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Linthicum Heights

MD 21090, USA



DAY-1

MONDAY, March 04, 2019

Keynote Presentation

Genomic Resources for Environmental Resilience and Species Restoration in Hardwood Forest Trees

John E. Carlson

Pennsylvania State University, Pennsylvania, PA

Abstract

Hardwood tree species in temperate forests, plantations, and urban plantings have been under assault for well over 100 years, due to accelerating threats from invasive insects, plants and microbes, pollution, climate change, and overharvesting. These forest health issues have resulted in major ecological disasters and general decline of ecosystem services required from temperate forests. This has presented an urgent need for tools to inform and accelerate tree management, improvement and reforestation efforts. In response, a concerted effort is underway to develop genetics and genomics resources to enable in-depth genome-wide investigations into forest health issues. In this presentation, an overview is provided of the genomics resources available, and underway, for a wide phylogenetic distribution of hardwood trees, the gaps remaining, and examples of how these resources are being brought to bear on addressing forest health issues.

Biography

John Carlson is a Professor of Molecular Genetics and Director of the Schatz Center for Tree Molecular Genetics at Pennsylvania State University. Dr. Carlson was a pioneer in molecular genetics with forest trees. He has contributed over 140 peer-reviewed papers in Genomics (transcriptomics, EST databases, DNA marker development, genetic linkage mapping, genome sequencing, metagenomics), Biotechnology (micropropagation and genetic engineering), and Conservation Genetics with forest trees, wildlife and bioenergy plants. He has held Visiting Professorships at Chonnam National University in South Korea, the Northeastern Forestry University in China, the Hong Kong University of Science & Technology, and Beijing Forestry University.

Circadian Regulation of Plant Innate Immunity

Hua Lu

University of Maryland - Baltimore County, Baltimore, MD

Abstract

Many living organisms on earth have evolved the ability to integrate environmental and internal signals to determine time and thereafter adjust their metabolism, physiology, and behavior. The circadian clock is the endogenous timekeeper critical for multiple biological processes, including responses to daily invasions by pathogens and pests in many organisms. A growing body of evidence supports the importance of the circadian clock for plant health. Plants activate timed defense to anticipate attacks of pathogens and pests with different lifestyles. Pathogen infection is also known to reciprocally modulate clock activity. Such a crosstalk likely reflects the adaptive nature of plants to coordinate limited resources for growth, development, and defense. I will report our recent progress in understanding of molecular basis underlying the crosstalk between the circadian clock and defense.

Biography

Hua Lu received her PhD in Biology from Texas A&M University in 1999. She joined UMBC as an Assistant Professor in 2006 and she is now a Full Professor. Her research focuses on elucidation of mechanisms of plant disease resistance. Her laboratory has identified a number of genes important for defense and revealed crosstalk between plant defense and other biological processes, including cell death, cell cycle progression, plasmodesmata function, alternative splicing, flowering time control, and the circadian clock. She is a dedicated teacher who provides mentoring to students inside and outside of the

classroom. She also contributes to the professional society by serving as editor and/or reviewer for international journals and funding agencies.

Innovative Forage-Based Management Systems for Producing Grass-Fed Beef

C. P. Bagley

Tennessee Tech University, Cookeville, TN

Abstract

Livestock markets in the US have primarily been focused on grain-fed, well-marbled beef products. Most lands in the US are more suited to forage production than to row crop and feed grain production. Further, feeding grains to livestock, and particularly to beef cattle (conversion rate of approximately 6 : 1 grain to beef), reduces potential food sources to the human population, a situation becoming more serious with increasing human population and demands for inexpensive food grains. An increasing number of customers are demanding “grass-fed” beef with the perception of this meat being more nutritious, natural, and environmentally friendly to produce. Several studies have proven the efficiency of grass-fed beef; however, newer forage species and greater knowledge of cattle genetics will allow us to even better match livestock genotypes to forage species as genetic studies have shown certain animal genotypes are more efficient on certain forages than are others. Additionally, spatial technologies allow us to begin to be able to “locate” and track cattle actively grazing. Lastly, newer by-product feeds that are not suitable for human consumption are becoming widely available as starch is extracted from corn for other purposes, generating millions of tons of these by-product feeds that can be supplemented to forage-based grazing during times of limited forage availability. Typically, consumers will not purchase frozen beef, creating the need for year-round grass-fed beef availability. Grass-fed beef with minimal by-product feeding can help meet world beef demands in an environmentally sustainable, consumer friendly production system.

Biography

C. Pat Bagley graduated from Virginia Tech University with a Ph.D. in Animal Science, and minor in Agronomy. His research career started with LSU, and is now with Tennessee Tech University. His research work has primarily focused on forage-based management systems for the efficient production of beef. Increasingly, there is more focus on forage-based, grass-fed beef using newer technologies; spatial technologies: improved forage species; and matching livestock genotypes with new forage selections. He has taken students on study-abroad trips to many Central and South American countries, and is taking his 14th group to Mexico in January, 2019.

Featured Presentations

Alternative Splicing is Crucial for Plant Abiotic Stress Responses

Jianhua Zhu

University of Maryland, College Park, MD

Abstract

Plants are sessile organisms and they have to cope with various ever-changing environmental abiotic stress conditions such as cold, heat, and soil salinity. In an effort to identify and characterize key genes for plant abiotic stress responses, we performed several forward genetic screens for mutants with altered responses to abiotic stress conditions. Three of the genes we identified through the forward genetic analyses encode proteins that are part of the spliceosome for alternative splicing. First, Regulator of CBF Gene Expression 1 (RCF1) is a DEAD box RNA helicase. We showed that RCF1 is essential for pre-mRNA splicing and is important for cold-responsive gene regulation and cold tolerance in plants. Second, Regulator of ABA Response 1 (ROA1) is a close ortholog of the human splicing factor RBM25. Our results indicated that RNA splicing is of particular importance for plant response to the phytohormone ABA and that the splicing factor ROA1/AtRBM25 has a critical role in this response. Third, the U1 small nuclear ribonucleoprotein complex protein AtU1A has a critical role as a regulator of pre-mRNA processing and salt tolerance in plants. In summary, we showed in our genetic analyses that alternative splicing is crucial for plant response to abiotic stress conditions.

Biography

Jianhua Zhu has completed his PhD at the age of 29 years from Purdue University, USA. He is the director of Plant Science Graduate Program and an Associate Professor in the Department of Plant Science and Landscape Architecture at the University of Maryland-College Park, USA. Currently, his research interests include elucidation of the molecular mechanisms by which plants cope with environmental adverse conditions such as cold, heat, drought, and soil salinity. He has 46 publications that have been cited over 5800 times, and his publication H-index is 32 and has been serving as an editorial board member of several reputed Journals.

Divergent Evolution for Fruit Chemistry in *Vaccinium*: Blueberry versus Cranberry

Nicholi Vorsa

Rutgers University, New Brunswick, NJ

Abstract

In many plant species, fruit serves as a vehicle for seed dissemination. In the genus *Vaccinium*, seed dispersal in blueberry is largely animal dispersed, whereas cranberry may have utilized water as a vehicle as well. The morphology and chemistry of *Vaccinium* fruit appears to reflect these various seed dispersal strategies. As a consequence, the evolutionary influences for seed dispersal have likely led to the fruit of *Vaccinium* species, particularly blueberry and cranberry, to be recognized for their potential to benefit human health due to being a rich source of phenolic compounds, especially the flavonoids. Three major *Vaccinium* flavonoid classes, anthocyanins, proanthocyanidins and flavonols are recognized as potent anti-oxidants, and may provide benefit to cardiovascular, urinary tract, and cognitive health, as well as having anti-aging properties. Cranberry has a higher content of both proanthocyanidins and flavonol glycosides than blueberry with largely A-type proanthocyanidins whereas in blueberry they are principally B-type. Quercetin and myricetin are the principal flavonol aglycones with galactoside as the principal sugar conjugate. Blueberry has a more diverse profile of anthocyanins in both aglycones and sugar conjugates. Cranberry has a higher level of organic acids including citric, malic, and quinic acids, while domesticated blueberry has principally citric acid. Other blueberry species have shikimic and quinic acids, and but lack citric acid. Cranberry is also unique in having benzoic acid. The species also contrast in their volatiles with blueberry having 'fruity' aldehyde, ketone and alcohol volatiles, e.g., linolool, whereas cranberry's principal volatile is 1- α terpineol.

Biography

Nicholi Vorsa received a BS from Rutgers University (1976), a MS degree (1978), and a PhD from Rutgers University (1985). He is Professor of Plant Biology, Rutgers University and Director of the PE Marucci Center, New Jersey AES. Dr. Vorsa's two major areas of research are genetic enhancement of blueberry and cranberry and the study of natural products in relation to human health. He has published extensively on cranberry genetics and published the first genetic map of cranberry. Currently his areas of focus areas are cranberry genomics, genetics of phytochemicals, fruit rot resistance breeding. He has eight patents.

The Use of Visual Markers to Aid in the Identification of CRISPR-Cas9 Multiplex Edited Plants

Cristian H. Danna* and Renyu Li

University of Virginia, Charlottesville, VA

The development of DNA editing tools to target specific genes has been a major breakthrough in plant biology in the past 10 years. *Arabidopsis thaliana*, despite being the second multicellular organism, and first plant, to have its genome fully sequenced in 2000, was not suitable for gene targeting until recently. Since 2013, CRISPR/Cas9 has been successfully used in *Arabidopsis* and other plant species for targeted mutagenesis. Despite the high specificity and ease of use of CRISPR/Cas9, the identification of edited individual *Arabidopsis* plants has remained difficult, particularly when multiple genes are targeted simultaneously. A typical selection protocol for CRISPR-Cas9 edited plants involves the screening of a large number of plants via PCR-sequencing and/or PCR amplification coupled to restriction endonucleases digestion of the targeted genomic DNA. To circumvent this problem, we have developed and successfully tested a strategy for the rapid identification of CRISPR-Cas9 edited *Arabidopsis* plants via the co-editing of a positive selection marker that is visually observable. This selection strategy facilitates the identification of CRISPR-Cas9 multiplex edited plants with low effort and low cost.

Epigenetic Variability among Saffron Crocus (*Crocus sativus* L.) Accessions Characterized by Different Phenotypes

Matteo Busconi¹, Licia Colli¹, Giovanna Soffritti¹, Marcello Del Corvo¹, Silvia Fluch², Elisabeth Wischnitzki², Eva Maria Sehr², Marcelino de los Mozos Pascual³ and Jose Antonio Fernandez⁴

¹*Catholic University of the Sacred Heart, Italy*

²*Austrian Institute of Technology GmbH, Austria*

³*Centro de Investigación Agroforestal de Albaladejito, Spain*

⁴*Universidad de Castilla—La Mancha, Spain*

Abstract

Saffron (*Crocus sativus* L.) is a sterile triploid a growing number of evidences support allopolyploidy as the most probable mechanism to have occurred. The crop vegetatively multiplies year by year by means of corms that does not generate genome variations with the exception of some spontaneous mutations that in a triploid saffron population are not easily detectable. In a characterisation of saffron accessions of the WSCC (World Saffron and Crocus Collection, Cuenca, Spain), characters related to phenology (date of sprouting and flowering), floral morphology (length of tepals, length of stamens, filaments and anthers) and saffron production (percentage of flowering corms, saffron spice weight per flower) were measured and a big variation detected. This raises the question about the origin of such phenotypic variability, and epigenetic variation could be a possible answer. In order to have a deeper insight in the epigenetic of saffron, the analysis of the DNA methylation among saffron accessions preserved in the WSCC collection was carried out by Methyl Sensitive AFLPs coupled with high throughput sequencing. The selected accessions had various geographic origin, different phenotypes and extremely low genetic variation. Despite of this, high epigenetic variability in DNA regions associated with gene expression was detected. Finally, the epigenetic stability of 17 WSCC accessions was followed during four consecutive years under open field conditions evidencing that, despite the cultivation in the same field, each accession maintained an epigenotype clearly different from the other accessions and just small intra-accession variability was detected suggesting a high stability of Saffron epigenome.

High-density Map Construction and QTL Identification for Horticultural Traits in a Diploid Blueberry Biparental Mapping Population

Lisa J. Rowland^{1*}, Xinpeng Qi¹, Elizabeth L. Ogden¹, Massimo Iorizzo², Daniel J. Sargent³, Hamed Boston² and Judson Ward⁴

¹United States Department of Agriculture, Beltsville, MD

²North Carolina State University, Raleigh, NC

³Driscoll's Genetics Ltd., United Kingdom

⁴Driscoll's Genetics Ltd., Watsonville, CA

Abstract

We previously constructed an F₁ interspecific mapping population of diploid blueberry by crossing the parent F₁#10 (*Vaccinium darrowii* Fla4B × diploid *Vaccinium corymbosum* W85-20) with the parent W85-23 (diploid *Vaccinium corymbosum*). Employing a Capture-Seq technology developed by RAPiD Genomics, with emphasis on probe design in predicted gene regions, 117 F₁ progeny, two parents, and two grandparents of this population were sequenced, yielding 138.64 Gbp raw sequenced reads. A total of 143,313 SNPs referenced to 7,162 blueberry genome scaffolds were called and filtered to arrive at a set of 81,067 high quality SNPs, which were then subjected to a parental-dependent sliding window approach to further genotype the population. Deduced bin markers were used to construct linkage maps using OneMap, and genetic distances were calculated by Kosambi's mapping function. As a result, twelve blueberry linkage groups (LGs) consisting of 3,090 bin markers were obtained, spanning a total genetic distance of 1107.69 cM, with the largest LG of 146.56 cM and the smallest LG of 32.48 cM. The population was evaluated for several horticultural traits, including important fruit quality (fruit color, scar size, firmness, flavor, and weight) and plant traits over multiple years, and a QTL analysis was performed. Significant QTL were identified for chilling requirement, cold hardiness, fruit color, scar size, and date of full bloom.

Biography

Rowland has been a scientist with the USDA-ARS for over 30 years. Her research interests in the Genetic Improvement of Fruits and Vegetables Laboratory are focused on molecular genetics and genomics of blueberry. The areas of research include transcriptome sequencing, development of molecular markers, use of molecular markers in construction of genetic linkage maps and identification of markers linked to horticulturally important traits. Furthermore, her laboratory conducts gene expression studies to identify genes associated with chilling requirement, cold hardiness, and fruit quality.

Cloning, Utilization and Protection of Pm21 Conferring Broad Spectrum Resistance to Wheat Powdery Mildew

Tongde Bie^{1*}, Huagang He², Shanying Zhu², Renhui Zhao¹, Zhengning Jiang¹ and Tiantian Chen¹

¹Yangzhou Academy of Agricultural Sciences, China

²Jiangsu University, China

Abstract

Genetic and breeding studies have shown that *Pm21*, originated from the wheat wild relative *Dasypyrum villosum*, confers broad-spectrum resistance to all reported isolates of the wheat powdery mildew pathogen *Blumeria graminis* f. sp. *tritici* (*Bgt*). The wheat-*D. villosum* translocation line T6VS.6AL carrying *Pm21* has been widely applied worldwide, and about forty varieties carrying *Pm21* were released in China. However, due to the lack of recombination between the *D. villosum* chromosome 6VS carrying *Pm21* and its wheat homoeologous counterpart, it has been very difficult to isolate *Pm21* in wheat background by map-based cloning strategy for many years. Thanks to the discovery of powdery mildew-sensitive *D. villosum* accessions, recently, *Pm21* was successfully cloned via map-based strategy and identified to encode a typical CC-NBS-LRR protein and confer broad spectrum resistance to powdery mildew, which was supported by VIGS, larger-scale mutagenesis, transgenic verification, and inoculation with diverse *Bgt* isolates. Interestingly, evolutionary analysis revealed that *Pm21* is a conserved gene in Triticeae, but all of its orthologs in wheat and closely related species lost resistance. This reinforces the value and importance of *Pm21* in improving the *Bgt* resistance of wheat crops. However, due to the overusing of *Pm* genes such as *Pm2*, *Pm4*, *Pm8*, have lost resistance to *Bgt* in many parts of China. So, as a classic RGA-like gene, will *Pm21* also be overcome by new evolved *Bgt* isolates? How can we protect *Pm21* in practical wheat breeding and production? We will discuss and give our suggestions.

Biography

Tongde Bie, head of wheat genomics and molecular breeding team, Yangzhou Academy of Agricultural Sciences, graduated from Nanjing Agricultural University with a doctorate of science in 2007, is now mainly engaged in wheat resistance gene discovery, cloning, marker development and molecular breeding work.

Gene Expression of Coffee Miraculin-like Genes in Response to Plant Stress

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³Institut de Recherche pour le Développement (IRD), France

⁴Universidade do Rio Grande do Sul, Brazil

Abstract

The root-knot nematode (RKN) *Meloidogyne incognita* is considered one of the most economically harmful pathogens to worldwide agriculture and devastating to coffee plantations. Genetic improvement strategies for introgression of R genes result in a breakdown of resistance, whereas nematocidal chemicals are considered to be inefficient or toxic. In previous works, we observed that a gene homologous to miraculin was overexpressed at 5 and 6 days after infection in coffee roots resistant to *M. incognita*. Samples of these roots were sequenced by RNAseq Illumina HiSeq 4000, generating more than 800 million length readings of 2x100 nt. Differential *in silico* expression analysis and GO enrichment results indicate that some gene families are strongly deregulated in the resistance response. Fourteen superexpressed genes of Kunitz type family protease inhibitors (PIs), similar to miraculin, have been identified. The evidence to date is that miraculin must be important in responding to coffee stresses, because the *CoMir* miraculin gene is overexpressed by the attack of the coffee beetle (*Leucoptera coffeella*). The present study shows the real-time expression analysis of the miraculin-like genes in coffee and the correlation of their expression patterns to other biotic or abiotic stress responses. These genes may be important actors in the coffee immune response and may be potentially used in biotechnology approaches for the control of nematodes and pests.

Biography

Erika Albuquerque has completed her PhD. at the Science Faculty of Université de Montpellier II - France and postdoctoral studies in nematode genomics at INRA (Sophia Antipolis - France). Currently working as principal investigator at the Brazilian Agricultural Research Corporation. She conducts research in phytopathology researching plant-pest interactions, especially with nematodes and insects. She has experience in the field of Biochemistry, with emphasis in Molecular Biology, studying mainly the following subjects: genomic, transcritômica, functional validation of genes, silencing by interfering RNA, genetic transformation of plants, genetic editing of plants.

The Abyssinian Pea (*Pisum sativum* ssp. *abyssinicum*) Appears to Have Been Produced from *P.s. ssp. elatius* x *P.s. ssp. sativum* Hybridization

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Abstract

The origin of the Abyssinian pea (*Pisum sativum* ssp. *abyssinicum*) has been a topic of considerable discussion since the taxon's scientific recognition in the early 1900s. It is cultivated in the Ethiopian highlands and Yemen, is not known from the wild, possesses a karyotype distinct from other domesticated forms, and exhibits reduced sterility in crosses with both domesticated and most wild peas. The taxon displays very little genetic variability, suggesting that it is of recent (<4000 years ago) origin and leading some to propose that the Abyssinian pea is of hybrid origin. We tested this hypothesis by

examining mitochondrial, plastid and nuclear DNA markers in a wide range of domesticated and wild *Pisum* germplasm. The results allowed a clear rejection of the possibility that this taxon was the immediate product of a *P. fulvum* x *P. sativum* hybridization, currently the most widely accepted hypothesis. Instead, the taxon appears to have been generated by the cross *P. sativum* ssp. *elatius* x *P. sativum* ssp. *sativum*, with the *elatius* germplasm being closely related to several accessions collected in Israel. These *elatius* accessions are some of the few with cytoplasmic markers identical to those characterizing *P. fulvum*. Hence, the previously observed similarity between certain markers in the Abyssinian pea and *P. fulvum* is most like due to a distant relationship through the maternal lineage.

“CANARY: A Rapid Technology to Help your Diagnostics Sing”

Andrew Flannery

Path Sensors Inc., Baltimore, MD

Abstract and Biography not Available

Integration and Visualization of Multi-Omic Data in Grapevine

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Abstract

It is now generally accepted that the analysis of a single level of biological information is not sufficient to achieve a deep understanding of the regulation of complex traits. Integrating data generated from multiple ‘omics’ provides a better view on how plants modulate their response to different environments. Difficulties arise when attempting to integrate large data sets, especially from non-model organisms such as grapevine (*Vitis vinifera*). One of the barriers hampering the use of multi-omic approaches is the high level of programming skills required to conduct such analyses. The development of user friendly analytical and visualization tools can help in overcoming these difficulties, by providing a interface in which the results from data integration can be visualized. The use the shiny framework on the programming language R allows for the methods used for data integration and co-visualization to be embedded within a visual analysis tool which any researcher can use without the need of coding expertise. Here the multi-omic analysis platform *InteGRAPE* (β-version) is presented. *InteGRAPE* permits for multi-omic data to be integrated and visualized through interactive plots. To showcase this tool, we present a case study integrating epigenetic (DNA methylation) and gene expression data within the context of 32 environmental variables and 35 phenotypic traits retrieved from 22 commercial vineyards planted within 6 sub-regions of the Barossa Wine Growing Region in South Australia.

Biography

Lopez graduated in Biology (Botany) at the University of La Laguna (Spain). Carlos did his postgraduate studies (MSc and PhD) at the University of Reading (UK). Since then he has worked as a Post-Doc in the IBV-CSIC (Spain), RJB-CSIC (Spain), Aberystwyth University (UK) and the University of Adelaide (Australia). Dr. Lopez currently leads the Environmental Epigenetics and Genetics Group at the Department of Horticulture, University of Kentucky (USA). His current research is focused in the field of environmental genomics including plant/microbiome and epigenome/environment interactions in crop and wild species. Carlos is also interested in biomarker discovery for human health, and agriculture.

Effect of Mercury on Pollen Germination and Tube Growth in *Lilium Longiflorum*

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²Istanbul University, Turkey

³University of Life Sciences in Lublin, Poland

Pollen development and germination was adversely affected by the presence of Mercury, whereas low concentrations germination stimulated the germination. Mercury caused morphological anomalies during the tube growth, characterized by irregularly increasing diameters and swelling tips. The main effect was the anomalous cell wall formation at the tip where a great number of organelles were found reducing the secretory vesicles. The dense organelle concentration caused a significant reduction of cytoplasmic movement integrity and the cytosol streaming was gradually reduced or stopped completely. Electron dense, multilamellar myelin-like structures (MMS) of membranous material were frequently present, in close contact with plasmalemma or away from it. A loose network of fibrillar material and spherical aggregates mostly at the tip region were observed which progressively were loosened into the surrounding medium. Elevated Mercury concentrations can affect plant reproduction, resulting in anomalies in gamete development and consequently loss of plant biodiversity.

Explanations for *Amaranthus retroflexus* Growth Suppression by Cover Crops

Judith Wirth* and Aurelie Gfeller

Agroscope, Switzerland

Abstract

Many growing cover crops successfully suppress weeds. Weed control can be due to resource competition and/or allelopathy and is often associated to CC biomass development and subsequent shading, but for certain CC other factors might be implicated. We therefore studied the factors responsible for amaranth (*Amaranthus retroflexus*) growth suppression by different cover crops (CC).

In field trials with two shading levels amaranth biomass was similar, demonstrating that light interception by CC was not the primary mechanism responsible for growth suppression. Below a threshold of 3 t/ha of CC biomass, amaranth growth suppression was negatively correlated with CC biomass ($R^2=0.41$) and this correlation was influenced by the CC species. Brassicaceae and black oat (*Avena strigosa*) did not follow this relation and effectively controlled amaranth even with a low biomass.

The effects of root interactions between amaranth and CC on amaranth growth were tested in the absence of resource competition under controlled conditions. Buckwheat suppressed growth of different weeds without physical root interactions, probably through allelopathic compounds. Root exudates were obtained from buckwheat (BK), pigweed (P) and a buckwheat/pigweed mixed culture (BK-P). BK-P root exudates inhibited pigweed root growth by 49 %. Metabolomic analyses of root exudates revealed that BK and BK-P had a different metabolic profile, suggesting that buckwheat changes its root exudation in the presence of pigweed indicating heterospecific recognition. Our findings might contribute to the selection of crops with weed suppressive effects for sustainable weed management.

Biography

Judith Wirth studied agricultural sciences at the TU Munich and at the University of Hohenheim in Germany. Subsequently she did a PhD at the INRA in France in the area of molecular plant physiology and a postdoc at the ETH in Switzerland with iron-biofortified rice. Since 2010, she is head of the research group Herbology in Field Crops and Viticulture in the research division Plant-Production Systems at the Swiss federal research station Agroscope. Her research interests are weed control through allelopathic cover crops, invasive plant species in agriculture and herbicide resistance. Moreover she is implicated in efficacy evaluation of herbicides.

Adding Locally Derived Effective Microorganisms (LEM): Effect on Soil Functions, Plant Stress and Wheat Grain Nutrient Density in Two Organic Systems

Dorcas Franklin¹, Kishan Mahmud¹, Laura Ney¹, Miguel Cabrera¹, Mussie Habtesslassie², Thomas Ducey³, Subash Dahal¹ and Anish Subedi¹

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²University of Georgia, Griffin, GA

³Coastal Plain Soil, Water and Plant Conservation Research, Florence, SC

Abstract

Soils are foundational to growing healthy plants and healthy biodiverse soils may have a more sustained ability to provide micro and macro plant nutrients. Adding bio-inoculates to improve soil and composting manures is becoming of more interest to organic and conventional producers. In these studies, we used composted organic broiler litter fortified with two bio-inoculants and a control (water only). The bio-inoculants were: 1) locally derived microbial inoculant (LEMs; predominantly *Bacilli*, *Pseudomonales* and *Rhizobiales*), 2) False-LEM; predominantly *Lactobacillaceae*. Our goal was to determine the potential of LEM and F-LEM to improve soil functions in Red Turkey hard winter wheat (*Triticum aestivum*) grain grown under two rotation systems, receiving different amounts of tillage as well as different amounts of fertilizer. Soil functions measured were: a) provisioning of plant available N, P, and other nutrients such as Ca, Mg, and Zn density in grain, b) resistance to stress and sensitivity to rotational management using soil nematode trophic level communities as a measure, and c) wheat yield. The nematode community structure-trophic index indicated that in the more stressed system, soils where LEM was applied had more complex food webs. In LEM treated wheat plots, for both systems, we found greater soil biodiversity in phosphorus solubilizing bacteria and nitrogen-utilizing bacteria and greater nutrient density in wheat grain in both cropping systems. Calcium and Zinc content in wheat grain was significantly greater ($P < 0.05$) in LEM treated plots even though there were no significant difference in the wheat biomass and yield between treatments for both systems. This indicates that these inoculums can build resistance to stress and improve nutrient density in both cropping systems.

Biography

Dory Franklin is a soil scientist working toward the development of more sustainable farming systems, healthy soil and clean water. Her participatory research in grass and crop systems focuses on retaining and recycling nutrients with management practices for better farm success. She is currently focused on bio-management to improve plant nutrient density and quality. She and her graduate students are exploring management practices such as strategic placement of farming equipment and farm inputs to distribute nutrients were needed and bio-inoculates to improve compost carbon, nitrogen, and phosphorus ratios and plant availability of nutrients in manures. She teaches Sustainable Agriculture Management from an agroecological perspective and an understanding of soil biology and morphology, nutrient balances and reduction of agricultural wastes.

Real Time Bacterial Chemotaxis in the Rhizosphere

Gladys Alexandre* and Lindsey O'Neal

The University of Tennessee, Knoxville, TN, USA

Abstract

Rhizosphere plant-microbe associations are diverse, spatially and temporally dynamic and are critical to plant health and crop productivity. Bacterial motility and chemotaxis are traits predictive of competitiveness in the rhizosphere and promote root surface colonization, in a range of plant-microbe associations. Here we describe novel tools and their application to the visualization of bacterial chemotaxis and root surface colonization in real time, over up to a week. We use the soil and plant-growth promoting bacterium alphaproteobacterium *Azospirillum brasilense* to track bacterial chemotaxis in the rhizosphere of wheat and alfalfa. Using novel assays and specific mutants, we show that *A. brasilense* displays positive chemotaxis to some regions of the roots and distinct negative chemotaxis to others and that this response pattern varies with the plant considered. Using a chemotaxis receptor mutant we also identify a major chemoattractant that modulates chemotaxis and surface colonization of wheat. We also establish that the chemotaxis response to the rhizosphere mirrors the subsequent colonization pattern of the root surfaces in *A. brasilense* and extend these observations to other motile soil bacteria.

Biography

Gladys Alexandre is a Professor in the Biochemistry & Cellular and Molecular Biology Department at the University of Tennessee, Knoxville. Her research addresses the molecular mechanisms of bacterial chemotaxis in species with multiple chemotaxis systems and their roles in plant-microbe associations. Her group has established the soil bacterium *Azospirillum brasilense* as a model to understand chemotaxis in soil and plant-associated bacteria. Alexandre and colleagues have identified several strategies by which motile bacteria couple metabolism with chemotaxis. Her research has been continually funded by the National Science Foundation since 2003 including through a prestigious CAREER award.

Drought and Salinity Effect on Plant-Plant Interaction in North African Dryland

Ghassen Chaieb^{1*}, Chedly Abdelly² and Richard Michalet²

¹University of Bordeaux, France

²Center of biotechnology of Borj Cedria, Tunisia

Abstract

The outcomes of plant-plant interaction along with environmental stress gradient have been widely studied during the last two decades. The study of positive and negative interactions within plant community is an important predictive tool for understanding ecosystem response to environmental change. Therefore, the significant variation of environmental change lead us to consider the key role of plant-plant interaction in mediating the response of natural systems and how this role might be influenced by the impact of environmental change processes.

This study was carried in north African dryland and study site were the continental saline soils under arid climate. A number of 8 sites were selected in two contrasting situations of the arid climate (Upper arid and lower arid). Saline soils are locally called (Sebkhas) in which vegetation is distributed according a topographical and saline gradient (Chaieb et al 2018). Plant-plant interaction experimental design was performed through transplanting species along salinity gradient in both vegetated areas and open areas (unvegetated).

We found a significant variation of plant-plant interaction according salinity. In the most stressful situation, there is a collapse of plant interaction (Michalet et al 2006). Plant facilitation was important in rainy season and changed to competition in dry season. There is also a temporal effect of plant-plant interaction collapse which became more important in dry seasons.

Aridity play a major role on plant-plant interaction; however, plant species show several strategies in mediating the increase of the combined effect of aridity and salinity by facilitation which operate the amelioration of abiotic stress.

In-situ Production of Low-Cost Agricultural Biochar

GuodongLiu* and Qifa Zhou

University of Florida, Gainesville, FL

Abstract

Application of biochar in crop production is effective to sequester atmospheric carbon and improve soil quality. Current pyrolysis and transportation costs are so high that biochar is too costly to be used in field scale. This study developed a new in-situ technique, "burn and soil cover" (B-SC), which can be used by farmers for biochar production with crop residue. In this study, the air-dried feedstock, elephant grass and corn residue, were burnt in situ for biochar production. After approximately 90% of the leaves were combusted, the burning process was dramatically slowed down by covering the feedstock with soil. The biochar yield averaged 18.0 ± 1.3 ($n = 15$) and 13.7 ± 1.3 ($n = 10$) kg per 100 kg of feedstock for the elephant grass and for the corn residue, respectively. The biochar properties were suitable for improvement of soil quality and health. The operational time for processing 10 kg of the corn residue by the individual farmer was 24.4 ± 4.1 minutes ($n=10$). As compared with the conventional field burning process, the B-SC process generated a significantly lower emission of smoke.

Biological Control Evaluation of the White Scale *Diaspis boisduvalii* Signoret, 1869 (Hemiptera: Diaspididae) in Conventional Banana Cultivation

Ndonkeu Tita Walter*, Juliet Daniela Aranibar Luna and Bert Kohlmann

Earth University, Costa Rica

Abstract

The objective of the project was to evaluate the efficiency of commercially available biological controllers *Cryptolaemus montrouzieri* Mulsant, 1853 (Coleoptera: Coccinellidae) and *Chrysoperla carnea* (Stephens, 1836) (Neuroptera: Chrysopidae) of the white scale of banana *Diaspis boisduvalii* Signoret, 1869 (Hemiptera: Diaspididae); in relation to possible native

controllers. Regarding possible native biological controllers, two predators and one parasitoid were identified; *Nacarina cordillera* (Banks, 1910) (Neuroptera: Chrysopidae), *Nacarina titan* (Banks, 1915) (Neuroptera: Chrysopidae) and *Plagiomerus Crawford*, 1910 (Hymenoptera: Encyrtidae), respectively. Of the three native controllers, the larvae of *N. cordillera* were used to compare their percentage of predation efficiency with commercial controllers, because it was the most common of all three native species. Abbott's (1925) formula for predation efficiency was used to compare the percentage of the results of the commercial and native controllers over a period of 6, 12, 18, and 24 hours at scale concentrations of 10, 25, and 40 specimens. *C. montrouzieri* obtained a percentage of predation efficiency of 13.5 %, *C. carnea* of 7.4 % and *Nacarina cordillera* of 75.5 %, respectively. It is therefore concluded that the native predator proved to be more effective than the commercially available ones, possibly because they are better adapted to the local ecological conditions than the commercial controllers.

Biography

Walter Ndonkeu Tita is a Pest Management expert/Entomologist. He graduated with a Ph.D. in Entomology from McGill University, Canada. Prior to becoming a professor at Earth University, Costa Rica, he worked in the agricultural industry in both Cameroon and Canada for many years. His research interest are in the areas of integrated pest management, parasitic and insect pathogenic nematodes, plantation agriculture, microbial pathogenicity, insect immunity, and insect-plant and pest-pathogen interactions. He is a member of the Canadian Society of Entomology, the Society of Invertebrate Pathology and the Canadian Society of Microbiologist.

Biology, Thermal Requirements and Estimation of the Number of Generations of *Hypothenemus hampei* (Ferrari, 1867) (Coleoptera: Curculionidae) and *Leucoptera coffeella* (Lepidoptera: Lyonetiidae) in the State of Sao Paulo, Brazil

Marisol Giraldo-Jaramillo*, José Roberto Postali Parra¹ and Audberto Quiroga²

¹National Coffee Research Center, Colombia

²Universidade de São Paulo (ESALQ-USP), Brazil

Abstract

Commercial coffee plantations are found between 20°N and 26°S worldwide. The optimal temperature is reported as 18–22 °C; temperatures below 12 °C and above 24 °C, are unsuitable for growth and productivity (Maestri and Barros 1977, Pereira et al. 2008). Coffee, one of the most important agricultural crops in Brazil, is strongly affected by climate changes (Camargo and Camargo 2001, Jaramillo 2018), as are the insects associated with coffee crops. The coffee berry borer (CBB) *Hypothenemus hampei* (Ferrari, 1867) (Coleoptera: Curculionidae) and the coffee leaf miner (CLM) *Leucoptera coffeella* (Lepidoptera: Lyonetiidae) are important insect pests of coffee worldwide (Parra and Reis 2013). The present study determined the climate zones for CBB and CLM in the state of São Paulo, based on their thermal requirements. The results showed that temperature affected the mean biological development times of CBB and CLM, which completed their life cycles more rapidly in increased temperatures until the 30 °C threshold, and more slowly above this temperature. Development time (egg-adult) was inversely related to temperature in the range between 18 and 32°C. The temperature threshold (Tt) and the thermal constant (K) were estimated for both species. These laboratory estimates of thermal requirements and the Geographic Information System (GIS) were used to generate insect life-span distribution maps for São Paulo. Higher pest incidences should coincide with both temperature increases and the availability of coffee fruit for infestation. The data obtained can be used to estimate the monthly and yearly number of generations of this pest, for use in integrated pest-management programs.

DAY-2

TUESDAY, March 05, 2019

Featured Presentations

Thiol Redoxomes in Plant Immunity – Pathways, Molecular Players and Structural Determinants

Sorina C. Popescu

Mississippi State University, Starkville, MS

Abstract

Plant stress caused by pathogen attack and deleterious environmental factors is one of the greatest challenges to overcome in agriculture. It is critical to understand how plants sense and integrate stress signals to elicit physiological responses for survival and to reach a predictive understanding of the adaptation mechanisms. Shifts in the cellular redox potential occur in the early stages of the plant effector-triggered immunity (ETI). Accumulation of reactive oxygen species leads to oxidative stress, which has a strong impact on the proteome. Susceptible residues in proteins are oxidized and, in the process, the activity and stability of oxidized proteins change significantly. The plant redoxome – the fraction of the proteome suffering oxidative post-translational modification (oxPTM) – remains largely unknown.

Previous work from our group focused on a family of peptidases, the thimet oligopeptidases (*TOPs*). Simulations of computational models postulated that *TOPs* mediate the cellular redox homeostasis and redox signaling during the ETI. In current work, we use state-of-the-art methods in systems biology and protein biochemistry to analyze *TOPs* oxidation states as potential redox switches in the plant defense and adaptive pathways. The reversible thiol redoxomes were characterized in the wild-type and *top1top2* null mutants in the early stages of the ETI. We identified oxidation-sensitive cysteine residues and highlighted significant differences between the redoxomes in the two genotypes. Our work significantly expands the space of the plant redoxome and can guide future systematic studies of oxPTM in immunity, and the development of photosynthetic organisms with improved fitness under adverse environmental conditions.

Biography

Popescu is faculty in the Department of Biochemistry, Molecular Biology, Entomology, and Plant Pathology at MSU. She earned her Ph.D. from Rutgers U. of New Jersey and continued as a postdoctoral associate at Yale U. in New Haven, CT. Her research revolves around utilization of various ‘omics’ and systems biology techniques to study plant response to pathogens and environmental stress. Her work has led to the development of high-throughput tools to characterize proteins and a better understanding of the properties of protein networks. Driven by a strong motivation of translating research findings from models to crops and expanded her research repertoire. Current topics in her lab include kinase and redox signaling in plant stress and biotechnology-directed applications in tomato, sweet potato, and cotton. She has authored over 20 peer-reviewed publications, reviews, and book chapters. She presented her work at numerous national and international scientific meetings and workshops.

Understand the Biological Specificity of MAPK Signaling Controlling Stomatal Development

Jin Suk Lee*, Hassan Damen, Raman Jangra and Farzaneh Tamnanloo

Concordia University, Canada

Abstract

As with all multicellular organisms, plants depend on cell-to-cell communication to coordinate both development and environmental responses across diverse cell types. Stomata, valves on the plant epidermis used for gas exchange with the atmosphere, are formed through a series of differentiation events according to positional cues mediated by extrinsic cell-to-cell signaling. Several members of the cysteine-rich peptide family that act in distinct stages of stomatal development have

recently been identified, but interestingly they all require the same downstream Mitogen-Activated Protein Kinase (MAPK) signaling components to function. Thus, an outstanding question in the field is: How do cells interpret different peptide signals using the same set of MAPKs to elicit unique responses. Some of our findings include new regulators of stomatal MAPK signaling, and the molecular mechanisms controlling distinct stages of stomatal development, will be discussed.

Biography

JinSuk has completed her masters in 1998-2000 in Agriculture and Life Sciences at Chungnam National University, South Korea and Doctor of Philosophy at University of British Columbia, Canada. She is a NSERC Postdoctoral Fellow of University of Washington and worked as HHMI Research Associate from 2012 – 2014. Currently she is working as Assistant Professor in Concordia University, Canada and also acting as Research Chair in Plant Science and Biotechnology.

MAC3A and MAC3B, Two Core Subunits of the MOS4-Associated Complex, Positively Impact miRNA Biogenesis

Bin Yu* and Shengjun Li

University of Nebraska-Lincoln, Lincoln, NE

Abstract

MAC3A and MAC3B are conserved U-box containing proteins in eukaryotes. They are subunits of the MOS4-associated complex (MAC) that plays essential roles in plant immunity and development in *Arabidopsis*. However, their functional mechanisms remain elusive. Here we show that MAC3A and MAC3B act redundantly in microRNA (miRNA) biogenesis. Lack of both MAC3A and MAC3B in the *mac3b mac3b* double mutant reduces the accumulation of miRNAs, causing elevated transcript levels of miRNA targets. *mac3a mac3b* also decreases the levels of primary miRNA transcripts (pri-miRNAs). However, MAC3A and MAC3B do not affect the promoter activity of genes encoding miRNAs (*MIR*), suggesting that they may not affect *MIR* transcription. This result together with the fact that MAC3A associates with pri-miRNAs *in vivo* indicates that MAC3A and MAC3B may stabilize pri-miRNAs. Interestingly, we show that MAC3A is phosphorylation-dependent ubiquitin E3 ligase and its activity is required for miRNA biogenesis. Furthermore, we find that MAC3A and MAC3B interact with the DCL1 complex that catalyzes miRNA maturation, promote DCL1 activity and are required for the localization of HYL1, a component of the DCL1 complex. Besides MAC3A and MAC3B, two other MAC subunits, CDC5 (a transcription factor) and PRL1 (a WD domain containing protein), also function in miRNA biogenesis. Based on these results, we propose that MAC functions as a complex to control miRNA levels through modulating pri-miRNA transcription, processing and stability.

Biography

Bin Yu is an associate professor in the School of Biological Sciences & Center for Plant Science Innovation at University of Nebraska, Lincoln, where he has been a faculty member since 2008. Bin completed his Ph.D at Michigan State University and his undergraduate studies at Shandong Agricultural University. He is interested in understanding the molecular mechanisms underlying the metabolism and function of small RNAs including microRNAs (miRNAs) and small interfering RNAs, which are negative regulators of gene expression.

Characterization of Proteins Involved in Chloroplast Targeting Disturbed by Rice Stripe Virus by Novel Protoplast-Chloroplast Proteomic

Jinping Zhao^{1,2*}, Jingjing Xu², Binghua Chen^{2,3,5}, Weijun Cui^{2,3}, Zhongjing Zhou², Xijiao Song², Zhuo Chen^{2,5}, Zhiping Deng², Hongying Zheng^{2,3}, Yuwen Lu^{2,3}, Jiejun Peng^{2,3}, Lin Lin^{2,3} and Fei Yan^{2,3}

¹Texas A&M University AgriLife Research Center at Dallas, Dallas, TX

²Zhejiang Academy of Agricultural Sciences, China

³Ningbo University, China

⁴Jiangnan University, China

⁵Guizhou University, China

Abstract

Rice stripe virus (RSV) is one of the most damaging rice pathogens, causing the general chlorosis symptom in host plants. The chloroplast changes associated with chlorosis symptom suggest that RSV interacted with the chloroplast. Proteomics have revealed the chloroplast related proteins with reduced accumulation after RSV infection. However, the chloroplast proteins whose translocation affected by RSV infection is remain unclear. Here, we revealed that RSV infection caused the malformation of chloroplast structure and the whole reduced levels of chloroplast membrane protein complexes in *Nicotiana benthamiana*. After the purity of chloroplast fraction was validated by WB, we then applied protoplast-chloroplast proteomics to establish the special filters to screen the nucleus encoded chloroplast proteins which do not transported to chloroplasts after RSV infection and obtained 66 candidate proteins. GO enrichment analysis of these 66 candidate proteins indicated that the RSV infection changed the relevant several biological process of protein targeting to chloroplast, and there were three interesting nucleus encoded chloroplast proteins (K4CSN4, K4CR23 and K4BXN9) involved in regulate the biological process of protein targeting to chloroplast. In addition to these three proteins, we discovered that 41 among 63 candidate proteins had chloroplast transit peptides. GO enrichment analysis of 41 proteins revealed very similar result with GO enrichment analysis of 66 candidate proteins. These results indicated that RSV infection changed the location of 66 nucleus encoded chloroplast proteins and was believed to regulate the relevant multiple biological process of protein targeting to chloroplast through the three interesting proteins.

Biography

Jinping Zhao is now a Postdoctoral Research Associate in Dr. Junqi Song's group at the Texas A&M University AgriLife Research Center at Dallas, Texas, USA. Dr. Zhao got his Ph.D. degree at Tsinghua University and have more than 15 years of experience in plant immunity, plant pathology, plant virology and plant biotechnology.

Species Revision and Speciation of *Orinus* (Poaceae) endemic to the Qinghai-Tibet Plateau

Xu Su^{1*}, Yuping Liu¹, AJ Harris² and Zhumei Ren³

¹Qinghai Normal University, China

²Oberlin College and Conservatory, Oberlin, OH

³School of Life Science, Shanxi University, China

Abstract

In this study, we used multiple approaches and lines of evidence to determine species boundaries for plants occurring in the Qinghai-Tibet Plateau (QTP), using the genus *Orinus* (Poaceae) as a model system. We sequenced four DNA fragments, three chloroplast DNAs (*matK*, *rbcl*, *trnH-psbA*) and one nuclear ITS. Six species previously recognized, statistical analyses based on character variation, molecular data and niche differentiation identified only two well-delimited clusters, together with a third possibly originating from relatively recent hybridization between, or historical introgression from, the other two. Based on the principle of the integrative species delimitation to reconcile different sources of data, our results together provide compelling evidence that the six previously recognized species of the genus should be reduced to two, with new circumscriptions, while the third, identified in this study, should be described as a new species. we report this new species,

together with a complete taxonomic revision of the genus, and a key to distinguish the three extant species.

Besides, we examined the speciation of three redefined *Orinus* species based on a total of biparentally inherited 10 SSR and 11 nuclear loci. The results showed that these *Orinus* species had a high interspecific divergence. The sustained uplifts and Quaternary climatic oscillations of the QTP, may have together drive the allopatric divergence in *Orinus* and introgression after divergence between them. The habitat differentiation due to the Pleistocene climatic changes may have led to the speciation of *Orinus*.

Biography

Xu Su, Male, 08-28-1980, Professor in Qinghai Normal University, Doctoral supervisor, Leader of Natural Science and Engineering in Qinghai Province. 2016-2017, Scholar Visitor in Smithsonian Institution. Primary Research Interests: (1) systematics and evolutionary relationship of the tribe Triticeae using the multi-subject research methods ranging from morphological characters, Ecological factors, and Geographical distribution. (2) the species delimitation, speciation and phylogeography of the endemic genus or species (i.e. *Orinus*, *Littledalea*, *Psammochloa villosa*) from the QTP by utilizing the research methods of generalized morphology and evolutionary biology.

The Hydration State of Fatty Acids Hydrocarbon Chains in Membrane Lipids Might be a Molecular Basis for Cold Stress and Tolerance

Chaim Frenkel

Rutgers University, New Brunswick, NH

Abstract

We posit that cold-induced changes in the hydration state of nonpolar domains determines the metabolic functionality of cellular macromolecules. We used water-fatty acid emulsions (water-in-oil) system to gage the effect of cold temperatures on the hydration state of fatty acid hydrocarbon chain, using gas chromatography. The results revealed precipitous water loss from hydrocarbon chains of fatty acids, ensuing at 25° C to around 15° C and consequent molecular ordering of fatty acids at lower temperatures. Cold-induced dehydration of fatty acids is biphasic and could account for Arrhenius plot discontinuity previously observed. Cold-induced lipid dehydration may arise from temperature-dependent periodicity in water affinity for nonpolar surfaces. Increased efficacy for water binding by fatty acids, created by double bond-induced polarity in hydrocarbon chains and, furthermore, double bond interaction with hydrated cations (e.g., ammonium ion) was shown to oppose cold-induced water expulsion. Accordingly, unsaturated fatty acids from cold-tolerant cucumber seedlings displayed a three-fold increase in hydration efficacy, compared with the control. We propose that cold-induced dehydration of fatty acid hydrocarbon chains and resultant molecular ordering might be a molecular basis for chilling stress whereas persistence of water homeostasis of fatty acids hydrocarbon chains might be a mechanism for cold tolerance.

Plant Nanobionics: A Case Study of Mechanisms Underline Cerium Oxide Nanoparticles Improved Plant Salinity Stress Tolerance

Honghong Wu^{1,2}, Lana Shabala³, Sergey Shabala³, Nicholas Tito¹ and Juan Pablo Giraldo¹

¹ University of California, Riverside, CA

² Huazhong Agricultural University, China

³ University of Tasmania, Australia

Abstract

Salinity is a widespread environmental stress that severely limits crop yield worldwide. Here, we demonstrate that applying designed cerium oxide nanoparticles (nanoceria) can augment plant ROS scavenging ability, modulate the activities of K⁺ efflux channels, improve K⁺ retention in leaf mesophyll cells, and eventually enhance salinity stress tolerance in *Arabidopsis thaliana* (Col-0). Briefly, we found that the designed negatively charged poly acrylic acid coated nanoceria (PNC;

hydrodynamic size, 10 nm) with low surface Ce^{3+}/Ce^{4+} ratio have the unique capability of catalytically reducing levels of stress-induced reactive oxygen species (ROS) including hydroxyl radicals ($\cdot OH$) that lack enzymatic scavenging pathways. Compared with plants without nanoparticles, plants embedded with these PNC exhibit an increase in photosynthetic performance such as quantum yield of photosystem II, carbon assimilation rates, and Rubisco carboxylation rates, and eventually the biomass under abiotic stresses e.g. salinity, high light, heat, and chilling. Also, catalytic $\cdot OH$ scavenging by PNC in *Arabidopsis* leaves showed about three-fold lower NaCl-induced mesophyll K^+ efflux compared to control leaves upon exposure to salinity stress, indicating a significant improvement in mesophyll K^+ retention, a key trait associated with salinity stress tolerance. Moreover, the ROS-activated plasma membrane nonselective cation channels (ROS-NSCC) were identified as the main $\cdot OH$ -inducible K^+ efflux channels which are tuned by PNC. Our study demonstrates a plant nanobionics approach of augmenting plant ROS scavenging by PNC for understanding and improving plant tolerance against abiotic stresses.

The Adaptive Role of Mitogen-Activated Protein Kinase (MAPK) Signalling in *Chlamydomonas Reinhardtii* Grown Under Paraquat Induced Oxidative Stress

Tímea V. Nádai^{1,2}, Ákos Boldizsár¹, Balázs Kalapos¹, Éva Darkó¹, Gabor Galiba^{1,2}, Katerina Bisova³ and Robert Doczi¹

¹Hungarian Academy of Sciences, Hungary

²University of Pannonia, Hungary

³Centre Algatech, Czech Republic

Abstract

In recent years algal biotechnology has become a rapidly developing field. Algae are currently exploited for the production of secondary metabolites as high value products for commercial usage: human and animal consumption, colouring agents, cosmetics, pharmaceutical raw materials. The production of next generation biofuels and the bioremediation of waste water (CO_2) are also among their possible usage.

In unicellular algae growth and cell cycle progression are tightly connected to the environmental conditions. Furthermore, adaptation to stress means significant changes in metabolism. In order to sense and regulate responses to environmental stimuli plants have evolved complex cellular signalling networks, like the mitogen-activated protein kinase (MAPK) phosphorylation cascade which have pivotal role in regulating stress responses, cell division and growth. Despite the high economic potential of microalgae very little is known about its environmental adaptation and signalling, and our knowledge on algal MAPK functions is almost nothing.

For the initiation of algal MAPK signalling studies we have utilised *Chlamydomonas reinhardtii*, an excellent laboratory model species, which is a well-established system to study cellular biological processes. For the functional analysis we cloned selected *Chlamydomonas* MAPK signalling genes and generated transgenic constructs. These *Chlamydomonas* lines along with the wide type and the insertion mutants are characterised in terms of oxidative stress responses. Furthermore, we carried out a transcriptome analysis for the better understanding of key MAPK functions in algae. Our results reveal a unique involvement of MAPK in modulating ROS response in *Chlamydomonas*. This work is supported by OTKA NN 114511.

Biography

Tímea V. Nádai received a bachelor's and a master's degree in biochemical engineering, with the specification of applied biotechnology, from Budapest University of Technology and Economics. Now she is a second-year PhD student at the University of Pannonia, Georgikon Faculty, Festic Doctoral School. The Department of Plant Molecular Biology, Institute of Agriculture, Centre for Agricultural Research, Hungarian Academy of Sciences gives place for her experimental laboratory work. Her research topic is the regulation of stress adaptation in cultured microalgae.

Climate change in Sugarcane Agriculture: Metabolic and Molecular Mechanism of Thermo-tolerance

R.Gomathi*, S.Kohila and K. Lakshmi

ICAR-Sugarcane Breeding Institute, India

Abstract

In tropical climates, excess of radiation and high temperatures are often the most limiting factors affecting plant growth and final crop yield. Sugarcane requires optimum temperature (32–34°C) for growth, productivity and yield expression and it known to tolerate temperatures approaching 40°C, and high temperature injury around 45°C is detrimental to sugarcane growth. Heat stress greatly changes the physiological and biochemical phenomena of sugarcane leading to growth and yield suppression. The adverse effects of heat stress can be mitigated by developing crop plants with improved thermo tolerance using various genetic approaches. A thorough understanding of physiological responses of plants to high temperature, mechanisms of heat tolerance and possible strategies for improving crop thermotolerance is imperative in the present situation. Globally, a first systematic study on thermo-tolerance for sugarcane was investigated through metabolomic, transcriptomic and proteomic approaches in seven commercial sugarcane genotypes and four wild species clones at two different growth phases. Control plants were grown under optimal conditions at 37/28 ± 2 °C day/night with a 12-h photoperiod. Heat stressed plants were grown at 45/32 ± 2 °C during the day/night with a 12-h photoperiod and for a total of 15 days, with 60–70% relative humidity, and light intensity 395–410 μmol m⁻²s⁻¹. Two sets of pot culture experiment were conducted simultaneously, one for formative phase (150 days) and another one grand growth phase (210 days). The experiment laid out Completely Randomized Block Design (CRD) with replication thrice. Normal recommended agronomic practices were performed for these experiments. Metabolomic approach: The study revealed that heat stress decreased chlorophyll content, chlorophyll stability index (CSI), SPAD value, maximum quantum efficiency of PSII photochemistry (Fv/Fm ratio), leaf gas exchange parameters, relative water content (RWC), and activities of nitrate reductase (NR), sucrose-metabolizing enzymes (SPS, SS, AI, NI) in all the genotypes and species clones. In contrast, elevated temperature induced an increase in proline, total phenolics content (TP), antioxidant enzyme activities (SOD and POX), lipid peroxidation (LP), membrane injury index (MII) and soluble sugar content in all clones. Based on the principal component analysis (PCA), physiological heat tolerance indexes could clearly distinguish sugarcane genotypes into three heat tolerance clusters. Noteworthy in comparison to the heat-sensitive varieties, sugarcane genotype that possessed higher degrees of heat tolerance (Co 99004) displayed higher chlorophyll content, CSI, antioxidant enzyme activities, NR activity, RWC, total phenols, sucrose-metabolizing enzymes, soluble sugar content and leaf gas exchange and lower level of lipid peroxidation and membrane injury index.

Effect of Rhizobacteria on Antioxidant Enzyme Activity in Soybean under Salt Stress

Humaira Yasmin*, Sana Naeem and Muhammad Nadeem Hassan

COMSATS University, Pakistan

Abstract

Soil salinity is one of the most adverse factors that hampered the growth, yield and physiological response in soybean. There is an increasing trend towards the use of plant growth promoting Rhizobacteria (PGPR) for plant growth promotion and alleviation of salt stress. The current study was conducted to investigate the physiological responses and protein profiling of soybean plants, inoculated with halotolerant PGPRs, under the salt stress. For this, a pot experiment was conducted, where *Bacillus subtilis* and *Pseudomonas* sp. were inoculated in hydroponically grown soybean plants under 100mM NaCl stress. Quantification of protein content, photosynthetic pigments, proline, MDA contents and Na⁺ and K⁺ concentration and activities of ROS scavenging enzymes was assayed in controlled, salt stressed and PGPRs inoculated conditions. Moreover, protein profiling was done by SDS-PAGE. Overall, inoculated treatments ameliorate the effects of salt stress by enhancing the activities of antioxidant enzymes, contents of proline and proteins, and photosynthetic pigments. It also reduced the Na⁺ concentration accumulated in the saline plants. However, antagonistic results were observed for K⁺ concentration.

Electrophoretic pattern of proteins demonstrated that *Pseudomonas* sp. caused induction of new proteins (38kDa) that can be associated with resistance to salinity stress in soybean plants. Hence, PGPRs inoculation enhanced the production of some defense proteins and antioxidant enzymes in the soybean plants that may in turn play a role in adaptation to saline conditions. Our results showed that salinity tolerance is more pronounced in *Pseudomonas* sp. as compared to *Bacillus subtilis* that for the protection of soybean plant under salinity stress.

Biography

Humaira Yasmin has strong background in the area of identification of plant growth promoting rhizobacteria for their abiotic stress tolerance potential in economically important crops. She did her Mphil and PhD in Plant physiology and Plant microbe interaction respectively, from Quaid i Azam University, Islamabad. She also did resaerch work in faculty of agricultural chemistry ,University of Sydney Australia under the supervision of well known poineer of Plant microbe interaction Emireatus Prof Ivan R. Kennedy. Under his supervisin , she has studied relative expression of drought and salt tolerant genes of *Pseudomonas* and *Bacillus* strains with repect to their native stressed and irrigated regions.

Molecular Characterization and Identification of Trichodorid Nematode Species from Multiple States in the USA

Guiping Yan¹ and Danqiong Huang

North Dakota State University, Fargo, ND

Abstract

Stubby root nematodes (SRN; *Paratrichodorus* and *Trichodorus*) in the family Trichodoridae are important plant pathogens that affect many crops. They can be particularly devastating to potato due to their ability to transmit *Tobacco rattle virus* causing corky ringspot disease on tubers. During 2015-2017, 184 soil samples and 16 nematode suspensions from eight states in the USA were examined for the presence of SRN. It were detected in 58% of the soil samples and 50% of the suspensions. Ribosomal DNA sequencing revealed the presence of four trichodorid species *Paratrichodorus allius*, *P. minor*, *P. porosus* and *Trichodorus obtusus*. The DNA sequences were characterized by analyzing D2-D3 expansion region of 28S rDNA, 18S rDNA, and ITS rDNA. Intra- and inter-species variabilities were higher in ITS than 18S and D2-D3. Phylogenetic analysis showed that four species formed a monophyletic group, with *P. allius* more closely related to *P. porosus* than *P. minor* and *T. obtusus*. Genetic variation was observed in ITS2 rDNA of *P. allius* populations from the same geographic regions. Traditional identification based on morphology is laborious and requires an extensive training in nematology. For efficient diagnosis, a multiplex PCR assay was developed to simultaneously identify these four species using one PCR reaction. A real-time PCR assay was developed for sensitively identifying *P. allius* from single nematodes and soil nematode communities. The genetic diversity provides important information for understanding the evolutionary relationships of SRN and the molecular assays provide rapid species identification for accurate diagnostics of these trichodorid nematodes found from the USA.

Biography

Guiping Yan is an assistant professor of Nematology in Dpartment of Plant Pathology, North Dakota State University, USA. Her current research is focused on detection, biology and management of plant-parasitic nematodes that threaten production of field crops. Her team has developed a series of new molecular assays for detecting, identifying and quantifying plant-parasitic nematodes from nematode individuals, communities and soil DNA. Recently she served as the Chair and Secretary of the North Central-1197 Nematology Committee, and currently is an executive member of the Society of Nematologists and the Chair of the American Phytopathological Society Nematology Committee.

Effects of Bio-Bactericide Treatment of Kiwifruit Infected with *Pseudomonas Syringae* pv. *Actinidiae* (Psa) on Host Gene Expression, Lesion Severity and Psa Populations

Kirstin Wurms¹, Huub de Jong², Tony Reglinski¹, Annette Ah Chee¹, Rachele Anderson¹, Joseph Taylor¹, Stephen Hoyte¹ and Philip Elmer¹

¹The New Zealand Institute for Plant & Food Research Limited, New Zealand

²Utrecht University, The Netherlands

Abstract

Pseudomonas syringae pv. *actinidiae* biovar 3 (Psa), which causes bacterial canker in kiwifruit, is one of the most serious global pathogens of this crop. Problems with existing controls, namely fungicide resistance and copper build-up in soils, drive the need for control alternatives such as bio-bacteriocides that contain elicitors, biocontrol agents (BCA) or antimicrobial natural products. This study investigated effects of use of Acibenzolar-S-methyl (ASM), an elicitor used in New-Zealand orchards to manage Psa, and a yeast BCA, (BCA-G2) on necrotic lesion severity, expression levels of plant defence genes and Psa populations. Tissue cultured *A. chinensis* var *deliciosa* 'Hayward' plantlets were treated with either ASM, BCA-G2, or a combination of both. ASM and BCA-G2 treatments significantly reduced lesion severity compared to the untreated control, and combining the treatments was significantly more effective than the individual treatments on their own. Genes associated with the salicylic acid pathway, namely PR1, β -1,3-glucosidase and PR5 in leaf tissue were significantly induced by treatments of ASM and BCA-G2. BCA-G2 treatments reduced epiphytic Psa populations on the leaf surface and combined treatments of ASM and BCA-G2 reduced endophytic Psa populations compared to the treatments applied alone. In conclusion, this study suggests that combining ASM with a BCA can significantly inhibit disease severity in kiwifruit after Psa infection.

Biography

Kirstin Wurms has been working as a scientist at Plant & Food Research, New Zealand for 18 years. Her research areas of interest are development of natural product bio-fungicides and host plant defence gene expression. She and her co-authors are part of a group that focusses on developing applied, environmentally-friendly solutions to plant disease control. The group has been responsible for taking 7 bio-pesticides from the point of conception to release on the market. Outside of work, Kirstin is often found at her kids' sports events, especially rhythmic gymnastics, or hanging out with her two Dalmatian dogs.

Advances in Crop Improvement of Goldenberry (*Physalis peruviana* L.) in Colombia

Victor M Nunez¹, Erika Sánchez², Francy Garcia¹, Franklin Mayorga¹ and Jaime Osorio Guarín¹

¹AGROSAVIA, Colombia

²University of Nebraska–Lincoln, Lincoln, NE

Abstract

Physalis peruviana L, known as cape gooseberry or golden berry, is an exotic fruit that belongs to the family Solanaceae and the genus *Physalis*. Originally from the Andes, it is a relatively new crop established as a commercial plantation in the mid-1980s, but its fruit is well known all over the world and highly prized for its nutritional value and its wide range of pharmacological properties and special bio-functional compounds. At present, Colombia is the main world producer, where it is the second most exported fruit, only behind the banana and plantain. The crop faces several limitations, such as wilt disease caused by *Fusarium oxysporum* f. sp. *physali* (Foph), fruit cracking and fruit quality uniformity among others. Most research on this crop is related to the development and improvement of cultivation techniques, therefore, genetic improvement approaches are in great need. The Colombian Agricultural Research Corporation (AGROSAVIA) started a crop improvement program in 2008 to develop fusarium resistant cultivars with better yield and low fruit cracking. The research program includes conventional approaches, molecular markers, bioinformatics, cytogenetics, genetic transformation,

double haploid technology, grafting, micropropagation and fruit quality traits analysis. So far, we have released the first two commercial cultivars with mass selection and doubled haploid technology. We expect to release the first fusarium-resistant cultivar with good yield, low fruit cracking and quality traits. The potential of using genome editing, isolated microspores culture and phenomics will be discussed.

Biography

Victor Manuel Nunez Zarantes is a colombian reseacher at the Corporación Colombiana de Investigación Agropecuaria (AGROSAVIA). Studied at the Universidad Nacional de Colombia, University of Minnesota and Iowa State, worked at the Centro Internacional de Agricultura Tropical CIAT, GARST Seed Company (ICI), Pioneer Hi-Bred. He has expertise in genetic transformation for corn, potato, pea, cotton and golden berry; in doubled haploid for rice, corn and golden berry; micropropagation in several tropical crops; molecular markers in papaya and cytogenetics in golden berry and blackberry. His present research interest includes crop breeding and biotechnology of golden berry and blackberry.

Identification of Seed Filling Gene (VmBS1) in Black Gram (*Vigna mungo* L. Hepper) Mutant Induced by Gamma Irradiation

Arulbalachandran Dhanarajan

Periyar University, India

Abstract

In recent years, the mechanisms regulating seed filling has advanced and significance due to the diversity of experimental approaches used. Genetic factors partially controlled the cultivars considerably vary in pod filling potential. Here the studies find out the identification of mRNA transcript of the mutant trait. The mutants were sampled based on the gamma irradiation doses used which from 200, 400, 600, 800 and 1000 Gy and non-irradiated sample as a control. The observed viable mutants of black gram have significantly bold size seed, chlorophyll mutants and tall and dwarf due to the effect of gamma irradiation with different doses and knock-down the *VmBS1* gene which reproduced during seed filling potential. The present study hypothesized that the *VmBS1* gene control the phenotypic characters such as increasing of leaf width, number of flowerings, pod size and seed size in black gram mutants. The increase of seed size by the mutation is by far the largest, compared to non-irradiated seeds. Thus, mutants and/or *VmBS1* gene knock-down of black gram reveals that it does not necessarily achieve the higher yield of total seed weight that means the seed filling probability achieve the economical value by the improvement of bigger seed size in leguminous crops.

Biography

D. Arulbalachandran is an Assistant Professor in the Department of Botany, School of Life Science, Periyar University, Tamil Nadu, India. He is focusing in the field of cytogenetics, mutation breeding and molecular analysis in crops. He completed a research project under UGC and board member for curricula in various institutions and member of various scientific societies such as ASPB, CSSA, USA and reviewer in various national and international journals and he has published research articles in national and international repute. He published books *viz.*, Ecology, Biodiversity and Mutation Breeding in Crop Plants and also published an edited book titled "Sustainable agriculture towards food security" and contributed some book chapters in Springer.

The Breeding of Glutinous Hybrid Rice

Zhang Shubiao

Fujian Agriculture and Forestry University, China

Abstract

The glutinous rice is the traditional food and some nationality's staple food, which is also important raw material for some food production. The farming of glutinous rice is an important cultural component of many countries and minorities. With the living standards' improved the market demanding of glutinous rice is increasing.

The rice breeding has entered into the super rice breeding stage and the good progress was made, but the glutinous rice breeding still mainly paused in the conventional rice breeding stage. It is important for us to develop glutinous hybrid rice for improving the yield of glutinous rice.

Induced mutants of *wx* were directly obtained after irradiation on maintainer (B), restorer (R) and photoperiod (temperature) sensitive genic male sterile lines (S) of hybrid rice. CMS(A) lines with *wx* (referred to as *wxA*), T(P)GMS lines with *wx* (referred to as *wxS*), restorer lines with *wx* gene (referred to as *wxR*) as well as hybrid rice with *wx* gene (referred to as *wx*-hybrids) were developed. By using the *wx*-hybrid rice breeding method, most of CMS(T(P)GMS) lines and R lines used in China were transferred to *wx*-CMS(*wx*-T(P)GMS) lines and *wx* R lines. Till now, 10 *wx*-CMS (T(P)GMS) lines and 7 elite *wx*-hybrid rice were released for commercial production. Compared with the traditional glutinous rice, the yield of the *wx*-hybrid rice was improved about 1,500 kg ha⁻²

The Use of Carbon Nanomaterials to Improve Boreal Seed Germination, Seedling Vigor and Growth

Jean-Marie Sobze¹ and Raymond Thomas²

¹Northern Alberta Institute of Technology, Canada

²Memorial University, Canada

Abstract

Seed germination constitutes a fundamental part of plant growth and development. However, the ability of seeds to germinate successfully hinges on numerous factors, though seed dormancy may arguably be one of the most difficult. Nanotechnology has the potential to revolutionize plant propagation and play an important role in food and crop production (Parisi *et al.* 2015; Servin *et al.* 2015). Several studies have demonstrated the beneficial effects of different nanomaterials in improving germination and growth in many agricultural plant species (Gao *et al.* 2011; Mondal *et al.* 2011; Morla *et al.* 2011; Smirnova *et al.* 2012). Single walled carbon nanotubes were shown to penetrate thick seed coats at relatively low doses, stimulate germination, and enhance growth of tomato plants (Khodakovskaya *et al.* 2010). Multi-walled carbon nanotubes were also shown to induce water and essential nutrient uptake thereby enhancing seed germination and plant growth (Villagarcia *et al.* 2012; Tiwari *et al.* 2014). Though nanotechnology has been used extensively on agricultural crops, to date this has not been widely tested on native boreal forest species, particularly in the context of improving seed germination and growth performance. In 2017, we conducted project to test the effectiveness of select carbon nanoparticles to improve seed germination and seedling vigor in boreal plants with seed dormancy issues. Using two native boreal species commonly used in land reclamation (green alder (*Alnus viridis*) and bog birch (*Betula glandulosa*)), our study revealed that nanoparticles increased seed germination up to 90% and 88 % respectively. This occurred concomitantly with significant improvement in seedling vigor compared to the control plants.

Biography

Jean-Marie Sobze is a professional forester with the Association of Alberta Forest Management Professionals (AAFMP) and NAIT's Plant and Seed Research Chair. He is responsible for developing practical methods and technologies for plant and seed delivery. He has over 16-years of experience in forest management and industry-related research. He recently co-

authored a comprehensive article on alternative seed deployment systems on industrial disturbed sites. He received a PhD and MSc in Forestry at the University of Gottingen, Germany, specializing in community-based forest management, and BSc in Forestry and Wildlife at the University of Dschang in Cameroon.

Methods for Estimation of Leaf Area Index: A Case Study from Central European Deciduous Stands

Cerny Jakub^{1*}, Haninec Pavel², Pokorný Radek² and Bednář Pavel¹

¹*The Forestry and Game Management Research Institute, Research Station at Opočno, Czech Republic*

²*Mendel University in Brno, Czech Republic*

Abstract

Fast and precise leaf area index (LAI) estimation is frequently needed for a wide range of ecological studies. In 2013, the LAI obtained by the semi-direct and indirect methods in three European beech stands and one sycamore maple stand were compared with LAI estimated by the direct method. Within each studied stand, the LAI was estimated using 15 litter traps with a capture area of 0.25 m², metallic sharp needle 1.5 mm in diameter on 100 randomly spaced sampling points, and by LAI-2000 PCA at 27 regularly spaced points within the perpendicular transects for direct, semi-direct and indirect methods, respectively. Seasonal LAI was estimated using an LAI-2000 PCA which showed similar trends among the stands and strongly corresponded to phenological phases of deciduous stands in Europe. Seasonal maximum stand LAI value was observed on June 19th (DOY 170) and reached 4.5–5.1, and 4.0 in the beech and maple stands, respectively. The summer months (DOY 140–240) are the best period for comparing LAI estimates by the distinct indirect methods. The needle technique significantly underestimated ($p < 0.05$) direct LAI on average by 22.0% and 40.0% in the beech and maple stands, respectively. The LAI-2000 PCA insignificantly underestimated ($p > 0.05$) LAI on average by 15.1% and 5.8% in the beech and maple stands, respectively. All used methods for LAI estimation at the stand level could be applicable in deciduous forest stands with a similar site and stand characteristics. However, calibration by direct method is necessary to obtain the required accuracy.

Biography

Cerny Jakub is a permanent staff of the Forestry and Game Management Research Institute, Research Station at Opočno and simultaneously a PhD student of Silviculture at Mendel University in Brno. The topic of the thesis is “LAI – quantifier of silvicultural measures”. He focuses on LAI of the main central European tree species, dendrochronology, physiology and vitality of forest stands. The research was funded by the Ministry of Agriculture of the Czech Republic, institutional support MZE-RO0118 and National Agency of Agricultural Research (Project No. QJ1620415).

Light Spectrum Dependent Circadian Regulation of Freezing Tolerance and Modification of Development and Yield Quality Applying LED Light Sources in Cereals

Gábor Galiba^{1,2*}, István Monostori¹, Krisztián Gierczik^{1,2}, Ákos Boldizsár¹, Aliz Novák¹, Ahres Mohamed^{1,2}, Éva Ádám¹, László Kozma-Bognár¹, Attila Vágújfalvi¹, Mariann Rakszegi¹ and Éva Darkó¹

¹*Hungarian Academy of Sciences, Hungary*

²*University of Pannonia, Hungary*

Abstract

It has been described that the photoperiod and the light quality are important regulators in the cold acclimation processes through the modulation of the CBF regulon. Photoreceptors perceive the incident light and regulates several metabolic and photomorphogenetic processes. Utilization of LED lighting technology provides a new flexible platform to study the effect of altered light spectrum and intensity on plant development and abiotic stress tolerance.

We applied LED lighting technology (1) to investigate the circadian regulated signaling pathway of the light-quality and

temperature dependent regulation of freezing tolerance in cereals. (2) Moreover, the effects of light intensity and spectral composition on plant development, metabolism and nutritional quality were also evaluated.

1) The reduced red/far-red ratio at 15°C induced the CBF gene expression and it also increased the freezing tolerance of winter wheat and winter barley. Most likely the photoreceptors phyA and phyB plays important regulatory role in this acclimatization process. From the CBF cluster only the *HvCBF4* subgroup genes expressed at room temperature (22°C) and these genes showed circadian rhythms in barley. The gene expression pattern of some representative components of the light regulatory signaling pathways upstream to CBF genes was revealed.

2) Comparing different spectral compositions and light intensities revealed significant differences in growth, development, and flour quality of wheat. Our results demonstrated through modification of light quality LEDs make it possible to manipulate the metabolism to obtain desired traits and products.

Acknowledgements for funding: OTKA K111879 and OTKA NN 114511.

Biography

Gábor Galiba, biologist (D.Sc.), is Head of Department of Plant Molecular Biology, Agricultural Institute, Centre for Agricultural Research, Hungarian Academy of Sciences, Martonvasar, Hungary and Professor at Fesztetics Doctoral School, Georgikon Faculty, University of Pannonia, Keszthely, Hungary. He is a Member of the Agricultural Biotechnology Committee of the Hungarian Academy of Sciences. He received Fulbright Research Fellowship and Hungarian-American Enterprise Scholarship Fund at UC Davis, California in 2003 and 2007. His recent research focus on light regulation of frost tolerance and indoor plant development and yield quality. Scientometrics: Cumulated Impact F.: 158,9. Number of independent citations: 3170; Hirsch-index: 36.

Developing a New Method for Assessing Plant Lodging and Canola Root System Architecture

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²*Northwest A&F University, China*

Abstract

Canola is a cool season crop and is susceptible to abiotic stresses, especially heat and drought during the flowering stage. Root plasticity is important for mitigating abiotic stresses and maintaining yield. An electrical capacitance method was assessed for estimating canola root morphological traits in relation to lodging resistance, susceptibility to heat and drought stresses, and the impact of agronomic practices and abiotic stress on lodging. Our data showed that heat stress greatly increases root lodging risk, and further makes root lodging even more prevalent than stem lodging, and electrical capacitance can be considered as a non-invasive technique for the in situ assessment of lodging resistance.

Biography

Ma is a recognized national and international authority in crop physiology, focusing on the abiotic stress physiology, crop production systems and nutrient management. He has co-authored more than 170 scientific journal publications and 18 book chapters / review papers. He has been awarded the Fellow of the American Society of Agronomy (2007), Fellow of Canadian Society of Agronomy (2011), and Fellow of Crop Science Society of America (2012).

Strategies Used to Detect Genetic Variability in Chickpea (*Cicer arietinum* L.)

Ernestina Valadez-Moctezuma

Universidad Autónoma Chapingo, México

Abstract

The chickpea (*Cicer arietinum* L.) is one of the main grain legumes grown in the world. A priority in the management and use of elite plant materials for breeding has been based on molecular markers or DNA sequencing of entire genomes, in order to perform genetic differentiation, which is still costly. Chickpea (*Cicer arietinum*) is one of the species with genomic and genetic monotony and very low polymorphism, because this crop presents a high level of autogamy, which makes difficult for the differentiation of elite genotypes, and its detection even with DNA markers has not been easy. In germplasm banks, the genetic distinction is a priority in order to use properly selected lines. In this study, was evaluated the variability of 57 genotypes from different geographic areas using morphological characters and molecular markers like RAPD (Random Amplified Polymorphic DNA), ISSR (Inter Simple Sequence Repeat), nrRAMP (non-radioactive Random Amplified Microsatellite Polymorphism) and SSR (Simple Sequence Repeat). RAPD markers even when they generated DNA profiles, these were not informative in chickpea. The ISSR and SSR techniques differentiated the 57 chickpea accessions, which makes them good candidates to characterize this crop. The nrRAMP technique was an effective and useful method to assess the genetic diversity and variability among closely related plants of chickpea; in addition, this technique can be easily implemented in laboratories.

Biography

Ernestina Valadez Moctezuma obtained a degree in Biology from the Universidad Nacional Autónoma de México. She has a Master of Science degree in Genetics from the Colegio de Posgraduados, Montecillo, México and a Ph.D. in Science from the Universidad Nacional Autónoma de México. She is currently a Professor and Researcher at the Universidad Autónoma Chapingo, Mexico of Molecular Biology, Genetic Molecular Markers and Biotechnology areas. Her current lines of research: Differentiation and analysis of genetic variation in *Opuntia*, *Agave*, *Apple* and some phytopathogens, mainly.

Identification and Quantification of Flavonol O-Glycosides with 3,5,4'-Trihydroxy-6,7-Methylenedioxyflavone as an Aglycone from Indigo Leaves and their Biological Activities

Kazushige Yokota¹, Shota Nakai², Tomoe Ishihara², Hideto Kimura² and Mitsuo jisaka¹

¹*Shimane University, Japan*

²*Kotobuki Seika Co., Japan*

Abstract

Polygonum tinctorium Lour. (indigo plant) has been valuable as a medicinal plant for the preparation of traditional herbal medicine. This study was undertaken to identify flavonol O-glycosides with different aglycones from indigo plant by ultra-performance liquid chromatography-electrospray ionization-time-of-flight/mass spectrometry^E together with other instrumental analyses and to quantify the individual components by reverse-phase high-performance liquid chromatography using the 80% methanol extracts from the seeds, sprouts, and aerial parts of indigo plant. The analysis revealed that flavonol O-glycosides with 3,5,4'-trihydroxy-6,7-methylenedioxyflavone (TMF) as an aglycone became mainly detectable in the sprouts and resulted in major constituents of flavonoids in the leaves although they are not detectable in the seeds. The polyphenolic fraction of the leaves exhibited anti-inflammatory effects on cultured macrophage-like cells stimulated with lipopolysaccharide. More potent anti-inflammatory activity was recognized with free TMF than flavonol-O-glycosides with its aglycone. Free TMF were detectable in the blood circulation in mice after oral administration of the fraction containing flavonol O-glycosides with TMF from indigo leaves. We also found that free TMF was as effective as quercetin, another aglycone of flavonols, to suppress the gene expression of pro-inflammatory factors. Moreover, administration of flavonol O-glycosides with TMF as an aglycone appreciably protected against ulcerative colitis in a murine model of inflammatory bowel disease, suggesting the effectiveness in vivo. Flavonol-O-glycosides with TMF showed higher antioxidant activities

than free TMF as evaluated by the assay of hydrophilic oxygen radical absorbance capacity. Taken together, our findings indicate additional health benefits of predominant species of flavonol-*O*-glycosides with TMF from indigo leaves.

Biography

Yokota studied Food Science and Biotechnology at Kyoto University, Japan and graduated as MS in 1980. On the basis of continued study in the doctoral course, he received his PhD degree in 1984 from the same institution. In 1982, he joined the Biochemical Laboratory of Prof. Yamamoto at Tokushima University School of Medicine and worked as an Assistant professor. He shifted to the Faculty of Agriculture at Shimane University, Japan in 1986. He is now a Professor of Institute of Agricultural and Life Sciences at Shimane University, Japan.

Effective Forms, Additive Effect, and Toxicities Scattering Effect of Pharmacodynamic Substances of Traditional Chinese Medicines

Shao-Qing Cai*, Feng Xu, Dong-Hui Yang, Ming-Ying Shang, and Xuan Wang

Peking University, China.

Abstract

The blood concentrations of the pharmacodynamic substances of traditional Chinese medicines (TCMs) are usually very low. How can they exert pharmacological actions? In which forms (original form, metabolite or the both) do they exert the actions? To answer these questions, we proposed a new concept of 'Effective Forms' of pharmacodynamic substances of TCMs and a hypothesis of additive effect of multiple constituents of TCMs. The hypothesis includes that the summation of all of the Effective Forms of pharmacodynamic substances of TCMs is the core material base of the efficacy of TCMs, and the additive effect of the blood concentrations of different Effective Forms is one part of the action mechanism {Cai et al. The 'Efficacy Theory' may help to explain the characteristic advantages of the TCMs. *China J Chin Materia Med* 2015; 40: 3435}. The additive effect of the different Effective Forms of the pharmacodynamic substances of TCMs means additive effect of its numerous constituents or/and metabolites on a target, and therefore the efficacy produced by the addition of the concentrations of all these compounds, which different from the synergy effect of multi-constituents on multi-targets. Those compounds having the similar structure are likely to have the same pharmacological effects on the same target. The synergistic effect based in the overall action of the additive effects of multiple constituents/metabolites on individual targets may be a very important part of the pharmacological mechanism of TCMs. We will give an explanation 'Toxicity Scattering Effect' for 'Why toxicities of TCMs are low'?

Biography

Shao-Qing Cai got his B.Sc. in 1982 at Beijing Medical College and his Ph.D. degree in 1989 at Toyama Medical and Pharmaceutical University in Japan. Since then he has been working at Peking University with research activities: Conservation and efficient utilization of medicinal plants; Effective substances of traditional Chinese medicine. He was vice dean of School of Pharmaceutical Sciences, Peking University and is vice-chairman of Specialty Committee of Medical Resources Utilization and Conservation, World Federation of Chinese Medicine Societies. He serves as member of the Chinese Pharmacopoeia Commission and associate editor of *J Ginseng Research*.

Xanthomonas oryzae p v. *oryzae* TALE Proteins Recruit OsTFIIA γ 1 to Compensate for the Absence of OsTFIIA γ 5 in Bacterial Blight in Rice

Gongyou Chen*, Wenxiu Ma, Lifang Zou, Zhiyuan Ji, Xiameng Xu and Zhengyin Xu

Shanghai Jiao Tong University, China

Abstract

Xanthomonas oryzae pv. *oryzae* (Xoo), the causal agent of bacterial blight (BB) of rice, uses transcription activator-like effectors (TALEs) to interact with the basal transcription factor gamma subunit OsTFIIA γ 5 (Xa5) and activates the transcription of host genes. However, how OsTFIIA γ 1, the other OsTFIIA γ protein, functions in the presence of TALEs remains unclear. In this study, we show that OsTFIIA γ 1 plays a compensatory role in the absence of Xa5. The expression of OsTFIIA γ 1, which is activated by TALE PthXo7, increases the expression of host genes targeted by avirulent and virulent TALEs. Defective OsTFIIA γ 1 rice lines show reduced expression of the TALE-targeted susceptibility (S) genes, OsSWEET11 and OsSWEET14, which results in increased BB resistance. Selected TALEs (PthXo1, AvrXa7 and AvrXa27) were evaluated for interactions with OsTFIIA γ 1, Xa5 and xa5 (naturally occurring mutant form of Xa5) using biomolecular fluorescence complementation (BiFC) and microscale thermophoresis (MST). BiFC and MST demonstrated that the three TALEs bind Xa5 and OsTFIIA γ 1 with a stronger affinity than xa5. These results provide insights into the complex roles of OsTFIIA γ 1 and OsTFIIA γ 5 in TALE-mediated host gene transcription.

Biography

Gongyou Chen, a Ph D professor of School of Agriculture and Biology at Shanghai Jiao Tong University, leads a working group on understanding molecular *Xanthomonas*-plant pathosystems. The major interests includes: (1) what are the plant targets by transcription activator-like effectors (TALEs) of *Xanthomonas* species, (2) How the pathogens use TALE proteins to switch the susceptibility and resistance in plants, (3) How to breed broad-spectrum resistant plants to control plant diseases.

Poster Presentations

Genome-to-Genome Crosstalk of Flowering-time Genes in Hexaploid Wheat

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¹Fukui Prefectural University, Japan

²Kobe University, Japan

Abstract

Bread wheat (*Triticum aestivum*) is an allohexaploid species with A, B and D genomes which were originated from the ancestral species. We made two synthetic hexaploid wheat lines (genome constitution AABBDD) by crossing of *T. turgidum* ssp. *durum* cv. Langdon (AABB) with early-flowering *Aegilops tauschii* accession AT80 (DD) or late-flowering *Ae. tauschii* accession PI508262 (DD). The synthetic hexaploid wheat line Syn6239 derived from AT80 showed early-flowering phenotype, but the synthetic hexaploid wheat line Syn6228 derived from PI508262 was late-flowering. It is noteworthy that the two synthetic lines share the same A and B genomes from a tetraploid cultivar Langdon. The difference of flowering-time of the two synthetic lines was due to the effect of different D genome from different *Ae. tauschii* accessions. We examined expression patterns of a florigen gene, *WFT* (*Wheat FLOWERING LOCUS T*), using a real-time PCR analysis with genome-specific primer sets for three homoeologs of *WFT* gene located on A, B and D genome, *WFT-A*, *WFT-B* and *WFT-D*, respectively. The expression level of *WFT-D* was higher in the early-flowering Syn6239 than in the late-flowering Syn6228, which were similar in *WFT* expression patterns of D genome donors, the diploid *Ae. tauschii* accessions AT80 and PI508262. Surprisingly, in the early-flowering Syn6239, *WFT-A* and *WFT-B* also showed higher expression levels than those in the late-flowering Syn6228. These results indicated that the expression of *WFT-A* and *WFT-B* located on A and B genome, respectively, were affected by some upstream genes in D genome; that is, the genome-to-genome crosstalk of flowering-time genes.

Biography

Koji Murai is a Professor in Department of Bioscience at Fukui Prefectural University.

Forest Structure and Successional Trends in Riparian Forest Stands in Southern Quebec Basins

Diane Saint-Laurent¹, Lisane Arseneault-Boucher¹ and Jean-Sébastien Berthelot²

¹University of Quebec at Trois-Rivieres, Canada

²Paré & Associates, Canada

Abstract

For riparian forest stands, variations in the water balance are an important factor affecting tree growth. In cold temperate regions, spring floods associated with the thawing of the snow cover create additional water stress as a result of a major inflow of water that floods the riparian areas, sometimes over a period of several days or weeks, which can hinder the growth of certain species or even cause them to die. Floods can also strip surface litter and uproot young shrubs and tree saplings not able to withstand the strong currents associated with high stream flows. All of these factors associated with successive floods necessarily create long-term change in tree composition and the structure of riparian forest stands affected by such special water conditions. Studies on riparian vegetation subjected to periodic flooding are rarer, especially for areas affected by successive flooding that causes alluvial plain aggradation. The physiological characteristics of forest communities may indeed vary depending on soil and sediment properties, as well as the microtopography of riverbanks, which are gradually shaped by successive floods. The aim of this study is to understand the dynamics of these wooded areas that are affected by frequent flooding, especially over the last 30 years and which take the form of an increase in the frequency of flooding. This

study could also serve to establish a frame of reference that could be used to monitor changes in these wooded areas, and possibly to recommend restoration measures for riverside areas.

Keywords: Riparian forest; floods; tree population; structure and composition; stand tree ages; southern Québec

Biography

Diane Laurent interests concern the study of riparian forests in relation to pedogenetic processes and climatic changes. Her work includes disturbances associated with frequent floods that alter forest ecosystems and riparian soils. The structure and composition of riparian tree stands and their dynamics and evolution are also part of my research interests.

Morphological and Molecular Characterization of *Cactodera cacti* from Idaho

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Abstract

The cactus cyst nematode (*Cactodera cacti*) is a widespread nematode infecting mainly the plants from the family Cactacea. It is distributed worldwide and is reported in several U.S. states. The soil samples were collected from a cactus garden collection field from Meridian, Idaho. Cysts were successfully recovered from the soil and the roots of the affected plants by sieving and centrifugation extraction method. After fixation, the cysts and juveniles (J2) recovered from cysts were examined molecularly and morphologically. The cysts were lemon shaped, abulate, circumfenestrate, light to dark or reddish brown in color and had a straight to wavy line type of cyst wall cuticular pattern. Measurements of second-stage juveniles included body, stylet, tail, and hyaline tail terminus length. Shape of stylet knobs were semi- rounded, convex anteriorly and posteriorly. The ITS 1&2 rDNA region was amplified with primers TW81 and AB28 producing PCR amplicons of 985 bp. The PCR products were cleaned and then cloned. Six clones representing three J2 were sequenced. Alignments of ITS rDNA sequences from *Cactodera* species and *Betulodera betulae* as an outgroup were also constructed and phylogenetic relationships were estimated with Bayesian interference. Both methods of analysis indicated the specimens were *Cactodera cacti*. To our knowledge, this represents the first report of this cactus cyst nematode in Idaho.

Biography

Mihail Kantor is currently an Established Researcher (ORISE Fellow) working in the Mycology & Nematology Genetic Diversity & Biology Laboratory at USDA ARS, Beltsville. My current research focuses on identification and curation of nematodes submitted from all over the world. His previous research work involved the use of genetic, genomic and metabolomics technologies to enhance disease and pest resistance in watermelon cultivars, a staple crop in the southern United States. In particular, I tried to understand the changes that occur in plants and how they react after being infected by nematodes.

Overexpression of *Solanum tuberosum* SIP1 in *Arabidopsis* Exhibits Stress Tolerance and Improved Photosynthetic Efficiency under Osmotic Stress

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¹United Arab Emirates University, UAE

²Seoul National University, Seoul, South Korea

³University of Geneva, Switzerland

Abstract

Transgenic *Arabidopsis* plants expressing a gene isolated from *Solanum tuberosum* that encodes a small basic intrinsic protein

(SIP1) were developed. In this study, these transgenic *SIP1* plants were subjected to polyethylene glycol (PEG) induced osmotic stress and assessed based on various physiological and photosynthetic parameters. Chlorophyll-a fluorescence induction kinetics was used to evaluate critical photosynthetic parameters like ratio of variable and maximum fluorescence (FV/FM), absorbance of photons per active reaction center (ABS/RC), trapping of photons per active reaction center (TRo/RC), electron transport per active reaction center (ETo/ RC), and performance index (PI). Our findings indicate that the PEG-induced damage was more prominent at the donor side rather than the acceptor side of PSII. Furthermore, *SIP1* plants showed increased proline accumulation, reduced accumulation of oxidants and increased specific activity of antioxidant enzymes. Overall, our findings demonstrate that constitutive expression of *SIP1* in Arabidopsis plants induces significant improvement in abiotic stress tolerance as well as in the photosynthetic parameters under PEG-induced osmotic stress.

Biography

Mayank Anand Gururani obtained his PhD in Molecular Biotechnology in the year 2013 from Konkuk University, South Korea. He worked as a postdoctoral researcher under the supervision of Prof. Pill Soon Song at Jeju National University, South Korea from 2013-2015. He later worked at the Yeungnam University, Gyeongsan, South Korea as an Assistant Professor for one year and moved to the United Arab Emirates in 2016. Currently, he is working as Assistant Professor in the Biology department of UAE University, UAE. His research interests are molecular biology of photosynthesis and abiotic stress physiology.

The Use of Bioreactors on In vitro Multiplication of Brazilian Giant Bamboo: *Guadua magna* Londoño & Filg., Family Poaceae

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¹University of Brasilia, Brazil

²Embrapa Recursos Genéticos e Biotecnologia/CPAB, Brazil

Abstract

Popularly known as "Brazilian Giant Bamboo", *Guadua magna* (Poaceae family) is a sympodial species from the Brazilian Savana. To limit the risk of genetic erosion due indiscriminate use, a rational production of plantlets is needed. This study compared the physiological and biometric responses of plantlets produced in different systems, using liquid culture medium supplemented with 20 g.L⁻¹ sucrose and 6.21 μM meta-Topolin as basic medium. The subcultures were realized every 30 days in four *in vitro* culture systems: Liquid Conventional (T1-LC), liquid under agitation (T2-LA), permanent immersion bioreactor (T3-PERIB) and temporary immersion bioreactor (T4-TIP). Each system received 50 mL of culture medium proportionally per explant used. After three subcultures, the plants were submitted to *ex vitro* acclimatization under greenhouse. After 90 days it was verified that TIP and PERIB presented the higher percentages of shoot survival (85.7%), number of shoots (31.5 and 28.8), shoot size (2.6 cm and 3.1 cm) and fresh mass (15.8 g and 11.8 g), as well as contents of chlorophyll *a* (11.94 μg.cm² and 12.86 μg.cm²), *b* (3.50 μg.cm² and 5.03 μg.cm²) and caratenoids (3.17 μg.cm² and 3.57 μg.cm²). Through electrolyte extravasation analysis, it was possible to verify that in all culture systems membrane damage was relatively low (≤ 33.45), except T2-LA (60,43). The optimal survival rates after acclimatization were observed in plantlets from T4-TIP (95.8%), followed by T3-PERIB (88.2%), T1-LC (66.67%) and T2-LA (0%), with occurrence of spontaneous adventitious rooting. The anatomical analysis of the shoots revealed developing multiple meristematic regions, conferring regular plant growth.

Biography

Fernanda Furlan Queiroz is a Brazilian Biologist, Master in Forestry and Environmental Sciences - UFMT, currently PhD candidate with scholarship in Botany at University of Brasilia - UnB, in the Research fields of Cell Culture and Plant Tissues and Genetic Transformation of Plants. She develops activities in EMBRAPA GENETIC RESOURCES AND BIOTECHNOLOGY - CENARGEN with clonal systems and *in vitro* vegetative reproduction of bamboo species of the Brazilian flora, focusing on genotypic evidence and physiological influences on the response in bioreactors, somatic embryogenesis and suspension cell culture.

Arabidopsis Scaffold Protein Rack1A Regulates Auxin Mediated Lateral Root Development Pathway

Shifaa Alshammari^{1*}, Sivanesan Dakshanamurthy² and Hemayet Ullah¹

¹Howard University, Department of Biology, Washington, DC, USA

²Georgetown University Medical Center, Washington, D.c.,

Abstract

RACK1 (Receptor for Activated C Kinase 1) is a WD-40 type scaffold protein family, conserved in single cell eukaryote yeast to human and plays regulatory roles in diverse signal transduction and stress response pathways. Loss of function mutant in the predominant isoform-RACK1A in *Arabidopsis*, indicates that it regulates diverse environmental stress resistance through negative regulation of stress hormone ABA and positively regulates auxin mediated diverse developmental pathways. It is hypothesized that chemical knock-out, as opposed to genetic knock-out, of RACK1A will provide a functional advantage in protecting plants from diverse stress and a small compound stabilizing RACK1 will be useful to promote auxin regulated developmental pathways. Dozens of small compounds based on our lab derived crystal structure of *Arabidopsis* RACK1A are isolated and functionally tested as their ability modulate the auxin signaling pathways. These functional modulators of RACK1A appear to regulate the auxin induced lateral root development process. In this pathway, the small compound inhibiting stable RACK1A expression appears to produce hyposensitivity to auxin. On the other hand, a RACK1A stabilizing compound provided hypersensitivity to the auxin induced lateral root development. The compound augmenting auxin mediated lateral root development has been found to promote diverse auxin responsive gene expression as well. Taken together, these results suggested that RACK1A may act as a modulator in the auxin signal pathways. This work may lead to understand the molecular interaction between RACK1A and auxin and the possible application of novel RACK1A modulating small compounds as fertilizers to promote auxin mediated developmental pathways safely in non- genetically modified crops.

Biography

Shifaa Alshammari is a 3rd year PhD student in the biology department at Howard University. She received a bachelor's degree in Biological Science from Dammam University, KSA and a master's degree in Biology from Tennessee's State University, USA. Her research interests include studying the molecular role of the Receptor for Activated C Kinase1 (RACK1) scaffold protein in modulating auxin signaling pathway and lateral roots development in the *Arabidopsis thaliana*.

Association Study Reveals Novel Genes Related to Yield and Quality of Fruit in Cape Gooseberry (*Physalis peruviana* L.)

Victor Nunez Zarantes¹, Francy Liliana García-Arias and Jaime Osorio Guarín

AGROSAVIA, Colombia

Abstract

Physalis peruviana L. is a tropical fruit, commonly known as cape gooseberry, in which its genetic breeding program has been focused in the improvement of yield and fruit quality. The association mapping approach can provide insights into the molecular basis of agronomic traits and assist the breeding program. In this study, we characterized a diverse panel of 100 cape gooseberry accessions for yield, fruit size-shape, and fruit quality traits. The Principal Component Analysis (PCA) and the Cluster Analysis (CA) classified the accessions into three different groups and seven accessions were identified for high yield and low cracking fruit. Genotyping-by-sequencing (GBS) conducted in the studied accessions identified 27,982 and 36,142 informative SNP markers based on the alignment against the two cape gooseberry reference transcriptomes, and 30,344 SNPs based on the alignment to the tomato reference genome. Genetic diversity and population structure analyses revealed a low differentiation level between subpopulations and a high genetic diversity. A total of 34 markers were identified related to 22 candidate genes among them, the candidate gene Solyc03g082690.2 was significantly associated with fruit weight (FW), fruit size traits (FS) and fruit weight per plant (FWP). In the future, these markers can be probably used to improve yield or fruit quality in cape gooseberry through marker-assisted selection (MAS).

Incidence of Female *Spodoptera frugiperda* (Noctuidae: Lepidoptera) on Capturing by Traps Baited with Sexual Pheromone from Conspicifics

Mariana Cruz¹, Norma Robledo¹ and Humberto Reyes²

¹Centro de Desarrollo de Productos Bióticos del Instituto Politécnico Nacional, Mexico

²Universidad Autónoma del Estado de Morelos -Jicarero, Mexico.

Abstract

Sexual chemical communication of lepidoptera is important for their reproduction; generally, females emit sexual pheromone (SP) to attract males, but likely females can be attracted to SP from conspecific as it was reported for lepidoptera, thus FS would perform as aggregation pheromone.

Spodoptera frugiperda is the main pest on maize crops in Mexico. This moth has been controlled by using a trap with FS formulated on (Z)-7-dodecenyl acetate, (Z)-9-tetradecenyl acetate and (Z)-11-hexadecenyl acetate. However, there are not reports about captured female moths or their ability to detect their own SP; therefore, this research focused on determining incidence of females captured by SP-baited traps and recognising their reproductive status.

After seeding, four traps/hectare were placed by one week; traps were distributed at 20 m from border of maize crop and 20 m among them; a no-stimulation trap was placed beside every SP-baited trap. Moths counting was registered as capture/trap/night (34 days). Identification of captured insects was carried out by taxonomic keys based on morphological characteristics of genitalia. Bursa copulatrix was dissected to recognise reproductive status: virgin or mated, then spermatophore were reviewed.

11,221 moths were captured, 21.31 % were females and 60 % of females were mated.

An aggregation pheromone trap system performs high impact to decrease population of pests on crops.

Biography

Mariana Cruz completed professional studies at the Instituto Tecnológico Nacional De Mexico where she obtained a degree in Biochemical Engineering with a specialty in Biotechnology and food technology. She is currently studying the third semester of the Master of Science in Agroecological Management of Pests and Diseases in the Centro de Desarrollo de Productos Bioticos del Instituto Politecnico Nacional and a research stay at the Universidad Autonoma del Estado de Morelos where I am working on a project based on the chemical ecology and sexual communication of the insect plague *Spodoptera frugiperda*.

Volatile Compounds from Papaya (*Carica papaya*) Fruit Oviposited and not Oviposited by *Toxotrypana curvicauda*

Mariana Cruz¹, Olga Lidia Ruiz and Norma Robledo

¹Centro de Desarrollo de Productos Bióticos del Instituto Politécnico Nacional, Mexico

Abstract

Toxotrypana curvicauda (Diptera; Tephritidae) oviposita in papaya fruits (*Carica papaya*), causing its deterioration and loss. The selection and acceptance of the host, generally depends on chemical stimuli that the females can identify at a distance. This profile of volatile compounds can change with oviposition. Therefore, the objective of this work was to know the volatile compounds present in the emissions of fruit oviposited and not oviposited. For the extraction of volatile compounds from fruit oviposited and not oviposited, it was carried out by solid phase microextraction and the compounds were identified by gas chromatography-mass spectrometry. The results showed that seven compounds were identified in the two states of papaya fruits, six isoprene derivatives and one more isothiosianate derivative. The Benzyl isothiocyanate was identified only in infested fruits, whereas α -Zingiberene, β -Caryophyllene, β -Curcumene, β -Bisabolene, β -Farnesane and β -Sesquiphellandrene were identified in fruit oviposited and not oviposited, differences in abundances among them.

β -Bisabolene is seven times lower in fruit oviposited compared to abundance in not fruit oviposited, while the abundances of β -Caryophyllene and β -Farnesane are higher in infested fruits. This investigation provides knowledge on the oviposition preference of *T. curvicauda*, which indicates that the Benzyl isothiocyanate could act as an oviposition repellent, likewise it is reported for the first time α -Zingiberene, β -Curcumene, β -Bisabolene and β -Farnesane, in papaya fruits.

Biography

Mariana Cruz completed professional studies at the Instituto Tecnológico Nacional De Mexico where she obtained a degree in Biochemical Engineering with a specialty in Biotechnology and food technology. She is currently studying the third semester of the Master of Science in Agroecological Management of Pests and Diseases in the Centro de Desarrollo de Productos Bioticos del Instituto Politecnico Nacional and a research stay at the Universidad Autonoma del Estado de Morelos where I am working on a project based on the chemical ecology and sexual communication of the insect plague *Spodoptera frugiperda*.

Self-mulch has no Effect on Cumulative Transpiration of Rain-fed East African Highland Banana

Godfrey Taulya¹, Peter Leffelaar², Van Asten Piet³ and Ken Giller²

¹International Institute of Tropical Agriculture, Uganda

²Wageningen University, The Netherlands

³Olam International, Uganda

Abstract

Mulching is reported to increase fresh bunch weight in the rainfed banana cropping systems of Uganda. This study tested the hypotheses that self-mulch: 1) reduces cumulative evaporation from the soil, 2) increases cumulative transpiration, and 3) increases fresh bunch yields in rain-fed EAHB cropping systems. A light interception and utilization-based potential production EAHB model was linked to a soil water balance module to simulate water-limited production. The water balance module has a layer of banana residue mulch (self-mulch) on the soil surface, which is switched on/off via a binary (1, 0) factor. The mulch layer was simulated as mulch area index computed from the biomass yield in the plant growth module and specific mulch area. Drought stress was quantified as the actual to potential transpiration ratio, which in turn was used to reduce dry matter accumulation in the plant growth module. Model calibration and testing was based on soil water storage, EAHB growth and yield data taken from fertilizer response trials on-station at Kawanda (central Uganda) and on-farm in Ntungamo (south-western Uganda). Soil water storage was recorded using a Diviner 2000. Weather data were collected using an automatic weather station. Self-mulch reduced cumulative evaporation from the soil by 40% but had no effect on cumulative transpiration and soil water storage. Self-mulch increased fresh bunch yield by 10% at Kawanda but had no effect at Ntungamo.

Keywords: *Evaporative demand, Light interception, Musa sp. Radiation extenuation, Soil water storage*

Biography

Godfrey Taulya has interest in improving sustainability and resilience of smallholder farmers' production systems without compromising environmental quality. Over the past 15 years he has been engaged in developing and testing best-fit agronomic practices for East African highland banana farming systems, with special focus on managing crop water and nutrient requirements, based on harnessing synergies and managing trade-offs at farming systems level in East and Central Africa.

Susceptibility of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) to some Entomopathogenic Fungi and Bacteria under Laboratory and Field Conditions

Ndonkeu Tita Walter^{1*} and Thabu Mugala

Earth University, Costa Rica

Abstract

The susceptibility of *Spodoptera frugiperda* to various strains of entomopathogenic fungi and bacteria were evaluated under laboratory and field conditions. The treatments used were commercial strains Beardox (Mogto4) and Beardox (Mogbv) containing 1 x 10⁹ spores/ml of *Beauveria bassiana*, Metafix containing 1 x 10⁹ spores/ml of *Metarrhizium anisopliae*, Cillium containing 1 x 10⁹ spores/ml of *Lecanicillium lecanii* and Btis containing 1 x 10⁹ spores/ml of *Bacillus thuringiensis* and a mixture of all fungi strains in combination with *Bacillus thuringiensis*. The results indicated that there was synergism between all the fungi and bacteria strains used. *Lecanicillium lecanii* produced low percentage mortality both under field and laboratory conditions as well as in combination with *B. thuringiensis*, producing a mortality of 60 % and 70 % respectively. There were statistical differences between treatments both under laboratory and field conditions with P<0.001. Under field conditions, the treatment *B. bassiana* (Mogto4), *M. anisopliae*, *B. bassiana* (Mogto4) + *B. thuringiensis*, *M. anisopliae* + *B. thuringiensis*, mixture of all fungal strain, mixture of all fungal strains + *B. thuringiensis* had mortality percentages of 86.67 %, 93.33 %, 96.67 %, 96.67 %, 96.67 % respectively. Under Laboratory conditions, *B. bassiana* (Mogto4) + *B. thuringiensis* and mixture of all fungal strains obtained the highest mortality of 100 % while the treatment with *B. bassiana* (Mogbv) had the least mortality of 70 %. The most common symptom of fungi and bacteria infestation on the insect was sporulation and mummification. Treatment with *L. lecanii* obtained the highest foliage damage index.

Biography

Walter Ndonkeu Tita is a Pest Management expert/Entomologist. He graduated with a Ph.D. in Entomology from McGill University, Canada. Prior to becoming a professor at Earth University, Costa Rica, he worked in the agricultural industry in both Cameroon and Canada for many years. His research interest are in the areas of integrated pest management, parasitic and insect pathogenic nematodes, plantation agriculture, microbial pathogenicity, insect immunity, and insect-plant and pest-pathogen interactions. He is a member of the Canadian Society of Entomology, the Society of Invertebrate Pathology and the Canadian Society of Microbiologist.

DAY-3

WEDNESDAY, March 06, 2019

Featured Presentations

Living with High Putrescine: Metabolic Engineering of the Interacting Pathways of Glu-Orn-Arg-Pro-Polyamines and GABA to Increase C and N Assimilation in plants

Subhash C. Minocha¹ and Rakesh Minocha²

¹University of New Hampshire, Durham, NH

²USDA Forest Service, Durham, NH

Abstract

Our research is focused on evaluating the feasibility of enhancing carbon as well as nitrogen assimilation in plants through genetic manipulation of the metabolism of polyamines – a group of aliphatic amines that play variety of roles in plant development, and abiotic and biotic stress responses. In addition to their role as stress-protective compounds, polyamines participate in key developmental processes mediated by specific signaling pathways involving γ -aminobutyric acid (GABA), NO, and ethylene. Using the techniques of HPLC, radioactive precursor feeding, transcriptomics and metabolomics, we found that increased accumulation of putrescine: (1) is not accompanied by similar increases in spermidine and spermine, (2) does not affect the turnover rates (half-life) of any of the three major polyamines, (3) is not accompanied by alterations in the expression of a broad spectrum of genes in the Glu-Orn-Put-Spd-Spm-GABA pathway; and (4) does not affect the production of Put via the Arg pathway. Many of the genes whose expression is altered in response to over production of putrescine are involved in transcription, translation, membrane transport, osmoregulation, shock/stress/wounding, and cell wall metabolism. The most noteworthy differences in metabolic makeup of the cells are in organic acids, carbohydrates and nitrogen-containing metabolites. There is also a net increase in total C and N accumulation and biomass production in transgenic cells of poplar and whole plants of Arabidopsis. The results provide valuable information about the role of polyamines in regulating both nitrogen and carbon assimilation pathways and guidance in designing transgenic plants with increased nitrogen use efficiency and carbon assimilation.

Biography

Minocha After receiving Ph.D. from University of Washington, Seattle (1972-1974) joined the University of New Hampshire where he is currently a professor of Plant Biology and Genetics. During his tenure at UNH, he has been involved in: (1) teaching a variety of courses in Plant Physiology, Plant Developmental Biology, Plant Biotechnology, Biotechnology and Society, Cell Culture, and Plant Growth Regulators, (2) research on a broad range of projects, like cytodifferentiation of xylem cells in culture in Jerusalem artichoke, somatic embryogenesis in carrot, tissue culture of over 10 plant species (as diverse as Venus fly trap and birches, poplars, pines, spruces, and willows, using techniques of biochemistry, DNA manipulation, genetic engineering, genomics, transcriptomics and metabolomics; (3) Establishing national and international collaborations in research through sabbatical leaves, all leading to joint publications, research grants, reciprocal visits of scientists and scholars from five continents, (4) and served as Department Chair (Botany and Plant Pathology for 6.5 years) and Program Director (Biology 7 years). He has mentored more than 35 graduate student and more than 250 undergraduate students for research. He has been the recipient of “Excellence in Public Service” award (1995), the “UNH Distinguished Professorship” (2002), and “Excellence in International Engagement Award” (2013). In addition, he has about 115 peer-reviewed publications and three (edited) books.

Biotechnological Potential of the Cell Death Conditional Regulators for Improvement of Plants Growth and Seeds Yield

Stanisław Karpiński¹, Maciej Jerzy Bernacki¹, Weronika Czarnocka¹, Anna Rusaczonek¹, Damian Witoń¹, Sergiusz Kęska², Janusz Czyż¹, Ireneusz Ślesak³, Joanna Dąbrowska-Bronk¹ and Magdalena Szechyńska-Hebda^{1,3,4}

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²Siedlce University of Natural Sciences and Humanities, Poland

³The Plant Breeding and Acclimatization Institute, Poland

⁴The Franciszek Górski Institute of Plant Physiology, Poland

Abstract

In *Arabidopsis thaliana*, *LESION SIMULATING DISEASE 1 (LSD1)*, *ENHANCED DISEASE SUSCEPTIBILITY 1 (EDS1)*, and *PHYTOALEXIN DEFICIENT 4 (PAD4)* proteins are conditional regulators of cell death in response to abiotic and biotic stresses. Hormones, such as salicylic acid (SA), and reactive oxygen species, such as hydrogen peroxide (H₂O₂), are key signaling molecules involved in plant cell death. We have demonstrated that silencing of these genes (separately or in combination) in poplar trees can be successfully used for amelioration of plant growth, of cell wall properties and wood quality for pulp production. The proposed mathematical model suggests that LSD1, EDS1 and PAD4 together with SA and H₂O₂ are involved in the regulation of plant water use efficiency (WUE), vegetative growth, and generative development. The analysis of *Arabidopsis* wild-type and single mutants *lsd1*, *eds1*, and *pad4*, as well as double mutants *eds1/lsd1* and *pad4/lsd1*, demonstrated the strong conditional correlation between SA/H₂O₂ and WUE that is dependent on LSD1, EDS1 and PAD4 proteins. Furthermore, we showed that WUE, vegetative biomass accumulation, and seed yield differ significantly in analyzed genotypes depending on the growing conditions, and therefore cannot be described by the same mathematical equation. However, we found a strong correlation between the SA/H₂O₂ homeostasis of 4-week-old *Arabidopsis* leaves and total seed yield of 9-week-old plants. Altogether, our results prove that SA and H₂O₂ are conditionally regulated by LSD1/EDS/PAD4 to govern WUE, biomass accumulation, and seed yield. Conditional correlation and the proposed model presented in this study can be used as the starting points in the creation of a plant breeding algorithm that would allow to estimate the seed yield at the initial stage of plant growth, based on WUE, SA, and H₂O₂ content.

Acknowledgments: This work was financially supported by the “CROPTECH” project granted to SK by the Polish National Centre for Research and Development and the “Maestro 6” project (2014/14/A/NZ1/00218) granted to SK by the Polish National Science Centre.

Light Absorption Efficiency, A Key Process Behind Leaf Economics Trade-Offs

Susana Enríquez

National Autonomous University of Mexico, Mexico

Abstract

A universal trade-off in leaf economics has defined leaves with quick or slow returns on their investments of nutrients and mass. Species with quick returns present leaves with high nutrient contents, high rates of photosynthesis and respiration per unit mass, short lifetimes and high leaf area per mass (SLA). In contrast, species with slow returns produce expensive leaves (high LMA=1/SLA) with longer lifetimes, low nutrient content and low rates of photosynthesis and respiration. The evolutionary driver of this trade-off has to affect central processes in the photosynthetic activity of plants, considering the universal spectrum of leaf economics. Here, I discuss the importance of light absorption and more specifically the variation in light absorption efficiency of the photosynthetic structure to explain the benefits and costs of this trade-off.

Biography

Susana Enríquez is originally from Spain where she received her Bch degree in Biology in 1986 at the Autonomous University of Madrid and also a PhD in Marine Biology in 1993. She spent more than three years at the University of Copenhagen (DK) supported by a UE Marie Curie fellowship, where she continued developing her Ph.D research on functional allometry of photosynthetic organisms. Since 1998 is working as researcher at the University National Autonomous of Mexico (UNAM) in a department nearby Cancun specialized in coral reef research, where she investigates the photobiology and ecophysiology of seagrasses, algae and corals.

Phenotyping of Soybean by UAS-Based Multi-Sensor Data Fusion

Monica Herrero-Huerta^{1,2,*} and Katherine M. Rainey²

¹Purdue University, West Lafayette, Indiana

²University of Salamanca, Spain

Abstract

Precise and functional phenotyping is a limiting factor for crop genetic improvement. However, because of its ease of application, imagery-based phenomics represents the next breakthrough for improving the rates of genetic gains in field crops. Currently, crop breeders lack the know-how and computational tools to include such traits in breeding pipelines. A fully automatic user-friendly data management together with a more powerful and accurate interpretation of results should increase the use of field high throughput phenotyping platforms (HTPPs) and, therefore, increasing the efficiency of crop genetic improvement to meet the needs of future generations.

The aim of this study is to generate a data fusion methodology to high throughput phenotyping from 2D and 3D information; based on temporal multispectral imagery (MSI) and visible data (RGB) collected from Unmanned Aerial Systems (UAS) in soybean crops. The approach will be developed in a novel and innovative way, ensuring flexibility and simplicity in data acquisition, automation in the process and high-quality results, using low-cost sensors. The non-invasive system proposed allows the determination of biophysical models and physiological growth analysis by combining close-range photogrammetry (quality) and computer vision (flexibility, automation and efficiency). During the growing season of 2017, a soybean experiment was carried out at the Agronomy Center for Research and Education (ACRE) in West-Lafayette (Indiana, USA). Periodic images were acquired by Parrot Sequoia Multispectral sensor and G9X Canon camera on board senseFly eBee.

The results confirm the feasibility of the proposed methodology, providing scalability to a comprehensive analysis of crop extension and affording a constant operational improvement and proactive management.

Biography

Civil Engineering with a PhD entitled 'Close-Range Photogrammetry applied to Agroforestry Engineering' from the University of Salamanca (Spain, 2016). Postdoctoral studies from Delft University of Technology (The Netherlands) in Geosciences and Remote Sensing (2015-2018). Active member from TIDOP research group (Geomatic Technologies for the 3D digitalization and modelling of complex objects) (Spain). Currently, research staff member at Purdue University in Agronomy developing Analytical Tools for Drone-based Canopy Phenotyping. Her research interests has been focused on close-range hyperspectral photogrammetry and LiDAR by alternative platforms and specifically in computer vision and deep learning analysis by multi-sensor data fusion applied to agro-forestry and plant science: monicaherrerohuerta.webnode.com

Gene Delivery into Plant Mitochondria

Alicja Ziemienowicz*, Trevor MacMillan, Fengying Jiang and François Eudes

Agriculture and Agri-Food Canada, Canada

Abstract

The ability to genetically engineer plant cell mitochondria has many important applications in cell biology and agricultural biotechnology. Mitochondria play a central role in cellular metabolism and are linked to important agronomic traits. Therefore, it is critical to gain a greater understanding of the mitochondria's role in the essential metabolic pathways and to learn how this knowledge can be applied to increase plant performance through breeding and genetic engineering.

Current mitochondrial research in plant and animal cells is restricted due to the limited ability to manipulate the mitochondrial genome in whole cells. Our studies resulted in discovery of a method for genetic engineering the mitochondria of plant

cells. The method was achieved by selecting short peptides that combine cell-penetrating properties with specific organelle targeting properties; thus, these peptides were named mitochondrial targeting peptides (mTPs). The mTPs were able to form nanoparticles in the presence of exogenous double-stranded DNA (dsDNA) and to deliver DNA reporter gene cassette to the mitochondria of triticale protoplasts and microspores. The mTP-delivered DNA was then expressed in the transfected cells and inserted into their mitochondrial genomes. Moreover, we demonstrated that microspores with exogenous DNA integrated into the mitochondrial genome can be regenerated into plantlets. This method represents the first successful gene delivery into crop plant somatic and germ cells. This new method can be used to study mitochondrial functions as well as to develop crop plants with novel traits relevant to agriculture.

Biography

Ziemiłowicz graduated with a Ph.D. (1995) in molecular biology from the University of Zurich, Switzerland. She held two post-doctoral positions (Friedrich Miescher Institute in Basel, Switzerland; University of Gdansk, Poland) - research on Agrobacterium-mediated plant transformation. She also led the Molecular Genetics Laboratory at the Jagiellonian University in Krakow, Poland, and continued her research on Agrobacterium. Dr. Ziemiłowicz was Associate Professor at the University of Lethbridge, Canada, from 2007 to 2012. In 2013 she joined the Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, where she leads the Novel Trait Development program focusing on factors limiting crop productivity.

Response of Soil CO₂ Emission and Spring Maize Growth to Ridge-Furrow Mulching in the Chinese Loess Plateau

Weiwei Li^{1*}, Yuncheng Liao¹, Wei Wu¹, Xiaoxia Wen¹, Juan Han¹ and Qianlai Zhuang²

¹Northwest A&F University, China

²Purdue University, West Lafayette, IN

Abstract

Ridge-furrow mulching system (RFMS), as a prospective rainwater harvesting system, has been widely adopted in arid and semi-arid areas, but its effect on soil CO₂ emission is still poorly understood. Field experiments were conducted in 2014 and 2015 to compare maize growth and soil CO₂ emissions among different RFMS practices (i.e., three different ridge/furrow ratios) and conventional flat planting (CK, without mulching). We found that RFMS practices significantly increased soil temperature of the ridge, promoted soil moisture of the furrow, and enhanced microbial diversity at the early crop growth stage, resulting in increased soil respiration. The ridge soils exhibited much higher soil respiration than the furrow soils under all three RFMS practices. Soil temperature rather than soil moisture explained the seasonal variation of soil respiration for both CK and RFMS. The improved hydrothermal characteristics of RFMS plots also led to early and stable seedling establishment, leading to higher grain yield and water use efficiency (WUE). Compared with CK, RFMS with ridge/furrow ratios of 40:70 cm, 55:55 cm, and 70:40 cm, significantly increased soil CO₂ emissions by 10.6%, 19.6%, and 20.4%, respectively, while increasing maize yield by 26.1%, 36.4%, and 50.3%, respectively, averaged over two years. Carbon emission efficiency (CEE) was significantly higher in RFMS than in CK in both years. This study suggests that, due to its high yield, WUE, and CEE, RFMS with a ridge/furrow ratio of 70:40 cm could be a highly promising strategy for sustaining crop productivity while minimizing environmental impacts.

Biography

Weiwei Li is a PhD candidate majored in Ecology at Northwest A&F University. Her research interests mainly focus on improving crop productivity with plastic film mulching in dryland areas, carbon exchanges between agricultural ecosystems and the atmosphere, and partition of soil respiration. In 2017-2018, she studied at Purdue University as a joint PhD student and was supervised by Prof. Qianlai Zhuang at the Ecosystems & Biogeochemical Dynamics Laboratory. During her visit, she tried to conduct O₃ impacts on crop yield in the US.

The Germplasm Resources and Utilization Status of Crataegus Plants in China

Dong Wenxuan

Shenyang Agricultural University, China

Transcription Factor SmWRKY1 Positively Promotes the Biosynthesis of Tanshinones in *Salvia miltiorrhiza*

Guoyin Kai^{1,2*}, Wenzhi Cao², Yao Wang¹, Xiaolong Hao² and Min Shi¹

¹Zhejiang Chinese Medical University, China

²Shanghai Normal University, China

Abstract

Tanshinones, one group of bioactive diterpenes, were widely used in the treatment of cardiovascular diseases. WRKYs play important roles in plant metabolism, but their regulation mechanism in *Salvia miltiorrhiza* remains elusive. In this study, one WRKY transcription factor *SmWRKY1* was isolated and functionally characterized from *S. miltiorrhiza*. Multiple sequence alignment and phylogenetic tree analysis showed *SmWRKY1* shared high homology with other plant WRKYs such as *CrWRKY1*. *SmWRKY1* was found predominantly expressed in leaves and stems, and was responsive to salicylic acid (SA), methyl jasmonate (MeJA), and nitric oxide (NO) treatment. Subcellular localization analysis found that *SmWRKY1* was localized in the nucleus. Over-expression of *SmWRKY1* significantly elevated the transcripts of genes coding for enzymes in the MEP pathway especially 1-deoxy-D-xylulose-5-phosphate synthase (*SmDXS*) and 1-deoxy-D-xylulose-5-phosphate reductoisomerase (*SmDXR*), resulted in over fivefold increase in tanshinones production in transgenic lines (up to 13.7 mg/g DW) compared with the control lines. A dual-luciferase (Dual-LUC) assay showed that *SmWRKY1* can positively regulate *SmDXR* expression by binding to its promoter. Our work revealed that *SmWRKY1* participated in the regulation of tanshinones biosynthesis and acted as a positive regulator through activating *SmDXR* in the MEP pathway, thus provided a new insight to further explore the regulation mechanism of tanshinones biosynthesis.

Biography

Guoyin Kai, Male, Philosophy Doctor (Ph.D.), now is a professor of plant biotechnology, head of Lab of Medicinal Plant Biotechnology in Zhejiang Chinese Medical University. He got his B Sc in biology education M Sc in crop breeding, Specialist in biochemistry and molecular biology, Philosophy Doctor's degree (Ph.D.) at Shanghai Jiaotong University, China. From 2012-2013, he worked in USA as a visiting scientist. Currently Dr. Guoyin Kai' researches focus on the plant metabolic engineering and TCM resource biotechnology. Studies on the mechanisms of biosynthesis and regulation of active compounds in medicinal plants. Now he has published more than 100 papers and applied more than 30 Chinese patents.

Effect of Flavonoids on Mycorrhizal Synthesis between *Arbutus unedo* L. In Vitro Plants and *Tuber borchii* or *Lactarius deliciosus*

Filomena Gomes^{1*}, Rita Santos¹, Joana Pereira¹, Fábio Castro¹, Patrícia Figueiredo², Inês Ferreira³, Helena Machado⁴ and João Nunes⁵

¹Polytechnic Institute of Coimbra/ CERNAS, Portugal

²GREENCLON LDA, Portugal

³Voz da Natureza LDA, Portugal

⁴National Institute for Agrarian and Veterinarian Research, Portugal

⁵BLC3 Association, Portugal

Abstract

Arbutus unedo L. is a Mediterranean species drought tolerant and fire resistant due to its low-level of combustibility and regeneration ability following fire occurrence. Fruits can be processed or consumed as fresh fruit. Adult plants were selected and micropropagated. New orchards were established considering the higher production of clones compared to seedlings. Mycorrhizal fungi as *Tuber borchii* or *Lactarius deliciosus* can produce edible mushrooms increasing the landowners's yield. Quercetin, among flavonoids, is known by stimulate the mycorrhization.

The objective of this study was to evaluate the effect of quercetin addition on mycorrhization. Two clones were tested during the *ex vitro* rooting. As mycorrhizal fungi a vegetative inoculum of *Lactarius deliciosus* and spores of *Tuber borchii* were used. Five quercetin levels (0.5 – 10 μ M) were tested after the addition to different media for inoculation (Knop medium compared to water distilled and sterilized). Perlite was used as substrate for inoculation. Six months after inoculation, plants were transferred to field containers and roots were analyzed.

When quercetin was added, a higher level of mycorrhizae establishment was observed compared to control. The mycorrhization level for both fungi was dependent of genotype, quercetin level and media culture (P<5%). Clones showed different response to quercetin level and inoculation media. However, similar genotype response was observed for both fungi tested. The highest level of quercetin showed a toxic effect. Roots were examined before field trial establishment, which intends to confirm long term persistence of mycorrhizae and to evaluate the fungal colonization level required to guarantee mushroom production.

Biography

Filomena Gomes is a lecturer at the Coimbra, Graduate in Forestry with Master and PhD in Plant Biology. Professional career began as a teacher of Soils and Fertility (1982-85). From 1985 to 1995 worked in tree breeding and plant propagation at Portucel Florestal. Since 1995, at ESAC as a teacher in the Forestry Department. Since 2005 has been working on plant breeding of *Arbutus* and Chestnut. Since 2012 has been collaborating in R&D European projects (ProDeR, FCT, PDR2020), with several partners, to improve vegetal material and cultural practices, collaborating with Research & Development Entities, Associations and Forest Producers.

21st Century Challenges to Food Security: An Attempt to Increase Crop Production through Transgenic and Genome Edited Approaches

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Abstract

The present status of global food security is alarming! The ever-increasing population coupled with various biotic and abiotic stresses brings toughest challenges and threatened for food production and sustainable agriculture. Recent development of molecular tools for precision gene manipulation for trait improvement is very much encouraging and has already been moved from laboratory curiosity to providing new varieties. Our strategies were to manipulate few key genes of interest to control notorious biotic stress weed as well as generate high yielding variety to meet the predicated food demand by 21st century. We have successfully introduced multiple distinct point mutations in the native copy of *OsALS* and *OsEPSPS* gene (major target for important herbicides) through homologous recombination using CRISPR/Cas9 platform. Alternate herbicide management is also important for minimum impact on the environment. Previously in our lab we separately generated over expressed mutated *OsEPSPS* dm and *PsPtXD Japonica* and *Indica* lines. Afterward, we have developed an *OsEPSPS* dm X *PsPtXD japonica* hybrid model for further evaluation of combined herbicidal effect of Glyphosate and Phosphite along with multi-utility effect of phosphite on crop management system.

Inflorescence development and architecture is key determinant of grain size, number and yield which are the most important traits and regularly used in plant breeding programs. Phytohormones cytokinins are known to have profound influence on these major agronomically important traits. We have targeted *OsCKX2* (negative regulator of cytokinins biosynthesis pathway) for attaining higher yield through CRISPR/Cas9. Respective edited and transgenic lines will be further evaluated for physiological and biochemical analysis and their potential commercial release.

Biography

Bhabesh Borphukan currently pursuing PhD in Plant Molecular Biology from International Center for Genetic Engineering and Biotechnology, New Delhi, India. He have completed my B.Sc. degree in Agri. Biochemistry and Plant breeding from Assam Agricultural University, India. He hold M.Sc. in Agri. Biotechnology for the evaluation of Shorghum minicore and expression profiling of *R*-genes for charcoal rot disease from University of Agricultural Sciences Dharward, India. His doctoral research work mainly focuses on the development of method for achieving homologous recombination based genome editing in rice along with increase yield and nitrogen use efficiency in rice.

Nativity and Ancestry of the Dessert Watermelon, *Citrullus lanatus*

Harry S. Paris

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Abstract

Watermelons, *Citrullus* species, are xerophytes native to Africa. Dessert watermelons, *C. lanatus*, are much loved worldwide. However, the nativity and ancestry of the dessert watermelon have befuddled many investigators. A common idea is that the colocynth, *C. colocynthis*, is the ancestor of the dessert watermelon. Although the fruits of the colocynth are small with bitter white or greenish fruit flesh, as would be expected for an ancestor, there are weak crossability barriers between it and the dessert watermelon. Another common idea is that the citron watermelon, *C. amarus*, is the ancestor. The citron watermelon grows wild in southern Africa and its fruits are hard, bland or bitter. However, there are weak crossing barriers between it and the dessert watermelon. A more recent idea, based on genomic analysis, is that the egusi watermelon, *C. mucospermus*, cultivated in western Africa for consumption of its seeds, is the ancestor. Here, too, there are weak crossing barriers between it and the dessert watermelon. A recent treatment of the genus, based on genomic analysis, confirms that the colocynth, citron, egusi, and dessert watermelons are indeed separate species that diverged from one another millions of years ago. A more recent analysis of archaeological and iconographic evidence from Egypt and Sudan, literary evidence from the classical period, and the modern distribution of small, primitive watermelons in Sudan and neighbouring countries overwhelmingly indicates that dessert watermelons are native to northeastern Africa and sweet dessert watermelons were selected in Mediterranean lands by no later than the second century CE.

Biography

Harry Paris is a senior scientist, recently retired, from the Agricultural Research Organization, Israel. His professional career, spanning over 40 years, was devoted to breeding cucurbits and exploring the mode of inheritance of some of their horticulturally important traits, and to researching the evolution and history of cucurbit crops.

Novelties on the taxonomy of *Senegalia* Raf. (Leguminosae): segregation of new genera

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Abstract

Morphological and genetic studies support that the genus *Acacia* Mill. (Fabaceae, Mimosoideae) is polyphyletic. The evidence for this is based on almost two decades of molecular studies that have elucidated major relationships of *Acacia* s.l. and other related taxa within the Mimosoideae. These studies confirm that *Acacia* s.l. is non-monophyletic and has led to a revised taxonomy of seven genera from the former *Acacia* s.l. This includes the retypification of the *Acacia* to the mainly Australian clade, which was approved at the XVII International Botanical Congress at Vienna. These genera mostly correspond to five formerly recognized infrageneric taxa of *Acacia* s.l.: the former subgenus *Acacia* (as the genus *Vachellia*), subgenus *Aculeiferum* sect. *Aculeiferum* (as genus *Senegalia* s.s.), sect. *Filicinae* (as the genus *Acaciella*), subgenus *Phyllodineae* (as the genus *Acacia*), and the genus *Mariosousa*. There remain two groups of previously poorly or unsampled species that we are proposing as new genera based on molecular biology and morphological characteristics: *Parasenegalia* and *Pseudosenegalia*. Although members of these two genera are distinct, previous taxonomic treatments have not dealt with them as separate units within *Acacia* subg. *Aculeiferum*. The species of *Parasenegalia* are widespread in the tropical areas of the Caribbean and scattered in Central and South America. Those of *Pseudosenegalia* are found in Bolivia. The authors wish to thank the financial support granted by Capes, CNPq, Fapemig, Fapesb, and CSIRO.

Biography

Vanessa Terra has been a professor at the Federal University of Uberlândia for almost 4 years. She is biologist (Federal University of Santa Maria (RS/Brazil) with master's degree and Ph.D. in Botany from the Federal University of Viçosa (MG/Brazil) with part of her Ph.D. carried out in CSIRO Plant Industry (Canberra/ACT/Australia). She works with taxonomy and phylogeny of Leguminosae with emphasis in the *Senegalia* species.

Anatomical Interpretation of the Phylogeny and Taxonomy of the Genus *Chamaecrista* Moench (Leguminosae) with Special Focus on Secretory Structures

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Abstract

Chamaecrista is a legume genus with ~330 species distributed across the tropics, being most diverse in the New World. The topography of the molecular phylogenetic tree disagrees with the traditional grouping of species based mainly on flower morphology and presence/absence of nectaries and secretory hairs. Our study aimed to anatomically characterize *Chamaecrista* species, identifying meaningful morphoanatomical characters that may shed light on the taxonomy and phylogeny. Standard light microscopy techniques were used to anatomically characterize leaves and flowers. Type, position and chemical nature of the exudates of the extrafloral nectaries are important for the taxonomy at the sectional level. The presence of mucilage, pectins, proteins, and polysaccharides is evidence for the complexity of such nectar. Although the morphology of the secretory glandular hairs varies, they usually consist of a short stalk and a large spherical-shaped glandular head with a beak-shaped filiform projection. An apical pore, formed as the result of the breaking of the tip projection, allows the immediate discharge of oleoresin-rich secretion. Several types of non-vascularized colleters were found. The colleter exudates is made up by a mixture of hydrophilic and lipophilic compounds. Osmophores were found in flowers of forest woody species. The position and type of stomata, type of mesophyll, presence/position of mucilage idioblasts and venation pattern of petiole/rachis also provided useful characters for discriminating species of *Chamaecrista*. Our data hold great taxonomic and phylogenetic potential. However, a broad molecular phylogeny of *Chamaecrista* is still required in order to understand how such morphoanatomical characters evolved within the genus.

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