magnus Group

4th Edition of Global Conference on

# PLANT SCIENCE AND MOLECULAR BIOLOGY

## September 19-21, 2019 - London, UK

## GPMB 2019

Theme:
To Unfold the Hidden Secrets of Plant Science and Molecular Biology for Better Now and Future

Venue: Park Inn by Radisson Hotel & Conference Centre,
London Heathrow Airport, Bath Road, Heathrow,
Middlesex. UB7 0DU, London, UK

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BOOK OF ABSTRACTS

4th Edition of Global Conference on

# PLANT SCIENCE & MOLECULAR BIOLOGY

*Theme:*
*To Unfold the Hidden Secrets of Plant Science and Molecular Biology for Better Now and Future*

SEPTEMBER 19-21, 2019
LONDON, UK

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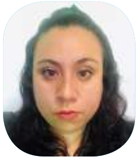

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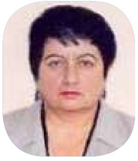

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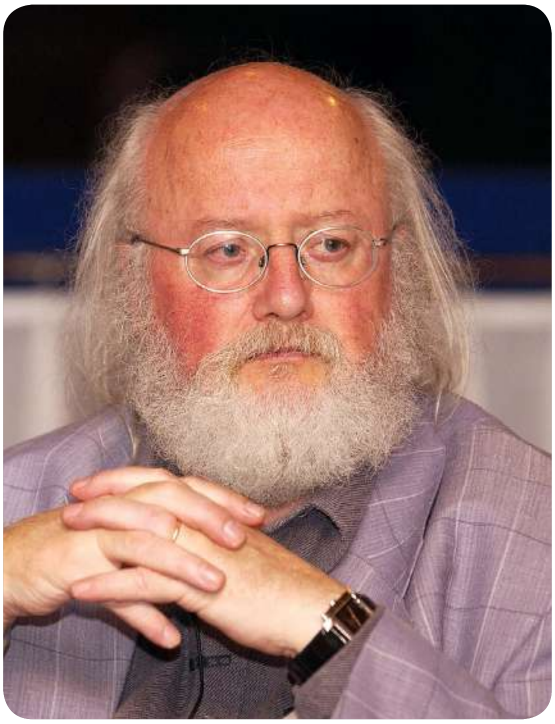
*Thank You*
*All...*

# Welcome Message



It is an honor and pleasure to write a welcome note. Biotechnology today provides every year new and unexpected progress: Truly innovative methods for faster and more precise plant breeding open new support unities to adapt to e.g. to the impact of climate change, especially drought damage, but also to achieve higher productivity and use more intelligent and differentiated methods to work against crop pests using less toxic substances. Even organo-transgenic strategies can be planned professionally. Monocultures are not basically a big problem, and this is not a coincidence, since most mass crops in agriculture originate from ancestral crops with huge monodominant stands.

Despite those advantages of new and extremely flexible breeding methods many people are fearful about such modernity – mainly due to a huge propaganda with false and filtered arguments of the opponent Organizations.

So, we need also better communication methods, contradicting straight-forward in an intelligent and discursive way the 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 a broad spectrum of participants in age and institutions, will hopefully provide professional and valuable information, helping to find new solutions and calm down the often-hefty debates.

Klaus Ammann

**Klaus Ammann**
University of Bern
Switzerland

# Welcome Message

Dear Participants of Plant Science and Molecular Biology 2019,

It is a pleasure for me to welcome you at the Global Conference on Plant Science and Molecular Biology, 2019, in London, UK.

This conference brings together people from different fields and different viewpoints, unified by the faith in scientific progress resulting from reliable and reproducible verification of relevant theoretical concepts. In a world of changing climate – but also of changing perception of information – it is the responsibility of scientists to uncover and evaluate facts and draw conclusions on societal consequences.

With plants being the only relevant primary produces of organic raw materials on our planet, plant science is of prime importance for global development. Embracing more than 20 sessions that span topics as diverse as evolution, biotechnology and environment interaction, GPMB 2019 accepts this responsibility and gives all of us the opportunity of learning and sharing knowledge that is badly needed.

With my own focus in plant metabolism and its responses to abiotic stress, I am excited to grasp recent information on, e.g., plant genetics, molecular biology, nutrition or hormonal regulation. Many other topics will be presented and will elicit inspiring discussions. I am sure that productive collaborations will be initiated at the conference, and this will pave the way to future scientific progress.

Situated in the city of London, GPMB 2019 will not only stimulate scientific exchange, but also fascinate the participants by the lively atmosphere of a megacity that itself faces dramatic change in 2019.

I look forward to meeting you in London!

**Arnd G Heyer**
University of Stuttgart
Germany

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*University of Bern*
*Switzerland*

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

# About GPMB 2019

Plant Science Conferences 2019 is scheduled to introduce and sum up the latest research activities and to project the scientific advances in the field of plant science and molecular biology. It serves as a forum for scientists, researchers and students to share and learn from colleagues through keynote, oral and poster presentations. Our main aim to become a bond in between the scientists and the world for improving the facts and give them different sight to imagine and reveal them. It serves as a resource to international research communities through important and timely discussions on areas related to plant science, plant biology, plant pathology, plant physiology, plant anatomy, plant genetics, plant and environment, soil sciences, plant nutrition, agronomy, plant biochemistry, plant biotechnology and many more interesting topics.

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# KEYNOTE FORUM

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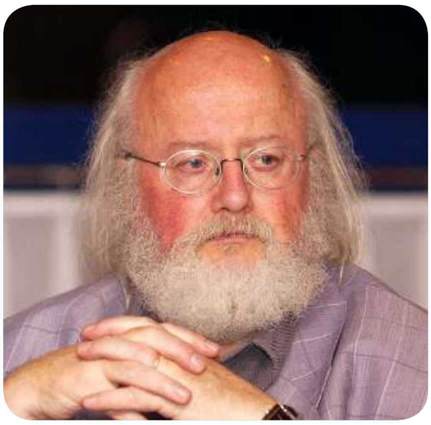

**Biography**

Prof. em. 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 and Missouri Botanical Garden. Member of www.prri.net, maintaining 650 reference bibliographies on botany, biotechnology and biodiversity, over 340 publications, and ca. 205 slide presentations, Editor, Co-Editor in journals from Elsevier, Springer and Landes. Member of numerous scientific committees, Fellow of the Royal Society of Biology etc.

# The regulation of GM crops in times of gene editing

**Klaus Ammann**

University of Bern, Switzerland

If we want to escape years-long fruitless debates on biotechnology and biodiversity, we have to do more than just to deplore the debate full of artificial (or imagined) contrasts; the main arguments are summarized below. The debate needs a professional discursive structure and we must embrace different kinds of knowledge, and future new solutions should not be excluded, on the contrary: in new regulatory structures they also have to be anticipated. Mutual understanding of the different views on agricultural strategies may stimulate the debate and lead to innovative solutions. The debate must embrace also the full set of social sciences.

**Audience Take Away:**

- A new understanding of professional Discourse will have to replace the fruitless and aggressive debates
- This new kind of discourse will help to understand colleagues from other faculties, specifically it could helpt to plan research and teaching in a broader perspective. It will also improve the accuracy of research design, or provide new information beyond the limits of the own faculty

## Biography

Dr. Michelle Jones studied agricultural biochemistry at Iowa State University for her BS and received her PhD in Horticulture with an emphasis in molecular physiology from Purdue University in 1997. She was on the faculty at Colorado State University and moved to The Ohio State University in 2001. She is currently a Professor in the Horticulture and Crop Science Department and the D.C. Kiplinger Endowed Floriculture Chair. She works with the Greenhouse Industry as a Floriculture Extension Specialist and conducts research in Horticultural Crop improvement.

# Identifying beneficial bacteria that enhance abiotic stress tolerance in horticulture crops

**Michelle L. Jones**
The Ohio State University, USA

Plant growth promoting bacteria can enhance growth and stress tolerance by improving the efficiency of nutrient uptake, producing plant growth promoting hormones, or reducing stress hormones like ethylene. Nutrient deficiencies and drought stress can have a negative impact on horticultural crop quality and yield. The application of beneficial bacteria in greenhouse production systems can increase stress tolerance under low water and nutrient conditions, and allows for the production of high quality crops with lower fertilizer inputs. A collection of 45 known Pseudomonas strains and a core lab collection of 1,100 bacteria isolates were screened using multiple in-lab assays to identify bacteria with the potential to enhance plant growth and stress tolerance. Polyethylene glycol (PEG) was used for the in vitro selection of osmotic stress tolerant bacteria, a trait correlated with the ability to alleviate drought stress in plants. The second bioassay identified bacteria that produce the enzyme 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase. ACC deaminase is capable of reducing the amount of stress ethylene produced by plants by degrading the ethylene precursor, ACC. Bacteria with the ability to solubilize organic phosphorus and potentially increase nutrient availability to plants were selected in a third assay. These three independent in-lab assays led to the selection of over 200 bacteria that were evaluated in greenhouse trials. Petunias were treated weekly by drenching the growing media with an equal concentration of bacteria. Young plants (two weeks after transplant) had water withheld until plants were severely wilted. Plants were then irrigated and recovery was assessed. Shoot biomass and flower number were measured to determine differences in the growth of bacteria-treated plants and untreated control plants. Petunias were also grown under nutrient deficient conditions to identify bacteria that could enhance plant growth above that of the untreated control (no bacteria) plants. Elite bacteria strains that promoted growth in greenhouse trials under both drought and low nutrient conditions were identified. Isolates selected from the core collection will be sequenced, and in addition to the known Pseudomonas strains, this information will be used to develop future experiments to investigate the potential modes of action for growth promotion under abiotic stress.

**Audience Take Away:**

- How in-lab assays can identify bacteria of interest so that in planta greenhouse trials can be conducted
- How to conduct high throughput greenhouse trials that evaluate thousands of plants for abiotic stress tolerance phenotypes
- How beneficial bacteria can be used in greenhouse production systems to enhance crop quality and abiotic stress tolerance

## Biography

Anabel RIAL B. Caracas 1965. PhD. Biodiversity conservation and sustainable use; strategy design/key conservation áreas, RAP Program. Tropical forest, wetlands, aquatic plants taxonomy and ecology. More than 100 projects in South America & Africa (EU, GEF, UNDP, CAF, CI, TNC, WWF, ECOFAC). Multidisciplinar/multicultural/interinstitutional teams. Former Scientific Director Conservation International Venezuela; Professor Masters on biodiversity (UNESCO MaB, Universities Spain, Colombia & Venezuela). Researcher La Salle Natural History Museum, Member Latin American Network Wetlands and Climate Change Impacts (CYTED). In Colombia since 2010 linked to Universities, NGO's, private and public sector. UNDP biodiversity consultant principal researcher Regional Strategy Equitable Management and Sustainable of the Hydrocarbons Sector. Oil Produced Water Reuse & Water Asset Management, Large land area master development. Currently independent consultant. Member UICN-SSC Freshwater Specialist Group. Guest lecturer at 40 international events. Author/editor of eigth books, over 50 scientific articles. Author of the two aquatic plants books of the Orinoco Basin (Venezuela and Colombia). Video-documentary Producer & scientific advisor.

# Aquatic plant useful concepts to delimit tropical wetlands (Orinoco basin case)

## Anabel Rial B.

Independent Consultant - Venezuela/Colombia
Member IUCN SSC Freshwater Plant Specialist Group

Aquatic plants are key organisms, useful to delimit and typify wetlands. In tropical floodplains, macrophytes are subject to flood pulse constantly, this driving force determin the expression of these organisms. After many years of observations, we have updated and introduced some useful concepts in order to better understand and preserve the aquatic ecosystems and their floras.

**Audience Take Away:**

- New concepts and approaches around aquatic plants
- How aquatic plants are useful to delimit and typify aquatic sistems
- Orinoco floodplains as an example of wetland dinamics and complexity

# DAY 1

# SPEAKERS

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# A universal genetic switch for increasing plant yields, stress tolerance and product shelf life

**Jerry Feitelson, Ph.D.**
Agribody Technologies, Inc., USA

Agribody Technologies, Inc. (ATI) uses genome editing with a highly validated pair of gene targets conserved across plant species to significantly improve seed and biomass yield and increase resistance to abiotic (drought, low nutrients, crowding) and biotic (pathogen) stress, while delaying post-harvest senescence. The efficacy of this technology was consistently proven in multiple crops in lab, greenhouse and field conditions. Two years of replicated field trial data in alfalfa have shown unprecedented 20-45% yield increase in an elite commercial variety with no loss of quality. Similarly, field trials in banana and greenhouse studies in tomato, lettuce and ornamentals have increased shelf-life by 2- to 3-fold. Currently, several licensing and co-development projects with innovative seed companies are currently underway in multiple crops. Results from these various studies will be discussed.

## Biography

Jerry Feitelson, Ph.D. is Co-Founder/CEO of Agribody Technologies, Inc., an agricultural biotechnology company partnering with innovative seed companies. He was previously CSO of Global Clean Energy Holdings & Sustainable Oils; Manager of Business Development, IP & Alliances at Beckman Coulter; VP of Technology and Business Development at GenWay Biotech; and Research Director at Akkadix. At Mycogen, his group discovered and patented most of the B.t. toxin genes. He was a Senior Research Microbiologist at American Cyanamid and Adjunct Professor at Rutgers University. Jerry is an inventor on 16 U.S. patents & author of 40 publications. His educational background includes a B.S in Life Sciences at MIT, a Ph.D. in Genetics with Joshua Lederberg at Stanford University School of Medicine, and an NIH postdoctoral research fellowship at the John Innes Institute, Norwich, UK in Streptomyces molecular genetics, where he cloned the first gene involved in antibiotic biosynthesis with a known biochemical role.

# Genome sequence of a *Bacillus* sp. with antimicrobial activity toward significant sorghum fungal pathogens

**[1]Enrique G. Medrano, Ph. D*., [2]Louis K. Prom, Ph. D.**
United States Dept. Agriculture – Agricultural Research Service, College Station, USA

The cereal *Sorghum bicolor* (L.) is the fifth most important crop with a range of uses from food, feed, fodder, and recently to a potential source of biofuel. Fungi are the primary disease agents that cause significant yield losses to sorghum. Currently, fungal infections of sorghum are controlled by chemical applications that pose both a toxic risk to the environment and potential resistance development by the microbes. Recently, we showed the effectiveness of a bacterium (Bacillus sp.) called LP16S recovered from sorghum that can thwart major fungal pathogens *(Fusarium, Colletotrichum, Curvularia* and *Bipolaris)* of the plant. Using next generation sequencing technology, the entire genome of strain LP16S was sequenced with the aim of mining for genes that encode products used to suppress fungal growth and development. Both shotgun and paired-end libraries were generated, sequenced and the data was used to construct the genome. The genome consisted of over 5 Mbp and extrachromosomal DNA was detected. For manual annotation, putative coding sequences were identified with the NCBI BLASTx program. The Prokaryotic Genome Annotation Pipeline program at the NCBI was used for computational gene prediction; both sets of results were manually curated. Annotation of the genome revealed several predicted gene products with antifungal activity that shall be discussed. Further, work to characterize the naturally produced biocontrol factors is in progress to ultimately eliminate or minimize fungal attacks on sorghum without the use of chemicals. This is the first whole genome sequence and annotation project of a bacterial biocontrol agent that can inhibit multiple sorghum fungal pathogens.

### Audience Take Away:

- Presentation attendants shall be informed of a novel *Bacillus* sp. biocontrol agent of sorghum fungal pathogens, bacterial biology knowledge will be gain, and genetically identified antimicrobials. Putatively identified antagonistic agents produced by the strain may be utilized in other disease control paradigms
- The information presented could likely be broadly applicable to other biocontrol systems for use by researchers and incorporated into plant pathogen courses. Generally, the whole genome sequence data could be used in comparative genomics work toward identifying key genes and their respective products utilized in management of fungal phytopathgens

### Biography

Dr. Medrano has 16 years research experience with the United States Department of Agriculture-Agricultural Research Service as a Research Scientist. 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 45 scientific publications and is known and respected by colleagues for conducting innovative and superior quality research. He has presented more than 66 papers, posters, and seminars at scientific conferences, many by invitation including 8 international conferences.

# Molecular regulation of food crop and medicinal plant biochemical pathways under mineral nutrient limitations

**Godson O. Osuji*, Aruna Weerasooriya, Peter Y. Ampim, Laura Carson, Paul M. Johnson**
Prairie View A&M University, Prairie View, USA

Plants naturally grow in degraded soils with mineral nutrient limitations. Close to 800 million people in the world live in rural areas and rely on crop production on degraded soil to put food on their dining tables. More than 500 million smallholder farmers and gardeners produce most of the world's fresh food, phyto-medicines, and feed. Limited resource farmers lack the financial power to purchase sufficient fertilizers and pesticides for their crops. But most of the time their crops and medicinal plants still produce lots of nutritious biomass food and feed stuff yields. Most studies in plant physiology had focused on the transcriptional and translational changes associated with mineral nutrient limitations but did not explain the molecular mechanisms that created the differential abundance of mRNAs, proteins, and enzyme activities. We have recently confirmed in both in vitro and in vivo studies how superfluous total RNAs are instantly degraded when plants are subjected to soil mineral nutrient limitations. The mechanism is that plant glutamate dehydrogenase (GDH) synthesizes specific panels of non-genetic code-based RNA enzymes in response to soil mineral nutrient compositions and concentrations, xenobiotics, soil pH and temperature changes etc. The nascent GDH-synthesized RNA enzymes swiftly cleanse out unnecessary and superfluous mRNAs, tRNAs, and rRNAs (genetic code-based RNAs) thereby minimizing the wastage of metabolic energy in the synthesis of unnecessary proteins, but optimizing the synthesis of needed amino acids, proteins and enzymes that assure development, nutritious biomass phytochemical accumulation and survival of the crop despite the harsh environment. The G+C contents of GDH-synthesized RNAs are wider and different from those of genetic code-based RNA, and are accordingly more stable electrostatically than total RNA; superfluous total RNA degradation being also different than the RNase, and the RISH/RITS-dependent double-stranded silencing of complementary RNAs (siRNA, miRNA, shRNA). GDH-synthesized RNA enzyme function is thus independent of, above and beyond the genetic code. When *Arachis hypogaea* was subjected to stoichiometric mineral nutrient limitations, the mRNA encoding phosphate translocator was degraded thus diverting chloroplastic triose phosphates to starch synthesis and export as maltose to the cytoplasm for utilization in cellulose biosynthesis biomass accumulation. Accordingly, the peanuts produced substantially more nutritious pod yields (9418-9822 kg per hectare) compared with the USA peanut producer yield (3184-5936 kg per hectare). The research project is helping smallholder farmers to further increase, double, and optimize nutritious crop yields that assure more farm income and more agriculture jobs. Superfluous total RNA degradation in *Zea mays, Vigna unguiculata, Arachis hypogaea,* and *Phyla dulcis* will be discussed as the biochemically proven molecular regulation that support the agriculture innovation capacity of gardeners and smallholder farmers. The discoveries especially help botany, ethno-medicinal pharmacology, agronomy, analytical biochemistry, and plant biology to reconfigure the design of plant projects and to more correctly interpret results, outcomes, and outputs because plant biochemical pathways are dramatically altered in response to the swift degradation of superfluous total RNAs; resulting to the massive accumulation of nutritious biomass and of human health beneficial phytochemicals.

**Audience Take Away:**

- Preparation and application of stoichiometric mixes of mineral salt solution
- Glutamate dehydrogenase Synthesis of RNA enzyme
- In vitro and in vivo identification of superfluous total RNAs in *Zea mays, Vigna unguiculata, Arachis hypogaea,* and *Phyla dulcis*
- Modified biochemical pathways in response to the degradation of superfluous total RNA
- Indigenous farmers marketing nutritious fresh cereals, pulses, vegetables, tubers, and medicinal herbs beneficial to human health
- The audience will be mainly plant system research scientists, professors, agriculture extension officers, agriculture policy makers etc who are also active in backyard gardening. They will learn how to prepare stoichiometric mixes of mineral salts and to apply them to their garden; thus the agriculture extension officers will expand their outreach programs. Plant system research scientists and professors will learn how to assay for superfluous total RNA and to differentiate RNA enzyme degradation of total RNA from siRNA, miRNA, and shRNA silencing of mRNAs; thus expand the comprehensiveness of teaching and research. Agriculture policy makers will become aware of the practical importance of superfluous total RNA degradation in the innovation capacity of smallholder farmers to increase, double, and optimize nutritious crop yields; and to increase farm income and jobs

## Biography

Godson O. Osuji studied Biochemistry and graduated PhD 1975 at the University of East Anglia, Norwich, England. His doctoral research was at John Innes Center, Norwich, England; Postdoc, 1976 supervised by Dr. Fred Sanger, MRC Laboratory of Molecular Biology, Cambridge. Returned 1977 to lecture at the University of Nigeria Biochemistry Department; rose to tenured Professor of Biochemistry 1982 at Nnamdi Azikiwe University, Nigeria. He became Fulbright Professor 1985 at USDA Research Laboratory, New Orleans. In 1989, he became research scientist (biochemistry) at Prairie View A&M University. He has authored more than 80 peer-reviewed papers on molecular regulation of biochemical pathways.

# Beyond *Arabidopsis:* Paving the way to commercial applications of Karrikin compounds

**Kenneth Tryggestad[1*], Santi Krisantini[1], Gavin R. Flematti[2], Jitka Kochanek[1]**
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Karrikins are a family of compounds derived from charred plant materials and smoke that were discovered in 2004 as the chemical cues that stimulate germination from seed banks for many fire-following species. The most universally active and abundant compound from smoke, karrikinolide or KAR1, was chemically synthesised in 2005 and subsequent research has determined that the karrikin perception system is fundamental in plant functioning throughout many angiosperms, including non-fire following plant species. Nonetheless, most of the recent work into karrikin functioning in plants has used the model plant *Arabidopsis thaliana.* Beyond seed germination stimulation, the proposed karrikin signal transduction mechanism in *Arabidopsis* can increase a seed's sensitivity to light, enhance seedling photomorphogenesis and accelerate leaf morphogenesis. Additionally, the very recent discovery in *Arabidopsis* that karrikins may behave as microprotectants, potentially having an important role in improving plant resilience to abiotic stress, makes karrikin research timely and suggests that crops could especially benefit from applications of this compound. Escalating climatic extremes are already making many crop varieties struggle to thrive under increasingly challenging abiotic conditions, such as heat waves and drought, but there is only limited evidence to suggest that karrikin effects in *Arabidopsis* translate to crop species, either under stressful or non-stressful conditions. Hence here we show a systematic approach to further karrikin research so these compounds can become useable for crops under field conditions and for other plant-related applications. Specifically, we use crops from the *Solanaceae* family to demonstrate a family-specific active dosage for karrikin compounds while concomitantly showing intra-specific variation for the magnitude of the karrikin response. Thus our results suggest that different varieties within a single crop are likely to require screening to determine their karrikin activity and for this we provide a simple laboratory method to screen for active dosages. For both KAR1 and KAR2, administered via seed priming, active dosages from laboratory assays are shown to effectively modify the plant phenotype and morphological characteristics until harvest. Thus this work provides a structured approach to further karrikin research, paving the way to making karrikin compounds useable for commercial plant applications.

### Audience Take Away:

The audience will gain new insights into applied karrikin research with a view to making these promising plant growth regulators useful for plant industry applications. Since the discovery of the most active karrikin in smoke in 2004, and laboratory synthesis of the pure compound in 2005, much research has been undertaken to understand the biological functioning of karrikins in plants, predominantly using Arabidopsis. However, karrikins have not been used successfully in commercial contexts due to complexity of their application, functioning and dosage-specific requirements. Thus this presentation will provide the audience with an understanding of the first steps towards a solution to problems hindering commercialisation of karrikin compounds by suggesting an effective framework to screen for karrikin responses and ensure successful delivery to plants

### Biography

Kenneth Tryggestad studied Agriculture Science with an emphasis in Agronomy at Western Illinois University, United States, and graduated in 2016 with a Bachelor of Science Degree. Ken then joined Dr. Jitka Kochanek's research group, The Plant Growth and Productivity Laboratory, at the University of Queensland, Australia as a Ph.D. student. He continues to work towards completion of his thesis 'Optimisation of Novel Plant Promoting Compounds and their Delivery Methods for the Australian Vegetable Industry' under the supervision of Dr Jitka Kochanek, Dr Robyn Cave and Prof Bhesh Bhandari.

# Interpreting of Circum-Euxinian (Russian Black-Sea to Turkey) disjunctive distribution of sub-Mediterranean pseudomaquis plant community

**Arnold Gegechkori**
Ivane Javakhishvili Tbilisi State University, Georgia

An understanding of the formation of scattered patches of the Mediterranean pseudomaquis along the coastal region of the Black Sea, requires consideration of the recent geological history of the two seas. The most important crises in the recent history of the Mediterranean Sea occurred during the 'Messinian Salinity Crisis', occurred in Early Pleistocene (5.96 to 5.33 mya) (Gautier et al., 1994). This event influenced the net of hydrological balance, climate, and biotas of the Mediterranean Sea's and Black Sea's adjacent terrestrial ecosystems.

The constantly humid climate conditions suitable in past geological time, according mentioned „crisis" converted into another, Mediterranean-type climate with hot, dry summer months and a cool, wet winter (Gratsianskii, 1971).

The moist subtropical laurel forests (laurisila) largely retreated and the present thermo-Mediterranean vegetation evolved, dominated by coniferous and flowering screlophilous trees and shrubs (Wulf, 1944).

During Early Pliocene the Mediterranean Region's climate and phytocenosis (first of all Mediterranean maquis) largely influenced to the adjacent regions with non-Mediterranean climate including the Black Sea Basin's regions (Wulf, 1944). Transformation of typical (primary) maquis into pseudomaquis in the circum-Euxinain region determined formation of patches (relict niches) of the Mediterranean enclaves in a narrow strip along the Black Sea coast.

This area is characterized by significant combination of Mediterranean and Euxinian (e.g., deciduous oak species) elements. Four disjunct populations of pseudomaquis relict patches in overstory and midstory still exists along the Black Sea region: (1) the northwestern part of Russian Black Sea coast (*Juniperus* spp., *Pistacia atlantica* (P. *mutica*), (2) easternward, isolate populations of pseudomaquis of Abkhazeti West Georgia *(Pinus brutia* var. pityusa), Arbutus andrachne and *Erica arborea,* (3) northern patch in southwestern Georgia, Adjara *(A. andrachne)*, (4) Turkish Black Sea region *(Pinus pinea, Arbutus andrachne,* and Erica arborea).

All these relict patches are vivid example of natural heritage of the Western Caucasus.

# Long-term effect of crop-rotations on weed dynamic and glyphosate consumption in the south of Buenos Aires province, Argentina"

**Istilart Carolina M**
Instituto Nacional de Tecnología Agropecuaria (INTA), Argentina

An estimated 80% of the crops are carried out under no-till systems in the south of Buenos Aires province (Argentina). Most agroecosystems have been characterized by undiversified cropping systems, where soybean is the main crop since 2004. This agricultural model tends to increase the evolution of herbicide-resistant weeds. In the current context, it is necessary to carry out an integrative weed management that includes cultural method as cover crops and rotations, in addition to chemical weed control. Diversified crop rotations break the weed cycle and prevent the weed adaptation. Moreover, these practices conduce to combine herbicides of several modes of action reducing risks of resistance. In the Argentinean Pampa, the temperate climate and rainfall distribution enable the production of pastures and crops in winter and summer. The aim of the current work was to evaluate the effect of three 6-year cycles of diversified crop-rotations on weed dynamic. In this sense, a long-term experiment was carried out in CEI Barrow (MAIBA-INTA), where was determined the effect of five crop sequences on weed species. Weed surveys were performed at the last year of every 6-year cycle. A randomized block factorial design (3 x 5) with four repetitions was applied. After every cycle, the effects of five crop rotations were evaluated: CR1- Conservationist agriculture; CR2- Crop-pasture rotation; CR3-Crop rotation for poor soil quality; CR4- Crop-pasture rotation including cover crops (oat-vetch) and CR5- Intensive crop rotation: two crops by year. A significant interaction was detected between cycles and rotations on weed density (pl.m-2), Shannon diversity index and floristic richness. The analysis of all weeds showed that the rotation with cover crops (CR4) had the lowest weed density (12 to 42 pl.m-2) every cycle, while was 19.4 pl.m-2 in the last year. The interaction between the last 6-year cycle and CR2 and CR3 showed the highest weed density, both treatments were significantly different from the rest. Weed diversity was higher in rotations of the first cycle than the last cycle. In contrast, floristic richness and weed diversity were similar in the sequence CR4. After 18 years of rotations, 16 weed species remained: Sonchus oleraceus and Polygonum aviculare were the most common, Avena fatua disappeared from all rotations and Lolium spp. was not registered in CR1, CR2 and CR4. Twenty six applications of glyphosate were carried out on CR4, while CR5 was associated to the highest consume of this herbicide (45 applications). No weeds have shown herbicide insensitivity under any rotation during 18 years.

### Audience Take Away:

- Crop rotation is an important tool for managing weeds in order to prevent the evolution of dominant weeds
- Low risk of herbicide-resistance is associated to diversified crop rotations
- A diversified crop rotation reduced the number of glyphosate applications needed for weed management

### Biography

Carolina Istilart studied Agronomic Engineering at National University of La Plata, Argentina. At the same institution, she attended postgraduate studies associated to weed sciences. She worked in the Department of Botany of National Institute of Agricultural Technology from Castelar (Argentina). She was professor of weed science in a postgraduate career at National University of Mar del Plata. Currently, she works in the Experimental Station of Barrow and her main lines of research are associated to integrated weed management in extensive crops (wheat, maize, sunflower and pastures), carry-over of herbicides and glyphosate-resistant Lolium spp. She won several award and recognitions related to her specialty and has published numerous research articles in science journals.

# Photosynthesizing while hyperaccumulating nickel: insights into the genus *Odontarrhena*

**Andrea Scartazza[1], Daniela Di Baccio[1], Lorenzo Mariotti[2], Isabella Bettarini[3], Federico Selvi[4], Luigia Pazzagli[5], Guillaume Echevarria[6], Piero Picciarelli[2], Ilaria Colzi[*3], Cristina Gonnelli[3]**
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Nickel (Ni)-induced changes in photosynthetic activity in edaphically contrasting species of *Odontarrhena* were investigated. Two Ni-hyperaccumulators *(O. chalcidica* and *O. moravensis)* and one non-accumulator *(O. muralis)* were grown in hydroponics and exposed to NiSO4 treatments (0.250 and 1 mM) for one week. Nickel effects on growth, root and shoot Ni accumulation and several photosynthetic parameters, through gas exchange and chlorophyll fluorescence analyses, were measured. The Ni-hyperaccumulators accessions showed a more efficient photosynthesis under Ni excess in respect to the non-accumulating species, at both the metal concentrations used in the case of O. chalcidica and at the lowest one in *O. moravensis.* Unexpectedly, Ni treatments in *O. chalcidica* increased not only the photochemical efficiency of PSII and the CO2 assimilation rate, but also the stomatal conductance. Moreover, the changes in the concentration of photosynthetic pigments was species-dependent in the two hyperaccumulators in response to the different Ni treatments. The increased efficiency in photosynthetic activity under high Ni levels was more striking in *O. chalcidica,* that also displayed the highest Ni tolerance and accumulation in respect of *O. moravensis. Odontarrhena muralis* showed reduced growth in the presence of Ni with the lowest levels of the metal in roots and shoots, thus underlining its higher sensitivity to this element; in the same condition, the decrease in the photosynthetic performance, already at the lower concentration used, was due to a combination of both stomatal and non-stomatal factors.

Our data represent the first report on the Ni effects on photosynthetic activity in Ni-hyperaccumulating plants. An unexpected positive effect of the metal excess on the photosynthetic performance was found in *O. chalcidica* and, to a lower extent, in *O. moravensis.* Therefore, beyond the already known Ni functions in plant nutrition, new research possibilities could be opened concerning the role of the metal in the photosynthetic machinery of hyperaccumulators.

### Audience Take Away:

- The audience will be able to acquire new knowledge about the physiology of some Ni-hyperaccumulator species
- The information that the audience will learn from the presentation are useful also for practical solution: only by learning about the physiology of the hyperaccumulator plants they could be used in the field for practical application, such as phytomining technique
- The results showed during the presentation could inspire the audience for new ideas in their research and projects

### Biography

Dr. Ilaria Colzi obtained a second level degree in Environmental Biology in 2008 and a European PhD in "Biosystematics and Plant Ecology" in 2012 at University of Florence, Italy. Between 2012 and 20218 she continued her research activity as research fellow at Department of Biology and DISPAA at University of Florence, and as post-doc fellow at London Institute for Mathematical Sciences. From 2018 she is a Temporary Researcher at the Department of Biology, University of Florence and she is lecturer of the course "Applied Plant Physiology" for the Master degree in Biology. She is author of 31 publications in referred international journals.

# Evaluation of the capacity of tris(3-hydroxy-4-pyridinonate) iron(III) complexes to correct iron deficiency chlorosis in soybean *(Glycine max L.)*

**Sofia Ferreira[1], Carla S. Santos[2], Andreia Leite[3], Tânia Moniz[3], Marta W. Vasconcelos[2] and Maria Rangel[1*]**
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Successful cultivation of crops with the best nutritional properties is an issue of paramount importance in the Agricultural and Health fields. Iron (Fe) is an essential nutrient for plants and legumes are one of the major sources of Fe in human diet. However the absorption of Fe by the roots of plants is compromised when grown in alkaline soil. As a consequence, plants may suffer from Iron Deficiency Chlorosis (IDC), characterized by chlorosis, yield losses, and lower concentrations of Fe in edible parts of the plant.

To address IDC, farmers must rely on supplementing their crops with Fe-chelates to avoid serious growth deficiencies. Compounds Fe-EDTA and Fe-EDDHA, are commercial products used in agricultural context and some drawbacks have already been reported. The limited number of distinct Fe chelates that are used as fertilizers calls for the identification of new ligands capable of producing Fe-complexes with properties that allow more efficient pathways for root uptake, root to shoot translocation and maintenance of metal homeostasis.

We considered that 3-hydroxy-4-pyridinones were eligible to formulate new Fe fertilizers and herein we report a study regarding the hydroponic growth of soybean (*Glycine max L.*) in which we tested two 3,4-HPO Fe-chelates in comparison with the commercial fertilizer Fe-EDDHA. Chlorosis development was assessed using SPAD measurements and total chlorophyll quantification. The amount of Fe was quantified in roots and leaves, using atomic absorption spectroscopy.

We found that 3,4-HPO Fe-chelates have great potential as new IDC correctors since plants were significantly greener and had increased biomass. In particular, plants supplied with one of the compounds, were able to translocate more iron from the roots to the shoots not eliciting the expression of the Fe stress related genes. The results suggest that 3,4-HPO Fe-chelates could be economically and environmentally favourable in agricultural contexts.

This work received financial support from the European Union (FEDER funds through COMPETE) and National Funds (FCT, Fundação para a Ciência e Tecnologia), under the Partnership Agreement PT2020 through project UID/QUI/50006/2019 (LAQV/REQUIMTE) and PTDC/AGRPRO/3515/2014-POCI-01-0145-FEDER-016599.

**Audience Take Away:**

- The presentation is focused on the design new Fe fertilizers. We will explain the concept
- The complexes are made in our laboratory and we have the possibility to tailor-made the ligands to adjust the properties of the Fe-chelates and improve efficacy
- One of the compounds improves Fe content both in roots and in leaves
- Application of the new fertilizer can be made either in soil or sprayed on leaves

## Biography

Maria Rangel (www.chel2life.org) is an Associate Professor at University of Porto. She is a Bioinorganic Chemist whose research interests are focused in the role of metal ions in living organisms. She has been working on the design of Iron chelators for: (a) novel strategies to fight Infection; (b) treatment of Fe Overload and (c) Fe Sensing. Her interest in Iron Biology has been extended to Plant Nutrition and she is currently developing projects that aim the understanding of mineral nutrition processes and the design of Fe-chelates to address agricultural problems related with Fe deficiency.

# Attempts to explain incompatibilities in the process of pollination and fertilization of blackberry flowers *(Rubus L. subgen.* Rubus)

**Agnieszka Orzeł*, Włodzimierz Lech, Joanna Jagła, Monika Bieniasz**
Niwa Hodowla Roślin Jagodowych Sp. z o.o., Niwa Berry Breeding Ltd., Poland

**Understanding the biology of flowering among studied blackberry genotypes derived from Niwa's berry breeding program.**

The course of pollination and fertilization of flowers of 5 cultivars and 15 breeding clones of blackberries were examined in this study. Blackberries are commercialized species within *Rubus* (Rosaceae). They are classified in the *Rubus* subgenus *Rubus* (formerly Eubatus) and typically don't have a species epitaph because the cultivated blackberries are nearly all derived from at least two or more species. Chromosome numbers in *Rubus* range have substantial variation in the wild and cultivated genotypes.

Reports provided information for this range from 2n=2x=14 to 2n=18 x =126 including odd-pliods and aneuploids (Thomson 1995 a, 1995 b, 1997, Meng and Finn 1999). Cultivated blackberries all contain multiple species in their backgrounds (Clark et al.2007) and thus variation in progenitor species chromosome number. The *Rubus* subgenus *Rubus* contains only 10% of diploid species. Most blackberries are tetraploids 2n = 4x = 28. Thus, blackberries are polyploids that tend to produce apomictic seeds (Gustafsson 1943 and Nybon 1988). The most common species and varieties are self-fertile, and some also self-pollinating, through the special construction of anthers (Nybom 1986 a, b). Embryos can be formed both from the egg cell through fertilization, as well as from diploid cells of ovule which give rise to the adventitious embryo.

In this case, there may be two embryos (Pratt and Einset 1955, Czapik 1983). Apomictic forms of blackberries are self-fertile and autogamous i.e pollination of foreign pollen induces the formation of apomictic embryos, (the need for the formation of endosperms) Nybon 1987. The fact that the resulting seeds are not dependent on the donor pollen report Haskell 1960, Jennings and Topham 1971.

The diploid varieties show no deviations in the meiosis process. Such abnormalities were observed in polyploid species (Pratt, Einset 1955). The flowers have a diameter of 2 to 4 cm, the petals of the crown are white or pink. They have a large number of stamens (from 50 to 200) and about 50 to 100 pistils (Strik and Finn 1996). Two ovules grow in the ovary, one disappears before flowering, just as with all drupes, one remains as the embryo sac Polygonum type. After fertilization, the ovary transforms into single fruit, several dozen of which form an aggregate fruit structure. They may even form a single ovule on the receptacle. The amount of seeds is strongly correlated with the viability of pollen. There is a high correlation between the viability of pollen and the amount of seeds (Nybon 1985). On the pollinated stigma there are from 50 to 200 pollen grains that germinate after 30 minutes, but most often after a few hours. After 18 hours, the pollen tube is growing to the base of the style. Fertilization is recorded after about 30 hours (Engelhardt and Stösser 1979).

In many older breeding works, great attention is paid to the ratio of the amount of good pollen to the number of ovules. Blackberries belong to the transitional species between kleistogamy and allogamy. They develop a rather less valuable pollen, which obviously affects the amount of seeds (Cruden 1977).

**Attempts to explain incompatibilities in the process of pollination and fertilization of blackberry flowers *(Rubus L. subgen.* Rubus)**

There are three dominant types of problems or incompatibilities that there are revealed in that research. These are sporophytic incompatibility, anatomical incompatibility caused by narrowing of the transmission tissue of the style, and incompatibility of selective fertilization, resulting from irregularities in the course of micro and macrosporogenesis. Among all of the tested varieties, only two of those got proper fertilization. Among all varieties being tested, the fertilization of the ovules ranged from 0 to 80%. 'Prime-Ark ®Freedom' and 'Apache' varieties are self-fertile, while 'Prime-Ark® 45' and 'Reuben' are not self- pollinating.

**Impact of revealed data during the study on blackberry breeding program carried out in the Niwa Berry Breeding Ltd.**

The purpose of the research is to show that fertilization of the ovules is a decisive factor in the selection of appropriate clones for further cultivation of blackberries. The presented method is easy and fast, and the assessment is very reliable. At the same time, we try to present the course of pollination and fertilization of blackberry flowers, taking into account the incompatibilities that occur in this process. The presented method of fertilization of ovules can significantly accelerate breeding work.

**Audience Take Away:**

- Biology of flowering within blackberries *(Rubus L. subgen.* Rubus)
- Three types of incompatibilities: sporophytic incompatibility, anatomical incompatibility caused by narrowing of the transmission tissue of the style, and incompatibility of selective fertilization, resulting from irregularities in the course of micro and microsporogenesis in blackberries *(Rubus L. subgen.* Rubus)
- The presented data can show how to accelerate breeding work within blackberries *(Rubus L. subgen.* Rubus)
- Plant and Environment
- I think the targeted audience will be
    - ✓ Provided in new information that help them in their fields
    - ✓ Provided in practical solution to challenge the blackberry breeding
    - ✓ Provided new ideas in their research fields
    - ✓ Ready to compose alliance to prepare new project

**Biography**

Dr. Agnieszka Orzel studied Agriculture Science at University of Agriculture, Krakow, Poland and graduated as MS in plant breeding science in 2001. She joined to the raspberry and blackberry breeding program headed by Dr. Jan Danek in the Fruit Experiment Station Institute of Horticulture in Brzezna, southern Poland. She is co-author of 6 raspberry and 6 blackberry cultivars which got a dominant position in polish fruit market production.

She received her PhD in 2011 at University of Agriculture from the thesis "Biology of the flowering within Rubus species as a preliminary study in obtaining primocane blackberries". She obtained a new position as *Rubus* breeder since 2012 in the private breeding program, Niwa Berry Breeding Ltd. which is also a co-founder. From this program, the latest early primocane raspberry 'Delniwa' was released in 2017.

# Stress factors influencing androgenesis of rye

**Janusz Zimny*., Oleszczuk S., Zimny A., Czaplicki A., Sowa S.**
National Research Institute, Poland

The achievements of many laboratories over the last 50 years have led to the practical use of doubled haploid (DH) system in plant breeding. Today, all strategies for hybrid varieties of cereals involve the use of DH at various stages of the breeding process. DH allow the use of homozygous lines in basic research as well. Offspring of such lines does not segregate in subsequent generations. The progress observed in plant breeding, which is made thanks to homozygous lines, leads to the conclusion that in vitro induced androgenesis is currently the most efficient biotechnology method used in breeding practice.

The basic advantage of androgenesis is that homozygous lines can be obtained in a short time. After many years of attempts, DH regeneration of rye, oats and wheat is still a challenge for researchers. Despite many efforts to develop an effective method of producing doubled haploid cereals, many problems remain unresolved. One of them is that the genotype remains the main factor that determines the effectiveness of androgenesis in in vitro cultures. Finding of such androgenic genotypes and selection of the applied stress changing the path of microspores development, led to DH regeneration of rye with very high efficiency. In presented experiments, the influence of various stresses on the microspore viability was studied. Many different stress combinations were used to induce androgenesis. The experiments were carried out on microspores and anthers of several winter rye breeding lines. The results showed a correlation between the genotype and stress used, and the level of induction of androgenesis and microspore mortality at an early stage of the culture. The survival rate of microspores was highest after pre-cooling of spikes at 4 ° C for two weeks, and further pre-culture of the anthers in a mannitol solution at 4 ° C for seven days. Pre-cooling of spikes for three weeks was equally effective. We postulate the possibility of accumulating the ability to efficiently induce androgenesis in subsequent generations of regenerants.

**Audience Take Away:**

- How to develop a highly efficient regeneration system in recalcitrant cereal plants
- How to produce homozygous lines from single microspores of rye
- What is the influence of stress on changing microspore gametophytic developmental pathway to the sporophytic one
- We present rye genotype with unprecedented efficiency of androgenesis. It will be used to search for genes responsible for the ability to rye androgenesis

## Biography

Prof. Janusz studied Agriculture at the Warsaw Agriculture University, Poland and graduated as MS. He then joined for two years the research group of Prof. Horst Lörz Max Planck Institute Cologne, Germany during Prof. Jeff Schell time. After he received his PhD degree he obtained a postdoctoral fellowship supervised by Prof. Horst Lörz at the Center for Applied Molecular Biology, University of Hamburg, Germany. In 1993 he obtained world's first transgenic Triticale plants. The current activities of his group is focused on shortening the breeding cycle of cereals through the regeneration of doubled haploids, somaclonal variation issues and coexistence problems related to GMOs in agriculture.
1999 – Present – Head of the Department of Plant Biotechnology and Cytogenetics (PBAI-NRI), Radzików, Poland.

# GABA Shunt Pathway in Germinating Seeds of Wheat *(Triticum aestivum* L.) and Barely *(Hordeum vulgare* L.) under Salt Stress

**Nisreen A. Al-Quraan PhD.**[1*], **Zakaria I. AL-Ajlouni PhD.**[2], **Dana I. Obeidat**[1]
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Soil salinity is one of the major abiotic stresses affecting seed germination, crops growth and productivity. In this study three wheat cultivars *(Triticum aestiveum* L) (Hurani75, Um Qayes and Sham1) seeds and three barley cultivars *(Hordeum vulgare* L.) (Rum, Acsad175, and Athrouh) seeds were treated with different concentration of slat stress (NaCl) to investigate the effect of such treatments on seed germination stage physiology and metabolism through the characterization of seeds germination pattern, GABA shunt metabolite levels (GABA, Glutamate and Alanine) and glutamate decarboxylase (*GAD*) expression using RT-PCR. A trend of decreasing germination percentage with increasing NaCl concentrations was observed in all cultivars. At 200 mM NaCl, the germination was highly inhibited. The inhibition in daily recorded pattern was high in wheat when compared to barley in all cultivars under all NaCl treatments. Under all salt stress treatments, our data showed significant ($P \leq 0.01-0.05$) increase with positive correlation ($r = 0.50-0.99$) between level of GABA shunt metabolites (GABA, alanine, and glutamate) and salt concentration in all wheat and barley cultivars daily for 5 days, and after 5 days, separately. Increased GABA levels were associated with a small but significant ($P \leq 0.01-0.05$) increase in the content of Ala and Glu daily and after 5 days in all wheat and barley cultivars. In all NaCl treatments, the transcription of *GAD* in term of RNA level showed significant ($P \leq 0.01-0.05$) increase in all cultivars with positive correlation ($r = 0.50-0.98$). At 200 mM NaCl, the level of *GAD* RNA transcripts was significantly ($P \leq 0.01-0.05$) decreased. There were increased changes in GAD expression with time because of increasing stress levels. Data showed an association between *GAD* RNA transcription and the response of germinating seeds to salt stress in terms of GABA shunt metabolites accumulation. The elevated expression of the *GAD* under salinity stress suggests the need for elevated activity of the *GAD*-mediated conversion of glutamate to GABA during seed germinating, which provides alternative metabolic routes to the respiratory machinery, balancing carbon and nitrogen metabolism and osmolytes synthesis in wheat and barley germinating seeds under environmental stress. Our study determine the effects of NaCl treatments on embryo development and GABA shunt pathway metabolism of germinating seeds in wheat and barley. Also, this study strongly showed the functional role of GABA shunt pathway during seed germination under salt stress treatments in Jordanian cultivated wheat and barley plants.

## 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 working as a 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 understanding the role of 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, Stress Physiology

# Tomato Yellow Curl Leaf Virus

**Gunay Talibova**
Plant Protection, Baku Agropark, Baku, Absheron, Azerbaijan

A TYLCV causes the most destructive disease of tomato, and it can be found in tropical and subtropical regions causing severe economic losses. This virus is transmitted by an insect vector from the family Aleyrodidae and order Hemiptera, the whitefly Bemisia Tabaci, commonly known as the silverleaf whitefly .The primary host for TYLCV is the tomato plant, and other plant hosts where TYLCV infection has been found include eggplants, potatoes, tobacco, beans, and peppers.[1] Due to the rapid spread of TYLCV in the last few decades, there is an increased focus in research trying to understand and control this damaging pathogen.

As Crop Protection agronomist, I always try to find non chemical ways to deal with several problems, including Bemisia and TYCLV in order to ensure food safety and protect environment and peoples' health. So, I want present my latest research.

Povidone iodine solution with special adjuvant -this is the disinfectant for greenhouse use; disinfection of equipment, seeds, and also spraying for profilaction of several plant diseases.

The instruction of the product does not say anything about treating of already infected plant. I decided to apply it to infected tomato plant with TYCLV. I conducted this research during 7 weeks .Sprayed ones in a week with 0,07 % solution of following product and took videos every week after treatment .Here is the result. Infected plant began to grow .There was no difference between health and infected plants' fruits and trusses .Only old curled leaves did not change their shape. On another word, old symptoms stay as it use to be. A new formed leaf was in normal shape.

How it works? The basis of antimicrobial action of iodine is the ability to disrupt the metabolic processes of pathogens. Penetrating into the protoplasm of cells, iodine interacts with the amino groups of proteins, suppresses vital enzyme systems. When iodine interacts with water of protoplasm of cells produces active oxygen, which has a strong oxidizing effect. This also explains the destructive effect of iodine on pathogens.

**Audience Take Away:**

- Audience, especially growers-agronomists can safe their crop from taking out because of following pathogen
- Since almost every greenhouse around the World suffer from this pest and as a result ,from following virus, this research will help them first of all to fight effectively and nonchemically ,also save the budget and increase the productivity of greenhouse and so on. It provides practical solution that simplifies job

### Biography

Gunay Talibova studied at Baku State University, Azerbaijan in 2006 . She earned her master's degree at Gandja State University, Azerbaijan in 2006. Moreover, she has taken Phytopathology course at Wageningen University. She is Plant Protection agronomist- Phytopathologist at Baku Agropark , 20 hectare tomato greenhouse.

# The influence of ambient temperature on the MDA and H2O2 production and antioxidant metabolism in *Hedera helix* leaves. One year study

**Maja Diljkan[1*], Siniša Škondrić[2], Ljiljana Topalić-Trivunović[2], Dino Hasanagić[2], Biljana Kukavica[2]**
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The cellular changes provoked by either high temperature or low temperature include reactions which lead to the excess accumulation of toxic compounds, especially reactive oxygen species (ROS). The consequence of ROS accumulation is oxidative stress. The main effects of ROS include autocatalytic peroxidation of membrane lipids and pigments, modification of membrane permeability and functions. Plants exposed to extreme temperatures use several non- enzymatic and enzymatic antioxidants to cope with the harmful effects of oxidative stress; higher activities of antioxidant defence enzymes are correlated with higher stress tolerance.

The plants in our region, where the climate is humid continental, are exposed to huge temperature oscillations. Hedera helix (Ivy) is one of those plants that successfully respond to sudden day-to-day temperature changes and not only during the yearly season change. The aim of our research was to detect the influence of ambient temperature on the MDA and $H_2O_2$ production and antioxidant metabolism in Hedera helix leaves throughout all four seasons (winter, spring, summer and autumn).

Leaves of five individual plants of the *Hedera helix,* were collected at the location Banj brdo (Banja Luka), Bosnia and Herzegovina, in the period from November 2017 to November 2018. Leaves were conserved in liquid nitrogen, from the moment of sampling to the moment of extraction in the laboratory. We have examined the specific activity of three antioxidant enzymes; superoxide dismutase (SOD), catalase (CAT) and peroxidase (POD). The content of total phenols, concentration of hydrogen peroxide ($H_2O_2$) and malondialdehyde (MDA) were also measured and examined during this one year study.

Results of our research showed that concentration and activity of the analysed parameters vary on the vegetation period and the ambient temperature. Each individual plant of these analysed reacts in a specific way. Activity of peroxidase and catalase was higher during the winter months when the temperature was lower, while their activity decreased and reached its minimum during the summer period. Level of total phenols was influenced by POD activity and level of $H_2O_2$ was in correlation with both peroxidase and catalase. Results have also showed that there are cyclic changes in concentration of plant pigments where we noticed that there is a significant interconnection of carotenoids on concentration of chlorophyll A and B, respectfully.

**Audience Take Away:**

- Influence of ambient temperature variations and seasonal cycle changes during one year on activity of enzymes of antioxidant defense in leaves of the plant *Hedera helix*
- Correlation of antioxidant parameters and their correlation to indicators of oxidative stress
- Individuality of plant response to one year changes in its environment
- Dynamic seasonal response of *Hedera helix* to environmental changes
- One year tracking of the antioxidant metabolism and the production of ROS in plants as sessile organisms for better general understanding of their way of survival

## Biography

Maja Diljkan is a Pharmacy student at the University of Banja Luka, Bosnia and Herzegovina. In November 2017, together with Prof. Biljana Kukavica at the Faculty of Natural Sciences and Mathematics, University of Banja Luka she started researching antioxidant metabolism in Hedera helix leaves. In 2018, she participated in the 3rd International Conference on Plant Biology in Belgrade, Serbia and 2nd Congress of Biology in Kladovo, Serbia. During the internship in Centro de Estudios Transdiciplinarios del Agua (CETA), University of Buenos Aires, Argentina she worked on the project Arsenic adsorption on iron modified montmorillonite: kinetic, equilibrium and surface complexes studies. Under scholarship within the JoinEU-SEE PENTA mobility scheme she spent academic 2013/14 year at the Faculty of Pharmacy, University of Granada, Spain.

# Biological management of bacterial blight of pomegranate using *Bacillus subtilis* based bioformulations

**Pavan kumar[1,2*], Manjunath Girigowda[2], Bharati S Meti[1]**
[1]Basaveshwar Engineering College (Autonomous), Bagalkot.
[2]University of Horticultural Sciences, Bagalkot

Pomegranate is an important commercial fruit crop of tropical and sub-tropical parts of the world, known for its rich medicinal and nutraceutical values. Productivity of pomegranate is compromised by a bacterial blight disease caused by *Xanthonomas axonopodis pv. punicae (Xap),* account for 60-80 % of yield loss. Use of biological management of this disease is prospective option, as antibiotics and synthetics have negative impact on non-targeted beneficial microflora and have consumer repercussions on health. In this context, a potential *Xap* antagonistic bio-agent *Bacillus subtilis* UHSBs11 (KX950669) was isolated from the rhizosphere of bacterial blight infected pomegranate. Using this bio-agent as an active ingredient, a liquid based formulation was developed by impregnating plant extracts, chitosan (a sea weed extract), and other substrate molecules that are required for improved bio-efficacy and long viability of candidate bio-agent. Application of this formulation as foliar spray (5 mL/L) recorded 88 % of disease protection under green house condition and 79 % under field when evaluated for two seasons. Foliar application of the formulation also imparts resistance against disease by inducing various defense responsive genes such as phenylalanine ammonia lyase, chitinase, callose synathse and pathogenesis related proteins at different time points of post pathogen inoculation. Prophylactic foliar application resulted in reduced disease compared to generally used chemicals such as streptomycin sulphate, copper oxychloride and Bronopol (2-bromo-2-nitropropane-1,3-diol) simultaneously decreasing cost of cultivation. Further, Bio-formulation improved the reproductive parameters such as total yield and average productivity when compared to control and regularly used synthetic antibiotic.

**Audience Take Away:**

- An effective *Bacillus subtilis* based liquid bio-formulation for management of bacterial blight in pomegranate was developed.
- Integrated disease management (IDM) module with this bio-formulation recorded low disease severity, found to improve the pomegranate yield and other fruit quality parameters
- Application of the bio-formulation has significantly reduced the use of Streptocycline (streptomycin sulphate), copper oxychloride and Bronopol (2-bromo-2-nitropropane-1,3-diol) leading to decreased cost of production and lesser residual toxicity to the environment
- Application of bioforluation also induced systemic resistance in pomegranate against bacterial blight in pomegranate

### Biography

Mr. Pavan Kumar is a Ph.D research scholar at Basaveshwar Engineering College and Senior research scholar of university of Horticultural Sciences, Bagakot . He completed his M.Sc in biotechnology from university of Mysore and bachelors in life sciences from Karnataka University Dharwad, India. He is currently working on enhancement of host resistance in pomegranate against bacterial blight caused by Xanthomonas axonopodis pv. punicae and its integrated management. During his research he developed novel bio-formulation for pomegranate bacterial blight management which are successfully being adopted in the field trial by farmers. He has two publication in SCI(E) journals and one technology and a patent under communication.

# A novel beneficial endophytic bacterium-mediated plant growth promotion

**Özlem Akkaya[1*], Mine Gül Şeker[1], Nil Türkölmez[1], Merve Albayrak[1], Ceyhun Kayıhan[2], Yelda Özden Çiftçi[1]**
[1]Gebze Technical University, Turkey
[2] Başkent University, Turkey

Bacterial endophytes, a group of bacteria that promote plant growth, can colonize some or a portion of the plant's internal tissues. These bacteria are able to stimulate plant growth through different mechanisms. Previously, our research laboratory had reported that the presence of a beneficial putative endophytic bacterium in the long-term in vitro cultured microshoots of fraser photonia (Şeker et al., 2017). Here, we showed that this bacterium has an endophytic character as well as host-independent. Moreover, the mechanisms that underlie the positive effects of the bacterium on plant growth, have been investigated regarding its plant growth-promoting traits. The results highlight the complex nature of plant-endophytic bacterial interactions and the potential of this novel bacterium to be used as bio-fertilizer. This study supported by the Scientific and Technological Research Council of Turkey (TUBITAK) (Project number: 117R002).

**Audience Take Away:**

- Endophytic bacteria, are a very important part of the plant microbiome. In order to use the beneficial plant-endophytic bacteria interactions in agriculture effectively, the key aspects that govern successful interactions need to be defined. This study will help to identify the genetic basis of plant-endophytic bacterial interactions
- Although bacteria observed in plant tissue culture are generally considered to be contaminants; this study demonstrated the potential for the discovery of novel microorganisms that are very useful for the plant
- We also state that the use of plant-beneficial bacterial interactions is a powerful approach to improving plant growth and development without the need for transgenic applications

## Biography

Dr. Akkaya received her PhD in Molecular Biology and Genetics in 2012 at Gebze Technical University. Then, she moved to the Spain (CNB/CSIC) where she spent over two years at the Molecular Environmental Microbiology Laboratory as a postdoc. After completion of her postdoc, besides her microbial researches, she made collaboration with Plant Biotechnology Group in Gebze Technical University for studying plant-bacterial interactions.

# Diversity of terpenes and n-alkanes in Pine species – chemotaxonomic implications

**Biljana Nikolić**
Institute of Forestry, Serbia

It is well known that the Pinus genus is the most numerous in the Pinaceae family (about 110 species) and divided into two subgenus: *Strobus* (with 5 needles per fascicle) and Pinus (with 2 needles per fascicle). In this study, the focus is on autochthonous, relict and endemic species: Bosnian pine, *P. heldreichii* and Macedonian pine, *P. peuce,* because there are disagreements of various authors in terms of taxonomy. In addition, the terpene composition of 10 autochthonous and allochthonous pine species from the territory of Serbia and Croatia was examined.

In most taxa (*P. mugo, P. nigra ssp. nigra, P. nigra ssp. dalmatica, P. peuce, P. pinea, P. sylvestris, P. strobus and P. wallichiana*) -pinene is the most abundant terpene compound, while the following terpenes are dominant in other species: -pinene (*P. ponderosa*), trans-caryophyllene (*P. halepensis*), germacrene D (*P. heldreichii*), and abietadiene (*P. pinaster*).

In 12 analyzed species the following n-alkanes dominate: C23 (*P. heldreichii*), C25 and C29 (*P. peuce*), C27 (*P. nigra*), C29 (*P. mugo*), C31 (*P. sylvestris or C35 (P. ponderosa*), etc. As in most cases the subjects of examination are individual trees, the obtained results direct us to population study in order to discover other chemotypes which are common in pines.

This work was supported by Grant No 173029 of the Ministry of Education, Science and Technological Development of the Republic of Serbia.

**Audience Take Away:**

- Plant Physiology and Biochemistry
- Plant Sciences and Plant Research
- Plant Ecology and Taxonomy
- Provided in new information that help them in their fields
- Provided new ideas in their research fields
- Ready to compose alliance to prepare new project

## Biography

Dr Biljana Nikolić is Principal Research Fellow of the Institute of Forestry, Belgrade, Serbia. She finished master studies on Faculty of Forestry, Belgrade, and phD studies on Faculty of Biology, Institute of Botany and Botanical garden 'Jevremovac', Belgrade, Serbia. Up to now, she published 40 international references through projects of basic sciences. Dr Biljana Nikolić is chief of Department of genetics, plant breeding, seed and nursery production, head of the Research Laboratory Department for genetics, seed production, plant physiology and plant breeding as well as coordinator of the projects in the area of basic research of the Ministry of education and science of the Republic of Serbia.

# Effect of adenine sulphate and two growth regulators on in vitro propagation of plantain cv. *Agbagba* (aab)

**Akin-Idowu P.E*, Aduloju A.O, Olagunju Y.O, Aderonmu O.I, Adebo G.U**
National Horticultural Research Institute, Nigeria

This study aims to establish the optimal conditions for in vitro micropropagation of plantain (Agbagba) by evaluating the synergetic effect of Adenine sulphate (AdS) on benzylaminopurine (BAP) in combination with indoleacetic acid (IAA). Apical meristem (1.5-2.0 cm) were excised from shoot tips of plantain and used as explants. For regeneration, Murashige and Skoog (MS) medium were supplemented with different concentrations of BAP (2.0, 3.0, 4.0, 4.5 mg/l) and IAA (1.8 mg/l) in combination with or without AdS (50, 100 mg/l). Eight explants per treatment with three replicates were used. It was observed that 83% of the shoots turned green 5 days after initiation on medium containing 4.0 mg/l BAP + 1.8 mg/l IAA + 100 mg/l AdS and highest shoot length (7.9cm) and shoot weight (5.74g) were recorded 28days after initiation. Explants obtained from regeneration medium were passed through several cycles of subculture on MS medium supplemented with BAP (3.0, 4.0, 4.5, 5.0 mg/l) and IAA (1.8 mg/l) in combination with AdS (50, 100, 150 mg/l). Highest mean number of shoots (23.33 per explant) and shoot length (5.87 cm per explant) were recorded on medium containing 4.5mg/l BAP + 1.8 mg/l IAA + 100 mg/l AdS at the third subculture. This was followed by medium containing BAP 3.0 mg/l + IAA 1.8 mg/l + AdS 150 mg/l which recorded 19.67 shoot/explant and shoot length of 6.03 cm/explant. A 3-fold increase was further observed at the fourth subculture with MS medium supplemented with 4.5 mg/l BAP + 1.8 mg/l 1AA + AdS 100 mg/l. Adenine sulphate in combination with BAP stimulates multiplication of Agbagba. An increase in AdS concentration did not result in significant increase in the multiplication and growth parameters of plantain plantlets.

## Biography

Dr Pamela Akin-Idowu is an Assistant director and a Research scientist at the National Horticultural Research Institute (NIHORT), Ibadan, Nigeria. She heads the biotechnology unit of NIHORT where she manages research laboratories and coordinates project activities. Pamela has a PhD in Biochemistry (specialization in plant molecular biology) from the University of Ibadan, Nigeria. Her current research focuses on developing and optimizing protocols for in vitro propagation of some horticultural crops for mass production of healthy planting materials to meet farmers need.

She has over 18 years' experience in plant tissue culture techniques and molecular characterization. Other areas of research interest are in the characterization of horticultural crops for conservation of germplasm for use in crop improvement programmes based on phenotypic (qualitative and quantitative methodologies) and DNA markers (RAPD, SSR, SDS-PAGE).

She is a recipient of many fellowships including the African Women in Agricultural Research and Development (AWARD) a Bill and Melinda gates scholarship programme, Nuffic-Netherlands Fellowship Programme (NFP) and MASHAV (Government of Israel) Scholarship Programme. She has attended much training locally, regionally and internationally where she gained knowledge and hands-on skills in both advanced tissue culture and molecular techniques.

Pamela has published in many peer reviewed journals and has presented papers in both local and international conferences. She has also organized training workshops on plant tissue culture technology where she has participated as resource person and course coordinator. She is also a member of professional bodies like the International Society for Horticultural Science (ISHS), American Society of Biochemistry and Molecular Biology (ASBMB), Biotechnology Society of Nigeria (BSN) and the Horticultural Society of Nigeria (HORTSON).

# DAY 2

# KEYNOTE FORUM

4TH EDITION OF GLOBAL CONFERENCE ON

# PLANT SCIENCE AND MOLECULAR BIOLOGY

SEPTEMBER
19-21, 2019

LONDON, UK

## 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 115 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, the Editor-in-Chief of the journal: Scientia Horticulturae, and the Special Issue Editor of Agronomy (MDPI). He was 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.

# In vitro culture and epigenetic variation in horticultural crop improvement

**Samir C. Debnath**

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

The multibillion dollar micropropagation industry is now well accepted in many countries of the world for commercial propagation of various plant species. Fruits and vegetables are very rich in health-promoting bioactive components. Although significant progress has been achieved in plant tissue culture of horticultural crops to multiply the true-to-type plants all the year around, genetic and epigenetic variations are a concern in commercial micropropagation. This review describes the progress in depth of various aspects micropropagation, clonal fidelity and epigenetic variation in micropropagated horticultural crops achieved at St. John's Research and Development Centre, Agriculture and Agri-Food Canada and in other laboratories. It also deals with different types of molecular markers that was used to study clonal fidelity and DNA methylation and with the possible application of epigenetic variation in the production of micropropagated horticultural crops

**Audience Take Away:**

- Plant tissue culture; molecular biology; genetic and epigenetic variations; micropropagated plants; DNA methylation
- Applications of plant tissue culture and epigenetics in horticultural crop improvement

## Biography

The biochemist Prof. Arnd G. Heyer obtained his degree in Tübingen and Berlin, going on to gain a doctorate at the Free University of Berlin on the subject of "The characterization of the phytochrome system in the potato" in 1991. From 1992 to 1995 he worked at the Institut für Genbiologische Forschung Berlin GmbH and from 1996 to 2004 at the Max Planck Institute of Molecular Plant Physiology in Potsdam. Heyer has been at the Biological Institute, University of Stuttgart, since 2004.

# Analyzing plant responses to extreme environments at different scales: From subcellular compartments to whole plants in soil

**Arnd. G. Heyer**
University of Stuttgart, Germany

Climatic factors and resource availability can constitute extreme environments, and among them, water availability, temperature and irradiation are most important. We have shown that accumulation of sugars in specific cellular compartments is a prerequisite of acclimation to low temperature, and based on mathematical simulations, we could show that establishment of freezing tolerance affords a sequence of transport events that re-allocate a large number of metabolites between plastids, cytosol and vacuole of a plant cell. A fast response to a temperature drop includes sequestration of sucrose into plastids, which is later replaced by raffinose, probably because of its minor importance in central metabolism. The capacity of sucrose synthesis in the cytosol correlates with freezing tolerance in the model plant Arabidopsis thaliana, most likely because accumulation of intermediates would inhibit secondary reactions of photosynthesis. Using chlorophyll fluorescence, it can be shown that cold sensitive accessions of Arabidopsis are incapable of maintaining linear electron flow at low temperature, ultimately resulting in the production of reactive oxygen species. A so far unanswered question is, why plants accumulate large amounts of hexoses in the cold. Using thermal imaging to control freezing processes in whole plants, we can show that hexoses reduce the amount of freezable water in leaf tissue, thus preventing dehydration of the protoplast, when ice forms in intercellular spaces. At high irradiance as well as low temperatures, electron transport to oxygen can lead to oxidative stress. Transfer of reducing equivalents from the plastids to mitochondria, where they can be safely oxidized, takes place via the transport of carboxylic and amino acids. Using the sugar sensor mutant gin2-1, we show that these processes are interlinked with sugar metabolism, resulting in high light sensitivity of a mutant plant that is not able to sense its sugar levels.

## Biography

**Jeremy Sweet** has spent the last 30 years conducting research on Crop improvement and plant diseases. Much of this work was conducted at NIAB Cambridge studying sustainable crop production, integrated disease management, environmental and agronomic impacts of GM crops, and gene flow to crops and wild relatives. He was coordinator of the UK BRIGHT project which studied herbicide tolerance, and he was also coordinator of the European Science Foundation programme “Assessing the Impact of GMOs” that brought together all the major research groups in this area in Europe. He was a coordinator of the EU SIGMEA project analysing data on gene flow and gene impacts and was a participant in the EU CO-EXTRA programme and the BBSRC Gene flow project. He was work package leader in the GRACE EU project on Systematic Reviewing of the impacts of GM plants and is Vice-Chair of the EU COST action iPLANTA studying RNAi in crop improvement and crop protection. He was an advisory Board member of the EU Pegasus project on GM animals, the EU Price Project on coexistence, the DEMETRA Life project, the EU COST Action on GM trees, the ESEGMO project in Finland and he served on the Steering Committee of the Swiss NFP59 programme on GMOs. He was a member of the EFSA GMO Panel for 12 years until 2018, providing scientific opinions on the risks associated with GMO applications in the EU. He has served as chairman of the Environmental, Post Market Environmental Monitoring and GM Fish Working Groups of the EFSA GMO Panel. He was a member of the GM Insects working group and has developed a number of the EFSA Guidance Documents on ERA and risk management. He was a member of the BBSRC/Phyconet Management Board and participated in the ALGEBRA project on GM algae and in an EFSA study of RNAi GM plants. He is an author in over 50 scientific papers on GMOs, numerous plant pathology papers and of 2 books.
He developed his own consultancy in 2004 and is director of JT Environmental Consultants Ltd which provides research and advice on GMOs and Plant Health to the European Commission, European governments, FAO/UNIDO/UNEP and scientific organisations and academies of several countries. He lectures on risk assessment of GMOs on postgraduate courses at the Universities of Marche (Ancona) and Ghent, and other training courses for FAO, UNEP, EC and other organisations. He has provided training and other advisory services in European, Asian and S American countries. He is vice-chair of the iPLANTA COST action studying RNAi applications in plant production and protection.

# Rnai: A great potential for crop production and protection

## Jeremy Sweet

JT Environmental Consultants Ltd., UK

RNA interference (RNAi) involves small naturally occurring molecules of double stranded RNA (dsRNA) targeting genes for expression knockdown by recognition of the target gene messenger RNA (mRNA) and interfering with the translation into protein. In this way, plant genes can be targeted to remove unwanted metabolites and in pests, pathogens and viruses, essential genes can be silenced leading to an effective control. Since these small RNAs recognize target gene mRNAs based on sequence complementarity, systems can be designed which target only genes with homologous sequences in a very narrow range of species. The exponential increase in available genomic and transcriptomic sequence data allows the specific design of these dsRNAs, minimizing the risk for off-target effects or silencing effects in non-target organisms.

RNAi has several unique features compared to other forms of crop biotechnology which offer unique opportunities to breeders for varietal improvements. One of these characteristics is the fact that RNAi leads to a knockdown effect, rather than a complete knockout. This could be important when lower levels of gene expression are required. dsRNA small molecules have high mobility through the plant vascular system and can move inside the plant from one point of application to the entire plant. Therefore, dsRNA produced in part of the plant (eg. rootstock) can spread in all parts (eg. canopy) so to confer resistance to disease to the full plant, including fruit that will result not genetically modified but protected by the presence of target specific highly degradable dsRNA small molecule. The dsRNA small molecule can be applied topically via a spray-based approach and/or via the application of modified micro-organisms and virus. This approach excludes the use of DNA recombinant technologies in plant so to not be classified as a GMO plant, as expected in many directives and in particular in the EU directive 2001/18.

Worldwide, several virus resistant plants have been approved (e.g. plum, squash and papaya) and many more applications are being developed. As with other technologies, pest and pathogen resistance management is important and new crop protection applications need to be accompanied by effective stewardship and resistance management plans. In addition, plant resistance to a wide range pests and diseases is being studied, particularly to insect vectors of pathogens and a range of fungal pathogens such as cereal rusts or fruit grey mould.

A more recent innovation is the use of topical applications of dsRNA to induce gene silencing as a new strategy for plant protection or growth regulation. Technical advances in the production of dsRNA and formulations to improve the efficacy, stability and persistence of extracellular dsRNA mean that it is now realistic to consider using dsRNA as a biopesticide. It can be applied as foliar sprays (spray induced gene silencing – SIGS) or as soil additives and there is considerable commercial interest in this because the cost of production, the specificity and improved biosafety compared with chemical pesticides and some alternative biocontrol strategies. SIGS are also being considered for weed control by targeting specific genes in a weed that do not occur in crops or other weed genera. Such a strategy would be very useful for controlling grass weeds in a range of graminaceous crops such as wheat and rice. Topical applications would typically contain dsRNAs which are produced in bacteria or synthesised in vitro. Thus they are not like other agrochemicals and are different from other biocontrol agents which exploit proteins such as peptides or Cry toxins. The sRNA may be produced using GM bacteria but the product can be formulated to not contain any GM material except the RNA molecule designed for a very specific gene target in a pest, pathogen or weed in order to avoid non-target effects and with limited persistence in the environment. Thus, it represents a novel type of (bio)pesticide and it is important that regulations governing plant protection products (PPPs) are adapted to allow introduction of this technology.

RNAi is a technology which is already being exploited and with great future potential in a range of areas of crop production and protection. It can make a major contribution towards integrated pest management and the sustainable agricultural strategies needed worldwide to secure current and future food production. GM RNAi plants are being assessed and regulated using existing regulatory frameworks. However SIGS needs to be classified in the regulatory framework as novel PPPs.

**Audience Take Away:**

- They can learn about some of the principles, mechanisms, activity, and applications of RNAi in crop protection. Information useful to teachers, lecturers, and to agronomists, crop protectionists, regulators, investors, agro-industry considering options for research, investment, opportunity and integrated pest management

DAY 2

# SPEAKERS

4TH EDITION OF GLOBAL CONFERENCE ON

# PLANT SCIENCE AND MOLECULAR BIOLOGY

SEPTEMBER
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LONDON, UK

GPMB-2019

# The estimate seagrass *(Zostera marina)* population genetics in Isles of Scilly and South of Coast, UK

**Alotaibi M. Nahaa[1&2*], Börger Luca[1], Bull C. James[2]**
[1]Swansea University, UK
[2]Princess Nourah bint Abdulrahman University, KSA

Seagrass is a group of flowering plants that live in shallow sheltered areas along the UK coastline where they form dense green meadows under the sea. It is one of the most significant sources of coastal primary production and it provides a critical habitat for juvenile reef fish and commercial fisheries.

Ongoing pollution of coastal waters and changes in water movement and climate may lead to declining populations and viability may be compromised further by loss of genetic diversity. Therefore, it is important to estimate the population genetic structure and genetic exchange in populations. Using an existing panel of 15 microsatellites, we estimated genetic variation in eelgrass, *Zostera marina*, at five sites around the Isles of Scilly and eighteen sites around south coast of the UK mainland. The over-arching goal of this study is to gain an understanding of the spatial population genetics of eelgrass, *Zostera marina.* Allelic richness was unexpectedly low within the Isles of Scilly, compared to the UK mainland. However, most sites were in Hardy-Weinberg equilibrium. To test the hypothesis of isolation by distance, we performed a Mantel test on the correlation between genetic distance (Fst) and geographic distance (m). There was no support for the hypothesis that pairwise genetic divergence correlates with distance in the Isles of Scilly. However, there was isolation by distance across the south coast.

Connectivity between populations is vital to the survival of extinction-prone plants, including those at risk from local environmental change, with globally important implications for applied plant ecology. The genetic information for *Z. marina* allows investigation of the genetic basis of physiological adaptation to extreme natural environments such as tidal flats.

### Audience Take Away:

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

### Biography

I am studying a PhD in the Department of Biosciences, Swansea University, UK. PhD project is looking at spatial structure in population genetics in UK seagrass, Zostera marina. Supervised by Dr James Bull and Prof. Luca Borger in the Department of Biosciences, Swansea University, UK

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

I am interested in many research areas such as: Population Genetics structure, Plant Ecology, Environment variable, Competition and Allelopathy in plant community. I have contributed and participated in several businesses as a volunteer.

# Does root structure affect phosphorous uptake in *Brassica napus*?

**Alexandra Batchelor*, Darren Wells, Neil Graham**
University of Nottingham, UK

Phosphorous is a vital element for plant growth and is a structural component of phospholipid cell membranes, nucleic acids, ATP etc. However it can be relatively difficult for plants to access the phosphorous they need from soil. This is due to phosphorous generally having low bioavailability in soils as it is easily fixed or adsorbed by other elements in the soil, for example it can be fixed by aluminium or iron in acidic soils or by lime in calcareous soils.

This often leads to farmers regularly applying fertilisers high in phosphorous to crops in order to increase available phosphorous. Phosphorous fertilisers are often expensive, obtained mainly from finites sources and have negative environmental impacts including eutrophication and contamination from other elements in the fertiliser. Due to this plants need to be made better at absorbing phosphorous already in soils.

Plants acquire nutrients from the soil through their roots, therefore if phosphorous uptake is to be made more efficient then the roots require extensive study. This study focuses on how root structure affects the uptake of phosphorous, focussing on *Brassica napus*. This study investigates if the physiological properties of roots, particularly root architecture and anatomy, differs between varieties with high and low phosphorous levels in their leaves.

The root architecture is being investigated using the pouch and wick phenotyping method to analyse 2D root structure. The 2D structure can then be analysed with the Root Nav image analysis software to identify a variety of traits which may be linked to the phosphorous levels within the plants (e.g. root lengths, number of laterals etc).

Sectioning of the roots and subsequent confocal microscope imaging is being used to look at the anatomical structure of the roots to investigate if the internal cellular arrangement of the roots is different between these lines. This is particularly interesting as the internal structure of Brassica roots has not been investigated in detail.

**Audience Take Away:**

- Recent developments in root phenotyping of architecture and anatomy
- Detailed structure and anatomy of roots on *Brassica napus*
- Role of root structure and anatomy in phosphorus uptake

### Biography

Alexandra Batchelor studied Biology at the University of Nottingham, graduated with an MSci in 2017. Started on the BBSRC Doctoral training program at the University of Nottingham in October 2017. Studying for her PhD under Dr Neil Graham.

# Improvement of plant immunity using RNA silencing-based plant protection strategies

**Aline Koch***, **Karl-Heinz Kogel**
Justus Liebig University, Germany

RNA silencing (also known as RNA interference, RNAi) is a conserved and integral aspect of gene regulation mediated by small RNAs (sRNAs) that direct gene-silencing on the level of transcription but also post-transcriptionally. At the transcriptional level, gene expression is inhibited via RNA-directed DNA methylation (RdDM) while at the post-transcriptional level (PTGS) direct mRNA interference causes inhibition of translation. Originally, RNA silencing is associated with protection against viral infection, control of epigenetic modifications, regulation of genome stability, curbing of transposon movement and regulation of heterochromatin formation (Koch et al. 2017). Besides its natural function, RNA silencing has emerged as a powerful genetic tool for scientific research over the past several years. It has been utilized not only in fundamental research for the assessment of gene function, but also in various fields of applied research, such as agriculture. In plants, RNA silencing strategies have the potential to protect host plants against predation or infection by pathogens and pests mediated by lethal RNA silencing signals generated in planta (Koch et al. 2013, Koch and Kogel 2014, Abdellatef et al. 2015, Gaffar and Koch 2019). In addition to the generation of RNA silencing signals in planta, plants can be protected from pathogens and pests by exogenously applied RNA biopesticides (Koch et al. 2016). Regardless of how target-specific inhibitory RNAs are applied (i.e. by endogenously or exogenously), the use of target-specific inhibitory RNAs (iRNAs) for plant protection is a potential alternative to conventional pesticides because iRNAs are i) highly specific and easy to produce and ii) can be developed against an unlimited range of pathogens possessing an RNA silencing machinery. Given its significant potential for environmentally safe agriculture, the overall scientific goal of my research is to study how RNA silencing in plants can be utilized/implemented as technology to improve plant disease resistance.

**Audience Take Away:**

- They will learn from our pioneering work in the field of  RNA silencing-based plant protection measures
- The benefits of RNA silencing-based plant protection measures
- Insides into a novel (GMO-free) technology called spray-induced gene silencing (SIGS)
- Research into the mechanistic basis of RNA silencing-based plant protection

## Biography

Dr. Aline Koch studied Biology at the Justus-Liebig University, Giessen and graduated as MS in 2010. Since then she joined the research group of Prof. Karl-Heinz Kogel at the Institute of Phytopathology. She received her PhD degree in 2013 at the same institution. At this time, she was one of the first scientists working in the field of RNAi-based plant protection. In the first year of her postdoc, she additionally developed a non-GMO RNA spray approach (SIGS) in cooperation with BASF. Since 2014 she is a group leader with the research focus: RNAi-silencing mediated plant immunity.

# Epigenes: Hereditary units with bimodular organization

**Oleg N. Tikhodeyev**
Saint Petersburg State University, Russia

Epigenetic inheritance is a rapidly growing field of Modern Biology, in particular, of Plant Genetics. However, all fundamental genetic concepts are still based on the hereditary role of DNA, thus resulting in multiple contradictions and terminological confusions. Moreover, only few mechanisms of epigenetic inheritance (namely, DNA methylation, histone modification, RNA interference and amyloid prionization) are usually considered, while their actual spectrum is far wider. These mechanisms may realize through (i) regulation of transcription by transcription factors, DNA methylation, and histone modifications, (ii) RNA splicing, (iii) RNA-mediated post-transcriptional silencing, (iv) inhibition of plastid translation, (v) protein processing by truncation, (vi) post-translational chemical modifications, (vii) protein folding, and (viii) homologous and non-homologous protein interactions. Basing on this list, we suggest that any regulatory mechanism participating in gene expression and/or gene-product functioning, under specific circumstances, may produce epigenetic inheritance. Although the modes of such inheritance are highly variable, stable allelic variants are clearly distinguishable in many epigenetic systems. Irrespective of their molecular nature, all these alleles have a principle similarity. Each of them is a bimodular hereditary unit: its features depend on (i) an epigenetic determinant (certain epigenetic mark in the DNA sequence or its product), and (ii) a DNA determinant (the DNA sequence itself; if this is absent, the corresponding epigenetic allele fails to perpetuate). These data mean that epigenetic inheritance do not reject the hereditary role of DNA. Meanwhile, the DNA theory of inheritance becomes now just a part of a significantly more complex genetic concept, wherein multiple additional mechanisms with no or almost no limitations to their variety are also included.

**Audience Take Away:**

- The audience will get very new information on synthesis between the DNA concept of inheritance and epigenetics.
- It will be shown that epigenetic inheritance is not limited to DNA methylation and histone modifications, even in plants.
- General principles of molecular organization of any epigenetic allele irrespective to their nature will be presented.
- This will help to overcome multiple contradictions and dramatic terminological crisis occurring in current genetics.

## Biography

Dr. Tikhodeyev graduated from Leningrad (at present, Saint Petersburg) State University in 1983. Initially, he specialized in Yeast Genetics, and his PhD thesis defended in 1990 was devoted to [PSI+] factor (yeast hereditary prion). Presently, he is Associate Professor at the same University. He teaches a wide spectrum of biological disciplines from Plant Genetics to Behavior Genetics. His current scientific interests mostly relate to Theoretical Biology and paradigm shift in Genetics. He has published more than 30 articles in scientific journals and 3 textbooks, including Introduction to Behavior Genetics, and Genetics of Plant Development.

# Effects of low cAMP levels on plant immunity after infection with an avirulent strain of *Pseudomonas syringae pv.* tomato

**Sara Cimini[1*], Wilma Sabetta[2], Elodie Vandelle[3], Vittoria Locato[1], Alex Costa[4], AndreaBittencourt Moura[3], Laura Luoni[4], Alexander Graf[5], Luigi Viggiano[6], Diana Bellin[3],Emanuela Blanc[o2], Laura De Gara[1], Maria Concetta de Pinto[6]**
[1]University of Rome, Rome, Italy
[2]Institute of Biosciences and Bioresources, Italy
[3]University of Verona, Italy
[4]University of Milan, Italy
[5]Max Planck Institute of Molecular Plant Physiology, Germany
[6]University of Bari "Aldo Moro", Italy

Plants had to constantly deal with several environmental factors such as biotic and abiotic stresses, which can alter the oxidative metabolism and photosynthetic efficiency thus affecting plant growth and development. Despite remarkable phenotypic and metabolic differences of defence responses implemented by plants after stress exposure, only few chemical species are involved in the signalling pathways inducing them.

Plant defence responses seem to be mainly regulated by the amounts, timings and cellular compartmentalization of the produced stress-related metabolites. Among the signalling molecules inducing the activation of defence pathways, calcium ions ($Ca^{2+}$), reactive oxygen species (ROS) and cyclic nucleotides (cNMP) play pivotal roles. Recent evidence suggests that specific calcium signatures, followed by $Ca^{2+}$-mediated apoplastic oxidative bursts, are likely involved in both local and long-distance signalling. The amount, timing and type of ROS produced under stress conditions as well as their cellular localization, seem to be also critical for activating defence pathways in response to environmental stresses. In particular, hydrogen peroxide ($H_2O_2$) is one of the most interesting ROS for its action as signalling molecule due to its stability, higher than that of other ROS, and its capability to cross biological membranes. In higher plants, the presence and the physiological relevance of 3'-5'-cyclic adenosine monophosphate (cAMP) was becoming known only in the last decades, whereas its mechanism of action is still poorly characterized.
In this study, a more reliable approach has been developed, by generating *Arabidopsis thaliana* plants overexpressing the 'cAMP-sponge' (cAS plants), with the aim to genetically and specifically buffer cAMP levels.

We decided to use this genetic tool to investigate on cAMP role in plant immune response triggered by the avirulent pathogen *Pseudomonas syringae* pv. tomato DC3000 carrying the avirulence gene *AvrB* (*PstAvrB*). A higher bacterial growth and a reduced hypersensitive cell death were observed in cAS plants compared to wild-type plants. The genetically controlled lowering of intracellular cAMP levels results in the inability of cAS plants to manage the correct equilibrium between ROS production and scavenging thereby inducing an impairment of the redox homeostasis after pathogen infection. Consistently, the low cAMP availability induces a significant delay in the timing of cytosolic $Ca^{2+}$ and $H_2O_2$ increase following *PstAvrB* exposure. Analyses at biochemical and molecular levels have been also carried out in both control and infected plants over treatment time. In particular, ascorbate (ASC) and glutathione (GSH) metabolisms, as well as expression and activity of redox enzymes involved in ROS scavenging were investigated in both genotypes 4 h and 24 h post-infection. Moreover, a comparative proteomic analysis performed on WT and cAS plants 24 h post-infection reveals the occurrence of a transcriptional reprogramming that involve a core set of proteins regulated in both genotypes and other proteins uniquely modulated in WT and cAS plants. Concluding, our data confirmed that low cAMP levels affect the timing and intracellular levels of key signalling molecules thus altering the induction of defence redox systems and consequently compromising the plant immune responses triggered by pathogen infection.

**Audience Take Away:**

- The audience will be able to improve their knowledge about the involvement of cAMP in plant defence mechanisms triggered by an avirulent strain of Pseudomonas syringae pv. tomato. In particular, the information that the audience will learn from my presentation aim at reveal the effects of a low cAMP levels on plant immune responses with a particular attention to the redox systems regulation
- In higher plants, the presence and the biological role of 3',5'-cyclic adenosine monophosphate (cAMP) have been, for a long time, a matter of debate. This situation is firstly due to its low concentration and to the technical difficulties related to its detection. Moreover, cAMP biosynthesis and catabolism is not fully characterized. This work represent a new reliable approach for the study of cAMP functions obtained by the production of transgenic Arabidopsis thaliana lines overexpressing the cAMP-sponge, a genetic tool that specifically buffers cAMP levels. The specificity towards cAMP of this genetic tool allowed the development of a more reliable and targeted approach than the pharmacological tool, to gain further insight into its role

- The use of transformed plants overexpressing the cAMP-sponge can be used by the researcher to investigate on cAMP biological functions in different experimental conditions such as in response to abiotic and biotic stresses but also during plant development. Therefore, this presentation may be useful for providing new solution to make the designer's job more efficient and to improve the accuracy of a design

## Biography

Sara Cimini received a master's degree in "Cellular and Molecular Biology" in 2009 at the University of Rome Tor Vergata. She then joined the research unit of Prof. Laura De Gara and she attained the PhD degree in "Biochemical and Technological Sciences Applied to Food and Nutrition" in 2013 at Campus Bio-Medico University of Rome and starting from 2013, she has a post-doctoral fellowship in Plant Biology and Physiology in this research unit. Furthermore, she obtained a graduate master's degree in Bioinformatics at University of Rome La Sapienza in 2010. She is interested in understanding mechanisms of plant resistance at molecular, cellular and physiological level in response to biotic and abiotic stress conditions with a focus on Reactive Oxygen Species (ROS) and ROS-mediated responses.

# Foliar traits flammability in native woody species from semiarid environments from Argentina

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Wildfires are increasing in several both natural and artificial environments of world due to climate change and accelerated land use changes. Areas with seasonal climate as semiarid environments are the most affected by wildfires. The Argentine Chaco region agrees with this global pattern and this environment is the second most forested area of South America with great interesting for conservation. The objectives of this work were: a) to evaluate flammability traits in 11 native woody species and to assess changes in specific leaf area (SLA) of 6 representative species of different forest strata, in response to anthropogenic disturbances. The study area is included in Western Chaco region, Argentina. The sampling sites were located in an experimental area of 8000ha, belonging to Instituto Nacional de Tecnología Agropecuaria (INTA), Province of Santiago del Estero. Plant flammability traits considered for this study were Leaf and Twig Dry Matter Content (LDMC, TDMC), Twig Drying Time (TDT), Degree of Ramification (DR), and growth habit (GH) and foliar persistence (FP) as traits of plant architecture. These traits were assessed in 6 individuals of each species, in plots emplaced an undisturbed forest the last 35 year (control), and in a forest disturbed by wildfires, rolling-chopper and logging. The SLA represents an ecological indicator of environmental changes generated by disturbances and this trait is one of the most important components to initiate fires. The SLA study was carried out in the same forests evaluated for plant flammability assessments. The variables on both objectives were recorded following protocols for functional traits studies in plants. Statistical analysis included ANOVAs, Principal Components Analysis (PCA) and Cluster Analysis (CA). Results indicated that the main factors of plant flammability were LDMC and TDMC and the 63% of species studied presented flammability degree (FD) from medium to very elevated. The functional traits considered allowed identifying three species groups with different FD. The non perennial trees with herbaceous leaves were less flammable species and perennial shrub with sclerophyllous leaves were the most flammable species. Disturbances had no effects in FD of species studied. The SLA increased significantly after disturbances in all studied species suggesting a high aptitude to recover the photosynthetic apparatus and to capture resources released by these events, with predominance of acquisitive traits as non perennial broad leaves. This resilient aptitude despite of medium to high FD agrees with the high fire tolerance observed in native woody species from Argentine Chaco region through resprouting strategy, which is probably related to foliar traits (persistence, SLA) and GH. Results will contribute to improve the post-fire evaluations and restoration activities in degraded areas.

**Audience Take Away:**

- The wide audience of congress will recognize common aspects and knowledge needs related to the vegetation management in fire prone ecosystems of the World
- The functional studies are considered the best approach for plant flammability assessments since allow to compare the role of wildfires in the dynamic of natural processes in seasonal climate areas of world
- Early results of this work can improve models about fire behavior and to guide restoration activities of burnt areas

## Biography

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

# Characterization of Salt Tolerance-Related Protein (STRP) of *Arabidopsis thaliana,* a new player in cold stress responses

**Anna Fiorillo, Maurizio Mattei, Patrizia Aducci, Sabina Visconti, and Lorenzo Camoni***
University of Rome, Italy

Cold is one of the critical environmental conditions that negatively affects plant growth and development. STRP is an A. thaliana poorly characterized protein identified in a proteomic screen of temperature stress-responsive proteins. Here we studied the role of this protein in the response mechanism to cold stress. Our experiments show a rapid increase of STRP into the cytosol after cold treatment caused by increased protein stability. By means of specific proteasome inhibitor we demonstrate that cold stress inhibits the proteasome-mediated degradation of STRP. Protoplasts transiently transformed with the fusion protein STRP-YFP show that STRP is located into the cytosol, in the nucleus and is associated to the membrane. Under cold stress protein levels into the nucleus and in the cytosol increase, whereas the fraction associated to the membrane decreases.

To clarify the physiological function of STRP and its role in response to cold stress, we studied the cold response in the strp knockout mutants. This mutant is smaller compared to wild type plants both under physiological and stress conditions and is more susceptible to the oxidative damages induced by cold stress. Furthermore, the analysis of Abscisic acid (ABA) effects on growth and development of strp plants demonstrates that the mutant displays an ABA hyposensitive phenotype. These evidences demonstrate the crucial role of STRP in cold stress response and in the regulation of ABA biosynthesis and signaling.

**Audience Take Away:**

- We identified a new protein involved in cold stress responses
- Studying the physiological role of STRP helps to unveil the complex signaling network regulating the plant response to abiotic stresses
- The analysis of *strp* mutant contributed to expand the knowledge on the signaling mechanism of abscisic acid

## Biography

Dr Camoni studied Biology at Sapienza, University of Rome, and graduated in 1994. In 1995-1997 was Research Fellow at the National Research Council (CNR), in 1997 he was for 4 months Research Fellow at tha Institute of Molecular Biology, University of Copenhagen, Denmark. In 1998 he was Research Fellow at the University of Rome Tor Vergata. In 2000 he obtained a position as Research Scientist of Plant Physiology at the University of Rome Tor Vergata, and since 2001 he is Assistant Professor of Plant Physiology in the same University. He has published more than 40 research articles (H index=19).

# Mechanisms underlying the tolerance of plants to a combination of heat stress and drought

**Nobuhiro Suzuki*, Ayana Kumazaki, Kohey Honda, Ruka Nakano, Misaki Endo**
Sophia University, Tokyo, Japan

Plants as sessile organisms are exposed to multiple abiotic stresses that simultaneously occur under natural environmental conditions. Studies deciphering acclimation of plants to stress combinations are however still scarce. Here, we report the characteristics of Arabidopsis mutants with enhanced tolerance to a combination of heat stress and drought.

ISOCHORISMATE SYNTHASE 1 (ICS1) is known as a crucial enzyme required for the synthesis of salicylic acid and phylloquinone, one of the components of the photosystem I complex in the chloroplast. We revealed enhanced tolerance of an Arabidopsis mutant deficient in ICS1 *(sid2-1)* to a combination of heat stress and drought, accompanied by enhanced H2O2-dependent stomatal closure and accumulation of total soluble sugars. In addition, *sid2-1* plants showed higher accumulation of reaction centre proteins in the photosystem II compared to WT plants as well as enhanced expression of transcripts involved in the turnover of these reaction centre proteins. Taken together, our findings suggest that maintenance of photosynthetic apparatus as well as prevention of excess water loss might enhance the tolerance of *sid2-1* plants to a combination of heat stress and drought.

Elm2 gene in Arabidopsis was previously shown to be up-regulated in response to a combination of heat stress and drought. Here, we demonstrated enhanced tolerance of an Arabidopsis mutant deficient in *Elm2* gene *(elm2)* to this stress combination. However, the mechanisms underlying this enhanced stress tolerance of *elm2* mutant might be different from that of *sid2-1* mutant. *elm2* mutant showed lower accumulation of oxidized lipid and superoxide compared to WT plants under a combination of heat stress and drought. In addition, expression of transcript encoding a ROS producing NADPH oxidase was lower in *elm2* mutant compared to WT plants under this stress combination. Thus, the enhanced tolerance of *elm2* mutant to combined stress might be due to attenuation of oxidative damage caused by superoxide.

Our researches demonstrated the different mechanisms that are significant for the tolerance of plants to a combination of heat stress and drought. It should be interesting to address how these different mechanisms are integrated in future studies.

## Audience Take Away:

- Information can be a clue to establish new strategies to enhance stress tolerance of plants
- Information can be useful for the elucidation of the wide varieties of stress response mechanisms involving ROS regulatory systems
- We will provide new approaches to link biology and agriculture
- New perspectives associated with plant hormone signaling and the maintenance of photosynthetic apparatus will be provided
- New mechanisms of ROS production will be provided

## Biography

Nobuhiro Suzuki obtained Master's degree from Kagawa University in Japan, and Ph.D from University of Nevada, Reno in USA. Then, he worked as a postdoctoral fellow in Prof. Ron Mittler's lab in University of Nevada, Reno and University of North Texas. He is currently working as an assistant professor in Sophia University, Tokyo, Japan, mainly studying response of plants to heat stress and stress combinations. He published 29 peer-reviewed article and 1 book chapter.

# Effects of Gamma rays irradiation on *Eucalyptus* clones

**N.K. Khanna, O.P. Shukla*, S.L. Narkhede and S. K. S. Chauhan**
JK Paper Limited, India

JK Paper Ltd. Unit: CPM, Fort: Songadh, India was earlier has put in pioneering efforts and working with the farming communities in Gujarat and Maharashtra states of India for meeting its raw material requirement by promoting short rotation pulpwood plantations on their farm lands. This has created a win-win relationship for farmers as well as industry by helping farmers realize value from their wastelands and helping industry meet its ever increasing demand for raw material on a sustainable basis.

JKPL had put in placed robust plantation R&D network for increasing wood productivity & pulping qualities through breeding, selection, Mutation, & other tree improvement initiatives with improved silvicultural practices for wood productivity & quality improvement like density, pulp yield, improved fibre morphology etc.

JKPL have studied effects of gamma rays irradiation with doses (0.01, 0.03, 0.05 and 0.10) of radioactive cobalt (CO 60) gamma rays on 10 nos of high productive, site specific & disease resistant Eucalyptus clones, which were irradiate in Nuclear Research Laboratory, Indian Agriculture Research Institute (IARI), New Delhi, India. Progeny trials planted at JK Paper Ltd, Unit: CPM, Fort: Songadh, Gujarat, India. All higher doses irradiated plants (0.03, 0.05 and 0.10) were died after 3-4 month of plantings. Smaller doses shows faster growth (volume increment) over its control planted under statistical design of experiment.

DNA fingerprinting studies using different polymers were done for 2 clones with positive mutants at JK Agrigenetics Ltd, Biotechnology Lab, Hyderabad India shows variation in PCR with its control. The chemical analysis of wood (2 year age) also shows improvement in wood density & fiber % in mutant clones over its control due to mutagenesis.

**Audience Take Away:**

- Audience can carry out the wood productivity research in various plants
- Quality of fruit and agriculture crops can be improved by using gamma rays
- Gamma rays can be used for species evolution of plants and animal kingdom in the benefits and interest of the world community

## Biography

Mr. Om Prakash Shukla studied M.Sc (Genetics) from School of Biological sciences, Bhopal in 1982 and completed his State Forest Rangers Course (SFRC) from Forest Rangers College, Jabalpur in 1985. He has started his career with Nepa Limited, Nepanagar as Officer trainee in 1983 and with vast knowledge and increasing experience he has served various paper companies like Sirpur Paper Mills Ltd, JK Paper Ltd, Rayagada, Ballarpur Industries Ltd, and as on date he is designated as Chief General Manager (RM) at JK Paper Ltd, Unit CPM. He has published various research papers India as well as in International Journals.

# Comparative Investigation on Two Different Populations of *Lamium garganicum* subsp. striatum var. microphyllum *(Lamiaceae)* distributed in Turkey

**Baran, P[1*], Özdemir, C[2]**
Usak University, Turkey
Manisa Celal Bayar University, Turkey

**The following points will be discussed:**

- How much do the two populations differ from Mill (1982)'s and Mennema (1989)'s descriptions and each other, morphologically?
- How much do the populations differ from each other anatomically?
- How much do the populations differ anatomically from the other investigated *Lamium taxa* in the family?
- What points should be taken into consideration unbiasedly in an integrative review of the genus *Lamium*?
- This study aimed to describe the morphological and anatomical characters of two different populations of L. *garganicum* subsp. striatum var. *microphyllum* in detail to be able to contribute to the systematic works of the investigated taxon or to an unbiased revision of the genus *Lamium.*

**How much do the two populations differ from Mill (1982)'s and Mennema (1989)'s descriptions and each other, morphologically?**

According to Flora of Turkey, Mill (1982) recorded that *L. microphyllum* and *L. sandrasicum* are endemic alpine species, respectively distributed on Honazdağ and Sandras dağı in Denizli. Mennema (1989) has regarded *L. microphyllum* and L. sandrasicum as synonyms of *L. garganicum* subsp. striatum var. microphyllum in the recent monograph of the genus Lamium. In the present study, the two populations are corresponded to the synonyms *L. microphyllum* and *L. sandrasicum,* respectively. We will present the detailed morphological descriptions by photographs, illustrations, tables and measurements in this section. The morphological data will be compared to Mill (1982)'s and Mennema (1989)'s descriptions to update information. According to our morphological data the two populations appear different enough from each other to be able to be evaluated in higher taxonomic categories.

**How much do the populations differ from each other anatomically?**

We will present detailed anatomical descriptions of the investigated populations by photographs, tables and measurements in this section. According to Metcalfe & Chalk (1972) a quadrangular stem and a well-developed collenchyma, supporting tissue at the corners of stem is the characteristic feature of Lamiaceae family. The two populations reflect general character of the family, having collenchymatous tissue at the corners of the stems, which, in particular, is clearly detectable in the hand blade sections.

However, certain anatomical differences were detected between the two populations besides so many similarities. Glandular hairs were classified according to Werker et al (1985) and Werker (1993) in this study. Glandular hair diversity is one of the most important differences between the two populations.

**How much do the populations differ anatomically from the other investigated *Lamium taxa* in the family?**

We will compare the investigated populations with the other investigated Lamium taxa, anatomically in this section. Lack of extraxilar sclerenchyma in the roots or stems is one of the most important common points for both the investigated populations and other *Lamium taxa* (Baran & Özdemir 2009, 2011, 2013, Özdemir & Baran 2012, Celep et al 2011, Atasagun et al 2015, Atalay et al 2016).

The presence of glandular hairs on the leaves, especially at the margins of calyx teeth is one of the conflicting points with Mennema (1989). On the otherhand, there have also been few conflicting anatomical points for the same taxa reported by Atalay et al (2016), the recently done comprehensive work on Turkish *Lamiums.* The possible reasons of the conflicting points are discussed.

**What points should be taken into consideration unbiasedly in an integrative review of the genus *Lamium*?**

This population study points out that there are some issues that need to be considered in order for anatomical studies to contribute to systematic knowledge, correctly.

- Long-term and intensive chemical treatment methods, such as the paraffin method, can lead to the erosion and loss of certain soft tissue types of systematic importance, leading to incomplete or inaccurate information about the plant taxa.
- Especially few layered collenchymatic tissues may have lost in alike methods.
- Hand-blade section, a conventional method, should not be neglected for Anatomical Studies.
- Particularly, it should be used to determine the types of collenchymatic tissue such as angular, plaque and lacunar.
- When examining glandular trichomes;
- Hand-blade sections should be used in light microscopy.
- The appropriate sample should be prepared from fresh material instead of dry material in scanning electron microscopy
- Secretion mode described by Werker et al (1985), Werker (1993) should be included in classification. This can make a greater contribution to illuminating systematic problems in the genus *Lamium.*
- In order to reveal the general anatomical features of a plant taxon and use it in taxonomy, it is necessary to examine different populations of the same taxa and also as many samples as possible in a population.

**Audience Take Away:**

- Morphological Research
- Anatomical Research
- Points to be Considered in the Contribution of Anatomical Research to Systematic Research
- Systematic Botanists may show greater demand and rigor for Anatomical Studies
- We think the targeted audience will be
- Provided with new information that can help them in their fields
- Provided with practical solution to challenge disadvantageous methods that could produce misleading and incomplete results in Anatomical Studies
- Provided with new ideas in their research fields
- Ready to form collaborations to prepare new projects

**Biography**

Dr. Baran studied Biology at Manisa Celal Bayar University, Turkey and graduated as MS in Science of Plant Anatomy and Morphology in 2005. She received his PhD in Science of Plant Anatomy, Morphology and Karyology in 2011 at Manisa Celal Bayar University. She has been an Assistant Professor at Usak University since 2011. She has published more than 20 research articles (12 of which are SCI-indexed).

# Roles of Potassium Transporters in Salt Tolerance of plants

**Yuichi Tada**
Tokyo University of Technology, Japan

**The following points will be discussed**

Halophytic wild turf grasses

Ion managements in plants under salt stress

Functions of potassium transporters from salt tolerant turf grass

Acquisition of potassium and sodium by potassium transporters

**Halophytic wild turf grasses**

Salinity stress is one of the most significant limiting factors in agricultural crop productivity. Hence, improving the salt tolerance of crops is essential for sustainable food production. Halophytes are widely spread over higher plant families and orders and exhibit a broad variety of adaptations to salt. Wild turf grasses are known to be relatively resistant to salt. We examined the salt tolerance of more than 30 species of wild turf grasses collected from all over Japan and showed that Sporobolus virginicus is the most salt tolerant among them, which tolerate up to 1.5 M NaCl (Tada et al. 2014).

**Ion managements in plants under salt stress**

Plants have been classified into two categories, salt includers and salt excluders, from how to deal with sodium ion. Salt includers take up sodium ion and translocate it to the shoot, where it is sequestered and used as vacuolar osmoticum to decrease the water potential, whereas salt excluders adapt to saline environments by avoiding sodium ion accumulation. Ion channels including potassium transporters play important roles in the ion management. In Arabidopsis, a salt excluder, AtHKT1;1 contributes to the retrieval of sodium ion from the xylem to repress accumulation of sodium ions in shoots. I found that most of wild turf grasses are salt includers and that they have diverse ion accumulation patterns.

**Functions of potassium transporters from a salt tolerant turf grass**

We have cloned genes for potassium transporters from S. virginicus and have been characterizing their functions in potassium/sodium transport. SvHKT2;1 and SvHKT2;2 mediate distinct outward and inward K+ and Na+ transport activity in plants (Tada et al. 2019). Constitutive expression of the SvHKT2s in transgenic Arabidopsis resulted in reduced salt tolerance but their specific expression in xylem parenchyma cell enhanced the plant growth under mild salinity. SvHKT1;1 mediate inward Na+ transport activity and is possibly the counterpart of AtHKT1;1. I will discuss the roles of these transporters in salt tolerance in relation to their tissue/organ specificity.

**Acquisition of potassium and sodium by potassium transporters**

I would like to discuss the possibility of modifying the availability of potassium and sodium as fertilizer in transgenic plants expressing *SvHKTs.*

**Audience Take Away:**

- Diversity of sodium/potassium ion management in salt-tolerant plants
- Functional diversity of potassium transporters in plants
- The targeted audience will join the information about plant salt tolerance mechanisms and acquisition of potassium as a nutrient
- I think the targeted audience will be
- Provided in new information that help them in their fields
- Provided in possible solution to challenge the salt stress problem
- Provided new ideas in their research fields
- Ready to compose alliance to prepare new project

## Biography

Dr. Tada studied Agriculture Science at the Tokyo University, Japan and graduated as MS in plant breeding science in 1988. He joined the research group of Plant Biotechnology at Mitsui Toatsu Chemicals, Inc., Japan in 1988 and worked on rice molecular breeding and rice conventional breeding. He received his PhD in Agriculture in 1992 at the Tokyo University. While he was working for Mitsui Toatsu Chemicals, Inc., he turned to Mitsui Plant Biotechnology Research Institute from 1996 to 1999. He moved to School of Bioscience and Biotechnology, Tokyo University of Technology, Japan in 2005. He has been working on Plant molecular breeding in stress tolerance and phytoremediation. He has published more than 40 research articles.

# Genomic structural variation in the self-incompatibility locus causes a transition from outcrossing to selfing in amphidiploid *Arabidopsis kamchatica*

**Takuma Ota[1]*, Yasuaki Kagaya[2], Go Suzuki[3], Masao Watanabe[4], and Keita Suwabe[1]**
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Self-incompatibility (SI) is a sophisticated mechanism for pollen selectivity to prevent self- fertilisation and is genetically regulated by two genes located in S-locus. S-locus receptor kinase (SRK) and S-locus cysteine rich protein (SCR) is female and male specificity genes, respectively, and physical interaction of these S determinant factors triggers the downstream signalling cascade and subsequently causes a rejection of self-pollen. *Arabidopsis kamchatica* is amphidiploid plant species originated from a natural cross between *A. lyrata* and *A. helleri.* While parental diploid species have SI, *A. kamchatica* is a self-compatible species, predictively due to a loss of function in the SI system. To elucidate why *A. kamchatica* does not have a SI system, we attempt to reveal two S-locus genomic structures in A. kamchatica, one from *A. lyrata* and other form A. helleri, using two types of Next Generation Sequencing technologies, the Ion Proton (Thermo Fisher) and the MinION (Nanopore) systems. Because an amphidiploid plant genome has a high similarity in homoeologous genomic regions which originated from each parental genome, we manually curated two independent S-locus contigs, one from *A. lyrata* and other form *A. helleri,* using CLC Gnomic Workbench 11. By several bioinformatics analyses, we obtained two S-locus sequences separately and found critical mutations in the S-specificity genes in both S-loci. This result suggests that self-compatibility in *A. kamchatica* is caused by disruptive mutations in the S-specificity genes and the genomic structure of S-locus would reflect a process of breakdown of SI and evolutional transition history of mating system, from SI to selfing mode in *A. kamchatica.*

## Audience Take Away:

- Plant genomics
- Plant ecology
- Plant reproduction
- The audience will be provided how to create novel nucleotide sequence information of target region(s) using different types of sequencing technologies, and also be able to learn an evolutional history of genomes in related species

## Biography

Takuma Ota graduated as BSc in plant molecular genetics and breeding, Mie University in 2019, and is currently PhD student of Mie University, Japan.

# Evaluation of genetic diversity among sixteen accessions of African Locust Bean (*Parkia biglobosa* Jacq.) using SDS-PAGE and RAPD markers

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Using protein and DNA fingerprinting to study genetic diversity among cultivars may provide useful information to plant breeders. Sixteen accessions of African locust bean *(Parkia biglobosa)* collected from different locations across Nigeria were assessed for variability based on polymorphism using sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) of seed storage proteins and Random Amplified Polymorphic DNA (RAPD) analysis. SDS-PAGE revealed a substantial degree of homogeneity in the protein banding patterns ranging from 10 - 180 kDa polypeptides. One major cluster of bands was observed between 36 – 53 kDa and two minor clusters were observed between 11 and 17 kDa and at 180 kDa. The absence of 14 kDa band was specific to cultivar NH/2016/P04. Jaccard's coefficient of similarity ranged from 0.846 to 0.923. Based on UPGMA cluster analysis, the 16 cultivars were separated into 2 major groups at 0.91. While most cultivars were clustered at a very narrow genetic distance (group 1), cultivars NH/2016/P03, NH/2016/P04 and NH/2016/P14 were clustered into group 2. This implies that most of the cultivars are closely related indicating that the genes of ALB are highly conserved. For the RAPD analysis, forty primers were screened for polymorphism out of which sixteen were polymorphic. The sixteen primers generated a total of 256 bands out of which 163 bands were polymorphic resulting in 63.67% polymorphism. The genetic diversity ranged from 0.4141 to 0.9297, while Polymorphic Information Content (PIC) ranged from 0.3874 to 0.9252. Dendogram generated from UPGMA cluster analysis separated the 16 ALB cultivars into six groups at 0.65. RAPD marker has the potential to discriminate cultivars with narrow genetic base.

## Biography

Dr Pamela Akin-Idowu is an Assistant director and a Research scientist at the National Horticultural Research Institute (NIHORT), Ibadan, Nigeria. She heads the biotechnology unit of NIHORT where she manages research laboratories and coordinates project activities. Pamela has a PhD in Biochemistry (specialization in plant molecular biology) from the University of Ibadan, Nigeria. Her current research focuses on developing and optimizing protocols for in vitro propagation of some horticultural crops for mass production of healthy planting materials to meet farmers need.

She has over 18 years' experience in plant tissue culture techniques and molecular characterization. Other areas of research interest are in the characterization of horticultural crops for conservation of germplasm for use in crop improvement programmes based on phenotypic (qualitative and quantitative methodologies) and DNA markers (RAPD, SSR, SDS-PAGE).

She is a recipient of many fellowships including the African Women in Agricultural Research and Development (AWARD) a Bill and Melinda gates scholarship programme, Nuffic-Netherlands Fellowship Programme (NFP) and MASHAV (Government of Israel) Scholarship Programme. She has attended much training locally, regionally and internationally where she gained knowledge and hands-on skills in both advanced tissue culture and molecular techniques.

Pamela has published in many peer reviewed journals and has presented papers in both local and international conferences. She has also organized training workshops on plant tissue culture technology where she has participated as resource person and course coordinator. She is also a member of professional bodies like the International Society for Horticultural Science (ISHS), American Society of Biochemistry and Molecular Biology (ASBMB), Biotechnology Society of Nigeria (BSN) and the Horticultural Society of Nigeria (HORTSON).

# Effect of faba bean cultivars and sowing dates on *Orobanche crenata* biomass and seed reduction by the biocontrol agent *Phytomyza orobanchia* (Diptera : *Agromyzidae)*

**Mohamed Awad Soliman Al-Eryan**
Alexandria University, Egypt

The following points will be discussed

- Economic importance of parasitic weeds *Orobanche* spp.
- Problems that face faba bean crop in Egypt.
- Biological control of *Orobanche* spp.
- Resistant faba bean cultivars to *Orobanche* infection and sowing dates
- Integrated *Orobanche* management

## Economic importance of parasitic weeds Orobanche spp.

Broomrapes ( Orobanche spp. of the family *Orobanchaceae* ) are chlorophyll lacking holoparasites which attach to roots, causing great losses in quantity and quality in yields of the heavily infested host plants such as faba bean *(Vicia faba* L.), peas *(Pisum sativum* L), lentil *(Lens culinaris* Medic.), chickpea *(Cicer arietinum* L.), carrot *(Daucus carots* L.) and tomato *(Lycopersicom esculentum* Mill.) ( Parker & Riches, 1993 ). *Orobanche crenata* Forsk. is a very aggressive parasitic weed of winter legumes in the Mediterranean area of West Asia and North Africa ( WANA ), the area of infested faba bean totals nearly 200,000 hectare or about 63% of the planted area (Sauerborn, 1991a). Reported yield losses of infested faba bean ranged from 5% to complete crop failure depending mainly on the *O.crenata* seed bank in the soil, agronomic practices and temperature, as well as soil moisture regimes during the growing season (Borg 1986, Linke et al. 1991a, Sauerborn 1991b).

## Problems that face faba bean crop in Egypt.

In Egypt, *O.crenata* is one of the major constraints to the production of faba bean, which is the most important food legume in breakfast and lunch diets ( El-Helaly et al., 1973 and Al-Menoufi, 1994, Al-Eryan and Zaitoun, 2015 ). In West Nile Delta region, the area infested with O.crenata was more than 25,000 feddan ( Zaitoun et al.,1991 ). It occurs in about 20 % of the total area cropped with faba bean, of which about half suffers low to moderate infestation ( less than 5 spikes per $m^2$ ) and the other half is infested with 5 - 20 spikes per $m^2$ or more. The loss in faba bean seed yield in El-Beheira governorate (West Nile Delta) was 20,000 tons or about 10 million dollars (Hassanein et al.,1996). Nowadays, Orobanche infestations forced Egyptian farmers to change faba bean crop by wheat or berseem and now Egypt introduce faba bean from outside.

## Biological control of Orobanche spp.

Biological control is a particularly attractive means of suppressing parasitic weeds in crops.The insect natural enemies of *Orobanche* spp. have been surveyed in different countries. The dipteran *Phytomyza orobanchia* Kalt. ( *Agromyzidae* ) is the only one of these insects that has received further attention. This fly is widespread in Europe ( except Scandinavia ), the Mediterranean Basin and eastwards through Saudi Arabia to Uzbekistan (Spencer, 1973). *P.orobanchia* was first found in Germany and described by Kaltenbach (1872). In Egypt, it was first recorded by Hammad et al. (1967). In this respect, the broomrape fly, *P.orobanchia* may be considered as the main bio-agent against *Orobanche* spp. due to its mono-phagous habit, the larvae are active feeding on the immature seeds of *Orobanche.* A reduction of *Orobanche* seed production can only be achieved if the natural population of *P.orobanchia* is strengthened. This can be secured either by the creation of better conditions for *P.orobanchia* to reproduce and increase in number or by mass-rearing and targeted releases at the beginning of the *Orobanche* flourish ( Linke, 1999 andTrenchev, 1981).

Field applications which have been developed in the former Soviet Union are the most suitable for bio-control of this parasitic weed. In Egypt, biological control trials of the weed *Orobanche crenata* was conducted by (kolaib, 1991; Al-Eryan, 1996; Al-Eryan and Zaitoun, 1998 & 2001; Zaitoun and Al-Eryan, 1999 and Abu-Shall, 2001). Although of the effectiveness of Phytomyza releases in reducing *Orobanche* seed production can reach 91.73%, the already infested soil in addition to new accumulated seeds will cause further infestations over the successive seasons. This finding should be undertaken in the future release programs of P.orobanchia (Abu-Shall, 2001 and Al-Eryan et al., 2004).

**Resistant faba bean cultivars to *Orobanche* infection and sowing dates:**

At the end of March 2004, broomrape, *O. crenata* spikes were collected from three faba bean cultivars ( Sabawy, Giza 3 and Egypt 1 ) during two sowing dates ( early in 1-15 October and late in 1-15 November ) at West Nile Delta. The size and weight of Orobanche parasite depend on the planted cultivars and sowing date, which reflects on the amount of produced seeds. Statistical analysis showed that *Orobanche* biomass significantly affected by faba bean cultivars and sowing dates. Results of this study should be undertaken during planning release programs to improve efficacy of *P.orobanchia* in *Orobanche* seed reduction.

**Integrated Orobanche management**

Control attempts on *O.crenata* have not been successful because the weed produces numerous resilient tiny seeds. Due to the intimate relationship of *Orobanche* with its host, herbicides can't be applied without crop damage (Linke et al. 1990). Integrated control is therefore an attractive alternative for suppressing broomrape. In the Nile valley in Egypt, Nassib et al. (1989) and Al-Eryan et al. (2011) reported that integration of the use of the tolerant Faba bean genotype Giza 402 with a slightly reduced rate of glyphosate application (60g/ha) and slightly delayed sowing (The first fortnight of November) resulted in a nearly 96% reduction in *Orobanche* infestation and 29.2% increase in faba bean seed yield.

**Audience Take Away:**

- Risk of parasitic flowering plants on economic crops
- How to use alternative methods to control *Orobanche* parasitic weeds such as biological control – resistance crops – sowing dates
- The targeted audience will join the information about parasitic flowering plants with their research fields, also I think the audience will think applying biological control methods against other parasitic weeds in other economic crops
- I think the targeted audience will
- Activate brain storm to solve agriculture problems
- Supplied with new information that help them in their fields
- Supplied with practical solution to solve stress problem of parasitic flowering plants.
- Supplied new ideas in their research lines
- Ready to compose research team to prepare new project

**Biography**

Dr. Al-Eryan studied Agriculture Science at Alexandria University , Egypt. He has got Msc. in biological control of insects in 1991. Also, he has got PhD in biological control of parasitic flowering plant, *Orobanche crenata* in 1996. He graduated in scientific positions as demonstrator in 1985 to Prof. up to date in dept. Applied Entomology. He has shared in several projects funded from EU, IDRC, WHO and Alexandria Uni. He has published 32 research articles. He has Scientific contributions in applied Entomology such as recording the Peach Fruit Fly, Bactrocera zonata as a new pest in Egypt in 1998 and recording the Red Palm Weevil, Rhynchophorus ferrugineus as a new pest in Lybia in 2009. He attended International Conferences in Entomology: CZECK REPUBLIC 1998 – BRAZIL 2000 - THAILAND 2011 - MALAYSIA 2013. He has got the Alexandria University Prize in Science in 2002.

# Secondary metabolites from *Tectona grandis* extracted by extrusion process

**Lucero Paola Chávez Salgado[1*], V. Vandenbossche[1] and G. Vilarem[1]**
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*Tectona grandis* L.F. (teak) is a tree species native to India, Myanmar, Thailand and Laos People's Democratic Republic1 although it was moved outside of its natural occurrence to several countries in Africa and America during the past century2. Teak is a very recognized timber due to their economic value and remarkable characteristics like strength, ease of working, beauty and decay resistance. This last quality is ascribed to the second metabolites presents in their extractives, such as anthraquinones and naphthoquinones. These chemical compounds exhibit fungicidal and termicidal bioactivity.

The conventional extraction methods as soxhlet and maceration as well as the organic solvents are the most used to get the bioactive molecules. Nevertheless, extrusion process can be perform the extraction of secondary metabolites using water as a solvent. This technology has been broadly studied to fractionate and pre-treat lignocellulosic biomass in a continuous way. In the extrusion process, the biomass is mixed, heated and sheared by the action of one or two screws that turn into a confined barrel3.

This work is focused on the identification and quantification of chemical compounds from teak sawdust extractives using water at subcritical conditions by extrusion process and the comparison with other extraction methods using common solvents. In addition, the use of raw material coming from a woodworking enterprise located in Mexico intend to valorise wood wastes. The identification of the chemicals compounds was made by the comparison between the authentic ones and the results from the analysis by HPLC-DAD and HPLC-MS. The antioxidant activity was measured by DPPH (α, α-diphenyl-β-picrylhydrazyl) method and the polyphenolic content by Folin-Ciocalteu assay. Besides, the Van Soest and Wine method was conducted to characterise the teak heartwood.

According to the results, the aqueous extractives obtained by extrusion contain 2-hydroxy-3-(3-methyl-2-butenyl)-1,4-naphthoquinone (lapachol), anthraquinone-2-carboxylic acid and 2-methyl anthraquinone. These molecules were not identified by the other methods. This approach suggest a promising way to add value to wastes from the timber industry by getting chemical compounds from them.

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**Audience Take Away:**

- Extrusion can be used as an alternative method for extraction of secondary metabolites instead of the traditional ones (soxhlet and maceration techniques).
- This technology is a practical solution to the problem of extraction by hazardous solvents since it allows getting extractives from lignocellulosic biomass using water
- Extrusion is a versatile method that permits a broad range of parameters and a continuous operation
- The extraction of bioactive molecules from teak sawdust could be a good way to valorise wood wastes

**Biography**

Ph.D. student Lucero studied chemical engineering at the National Autonomous University of Mexico (UNAM), Mexico and graduated in 2007. She then received her Master degree of chemical engineering in 2014 at the same institution. She is studying currently at the Laboratory of Agro-industrial Chemistry, INP Toulouse, France supervised by Dr Vilarem.

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# DAY 2

# POSTERS

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# Critical time for weed removal in soybean as influenced by pre-emergence herbcides

**Stevan Z. Knezevic[1]*O. Adewale Osipitan[2]**
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By definition, the critical timing for weed removal (CTWR) is the maximum amount of time early season weed competition can be tolerated by the crop before the crop becomes subject to an irrevocable yield reduction. The concept of CTWR has been shown to be useful tool for determining the timing of weed control operations in agronomic crops. However, it has been speculated that CTWR can be influenced by the production practices. Therefore, field experiments were conducted in 2015 and 2016 at Concord, Nebraska, to evaluate the CTWR in soybean, as influenced by pre-emergence (PRE) herbicides. The studies were laid out in a split-plot arrangement with herbicide regime as the main plot and weed removal timing as the subplot. The herbicide regimes included; without PRE-herbicide and premix of saflufenacil plus imazethapyr at the rate of 280 g ai ha-1 or 420 g ai ha-1. The weed removal timings were at V1, V3, V6, R2 and R5 soybean stages, as well as weed free and weedy season-long control. The CTWR was based on 5% acceptable yield loss. CTWR started at V1 soybean stage (21 days after emergence (DAE)) without PRE herbicide, while the application of PRE-herbicide delayed the CTWR to V5 soybean stage (34 DAE) in 2015 and to R1 soybean stage (46 DAE) in 2016. These results suggested that the use of PRE-herbicide in soybeans could delay the need for post-emergence weed control by 2 to 5 weeks.

**Keywords:** Weeds, Pre-emergence, Post-emergence, critical, time

# Salicylic acid-cryotherapy treatment for elimination of potato virus s from *Solanum tuberosum*

**Humberto A. Lopez-Delgado, Diana R. Ruiz-Sáenz*, Diana D. Ayala-Hernández**
Programa Nacional de Papa, Instituto Nacional de Investigaciones Forestales Agropecuarias y Pecuarias, Conjunto SEDAGRO, México

Potato virus S (PVS) is one of the most difficult viruses to eliminate by thermotherapy due to its thermal deactivation point. Pre-treatment methods involving salicylic acid (SA) have been successfully carried in conjugation with cryogenic methods to reduce oxidative damage and eliminate viruses. In the present investigation, the effect of SA to protect Solanum tuberosum plants infected with PVS from oxidative damage from subsequent cryotherapy was studied. Vulnerable genotypes to cryogenic protocol were selected, with two SA treatments examined. Potato clones were pretreated with SA (0, 10-5, and 10-6 M), plant development was evaluated and then exposed to cryotherapy. This was followed up by a plant development evaluation and virus testing. After the initial treatment with SA, the plants exhibited an increase in the variables evaluated before cryotherapy. After cryotherapy, between 66.6% and 100% of the treated plants were found to be virus-free compared to control plants which exhibited 0% survival. Thus, the SA-cryotherapy treatment combination described appears to enhance plant survival and eliminate PVS from potato plants.

## Biography:

Biotechnology Engineer in UPVT (Universidad Politecnica del Valle de Toluca) in Toluca State of Mexico ,Mphil in Botany in COLPOS (Colegio de Postgraduados) in Texcoco State of Mexico INIFAP researcher in campus Metepec in Potato program since 2015, author and coauthor in different research publications.

# RNAi- mediated plant protection: Unraveling the molecular mechanisms underlying Identification of the molecular components of the the HIGSHost-induced gene silencing technology pathway

**Timo Schlemmer**
Justus-Liebig-University, Giessen, Germany

In plants, RNA silencing strategies have the potential to protect host plants against predation or infection by pathogens and pests mediated by lethal RNA silencing signals generated in *planta* (Koch et al. 2013). In addition to the generation of RNA silencing signals in *planta,* plants can be protected from pathogens and pests by exogenously applied RNA biopesticides (Koch et al. 2016).

Despite the promising potential of RNA silencing-based disease control and its benefits for agronomy and the ecosystem, the mechanisms underlying HIGS and SIGS technologies are virtually unresolved. There is little information about the contribution of either plant or fungal silencing machineries in cross-species RNA silencing (,i.e. plant and fungus) or the nature of the inhibitory RNA that translocate from the plant to the fungus after its transgenic expression or spray application. Addressing these questions is a central scientific goal of our research and key for making RNA silencing-based strategies a realistic and sustainable approach in agriculture.

Therefore, we currently aim to identify and further characterize plant and fungal RNA silencing-associated factors that are involved in HIGS and SIGS. In this context, we are testing Arabidopsis RNA silencing mutants expressing CYP3RNA to elucidate their role in the mechanistic basis of HIGS. Moreover, as we have shown that the fungal RNA silencing machinery also contributes to SIGS (Koch et al. 2016, Gaffar et al. 2018), we systematically included fungal *FgAGO* and *FgDCL* knock-out mutants in our HIGS and SIGS assays. In addition to this genetic approach, we aim to determine the specific *Arabidopsis,* barley as well as *Fusarium* AGO protein(s) that is/are associated with HIGS and SIGS using a biochemical approach.

## Biography

T. Schlemmer did his bachelor's in biology and his master's in crop science between 2013 and 2018. Since 2018, he joined the Institute of Phytopathology at the Justus-Liebig-University Gießen for doing his Ph.D. He focuses on the mechanistically basis of RNAi mediated resistance of *Arabidopsis thaliana* towards the crop pathogen *Fusarium graminearum.* For example, which components are necessary for double stranded RNA processing, packaging and transport into fungal cells.

# Evaluation of the wheat photosynthetic pigments content by spectral absorption of leaves determined using a smartphone

**Eduard A. Shuralev**[1, 2*], **Oleg V. Nikitin**[1], **Amir Mardanov**[1], **Konstantin A. Osyanin**[2]
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[2]Federal Center of Toxicological, Radiation and Biological Safety, Kazan, Tatarstan, Russian Federation

Various direct and indirect methods are used to determine the content of chlorophyll and carotenoids in plants. Among direct methods, the most widely used ones are the spectrophotometric determination of chlorophyll, after its extraction with various solvents. The disadvantage of this approach is the complexity of the procedures performed and the need for a laboratory base. Therefore, at present, methods of indirect registration of parameters of photosynthetic activity have become widespread. Fluorimetric and spectral research methods are most widely used for such registration. However, such approaches are also not without drawbacks, including due to the high cost of equipment. Therefore, the search continues for approaches aimed at registering the photosynthetic activity of plants by alternative methods, in particular, by attracting funds available to a wide range of people, in particular smartphones. In this connection, the purpose of this work is to assess the content of photosynthetic plant pigments by the spectral absorption of leaves, determined using a smartphone.

The hypothesis was put forward: characteristics of a photographic image of a wheat leaf plate, obtained using a smartphone after passing light through it (spectral absorption), allows us to indirectly judge the content of photosynthetic pigments and photosynthetic activity of plants.

Results were as fallowing. The content of chlorophyll a varied in the range of 0.34–2.08 mg per gram of raw wheat biomass, the content of chlorophyll b was 0.11–0.56 (at a ratio of 1.5–9.1), and the amount of carotenoids was in the range of 0.06–0.45. Significant differences between the variations of the trials were not observed. The soil-plant analysis development (SPAD) value varied between 22.13 and 47.93 units, averaging 37.19 units. The chlorophyll content, estimated by this parameter, was in the range of 187–615 μmol m–2. Indicators of the spectral absorption of a leaf plate of wheat, obtained by different models of smartphones (Samsung A5 and iPhone 5s), are statistically significantly correlated with indicators of the photosynthetic activity of plants, estimated by the parameter SPAD, and directly ($r = 0.68–0.86$ and 0.41–0.67). The highest values are noted for the GMR and VARI spectral indices. The correlation values with photosynthetic pigments, obtained using smartphones, are generally identical to those obtained using the SPAD indicator. The verification of the method demonstrated good convergence of the results on the definition of photosynthetic pigments, found from the obtained dependencies and determined by direct spectrophotometric method. The error of determination was within 20%, which corresponds to the errors of traditional methods of chemical analysis.

### Audience Take Away:

- The presentation will demonstrate the possibility of using widely used devices (smartphones) for quick and inexpensive determination of the content of photosynthetic pigments (chlorophyll, carotenoids) in plants
- The results obtained are comparable to data obtained using other, but more complicated (spectrophotometry) and expensive methods (fluorimetry)
- Given the high availability of smartphones in the modern world, this approach can be used by a wide range of people
- The proposed solution can be used for applied purposes in agriculture, science and education

### Biography

Dr. Eduard A. Shuralev studied at the Kazan State Academy of Veterinary Medicine, Russia and graduated as DVM in 1996. He then joined the research group of Prof. K. Salmakov at the Federal Center of Toxicological, Radiation and Biological Safety, Kazan, Russia. He received his PhD degree in 2000. Since 2011 he is Associate Professor at the Institute of Environmental Sciences, Kazan Federal University, Russia. Since 2013 he is also Leading Research Fellow at the Federal Center of Toxicological, Radiation and Biological Safety, Kazan, Russia. He has published more than 35 research articles in SCI(E) journals.

# Influence of different priming materials on germination of sorghum hybrıds (*Sorghum bicolor* l. moench. x *Sorghum sudanense* staph.) seeds

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Maximum germination percentage achieves immediately after harvesting and gradually decreases with storage time. Seed aging is the main problem of seed storage. Seed priming enhances seed germination performance after aging and able to promote rapid and more uniform seed germination and plant growth.The purpose of this Communication is to compare the efficacy of different seed priming osmotica on the germination of aged and unaged hybrid silaj sorghum seed. Sugar Grazer II and Digestivo hybrid silage sorghum cultivars were used as the plant material. As the priming material, 5 different chemicals (8 mg/L putrescine, 2 mg/L jasmonic acid, 100 mg/L kinetin, 50 mg/L KNO3 and 4.5 mg/L salicylic acid) were applied to aged and unaged seeds. Under laboratory conditions, the greatest first count germination (98.00%) was obtained from jasmonic acid-treated aged Sugar Grazer II seeds and the greatest first count germination in Digestivo cultivar (98.00%) was obtained from KNO3 treated unaged seeds. The greatest germination percentage (97.33%) was obtained from jasmonic acid-treated aged Sugar Grazer II.

**Key words:** Accelereted Aging, Germination, Priming, Seed, Sorghum.

**Audience Take Away:**

- Sorghum seeds generally lose their biological characteristics very quickly. In such a case this influences plant genetic characteristics and storage conditions. Sorghum seeds generally have 1000-seed weights of between 12-40 g and they need a well prepared seed bed for production. Therefore, when the sowing is not made in mellowed soil in a shallow fashion, germination and emergence rates will be quite low. On the other hand, since seed vigor is lost rapidly, sorghum seeds should be preserved under quite good conditions
- This method (priming) is a technical term that reduces the effects of aging by reducing Malondialdehyde (MDA) and free radicals production and maintenance of antioxidant activities and improve germination
- Also this is not an expensive method and can be implement by seed companies

## Biography

Dr. Negar EBRAHIM POUR MOKHTARI studied Agriculture at the Tabriz Islamic Azad University, Iran and graduated as MS in 2008. She received her PhD degree in 2014 at the Agronomy and Field crops Department of Ankara University, Turkey. After one year postdoctoral fellowship supervised by Prof. Dr. Mustafa Kizilsimsek at the Sutcu Imam University, Turkey she obtained the position of an Assistant Professor at the Gaziantep University.

# Isolation and identification of molds associated to dry-cured meat products

**Klara Čuljak*, Željko Jakopović, Ksenija Markov, Jadranka Frece, Deni Kostelac, Iva Čanak**
Klara Čuljak*, Željko Jakopović, Ksenija Markov, Jadranka Frece, Deni Kostelac, Iva Čanak

Dry-cured meat products are the oldest form of processed meat and very popular food around the world where different cultures contribute to their texture, flavor, and safety. The production of dry-cured meat products goes back thousands of years because it was quickly discovered that drying meat reduce intrinsic moisture and thus prevent the activity of microorganisms and prolong product durability. Specific microbiota in dry-cured meat products involves complex microbial ecosystems that combine bacteria, yeasts, and molds which are responsible for many of the characteristics of these products. The most frequently isolated fungi from dry-cured meat products are from *Penicillium, Aspergillus* and *Erotium* genera. For example *P. chrysogenum, P. commune, P. nalgiovense, P. olsonii, P. crustosum, A. niger, A. fumigatus, A. ochraceus, E. repens.* Some strains may produce highly toxic secondary metabolites, mycotoxins, and mold growth on sausage surfaces can lead to both desirable and undesirable effects. Preferred properties lead to the desired taste and texture of the product. The undesirable effects are usually connected to growth of undesirable molds which can lead to the defect in the quality and appearance. One of the possible solution is the use of the mold starter culture which will prevent the growth of undesirable wild mold population. The aim of this research was to isolate mold from fermented meat products in order to identify the indigenous flora of molds, the so-called houseflora. During the research, from 10 samples of dry-cured meat products, 3 different molds were isolated by classical microbiological methods. Each sample was inoculated in a 5 different mediums: Czapek yeast extract agar (CYA), malt extract agar (MEA), Sabouraud agar (SAB), potato dextrose agar (PDA) and potato dextrose agar prepared by cooking potatos and adding agar. Samples were incubated for 5 days at 28 °C. After the growth of molds, reverse and averse side of colonies are observed as well as color and exudate. Also the microscopic images were made. After obtaining microscopic images, samples were identified according to the identification key (Pitt and Hocking, 2009). Finally, analysing the results, it was concluded that isolated molds belong to *Penicillium* (2) and *Aspergillus* (1) genera and that they show different growth on different medium under same cultivating conditions. These findings can be helpful for further identification of molds on dry-cured meat products.

**Audience Take Away:**

- How to isolate mold from meat products
- Which microbiological methods to use to identify mold
- To identify molds based on growth on various nutrient media, colored colonies, exudates, microscopic images

**Biography**

Klara Čuljak is a student of Biotechnology at Faculty of Food Technology and Biotechnology, University of Zagreb, Croatia. She did her bachelor thesis at the Department of Biochemical Engineering at Laboratory for General Microbiology and Food Microbiology. For her bachelor thesis she did the research about isolation and identification of fungi from the surface of dry-cured ham. Finally, she has become a Bachelor of Biotechnology in September this year.

# Study on genetic diversity and physico-chemical characteristics of theichhungsen *(Haematocarpus validus* (miers.) bakh. f. ex. forman), a potential source of natural food colour from Mizoram

**PB Lalduhawma, Vanlalvenhima, Elija Lalrindika, Chhungpuii Khawlhring***
Mizoram University, India

An investigation was carried out between March to June, 2019, to identify superior genotypes of the fruits of Theichhungsen *(Haematocarpus validus* (Miers.) Bakh. F. ex. Forman), which is a potential source of natural food colour, from the state of Mizoram, North East India. The fruits were collected from different locations and various morphological features such as fruit weight and size, peel weight and thickness, pulp weight, seed weight, length and breadth, as well as physico-chemical characteristics such as TSS, titratable acidity, total sugar, reducing sugar, anthocyanin content, vitamin 'C', protein, carbohydrate, starch and phenolic contents were analysed. The fruit samples collected from different locations have varying weight on their fruit, seeds and pulp ranging between 14.81gm to 37.01 gm (fruits), 3.65 gm to 13.61gm (seed), and 1.84gm to 8.95 gm (pulp).

The study also reveal that fruits collected from Darlawn village has maximum average fruit weight(33.04 gm), maximum peel and pulp weight, maximum seed length and weight, highest reducing sugar (9.28%), lowest titratable acidity (2.22%) and highest starch content (1.93 mg/100gm). On the other hand, fruits collected from Tachhip village showed minimum average size in fruit length and breadth, fruit weight (18.61 gm), pulp weight (1.09 gm), seed weight (14.36gm) and seed length and breadth. Also fruits from Tachhip village have lowest TSS content (10.00 Brix ), lowest reducing sugar, highest titratable acidity (6.48%), highest vitamin 'C' content (17.94 mg/100gm), highest protein content (1.6 mg/100gm) and lowest phenol content (0.52 %). Fruits from Seling village have maximum peel thickness (4.81mm), maximum seed breadth, highest total sugar content, highest anthocyanin content (273 mg/100gm) and highest carbohydrate content (9.66 mg/100gm). Thus, the fruits from Darlawn are found to be best in terms of size, the fruits from Tachhip eventhough small in size, have high score in physico-chemical contents, whereas the fruits from Seling maybe most suitable for anthocyanin pigment extraction.

**Keywords:** Theichhungsen, blood fruit, natural food colour, anthocyanin.

# Urban organic gardening in Croatia

**Tanja Gotlin Čuljak [1*], Ivan Juran [1], Vesna Židovec [1], Tihomir Miličević [1], Branka Mrakužić [3], Klara Čuljak [2]**
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Urban gardening probably exists since the founding of cities, and its revival could be the key to sustainable cities of the future, but also for a sustainable future on Earth. Urban organic gardening is not a relic of the past. It is an integral part of the urban system of the human population. Food production in urban gardens should be in accordance with the principles of organic production. Urban gardening in the Republic of Croatia has existed for decades, and since locally grown food in urban gardens represents an ecological and social step forward for the inhabitants of our cities, their number increases considerably each year with strong support from local government. So far, formal urban gardens have been established in a large number of Croatian cities, in Zagreb, Varaždin, Osijek, Samobor, Rijeka, Velika Gorica, Karlovac, Ozalj, Split, Ivanić Grad, Virovitica, Koprivnica and others. Initiatives for the formation of urban gardens were initiated by citizens allied to different associations and informal groups of citizens. Also, the formation of urban gardens was initiated by the local authorities with the aim of putting into function the untreated and abandoned land, owned by the city where people can grow vegetables, flowers, medicinal herbs, berry fruit etc. In the City of Zagreb there are currently 12 city gardens with more than 2100 garden plots in the area of 22.20 ha. Garden parcels cover the area of 50 m2, and they are provided for use by public and based on certain criteria without a fee. The funds which are needed for the arrangement and establishment of urban gardens, also, their maintenance and communal services, the city ensures through the city budget and thus contributes to their financial sustainability. The main strategic goal of Croatian cities is to improve spatial quality and function of cities. Organic food production, enhancement and preservation of biodiversity as well as educational programs for gardeners, citizens, pre-school and school children were the specific goals of local government and the University of Zagreb Faculty of Agriculture co-operation. During three years of investigation of biodiversity, 258 plant species, 69 pathogens and 201 insect species have been identified in gardens. In total, 528 species of organisms in the gardens have been identified only by visual inspection. The estimated number of organisms in the garden is surely higher. The number of pollinators and natural enemies has increased considerably by implementation of flower strips and the installation of ''hotel for insects''. Also, yields of individual cultures has increased by up to 30%. A total of 45 lectures were held for gardeners and six important topics of ecological gardening were discussed; 70 workshops were held for preschool children, and 22 topics were discussed; 49 workshops were held for schoolchildren, and 16 topics were discussed. During the cooperation, a total of 164 lectures/workshops were held and 44 topics of ecological gardening and biodiversity were covered.

### Audience Take Away:

- Urban organic gardening: what and why?
- How to make space for gardening in urban areas?
- How to increase biodiversity in urban areas?

### Biography

Full professor Tanja Gotlin Čuljak has been working for more than 20 years at University of Zagreb Faculty of Agriculture. She has received PhD in 2006 at the same Faculty with thesis of distribution and identification of different aphid species in Croatia. She was leader of one international and seven national science projects. She is author or co-author of more than 60 scientific articles.

# Morphological aspect and molecular mechanism of pollen hydration on pollination in *Arabidopsis thaliana*

**Keita Suwabe[1]*, Maho Takada[1], Takuma Ota[1], Yohei Mizoguchi[1], Mei Ando[1], Yasuaki Kagaya[2], Go Suzuki[3], Masao Watanabe[4]**
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In flowering plants, sexual reproduction is a complex and orchestrated series of events regulated by multiple processes for successful seed production, including capturing and adhesion of pollen grains onto a surface of stigmatic papilla, foot formation to strengthen pollen–stigma interaction, hydration and germination of pollen grains, pollen tube elongation into the stigma and style, pollen tube guidance towards the ovule, and fertilization of egg cells and central nuclei, termed double fertilization. Among them, pollination is the first important step in plant reproduction to bring together the male and female gametophytes. In Arabidopsis thaliana, it occurs at a surface of the stigmatic papilla cell. After pollen recognition, accepted pollen grains rapidly start hydration and germination, and pollen tube exactly penetrates into the stigmatic surface, elongates through stigma and style, and finally fertilizes with a female gametophyte in the ovule. While it has been studied for many years, the knowledge base about molecular mechanisms underlying these sequential pollination events are still largely unclear. In this study, we focus on the pollen hydration process, as a mid-pollination appearance for successful reproduction. Coupled with the time-series imaging analysis of pollination and the gene expression information obtained via lasermicrodissection-RNA sequencing analysis of Arabidopsis papilla cell, we found that pollen hydration starts within 5 min and completed in approximately 45 min after pollination and the membrane bound-water channel proteins, belonging to the Major Intrinsic Protein family, would be key players of water transport from the pistil to pollen grains for successful pollen hydration.

**Audience Take Away:**

- Plant reproduction
- Molecular mechanism
- Seed production
- Target audience will be provided a novel knowledge of molecular mechanism of plant reproduction and new insight into successful seed production in Agricultural field

## Biography

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

# Identification of two helicases as potential targets for mitigating drought stress in rice

**Mouboni Dutta[1]*, Mazahar Moin[2], Anusree Saha[2], Achala Bakshi[2] and P.B. kirti[1]**
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Rice is consumed as a staple cereal crop by more than 3.2 billion people worldwide. But the constraint lies in the fact that rice cultivation requires about 35-43% of the world's total irrigation. Due to global climatic changes, abiotic stress factors like drought and soil salinity are hampering its productivity and sustainability. Moreover, in addition to the already existing high demand, the escalating global population estimates that rice productivity must be increased by 26% in the next 25 years. Hence, with the help of improved genome engineering techniques, we have developed water use efficient (WUE) rice varieties which can withstand abiotic stress conditions like drought without compromising its yield. We have developed gain-of-function rice mutants via activation tagging. Analysis of these mutants under water deficit conditions, and further in silico studies led to the identification of two important helicases (SEN1 and XPB2) as potential targets for gene manipulation to develop stress tolerant varieties of rice.

The drought tolerant attributes of SEN1 and XPB2 helicases has not been much explored. SEN1 and XPB2 are mostly associated with abnormal transcription termination and DNA repair respectively. A detailed study of the activation-tagged lines has provided us with an insight on the probable role of these genes in drought stress tolerance.

The expression analysis of the tagged mutants showed significant upregulation of the two genes in response to multiple simulated stress cues like salicylic acid, jasmonic acid, NaCl, polyethylene glycol (PEG), abscisic acid (ABA), and heat. We have also examined their expression patterns in response to infection with prominent rice pathogens such as Xanthomonas oryzae pv. oryzae and Rhizoctonia solani, which cause bacterial leaf blight and sheath blight respectively. Although not much significant upregulation was observed under biotic stress conditions, there was a noticeably high expression under ABA treatment. The lines showed better phenotypic and physiological characteristics in terms of increased fresh weight, root and shoot length, chlorophyll and proline content, photosynthetic performance, and yield when exposed to simulated stress factors. We have used ABA and PEG in order to mimic osmotic and drought stress conditions. Similar phenotypic traits were observed when the mutants were subjected to field-level drought stress. Further analyses of these plants are currently underway. We are also generating independent transgenic overexpression lines of these genes in rice for their further characterization. Taken together, our studies firmly establish that SEN1 and XPB2 can be considered important candidate genes for synthesizing tailor-made varieties of rice tolerant to drought stress.

## Audience Take Away:

- We have used Ac/Ds based activation tagging technique in order to generate gain-of-function mutants in rice. Since this is an emerging technique in the field of plant biotechnology, a discussion on its application will definitely encourage the audience working in similar areas to implement it
- We have predicted the probable role of two important helicases as potential targets for gene manipulation in rice. Although there are several reports on other helicases (especially the DEAD box helicases), this is the first kind where helicases without the DEAD-box domain are being reported to have important role in abiotic stress tolerance. This might be intriguing to other researchers to carry out a detailed analysis of the mode of action and other interactive pathways of the helicases in order to unveil their diverse functions
- Since rice is an important model cereal crop and it shows syntenic relationship with other cereals, characterisation of these two helicase genes might lead to comparative genomic studies including major other crops. Hence, there is a scope of exchange of ideas with scientists working on cereals crops other than rice
- The work will give the audience an idea about the significance of drought stress and urgency to act upon the issue. In essence, to mitigate the loss of yield and cope up with the increasing demand, it is important to identify novel genes and develop and commercialise improved varieties of rice. This piece of work thus creates new avenue for dealing these concerning issues

## Biography

Ms. Mouboni Dutta graduated with Botany honours in 2013 from Presidency College, Calcutta University, India. She then joined the University of Hyderabad for her Master's degree (2015) in Plant Biology and Biotechnology. In 2015 she joined Prof. P.B. Kirti's group at the University of Hyderabad for her PhD. Currently she is in her 4th year of PhD. She got selected for Newton-Bhabha fellowship and presently carrying out a part of her research at the University of Essex with Dr. Ulrike Bechtold for 4 months. She has successfully published 2 research papers and 1 review article in international journals as co-authors.

# Real-time quantitative PCR based method for quantification of *Xanthomonas axanopodis* pv punicae in pomegranate

**Pavan kumar[1, 2*], Pushpa Doddaraju[2], Manjunath Girigowda[2], Bharati S Meti[1]**
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Pomegranate is one of the important commercial fruit crops of India, known for its high nutritive and remunerative value. Cultivation of pomegranate is severely affected by bacterial blight caused by *Xanthomonas axanopodis* pv punicae (Xap). Under epidemic condition bacterial blight drastically reduces the yield and deteriorates the quality crop produce up to 80% under field condition. Breeding for developing resistant lines is the most appropriate strategies for effective management of plant disease. Therefore screening of a large genotype is very necessary for identification of resistant or tolerant type for resistant breeding. However, existing protocols for screening of different genotype green house and field often results in high experimental error leading to inconsistent disease scoring. In post-genomic era, early diagnosis and accurate quantification of pathogen is very crucial in identification of resistant cultivar. for identification of candidate gene inferring resistant. Hence, in the present study, we screened a large number of pomegranate accession for identification of resistant or tolerant lines. Further, accessions exhibiting highest disease tolerance were quantified using *Xanthmonas* specific primer XOPQ. The relative pathogen quantification was successfully conducted on 7 tolerant line IC318762, IC318735, IC318724, IC318734, IC318707, ACC8, IC318706 and two susceptible wild type Nana, Daru and one highly susceptible commercial cultivar Bhagwa selected from screened lines. The primer found to be specific to *Xanthmonas,* the sensitivity was analyzed using PCR coupled with agarose gel electrophoresis (PCR-AGE), PCR coupled with capillary electrophoresis (PCR-CE) and Real Time quantitative Polymerase Chain Reaction. The Conventional PCR-AGE useful in quantifying the pathogen with detection limit of 10 pg, followed by High resolution PCR-CE and RT-qPCR with 100fpg and 10 fg respectively. This approach can be employed for screening large number of pomegranate accession for breeding programmers to differentiate quantative resistant among genotypes.

**Key words:** Pathogen quantification, Pomegranate Bacterial blight, Real Time quantitative Polymerase Chain Reaction (RT-qPCR), Capillary gel free electrophoresis system.

**Audience Take Away:**

- Bacterial blight (BB) is the one of the most compromising factor in pomegranate cultivation, leading to huge economic loss.
- There are no resistant lines available for BB, breeding for resistance is one of the best and eco-friendly strategies for management of BB disease in pomegranate.
- Quantification of pathogen is very crucial in identification of resistant cultivar. Since, traditional methods are often results in high experimental error, leading to inconsistent disease scoring.
- In the present research real-time quantitative polymerase chain reaction (qPCR) was used for quantifying Xap biomass in pomegranate for discrimination pomegranate genotypes.
- This technique can be employed for screening large number of accession for resistant breeding programmers in pomegranate against BB.

## Biography

Mr. Pavan Kumar is a Ph.D research scholar at Basaveshwar Engineering College and Senior research scholar of university of Horticultural Sciences, Bagakot. He completed his M.Sc in biotechnology from university of Mysore and bachelors in life sciences from Karnataka University Dharwad, India. He is currently working on enhancement of host resistance in pomegranate against bacterial blight caused by Xanthomonas axonopodis pv. punicae and its integrated management. During his research he developed novel bio-formulation for pomegranate bacterial blight management which is successfully being adopted in the field trial by farmers. He has two publication in SCI (E) journals and one technology and a patent under communication.

# Development of a fertility restorer for novel *inap Brassica napus* CMS by genetic introgression of one Chinese woad chromosome

**Pengfei Li*, Lei Kang, Aifan Wang, Xianhong Ge, Zaiyun Li**
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The following points will be discussed

- Concept and Principle of Cytoplasmic male sterility and fertility restoration
- Production of novel inap *Brassica napus* CMS via somatic fusion with Chinese woad
- Development of a restorer for inap CMS through genetic introgression
- The organisations interested in CMS and Restorer
- Concept and Principle of Cytoplasmic male sterility and fertility restoration

Cytoplasmic male sterility (CMS) can occur either in natural plant populations by the natural mutation of mitochondrial loci (autoplasmy CMS), or as a result of crosses in which the nuclear genome of one species has been moved into the cytoplasmic background of another (known as alloplasmy CMS). Generally, the expression of CMS gene can be suppressed by special nuclear gene named as *restorer of fertility* (RF, or restorer) gene(s) derived from cytoplasm donor species. A CMS fertility restoration system has been widely used as an excellent pollination control system to facilitate hybrid seed production for many crops, including oilseed rape (*Brassica napus* L.).

Though a large number of alloplasmics for Brassica crops have been produced, only *Ogura*-INRA *B. napus* CMS with the wild radish cytoplasm and *Mori B. juncea* CMS produced from somatic fusion with *Moricandia arvensis*, were successfully exploited for commercial seed production on a large scale after systematic improvement of developmental abnormalities, including leaf chlorosis.

- Production of novel inap B. napus CMS via somatic fusion with Chinese woad

The intertribal somatic hybrids (2n = 52, AACCII) between B. napus (2n = 38, AACC) and *Isatis indigotica* Fort. (Chinese woad; 2n = 14, II) of the *Isatideae* tribe were obtained (Du et al., 2009) and backcrossed continuously to B. napus, resulting in the development of one novel *B. napus* CMS with carpelloid stamens (named inap CMS) (Kang et al., 2017).

- Development of a restorer for inap CMS through genetic introgression

RF gene(s) for *inap* CMS existed in one particular woad chromosome which was carried by one fertile monosomic alien addition line (MAAL) of rapeseed. The selfed progenies of this MAAL were selected and analyzed to screen the rapeseed-type plants (2n=38) with good male fertility and produce their doubled haploid (DH) lines by microspore culture. From the investigation of fertility restoration in the $F_1$ hybrids with *inap* CMS, one DH line was identified to restore the male fertility well and likely carried one dominant RF gene. This restorer produced the brown pollen grains as the woad and this MAAL did, suggesting that this trait was closely linked with *RF* gene(s). This restorer contained 38 chromosomes of rapesee. The successful breeding of the restorer for *inap* CMS rendered this new pollination control system feasible for rapeseed hybrid production, after *Ogura* CMS system in *B. napus* and *Mor* CMS system in *B. juncea*.

**Audience Take Away:**

- Agronomy and Agricultural Research
- The targeted audience will join the information about new CMS and fertility restoration in rapeseed
- Provided in new information that help them in their fields
- Provided new three-line materials in their research fields

**Biography**

Pengfei Li is now a doctoral student in College of Plant Science and Technology, Huazhong Agricultural University (2013-). Research interest: Brassica interspecific hybridizations, molecular cytogenetics, genome evolution.

# Systematic review on the anti-cancer effect of Chinese medicines in metabolomics perspective

**Wei Guo*, Yibin Feng**
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As one of the most prevalent diseases all over the world, cancer is a complex disease with multiple genetic and environmental risk factors. The mortality rate of cancer is equal to its incidence rate and the prognosis is poor. So far, due to serious side effects and increasing drug resistance, most chemotherapeutic agents for cancer are ineffective. Therefore, it is urgently needed for us to develop novel therapeutic strategies. The pure compounds, herb extracts and formulations from Chinese Medicine has been widely used in clinic not only in China but also throughout the world. Numerous successful medical record in treating cancer with Chinese Medicine have indicated it as an excellent source for cancer treatment as a complementary and alternative approach. However, due to its unique medical system with multicomponent nature, the underlying mechanisms how it works remain to be fully elucidated. Metabolic reprogramming is one of hallmarks to cancer. To support their high proliferation rates, cancer cells own a substantially unique metabolic phenotype. Metabolism-targeting therapies for cancer can be highly specific and effective, which are becoming a new therapeutics and drawing researchers' great attention. Metabolomics, one of the "Omics", systematically investigates the small molecule metabolites and provide us novel insights into dynamically metabolic responses of living systems. Besides, in accordance with the holistic perspective of Chinese medicines, metabolomics opens up a unique and novel insight into efficacy evaluation and action mechanism exploration of Chinese medicines as adjuvant therapies for cancer prevention and treatment. In this review, we systematically reviewed recent studies on the potential of metabolic treatment with pure compounds, herb extracts and formulations from Chinese medicines from the following aspects: glucose, lipid, amino acid, nucleotide metabolism and other altered metabolisms. The trends of future development of metabolism-targeting anti-cancer therapies were also discussed. Overall, the elucidation of the underlying molecular mechanism of anti-cancer Chinese Medicine in metabolomics perspective will provide us a new insight to develop novel therapeutics for cancer treatment.

## Audience Take Away:

- Introduce the audience what is the Chinese Medicine and its application in cancer treatment
- Introduce the audience what is metabolomics and its application in medical research
- Provide the audience a new insight to employ metabolomics to investigate the mechanism of complex mixtures

## Biography

Miss Guo studied biology science at Chong Qing University, China and graduated as bachelor in 2013. Then she came to Peking Union Medical College, Tsinghua University, China and majored in pharmaceutical analysis. After graduated as master in 2016, She then joined the research group of Prof. Feng to study pharmacology of Chinese Medicine on cancer treatment at the University of Hong Kong. Now she is in the third year of her PhD study. During her research career, she has published 4 research articles as first author in SCI(E) journals.

# Change of optimal transplanting date caused by heat wave in 2018 in Korea

**Jeonghwa Park*, Jongseo Choi, Shingu Kang, and Woonho Yang**
National Institute of Crop Science, Rural Development Administration, Suwon, Korea

The temperature over the globe has been rising due to global warming. Much like Europe, Korean peninsula is suffering from severe heat wave recently. In South Korea, average summer temperature for recent 5-year (Jul-Aug, 2014-2018) was 25.1°C,which is 0.9°C higher compared to the 30-year average (Jul-Aug, 1988-2013). In 2018, average temperature reached 26.5°C during summer as a result of heat wave. Heat waves are expected to become more frequent due to climate change, and it can affect the productivity and quality of crops.

This study was conducted to investigate the change of rice yield by transplanting dates (10-day intervals from 10-May to 20-June) over different maturity types (early maturing, mid-maturing and mid-late maturing) in several agricultural zones (plain, inland, sub-alpine, coastal).

In plain regions, the highest head rice yield was obtained from 15-Jun and 30-May transplanting date (4.6 and 5.4 t ha-1 respectively) for mid-maturing and mid-late maturing cultivars, respectively. This result shows the optimum transplanting dates in plain area were delayed 20 and 12 days compared to the transplanting date recommended for mid-maturing and mid-late maturing cultivars in normal years, respectively. Meanwhile, the yield of early maturing cultivars increased with delaying transplanting time.

In sub-alpine regions, the highest head rice yield was obtained from 21-Jun transplanting date (4.8 t $ha^{-1}$) for early maturing cultivars, which indicate 30-day delay of recommended transplanting date. The yield of mid-maturing cultivars increased with delaying transplanting time. Although mid-late maturing cultivars are not adaptable to sub-alpine regions in normal years, the highest grain yield in mid-late maturing cultivars in 2018 (5.2 t $ha^{-1}$) was greater than that in early or mid-maturing cultivars.

The effect of transplanting date on head rice yield was not clear in inland and coastal regions.

In conclusion, heat wave condition caused 12 to 30-day delay of optimum transplanting date for maximum head rice yield compared to current recommendation dates, as well as the increase of cultivation areas for mid-late maturing cultivars.

### Audience Take Away:

- Heat wave affected rice yield production according to transplanting time. Transplanting time should be delayed for high production under elevated air temperature
- Heat wave condition in 2018 caused 12 to 30-day delay of optimum transplanting date for maximum head rice yield compared to current recommendation dates
- Ongoing global warming is expected to enlarge the rice cultivation area of mid-late maturing genotype in the sub-alpine area of South Korea

### Biography

Jeonghwa, Park studied Agriculture at the Dongguk University, Seoul, Korea and graduated as MS in 1988. He then worked at Rice Cultivation Division, Crop Experiment Station, Rural Development Administration as a research scientist in 1990. He is now engaged at the Crop Cultivation and Environment Research Division, National Institution of Crop Science, RDA.

# Characterization of begomovirus associated with yellow mosaic disease of ridge gourd *[Luffa acutangula* (L.) Roxb]

**Premchand U*, Shankarappa. K. S and Mesta R. K**
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Ridge Gourd *[Luffa acutangula* (L.) Roxb.] It is commercial crop in the south and east India and commonly grown all over India particularly in states like Andhra Pradesh, Tamil Nadu, Gujarat, Konkan region of Maharashtra, Assam, West Bengal and Karnataka. It gives good yields up to 100-200 quintal per hectare and fetching good returns. This crop is known to get affected by many diseases. But in recently yellow mosaic disease on ridge gourd reported in southern states of India. It seems to be a newly emerged disease particularly in hot season. Roving survey in southern states of major ridge gourd growing areas during March to April 2015 revealed that disease incidence ranged from 30-100 per cent. A total of 63 samples out of 66 samples collected during surveys were found detected for both DNA-A and DNA-B components of begomovirus indicating that all detected samples were associated with bipartite begomovirus. PCR analysis of surveyed samples with beta and alpha-DNA satellites specific primers revealed that absence of both satellite DNAs in all the samples.

Representative surveyed sample was subjected to molecular characterization by sequencing the complete genome of the virus. The isolate has both DNA-A and DNA-B components. The DNA-A component consisted of 2,739 nt and DNA-B of 2,693 nt, which was approximately similar to other begomoviruses (ToLCNDV). Phylogenetic analysis of complete nucleotide sequence of both DNA-A and DNA-B of ToLCNDV-[IN:Kar:Bgk:Rid:15] with other selected begomoviruses showed the clustering of virus with ToLCNDV isolates and formed separate branch with ToLCNDV-[IN:Kar:Bel:Rid:14] a Belagavi isolate. The heat map indicated that the virus isolated from the ridge gourd had highest sequence similarity with the ToLCNDV species and Belagavi isolate with respect to both DNA-A and DNA-B components and which proved that the virus is a new strain of ToLCNDV species and variant of Belagavi isolate. The recombination analysis through Splits-Tree version 4 and RDP software indicated that the virus isolated from ridge gourd has derived through genetic exchanges from ToLCNDV-[TH:Mus:07] and ToLCNDV- [IN:Bah:Chi:07]. Results indicated that the virus has evolved as intraspecific recombinant begomovirus.

LAMP assay was established for the detection of begomovirus associated with yellow mosaic disease in ridge gourd and has higher sensitivity compared with conventional PCR.

Host rang study revealed that, of the 26 plant species tested, none have showed symptoms. While 21 varieties and seven hybrids of ridge gourd tested against disease, showed highly susceptible reaction.

### Audience Take Away:

- Sequencing of the viral genomes will give an exact picture of the diversity of virus in turn which will be helpful to design the management strategies.
- Diagnostic tool helpful in early detection of virus and the disease which in turn helps in early planning of disease management practice.
- In-silico analysis of genes and proteins will be useful for designing antiviral agents and docking studies.
- Reservoirs hosts are helpful in epidemiology and management of disease.

### Biography

Mr. Premchand U is a Ph.D. research scholar at University of Horticultural Sciences Bagalkot, India. He completed his M.Sc. in Plant Pathology from University of Horticultural Sciences Bagalkot, India. He is awarded with Mohit Subba Memorial COBACAS Best Thesis Award at National Conference, Cooch Behar Association for Cultivation of Agricultural Science (COBACAS) in collaboration with UBKV, Westbengal, India and University gold medal for his MS.c studies and His research contributions during Master's programme have reported diversity in newly emerged yellow mosaic disease on ridge gourd [Luffa acutangula (L.) Roxb.] in southern states of India. He is currently engaged with whole genome sequencing and diversity analysis of different viruses infecting Papaya (Carica papaya) in Southern states of India. He has one publication in Virusdisease journal.

# Unraveling the role of mirnas in combined heat and drought stress in tomato

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Plant microRNAs (miRNAs) control entangled gene regulatory networks and have been implicated in important developmental switches as well as in different stress responses. Adverse climatic conditions like high temperature, water deficit, osmotic imbalance, etc., negatively affect agricultural food production world-wide. In nature, a number of different stresses can occur simultaneously and studies have revealed that the response of plants to a combination of different stresses is unique and cannot be directly deduced by analyzing the response of plant to each of the different stresses applied individually. The effect of combined stresses may in fact be either additive or retrograde in nature. Combination of heat and drought stresses has adverse effect on the plant's physiological status, growth and productivity and represents an excellent example of simultaneous occurrence of two different abiotic stresses in nature. While differential mRNA transcript profiles in response to combined heat and drought stresses have been evaluated in some plants, studies on involvement of miRNAs in combined stress is completely lacking. In the present study, we identified the core miRNome involved in combined heat and drought stress in tomato (Solanum lycopersicum L.) leaf tissue. We identified miRNAs that showed up- regulation at both mature and precursor levels in individual heat, drought and combined stress like miR172b. We thus chose to characterize MIR172 family in-depth. In-house developed bioinformatics screening pipeline revealed five new putative loci for miR172 apart from the four loci reported at miRBase for tomato. Out of above five loci, four loci have been validated by cloning and sequencing. All these miR172 isoforms show different degree of stress- inducibility in individual and/or combined stresses at mature as well as precursor level pointing to specific stress-responsive roles. Transient assays in Nicotiana benthamiana revealed that different miR172 precursors exhibit different processivity to yield mature miRNA. Moreover, the same mature form exhibits variable target cleavage efficiencies when different targets were assessed. The main targets of miR172 are genes that encode AP2-like transcription factors. With the help of degradome data we identified HSF18 as a novel target of miR172. We find that upon HS, miRNA172 is up-regulated which in turn decreases HSF18 transcripts. Functional characterization of HSF18 by knocking-down its expression using virus induced gene silencing (VIGS) in tomato established its role as a negative regulator of HS-tolerance. Interestingly, miR172 promoter analysis identifies cis-regulatory elements for binding of AP2s as well as HSFs. Yeast one hybrid screen confirms HSF-mediated transcriptional control of miR172. Experiments to establish a possible feedback regulatory loop between AP2s, HSFs and miRNA are underway. Using short tandem target mimic (STTM) constructs against different isoforms of miR172 and miR-resistant version of HSF18, will help elucidate the role of miRNA172 in the regulatory networks involved in individual and combined stress response.

## Audience Take Away:

- Present investigation identified and characterized stress-responsive miRNAs in tomato and dissects out the regulatory networks that are responsive to combined heat and drought abiotic stress using over-expression, STTM and resistant-target approach. This would provide clues to better understand stress signaling and stress tolerance
- This study has shown for the first time HSF18 as a novel target of miR172
- The study has established miRNA:target modules that can be harnessed for crop improvement in future

## Biography

Chandni Bansal did her Masters in Biotechnology from Department of Biotechnology, University of Pune, Pune. During her masters she did summer training (May 2013-June2013) at National Institute of Immunology, New Delhi through IAS-SRFP (Indian Academy of Sciences- Summer Research Fellowship Programme). She is currently pursuing her Ph.D. degree with Dr. Saloni Mathur at National Institute of Plant Research (NIPGR), New Delhi through CSIR-UG
NET-SRF fellowship. The lab is interested in understanding the role of miRNAs in tomato in response to abiotic stresses.

# The challenge of agricultural research in Mexico

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The following points will serve for reflection.

1. Definition of the Ejido.

2. Definition of the distribution and possession of the land.

3. Amendment to Article 27 of the Constitution.

4. The Tax System in the field.

5. The new agricultural extensionism.

6. Challenges of agricultural research.

I. Definition of the Ejido.

In the establishment of the starting point it is fundamental to define the ejido, according to Flores-Rodríguez (2008). "The ejido is a system of distribution and possession of the land that was institutionalized after the Mexican Revolution and that consists of granting land to a group of people for exploitation

II. Definition of the distribution and possession of the land

In the first instance, the distribution and possession of the land will be discussed to begin the explanation of the subject, and this is established by Trejo-Sánchez (2012); "Since evolution is a constant phenomenon that brings social changes as consequences; It should not be forgotten that agrarian property is immersed in these changes and its development is impacted by constant economic and legal transformations. Hence, it is necessary that this does not continue in the lag and can be promoted as a source of national wealth, with which all Mexicans benefit.

In Mexico there is the National Institute of Geography and Informatics (INEGI) and Consulta Mitofsky (2008), mentions that the Mexican population is 106.7 million inhabitants; where 50.8% are women and the remaining 49.2% are men; and 76% of the Mexican population is urban and the remaining 24% is rural at the present time of 2018. These population data are of the following order: 123.5 million Mexicans; of which 51.2 are women and 48.8 are men (INEGI, 2017), the trends of the 2005 population and housing census are maintained; that is to say; Mexico has more than 25 million Mexicans who have to do directly and indirectly with the country's agricultural issue.

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This is why it is important to take into account the rural population as reported by Robles B.H. (2006); "In rural areas we have more than 5 million holders of land that have more than 185 million hectares; that is to say 5% ": At present the ejidal plot can be rented and even sold to other ejidatarios or residents of the same population nucleus; to be sold to a private individual, a step must be taken whereby the ejido accesses the full domain. Said process is carried out in a qualified general assembly where, in the presence of a public notary and a representative of the Agrarian Procurator's Office, 75% of the ejidatarios attend and are in agreement with the change, two-thirds of the participants (Morett-Sánchez and Cossio-Ruiz, 2017).

III. Reform to Article 27 of the Constitution.

Perez-Castañeda and Mackinlay (2015) question that the agrarian property in Mexico still has something of "social" and they express it in the following way: "from the moment in which the amendment of the constitutional article 27 ended the distribution of the land Upon entering into force on January 6, 1992, the agrarian reform process in Mexico was completed. Three quarters of the 20th century witnessed the gradual

conversion of more than half of the national soil to the heat of the creation of ejidos and the restitution or confirmation of communities. The 1992 reform of agrarian legislation caused the metamorphosis of the Mexican ejido. From that moment on, legal features were lost and, therefore, it ceased to be one of the modalities of social ownership.

And it is in the characteristic of imprescriptible where the social of the ejido differs from the private; then, the reference authors minimally give the ejidos of Mexico the property of a private property in Moderate domain. which reflects in the faculty of the ejidatarios of:

- Transmit the use and usufruct of the land Law Agaria (LA, article 45)
- To contribute the land to the social capital of a company (LA, article 75)
- To be able to offer the lands under guarantee (LA, article 46)
- To convert lands to full dominion (LA, art 23, fraction IX)
- To agree on the termination of the ejidal regime (LA, art.23, section XII)

IV. The Tax System in the field.

Once the phases of the distribution and possession of the land have been established, the land exploitation phase begins where the Mexican government in the revenue law for 2014 sought, among other things, to increase tax collection as established by Núñez Sánchez A. (2014). "In Mexico there are 118 million inhabitants of which Chiapas has more than 5 million of those 118; 53 million constitute the economically active population; that is, they are people who have the physical and productive capacity, and who perform some economic activity. Of these 53 million inhabitants, 29.6 million are in the informal economy, that is, in Mexico there are more informal workers than formal workers. There are 26 million captive salaried Mexicans who every 15 days make a withholding of income tax (ISR) on their payroll. These captives contributed last year with 401 billion pesos for public finances

However, although it is said that the fiscal incorporation regime (RIF) is a new issue of optional taxation (Núñez Sánchez A., Op.Cit) it must be given as a reading that it is obligatory for the agricultural and fishing sector; only with the fiscal discharge of the Ministry of Finance and public credit can the producers register to the government programs to support the production and / or purchase of productive assets such as tractors, harrows, plows, new breeding feet and transport equipment to move production.

When establishing the Mexican system of fiscal obligations in the rural sector, it is considered important to establish how to comply with fiscal obligations, but also how to increase agricultural production using the extension and rural training that is offered as government support.

**V. The new agricultural extensionism.**

Engel, (2000) states: "Extension is no longer enough as a vehicle to transmit the results of technological research to agricultural producers, extension should be positioned as an instrument to strengthen the self-learning and permanent innovation capacity of rural communities towards competitiveness and The sustainability".

According to the OECD (2010) in the early eighties in the Ministry of Agriculture, Livestock, Rural Development, Fisheries and Food (SAGARPA) there were about 25 000 government extension agents, in the nineties the Mexican government proposes implement a new extension system, which before the new millennium is transitioned from the process of classical extension to the private professional system, being in this scheme where the incorporation of knowledge capital generated by universities, research centers to carry out an efficient technology transfer.

It is essential not to focus exclusively on extensionism, because it is not only the transfer of technology that increases production in the field, but also the process of training current or existing technology where farmers are rarely observed. or rural day laborer make use of it, so it is necessary to address the issue of rural training.

Currently, the aim is to promote a new agricultural extension, because technical assistance and training services are disconnected from the results, and modern advisory services need new capacities to respond effectively to new ones. This new extension system is based on the hiring of PSP, which employs around ten thousand professionals per year.

In accordance with the rules of operation of the concurrency fund program and which is linked to the National Development Plan 2013-2018, which through the national program of crusade against hunger recognizes that "the field is a strategic sector , because of its potential to reduce poverty and affect regional development ", and that" the capitalization of the sector must be strengthened ", so that government resources destined to the agricultural, fishing and aquaculture sector should be used in a more efficient to address the problems in which the sector is immersed, because producers face constraints due to low levels of investment, productivity and lack of strategies for the aggregation of value in their economic units for primary activities.

The government established the figures of a Professional Services Provider (PSP or, as the case may be, a group of Social Services Providers (PSS).) To evaluate the transfer of technology and training of the rural sector.

## SAW. CHALLENGES OF AGRICULTURAL RESEARCH IN MEXICO

1. Increase the level of technology transfer provided by PSPs, where production is significantly influenced by the acceptance of new technologies as well as the productive and organizational training of ejido groups.

2. The programs of concurrent funds established in the federal government should be more efficient.Administratively to avoid bureaucracy in the process of assigning projects and economic resources.

3. The results of agricultural research must be consistent with the technician's assignment since currently the PSP is assigned untimely and considering that the productive processes are carried out throughout the year.

4. Considering that the new global environment demands to increase the access of producers to advances and technological changes, to the diffusion of innovation, to the new agrifood policies of investment in the sector, and to consider it as a basic principle to the development of capacities of the rural population.

5. The scientific research carried out in universities and experimental fields should be linked to the real problems of the field and focus on the solution of problems in the agricultural sector.

6. The processes of innovation of technology or cutting-edge technology are put into practice permanently within the sector and the beneficiary himself is the one who perceives the productive changes.

# Wheat *(Triticum aestivum* L.) photosynthesis is site-specifically and temporally varied between genotypes

**Prabuddha Dehigaspitiya[1]*, Anke Martin[1], Gavin Ash[1], Dananjali Gamage[3], Kiruba Shankari[1], Saman Seneweera[1, 2]**
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Wheat is one of the most important cereals for global food security and has been targeted for yield improvement for decades. Understanding the underlying physiological and molecular processes of crop plants is critical to improving photosynthetic efficiency. In our study, we investigated the comparative physiological and molecular mechanisms of photosynthesis, the biological capacity of carbon assimilation (Vcmax and Jmax) and the sucrose metabolism between wheat spikes and flag leaves using three wheat genotypes grown under glasshouse conditions. Spike dry weight, spike and flag leaf photosynthetic area and nitrogen (N) concentrations of the photosynthetic organs were measured at different growth stages. Furthermore, Vcmax and Jmax were calculated in flag leaves and wheat spikes using carbon dioxide response (A-Ci) curves at four different growth stages. Molecular level changes in photosynthesis and sucrose metabolism were assessed using gene expression analysis from real-time, quantitative-PCR using key genes related to photosynthesis (rbcL and rbcS) and sucrose metabolism (SPS1, SUS1 and SPP1). We observed a significant genotypic, site-specific and temporal variation in Vcmax and Jmax. Interestingly, the Vcmax and Jmax between wheat spikes and flag leaves at late-grain filling across all genotypes was not statistically significant. Further, a significant difference was observed in the expression of photosynthetic genes between wheat spikes and flag leaves showing much higher expression in flag leaves across all growth stages. However, both the organ types (pericarps and flag leaves) displayed a similar expression pattern across considered growth stages. The N content of the photosynthetic organs revealed that the highest Rubisco content in wheat pericarps may be present at the grain enlargement phase although the photosynthetic gene expression indicated the contrary. The expression of key genes related to sucrose metabolism (SPS1, SUS1, and SPP1) in wheat pericarps revealed that there were strong positive correlations between the biological capacity of carbon assimilation and SPS1, SUS1 and SPP1 expression during the heading to grain enlargement phase. Moreover, our results suggested that metabolic processes of wheat spikes may perform a major role in grain filling and thus total yield.

### Audience Take Away:

- Metabolic activities of plants vary in a site-specific manner. The biological role of plant organs changes over time and these changes are highly sensitive to the genetic makeup of the plant. However, the mechanisms and regulation factors behind site-specific, temporal and genetic variation of plant metabolic processes are not well understood
- An approach to improving the yield potential of critical C3 crops by improving the efficiency of photosynthesis/ changing the mode of photosynthesis (transforming C3 into C4) of crop plants
- Knowledge of site-specific and temporal variation of photosynthesis, coupled with site-specific regulation of gene expression, may enhance the productivity of economically critical C3 crops

### Biography

Mr. Prabuddha Dehigaspitiya studied Agricultural Biology at the University of Ruhuna, Sri Lanka and graduated as BSc in Agricultural Biology in 2016. Also, he studied Computer Science at the University of Colombo, Sri Lanka and graduated as BIT. He then joined the Department of Agricultural Biology, Faculty of Agriculture, University of Ruhuna as an assistant lecturer. In 2016, he got the opportunity to join the Centre for Crop Health, University of Southern Queensland, Australia for his Ph.D. His study area is site-specific and temporal variation in photosynthesis of crop plants.

# The effect of bio augmentation and biochar-stimulation on metal (loid) s contaminated soil and plant growth

**Melissa Simiele[1]*, Antonio Bucci[1], Manhattan Lebrun[1,2], Gabriella S. Scippa[1], Sylvain Bourgerie[2], Domenico Morabito[2], Gino Naclerio[1] and Dalila Trupiano[1]**
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Nowadays, environmental contamination by metal (loid) s is a major problem worldwide and poses severe scientific challenges. Metal (loid) s are natural constituents of the environment, but indiscriminate use for human purposes has altered their geochemical cycles and biochemical balance. This results in excess release of metal (loid) s into natural resources like the soil (Tang et al., 2015). Therefore, the removal of metal (loid) s from contaminated soils is imperative in order to minimize their impact on the ecosystems.

In the last decade, several efforts were carried out by scientific community to improve the green technologies effectiveness in soil management. The use of biological methods avoids physico-chemical strategy limitations: i) changes in native soil flora; ii) irreversible alterations in soil properties; iii) secondary pollution; iv) intensive labor; and v) high cost (Zubair et al., 2016). In fact, biological approach (bioremediation) may be an attractive alternative to physico-chemical methods: it is an environmentally friendly and economical strategy that uses organisms (microorganisms or plants) for polluted soils remediation and has high public acceptance (Kang et al., 2016).

Success of bioremediation depends on the proper selection of metal(loid) tolerant organisms. Various studies have focused on bioremediation effectiveness by addition of nutrients (biostimulation) or introduction of microorganisms to contaminated sites (bioaugmentation). Biostimulation involves the modification of the environment to stimulate the growth and activities of native microorganisms involved in the remediation process and thus this increases the efficiency of bioremediation. This can be done by addition of various forms of limiting nutrients and electron acceptors (da Conceicao Gomes et al., 2016). Often in biostimulation systems, both organic fertilizers and organic amendments of different origins have been proposed for decontaminating metal(loid) polluted soils. An organic amendment that can be utilized as a fertilizer and a metal(loid) stabilizer is biochar. It is a carbonaceous material produced from oxygen-limited pyrolysis of biomass under low temperatures (Trigo et al., 2014). Bioaugmentation involves the introduction of microorganisms isolated from the contaminated site or carefully selected and genetically modified to support indigenous organisms to remediate contaminated sites (Hamdia et al., 2007). At times, nutrient addition or microbial augmentation alone is not sufficient for a successful remediation of metal(loid) polluted soils. Recent studies show that a combined technology of bioaugmentation assisted by biostimulation is a high-efficiency and promising approach for the bioremediation of metal (loid) contaminated soils (Mahbub et al., 2017; Rojjanateeranaj et al., 2017; Wang et al., 2017).

In this context, the present study aims to evaluate the effect of the bioaugmentation and biostimulation strategies, alone and combined, in a metal (loid) contaminated site by using Arabidopsis thaliana model plant. The general purposes of the study presented here are: i) to isolate and characterize a metal(loid) resistant bacteria strain, ii) to analyze how metal(loid)s, biochar and the resistant microorganism could influence plant development and growth and iii) to understand the mechanisms involved in plant metal(loid)s tolerance.

**Audience Take Away:**

- Different bioremediation strategies
- Plant and environment interaction
- Plant ability/capability to growth on polluted soil
- Audience will acquire a deeper knowledge on how biostimulation assisted by bioaugmentation influence soil metal (loid) mobility/availability and the corresponding effect on plant tolerance, development and growth strategies. A better understanding of these strategies is necessary to comprehend ecosystem dynamics, guarantee the protection and efficiently manage territorial resources. Therefore, this is an area for future discoveries that will reveal the evolution of diverse metal(loid) tolerance mechanisms that could be valuable for the design of improvement strategies including for climate change challenges. More in general, this research will provide: new ideas in bioremediation research fields, practical solution(s) to challenge the environmental contamination and research and/or teaching activities updating on bioremediation topic

## Biography

Since 2014, Mrs. Melissa Simiele is graduated as MS in Molecular and Cellular Biology at University of Molise (Italy). She worked for the Regional Agency for Environmental Protection of Molise (ARPA Molise) in 2017 and currently, she is a PhD student at University of Molise. Her research interests are focused on bioremediation of metal(loid)- and/or organic- contaminated soils by using plants and bacteria synergic association. In detail, integrated analyses are used to elucidate/monitor the effect of different strategies on physico-chemical soil characteristics, metal and/or organic compound mobility/availability, soil microbial community diversity, plant morphological traits and proteomic profiles.

# Transcription factors as targets for ustilago maydis effectors

**Denise Seitner*, André Alcântara, Khong-Sam Chia, Armin Djamei**
Gregor Mendel Institute (GMI), Austrian Academy of Sciences (OEAW), Austria

Ustilago maydis, the causative agent of corn smut disease, infects one of the most important crops worldwide – Zea mays. To successfully colonize its host U. maydis secretes proteins, known as effectors, that suppress plant defense responses and facilitate the establishment of biotrophy.

Perception of pathogens by the host involves transcriptional reprogramming towards defense. This makes plant transcription factors (TFs) putative targets of fungal effectors. The aim of this project is to identify U. maydis effector candidates that target maize transcription factors, by yeast two-hybrid screening against a maize transcription factor library. Here we present our latest findings on one interesting interaction pair identified by this screen: The effector candidate Kxe1 and the KNOX transcription factor family.

## Biography

Denise Seitner studied Molecular Biology at the University of Vienna. For her master's degree she moved on to the University of Natural Resources and Life Sciences in Vienna to study Plant Pathology and Plant Protection. She then joined the research group of Armin Djamei at the Gregor Mendel Institute in Vienna for her PhD.

# Effects of non-steroidal anti-inflammatory drugs on the ultrastructure and composition of autochthonous vegetables

**Ocsana Opriş[1]*, Maria Loredana Soran[1], Ildikó Lung[1], Alexandra Ciorîţă[1], Lucian Copolovici[2]**
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In the recent years, the presence of pharmaceutical products in the environment is known under the name of "emerging contaminants" and is among the most important environmental concern at world level. Among the environmentally emerging contaminants are included the non-steroidal anti-inflammatory drugs (NSAIDs), which are one of the most relevant therapeutic classes for their properties. Therefore, we aimed to study the influence of diclofenac, ibuprofen and naproxen on plants growth. We chose three important autochthonous vegetables *(Atriplex patula* L., *Spinacia oleracea* L. and *Lactuca sativa* L.) that were watered with different concentrations of aqueous solution of drugs (0.1-1 mg L-1). After eight weeks exposure of the plants to NSAIDs we determined the chlorophylls and carotenoids content by high performance liquid chromatography coupled with photodiode array and mass spectrometer detectors, total polyphenols and antioxidant capacity by ultraviolet-visible spectroscopy. Also, the ultrastructural analyses of the vegetables were performed using transmission electron microscopy in order to assess the influence of the selected NSAIDs on cellular organisms, mainly photosynthetic organisms (chloroplasts), energy supply organisms (mitochondria) and nucleus as a cellular metabolism coordinator. In general, the plants exhibited linear decreased values of chlorophylls and total polyphenols with increased NSAIDs concentrations. In comparison with the controls, the autochthonous vegetables treated with NSAIDs had irregular growth of glandular trichomes on the surface of the adaxial side of the leaves. Also, less stomata were observed, the cells had less cytoplasm, the cell walls were irregular, and the chloroplasts were irregular distributed. Such investigations contribute for a better understanding of the impact of NSAIDs on the selected vegetables.

## Audience Take Away:

- The aim of the poster presentation fits within the frame of an international research priority concerning the environmental pollution, namely the impact of pharmaceutical residues on plants with important nutritional value
- The results contribute for a better understanding of the effects of important NSAIDs on composition and ultrastructural modifications in plants, data which are still limited especially at environmentally relevant concentrations
- The present researches will awareness a responsible consumption of drugs

## Biography

Dr. Opriş studied Chemistry at "Babeş-Bolyai" University of Cluj-Napoca (Romania). She obtained her PhD degree (2013) in Environmental Science at the same institution. Dr. Opriş works as senior researcher III at INCDTIM (Cluj-Napoca, Romania) and has a postdoctoral fellowship supervised by Prof. Copolovici. Her research interest are focused on chromatographic analysis of the environmental pollutants from different complex matrices; applications of nanoparticles in water decontamination; assessing the impact of abiotic stress on plants; extraction, chromatographic and spectroscopic analysis of bioactive compounds from plants. (Web of Science ResearcherID: Q-2771-2019)

# Insecticides susceptibility of the most important pests in greenhouse vegetable production in Croatia

**Ivan Juran[1], Tanja Gotlin Čuljak[1]*, Katja Žanić[2], Marija Mandušić[2], Elda Vitanović[2]**
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Insecticide resistance is the global problem in the production of agricultural crops which is particular important in greenhouses production where producers do not have adequate solutions in pest control. Two the most important pests in greenhouse vegetable production, western flower thrips *(Frankliniella occidentalis)* and greenhouse whitefly *(Trialeurodes vaporariorum)*, are polyphagous organisms with high reproductive potential and vast number of generation per year. According to the APRD database insecticide resistance of these pests was recorded worldwide. To help producers in pest control, programme of resistance monitoring of the economically important agricultural pests was developed in Croatia from 2017 until 2020. This programme includes major pests (insects, mites, plant pathogens and weeds) in arable crops, greenhouse production, orchards and vineyards. The aim of this research was to test insecticides susceptibility of western flower thrips and greenhouse whitefly. Populations of these pests were collected during 2018 at 16 locations at different part of Croatia and were tested according to the IRAC test methods No. 010 and No. 015 in laboratory conditions. Populations of the western flower thrips were tested on lambda-cyhalotrin, thiamethoxam and spinosad and greenhouse whitefly populations were tested on deltamethrin, alphacypermethrin, pyriproxyfen, imidacloprid and thiamethoxam. All tested populations of western flower thrips were resistant on lambda-cyhalotrin and thaiamethoxam and only two populations were susceptible on spinosad. Tested populations of greenhouse whitefly were resistant on deltamethrin, alphacypermethrin and pyriproxyfen. Only four populations were susceptible on imidacloprid and on thiamethoxam only one. According to the obtained results producers should utilize integrated measures in pest control and the only effective measure is biological control using natural enemies.

## Audience Take Away:

- Level of resistance of two most important greenhouse pests
- Distribution of resistant and sensitive populations of western flower thrips and greenhouse whitefly in Croatia
- Practical solutions how to control populations of tested organisms below economic threshold

## Biography

Full professor Tanja Gotlin Čuljak has been working for more than 20 years at University of Zagreb Faculty of Agriculture. She has received PhD in 2006 at the same Faculty with thesis of distribution and identification of different aphid species in Croatia. She was leader of one international and seven national science projects. She is author or co-author of more than 60 scientific articles.

# Whole genome sequencing and comparative genomics of *Ceratocystis fimbriata* and integrated disease management strategies against wilt in pomegranate

**Abhishek Gowda*, Manjunatha G, Pavan Kumar and Lokesh V**
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Pomegranate *(Punica granatum* L.), an important fruit crop of India, is commercially cultivated in the states of Maharashtra, Karnataka, Andhra Pradesh, Gujarat, Rajasthan and Tamil Nadu. Pomegranate is affected by many serious diseases, among them pomegranate wilt disease caused by Ceratocystis fimbriata has been appearing in devastating form. Whole genome sequencing libraries were prepared and sequenced using Illumina NextSeq500 Paired-end sequencing with 150*2. De-novo assembly of Illumina PE data was performed using SPAdes assembler. Gene prediction was carried out using the tool Augustus- 3.1 and a total of 7773 genes were found in the assembled scaffold. Genes were annotated using NCBI BLAST 2.2.29 with the proteins of Fungi kingdom taken from Uniprot database. Pathway analysis was done by using KAAS Server using reference fungus organisms. The present genome analysis is used for comparative analysis with that of the draft genome sequence of the available CF (sweet potato isolate) and the other two species of Ceratocystidaceae family, C. manginecans and C. albifundus and possible identification of isolate/ species specific genes. The identification of resistant rootstock will pave the new ways for developing durable resistance and to reduce the expenditure of management, few of the accessions recorded delayed disease expressions up to 180 days. Only three cultivars Bedana Sur, Yercaud and Yercaud local display no wilting symptom post one year post pathogen inoculation. The tolerant lines will be used for further crop improvement programme. Disease can be managed effectively by adopting integrated management practices including sanitation, cultural methods, chemical control and use of resistant cultivars.

## Research highlights

- Huge amount of genome-scale functional data like transcriptomes and proteomes of fungi provides an opportunity to systematically examine the pathophysiology of pathogen and also It gives clue for the specific genes or signature to be targeted.
- The similarity/diversity within Ceratocystidaceae family memebers would reveal the evolution lineage of the family.
- Wilt resistant rootstock will be identified to evolve suitable wilt resistant variety to ensuring more economical, feasible and effective wilt management approach.
- Prophylactic treatments using bioconsortia and treatments targeting the causal agents in association with wilt in advance before expression of the wilt symptoms could be potential means of wilt management.

## Biography

Mr. Abhishek Gowda is a Ph.D. research scholar at University of Horticultural Sciences Bagalkot, India. He completed his M.Sc. in Plant Pathology from University of Horticultural Sciences Bagalkot, India. His research contributions during Master's programme have paved the path identifying host defense inducers (Isonicotinic acid, methyl jasmonate and eugenol) and consortia of bio-agents (Pseudomonas spp. and Bacillus spp.) against pomegranate bacterial blight disease. He is currently engaged with whole genome sequencing and comparative genomics of Ceratocystis fimbriata (causal agent of Pomegranate wilt) for identification of virulence genes and their corresponding R/S genes in the host and integrated disease management of wilt in pomegranate. He has one publication in SCI(E) journal.

# Mapping and validation of QTLs for cabbage black rot resistance

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Black root (BR), a main serious disease of cabbage *(Brassica oleracea* L.), is caused by the bacterial *Xanthomonas campestris* pv. campestris. To identify QTLs for resistance to BR, we constructed a cabbage genetic map using 303 SSR markers with an average interval of 2.77cM based on RILs developed from R4-P1 (resistant) and R2-P2 (susceptible). Race1 of Xcc were used to spray inoculation the RILs seedings, the disease indexs (DIs) were collected two weeks after inoculation based on infected leaf area. Using IciMapping 3.2, 11 QTLs were detected, only one major stable QTL on chromosome 7 was associated with resistance in both two mapping population. The QTL was located in a 2.91Mb interval based on the R2-P2 reference genome sequence defined by simple sequence repeat (SSR) markers M35 and M25. Nine annotated resistance genes in this region were collected, then these genes were sequence aligned and the expression level in different time stages after inoculation were analysed between two parents. According to the sequence differences and expression levels of these candidate genes, we concluded that Bo7g111290 is more likely the BR resistance gene to Race1 of Xcc in R4-P1. Our results provide a basis for further QTL fine mapping and candidate genes cloning, will promote pyramiding Xcc resistance genes in cabbage.

**Key Words:** *Brassica oleracea* L., black root resistance, *Xanthomonas campestris* pv. Campestris, QTL, chromosomal segment substitution line.

# Dissection of heat induced morphological changes of reproductive tissues in *Arabidopsis thaliana*

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Heat stress can seriously impact on yield production or quality of crops. Many studies uncovered the molecular mechanisms that regulate heat stress responses in plants. Nevertheless, detailed morphological changes of heat treated plants were still not extensively studied.

In this study, we observed the detailed morphological changes of reproductive tissues in *Arabidopsis thaliana* caused by heat stress. Larger area of stigma, and shorter length of anther, filament and petals were observed in heat treated plants compared to those in controlled conditions. Furthermore, we observed reproductive tissues of plants grown under controlled or heat stressed conditions by scanning electron microscopy (SEM). Although previous studies indicated that pollen is more sensitive to heat stress compared to other tissues, pollen morphology under heat stress condition was almost comparable to that in controlled conditions. In addition, we revealed that pollen attachment to stigma was clearly decreased by heat stress. Furthermore, a length of papilla cells with no pollens seemed to be larger than that with pollens.

According to these results, we hypothesized that pollen attachment is involved in size reduction of stigma. To test this hypothesis, we analysed proportion of pollen attachment area on stigma and stigma diameter under controlled and heat stressed conditions. We classified patterns of pollen attachment on stigma into 4 types (type1: pollens on whole stigma, type2: pollens on a half of stigma, type3: pollens only on an edge of stigma, type4: few pollens on stigma). Approximately 60% of stigmas indicates type1 under the controlled conditions. In contrast, approximately 60 % of stigma under heat stressed condition indicates type 4. Furthermore, we compared the diameters of stigma with or without artificial pollination under controlled and heat stressed conditions. We observed enlargement of stigma without pollen, but, size reduction of stigma with pollens under both conditions, suggesting that pollen attachment is clearly involved in stigma size reduction.

Finally, we investigated the distribution of O2- and Ca2+, which are involved in pollen-pistil interaction before or after pollination under controlled and heat stressed conditions. Before pollination, O2- accumulated in stigma, and Ca2+ accumulated in anther under both conditions. After pollination, O2- accumulation spread to style and ovary, but, decreased in stigma under controlled conditions. In addition, under heat stressed condition, O2- accumulation was observed in style, but no O2- accumulation was found in ovary. Interestingly, despite the decrease of O2- accumulation in stigma under both conditions after pollination, Ca2+ highly accumulated in stigma after pollination under both conditions. These results indicate that O2- and Ca2+ might be involved in enlargement and reduction of stigma before or after pollination, respectively.

Thus, we concluded that heat stress caused the enlargement of stigma that might be associated with decreased pollen attachment to stigma. Furthermore, O2- might be involved in enlargement of stigma before pollination, and Ca2+ might be involved in reduction of stigma size after pollination.

## Audience Take Away:

- We provide a new perspectives of heat responses of reproductive tissues of model plant, based on the morphological analyses rather than molecular biological approaches
- Audience can investigate more accurate heat response mechanisms based on the output of our research
- Morphological and physiological approaches would be useful for elucidation of heat response as much as molecular biological approach
- Heat responses were analyzed by detailed morphological analyses, rather than the molecular biological approaches
- Decrease in seed production under heat stress might be associated with morphological changes in reproductive tissues
- Therefore, the information should be useful to link biological researches to Agriculture

## Biography

Kazuma Katano has completed his Master's degree program in Sophia University, Japan. He is currently working as doctoral student in Dr. Nobuhiro Suzuki laboratory in Sophia University. He has published an original article in Plant Physiology and Biochemistry in December 2017. He has also published review article in Frontiers in Plant Science as a second author in March 2018, and a review article in International Journal of Molecular Science as a first author in October 2018. He presented his research in the meeting of American Society of Plant Biologists, and in the meeting of Japan Society of Breeding (in Japanese).

# Genomic architecture of biomass heterosis in Chinese cabbage

**Fenglan Zhang, Deshuang Zhang, Shuancang Yu, Peirong Li*, Weihong Wang, Yangjun Yu, Xiuyun Zhao**
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Heterosis is a complex biological phenomenon in which hybrids exhibit superior phenotypic characteristics, such as enhanced biomass production, developmental rates, grain yields and stress tolerance. Chinese cabbage *(Brassica rapa)* is a major edible leafy-producing crop, and its F1 hybrids have been widely used in commercial production for many years. In this study, we generated 135 intraspecific hybrids by crossing 28 Chinese cabbage accessions. The agronomically important traits were evaluated comprehensively, including yield of whole plant gross weight, net weight, leaf weight, leaf number, plant height, head height, head width, head leaf number, plant diameter and head core length, at 70 d after sowing (DAS). We observed strong positive correlations among biomass, leaf weight and net weight in hybrids, indicating that both net weight and leaf weight were the main contributors to hybrid biomass. To identify loci or genes with the potential contribution to Chinese cabbage biomass heterosis, we conducted large-scale genome-wide association study (GWAS) analyses on heterosis for the complex agronomic traits using an algorithm for compressed mixed linear model in GAPIT software. A total of 764 protein-coding genes within the 10-kb genomic regions surrounding the heterosis-associated SNPs were identified and thought to be candidate genes for biomass heterosis in Chinese cabbage. Of the 764 genes, 547 genes had functional annotations for biological process categories in the GO database. These genes were divided into diverse functional categories, including the generic categories such as cellular processes, intracellular part, metabolic processes and developmental processes, and the specific categories such as photosynthetic membrane, nitrogen compound metabolic process, unidimensional cell growth, cell division, reproductive process, cell proliferation, indicating the collective contribution of these biological pathways to biomass heterosis in Chinese cabbage.

# Efficient CRISPR/Cas9-based gene knockout in Chinese cabbage *(Brassica rapa* subsp. pekinensis)

**Tongbing Su[1, 2, 3, 4*], Peirong Li[1, 3, 4], Weihong Wang[1, 3, 4], Yangjun Yu[1, 3, 4], Deshuang Zhang[1, 3, 4], Xiuyun Zhao[1, 3, 4], Shuancang Yu[1, 3, 4], Fenglan Zhang[1, 3, 4]**
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Genome editing offers great advantage to reveal gene function and generate agronomically important mutations to crops. Here, we report the genome of Chinese cabbage *(Brassica rapa* subsp. pekinensis, AA genome, 2n=20), an important leafy crop, can also be precisely edited by CRISPR/Cas9 system. CRISPR/Cas9 system performed genome editing, such as insertions or deletions at the expected positions of the candidate genes in transgenic Chinese cabbage plants. Furthermore, there were very likely no off-target mutations, indicated by examining regions that were highly homologous to sgRNA sequences. Our results show that CRISPR/Cas9 system is a powerful tool to effectively create knockout mutations in Chinese cabbage.

# Identification and fine-mapping of a major QTL qSB.A09 that controls shoot branching in *Brassica rapa* ssp. chinensis Makino

**Shuancang Yu*, Pan Li, Tongbing Su, Bin Zhang, Peirong Li, Xiaoyun Xin, Xiaozhen Yue, Weihong Wang, Xiuyun Zhao, Yangjun Yu, Deshuang Zhang, and Fenglan Zhang**
Beijing Vegetable Research Center (BVRC), Beijing Academy of Agriculture and Forestry Science (BAAFS), China

Shoot branching is a complex quantitative trait that contributes to plant architecture and ultimately yield, yet the genetic control of shoot branching in Brassica rapa L. subsp. chinensis remains poorly understood. In this study, a major QTL for shoot branching, designated shoot branching 9 (qSB.A09), was detected on the long arm of chromosome A09 in Brassica rapa L. subsp. chinensis using bulked segregant analysis (BSA) of an F2 population. Traditional QTL mapping of the F2 population was also carried out, revealing six QTLs in different regions. Of these, the mapping region on chromosome A09 was consistent with the results of BSA-seq analysis as well as being stable over the 2-year study period, contributing to 19.37 and 22.18% of the phenotypic variation across multiple genetic backgrounds. Using extreme recombinants, qSB.A09 was further delimited to a 127-kb genomic region harboring 28 annotated genes. The GRAS transcript factor Bra007056, an ortholog of MONOCULM 1 (MOC1), which is the key gene controlling tillering in rice, was subsequently identified as a potential candidate gene. Quantitative RT-PCR further revealed that expression of Bra007056 was positively correlated with the shoot branching phenotype. Furthermore, an Indel marker specific to Bra007056 co-segregated with the shoot branching trait in the F2 populations. Overall, these results provide a foundation for uncovering the molecular mechanism of shoot branching in Brassica rapa ssp. chinensis Makino

**Keywords:** Non-heading Chinese cabbage, shoot branching, QTL, fine mapping, candidate gene

# A monomeric peroxiredoxin plays dual role in *Deinococcus radiodurans* R1 and exhibits resistance against heat and oxidative stress

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Peroxiredoxins are one of the enzymatic antioxidants that play a protective role against damage caused by reactive oxygen species (ROS). Deinococcus radiodurans R1 is a highly resistant bacterium against ionizing radiation and oxidative stress conditions. The phylogenetic analysis indicated that all the four putative peroxiredoxins (DR0846, DR1208, DR1209, and DR2242) in D. radiodurans belongs to PrxQ group which plays an important role in stress resistance. DR0846 was selected as a PrxQ candidate in this study on the basis of expression analysis in response to H2O2 and gamma radiation. AMS shift assay, size exclusion chromatography (SEC) and native-gel results corroborated that DR0846 exists in monomeric form with an intramolecular disulfide bond between the two cysteine residues. In this study, we found that DR0846 plays dual role by functioning as a molecular chaperone as well as a peroxidase. Site directed mutagenesis confirmed that both the cysteines are important for peroxidase activity. A double deletion mutant deficient in catalase DR1998 and peroxidase DR0846 exhibits sensitive phenotype to heat and oxidative stress as compared to single mutants and wild type cells. This study demonstrates that DR0846 is an important antioxidant enzyme with dual functions as it contributes to resistance against heat and oxidative stress in D. radiodurans.

## Audience Take Away:

- This study provides novel insights in the multi-functional aspects of PrxQ but the molecular mechanism behind chaperone activity of PrxQ needs further studies.
- Additional roles of PrxQ prove that Prx and its interactors act as modules in defense and signalling.
- DR0846 provides resistance against heat and oxidative stress. However, the role of other Prxs under different stress conditions can provide useful information regarding redox metabolism in Deinococcus.
- Post-translational modifications of Prxs in Deinococcus need to be investigated in detail for better understanding of Prx functions.

## Biography

Shubhpreet Kaur is pursuing her Ph.D. from Korea University of Science and Technology, South Korea. She has graduated with Honors degree in botany from Panjab University, Chandigarh, India. She was gold medalist during her graduation.

# Expression of hairpin RNA of root knot nematode pola1 gene in *solanaceae* hosts reduced nematode multiplication and improved agronomic characters

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[2]Laboratory of Plant Pathology, Chiba University, Matsudo, Japan
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Engineering nematode resistance via in planta expression of double stranded RNA (dsRNA) having sequence homology with essential root knot nematode genes promises a comparatively more beneficial and lower risk management strategy than integrated use of nematicides, resistant crop varieties and good cultural practices currently employed. Expression of hairpin RNA of a targeted essential nematode gene in suitable host plants is known to trigger gene-specific RNAi pathway in the plants and/or infecting nematode parasites which can ultimately lower transcript levels of such targeted gene in the nematodes. Silencing the expression of essential nematode genes may produce lethal effects in the parasites and confer protection on the expressing host plant. Thus, the selection of such appropriate target gene is a key consideration for success of this strategy. Plant parasitic nematodes such as Meloidogyne spp. are among the most significant constraints to sustainable agriculture and responsible for huge yield losses in various crop species running into several million dollars worldwide but particularly in developing countries. Our study, therefore, evaluated the potential effectiveness of root knot nematode PolA1, an essential single copy nuclear gene encoding the largest subunit of RNA polymerase I enzyme as a target in conferring nematode resistance on Agrobacterium tumefaciens-transformed tobacco plants. We cloned a 472 bp sequence of M. incognita PolA1 via an entry vector into pANDA35HK RNAi binary vector which had the target gene in sense and anti-sense orientations. We transformed tobacco and tomato explants with Agrobacteria EHA 105 cells carrying this construct and characterized resulting putative transgenics. Selected T0 plants and their T1 progeny lines expressing double stranded RNA of the PolA1 target gene were then subjected to M. incognita infection at the end of which nematode parasitic success and key agronomic traits were evaluated. Nematode challenge bioassay showed reduction in nematode galling, female nematode fecundity and amount of nematode juveniles in soil among the transgenic plants. Transgenic plants also showed reduced progression of overall disease condition as well as improved agronomic characters compared to wild type plants. Transcript level of PolA1 was reduced in adult female nematodes feeding on transgenic roots suggesting that RNAi machinery may have been activated in the nematodes following ingestion of either PolA1 dsRNA or resulting siRNAs. Put together, our results indicate that M. incognita PolA1 gene is a potentially effective target for host induced silencing-mediated reduction of root knot nematode damage on the Solanaceae host plants although further molecular evaluation and resistance assessment are necessary.

### Audience Take Away:

- Essential genes, like PolA1, not related to parasitism can also be used as effective targets for host-plant mediated silencing to confer protection against nematodes
- Different host plants expressing same silencing construct against nematodes may differ in their response to infection and degree of resistance

### Biography

Peter Nkachukwu Chukwurah graduated with a Master of Science in Plant Biotechnology from the University of Calabar, Nigeria. He won the Japanese Ministry of Education, Culture, Sports, Science and Technology (MEXT) scholarship for doctoral studies in 2016 and then joined the research group of Prof. Ikuo Nakamura at Laboratory of Plant Cell Technology, Chiba University, Japan where he is currently a PhD student.

# Identification of cis-regulatory elements in response to ionizing radiation and genotoxin treatment in *Arabidopsis Thaliana*

**Prapti Prakash[1, 2*], Shubhpreet Kaur[1, 2], and Sungbeom Lee[1, 2]**
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[2]Department of Radiation Biotechnology and Applied Radioisotope Science, University of Science and Technology, Republic of Korea

Various environmental and endogenous cellular stresses may lead to the generation of DNA damages ((e.g., DNA double-strand breaks (DSBs)) in plant genome, which are detrimental for plant genome integrity and cell survival, if left unrepaired. Therefore, plants have evolved efficient repair mechanisms for the repair of DSBs such as non-homologous end joining (NHEJ) and homologous recombination (HR). HR requires the DSB-induced small RNAs (diRNAs), which aid in the recruitment of a repair machinery to DSB sites. Argonaute 2 in A. thaliana (AtAGO2) plays an important role in guiding diRNAs to DSB sites. The molecular mechanisms underlying the AtAGO2 expression in response to DSBs have been remained unclear. Using stable transgenic Arabidopsis plants expressing a sequentially deleted promoter fragment fused with the β-glucuronidase reporter gene, we identified a DSB-responsive 20 bp cis-regulatory region spanning from -391 bp to -371 bp from 1.3 kb 5' UTR of AtAGO2. An in silico analysis using the AthaMap predicted putative cis-regulatory sequences, AAACCACACC, in the 20 bp region. An electrophoretic mobility shift assay further demonstrated that the nuclear proteins extracted from the zeocin-treated A. thaliana have preferred binding activity with the predicted 10 bp nucleotides, but not with that of control plants. Together, we propose that the 10 bp sequences contain cis-regulatory elements required to activate the expression of AtAGO2 in response to DSBs.

### Audience Take Away:

- Information on the transcriptional regulation of AtAGO2 gene that is one of key molecules to repair DSBs in response to ionizing radiation and genotoxin treatments
- Information on the plant-derived novel cis-elements that are required to AtAGO2 expression
- Fundamental information to identify a transcription factor for AtAGO2, as well as to study unknown molecular mechanisms in the repair of DSBs in plants

### Biography

Prapti Prakash studied Biotechnology at the Gautam Buddha University, India and graduated as MTech in 2013. She then joined Indian Agriculture Research Institute (IARI), New Delhi as a senior research fellow. She is currently a PhD student in the University of Science and Technology, South Korea, in affiliation with the Korea Atomic Energy Research Institute (KAERI).

# DAY 2

# E-POSTER

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# Morphological particular properties of the varieties *Sesamum indicum* L. for the conditions of Pridnestrovie

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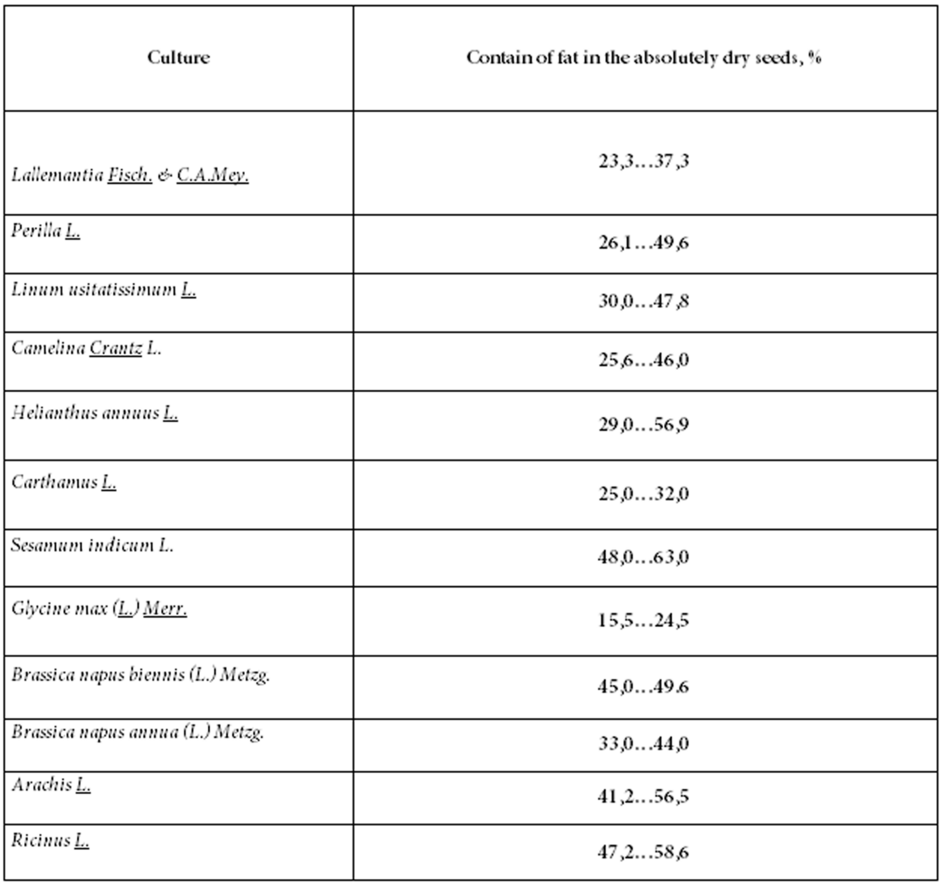
*Sesamum indicum* L. is a valuable oilseed plant. Its seeds contain from 48,0% up to 63,0% of fat (table 1).

**Table 1. Contain of fat in the seeds of the oilseed plants and the quality of fat**



| Culture | Contain of fat in the absolutely dry seeds, % |
|---|---|
| *Lallemantia* Fisch. & C.A.Mey. | 23,3…37,3 |
| *Perilla* L. | 26,1…49,6 |
| *Linum usitatissimum* L. | 30,0…47,8 |
| *Camelina* Crantz L. | 25,6…46,0 |
| *Helianthus annuus* L. | 29,0…56,9 |
| *Carthamus* L. | 25,0…32,0 |
| *Sesamum indicum* L. | 48,0…63,0 |
| *Glycine max* (L.) Merr. | 15,5…24,5 |
| *Brassica napus biennis* (L.) Metzg. | 45,0…49,6 |
| *Brassica napus annua* (L.) Metzg. | 33,0…44,0 |
| *Arachis* L. | 41,2…56,5 |
| *Ricinus* L. | 47,2…58,6 |

The relevance of the breeding work of the *Sesamum indicum* L. for the conditions of Pridnestrovie is a consequence of the aridization of climate and the wide use of seeds in the food industry. For Pridnestrovie *Sesamum indicum* L. is an introducer. The conditions of introduction is significantly different from the conditions of the center of origin of this culture.

Town Tiraspol (capitol of Pridnestrovie) were the tests are being held is situated at 46 degrees north latitude and has the conditions of the continental climate. The center of origin is administrative regions of north and north-west of Ethiopia: Tigray with the center in Mekel and Amhara with the center in Bahr Dar that are situated in the tropical zone (13 degrees and 11 degrees of the north latitude).

Among features of the model of the variety *Sesamum indicum* L. is a sustainability to the most often diseases (table 2).

**Table 2. Model of the variety Sesamum indicum L. for the conditions of Transnistria**

| Feature | Units | Value |
|---|---|---|
| The period of the growing season | Days | < 145 |
| Quantity of branches from the central stem | Pieces | 8-12 |
| Density of positioning of seed boxes | Pieces/10cm of the length of the plant shoot | > 6 |
| Productivity | Grams from one plant | 45-50 |
| The way of location of the plant shoots | Degrees regarding to the central plant shoot | < 30 |
| Sustainability | Points | Regarding to the often met diseases and pests and to the shedding of seeds |

On the territory where the tests are being held there are noticed phytoplasmic diseases on the different cultivated and wild plants (fig. from 1 up to 8).

Fig. 1, 2. Phytoplasm on *Foeniculum vulgare Mill. (there is an affected plant on the left side, and healthy plant on the right side)*

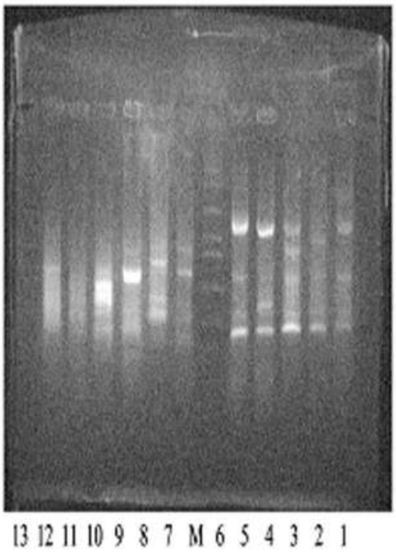
Fig. 3, 4. Phytoplasm on *Calendula officinalis L.*
*(there is an affected plant on the left side, and healthy plant on the right side)*

Fig. 5, 6, 7, 8. Phytoplasm on *Cirsium arvense* (L.) Scop.
*(there is an affected plant on the left side, and healthy plant on the right side)*

Research works of N.N. Balashova, A.P. Harkova, O.O. Timina showed a high prevalence of viruses: tobacco mosaic virus, cucumber mosaic virus, potato Y-virus, bronze virus of tomatoes, as well as phytoplasmic diseases. Exploratory research works in the conditions of Pridnestrovie confirmed the susceptibility of *Sesamum indicum L.* by viruses and phytoplasmic diseases (fig. 9, 10, 11).

Fig. 9, 10, 11. Phytoplasm on *Sesamum indicum* L. *(there is an affected plant on the left side, and healthy plant on the right side)*

The results of polymerase chain reaction analysis confirmed the susceptibility of Sesamum indicum L. by phytoplasm in the conditions of holding of breeding work (fig. 12).



strips 2, 3 – confirmatory test (phytoplasm) - sample 10;
strips 4, 5, 6 - confirmatory test (phytoplasm) - sample 11;
M - molecular weight marker, size of amplification fragment is 800 p.o. (Fermentas, Lithuania);
strips 7, 8 – refutive test, variety «Lebed»;
strips 9, 10 – refutive test, variety «Lebed»;
strips 11, 12 refutive test, variety «Mulatka»;
strips 1, 13 – negatory control (deionized water)

Fig. 12. Results of the testing of *Sesamum indicum L.*

Sustainable breeding samples morphologically differ from those affected by phytoplasm. Sustainable samples have significant pubescence of organs of plants, and not sustainable samples have insignificant or missing pubescence (fig. 13, 14, 15, 16). Insects, that transfer the diseases, do not live on very pubescent plants.

Fig. 13, 14, 15, 16. Particularities of morphological structure of not sustainable and sustainable samples of *Sesamum indicum L.* (on the left side there is not significant pubescence on susceptible samples, on the right side there is a presence of pubescence on sustainable samples)

In the process of creating of sustainable varieties of *Sesamum indicum L.* it is possible to use the selection of pubescent plants. The selection should be made at the early stages of plant growth, when the seeds are germinating (fig. 17).

Fig. 17. The appearance of pubescence on the seedling of *Sesamun indicum L.*

It is making the breeding process faster

## Biography

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

# Differences in lignification of early and late tracheids during wood formation in Scots pine stem

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Physical and mechanical properties of wood depend on cell development during the successive processes their production by cambium, growth of primary walls and deposition of substances in secondary cell walls. The each of these processes is under external factors, which originally act on physical events into cells (in particular, on membrane level) and then on cellular metabolism (physiological processes) that radically affects morphogenesis of cells and, as consequence, their parameters. Different combination of external factors, foremost of which are the temperature and moisture availability, especially the last, initiates the formation in annual ring of conifers of two types of tracheids, early and late, which are distinguished by radial diameters and cell wall thickness. Lignin is one of principal cell wall components of woody plants, taking part in the rigidity of plant, strengthening of their mechanical structure, improves the transport of water and prevents cell collapse under the tension of water transport.

The purpose of this work was to study the process of lignification on successive stages of development of secondary walls of tracheids during the formation of early and late wood in the trunks of pine-trees and the changes in the composition and structure of lignin at these stages. Lignin was isolated by the thioglycolic acid method from the layers of xylem cells with different degree of secondary wall development, which were obtained from the stems of 25-year old pine tree at the end of June and in early August, when the cells in differentiation zones were either early or late type. The metabolites, accompanying the development of cell walls (carbohydrate, hydroxycinnamic acids, being the precursors of monolignols and ascorbic acids, as the participant of redox reactions) were assessed. Low- (alcohol-soluble, LTGA-I) and high molecular weight (alkali-soluble, LTGA-II) fractions have been received. The fractions LTGA-II, as the main part of isolated lignins, were analyzed. In the early xylem lignification of the walls has been found to be gradually amplified during tracheid maturation, whereas in the latewood intensive synthesis of lignin occurs at the beginning of the process. The methods of alkaline oxidation, alkaline and acid hydrolysis's showed the differences in lignin structure both at the each stage of lignification and in dependence on wood type. The content and molar ratio of p-hydroxyphenyl (H), guaiacyl (G), and syringyl (S) subunits in lignins changed in earlywood compared with latewood oppositely. The type bonds of lignin macromolecules with carbohydrates (ether and ester) also were modified during lignin deposition. Hemicelluloses, included in such bonds, contained mainly the residues of arabinose and xylose and their content varied in dependence on lignification stage. Hydroxycinnamic acids, taking part in such linkages, also changed in dependence on lignification stage and on wood type. The content and composition of hydroxycinnamic acids (original monolignol precursors) and ascorbic acid content (redox-state) were in agreements with the changes in the composition and the structure deposited lignins. Observed differences correspond to different organization of intercellular spaces of two cell types and point to different conditions of precursor lignin polymerization.

## Audience Take Away:

The presentation will show significant changes in lignin structure during development of cell walls of the xylem in conifers under the influence of external factors, mainly the availability of moisture, in Scots pine stem. The study is important for understanding of biochemical and physiological processes of cell growth and development during wood formation in trees

## Biography

Dr Galina Antonova studied on chemical-technological faculty at Siberian Technological Institute (Krasnoyarsk, USSR) and graduated as engineer in 1959. With 1959 she works in V.N. Sukachev Institute of Forest (early - Institute of Forest and Wood) of Siberian Branch of Russian Academy of Sciences, at the beginning as Junior researcher, then senior researcher. She received Ph degree in 1972 and Dr degree in 1995 at the same Institute. Now she is Leading researcher at the Physicochemical Biology of Woody Plants Laboratory. She has published more than research articles in journals, 1 book and 4 chapters in books.

# Ribosomal protein genes emerging as potential targets for manipulating stress tolerance in crop plants

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[2]ICAR- Indian Institute of Rice Research, India
[3]School of Biological Sciences, University of Essex, United Kingdom

Ribosomal proteins have long been known primarily for their housekeeping functions including protein translation, ribosome assembly and other developmental processes. But lately, there have been reports of their extra-ribosomal activities in various systems. In Arabidopsis, aberrant expression of ribosomal protein S6 leads to a deleterious effect on survival of cells indicating their role in regulation of translation whereas semi-dominant mutations of RPL27aC results in critical developmental abnormalities viz, leaf patterning, inflorescence, seed set etc.

However, the role of ribosomal proteins particularly in stress responses has not been explored extensively. Recently, through activation tagging carried out for enhanced water use efficiency in indica rice, our research group could identify some Ribosomal Protein Large Subunit (RPL) genes (RPL23A and RPL6) to be significantly upregulated. Following this cue, when we studied the regulatory role of all the RPL genes under different external stimuli, we observed significant up-regulation of considerable number of RPL genes under several stress.

Subsequently, this led us to explore the developmental and stress regulated expression patterns of ribosomal protein small subunit (RPS) genes using real time quantitative PCR. We have

selected four abiotic stress conditions (ABA, PEG, NaCl and H2O2 mimicking drought, osmotic, salinity and oxidative stress conditions and two biotic stress conditions including infection with important rice pathogens, Xanthomonas oryzae pv. oryzae and Rhizoctonia solani causing bacterial leaf blight and sheath blight respectively in rice. A vast number of RPS genes exhibited significant upregulation under all the stress conditions at different time points. We also performed several in silico analysis to gain insight into the gene structure, cis-elements in upstream regulatory regions, protein properties and phylogeny of individual RPS genes. Our gene expression data was backed up by the in silico data. We observed that Ribosomal Protein genes not only became up-regulated but also exhibited an overlap in response to multiple stress conditions. This significant up-regulation and overlap in the expression of Ribosomal protein (RP) genes have been correlated with the presence of stress and signal-responsive elements in their putative promoter regions. Based on these findings, few RPS genes were identified to be promising for orchestrating abiotic stress tolerance in rice. To further affirm their stress responsive attributes, we have selected few RPL and RPS genes (including RPL6, RPS4 and RPS6A) for overexpression in rice. Detailed investigation of the transgenic plants overexpressing these genes using several biochemical, physiological and proteomic analyses is ongoing. Detailed functional analysis of RPL and RPS genes will confirm the stress responsive attributes of the RP genes and hence this will prove to be helpful to enhance the genetic makeup of crop plants to combat harsh environmental conditions. As rice has a close evolutionary relationship with other cereal crops, genes identified and characterized for improvement of rice cultivation can extensively be used for other important crops as well.

**Audience Take Away:**

- A detailed functional analyses of Ribosomal protein (RP) genes mentioned in the abstract will provide useful insight for further exploration of these genes in manipulating stress tolerance in crop plants
- Not much emphasis has been given previously to elucidate the extra-ribosomal functions of ribosomal protein genes in terms of stress tolerance. Since, sufficient background information has been generated in our laboratory that supports the involvement of RP genes in stress responses, these can be utilized to improve the productivity potential of crops. This might have a significant economic value in developing countries
- We know, it is of great significance to find genes in plants that might have a role in combating stress conditions so that they can be utilized wisely to enhance the genetic makeup of the plants. Hence, this research is important as it identifies few RP genes to have fair prospects to be exploited for crop improvement. Audiences working on similar area can be benefitted to know that although RP genes have been mostly considered as housekeeping genes, they can also be exploited in manipulating stress tolerance in plants
- As rice has a close evolutionary relationship with other cereal crops, genes identified and characterized for improvement of rice cultivation can be extensively used for other important crops as well. Thus, not only rice, scientists working on other crops can also be able to expand their knowledge on these specific genes and can also utilize them to manipulate other crops better yield and stress tolerance

## Biography

Anusree Saha studied botany at Presidency College, University of Calcutta, India and graduated with Botany honors in 2013. Subsequently, she went to University of Hyderabad and obtained Masters degree in Plant Biology and Biotechnology in 2015. Same year, she joined Prof. P.B.Kirti Laboratory at University of Hyderabad for her doctoral studies. She is currently a fourth year Ph.D student. She got selected for Newton Bhabha PhD placement and worked with Prof. Christine Raines at University of Essex, UK for four months in 2017. She has published 1 first authored and 3 co-authored research articles in international journals.

magnus
Group

# DAY 3

# KEYNOTE FORUM

4TH EDITION OF GLOBAL CONFERENCE ON

# PLANT SCIENCE AND MOLECULAR BIOLOGY

SEPTEMBER
19-21, 2019

LONDON, UK

GPMB-2019

## Biography

Dr. Wang completed his PhD at the University of British Columbia in 1999. He joined Agriculture and Agri-Food Canada as a Research Scientist in 2003. He has authored over 100 peer-reviewed papers and 25 book chapters and edited five books. His work not only advances knowledge in fundamental plant virology but also opens new avenues to crop improvement for the control of viral diseases. Dr. Wang is the recipient of various awards including this year's Ruth Allen Award from the American Phytopathological Society to honor him for having made outstanding, innovative research contributions to the field of plant virology.

# Understanding of the molecular plant-virus interactions and development of novel antiviral strategies

**Aiming Wang**
Agriculture and Agri-Food Canada, Canada

Plant viruses are obligate intracellular parasites that infect many agriculturally important crops and cause severe losses each year. Genetic resistance is considered the most effective means to control these viruses. However, extensive screening of germplasms for natural genetic resistance only identifies a few resistance (R) genes. Due to the frequent occurrence of resistance breaking isolates, the resistance conferred by these R genes is often not durable. To develop novel antiviral strategies, we have employed classical molecular and biochemistry tools as well as cutting edge technologies to study molecular virus-plant interactions. Since potyviruses are the largest group of known plant viruses including a number of notorious viruses such as plum pox virus (PPV), turnip mosaic virus (TuMV), soybean mosaic virus (SMV), potato virus Y (PPV) and papaya ringspot virus (PRV), we chose potyviruses as our major research target. We have been concentrated on the molecular identification of host factor genes that are essential for infections by TuMV, PPV and SMV, and functional characterization of their roles in the infection process. We have identified over ten host factor genes and conducted proof-of-concept experiments in manipulation of them for disease control using PPV as a case study. In collaboration with colleagues, transgenic plum highly resistant to PPV was successfully developed by targeting either the PPV genome or the plum eIF(iso)4E gene, a host factor gene of PPV. Since peach, the primary host of PPV, is recalcitrant to genetic transformation, established technologies such as precise genome editing and RNA silencing (RNAi) that require genetic transformation are not applicable. We thus studied the possibility to create PPV resistance by silencing a host factor gene of PPV through virus-induced gene silencing (VIGS) as well as by generation of a peach mutant population for screening for target gene mutants. For the VIGS approach, we found that Prunus necrotic ringspot virus (PNRSV) was highly endemic on stone fruit trees in Canada, and no obvious phenotypic differences were observed among PNRSV-positive or negative trees. We developed a PNRSV-based vector and further modified the vector to target the eIF(iso)4E gene. This modified vector knocked down the expression of eIF(iso)4E and prevented PPV infection in peach. The modified PNRSV vector is ready for field test. For the mutagenesis approach, we have developed a novel protocol to generate peach mutants and developed a peach mutant population consisting of more than 2,000 lines. Our current research focus is on screening for and molecular characterization of peach mutants resistant to PPV.

**Audience Take Away:**

- New concepts and theories of plant-virus interactions
- Advanced biotechnologies for the control of viral diseases
- Future research directions in plant-virus interactions

## Biography

Dr. Usha Palaniswamy holds a PhD in Plant Science (University of Connecticut, USA), MBA (Webster University, USA) and MEd in educational administration (M.K. University, India). Her academic career includes positions as Faculty of Allied Health and Asian American Studies, and in academic higher administration as the dean and associate dean. She served as a Project Manager at the World Vegetable Center in Taiwan and implemented school gardens in six countries in Asia and Africa. She is a recipient of several teaching, research and volunteer service awards. She is a Technical Advisory Committee member of Prem Nath Agricultural Science Foundation (PNASF) and serves on the PhD Board of Examiners of several Universities in India. She has authored four books and published over 55 research articles and several book chapters and review articles. She is the Editor-in-Chief of the Journal of Herbs, Spices and Medicinal Plants (Taylor and Francis, USA).

# Approaches to curing plant blindness in Communities

## Usha R. Palaniswamy

Maria College, USA

"Plant blindness" among the young and the old is a major concern in many communities. Plants are critical to the future of the planet, however absent from the minds of most people. This poses a challenge to the entire field of plant sciences. The benefits of plants are many spread across all human experiences and the role of plant foods in the daily diet and in biomedicine has enhanced overtime. The elevated status of fruits and vegetables in the daily diet is a major focus in finding a solution to nutrition security, human health promotion and disease prevention. Edible plant vaccines have been developed for oral administration against many allergies. New uses of plants include as tools in biomedical engineering such as the use of spinach leaf vascular network as a biomaterial for heart tissue regeneration and the possibility of using wood to help fix human bones. Plants are tapped into as "energy crops" the can be used to produce renewable biofuels that are cleaner than fossil fuels, releasing fewer pollutants and greenhouse gases. This presentation will explore ways of how plant blindness is currently being addressed in the US and in other parts of the world at the community and national levels with specific examples from Indonesia. Age and community-specific plant education to cure plant blindness in local communities is discussed in greater detail.

**Audience Take Away:**

- The audience will be able to apply what they learn to their own programs, homes and communities
- This is a topic that will be helpful to academics in research and teaching in spreading the importance of plants and plant sciences in the academic curriculum. It gives examples of how this problem of plant blindness is being addressed by others, giving examples that are easy to relate to. It will certainly improve the design of a similar program that the audience may be involved at the present time or have plans to engage in the future

## Biography

Dr Laura De Gara is Full Professor of Plant Physiology at the Campus Bio-Medico University of Rome. Member of commissions of the Italian Ministers of University and Research and of Agriculture. From 2007 to 2009 President of the Plant Oxygen Group (https://www.plantoxygengroup.eu/), From 2015 to 2017 President of the Evaluation Committee of the Research Centers of MIPAAF. In July 2018 elected Secretary General of the Federation of the European Societies of Plant Biology.

# $H_2O_2$ signature and antioxidative profile as key players of rice responses against salt stress

**Laura De Gara**
Campus Bio-Medico University, Italy

Plants are continuously faced with adverse environmental conditions, which affect the oxidative metabolism and photosynthetic efficiency, thus leading to the over-production of Reactive Oxygen Species (ROS). Despite their harmful nature, ROS also acts as powerful signalling molecules involved in responses to stress stimuli. A complex and differentiated redox network modulated by different environmental stimuli is responsible for the generation of ROS signature that is pivotal for the activation of homeostatic responses against stresses and for guaranteeing plant fitness in the resistant species or varieties.

According to the intensity and kind of stress, as well as plant developmental stage, resistant plants are able to maintain a normal phenotype by increasing detoxifying pathways (ROS – scavenging systems, molecular chaperons, compatible solutes etc.). In other cases, they can block cell division and growth in order to reduce the occurrence of genetic alterations that could negatively affect the progeny survival. Furthermore, Programmed Cell Death (PCD) of specific cellular districts is another defence strategy activated by tolerant/resistant plants in response to different abiotic stresses.

The comprehension of plant resistance mechanisms, defined at molecular, cellular and physiological level and activated in response to stress conditions related to climatic changes, represents a crucial area of plant science also due to its implications in food security. In fact, adverse climatic factors, such as drought, waves of temperatures far from the optimal ones and soil salinization drastically affects crop growth and productivity worldwide.

In this context, rice plays a central role since it is one of the main source of food for humans and is one of the most sensitive cereals to abiotic stresses, salinity first but also extreme temperatures and water scarcity.

In order to reach an advancement of knowledge regarding the signalling pathways triggering defence responses against salt stress two rice varieties showing contrasting salt sensitivity have been investigated. Analysis of key metabolites and related genes/enzymes have been performed on cell cultures derived from the two varieties, as well as on leaves and roots of the two varieties subjected to salt stresses of different intensity. An in-depth study centred on ascorbate and glutathione metabolism, cellular redox state and markers of cell viability and death has been carried out over treatment time. Moreover, redox-dependent regulatory mechanisms, such as post-translational modifications, i.e. thiol-disulphide switch, glutathionylation and S-nitrosylation, modulating enzyme activity and gene expressions, have been analysed in responses to salt stress.

These results wish to described ROS signatures and different antioxidative pathways as a part of a complex redox network activated in rice after salt stress exposure in order to draw effective strategies aimed at increasing rice resilience toward salt stress.

**Audience Take Away:**

- Redox biology and the complex regulatory networks that enable ROS to act as signaling molecules
- Redox pathways involved in the tolerance/responses to salt stress, an environmental condition related to climatic changes that affects plant productivity in increasing areas of our planet
- The involvement of different levels of metabolic regulation mechanisms and their interplay (gene expression, post-translational modification of enzyme, catalytic activity)
- Redox biology is a hot topic in plant physiology, redox homeostasis and signals based on redox alteration at metabolite and protein levels is involved in stress responses as well as in plant/cellular development/differentiation. The information here given will help the audience to understand better the relevance of the metabolic redox network for increasing plant fitness and productivity under climatic changes challenges. Discussion concerning why specific parameters have been chosen as key aspects for elucidating specific metabolic changes and responses, will help, in particular, young participant to improve their capability to design research activities

## Biography

Dr. Arunachalam Muthiah studied Agricultural Science at Tamilnadu Agricultural University(TNAU), Coimbatore, India during 1970—74. Graduated as Master of Science (1976) and Doctor of Philosophy in Plant Breeding and Genetics in 1990 at TNAU. He joined the research group in grain legumes in 1995 and worked nearly for two decades in improvement grain legumes specifically for pigeonpea improvement with higher yield potential coupled with biotic resistance for gram pod borer (Helicoverpa armigera ) and he is responsible for the development of pigeonpea cultivar CO8, maturing in 170 – 180 days with average grain yield of 1600 kg /ha under rainfed conditions , drought tolerant and moderately resistant to pod borer complex. This variety is released for general cultivation in 2017 in India. PPV and FR authority of India is provided with DNA finger printing profile for this cultivar. During the year 2013, Dr. Arunachalam Muthiah obtained the position of Director, Centre for Plant Breeding and Genetics Tamil Nadu Agricultural University, Coimbatore, India.

# Molecular characterization in pigeonpea for genetic diversity in cultivated and wild relatives for certain economic traits

**Arunachalam Muthiah**

Tamil Nadu Agricultural University, India

Plant genome – their size – difficulties in plant genome assembling – pigeonpea genome sequencing – molecular marker development

Pigeonpea – Narrow genetic base in the cultivated varieties

Wild relatives of pigeonpea and the useful characters present in them for introgression into cultivated genotypes.

Molecular markers with emphasis on Single Sequence Repeats (SSR) markers / microsatellite markers in detecting genetic diversity. Pigeonpea and its wild relatives for certain economic traits.

Economic traits viz. cytoplasmic genic male sterility, quality traits like seed/grain weight, protein content, determinant plant types for early flowering and uniform maturity, pod borer resistance etc- their molecular characterization and their impact in genome assisted breeding (GAB).

Inheritance and mapping of protein markers for pod borer resistance in pigeonpea, polymorphism among Cajanus cajan and Cajanus scarabaeoides genotypes with contrasting host response.

Plant Variety Protection (PVP) and farmer's Right (FR) – PVP and FR authority demanding submission of details of molecular markers associated with the newly released cultivar , so that admixture, if any, in seed lots could be identified – a practical application of molecular markers.

**Audience Take Away:**

- General concepts in plant genome assembling
- Pigeonpea – genetic base, wild relatives of pigeonpea and useful characters they possess
- Molecular markers wildly used in characterization of certain economic traits in Pigeonpea and in their wild relatives
- Genome Assisted Breeding for development of new cultivars utilising marker assisted selection
- Albumin and globulin markers linked to pod borer resistance and their use in marker assisted introgression of pod borer resistant allele

# DAY 3

# SPEAKERS

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# Harvest weed seed control in the United States

**Lauren M. Lazaro**
Louisiana State University AgCenter, USA

The loss of herbicides due to resistance threatens the future of the highly productive conservation cropping systems has been the motivation for growers to develop and adopt alternate systems. Subsequently, one of these alternative approaches, harvest weed seed control (HWSC), was developed to target weed seed passing through the harvester during grain harvest. The United States has just begun to implement HWSC tactics in the past decade, although this weed management tactic has been around for nearly 30 years. In addition to the efficacy of various HWSC methods, understanding the basic biology of the weeds present at harvest is imperative. There is little research on the quantity of seed that is retained on different weed species at harvest time, especially over large geographic ranges. As the adoption of HWSC systems continues to grow there will be an increasing demand for more refined systems that are easier to use and have minimal impact on harvest efficiency. Similarly, with HWSC now being considered in a range of global cropping systems, there is an increasing need for the adaptation of HWSC systems for these situations.

**Audience Take Away:**

- With the increase of herbicide resistant weeds, what is the future of weed management? Chemical weed management may not be the entire answer after all
- Long-term weed management strategies need to be implemented for the success of weed control
- Harvest weed seed control is a nonchemical integrated weed management tactic that targets weed seed present at harvest
- The use of HWSC is relatively new to weed management and has shown to be highly effective in specific cropping systems
- There is still a lot of research and room for growth in this area of weed management

## Biography

Dr. Lazaro studied Plant Biology, with an emphasis on Weed Science, at Southern Illinois University, Carbondale, USA under Drs. David Gibson and Bryan Young and graduated with her PhD in 2015. After two years postdoctoral fellowship supervised by Dr. Jason Norsworthy at the University of Arkansas, USA, she obtained the position of an Assistant Professor of Agronomy and Weed Science at Louisiana State University. She has published 20 research articles in peer-reviewed journals, two book chapters, and received the award for Outstanding Paper of the Year in Weed Science in 2016.

# Plant metabolic engineering for sustainable agriculture

**Lalithakumari Janarthanam**
ACELABIOTEK, USA

Catering the Plant metabolism through engineered microbes leads to Plant health, environmental health, animal health there by Universal health.

The present report is very simple and is purely an Application oriented Technology. In this technology beneficial microorganisms are engineered using their functional characteristics to catalyse the plant metabolism including nitrogen fixation,phosphate solubilization and uptake, potassium and other mineral elements solubilization and uptake,,phytohormone induction, stress tolerance, and water retention useful for a broad spectrum of crops including all grain crops, vegetables, fruites, flowers,forage grasses, grown under diverse soil and wide range of temperature.

Beneficial microbes isolated from diverse soil, crop roots, root nodules in USA are discussed on their isolation purification and grouping based on functional characteriztion to design a potential consortium containing multiple microbes.

Tested under Green house and field trials across US and also in many International trials. Recent Results on Almond, Olive Golf course Vegetable etc in California are also included in the presentation.

How this Poly microbial consortium helps in Soil Agregation creating air spores for water infiltration and retention will be discussed. Build up of Organic matter with increased Cat ion exchange capacity will be discussed. Plants are activated for stress mechanism ( Drought and Frost+pest and disease reduction ) Aqua porin a short lived proteins in stomatal pores will be correlated to the transpiration rate and stress.

The Plants are metabolically activated to yield nutrient rich quality products with increased BRIX VALUE (MINERAL DENSITY),flavor, sweetness and long keeping quality.

Most important cost economics to the farmers will be discussed.

Catering the Plant metabolism through engineered microbes leads to Plant health, environmental health, animal health there by Universal health.

## Biography

Dr. Lalithakumari Janarthanam, a distinguished microbiologist and plant pathologist has several years of experience in Research,Teaching and Administration in Agricultural sciences and Environment since 1965 till date. Her work presented a new concept of the Microbial relationships with Plant metabolism. Her US patented(US PATENTS 8822190 AND 9615584) Polymicrobial Formulation received the Popular Science Grand Prize Award for its forage boost and multi-functional benefits. It was chosen for "Best of What's New" & Grand Award winner in the Green Tech Category for its ability to increase crop yields, conserve water, and improve the environment, while eliminating fertilizer dependence(BSEI). She held various high level positions in India, University of Guyana, South America, Michigan State University East Lansing, USA. Director of Research and Development in Bio Soil Enhancers Inc. Hattiesburg, Mississippi.and Chief Technology Officer, Acela Biotek, California.

# Quality improvement in agronomy by no linear design of experiments and repeated measurements analysis

**Martha Elva Ramírez Guzmán**[1*], **María de Lourdes Arévalo Galarza**[2]
[1]Applied Statistics Department, Colegio de Postgraduados, México
[2]Fruit Department, Colegio de Postgraduados, México

Mexico has 16 thousand hectares dedicated to the cultivation of ornamental flowers. They produced approximately 83 thousand tons by year. Given the importance of this crop, there is interest on improving the quality of roses by identifying the best cultivars and periods of production. A feature highly valued in this industry is the stem length of the roses (50-70 cm). In this research, generalized Linear models (GLM), generalized linear mixed models (GLMM), generalized additive models (GAM), generalized additive mixed models (GAMM) and vector generalized lineal models (VGLM), were fitted to explore the possible effect of heat units, relative humidity and light over the stem length of two cultivar of roses during two periods. GAM model showed no linearity effect of heat units and relative humidity on stem length. The best conditions to produce plants between 50 and 70 cm were 650 to 830 of heat units and 82.5 to 85 % of relative humidity. GAMM model with repeated measurements ( 1, 7, 14, 21 and 28 days) identified that the best conditions to produced roses with the required characteristics, they were period 1 with cultivar 2. It was concluded that recently developed new statistical models can be very useful to show nonlinear effects "overshadowed" by the indiscriminate use of linear models.

**Palabras Clave:** Generalized Linear Mixed Model, Generalized Additive Mixed Model, Vector Generalized Lineal Models, quality control, flower production.

**Audience Take Away:**

- The audience will learn how to improve the statistical analysis considering the nature of the data
- It will be explained which are the new statistical methods which can be used with no normal distributions, no linear models and repeated measures
- The audience will be able to use the statistical methods through free software like R
- People will learn how new graphics will show no linear effects between response and explanatory variables
- Participants will learn how easy is to consider no normal distributions in the model
- The audience will learn how to take advance of repeated measures taking through time

## Biography

Dr. Martha Elva Ramírez Guzmán is a statistical consultant of the National Service for Agrifood Health, Safety and Quality (SENASICA) of Mexico. She was invited as speaker by Stephanie Bloem, Chief Executive of the North American Plant Protection Organization (NAPPO, Mexico-USA-Canada) for the International Symposium for Risk-Based Sampling during june 26 – 30, 2017 in Baltimore, Maryland. The research presented was Predictive phytosanitary model for quarantine pests. Her research can be found in https://www.researchgate.net/profile/M_E_Ramirez_Guzman/research.

# Ethnobotanical Value of *Cephalaria syriaca*

**Tamar Kacharava*, Tinatin Epitashvili**
Georgian Technical University, Georgia

Unique Plant Genetic Resources - unique species of **Useful Plants** (medicinal, aromatic, spices, dye and poisonous) are distributed in Georgia which cannot be found anywhere in the world. By today's state, many of these plants belongs to endangered species and are included in the Red Data Book of Georgia. Due to erosion of genetic resources and uncontrolled utilization, ***ex-situ*** and ***in-situ/on farm*** conservation of biodiversity is critical. It is also important intensification of mechanisms of popularization of ethnobotanical traditions and phyto products considering centuries-old traditions and todays priority status of phytopharmacy in Georgia.

During the investigation for enrichment of existing our data base of ethno botanical characteristics of Georgia, it has been identified that in some regions of our country for improvement of quality and taste of bread is valuable with natural phyto supplements such as cephalaria *(Cephalaria Syriaca)*. Adding cephalaria to the bread gives a pleasant scent and makes it soft, increases the duration of storage. This interesting natural phenomenon was the basis for our research direction, because of the negative effect of chemical compounds in our daily life, natural products have recently been in high demand.

*Cephalaria syriaca* is a herbaceous species of the family *Dipsacaceae*, mostly distributed in Europe, western and central Asia, and northern and southern Africa. Many of Cephalaria species are used traditionally for different purposes in various part of the world. Phytochemical studies support this genus with extremely rich chemical sources including novel phenolic, flavonoid, iridoid and triterpene-type glycosides together with biologically active glycosides and fatty acid.

Some species of this genus have scientific interest. For example - *Cephalaria syriaca*, an important oil yielding plant. Economic and medicinal studies support that *Cephalaria syriaca*, as an additive increases the strength of wheat flour dough in bread making and as a medicinal purposes it's used for their antimicrobial, antifungal, antioxidant, hypothermic, relaxant, insecticidal, herbicidal and cytotoxic activities.

Cephalaria syriaca is considered as weeds grown in wheat fields. Cephalaria`s height is same as wheat, on the stem it develops 4 branches, seed looks like wheat grain, with bitter taste. We have studied chemical composition of *Cephalaria syriaca* seed, where results was: protein – 18,46%, fats – 17,76%, carbohydrates – 43,43%, energy value in 100 g product – 422 kkal.

Today, due to adaption within wider bioclimatic habitat, rustic in nature, human domestication, inheritance of rich phytochemical compound, cephalaria is an important and actual plant material to study for a diverse area of science.

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Nusrat Sultana, Ahmet L. Tek, Sedat Serce. Karyotype analysis of Cephalaria syriaca cv. Karahan, a new cultivar developed from a wild population. Materials of International Symposium on Medicinal Aromatic and Dye plants, 5-7 October 2017, Malatya/Turkey.

**Audience Take Away:**

- The audience can acquire modern situation about useful plants in Georgia, practical knowledge and recommendations and their use
- The researchers will learn more about useful plants, especially plants that can be used as natural supplements and preservatives; they will be able to successfully apply the acquired knowledge in their future researches and studie

## Biography

Doctor of Agricultural Sciences, Professor of Georgian Technical University, Chief Scientific Worker of Biotechnology Center of Georgian Technical University, Chairman of Scientific Board, head of the Scientific – Educational Centre "Biodiversity & Ethnobotanic Features Rational Explotation" of Georgian Technical University, ECP / GR and Asia-Ocean countries of the European Corporation - "Genetic resource of medicinal and aromatic plants" - representative in Georgia. Project leader - "Create and improve pharmacological genebank of Medicinal, aromatic, dye, spicy and poisonous plants". Author of more than 140 scientific works in the direction of medicinal, aromatic, dye, spicy and poisonous plants. Participating in more than 25 international congresses and conferences. Supervisor of 7 Academic Doctor, 18 Masters and 2 Ph.D. student.

# Durability of the Genetic Resistance to the Coffee Rust (*Hemileia vastatrix*) in Improved Varieties in Honduras 2019

**Yonis Alberto Morales Reyes**
Honduran Coffee Institute, Honduras

Coffee rust (Hemileia vastatrix) is the main fungal disease of the crop worldwide, causing losses of 25 to 30% of production during protracted epidemics. To address this disease, several research efforts have been made aimed at understanding the pathogen, its interaction with the plant and climate and identifying resistance genes for the development of improved varieties, writing to date 9 resistance genes (SH1 to SH9) and 9 virulence genes (v1 to v9) using the differentiating plants initiated by Mayne in 1932 and continued by the International Coffee Rust Research Center (CIFC) in Portugal where they started crossbreeding between the Timor Hybrid 832/1 and 832 / 2 with Caturra and Villa Sarchi that derived in early generations from Catimores and Sarchimores sent to Honduras by PROMECAFE, for evaluation and release after a rigorous selection process producing varieties such as IHCAFE 90 in 1990, Lempira (1998) and Parainema in 2004, which have replaced susceptible varieties such as Pacas, Typical, Borbon and Catuai, dominating 65% of the cultivated area by 2012 where about 45% is Lempira variety that contributed to increased national productivity but created high vulnerability to emerging epidemics due to mutation effects, dispersion and genetic recombination of the fungus, favored by the low genetic diversity of resistance in the field. To minimize the risk, the genetic improvement program of the IHCAFE monitors plots of mother plants, seed foundation, research trials and farms of producers, registering the presence or absence of coffee rust, this allowed from 2007 to date to identify early and progressive the loss of resistance in the Lempira variety released in 1998 due to a low sporulation coffee rust in La Fé Peña Blanca Cortes and in 2015 the complete susceptibility of the F1 Millennium, Icatu 48 and Icatu 75. In 2017, identifying Lempira as susceptible after 17 years to be released before new coffee rust population with 5 new virulence genes (V1,4,6,7 and 9) identified by differentiating plants inoculated with coffee rust mass samples that in turn affect 20% of the IHCAFE 90 variety released in 1990, said study identified that only H27, Parainema, Centroamericano, Anacafe 14 and Batian are immune to the new coffee rust in 2017. With the exception of the H27 Susceptible in 2018 and the Centroamemricano in 2019. For the previously documented in Honduras the durability of the coffee rust resistance can vary between 8 and 25 years but the exact time can not be predicted, therefore it is necessary to increase the durability incorporating more major genes of resistance such as the SH3 gene present in Coffea liberica, consider the crossing of genera, induction of mutations and implement test crosses and study of progenies F2 as a prerequisite to the release of new resistant varieties of greater complexity of genetic resistance developed to limit the opportunities to fix pathogen mutations and the frequency of epidemic events in the coffee producing country or region.

## Audience Take Away:

- With the development of this presentation the audience will have a scientific support with field experiences of the importance of knowing the behavior of the pathogen and because the resistance is not permanently in the improved varieties, applying this knowledge to sustain the continuity of the processes of selection and search for new and better sources of resistance for future improved varieties
- This work can be considered to evaluate the level of risk of epidemics in diverse crops that have development and selection programs similar to coffee, and can implement the recommendations raised in their work
- The lessons learned in this work can be replicated by other programs and institutions where the genetic improvement of the crop is focused on genetic resistance to diseases
- This work demonstrates the most effective method to know all the diversity of virulence genes of a fungus that affects the crop, effectively identifying the susceptible genotypes and selecting in the shortest possible time the resistant genotypes that can be considered for release or the creation of new varieties resistant to future the cultivation of interest
- This work highlights the need to modify breeding schemes incorporating new sources of resistance present in other species and induced genotypes or mutations ending the work with crossings of tests and evaluation of their F2 progenies to select and release the varieties that have the greatest complexity genetics for resistance to the pathogen, reducing to the maximum possible the frequency of epidemics in the crop

## Biography

The Master of Science Yonis Morales graduated in Plant Breeding of the Antonio Narro Agrarian University Mexico 2014, he has experience in study of Genetic Diversity, association of Molecular Markers, is coordinator of the plant breeding program of the Honduran Coffee Institute, conducting research as the first study to identify virulence genes responsible for the loss of resistance to coffee rust in improved varieties, selection of resistant, early release of improved varieties, double haploid induction, giving talks in events such as the International Symposium on Plant Breeding and Induced Mutations in Vienna Austria 2018, SCAA 2018 and others.

# Seeds technologies to improve crop yielding

**Juan J. Narvaez-Reinaldo*, Estévez-Geffriaud V, Vergara-Fontova G1, Ballester J**
Seed Technology & Quality Process, Spain

Excessive nitrogen fertilization has led to a widespread problem of nitrate contamination of aquifers. For example 41% of aquifers from catalan region are contaminated by nitrates. With the aim to attenuate this problem, EU announced as a priority environmental objective to decrease the level of nitrate fertilization based on the Directive 91/676/ECC1.

Different studies have shown that the use of plant growth promoting microorganism and (among them) nitrogen fixers microorganism, they are a powerful tool to reduce the level of external & chemical nitrogen fertilization. In this sense, it is possible to find different successful experiences in the state of the art through the use of bioaugmentation (inoculation of nitrogen fixer microorganisms) and biostimulation (promotion of natural nitrogen fixer microorganisms from soils) techniques2.

Seed technology is the technical area composes by different techniques that facilitate the sowing process with the aim to improve the establishment of germinated seedlings. One of those techniques is the seed treatment or seed coating. There are different types of seed treatments: film coating (where seeds keep their original size and weight), encrusting (seeds keep original shape but suffer an increase of their weight) and pelleting (seeds becomes completely spherical and suffer a relevant increase of their weight). In all of them, it is possible to add different active substances (fertilizers, microorganisms or/and phytosanitaries)3

In the current oral communication, we present the results of two seed treatments developed by Semillas Fitó with the ability to facilitate the nitrogen fixation. The combination of FitoPower™ and FitoOptima™ by encrusting, they allow the bioaugmentation on lucerne/clover seeds with rhizobium and they ensure the nodulation of leguminous crops. On the other hand, the seed treatment named as RootMaximizer™ for broad bean seeds, it has the ability to biostimulate the natural population of rhizobium from soils and, as a consequence, to increase the final yielding.

# Endophytic *Bacillus Subtilis*-Mediated Drought Stress Tolerance in Wheat

**Oksana Lastochkina[1,2*], Liudmila Pusenkova[2], Darya Kulabuhova[2]**
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Abiotic factors leading to drought significantly limit major agricultural crops production worldwide. Under rapid growth population and climate change, it is important to ensure food security that is mainly possible through the increase of major cereal crop productivity, including wheat, commonly used for human consumption in many areas worldwide and supplying more than 50% of humanity's dietary energy. Beneficial plant growth-promoting bacterium *Bacillus subtilis* are considered as a sustainable and eco-friendly strategy to cope with the adverse effects of abiotic stresses on plants. To date, the growth-stimulating and protective effects of *B. subtilis* under different abiotic stresses have been discovered in varied plants, including wheat. The mechanisms of such physiological actions of B. subtilis on hosts are not completely understood and required detailed investigations for fully use the potential of these microbes as a component of organic agriculture to increase plant productivity. In this regard, our study is focused on the revealing and understanding the mechanisms of interaction in the systems "endophytic *B. subtilis* – host plants – abiotic stresses" leading to the increase of plant growth and tolerance. It was revealed that endophytic B. subtilis 10-4 exert a protective effect on *Triticum aestivum* L. (wheat) (Cv. Bashkirsky-26) under water deficiency which is implemented in enhancing growth of seedlings (roots and shoots), their biomass accumulation, and increasing water-holding capacity in leaves both under normal and stress conditions in compare to non-inoculated control plants. The realization of wheat drought tolerance by *B. subtilis* 10-4 is connected with the ability of the bacterium to decrease stress-induced oxidative and osmotic damages in seedlings with involving salicylate-signaling defense pathways were found. Interestingly, farther investigations allowed discovering that wheat cultivars belonging to different ecological groups (ecotypes) of Russia (namely, forest-steppe West Siberian and steppe Volga) demonstrate different drought tolerance when inoculated by the same strains of B. subtilis in the same growth conditions. In particular, *B. subtilis* 10-4 promoted better growth (seeds germination, elongation of seedlings, biomass accumulation) of the Cv. Saratovskaya-55 (representative of the steppe Volga ecotype) under the conditions of the simulated drought and, in the opposite scenario, had an inhibitory effect on the same growth parameters of the Cv. Omskaya-35 (representative of the forest-steppe West Siberian ecotype). Under the drought stress, the influence of B. subtilis on the tolerance of wheat cultivars in different ecotypes was observed at the initial stages of ontogenesis, which, apparently, is associated with different adaptation strategies used against drought by wheat having as is known a great adaptive potential allowing it to widely spread over the globe. Thus, the effects triggering by endophytic *B. subtilis* could be varied, diverse, intertwined, and often specific. Understanding the specific features of protective mechanisms implementation under the influence of B. subtilis in different ecotypes of wheat with different strategies of adaptation to drought is of great relevance. This will help to reveal the potential of *B. subtilis* and increase the productivity of wheat, growing in different ecological and geographical regions worldwide.

The reported study was funded by RFBR according to the research project № 19-016-00035.

**Audience Take Away:**

- The current state of knowledge of the fundamental physiological and biochemical mechanisms of B. subtilis-induced drought stress tolerance in wheat will be presented. The information about endophytic B. subtilis efficiency on drought tolerance induction in wheat according to their ecological groups (ecotypes) will be presented as well
- The results of work could be useful for the development of new endophytic *B. subtilis*-based biological products to protect wheat plants against abiotic stresses leading to drought and increase its yield/productivity
- The targeted audience will be provided by the information expanding the knowledge about the regulatory action of endophytic bacterium *B. subtilis* on tolerance of wheat to drought stress that could help them in their research fields, in a practical solution to challenge the stress problem and climate change

## Biography

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

# Disruption of microbial cell morphology by extracts from *Buxus macowanii*

**B Ngobeni[1], SS Mashele[1], NJ Malebo[2], E van Der Watt[3], and IT Manduna[4*]**
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[3]Department of Soil, Crop and Climate Sciences, University of the Free State, South Africa
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Microbial infections are a major cause of death all around the world. This is exacerbated to the rising costs of primary healthcare and its inaccessibility especially in developing countries. Moreover, there has been an increase in microbial strains that have reduced susceptibility to antimicrobial drugs. Research on the antimicrobial properties of medicinal plants, which may address these challenges, has become more important as they may present cheaper alternatives and different mechanisms of action. This study evaluated the antimicrobial properties of a methanolic extract from the leaves and twigs of Buxus macowanii in order to assess its potential for use in the development of novel antimicrobial drugs. Antimicrobial activity of the extract was evaluated using the broth microdilution method and electron microscopy. The detection of antimicrobial compounds was performed using the GCMS. The extract showed antimicrobial activity against all the microbial species used. Microscopic examination of the cells of B. cereus treated with Buxus macowanii showed some changes in morphology such as damage of the cell wall, swelling of the cells and incomplete cell division that eventually resulted in cell death. An antimicrobial compound, neophytadiene was detected in the extract. The results of the present study indicate that B. macowanii has antimicrobial activity due to morphological disruptions of the bacterial cell wall.

## Biography

Dr IT Manduna has a MSc in Botany (University of Fort Hare South Africa) and DSc in Botany from Colegio de Postgraduados (COLPOS, Mexico). She is an ethnobotanist with special interest in agro-processing African traditional medicine and indigenous vegetables. She has worked as a lecturer at Walter Sisulu University, South Africa and is currently a researcher in the Centre for Applied Food Sustainability and Biotechnology (Central University of Technology, South Africa).

# Production of medicinal functional rapeseed with alien chromosomes of Chinese woad

**Zaiyun Li**
Huazhong Agricultural University, China

The crucifer Chinese woad *(Isatis indigotica,* 2n=14, genomes II) is an ancient dye and medicinal plant in China. Its root *(Radix Isatidis)* is the most common and effective natural medicine for influenza, but the genetic control of its bioactive compounds and biosynthesis pathways remain to study. Through protoplast fusions between oilseed rape *(Brassica napus,* 2n=38, genomes AACC) and Chinese woad, somatic hybrids (2n=52, AACCII) were produced and backcrossed to oilseed rape, and seven alien additional lines (AALs) of oilseed rape carrying each of seven woad chromosomes were obtained. In cell culture, some AALs showed stronger inhibition to the propagation of AIV H5N6 and vesicular stomatitis virus than the woad, comparable to the NA inhibitor Oseltamivir. In mice, some MAALs still demonstrated stronger inhibition of H5N6 propagation than the woad. The expressions of most woad genes, especially some involved in the biosynthesis pathways of bioactive compounds were up-regulated. The AALs with the increased virus resistance also contained more types and higher contents of the bioactive compounds than the woad. These AALs had larger biomass than woad and provided novel vegetable for human and fodder or feed additives for livestock.

**Audience Take Away:**

- Plant Genetics and Genomics
- Plant Biotechnology
- Plant Metabolic Engineering
- The targeted audience will join the information about medicinal functional rapeseed highly resistant to viruses and the potential implications as human vegetable and animal fodder.
- I think the targeted audience will be
- Provided in new information that help them in their fields
- Provided new ideas in their research fields

## Biography

Dr. Li studied Agriculture Science at Southwest University, China and graduated as BS in Agronomy in 1983. He received his MS in Agronomy in 1988 at Nanjing Agricultural University, and PhD in Botany in 1992 at Sichuan University. He worked as post-doctor (1992-1994), Assistant Professor (1994-1999) and Professor (2000-) at Huazhong Agricultural University. He has granted many local and national projects on rapeseed. He has published more than 50 research articles.

# A Comparative Investigation On Two Different Populations of *Papaver pilosum* subsp. spicatum *(Papaveraceae)* endemic to Turkey

**Baran, P[1]*, Altan, Y**
Usak University, Turkey
Manisa Celal Bayar University, Turkey

The following points will be discussed:

- How much do the populations differ from each other morphologically?
- How much do the populations differ from each other anatomically?
- How much do the populations differ anatomically from the other investigated *Papaver* taxa and some other members of the family Papaveraceae?

This study aims to describe the morphological and anatomical characters of two different populations of *P. pilosum* Sibth. & Sm. subsp. *spicatum* (Boiss. & Balansa) Wendt ex Kadereit, which is endemic to Turkey, in detail to be able to contribute to the systematic work of that Turkish Papaver taxon and to an unbiased revision of the genus *Papaver* L. section *Pilosa* Prantl.

**How much do the populations differ from each other morphologically?**

The two populations in the present study correspond to *P. spicatum* Boiss. & Balansa var. *spicatum* and var. luschanii Fedde, respectively, described by Cullen (1965) in the first volume of the Flora of Turkey. P. *spicatum* Boiss. & Bal. has been regarded as synonym of P. *pilosum* subsp. *spicatum* by Kadereit (1996) in the last volume of the Flora of Turkey (Özhatay 2000). According to the recent treatment of the genus Papaver sect. Pilosa (Kadereit 1996), the two varieties have been combined in a new status, P. *pilosum* subsp. *spicatum.*

In this section, we will present detailed morphological descriptions by photographs, illustrations and measurements on the two populations. In order to understand how much they differ from each other morphologically, we will make a morphological comparison between the two populations under the treatments of Cullen (1965) and Kadereit (1996). The number of flower in spike-like raceme, the peduncles of flowers, the posture of peduncles, the indumentum and shape of capsules are significantly different. We think that the two populations appear different enough morphologically from each other to be evaluated in different taxonomic categories.

**How much do the populations differ from each other anatomically?**

We will present detailed anatomical descriptions of the investigated populations of *P. pilosum* subsp. *spicatum* by photographs and measurements in tables. The two populations had laticifers reflecting general characteristics of Papaveraceae family and the genus *Papaver* described by Metcalfe & Chalk (1950). However, certain anatomical differences were detected between the two populations, such as distribution of the xylem vessels in central cylinder of the roots, arrangement of vascular bundles in both the stems and the peduncles and density of trcihomes. Anatomical differences between the two populations support the morphological differences.

**How much do the populations differ anatomically from the other investigated *Papaver taxa* and some other members of the family Papaveraceae?**

In this section, we will compare the populations with the other investigated *Papaver* taxa, anatomically. There are very few anatomical studies on the genus *Papaver* in the literature. Our anatomical results are to some extent comparable with those of *P. somniferum* L., *P. rhoeas* L., *P. orientale* L., *P. dubium* L. and some other members of the family Papaveraceae. Xylem groups, pericycle, vascular bundles, hairs, stomata, mesophyll, petioles in transverse sections, laticiferous tubes, and anatomical structure of the peduncles are discussed.

**Audience Take Away:**

- Morphological Research
- Anatomical Research
- The Contribution of Morphological and Anatomical Research to Systematic Research
- Systematic Botanists should evaluate the Morphological and Anatomical Studies together in order to contribute more to the Systematic Studies
- We think the targeted audience will be
- Provided with new information that could help them in their fields
- Provided with practical solution to challenge the systematic problems
- Provided with new ideas in their research fields
- Ready to form collaborations to prepare new projects

**Biography**

Dr. Baran studied Biology at Manisa Celal Bayar University, Turkey and graduated as MS in Science of Plant Anatomy and Morphology in 2005. She received his PhD in Science of Plant Anatomy, Morphology and Karyology in 2011 at Manisa Celal Bayar University. She has been an Assistant Professor at Usak University since 2011. She has published more than 20 research articles (12 of which are SCI-indexed).

# Phytomedicinal compounds from the wild grape *Ampelocissus latifolia*

**Vidya Patni*, Deep Chhavi Anand**
Department of Botany University of Rajasthan Jaipur 302004 Rajasthan, India

*Vitaceae*, also known as Grape family has many plants with dietery, medicinal, and industrial significance. Some important medicinal plants of the family include, *Cissus quadrangularis, Cissus repanda, Cayratia trifolia, Ampelocissus latifolia* , all having various health benefits especially in bone health. Most of them are used in bone healing especially *C. quadrangularis*, which is locally known as" hadjod" meaning Bone joiner. The *in vitro* callus has been raised and maintained on MS medium supplemented with growth regulators. . The plant *Ampelocissus latifolia*, also known as wild grape has many medicinal properties and is used for curing simple body aches and fever to highly complicated disorders and bone fractures. *In vivo* and *in vitro* studies have been done in the plant and it was found to be rich in phytochemicals and metabolites. Further biochemical studies like GC-MS, FTIR and HPTLC revealed the presence of various important plant metabolites like beta-sitosterol, Campesterol, Stigmasterol, Caryophyllene, Tocopherol, Squalene, Bergamol, Behenylbehenate, Betulin, Longifolene, Ergosterol, 5-Hydroxy methyl furfural etc. The bioactive secondary metabolites such as flavonoid daidzein and terpenoid lupeol have been identified, isolated and quantified from different plant parts using HPTLC. Daidzein has been reported as both a phytoestrogen and antioxidant, and it is most often used to treat conditions affected by a decrease in estrogen levels in the body like menopause, including osteoporosis and increased risk of heart disease. These plant based estrogens are devoid of harmful side effects. Lupeol has various pharmacological activities displaying anti-protozoal, anti-microbial, anti-inflammatory, antitumor and chemo-preventive properties. Various functional groups of different activities have been identified through FTIR spectroscopy. They also possess high antioxidant and antimicrobial activity which can be correlated with their medicinal value.

### Audience Take Away:

- The techniques listed in this investigation can be used by faculty and researchers Any other plant containing phytoestrogen can be exploited for research
- Further enhancement in vitro with the addition of precursors can be done
- Academicians can adopt these techniques in teaching and Researchers can search for novel
- metabolites which may replace harmful side effects of estrogen

### Biography

Dr Vidya Patni Graduated from Stella Maris College Chennai and did her post graduation in Botany from Universiy of Rajasthan Jaipur, India and obtained a gold Medal for her first position in the University,in order of merit .She completed her PhD in Botany at the same University.She obtained the position of Associate Professor in 2008 and has published more than ninety Research papers in National and International Journals. She is also recipient of Y.S.Murthy gold Medal of Indian Botanical Society for her Research contribution in Tissue Culture.. Dr Vidya has been a council member of the Indian Science Congress Association and is an active life Member of several committees and Societies in Botany. .Besides ,she is coordinator of the University Innovation Cluster ad the IPR Cell of the University.

**In vitro** callus establishment by media composition variation can be used in teaching

The researchers and academicians can search for phytoestrogens from other plants especially Vitaceae to replace estrogen from other sources

# A slide talk with a short note on the Flora of Nepal

**Pushpa Man Amatya**
Purbanchal University, Nepal

The federal republic of Nepal is situated in the central Himalaya covering one third of its total length from east to west with the latitude of 26°22` to 30° 27` N and longitude of 80° 40` to 88° 12` E. It lies between two countries like China on its North and India on its East, South and West making it as a landlocked country. But however due to its wide variation in altitude, latitude, topography, snow fall pattern etc, it has wide variation in plant and animal distribution which is nowadays called biological diversity.

From the floristic point of view Nepal falls within two biogeographical realms: Indo Malayan and Paleo- arctic. Phytogeographically Nepal lies at the cross roads of six floristic regions – central Asiatic in the North, Sino-Japan in the east, South East Asia Malayan in the south east, Indian in the south, Sudano- Zambian in the south west and Irano-Turanian in the west. Hence the distribution of vegetation in the east is different from the west as compared to the rainfall pattern and shows their interrelationship and affinities with the floras of adjoining countries.

Hence different scientists have proposed the different types of vegetation in different periods. Here the vegetation is given in simplified form from the tropical area to the alpine and even arid areas where there is possibility of growing the mosses and lichens found on the crevices of stones.

For this many photographs of different flowering plants have been recorded along with Conifers, Rhododendrons which are available in different altitudes. Lots of wild plants with their edible, medicinal values are also described as per their vegetational zones. Rare plants which are in the record of CITES are also shown with photographs collected from the forest of temperate and subalpine zones.

**Audience Take Away:**

- The audience will learn the about the phytogeography of Nepal with respect to the growth and distribution of Himalayan flora
- One can have an idea about how the distribution of plants is dependent upon the altitude, latitude, and rainfall pattern and physiography of the country
- To discuss about use of medicinal plants and the wild Himalayan cherries like Pronus undulate, P.venosa, P. himalica

## Biography

Born on 11th March 1945. He completed M.sc from Tribhuwan University 1972. He joined Department of medicinal plants for 16 years, after teaching in different colleges and schools of Nepal from 1963 onwards. Specialized in Japanese Cherry blossoms from JICA, Tokyo 1978-1979. Introduced Bonsai and cut flowers in Nepal 1980 and Santalum album in Nepal from Srilanka in 1984. He worked in developing landscaping and gardening, Bioengineering 1986 onwards. He established private college as Kantipur Valley College -2001. He published books- flowering Cherries of Japan-1979 from JICA , Flowering cherries of Japan and Nepal- 2007, and My remembrance( A collection of about 20 articles published in Journals and other papers). And he is the member of Royal Horticulture Society (RHS) in UK, Membership Number – 19774994. Royal tutor for late Prince Nirajan of Nepal in Eton college, Winsore UK ( 1998-1999).

# Plant Tissue Culture in Azerbaijan

**Gulnara Balakishiyeva**
Grand-Agro Invitro LLC, Azerbaijan

In vitro plant propagation allows obtaining in several crops a higher reproduction rate than the classic vegetative propagation methods. Micropropagation enables vegetative production of large numbers of plantlets in a short period of time. It permits to reduce the surface of the area designated for producing the mother plants and for rooting the cuttings. Moreover, it produces in principle vigorous and healthy propagules. In addition, in vitro rooted clones could be more easily transported and shipped abroad due to its sterility. The most common method is axillary branching in which multiplication is achieved by forced outgrowth of axillary buds into new shoots. In Europe, the production of high-quality fruit varieties and rootstocks from commercial micropropagation accounts for over 70 million plants per year. France, Spain, Italy, and Greece are the main producers. Micropropagation, however, is highly labour oriented and, for this reason, outsourcing of in vitro plant production is shifting today to other European countries, having a lower production cost, such as Check Republic, Romania and Turkey. In Azerbaijan, plant tissue culture research is conducted mainly by the universities and also by governmental agricultural research institutes. Our company is the first in Azerbaijan, which is commercially related with plant tissue culture issues. Our plant tissue culture production laboratory has a very modern infrastructure. There are cutting room equipped with 10 sterilized laminar cabin, 3 incubation rooms with 4 million plant capacity and research and development unit performing various projects and the research findings generated by this laboratory every year reveals the quality of the work done in the plant tissue culture laboratory. Our staff has knowledge and experience to overcome the technical difficulties that may be encountered in tissue culture works from the sterilization stage to the rooting stage. The attention of our company is directed towards the modernization of laboratory equipment, the improvement of protocols of economically important species with low proliferation and/or rooting potential, the efficient conservation of shoot cultures in slow growth storage, aimed to increase the laboratory offer of species and cultivars. The development and rapid multiplication of new selected cultivars are required to meet the demand of consumers all year round.

## Biography

Dr. Gulnara Balakishiyeva studied Biology at the Baku State University, Azerbaijan and graduated as MS in 2006. She obtained PhD degree in Molecular Biology in the frame of the collaboration between Department of Fundamental Problems of Biological Productivity, Institute of Botany, NAS of Azerbaijan and UMR-1332 Biologie du Fruit et Pathologie INRA – Université de Bordeaux, France. After the completion of PhD research, she came back to Azerbaijan where she is currently engaged at the Grand-Agro Invitro LLC in Baku, as Laboratory Production Team Leader. She has published more than 30 research articles in different SCI(E) journals.

# Impact of oxidative stress on plant proteins modifications: relevance for plant allergens

**Katarina Smiljanic, Jelena Mihailovic, Teodora Djukic, Tanja Cirkovic Velickovic***
University of Belgrade–Faculty of Chemistry, Centre of Excellence for Molecular Food Sciences, Belgrade, Serbia;
Ghent University Global Campus, Incheon, South Korea; Ghent University

Novel tools are needed in order to address an important issue of how environmental pollution affects the structure and functionality of plant proteins. The impact of pollution and environmental oxidative stress, as well as heating at the molecular level have been studied by means of quantitative proteomics and global profiling of post-translational and chemical modifications by mass spectrometry and immunoblotting.

An increased phenolic content and release of sub-pollen particles was found in pollen samples from the polluted area, including a significantly higher content of mercury, cadmium, and manganese, with irregular long spines on pollen grain surface structures. Antioxidative defense-related enzymes were significantly upregulated and seven oxidative PTMs were significantly increased (methionine, histidine, lysine, and proline oxidation; tyrosine glycosylation, lysine 4-hydroxy-2-nonenal adduct, and lysine carbamylation) in pollen exposed to the chemical plant and road traffic pollution sources. Oxidative modifications affected several Timothy pollen allergens; Phl p 6, in particular, exhibited several different oxidative modifications. The expression of Phl p 6, 12, and 13 allergens were downregulated in polluted pollen, and IgE binding to pollen extract was substantially lower in the 18 patients studied, as measured by quantitative ELISA. Quantitative, unrestricted, and detailed PTM searches using an enrichment-free approach pointed to modification of Timothy pollen allergens and suggested that heavy metals are primarily responsible for oxidative stress effects observed in pollen proteins.

High temperature of roasting of peanut proteins results in several modifications of amino-acid residues that could be detected by mass spectrometry and immunoblotting. The most prominent allergen in peanut found to undergo several modifications was Ara h 1, a storage protein of peanut.

The results show that there are qualitative and quantitative differences in modifications of amino-acid residues of relevant plant allergens (relevant in respiratory and food allergens) in response to external stimuli and in relation to the level of inorganic and organic pollutants, as well as high temperature heating (in case of food roasting). The most frequently found modifications are oxidative modifications of amino-acid residues. Those modifications can affect IgE binding, as well as digestibility, processing and uptake of plant proteins in human digestive tract.

# Plant tissue culture as a tool in Papaya breeding

**Blanca Moreno*, Cuauhtemoc Navarro**
[1]R&D Plant tissue culture, NSIP, Frontera Hidalgo, Chiapas, México
[2]Director, In Vitro Division, Frontera Hidalgo, Chiapas, México

The increases in world food demand due to population grow and climate change necessitates the continuous genetic improvement of crop species. Moreover, for maximal effect in perennial species, this genetic improvement must be integrated with the latest high throughput in vitro propagation techniques. Mexico is the third largest producer and the number one exporter of papaya worldwide. We report herein the application of latest genetic and in vitro propagation technologies to facilitate both short- and long-term genetic improvement of this crop. Traditionally, papaya has been propagated by seeds. However, there are three drawbacks to seed propagation: 1) genetic heterogeneity (unless the varieties have been inbred for many generations, which is time consuming). 2) segregation of sex chromosomes in seed propagated papayas resulting in different morphological forms: males, females, and hermaphrodites. This is problematic in that only the hermaphroditic plants produce fruit of the size, shape, weight and quality desired by consumers. Consequently, all non-hermaphrodites must be manually removed from commercial plantings. 3) papaya seeds have relatively short viability, requiring frequent regeneration of seed inventories. Working with Agromod-Frescos, NSIP has developed and deployed a genetic improvement strategy for papaya for which in vitro propagation plays a central role. Specifically, we have pursued three goals. (1) Development and testing of a reliable micropropagation protocol for commercial production. In a pilot project we have produced more than 70,000 clonal plants of elite genotypes via shoot tip organogenesis that, when trialed, produced 100 % hermaphroditic, homogeneous, virus free plants (2) Development of an embryo rescue technique to produce interspecific hybrids from embryos harvested from 30 to 90 days after-pollination resulting in F1 clones via somatic embryogenesis or in vitro germination for field evaluation of morphology traits, resistance or tolerance to virus and fertility. (3) Development of cryopreservation protocols allowing the long-term preservation of genetic diversity in papaya. In this regard, we have made extensive collections of both wild and cultivated papaya germplasm worldwide, DNA sequenced (GBS) the materials, and used NSIP's optimization algorithms to define Optimized Core Collections that capture the majority of both allelic and haplotype diversity in papaya worldwide. Cryopreservation methods were developed and tested for both shoot tips and embryogenic calli, which were tested to determine their regeneration and normal development in response to different cryopreservation techniques: vitrification and slow freezing methodologies. By combining new breeding methods with the in vitro methods described herein we anticipate both an increase in the rate and efficiency of genetic improvement in papaya.

*Keywords: Carica papaya L.,* micropropagation, organogenesis, somatic embryogenesis, embryo recue, cryopreservation.

**Take Away Notes:**

- The audience would be seeing the wide application and advantages of plant tissue culture, as can be develop new strategies to the breeding process
- Papaya micropropagation
- They could be considering whatever issues for scaling up the micropropagation

**Biography:**

MS. Blanca Moreno studied Biotechnology at the UNACH, Chiapas University, Mexico and graduated as MS in 2011. She then joined the Company AGROMOD in Micropropagation and Greenhouse group. She received her master's degree in 2011 at the CICY, Research Center. After 5-year research fellowship supervised by Dr Navarro at the micropropagation Laboratory, she obtained the position as R&D plant tissue culture Manager at NSIP (before AGROMOD).

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