conferenceseries.com
549th Conference

4th International Conference on

Plant Genomics

July 14-15, 2016 Brisbane, Australia

Scientific Tracks & Abstracts

(Day 1)

Track 6, 12 & 13

Day 1 July 14, 2016

Track 6: Plant Genomics Applications
Track 12: Plant Physiology
Track 13: Plant Pathology

Session Chair
Grace Chen
USDA-Western Regional Research Center, USA

Session Co-Chair
Jasdeep Chatrath Padaria
National Research Centre on Plant Biotechnology, India

Session Introduction

Title: **The nitrate inducible NAC transcription factor TaNAC2-5A controls nitrate response and increases wheat yield**

Xue He, Chinese Academy of Agricultural Sciences, China

Title: **Molecular regulation of nitrate in plants**

Yong Wang, Shandong Agricultural University, China

Title: **The rpg4/Rpg5 integrated decoy resistance to wheat stem rust race *TTKSK* in barley: Towards effector identification**

Robert Saxon Brueggeman, North Dakota State University, USA

Title: **Presence of endogenous Badnavirus sequences in yam genome: Implication for tropical crops exchange**

Marie Umber, French National Institute for Agronomic Research, West Indies

Title: **Analysis of olfactory genes in Sitobion avenae by antennal transcriptome**

Julian Chen, Chinese Academy of Agricultural Sciences, China

Title: **Phytochemical constituents and bioactive properties of *Glinus oppositifolius* (L) Aug. DC., against bacterial pathogens**

Juliana Janet R Martin-Puzon, University of the Philippines, Philippines

Title: **Induced defense responses in hop-Verticillium interactions as revealed by proteomic and transcriptomic analysis**

Branka Javornik, University of Ljubljana, Slovenia

Title: **Transcriptome analysis of *Lesquerella*: A potential industrial oilseed crop for hydroxy fatty acid production**

Grace Chen, USDA-Western Regional Research Center, USA

Title: **Plant response to biotic stress: Insights from transcriptomics and structural genomics**

Ana Maria Benko Iseppon, Federal University of Pernambuco, Brazil

Title: **Compartmentalized metabolic engineering of plant for rational drug biosynthesis and oral delivery of whole plant material facilitated cost effective malaria treatment**

Shashi Kumar, International Centre for Genetic Engineering and Biotechnology, India

Title: **Genome-wide association for pollen viability and silk receptivity under heat stress in tropical maize**

Ayyanagouda Patil, University of agricultural Sciences, Raichur, India

Title: **Transcriptome profiling for identifying genes to develop abiotic stress tolerant transgenic wheat**

Jasdeep Chatrath Padaria, National Research Centre on Plant Biotechnology, India

Title: **Differential metabolic profiles and transcriptomic profiles during different color stages of albino tea plant (Camellia sinensis)**

Liang Chen, Tea Research Institute of the Chinese Academy of Agricultural Sciences, China

Title: **Studying host-insect interactions using viral induced gene silencing and siRNA**

Anna-Maria Botha Oberholster , Stellenbosch University, South Africa

Title: **Dissection of the network underlying agronomic traits in soybean**

Zhixi Tian, Chinese Academy of Sciences, China

Title: **Adaptive ecological incipient sympatric speciation of wild barley at "Evolution Canyon"**

Eviatar Nevo, University of Haifa, Isreal

Xue He et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

The nitrate inducible NAC transcription factor TaNAC2-5A controls nitrate response and increases wheat yield

Xue He, Wenjing Li, Baoyuan Qu, Xueqiang Zhao, Wenying Ma, Bin Li, Zhensheng Li and **Yiping Tong**
Institute of Genetics and Developmental Biology-CAS, China

Nitrate is a major nitrogen resource for cereal crops, thus understanding nitrate signaling in cereal crops is valuable for engineering crops with improved nitrogen use efficiency. Although several regulators have been identified in nitrate sensing and signaling in Arabidopsis, the equivalent information in cereals is missing. Here, we isolated a nitrate inducible and cereal specific NAC transcription factor TaNAC2-5A from wheat (*Triticum aestivum*). CHIP-SEQ (Chromatin Immunoprecipitation based Sequencing) dates indicated that TaNAC2-5A could bind to the genes encoding nitrate transporter and glutamine synthetase and the genes involving auxin signaling pathway. And a RING Zinc-finger protein that was screened by yeast two-hybrid may regulate the response of TaNAC2-5A to nitrate. Overexpression of TaNAC2-5A in wheat enhanced root growth and nitrate influx rate and hence increase root ability to acquire nitrogen. Further, we found that TaNAC2-5A over-expressing transgenic wheat lines had higher grain yield and higher nitrogen accumulation in aerial parts and allocated more nitrogen in grains in a field experiment. These results suggest that TaNAC2-5A is involved in nitrate signaling and show that it is an exciting gene resource for breeding crops with more efficient use of fertilizer.

Biography

Xue He has completed her PhD from China Agriculture University in 2007 and joined the Tong Fellow at Center for Molecular Agrobiology, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences. Her interest focuses on the genetic improvement of nitrogen use efficiency of wheat. She has published research results in *Plant Journal, Plant Physiology, New Phytologists*, etc.

hexue@genetics.ac.cn

Notes:

Yong Wang, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Molecular regulation of nitrate in plants

Yong Wang
Shandong Agricultural University, China

We identified a novel gene named Nitrate Regulatory Gene 2 (NRG2) by using forward genetics, which mediates nitrate signaling in Arabidopsis. *NRG2* mutants showed inhibited induction of nitrate responsive genes after nitrate treatment by an ammonium independent mechanism. The nitrate content in roots was significantly lower in the mutants than in WT, which may have resulted from reduced expression of *NRT1.1* and up-regulation of NRT1.8. Genetic and molecular data suggest that *NRG2* functions upstream of *NRT1.1* in nitrate signaling. Furthermore, *NRG2* directly interacts with NLP7 in the nucleus but does not affect the nuclear retention of NLP7 in the presence of nitrate. Transcriptomic analysis revealed that genes involved in four nitrogen related clusters were differentially expressed in the *NRG2* mutants. A nitrogen compound transport cluster was regulated by both *NRG2* and *NRT1.1*, while no nitrogen related clusters showed regulation by both *NRG2* and NLP7. Thus, *NRG2* plays a key role in nitrate regulation in part through modulating *NRT1.1* expression and may function with NLP7 via their physical interaction. *NRG2* family consists of 16 members and each protein contains two uncharacterized functional domains: DUF630 and DUF632. We further investigated the role of NRG2.10 and NRG2.15 in regulating nitrate signaling in Arabidopsis. The results showed that the induction of nitrate responsive genes after nitrate treatments and the nitrate accumulation in seedlings were affected in both NRG2.10 and NRG2.15 mutants. These findings demonstrate that *NRG2* family members play important roles in nitrate signaling.

Biography

Yong Wang has obtained his PhD degree from University of Lausanne in Switzerland in 2006 and Postdoctoral studies from the University of California, San Diego in USA. He has been working as a Professor at Shandong Agricultural University in China since 2010. He has published many papers in reputed journals including The Plant Cell and Plant Physiology etc.

wangyong@sdau.edu.cn

Notes:

conferenceseries.com

4th International Conference on
Plant Genomics

July 14-15, 2016 Brisbane, Australia

The *rpg4/Rpg5* integrated decoy resistance to wheat stem rust race *TTKSK* in barley: Towards effector identification

Robert Saxon Brueggeman[1], **Roshan Sharma Poudel**[1], **Shyam Solanki**[1], **Shiaoman Chao**[2] and **Jonathan Richards**[1]
[1]North Dakota State University, USA
[2]United States Department of Agriculture-Agricultural Research Service, USA

The barley *rpg4/Rpg5* locus confers resistance against wheat stem rust caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*) including race *TTKSK* (A.K.A. *Ug99*). The 70 kb region harbors two NLR R-genes, *Rpg5* and *HvRga1* that are required together for resistance. *HvRga1* and *Rpg5* contain typical NLR resistance-protein structure; however, *Rpg5* has an additional C-terminal serine threonine protein kinase (STPK) domain. The transcription factor, *HvVOZ1* was identified by yeast-two-hybrid of a library constructed from RNA of the *rpg4/Rpg5+* line Q21861; 48 hours post inoculation, utilizing the Rpg5-STPK domain as bait. We hypothesize that the Rpg5-STPK acts as an integrated decoy that HvVOZ1 binds to negatively regulate defense activation or binds after activation as part of a signaling complex. The second NLR, HvRga1, may guard theHvVOZ1-Rpg5 interaction or surveil the *Rpg5*-STPK domain for *Pgtrpg4/Rpg5*-Avr (*r45-Avr*) effector manipulation. Thus, *HvRga1* is possibly the guard that detects manipulation of the *Rpg5* STPK or possibly HvVOZ1 by the *r45-Avr* effector eliciting a strong effector triggered immunity defense response. The *r45-Avr* needs to be identified to thoroughly investigate these mechanisms and test our hypothesis. To accomplish this a panel of 37 wheat stem rust isolates collected in North Dakota, many with differential race typing on the wheat differentials and differential reactions on *rpg4/Rpg5* and *Rpg1* in barley were genotyped using restriction site associated DNA-genotyping-by-sequencing (RAD-GBS). This RAD-GBS produced 4,919 informative SNPs and this initial genotyping was used to select 24 diverse isolates (16 *avrRpg4/rpg5* and 8 *Avrrpg4/Rpg5+*) that were used to conduct in planta RNA-seq analysis during *Pgt* colonization 5 days post inoculation on the susceptible barley cultivar Harrington. The RNA-seq data was utilized to identify ~181,000 variant calls (SNPs and indels) within these *Puccinia graminis* transcriptomes during the infection process. The robust genotyping and phenotyping on these diverse differential isolates should allow us to identify candidate *r45-Avr* genes utilizing association mapping.

Biography

Robert Saxon Brueggeman has completed his PhD in 2009 from Washington State University and Postdoctoral studies also from Washington State University Department of Crop and Soil Science. He is currently an Associate Professor at North Dakota State University as the Barley Pathologist/Molecular Geneticist. He has published more than 32 papers in reputed journals covering the topics of the cloning and characterization of barley disease resistance genes and fungal effectors.

Robert.Brueggeman@ndsu.edu

Notes:

Marie Umber, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Presence of endogenous *Badnavirus* sequences in yam genome: Implication for tropical crops exchange

Marie Umber
French National Institute for Agronomic Research, French West Indies

The French West Indies Biological Resources Centre for Tropical Plants (CRB-PT) maintains several germplasm collections of tropical crops and wild relatives, including a collection of more than 450 yam accessions (*Dioscorea spp*). The purpose of this Centre is to conserve and distribute virus-free germplasm to end users. Yam is the third most important staple food crops in French Caribbean islands, after banana and sugarcane. Cultivation of this crop is almost exclusively by vegetative propagation, which presents challenges in the sharing and exchange of plant material because of the vertical transmission of viruses. To this aim, virus populations infecting conserved accessions are characterized and appropriate detection tools are created or optimized, then implemented for the sanitation of infected germplasm. Several *Badnavirus* species have been reported in yams. Recently, endogenous Dioscorea badnaviral sequences (eDBVs) were described in the genome of African yams of the D. cayenensis subsp., rotundata complex. The genome of the other two main cultivated yam species, D. alata and D. trifida has also been investigated by the analysis of BAC libraries. The major constraint of these sequences is to interfere with *Badnavirus* PCR-based detection methods and prevent from the accurate diagnostic of *Badnavirus* in yams. Moreover the occurrence of endogenous sequences from extant *Badnavirus* species in yams should suggest that some eDBVs could be infectious as some eBSV (endogenous Banana streak virus) sequences in banana. Conversely, molecular evidence supporting the role of these EVEs (endogenous viral elements) in antiviral defense will also be presented.

Biography

Marie Umber has completed her PhD from Strasbourg University in France and Postdoctoral studies in Guadeloupe (French West Indies), working on endogenous viral sequences in yam and banana. Since 2013, she is the person in charge of the viral sanitation of the yam collection from the Biological Resources Centre for Tropical Plants (CRB-PT) in the French National Institute for Agronomic Research (INRA).

marie.umber@antilles.inra.fr

Notes:

Julian Chen et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Analysis of olfactory genes in Sitobion avenae by antennal transcriptome

Julian Chen, Wenxin Xue, Jia Fan and **Jingrui Sun**
Chinese Academy of Agricultural Sciences, China

Olfaction is the essential sense of insect's feeding and mating. It achieves semiochemical and pheromone perception through olfactory pathway which coupled components by expressing series olfactory genes, distributing in antenna. transcriptome of antenna is a good way to understand the complicated olfactory system components. Analysis of chemical sensing system is a crucial basic work for studying the olfactory physiology of aphids and developing biological control technologies. In this study, we sequenced winged and wingless antennae transcriptome of Sitobion avenae (Fabricius), one of the most serious pests of cereals using IlluminaHiSeqTM2500/MiseqTM technology and Trinity assembly. A total of 133,331 unigenes were obtained with an average length of 594 bp. To annotate the transcripts, we searched against the Nr, Nt, Pfam, KOG/COG, Swiss-prot, KEGG and GO databases and 100,345 unigenes (75.26%) were annotated in at least one database. There were 1,517genes (1,107 up-regulated and 410 down-regulated genes) differentially expressed between wingless and winged antennae, respectively. Nine of them are associated with odour binding pathway. 13 OBPs, 5 CSPs genes were identified from S. avenae. All of these transcripts have the typical structural features of insect (six conserved cysteines for OBPs and 4 for CSPs). Through multiple comparisons phylogenetic tree constructed of OBPs across several aphids, we can see that there is a high similarity between orthologs within a range of aphid species. Besides, 48 Ors (odorant receptors) were annotated as well and further studies are in progress.

Biography

Julian Chen has completed her PhD at Graduate School & Institute of Plant Protection, Chinese Academy of Agricultural Sciences (IPP-CAAS). She is a Group Leader of Wheat Insect Pest Research Group, IPP-CAAS. She has published more than 110 papers in reputed peer-review journals.

jlchen@ippcaas.cn

Notes:

Juliana Janet Martin-Puzon et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Phytochemical constituents and bioactive properties of *Glinus oppositifolius* (L) Aug. DC., against bacterial pathogens

Juliana Janet Martin-Puzon[1], **Demetrio L Valle, Jr**[1, 2] and **Windell L Rivera**[1]
[1]University of the Philippines, Philippines
[2]Makati Medical Center, Philippines

This study aimed to determine the presence of bioactive phytochemical constituents and evaluate the *in vitro* antibacterial activities of *Glinus oppositifolius* or carpet weed, a plant valued for its use in traditional medicine and as a vegetable. The leaves, stems and roots were extracted using chloroform, ethanol and methanol. Phytochemical screening revealed that the entire *G. oppositifolius* plant, i.e., roots, stems and leaves, is a rich source of alkaloids, flavonoids, glycosides, saponins, sterols, tannins and triterpenes. The antibacterial activity of the leaf and stem extracts were evaluated through disc diffusion, minimum inhibitory concentration and bactericidal concentration assays against methicillin resistant *Staphylococcus aureus* (MRSA), vancomycin resistant *Enterococcus* (VRE), extended spectrum β-lactamase producing (ESβL+), carbapenem resistant Enterobacteriaceae (CRE) and metallo-β-lactamase producing (MβL+) *Pseudomonas aeruginosa* and *Acinetobacter baumannii.* The leaf extracts revealed antibacterial activities, inhibiting the growth of non resistant and multidrug resistant (MDR) strains of the Gram negative bacteria *E. coli, P. aeruginosa* and *A. baumanii.* In conclusion, the various biological activities of *G. oppositifolius*, including its antibacterial activity, are due to the presence of diverse bioactive secondary metabolites. The presence of phytochemical compounds in *G. oppositifolius* is scientific evidence on its use for treatment of many ailments. Thus, the results demonstrate the great potential of the plant as a new, alternative source of antimicrobials and other components with therapeutic value.

Biography

Juliana Janet Martin-Puzon is currently an Assistant Professor in the Institute of Biology, College of Science, University of the Philippines, Diliman, Quezon City. She has complted her MS in Botany and PhD in Biology majoring in Plant Physiology at the Institute of Biology, College of Science, University of the Philippines and her BS degree in Biology major in Microbiology at the College of Arts and Sciences, University of the Philippines Los Baños. Recently, she has completed a Research Fellowship under the University of the Philippines, Natural Sciences Research Institute, Department of Agriculture, Bureau of Agricultural Research (UP-NSRI/DA-BAR) Post-Doctoral and Senior Scientist Research Fellowship Program. She has published numerous scientific papers in international peer-reviewed journals dealing on her research interests, namely, plant and cell physiology, plant stress physiology, phytoremediaion, secondary metabolism (natural products and their bioactivities) and controls of plant growth and development. Notably, she has presented her works through platform and poster presentations in various conferences, both internationally and locally. She has given local seminar-workshops emphasizing on research methods in physiology, particularly the assessment of heavy metal stress tolerance in plants, among others. She also serves as a Referee of papers dealing with her areas of expertise submitted for publication in scientific journals.

janetmpuzon@gmail.com

Notes:

Branka Javornik et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Induced defense responses in hop-*Verticillium* interactions as revealed by proteomic and transcriptomic analysis

Branka Javornik[1], **Vasja Progar**[1], **Stanislav Mandelc**[1], **Jernej Jakse**[1], **Natasa Stajner**[1], **Andreja Cerenak**[2], **Sebastjan Radisek**[2] and **Sabina Berne**[1]
[1]University of Ljubljana, Slovenia

[2]Slovenian Institute for Hop Research and Brewing, Slovenia

Verticillium wilt caused by soil borne vascular tissue infecting species of the *Verticillium* genus is a devastating disease in many crops. Host resistance and phytosanitary measures are the best options for controlling the disease so elucidation of plant wilt resistance can undoubtedly enhance resistance breeding. We study Verticillium wilt in hop caused by a highly virulent strain of *V. nonalfalfae,* which has recently become a serious threat to hop production in Europe. The first QTL for hop resistance against Verticillium wilt has been identified, opening up possibilities for investigation of the genetic basis of hop resistance source, as well as markers development and their exploitation in MAS resistant breeding. Transcriptomics and proteomics were employed in a time course experiment comparing infected and control plants of resistant and susceptible hop cultivars to characterize hop-*Verticillium* interactions. The expression patterns of most studied genes and the decline of fungal biomass in the infected resistant cultivar suggest that the defense response in the resistant cultivar is strong enough at 20 dpi to restrict further fungus colonization. The results so far have shown strong expression of genes encoding PR proteins in both interactions, strong up regulation of genes implicated in ubiquitination and vesicle trafficking in the incompatible interaction and their down regulation in susceptible plants. Additionally, the identification and high abundance of two mannose/glucose specific lectin isoforms and dehydrins present only in the roots of the resistant cultivar implies a putative function of these proteins in hop resistance against *V. nonalfalfae*.

Biography

Branka Javornik is working as Head of Biotechnology Studies in Biotechnical Faculty at University of Ljubljana, Slovenia. Her international experience includes various programs, contributions and participation in different countries for diverse fields of study and interests reflect in wide range of publications in various national and international journals.

Branka.Javornik@bf.uni-lj.si

Notes:

Grace Chen, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Transcriptome analysis of *Lesquerella*: A potential industrial oilseed crop for hydroxy fatty acid production

Grace Chen
United States Department of Agriculture-Agricultural Research Service, USA

Seed oil of *Lesquerella* (*Physaria fendelri*) contains 55-60% hydroxy fatty acid (HFA) that has important industrial application. A high throughput, large scale sequencing of transcripts from developing *Lesquerella* seeds was carried out by 454 pyrosequencing to generate a database for quality improvement of seed oil and other agronomic traits. Deep mining and characterization of acyl lipid genes were conducted to uncover candidate genes for further studies of mechanisms underlying HFA and seed oil synthesis. A total of 651 mega bases of raw sequences from an mRNA sample of developing seeds were acquired. Bioinformatic analysis of these sequences revealed 59,914 transcripts representing 26,995 unique genes that include nearly all known seed expressed genes. Based on sequence similarity with known plant proteins, about 74% (19,861) genes matched with annotated coding genes. Among them, 95% (18,868) showed highest sequence homology with *Arabidopsis* genes, which will allow translation of genomics and genetics findings from *Arabidopsis* to *Lesquerella*. Using *Arabidopsis* acyl lipid genes as queries, we searched the transcriptome assembly and identified 615 *Lesquerella* genes involved in all known pathways of acyl lipid metabolism. Further deep mining the transcriptome assembly led to identification of almost all *Lesquerella* genes involved in fatty acid and triacylglycerol synthesis. Moreover, we characterized the spatial and temporal expression profiles of 15 key genes using the quantitative PCR assay. The information obtained from data mining and gene expression profiling will provide a resource not only for the study of HFA metabolism but also for the biotechnological improvement of HFA production in *Lesquerella*.

Biography

Grace Chen has obtained her PhD from University of Wisconsin at Madison and did her Postdoctoral studies from University of California, Plant Gene Expression Center. She has published more than 35 papers in reputed journals and she is globally recognized as an expert on oilseed biotechnology.

Grace.Chen@ARS.USDA.GOV

Notes:

Ana Maria Benko-Iseppon, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Plant response to biotic stress: Insights from transcriptomics and structural genomics

Ana Maria Benko-Iseppon
Universidade Federal de Pernambuco, Brazil

The comprehension of the plant response to pathogen attack is essential for the development of strategies to improve resistance and diminish yield losses. Besides the desired resistance, the crosstalk between plant reaction to biotic and abiotic stresses is also a central question, especially considering the predicted global warming scenario. In this regard, the use of strategies involving omics analysis and bioinformatics can bring interestingevidence, useful for molecular breeding, crop selection and generation of genetically modified plants. Our group has been studying key gene families associated to plant defense in different plant groups including crops (e.g., cowpea, soybean, castor bean, grape, etc.) and medicinal plants with a focus on the families Euphorbiaceae, Fabaceae and Curcubitaceae, using transcriptomics (RNA-Seq, RT-qPCR, transgenesis) and bioinformatics approaches. Gene families studied include R (Resistance), PR (Pathogen Related), TF (Transcription Factors) and Kinases, evaluated under biotic (pathogen inoculation) and abiotic (water deficit and salinity) stresses. Besides the expression profiling, aspects of gene and protein structure and genomic evolution have been analyzed. In case of resistant or tolerant plants (depending on the stress type), a constitutive or earlier induction of given genes has been recognized, indicating that the early stress perception and the precocious induction of other stress associated genes is a key defense mechanism. Particularly for some TF, PR and Kinase genes, a dual role in response to biotic and abiotic stresses has also been recognized.

Biography

Ana Maria Benko-Iseppon is a Biologist with PhD in Plant Genetics from University of Vienna, Austria and Post doctorate in Plant Molecular Biology from the University of Frankfurt. She is working as full Professor in the Department of Genetics, Federal University of Pernambuco and as Head of the Laboratory of Plant Genetics Biotechnology. She has experience in the field of plant genetics with emphasison plant molecular biology, genomics, transcriptomics and bioinformatics as well as in cytogenetics, genetic mapping in plants and bioprospection of therapeutic molecules from plants.

ana.benko.iseppon@pq.cnpq.br

Notes:

Shashi Kumar, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Compartmentalized metabolic engineering of plant for rational drug biosynthesis and oral delivery of whole plant material facilitated cost effective malaria treatment

Shashi Kumar
International Centre for Genetic Engineering and Biotechnology, India

The rapid progression of malarial illness and drug-resistant parasites threatens nearly half the global population. Artemisinin, a drug native to Artemisia annua, is highly effective against drug-resistant malarial parasites. Insufficient supply of artemisinin and lack of an anti-malarial vaccine requires development of new alternative sources of production. Furthermore, prohibitively expensive purification process underscores the need for alternative ways of drug delivery. In this study, the chloroplast genome of tobacco was engineered to express the yeast mevalonate (MEV) biosynthetic pathway. The dihydroartemisinic acid (DHAA) biosynthetic pathway was expressed in the same plant via the nuclear genome transformation. Double transgenic (DT) lines with confirmed transgene integration/expression showed 2-3 folds increase in IPP. A high level of an intermediate volatile metabolite amorphadiene (committed precursor to artemisinin) targeted to mitochondria was detected by GC-MS. Efficient conversion of DHAA to artemisinin by photo-oxidation was confirmed by LC-MS/MS analysis. The DT lines grew normally, flowered and set seeds like untransformed plants. The partially purified artemisinin extracts from DT leaves inhibited in vitro growth progression of red blood cells (RBCs) infected with the malaria parasite Plasmodium falciparum. Most importantly, oral feeding of dried plant cells expressing artemisinin reduced the parasitemia levels in challenged mice, facilitating low cost production and delivery of this important life-saving drug. Thus, metabolic engineering utilizing different cellular compartments in plant cells and a synergistic drug delivery approach utilizing bioencapsulation is a novel concept that could be employed in a number of other metabolite based drug studies.

Biography

Shashi Kumar is a Team Leader at ICGEB in New Delhi, India. He has graduated in Genetics from the University of Delhi, 1998, Postdoctoral research at University of Virginia, University of Central Florida, University of California Berkeley and Scientist at Yulex Inc., USA and USDA, Albany, USA. He has participated in establishing the "Centre for Advanced Bio-Energy Research" supported by the Department of Biotechnology, Government of India. His area of interests include metabolic engineering for drug biosynthesis, metabolic engineering of rubber plant for hypoallergenic latex, DNA barcoding, development of sustainable algal biofuel technology and genetic engineering of marine algae for higher lipid and biomass.

skrhode@icgeb.res.in

Notes:

Ayyanagouda Patil, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Genome-wide association for pollen viability and silk receptivity under heat stress in tropical maize

Ayyanagouda Patil
University of Agricultural Sciences, India

Heat stress is a one of the major abiotic stresses which has profound impact on pollen viability and silk receptivity intern affect maize yields. Heat stable lines can be identified based on pollen viability and silk receptivity under high temperature condition. The present study is first of its kind to conduct genome wide association study for identification of genomic loci associated with pollen viability and silk receptivity under heat stress in tropical maize using genotyping by sequence data (GBS) with 239,594 SNP markers (MAF≥0.05) used for marker trait association in a panel of maize inbred lines. The pollen viability and silk receptivity of the inbred lines was assessed based on seed set percent. Association analysis was conducted using a mixed linear model involving both population structure and kinship to control false positives. The average physical distance between pairs of markers was 27.7 kb with mean LD estimation (r2) of 0.36 across genome and LD decay of 6.34 kb at r2=0.2. Out of 239,594 SNPs, 44 SNPs were significantly (P≤0.0001) associated with pollen viability and 69 SNPs were significantly associated with silk receptivity under heat stress. Candidate gene based analysis was used to predict the putative function of the associated genes. Of the many SNP makers, the gene associated with SNP marker (S6_156252525) is homologue of rice Osg1 gene which code for β-1,3-glucanases associated with pollen fertility. The SNP (S10_120824169) for silk receptivity was associated with protein phosphatase 2C, which has an important role in phosphorylation/dephosphorylation of heat shock proteins, possibly promoting the silk to survive under high temperatures. The SNP marker S3_220855063 was found to be associated with hydroxyproline-rich glycoproteins, which plays an important role pollen tube and silk growth. These SNP markers linked to the functionality of silk and pollen may be the ideal candidate for developing heat tolerant hybrids.

Biography

Ayyanagouda Patil has completed his Masters in Genetics and Plant Breeding from University of Agricultural Sciences, India and later pursued his Doctoral degree in the Department of Plant Biotechnology. He has worked extensively on genomics & transcriptomics plant improvement for his doctoral studies. He has later joined the University of Agricultural Sciences, Raichur as an Assistant Professor of Biotechnology in the year 2011. He was nominated as Head of the Department of Molecular Biology and Agricultural Biotechnology in University of Agricultural Sciences, Raichur on 2014 and continuing till date. He has published more than 25 research papers and abstracts.

ampatil123@gmail.com

Notes:

Jasdeep Chatrath Padaria, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Transcriptome profiling for identifying genes to develop abiotic stress tolerant transgenic wheat

Jasdeep Chatrath Padaria
National Research Centre on Plant Biotechnology, India

Wheat (Triticum sp.) stands as the second largest staple crop of the world with 17% of the total cultivatable land under wheat production. Global annual wheat production needs to be increased at quantum leaps from the present production of more than 650 million metric tons so as to feed the ever burgeoning world population. Unfortunately, with the changing global climate, various abiotic stresses further hamper the wheat productivity. Development of abiotic stress tolerant cultivars is necessary to achieve the goal of enhanced wheat productivity. With the available gene pool within a species becoming limited, it becomes imperative that we search genes responsible for abiotic stress tolerance across the, genus, species and even kingdom and using rDNA technology develop transgenic wheat tolerant to abiotic stresses. The present study involved identification of abiotic stress responsive genes from tolerant plant systems as *Penniseteum glaucum, Triticum aestivum, Ziziphus nummularia* and *Prosopis cineraria* using Roche 454 and Illumina sequencing platforms. De novo assembly and transcriptome annotations were preformed to have insight about genes, gene family and transcriptional factors related to abiotic stress. Further analysis for change in expression level of known and unknown genes, SNP detection and SSR marker detection have been carried out to identify stress responsive genes and stress tolerance linked markers. A few stress responsive genes as NAC, P5CS, WRKY, HSP, MYB, ASR, DREB etc have been identified and characterized. These genes are further functionally validated and have been transformed in elite Indian bread wheat for development of transgenic wheat tolerant to abiotic stress.

Biography

Jasdeep Chatrath Padaria has completed her PhD from Indian Agricultural Research Institute and Postdoctoral studies in the area of Gene expression profiling with respect to abiotic stress tolerance at Department of Horticulture and Landscape Architecture, Purdue University, USA. She is working as a Principal Scientist in the area of Biotechnology and Climate Change at National Research Centre on Plant Biotechnology, a premier institute in the area of plant molecular biology and biotechnology. She has published more than 25 papers in reputed journals and has guided 15 MSc and PhD students.

jasdeep_kaur64@yahoo.co.in

Notes:

Liang Chen, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Differential metabolic profiles and transcriptomic profiles during different color stages of albino tea plant (Camellia sinensis)

Liang Chen
Tea Research Institute of the Chinese Academy of Agricultural Sciences, China

Anji Baicha is an elite albino tea cultivar of very high quality and popularity in China, with white shoots at low air temperature and green shoots at high temperature in early spring. Metabolomic analysis found that the main differential metabolic pathways between the albescent stage and the green stage included carbon fixation in photosynthetic organisms and the phenylpropanoid and flavonoid biosynthesis pathways. Compared with the green stage, the carbohydrate and amino acid metabolic pathways were disturbed during the albescent stages. There were higher levels of β-carotene and theanine but lower level of chlorophyll a, in the white stage than in the green stage. During the albescent stages, the sugar (fructofuranose), sugar derivative (glucose-1-phosphate) and epicatechin concentrations decreased, whereas the amino acid (mainly glycine, serine, tryptophan, citrulline, glutamine, proline, and valine) concentrations increased. Transcriptomic analyses were applied to analyze the expression profiles changes in the different color stages. The transcriptomes of the plant leaves were highly divergent between different colors stages, as approximately three-quarters of all unigenes were differentially expressed between different color stages. Functional classification based on Gene Ontology enrichment and KEGG enrichment analyses revealed that these differentially expressed unigenes were mainly involved in metabolic pathways, biosynthesis of secondary metabolites, phenylpropanoid biosynthesis and carbon fixation in photosynthetic organisms. Furthermore, differentially expressed unigenes involved in carotenoid biosynthesis, chlorophyll biosynthesis and theanine biosynthesis were identified. These results provide a further understanding of the molecular mechanisms underlying albino phenomena.

Biography

Liang Chen has completed his PhD in Tea Science from Zhejiang University, China and Postdoctoral studies from Cornell University, USA. Presently, he is the Associate Director of National Center for Tea Improvement, TRICAAS. He has published more than 30 papers in reputed journals and has been serving as an Editorial Board Member of repute.

liangchen@tricaas.com

Notes:

Anna-Maria Botha-Oberholster, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Studying host-insect interactions using viral induced gene silencing and siRNA

Anna-Maria Botha-Oberholster
Stellenbosch University, South Africa

Wheat Dn genes afford resistance to the economically important pest, Diuraphis noxia (Kurdjumov, Russian wheat aphid, RWA) and have been the topic of transcriptomic and proteomic studies aimed at unraveling the pathways involved in resistance. However, despite numerous efforts to isolate these Dn genes, none of them had been cloned and sequenced and this can partly be ascribed to the complexity and size of the bread wheat genome, as well as the apparent centromeric location of these genes. To date, several R-gene targets were investigated using viral induced gene silencing (VIGs) in wheat. However, the availability of the complete genome of the pest has opened up new avenues of study to unravel the complex interaction between these organisms. The current study explores both avenues. Candidate plant resistance genes were silenced *in planta* and aphid response assessed, while candidate aphid effectors were also delivered *in planta* to assess their respective functions during host-pest interactions. In all cases, the aphids were allowed to feed, where after reproduction was recorded. The ectopic expression of the gene targets was also quantified using RT-PCR analysis.

Biography

Anna-Maria Botha-Oberholster has received her training in Plant Genetics at the Weizmann Institute of Science, Israel and the Salk Institute of Biological Science, USA. From 1994, she actively mentored students and has been affiliated to several academic institutions globally. Highlights in her career spanning more than 20 years, include representing Africa at the initiation meeting that started the International Wheat Genome Sequencing Consortium in Washington DC, in 2004 and at IBSA (now BRICS) in Brazil in 2008. Her research outputs include more than 100 peer-reviewed papers in accredited international journals, 5 book chapters, numerous peer-reviewed conference proceedings, technical reports and popular articles.

ambo@sun.ac.za

Notes:

Zhixi Tian, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Dissection of the network underlying agronomic traits in soybean

Zhixi Tian
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China

Many agronomically important traits exhibit modularity and tend to be tightly integrated. The understanding of how traits become associated or correlated is essential in the improvement of complex traits. Soybean (*Glycine max* L Merr) is a major crop of agronomic importance as the predominant source of animal feed protein and cooking oil, which was domesticated from wild soybean (G. soja Sieb & Zucc) in China 5,000 years ago. Understanding soybean domestication and improvement and a comprehensive dissection of the genetic basis of agronomic traits is important for soybean improvement. By analysis of several hundred re-sequenced wild, landrace and improved soybean accessions, we detected 230 selective sweeps and 162 selected copy number variants. Combined with previous quantitative trait loci (QTL) information, we find that, of the 230 selected regions, 96 correlate with reported oil QTLs and 21 contain fatty acid biosynthesis genes, 96 of which correlate with reported oil QTLs. Moreover, we detected more than two thousands association signals via a comprehensive GWAS for dozens of agronomic traits. Through modeling analysis, we find that amount of association sites are tightly linked and form a complex network to regulate the modularity of different complex traits. This study provides valuable resources for genomics-enabled improvements in soybean molecular breeding.

Biography

Zhixi Tian has completed his PhD from Institute of Genetics and Developmental Biology, Chinese Academy of Sciences and Postdoctoral studies from Purdue University, USA. He is a Principle Investigator of Institute of Genetics and Developmental Biology. His research interests focus on functional genomics and genetics of soybean. He has published more than 27 papers in reputed journals.

zxtian@genetics.ac.cn

Notes:

Eviatar Nevo, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Adaptive ecological incipient sympatric speciation of wild barley at "Evolution Canyon"

Eviatar Nevo
University of Haifa, Israel

Sympatric speciation (SS), the origin of new species within a free breeding population or contiguous populations has been under continuous controversy since first proposed by Darwin in his Origin. "Evolution Canyon" (EC) at Mount Carmel, Israel has been a fruitful microclimatic natural model for unraveling incipient adaptive ecological sympatric speciation across life from bacteria through plants and animals. EC consists of hot and dry, south facing, savannoid "African" slope (AS) abutting with a cool and humid, north-facing, forested "European" slope, separated on average by 250 meters. Here, I describe incipient adaptive SS in wild barley, *Hordeum spontaneum*, the progenitor of all world cultivated barley at EC, based on inter-slope divergent adaptive complexes, inferior inter-slope crosses than intra-slope crosses and sharply divergent RNA-seq and whole genome inter-slope contrasts. Inter-slope adaptive complexes include phenotypically, interslope divergent flowering time, early at AS and late at ES and genotypically, higher genetic polymorphism of allozyme and DNA diversities on AS, higher drought resistance on AS, based on dehydrins, rhizosphere bacteria, and EibiI gene and higher resistance against rust fungi on ES. Wild barley at EC was domesticated by humans in Neolithic times and harbors important abiotic and biotic genetic resources for future cultivated barley improvement.

Biography

Eviatar Nevo has conducted local (in four natural laboratories of "Evolution Canyons" in Israel), regional (in Israel and the Near East Fertile Crescent as natural genetic laboratories), and global (across all continents as genetic labs) genetic studies, interdisciplinary linking genetics and ecology in terms of ecological genetics and ecological genomics, bridging genotypes and phenotypes, integrating molecular and organismal biology, organism-environment relationships and elucidating the patterns and causation of genetic diversity in nature. He has established the Environmental Theory of Genetic Diversity proposing that, generally, genetic polymorphism at all scales, local, regional and global, and across life, is positively correlated with and predictable by environmental stress. He has founded (1973) and directed the Institute of Evolution at the University of Haifa till October 2008. In 2005, he has established the International Graduate Center of Evolution with 77 PhD students from 13 countries, thus cultivating the future world leaders of biodiversity including genetic diversity. He has studied the effects of atomic radiation at the Chernobyl disaster and found numerous molecular mutations associated with cancer in the offspring of liquidators who cleaned the site and in those who were born after the event, indicating that the mutations have passed through the germ line from parents to offspring.

nevo@research.haifa.ac.il

Notes:

conferenceseries.com
549th Conference

4th International Conference on

Plant Genomics

July 14-15, 2016 Brisbane, Australia

Scientific Tracks & Abstracts

(Day 2)

Track 1, 7, 10, 17 & 19

Day 2 July 15, 2016

Track 1: Plant Molecular and Cellular Biology
Track 7: Plant Tissue Culture
Track 10: Plant Stem Cells
Track 17: Cereals and Crops
Track 19: Bioinformatics

Session Chair
Wen Yuan Song
University of Florida, USA

Session Co-Chair
Rakhi Chaturvedi
IIT Guwahati, India

Session Introduction

Title: **Application of next-generation sequencing, genome sequencing, and whole genome re-sequencing to practical plant breeding: Case studies on lupin**
Huaan Yang, Department of Agriculture and Food Western Australia, Australia

Title: **C2Pe: A new open source qPCR algorithm and web interface for raw data analysis**
Juan Pablo Matte, Pontificia Universidad Catolica de Chile, Chile

Title: **Developing climate resilient wheat**
Kulvinder S. Gill, Washington State University, USA

Title: **Drought tolerance mediated by the rice ubiquitin ligase OsDt1**
Wen Yuan Song, University of Florida,USA

Title: **Evaluation of irrigation in triple-cropping of sugarcane**
Jamal Saudi, Dehkhoda Sugarcane Agro-Industry Co, Iran

Title: **Understanding the molecular mechanisms underlying high grain calcium content in finger millet (*Eleusine coracana*): Paving way to calcium biofortification**
Neelofar Mirza, National Bureau of Plant Genetic Resources, India

Title: **Molecular and cytological studies on pollen development in autotetraploid rice**
Muhammad Qasim Shahid, South China Agricultural University, China

Title: **Screening of mung bean (Vigna radiata) genotypes for nutrient stress tolerance**
Md Altaf Hossain, Soil Resource Development Institute, India

Title: **Known proteins, unexpected functions: A new insight into the transport mechanism of arsenite and cesium**
Abidur Rahman, Iwate University, Japan

Title: **Phylogenic analysis of genera *Bellevalia, Leopoldia, Muscari* and *Pseudomuscari* species (Hyacinthaceae) in Iran based on four plastid DNA regions**
Azarnoosh Jafari, Islamic Azad university, Iran

Title: **Screening and bioactivity measurement of high altitude medicinal plants**
Deepak Sharma, Kathmandu University School of Science, Nepal

Title: **Reaping the benefits of genome sequence and re-sequence information for chickpea improvement**
Mahendar Thudi, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India

Title: **PRL1 modulates root stem cell niche activity and meristem size through WOX5 and PLTs in Arabidopsis**
Xia Li, Huazhong Agricultural University, China

Title: **Studies on nutrient uptake and culture conditions for synthesis of caffeine, (+)-catechine, (-)-epicatechin and (-)-epigallocatechin gallate in anther derived haploid cell lines of tea Camellia sinensis L**
Rakhi Chaturvedi, IIT Guwahati, India

Title: **The plant regeneration and genetic improvement of Sapium sebiferum: An important bioenergy tree**
Lifang Wu(Jinyan Hou), Hefei Institute of Physical Science, CAS, China

Title: **Title:WSC remobilization to grain under drought in wheat**
Jingjuan Zhang, Murdoch University, Australia

Title: **Genetics of root-lesion nematode resistance in wheat: A review**
Rebecca S. Zwart, University of Southern Queensland, Australia

Title: **Breeding biofortified crops to alleviate micronutrient malnutrition**
Parminder Virk, International Centre for Tropical Agriculture, Colombia

Huaan Yang, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Application of next-generation sequencing, genome sequencing and whole genome re-sequencing to practical plant breeding: Case studies on lupin

Huaan Yang
Department of Agriculture and Food Western Australia, Australia

Next-generation sequencing (NGS) and whole genome sequencing bring us a deluge of genome and genetic variations. In lupin, we are applying NGS and genome sequencing technologies to help practical plant breeding through four avenues. (1) NGS as DNA fingerprinting for rapid trait-marker association discovery. Markers closely linked to disease resistance genes were successfully discovered by NGS-based RAD sequencing and were applied to marker assisted selection (MAS) in lupin. (2) Genome sequencing for developing functional markers. We completed the draft genome sequence of lupin; a diagnostic marker linked to anthracnose disease resistance gene was developed by gene annotation and further confirmed by genetic mapping. (3) Genome sequencing to developed cost-effective markers. In the last 15 years, DAFWA has developed over a dozen of gel-based InDel markers linked to various genes of agronomic traits of interest in lupin. Using the draft lupin genome sequence as templates, all previously developed InDel markers were converted into a cost-effective SNP markers to suit modern SNP genotyping platform. (4) Whole genome re-sequencing for developing diagnostic markers for MAS. We recently resequenced the whole genomes of17 lupin lines; several million markers were documented and 207,887 markers were anchored on the lupin genetic linkage map. We demonstrated two protocols of using whole-genome resequencing data for rapid development of diagnostic markers for MAS. In conclusion, the cases in lupin represent one of a few successful cases where NGS and genomes sequencing have been used as routine tools for molecular plant.

Biography

Huaan Yang is a Plant Pathologist by training with BSc in 1982 and MSc in 1985. He has completed his PhD from University of Western Australia in 1992. He became a Molecular Geneticist following his development of a DNA fingerprinting technology called “MFLP” in 2001. His lab has been the only lab for large-scale application molecular markers on MAS in plant breeding on legume grain crops in Australia since 2004. Since 2011, his lab has been fully switched into NGS and genome sequencing based approaches for pre-breeding in lupin.

huaan.yang@agric.wa.gov.au

Notes:

Juan Pablo Matte et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

C2Pe: A new open source qPCR algorithm and web interface for raw data analysis

Juan Pablo Matte[1], **J Padarian**[2], **R Siqueira**[3], **N Wilson**[2] and **B Jones**[2]
[1]Pontificia Universidad Catolica de Chile, Chile
[2]The University of Sydney, Australia
[3]University of Lausanne, Switzerland

The determination of transcript levels via quantitative polymerase chain reaction (qPCR) is now widespread and instrumental in research, medicine and a broad range of other areas. The standard method of analysis is delta Ct, that is simple to use, but has a high probability of deviating from the true value. Several alternative approaches that give more consistent results have been presented but they are all complex to use. The C2Pe method we have developed can improve on the delta Ct method by 51%, using the PCR curve to estimate the efficiency of each reaction. The main innovations are that the embedded equations use the second phase of the curve to add a quality value to the data to correct the information given by the exponential phase. We have also incorporated revised statistics to improve the robustness of the analysis and constructed a web-based interface to give a straightforward, streamlined qPCR experience.

Biography

Juan Pablo Matte has studied both, Forestry Engineering and Biological Science degree in the Pontificia Universidad Catolica de Chile. He has completed his PhD in 2013 and Postdoctoral studies in 2015 from The University of Sydney, Australia. Currently he is an Associate Researcher at the Pontificia Universidad Catolica de Chile, under the PAI project number 82140040 from CONICYT.

jpmatte@uc.cl

Notes:

Kulvinder S Gill, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Developing climate resilient wheat

Kulvinder S Gill
Washington State University, USA

To meet the food security demands of growing human population, yield of majority of the crop plants needs to be doubled by 2050 while dealing with the climate change. With the increasing temperature trends and unusual climatic changes, crops in future climates will experience frequent temperature extremes causing significant yield losses. Heat stress is a serious challenge to wheat production as every 1 °C increase above the optimal temperature results in 4-5% yield loss. Rainfed areas of the US are projected to decrease wheat production by 20-40% due to climate change. Thus, developing climate resilient wheat is crucial in today's context. As a public-private partnership, Feed the Future Innovation lab-Climate Resilient Wheat is developing heat tolerant varieties by exploiting natural variation. A short period of heat stress during germination had serious and long-term effect on plant development and yield. A ten-day heat stress at germination reduced germination percentage, coleoptile length and yield. Sugars availability maybe a reason for the effect on germination as external application of sucrose showed significant recovery in germination percentage and coleoptile length. Heat stress during vegetative phase significantly affected tiller number, flowering time, pollen fertility, plant height and yield. During the reproductive stage, heat stress adversely affected photosynthesis and increased membrane disintegration due to decreased chlorophyll index and increased ROS and lipid peroxidase activity. The identified heat tolerant lines will be used to transfer the trait into wheat cultivars by simultaneous detection and utilization of QTLs. Various molecular and physiological studies for the trait are underway and update will be presented.

Biography

Kulvinder S Gill has completed his PhD from Kansas State University followed by Postdoctoral studies at the same university for about 3 years. He is the Professor and Director of the Feed the Future Innovation Lab: Climate Resilient Wheat. He has published more than 100 papers in reputed journals. His research program focuses on understanding and utilizing chromosome pairing control in polyploids, developing alternate dwarfing gene systems for wheat and on using modern tools and technologies for crop improvement.

ksgill@wsu.edu

Notes:

Wen-Yuan Song et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Drought tolerance mediated by the rice ubiquitin ligase OsDt1

Wen-Yuan Song, Xiaoen Huang, Xiuhua Chen, Sisi Gang and **Sixue Chen**
University of Florida, USA

Drought stress is a major limitation to crop production in the worldwide. We have identified ubiquitin ligase OsDt1 that can aid drought survival of rice. The OsDt1 gene is strongly induced by water deficit. While down-regulation increases drought sensitivity, overexpression of OsDt1 allows plants to confer strong tolerance to water stress. RNA-seq assays identified a total of 307 differentially expressed genes (DEGs) between the OsDt1 overexpression line OXDt1-70 and the empty-vector control line A36 under normal conditions. Among them, 24% (50 up-regulated and 24 down-regulated) DEGs have been reported previously to be associated with water stress or drought regulators. The OsDt1 protein localizes to both the plasma membrane and nucleus in rice cells. Protein blot analysis suggests that the ubiquitin ligase activity of OsDt1 might be active in the nuclear pools. Yeast two-hybrid analysis shows that OsDt1 interacts with a negative regulator of drought response. These results suggest that OsDt1 function as a key regulator of drought survival in rice.

Biography

Wen-Yuan Song has completed his PhD in 1995 from the Institute of Genetics, Chinese Academy of Sciences, China and Postdoctoral studies from the University of California-Davis, USA. He is currently an Associate Professor at the University of Florida, USA. His research mainly focuses on plant response to biotic and abiotic stresses.

wsong@ifas.ufl.edu

Notes:

Jamal Saudi, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Evaluation of irrigation in triple-cropping of sugarcane

Jamal Saudi
Dehkhoda Sugarcane Agro-Industry Co, Iran

Sugarcane is one of the important plants in tropical and semi-tropical regions that need plentiful water, these plants cultivates in extended area in Khuzestan province of Iran. In this study, triple-cropping of sugarcane cultivar Cp69-1062 on the ridge was evaluated and compared to double-cropping of sugarcane cultivar Cp69-1062 on the ridge that is current planting region. Results showed that in spite of higher dense planting in triple-cropping, in leaf sheath moisture, leaf nitrogen, ridge EC, qualitative situation of cultivar, plant height, stem diameter and number of shoots, there was not any significant difference between triple-cropping with double-cropping of sugarcane on the ridge. However, the difference between numbers of stem per m^2 in triple-cropping with double-cropping of sugarcane was significant at 5% level. Also, water use efficiency (WUE) and the mean yield of sugarcane and sugar in triple-cropping were more than double-cropping of sugarcane.

Biography

Jamal Saudi is currently a PhD student in Soil Fertility & Chemistry from Islamic Azad University (IAU), Khuzestan Science & Research Branch. He has completed his MSc in Agriculture Engineering from Islamic Azad University, Khuzestan Science & Research Branch, in 2011 and was graduated in Agrology from Shahid Chamran University of Ahvaz in 1992. He is presently the Director of Applied Research at Dehkhoda Sugarcane Agro-Industry Co, in Iran.

saudijamal@gmail.com

Notes:

Neelofar Mirza, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Understanding the molecular mechanisms underlying high grain calcium content in finger millet (*Eleusine coracana*): Paving way to calcium biofortification

Neelofar Mirza
National Bureau of Plant Genetic Resources, India

Understanding the molecular mechanisms underlying the uptake, transport, accumulation and of the existing genetic variation for storage of minerals in grains is of utmost importance for development of biofortified crops. Finger millet (*Eleusine coracana*) has an immense potential as a food security crop due to its high nutritional profile and exceptionally high calcium (Ca) content. Seeds, tubers and fruits are generally low in Ca content however, finger millet grains has been reported to contain Ca as high as 376-515 mg/100 g. In order to understand the molecular machinery associated with this high Ca accumulation and to identify the candidate genes and proteins, a combination of biochemical, functional genomics and proteomics approaches were used. Genotypes with contrasting grain Ca content were selected. Members of calcium transporters and sensors i.e., Calmodulin and CaM/Ca dependent kinases were isolated and transcriptional expression analysis of these genes was carried out in various tissues i.e., from root tips to different stages of developing spikes amongst the contrasting genotypes. Calmodulin (CaM) protein was also assessed in their grains using anti-CaM antibodies. Results correlated the variable Ca accumulation in different tissues to differential expression of these genes. Immmuno-detection showed higher CaM in the grains of high Ca accumulating genotype. Also, higher transcript levels of CaM and Ca transporters was seen in the high Ca accumulating genotype, which might cause greater stimulation of the downstream calcium transport machinery leading to elevated calcium accumulation. The results provide a model for explaining the mechanism of elevated calcium accumulation in finger millet and pave way for development of nutraceuticals or designer crops.

Biography

Neelofar Mirza has completed her PhD in Molecular Biology & Biotechnology from G. B. Pant University of Agriculture & Technology, India and has since been involved in Teaching and Research in Jamia Millia Islamia University and Indian Agriculture Research Institute. She is currently working as a Research Associate on crop related NGS technology at National Bureau of Plant Genetic Resources, New Delhi, India. She has six publications to her credit and has won the USSTC Young Scientist Award in 2013.

mirzabiotech2000@gmail.com

Notes:

Muhammad Qasim Shahid et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Molecular and cytological studies on pollen development in autotetraploid rice

Muhammad Qasim Shahid and **Liu Xiang-Dong**
South China Agricultural University, China

Autotetraploid rice has a great genetic potential to increase the rice production but lower pollen fertility is a major barrier in its utilization. Intersubspecific autotetraploid rice hybrids showed greater genetic variation compared to their diploid counterparts. Here, we observed the pollen development and its relation with seed set in autotetraploid rice. Microgametogenesis in autotetraploid rice was similar to diploid rice but different kinds of abnormalities, including microspores degeneration, cytoplasm shrinkage and abnormal cell walls were found in autotetraploid rice. Many different kinds of chromosomal abnormalities were found during various development stages of pollen mother cell meiosis such as chromosome lagging, chromosome straggling, pre-separation of two chromosome set, randomly arranged chromosome on the equator, abnormal spindle and incomplete/no separation of cytokinesis. We identified 55 meiosis related or meiosis stage specific genes and 7 genes related with photosynthesis system I that were down-regulated in autotetraploid rice. Gene ontology analysis on the targets of up-regulated DEM showed that they were enriched in transport and membrane in pre-meiotic interphase, reproduction in meiosis and nucleotide binding in single microspore stage. Quantitative RT-PCR was used to validate differentially expressed genes and microRNAs selected from functional categories based on the gene ontology analysis. The results showed that their expression patterns were consistent with the microarray data and high-throughput sequencing, respectively. These stably expressed genes not only related to the pollen development genes but also involved in cell metabolism, cell physiology, binding, catalytic activity, molecular transducer activity and transcription regulator activity. These findings provide a foundation for understanding the effect of polyploidy on meiosis related genes and miRNAs expression patterns during pollen development that lead to low pollen fertility in autotetraploid rice.

Biography

Muhammad Qasim Shahid has completed his PhD from South China Agricultural University and Postdoctoral studies from South China Agricultural University and Istanbul University. He is working as an Associate Professor in South China Agricultural University. He has published more than 25 papers in reputed journals such as *Plant Physiology, Journal of Experimental Botany, PLOS ONE and Crop Science.*

qasim@scau.edu.cn

Notes:

Md Altaf Hossain, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Screening of mung bean (Vigna radiata) genotypes for nutrient stress tolerance

Md Altaf Hossain
Soil Resource Development Institute, Bangladesh

Generally nutrient deficiency of a soil is corrected through application of chemical fertilizers. Fertilizers on one hand are costly and on the other hand it may lead to water pollution by nitrogen and phosphorus from agricultural land. Screening of genotypes for nutrient stress tolerance could be the best alternative to overcome the situation. The present study evaluates the plant growth characters with emphasis on root growth and nutrient uptake of selected mung bean genotypes and examines the efficiency of certain growth parameters for predicting their adaptation in sub-optimal nutrient environment. Some genotypes (VC 6153B, GK3 & VC 6144A) were found to be high nutrient acquiring genotypes and some (PDM 54, IPSA 25 & VO 1443 A-G) were low nutrient acquiring genotypes.

Biography

Md Altaf Hossain is a PhD in Agronomy from Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh. He is a public servant of Bangladesh. He has published 15 scientific papers in reputed journals in home and abroad. He is acting as a Principal Scientific Officer in the Soil Resource Development Institute (SRDI) under the Ministry of Agriculture, Government of Bangladesh.

altajolly63@yahoo.com

Notes:

Abidur Rahman, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Known proteins, unexpected functions: A new insight into the transport mechanism of arsenite and cesium

Abidur Rahman
Iwate University, Japan

Toxic metals in the soil are a major environmental concern for agriculture industry. The translocation of these metals from root to the reproductive organs is the major source of food chain contamination. One of the best methods to reduce the soil contamination is phytoremediation. However, appropriate use of phytoremediation needs the basic mechanistic information of the transport of toxic metals. Hence, identifying the transporters and understanding the cellular transport mechanism are a prerequisite to engineer plants capable of phytoremediation. This talk will be focused on transport mechanisms of two metals, arsenic and cesium. Arsenic exists in two natural forms; arsenate and arsenite. Arsenate is the predominant form in the soil and transported by phosphate transport carrier system. Once arsenate gets inside the plant, it is readily converted to more toxic form arsenite by arsenate reductase. The uptake of arsenite is regulated by aqua glycero proteins or aquaporins. However, the efflux of arsenite remains obscure. Using molecular and cellular approaches, we found that intracellular arsenite and auxin responses are connected and one of the auxin efflux carriers also functions as an arsenite efflux carrier. I will also introduce our recent work on cesium transporters and provide evidence that cesium transport is regulated by carriers that are not linked to potassium transport system.

Biography

Abidur Rahman has completed his PhD from Kobe University, Japan and Postdoctoral studies from University of Massachusetts, Amherst, USA. He is currently working as an Associate Professor in the Faculty of Agriculture, Iwate University, Japan. He has published more than 25 papers in high impact journals and has been serving as Editorial Board Member of several reputed journals.

abidur@iwate-u.ac.jp

Notes:

Azarnoosh Jafari et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Phylogenic analysis of genera *Bellevalia, Leopoldia, Muscari* and *Pseudomuscari* species (Hyacinthaceae) in Iran based on four plastid DNA regions

Azarnoosh Jafari[1], **Jamil Vaezi**[2], **Mohammad Mahdi Forghanifard**[3], **Mohammad Farsi**[4], **Maryam Behroozian**[2] and **Felix Forest**[5]
[1]Islamic Azad University, Mashhad, Iran
[2]Ferdowsi university of Mashhad, Mashhad, Iran
[3]Damghan Branch, Islamic Azad University, Damghan, Iran
[4]Ferdowsi university of Mashhad, Mashhad, Iran
[5]Royal Botanic Gardens, Kew, UK

In the present research, a phylogenetic study of the Iranian species of *Bellevalia*, *Leopoldia*, *Muscari* and *Pseudomuscari* (tribe Hyacinthaceae, Asparagaceae) was performed based on the plastid regions *rbcL*, *matK, trnL* intron and *trnL-F* spacer. The four sections of genus *Bellevalia* i.e. *Nutans, Patens, Conica* and *Oxydonta* are found in Iran. Traditionally, flower colour and shape, the ratio of leaf to scape length were used to delimit sections, subsections and species, while an overlap in these features was sometime observed and flower color and shape change in fresh and dried specimen. Regarding *Muscari*, Davis and Stuart believed that *Pseudomuscari* and *Leopoldia* were subgenera of this genus while Garbari and Greuter treated them as distinct genera. These three genera are distinguished based on flower color, shape and throat contraction. *Leopoldia* is similar to *Bellevalia* and *Muscari* is similar to *Pseudomuscari*. So, in order to determine the exact circumscription of sections and genera, a phylogenetic analysis based on four plastid DNA regions was performed. For this 91 specimens including *Hyacinthus* as out group taxon were evaluated. The results showed that *Bellevalia* is a monophyletic clade but that its sections are not. Also, some *Leopoldia* species are placed in the *Muscari* clade. Moreover the two possible positions of *Muscari* and *Leopoldia* shown here can be explained by hybridization between these two genera. Thus, based on these results, *Leopoldia* could be considered as an infrageneric rank of *Muscari*. Since, no decisive point was observed in genera and sections circumscription, it is recommended that this molecular analysis is expanded to investigate further the relationships among species of Hyacinthaceae in Iran.

Biography

Azarnoosh Jafari has completed her PhD in 2004 from Research and Sciences of Tehran Branch, Islamic Azad University. She is the Director of the project and she has published more than 50 papers in English and Persian.

Azarnoosh_djafari@mshdiau.ac.ir

Notes:

Deepak Sharma, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Screening and bioactivity measurement of high altitude medicinal plants

Deepak Sharma
Kathmandu University School of Science, Nepal

Ten different medicinally important plants collected from Khaptad National Park were found to have high antimicrobial, cytotoxic and high antioxidant properties. Among the samples *P. edgeworthii* were found to exhibit greatest antimicrobial properties with ZOI-10 mm at 200 mg/ml extract concentration against *S. aureus* which is in accordance of their traditional uses. A. spectabilis were found with highest cytotoxic property with LC50 value 6.14 ppm, among B. diffusa, *T. foliolosum and E. strobilifera* 13.59 ppm, 64.50 ppm, 223.46 ppm respectively. The high antioxidant properties observed in the plants *E. strobilifera* (5.46 µg per ml) using DPPH bioassay method indicate their anticancer properties. A series of research is thought to be continued for the future which can lead for the development of drugs.

Biography

Deepak Sharma has completed his Masters in Biotechnology from Rajasthan University with Silver Jubilee Scholarship of Government of India (2008-2010) and pursuing Doctoral studies from Kathmandu University School of Science from 2014 to till date. He is also a Research Assistant of Seoul National University's funded project of KOIKA AP1 in supervision of Professor Dr. Janardan Lamichanne at Kathmandu University.

deepakshrm59@gmail.com

Notes:

Mahendar Thudi et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Reaping the benefits of genome sequence and re-sequence information for chickpea improvement

Mahendar Thudi[1], Annapurna Chitikineni[1], Xin Liu[1], Weiming He[2], Manish Roorkiwal[1], Wei Yang[2], Jianbo Jian[2], Dadakhalandar Doddamani[1], Pooran M Gaur[1], Abhishek Rathore[1], Srinivasan Samineni[1], Rachit K Saxena[1], Dawen Xu[2], Narendra P Singh[3, 4], Sushil K Chaturvedi[4], Gengyun Zhang[2], Jun Wang[2], Swapan K Datta[5], Xun Xu[2] and Rajeev K Varshney[1]

[1]International Crops Research Institute for the Semi-Arid Tropics, India
[2]Beijing Genomics Institute, China
[3]All India Coordinated Research Project on Chickpea-ICAR, India
[4]Indian Institute of Pulses Research-ICAR, India
[5]Visva-Bharati University, India

Chickpea (*Cicer arietinum* L.) is one of the most important annual pulse crops cultivated by resource poor farmers across the globe. Besides being the rich source of human dietary proteins, it improves the soil heath through symbiotic nitrogen fixation. Globally it is cultivated on over 13.2 Mha with an annual production of 13.1 million tons and productivity is less than 1 ton per ha much less than estimated potential of 6 t/ha under optimum growing conditions. In order to understand the impact of breeding on genetic diversity and gain insights into temporal trends in diversity in chickpea, a set of 100 chickpea varieties released in 14 countries between 1948 and 2012 were re-sequenced. For analysis, the re-sequencing data for 29 varieties available from an earlier study was combined and genome analysis was conducted for 129 genotypes. Linkage disequilibrium decay was higher in landraces than in breeding lines. Re-sequencing of a large number of varieties has provided opportunities to inspect the genetic and genomic changes reflecting the history of breeding, which we consider as breeding signatures and the selected loci may provide targets for crop improvement. In addition, the analysis provided insights into population structure, genetic diversity, gene loss, domestication and selection sweeps in this crop that is important for global food security in developing countries.

Biography

Mahendar Thudi has obtained his PhD in Plant Sciences from University of Hyderabad, India. His seminal contribution includes genome sequences of chickpea, molecular breeding products in chickpea, genetic resources like TILLING populations (in chickpea and pearl millet) and genomic resources like SSR markers, genetic maps (in chickpea and pearl millet) and high-throughput DNA fingerprinting, genome diversity analysis, marker-trait associations and chickpea physical map. His research articles (>40) are published in high-impact factor journals including, *Nature Biotechnology*, *Scientific Reports*, *PLoS ONE*, *Theoretical and Applied Genetics*, etc. that are widely read and cited.

t.mahendar@cgiar.org

Notes:

Xia Li, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

PRL1 modulates root stem cell niche activity and meristem size through WOX5 and PLTs in Arabidopsis

Xia Li
Huazhong Agricultural University, China

The stem cell niche in the root meristem maintains pluripotent stem cells to ensure a constant supply of cells for root growth. Despite extensive progress, the molecular mechanisms through which root stem cell fates and stem cell niche activity are determined remain largely unknown. In *Arabidopsis thaliana*, the Pleiotropic Regulatory Locus 1 (PRL1) encodes a WD40-repeat protein subunit of the spliceosome-activating Nineteen Complex (NTC) that plays a role in multiple stress, hormone and developmental signaling pathways. In this study, we show that PRL1 is involved in the control of root meristem size and root stem cell niche activity. PRL1 is strongly expressed in the root meristem and its loss of function mutation results in disorganization of the quiescent center (QC), premature stem cell differentiation, aberrant cell division and reduced root meristem size. Our genetic studies indicate that PRL1 is required for confined expression of the homeodomain transcription factor WOX5 in the QC and acts upstream of the transcription factor PLETHORA (PLT) in modulating stem cell niche activity and root meristem size. These findings define a role for PRL1 as an important determinant of PLT signaling that modulates maintenance of the stem cell niche and root meristem size.

Biography

Xia Li has received her PhD from Purdue University in the United States and then joined in the Vector Tobacco Inc., as a Research Scientist from 2001-2004. In 2004, she was selected as one of the “One Hundred Talents” of Chinese Academy of Sciences (CAS) and became a Principal Investigator in the Institute of Genetics and Developmental Biology, CAS. She has moved to Huazhong Agricultural University as Professor since September, 2015. She has published more than 50 papers in reputed journals and has been serving as an Editorial Board Member of repute.

xli@genetics.ac.cn

Notes:

Rakhi Chaturvedi et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Studies on nutrient uptake and culture conditions for synthesis of caffeine, (+)-catechine, (-)-epicatechin and (-)-epigallocatechin gallate in anther derived haploid cell lines of tea Camellia sinensis L

Rakhi Chaturvedi, Mishra Vijay K and **Ruchira Bajpai**
Indian Institute of Technology IIT Guwahati, India

Tea is a perennial, evergreen tree of the family Theaceae. It is most consumable non-alcoholic caffeine containing beverage in the world due to its pleasant taste, attractive aroma and its medicinal property. Tea contains large amount of catechins (a group of very active flavonoids) which have anticancer, antidiabetic, antiviral, antimalarial, hepatoprotective, neuroprotective and cardio protective effects. Present study aims to study batch kinetics of androgenic haploid cell lines established from pollen grains in anther cultures of TV21 cultivar of tea. The haploid status of these cell lines were confirmed by flow cytometry. Cell suspension cultures were raised from fresh friable and high proliferating calli established on semi-solid medium. Dynamic changes of parameters, such as pH, fresh and dry cell concentrations, consumption of major nutrients, carbon source and agitation speeds, were studied to understand the culture characteristics. Maximum viable cultures were obtained at a rotation speed of 120 rpm. Identification and quantification of caffeine, (+)-catechine, (-)-epicatechin and (-)-epigallocatechin gallate were performed by HPLC which were further confirmed through mass spectrometric data analysis. Maximum yield of 2.7% caffeine, 0.26 % (+)-catechin, 0.92% (-)-epicatechin and 10.36% (-)-epigallocatechin gallate per gram dry weight was obtained from cells in suspension culture at 24th day. Compare to this, leaves from parent plant produced 3.14% caffeine, 0.48 % (+)-catechin, 1.3% (-)-epicatechin and 11.3% (-)-epigallocatechin gallate per gram dry weight which was marginally higher. The optimized conditions and parameters of the present study would be useful for further scale-up process by using suitable elicitors/precursors.

Biography

Rakhi Chaturvedi is the Professor at Biosciences and Bioengineering (BSBE) Department, IIT Guwahati, Guwahati. She has obtained her Bachelor's and Master's degrees from University of Allahabad, Uttar Pradesh, India. Subsequently, she has received MPhil and PhD degrees from University of Delhi, India in 1996 and 2001, respectively. After completing her Postdoctoral studies from Jawaharlal Nehru University, she has joined IIT Guwahati in the year 2004 as an Assistant Professor in the Department of BSBE. She has held important academic and administrative positions. She has served as Vice-Chairperson GATE-JAM 2013, Chairperson GATE-JAM 2014, Chairperson GATE-2015 and Organizing Chairperson JAM-2015 examinations. Currently, she is the Associate Dean of Alumni Affairs and External Relations at IIT Guwahati.

rakhi_chaturvedi@iitg.ernet.in

Notes:

Lifang Wu, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

The plant regeneration and genetic improvement of *Sapium sebiferum*: An important bioenergy tree

Lifang Wu
University of Science and Technology of China, China

Sapium sebiferum Roxb., a monoecious deciduous tree of the Euphorbiaceae family, is an economically important multipurpose woody plant species in tropical and subtropical region, considering the huge potential of this species for ornamental, biomass and biodiesel producing. It is essential for *S. sebiferum* to establish high efficient plant tissue culture procedures which can be used for large scale propagation and genetic improvement. We have established high efficient plant regeneration systems through different pathways by using different parts of *S. sebiferum* as explants. And based on those plant regeneration systems, we have established a high efficient genetic transformation system. Our results provide critical information for the propagation and the genetic improvement of *S. sebiferum*.

Biography

Lifang Wu has obtained her PhD from Hefei Institutes of Physical Science, Chinese Academy of Sciences, Hefei, China and her Postdoctoral studies from National University of Singapore. She has published more than 50 papers in reputed journals such as *Nature, Plant Physiology & Genes and Development* etc. She is globally recognized as an expert in molecular breeding of woody bioenergy plant species.

lfwu@ipp.ac.cn

Notes:

Jingjuan Zhang et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

WSC remobilization to grain under drought in wheat

Jingjuan Zhang[1], **Yunji Xu**[2], **Wei Chen**[3], **Bernard Dell**[1], **Rudi Appels**[1], **Wujun Ma**[1], **Rudy Vergauwen**[4], **Ben Biddulph**[5], **Nusrat Khan**[1], **Xinmin Zhang**[1], **Hao Luo**[1], **Australian wheat NVT group**[5] and **Wim Van den Ende**[4]
[1]Murdoch University, Australia
[2]Yangzhou University, China
[3]Chinese Academy of Science and Ministry of Water Resources, China
[4]Katholieke Universiteit Leuven, Belgium
[5]Department of Agriculture and Food Western Australia, Australia

Stem water soluble carbohydrate (WSC, mainly fructan), as a main storage carbon source before anthesis, can contribute up to 57% of wheat grain yield under terminal drought stress. However, the remobilization of stem WSC varies depending on the growth stages, conditions and genotypes. Therefore, it is worthwhile to further investigate the attributes on high remobilization efficiency of stem WSC. In recent study, two wheat varieties: Westonia, Kauz and their derived 20 double haploid (DH) lines with large genetic variations were used in field drought experiments. The results clearly showed that the genetic variation is involved in stem WSC remobilization to grain under drought; a key enzyme (1-FEH w3) degrades 2-1 linkage fructan and contributes the stem WSC remobilization; a marker generated within auxin response element (AuxRE) in the promoter region of 1- FEH w3 correlates with high stem fructan remobilization capacity and the 1-FEH w3 Westonia allele is associated with high grain weight under drought. In the stem segment analysis, fructan remobilization occurred earlier in lower parts of the stem and sheath under drought, which was associated with an earlier increase of grain weight and thousand grain weight in earlier mature lines. Root WSC and fructan were one third of the levels in stems. The significant correlation between root fructan levels and grain assimilation indicate that under terminal drought, root WSC represents a redistributed carbon source for grain filling rather than deep rooting. Our results further confirmed that β-(2-6) linkage predominate in wheat, which leads the future study.

Biography

Jingjuan Zhang has completed her PhD from Murdoch University in 2008 and followed by Postdoctoral studies. She has 25 years of work experience in wheat and has published 16 papers in reputed journals and the recent seven first authored papers and one co-authored paper are relevant to water soluble carbohydrate remobilization in wheat.

J.Zhang@murdoch.edu.au

Notes:

Rebecca S Zwart, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Genetics of root-lesion nematode resistance in wheat: A review

Rebecca S Zwart
University of Southern Queensland, Australia

Root-lesion nematodes (RLN) are one of the most widespread and devastating plant parasitic nematodes species globally. In Australia, RLN species *Pratylenchus thornei* and *P. neglectus* are particularly important biotic constraints to wheat production. The most efficient and effective strategy for improving on-farm RLN management relies on providing wheat growers with cultivars with better levels of resistance to RLN to ensure high yields and reduce the build-up of nematode populations to invade subsequent crops. Current research efforts in Australia are focused on the genetic characterization and introgression of superior sources of resistance into commercial wheat cultivars. Studies on the inheritance of *P. thornei* resistance in wheat have revealed polygenetic and additive gene action. Superior resistance has been identified from a wide range of backgrounds, including landrace and synthetic hexaploid wheats (ABD genomes), and wild diploid (D and A genomes) and tetraploid (AB genomes) genome donors. Effective sources of dual resistance to *P. thornei* and *P. neglectus* have been identified in synthetic hexaploid wheat. A single gene conferring resistance to *P. neglectus*, Rlnn1, has been mapped to chromosome 7AL. QTL analysis in several bi-parental mapping populations has identified major QTL for *P. thornei* resistance on chromosomes 2BS, 6DS and 7BL, which have been verified in sources of resistance from diverse backgrounds. Genotyping-by-sequencing has provided closely linked flanking markers that are now available to Australian breeders through the Australian Wheat and Barley Program to implement marker-assisted selection. Further fine mapping using large segregating populations will allow map-based cloning approaches to identify candidate genes underlying these QTL for RLN resistance.

Biography

Rebecca S Zwart has completed her PhD from University of Queensland, Australia on the genetics of root-lesion nematode resistance in wheat. She is a Senior Research Fellow (Crop Nematology) at the University of Southern Queensland, Australia. She has held Postdoctoral positions investigating the genetics and nature of inheritance of genes conferring host resistance to wheat diseases in Australia, Belgium and India.

rebecca.zwart@usq.edu.au

Notes:

Parminder Virk, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Breeding biofortified crops to alleviate micronutrient malnutrition

Parminder Virk
International Centre for Tropical Agriculture, Colombia

Micronutrient malnutrition affects more than half of the world population. Biofortification, the delivery of micronutrients via micronutrient dense crops, offers a cost effective and sustainable approach. HarvestPlus and its partners breed and disseminate new, more nutritious varieties of staple food crops that provide higher amounts of pro vitamin A, iron or zinc, the three micronutrients identified by the World Health Organization as most lacking in diets globally. Crop improvement activities focus on exploring the available natural genetic variation. To date, HarvestPlus has established productive research networks that link national research programs in target regions of the developing world with advanced agriculture and nutrition research institutes around the globe with more than 100 biofortified crop varieties released. To accelerate breeding process state of art genomic approaches namely genetic mapping and genome wide association studies for the identification of candidate genes for mineral uptake and homeostasis and functional markers associated with favorable alleles for enhanced micronutrients. Recently, with the advent of high throughput cost effective molecular genotyping, genomic selection models are being explored to enhance breeding efficiency. Conventional breeding alone is not always an option in particular where there is limited genetic variability or the target trait is altogether absent in the edible part (e.g. iron and pro vitamin A in rice endosperm). Under these circumstances transgenic approaches are in development. Their practical application, however, also demands visionary changes in regulatory policies and a broader consumer acceptance.

Biography

Parminder Virk is the Head of Crop Development and responsible for the development of biofortified staple food crops. He spent most of his career at the International Rice Research Institute (IRRI), Los Banos, as lead Rice Breeder for productive environments, biofortified rice and transgenic breeding. Together with his team he has developed 27 rice varieties for major rice growing countries. He has extensive experience in international collaboration with public and private sectors in germplasm development, distribution/testing, research, training, technical assistance and consulting and technology transfer.

p.virk@cgiar.org

Notes:

Track 14 & 18

Day 2 July 15, 2016

Track 14: Plant Breeding
Track 18: Plant Science

Session Chair
Hailing Jin
University of California, USA

Session Co-Chair
Rebecca S. Zwart
University of Southern Queensland, Australia

Session Introduction

Title: **QTL identification for reproductive-stage salinity tolerance in rice using novel phenotyping technique**
Rakesh K Singh, International Rice Research Institute, Philippines

Title: **Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerances in rice (*Oryza sativa L*)**
Jianlong Xu, Chinese Academy of Agricultural Sciences (CAAS), China

Title: **Breeding of drought tolerant canola: From laboratory to the field**
Guangyuan Lu, Chinese Academy of Agricultural Sciences, China

Title: **Cross kingdom RNAi in plant pathogen interactions**
Hailing Jin, University of California, USA

Title: **Faba bean (*Vicia faba*) seed gene function expression profile study**
Shi Ying Yang, The University of Adelaide, Australia

Title: **Chemical triggered defense mechanisms against *Phytophthora infestans***
Gefu Wang-Pruski, Dalhousie University, Canada

Title: **Maize responses to photoperiod changes under controlled conditions**
You Zhi Li, Guangxi University, China

Title: **The effect of biofuel production on sustainability of agriculture**
Andrzej Wasiak, Bialystok University of Technology, Poland

Title: **Genomics to detect and measure departures from autogamy in domesticated tomato**
Thomas Orton, Rutgers University, USA

Title: **Resistance of different Musa varieties to some strains of *Fusarium oxyporum f. sp. cubense* (Foc) with particular focus on Foc Tropical Race 4 (Foc TR4) in the Philippines.**
Agustin B. Molina, Bioversity International, Philippines

Title: **Understanding redox sensing and signaling through the identification and functional characterization of redox-sensitive proteins**
Yiji Xia, Hong Kong Baptist University, Hong kong

Title: **Translating advances in pearl millet genomics to farmer preferred cultivars**
Rakesh K Srivastava, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India

Title: **New insights into genome-wide change of DNA methylation and its association with gene expression in cadmium-exposed rice (*Oryza sativa*)**
Zhi Min Yang, Nanjing Agricultural University, China

Title: **Electron treatment of seed**
Frank-Holm Roegner, Fraunhofer Institute for Organic Electronics, Germany

Title: **Molecular analysis of bioengineered rice: A proteomic and transcriptomic approach**
Soumitra Paul, University of Calcutta, India

Title: **An insight into the molecular mechanism of glutathione-ethylene interplay in plant defense**
Riddhi Datta, Govt. General Degree College, Kolkata, India

Title: **Selection of barley Genotypes fornutritional composition vis-à-vis malting trait for improvement**
Alka Vasan, CCS Haryana Agriculture University, Haryana, India

Rakesh K Singh et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

QTL identification for reproductive-stage salinity tolerance in rice using novel phenotyping technique

Rakesh K Singh[1], **Mostafa Ahmadizadeh**[1, 2] and **Naireen A Vispo**[1]
[1]International Rice Research Institute, Philippines
[2]Sari Agricultural Sciences and Natural Resources University, Iran

Rice responds differentially at different stages of development. The seedling and reproductive stages are the most sensitive growth stages with very weak association, suggesting that they are regulated by different processes and sets of genes/QTLs. There are hardly any studies exist on reproductive-stage salinity tolerance mainly because of the lack of reliable reproductive-stage-specific phenotyping techniques and incomplete knowledge of the stage-specific mechanisms of salinity tolerance. Two major challenges for screening exclusively for the reproductive stage are; how to stress plants at the reproductive stage without stressing them at the seedling or late vegetative stage; and how to impose the stress on different genotypes or mapping populations at equivalent growth stages of development because of the variability in the progression of growth rate through developmental stages. We standardize a methodology that allows salt translocation to the reproductive organs such as the flag leaf (the largest source for the sink) and panicle as quickly as possible just at the initiation of booting when the genotypes are at the same stage of tissue/organ development rather depending on age of the plant. A mapping population derived from CSR28/Sadri was used QTL identification using the novel phenotyping technique and 6K illumina SNP platform. Salt stress equivalent to EC 10 dSm-1 was imposed on rice plants with trimmed leaves starting from boot leaf emergence up to 20 days in an experiment. Stage-specific effect of salt stress was verified by observing salt-sensitive and salt-tolerant genotypes. Details will be presented.

Biography

Rakesh K Singh is a Rice Breeder in Plant Breeding Division at IRRI, Philippines. His expertise is on breeding rice varieties for abiotic stress tolerance with special reference to salt-affected soils (saline and alkaline soils), as well as zinc deficient and iron toxic soils. He has completed his MSc and PhD degree from GB Pant University of Agriculture and Technology, Pantnagar, India and started his research career in 1986 as a Scientist at Central Soil Salinity Research Institute (Indian Council of Agricultural Research), Karnal (India), where he strengthened the rice breeding program for salt-affected areas. He has moved to IRRI Philippines in 2005 and led the salinity breeding group to developed salinity tolerant and first time multiple stress tolerant (salinity+submergence tolerant) rice genotypes at IRRI using molecular marker technology that are released and/or under advance stage of testing for release in various south and SE Asian countries. He has published more than 75 papers in peer reviewed journals and guided many MS and PhD students from India, Philippines, Myanmar, Iran, Burundi, Madagascar and Egypt. He is also serving as an Adjunct Associate Professor of Plant Breeding and Genetics at the University of the Philippines at Los Baños, Philippines.

r.k.singh@irri.org

Notes:

Jianlong Xu, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerances in rice (*Oryza sativa L*)

Jianlong Xu
Chinese Academy of Agricultural Sciences, China

Low and unstable productivity from multiple abiotic stresses are characteristic in the rice production of most rain fed areas of Asia and Africa. In 2007, we initiated backcross (BC) breeding procedure for improving yield and tolerances to multiple abiotic stresses. Using 8 BC1 populations derived from a widely adaptable and high yielding recipient and 8 donors plus two rounds of phenotypic selection, we were able to develop 496 introgression lines (ILs) with significantly improved yields under drought, salt and/or non-stress conditions. From these ILs, 6 new varieties were released for the rain fed and irrigated areas of Philippines and Pakistan and many more are in the pipeline to be released in several countries. Genetic characterization by SSR markers reveal three interesting aspects of donor introgression in the selected BC1F2 plants and BC1F3 lines: Introgression frequency in BC progenies was characteristic to specific crosses; donor introgression at different genomic regions of the selected ILs varied considerably across the genome resulting at least partially from strong selection for target traits; there was greatly reduced heterozygosity in the selected BC progenies, particularly with selection under drought and salinity. The strong phenotypic selection for abiotic stress tolerances at early segregating generation appeared to offer major advantages over the conventional pedigree breeding approach by not only allowing one or more abiotic stress tolerances integrated into elite backgrounds but being able to achieve quicker homozygosity in the selected progenies. The trait specific IL's are good materials for discovery of genes/QTL underlying the target and non-target traits and for highly efficient development of Green Super Rice by designed QTL pyramiding.

Biography

Jianlong Xu has obtained his PhD from Zhejiang University in China and his Postdoctoral career at PBGB Division of International Rice Research Institute (IRRI). He is majoring in molecular designing and genomic breeding of green super rice and has published more than 60 papers in reputed international journals, obtained eight patents and developed ten rice varieties.

xujlcaas@126.com

Notes:

Guangyuan Lu, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Breeding of drought tolerant canola: From laboratory to the field

Guangyuan Lu
Chinese Academy of Agricultural Sciences, China

The production of oilseed rape, a globally important oil crop, is tremendously limited by drought stress. To cope with this issue, the breeding of new cultivars with improved ability to drought stress is of great interest. To this aim, we carried out experiment-1 to establish selection criteria for drought tolerance at different developing stages. The impacts of water deficit establish at the germination stage on biological traits of 37 semi-winters rapeseed cultivars was first analyzed. The results proved that osmotic stress induced by 14% polyethylene glycol (PEG-6000) had a substantial impact on seed germination and caused a significant reduction in plant growth and seed vigor. Relative water content was identified as an indicator for early screening of drought tolerance. At the reproductive stage, seed yield, 1000-seed weight, height of the first branch, plant height and number of pods per plant were all markedly reduced under the exceptionally long (>100 d) and severe drought condition (a total of 162 mm precipitation during rapeseed life cycle, 52% reduced). Out of top three two of the tolerant genotypes at the germination stage were also shown to be tolerant based on drought susceptibility index of yield. Path analysis and phenotypic correlation were employed to rank the relative importance of other agronomic traits with regard to seed yield under drought conditions the important contributors to seed yield, in descending order, were as follows: 1000-seed weight, days to maturity, number of pods per plant and plant height. By taking this concept in mind, we have recently bred a new drought-tolerant cultivar (YG85) that can be grown in the drought-prone environments in the Northwest of China. To facilitate the breeding of drought tolerance with the aid of molecular markers, we conduct experiment-2 with a panel of 101 lines, which had previously been analyzed by RNA-Seq. The evaluation of drought tolerance at seedling stage resulted in the identification of 7 drought tolerant lines that could be incorporated into breeding program. The ongoing genome-wide Associative Transcriptomics analysis is expected to bring about the discovery of some candidate genes underlining drought tolerance and the development of functional markers.

Biography

Guangyuan Lu has completed his PhD from Huazhong Agricultural University, China and worked as a Visiting Scholar in John Innes Centre, UK during 2013-2014. He is the Group Leader of 'rapeseed molecular breeding' section, Oil Crops Research Institute, CAAS, a premier crop innovation organization. He has published more than 43 papers in reputed journals and has been serving as a Reviewer of *Molecular Breeding*.

luwiz@163.com

Notes:

Hailing Jin, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Cross kingdom RNAi in plant pathogen interactions

Hailing Jin
University of California, USA

Small RNAs (sRNAs) are a class of short non coding regulatory RNAs that are present in almost all the eukaryotes and mediate gene silencing in a sequence specific manner. Studies from my lab and others have shown that plant endogenous sRNAs play a critical role in host immune responses against pathogen attacks. We have also demonstrated that some sRNAs from eukaryotic pathogens, such as Botrytis cinerea, the fungal pathogen that causes grey mold disease on more than 200 plant species could be translocated into host plant cells. These sRNAs act as effector molecules to suppress host immunity genes for successful infection. This finding represented the first example of naturally occurring Cross kingdom RNAi during the host pathogen interactions. Similar phenomenon was recently reported in mammalian system, where a gastrointestinal nematode *Heligmosomoides polygyrus*, also delivers sRNAs to mammalian cells and target host genes involved in innate immunity. Thus, Cross kingdom RNAi was used as an aggressive virulence mechanism by both plant and animal pathogens and pests. Furthermore, we have found that transgenic plants that expressing sRNAs that targeting fungus Botrytis Dicer like genes could effectively block the generation of sRNA effectors and suppress disease symptom. These results suggest that sRNA trafficking is bidirectional; sRNAs could be also transferred from the host plants to the interacting pathogens.

Biography

Hailing Jin is currently working as a Professor and Director to Genetics, Genomics and Bioinformatics Graduate Program and Vice Chair to Plant Pathology & Microbiology Department and has obtained PhD degree in 1996 from Shanghai Institute of Plant Physiology and Ecology and her areas of expertise on Small RNA-mediated Gene Regulation; Plant Immunity. She has received many awards like 2010-15 NIH R01 Award, 2007-12 NSF Career Award, 2008-09 UCR-LANL Collaborative Award, 2006-09 UC Discovery Award, 2006-10 Awards from California Citrus Research Board, 2007-08 Interdisciplinary Research Award, Institute for Integrative Genome Biology, 2004, 2006 UC Regents' Faculty Development Award.

hailingj@ucr.edu

Notes:

Shi Ying Yang, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Faba bean (*Vicia faba*) seed gene function expression profile study

Shi Ying Yang
The University of Adelaide, Australia

Faba bean (*Vicia faba*) is one of the important grain legume crops worldwide, which is commonly consumed as human food and animal feed. The faba bean (2n=12) genome is approximately 13.4 Gb, the largest genome in the grain legume family. The faba bean seeds size is the biggest one in all of the grain crops. Our study applying RNA-Seq technology to construct the first faba bean genome de novo assembling. There was a total number of 47621 All-Unigene discovered in faba bean seeds by RNA-Sequence, length 27605508 bp. And then investigated the faba bean seed genes function expression profile on comparison of the following traits: Hydration index, rust resistance, photoperiod response, seed staining and ascochyta blight pathogen resistance.

Biography

Shi Ying Yang has completed her PhD from Charles Stuart University, Australia. She has been an Associate Professor at Guangxi Academy of Agricultural Sciences, China until 2009. Currently she is a Research Officer at School of Agriculture, Food and Wine, The University of Adelaide, Australia. Her major research work on the germplasm evaluation, grain legume crops breeding and molecular marker, herbicide selection and genomic study. She has published two book chapters with colleagues and 30 refereed journal papers.

shi.yang@adelaide.edu.au

Notes:

Gefu Wang-Pruski, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Chemical triggered defense mechanisms against *Phytophthora infestans*

Gefu Wang-Pruski
Dalhousie University, Canada

Late blight is the most devastating disease in potato production around the world. It is caused by *Phytophthora infestans* which mutates rapidly. Renewed control strategies aimed at higher efficiency and lower environmental impact are urgently required. Research carried out for a decade in our laboratories demonstrated that we can prime potato plants to boost diverse defense functions against *Phytophthora infestans*. Priming could reduce the use of fungicides and pesticides and ensure the protection of human health and the environment. In this talk, I will present our knowledge about the molecular mechanisms of priming against P. infestans based on our studies using proteomics, metabolomics and gene expression profiling tools.

Biography

Gefu Wang-Pruski has received her PhD from University of Alberta in Canada and completed her Post doctorate from Loma Linda University in Southern California. She has over 30 year's research experience. She is currently a full Professor at Dalhousie University. She has been leading over 20 national and international research programs in the past 15 years and generated over 50 peer-reviewed publications. She has been serving as an Editorial Board Member for many journals.

gefu.wang-pruski@dal.ca

Notes:

You-Zhi Li, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Maize responses to photoperiod changes under controlled conditions

You-Zhi Li
Guangxi University, China

Response of maize to photoperiods affects adaption of this crop to environments. Sensitivity towards photoperiod changes has limited integration of tropical and temperate maize germplasm into existing breeding programs. We characterize the phenotypes of four temperate-adapted maize foundation parents, Huangzao 4, Chang 7-2, Ye 478 and Zheng 58 and two tropically adapted maize foundation parents, M9 and Shuang M9 throughout the growth stage under three constant photoperiod regimes in a daily cycle of 24 h at 28 °C and analyzed expression of 48 photoperiod response associated genes. Consequently, long photoperiod (LP) repressed development of the tassels of photoperiod sensitive maize lines at V9 stage and caused subsequent failure in flowering; failure of photoperiod sensitive maize lines in flowering under LP was associated with lower expression of flowering related genes; photoperiod changes could make a marked impact on spatial layout of maize inflorescence. The larger oscillation amplitude of expression of photoperiod responsive genes occurred in LP sensitive maize lines. In conclusion, failure in development of tassels at V9 stage under LP is an early indicator for judging photoperiod sensitivity. The adaptation of temperate adapted maize lines to LP is due to the better coordination of expression among photoperiod sensing genes instead of the loss of the genes. High photoperiod sensitivity of maize is due to high expression of circadian rhythm responding genes improperly early in the light.

Biography

You-Zhi Li is a Professor at the College of Life Science and Technology, Guangxi University, China. He has obtained his PhD degree in Microbiology from the Huazhong Agriculture University and Master degree in Plant Pathology from the North West Agriculture and Forestry University (formerly named Northwestern Agricultural University). His research interests are very broad but the focus is on maize environmental adaptability. He is presently serving as the Associate Dean of the College of Life Science and Technology as well as a Principle Investigator of the State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources, Guangxi University, China.

dyzl@gxu.edun.cn

Notes:

Andrzej Wasiak, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

conferenceseries.com

4th International Conference on
Plant Genomics

July 14-15, 2016 Brisbane, Australia

The effect of biofuel production on sustainability of agriculture

Andrzej Wasiak
Bialystok University of Technology, Poland

During recent years biomass become considered as a resource that should satisfy various needs of human society. The food, construction materials as well as energy are supposed to be harvested from this resource. Obviously not total demand can be covered basing only on biomass, but its contribution is expected to increase. It is worth, therefore, to estimate limits of this growth, as well as factors determining those limits. The present paper is confined to the analysis of biomass as a source of energy. The main task is to estimate energetic efficiency of agricultural processes. The energetic efficiency is understood as the ratio of the amount of energy obtained from biofuels, produced basing on crops from particular region, to energy inputs required to facilitate all subsidiary processes assuring functioning of production processes. Based upon earlier works conducted by the present author, the mathematical model of energy efficiency of biofuel production is extended to more general form aiming to describe the effects of exclusion of a fraction of crops from food production towards biofuel production. The derived model gives quantitative relations between energy efficiency of "energetic plantations", energetic efficiency of industrial biofuel processing plants and energy demand of other types of agricultural production. Investigations are aimed towards determination of the role of biomass as a source of energy and the possibility of assuring energetic self-sufficiency of agriculture, as well as its effect on global energy demand. The potential role of modern biotechnology applied to "energetic" biomass production is also considered.

Biography

Andrzej Wasiak has completed his MS in 1961 in Chemistry (X-ray Crystallography) from Polish Academy of Sciences, PhD in 1974 in Technical Sciences/Polymer Physics, DSc in Materials Science (2000) from the University of Warsaw, Poland. He has also worked at Research Institute of General Chemistry in Warsaw (1964-67), Institute of Fundamental Technological Research (1968-2000). Since 2000, he is a Professor at Bialystok Technical University and Visiting Scientist at the University Massachusetts, USA, Kyoto University, Japan, the University of Duisburg and also a Fellow of the Committee of Production Engineering Polish Academy of Sciences. His scientific interest includes experimental studies and mathematical modeling of transitions occurring in technological processes like energy demand, material's structure formation, etc.

andrzej.wasiak@gmail.com

Notes:

Thomas Orton et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Genomics to detect and measure departures from autogamy in domesticated tomato

Thomas Orton, Peter Nitzsche, Josh Honig and **Veysel Donderalp**
Rutgers University, USA

Evidence that genes exist in cultivated tomato germplasm that promote outcrossing was obtained during the course of a traditional breeding program, specifically the recapitulation of the iconic variety 'Rutgers'. This open-pollinated variety was bred during 1926-1932 and released publically in 1934. Following an impressive run as an enormously popular world-wide fresh market and processing variety in the mid-10th century, 'Rutgers' was rendered obsolete by emerging F1 hybrid varieties and new processing methods and varieties. We (Rutgers University and the Campbell Soup Co.) sought to recapitulate an updated version of 'Rutgers' starting in 2010, using the same general approach (modified pedigree program) as the original 1934 release that culminated in the development of 'Rutgers 250', an open-pollinated garden variety released in 2016. The new variety possesses vine and fruit attributes that transcend the range embodied by the seminal parents, 'JTD' and 'Marglobe' (both prominent heirloom varieties from the early 20th century). When we contrasted 'Rutgers 250' with the parents with respect to SSR genotypes, we discovered many non-parental configurations and hypothesized that an outcrossing event occurred at or about the F2 that introduced some of the genes that were selected during the breeding program and present in the finished variety. We discovered in 2015 that the parental variety 'JTD' exhibited exerted stigmas, a trait common to wild outcrossing populations, while flowers of 'Marglobe' were inserted. All F1 individuals were exerted, suggesting the presence of dominant allele interaction. The F2 is currently under study. The total array of breeding germplasm in our program was subsequently screened for presence of exerted stigmas. Nine of 165 populations grown out in summer 2015 exhibited flowers with at least 50% exerted stigmas, or 5.45%. Most others were totally devoid of exerted stigmas. This strongly suggests that genes that profoundly affect mating system may be present in tomato breeding programs and that the presumption of autogamy should be verified before and during breeding efforts that include uncontrolled mating.

orton@aesop.rutgers.edu

Notes:

Agustin B Molina et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

conferenceseries.com

4th International Conference on

Plant Genomics

July 14-15, 2016 Brisbane, Australia

Resistance of different Musa varieties to some strains of *Fusarium oxyporum f. sp. cubense (Foc)* with particular focus on Foc Tropical Race 4 (Foc TR4) in Philippines

Agustin B Molina[1], **Vida Sinohin**[3], **Merlina Juruena**[4], **Emily G Fabregar**[2] and **Fe dela Cueva**[5]
[1]Bioversity International, Philippines
[2]Office of the Provincial Agriculturist, Philippines
[3]University of the Philippines Los Banos, Philippines
[4]Lapanday Foods Corporation, Philippines
[5]Bioversity International, France

Musa cultivars of different genomic groups were tested in the field and screenhouse against Foc strains. Three Vegetatively Compatible Groups (VCGs) namely, VCG 1213/16 (Foc TR4 strain), VCG 0123 and VCG 0126 were tested against 5 banana cultivars. Resistance was assessed on incidence of plants showing external symptoms and internal vascular discoloration index. Results showed that common commercial Cavendish (AAA) and local cultivar Lakatan (AAA) were susceptible to VCG 1213/16 but resistant to VCG 0123 and VCG 0126. On the other hand a local cultivar Cardaba (BBB) was resistant to VCG1213/16 but susceptible to VCG 0126 (Race 1 strain). This indicates a variety by Foc strain interaction. Results of field trials where more varieties were assessed against VCG1213/16, showed that genomic constitution based on balbisiana or acuminata, in diploid or triploid forms were not clearly related to resistance nor susceptibility to Foc TR4. Some AA diploids were highly resistant while some were susceptible. Similarly AAA, AAB and ABB triploids responded differently to Foc TR4 in the field. While VCG 1213/16 is highly virulent to many commercial cultivars, several cultivars were highly resistant. The variety by strain interaction is contrary to earlier belief that varieties susceptible to Race 1 strain are also susceptible to Race 4, pointing to the deficiency of the old Race classification system. This underscores the importance of more studies to understand field resistance of the many banana cultivars in relation to different Foc strains in different agroecosystem for practical purposes.

Biography

Agustin B Molina was a Senior Scientist and Regional Coordinator for Asia of Biodiversity International since 1998 and is currently an Honorary Research Fellow and Acting Regional Coordinator after his retirement in 2014. He spent more than 15 years of research on banana Fusarium wilt with regional partners in the Banana Asia Pacific Network. His career transcended the academe, industry and international R&D. He was a Plant Pathologist/Director of Research of Chiquita Brands Inc in Central America for 10 years; Former Professor and Chair of Department of Plant Pathology at University of the Philippines, Los Banos. He has obtained his PhD degree in Plant Pathology at Pennsylvania State University in 1983. He has published and presented many papers in his field.

A.MOLINA@cgiar.org

Notes:

Yiji Xia et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Understanding redox sensing and signaling through the identification and functional characterization of redox-sensitive proteins

Yiji Xia, Yimin Li, Pei Liu, Huan Zhong, Shuying Pang and **Hailei Zhang**
Hong Kong Baptist University, Hong Kong

A common physiological response to various environmental stresses in plants is accumulation of reactive oxygen species (ROS). ROS can cause oxidative damage to macro biomolecules. On the other hand, ROS have increasingly been recognized as important regulators in physiological and developmental pathways. ROS signaling is mediated largely through actions on redox-sensitive proteins that undergo oxidative modifications in response to perturbation of cellular redox states. We have developed gel-based and gel-free (OxiTRAQ) quantitative redox proteomics methods to identify Arabidopsis proteins whose thiols underwent oxidative modifications in response to treatments of ROS and the defense elicitors (salicylate and flagellin). The redox-sensitive proteins are involved in a variety of biological processes including chromatin remodeling and transcription, mRNA processing, post-translational modifications and primary and secondary metabolism. A redox-sensitive bZIP transcription factor in Arabidopsis has been found to act as a redox sensor and mediate expression of oxidative stress responsive genes through its oxidation/reduction. Our progresses in developing redox proteomics methods and in characterizing the role of the transcription factor in redox sensing and stress responses will be presented.

Biography

Yiji Xia is currently a Professor and Head of Department of Biology at Hong Kong Baptist University. He has received his PhD in Genetics from Iowa State University in 1997 and was a Joint Postdoctoral Associate at Salk Institute/Noble Foundation from 1997 to 1999. After working at Akkadix Corporation (San Diego, USA) as a Senior Scientist from 2000 to 2001, he has joined Danforth Plant Science Center (St. Louis, USA) as Principal Investigator. Since 2009, he has been working at HKBU. He has published over 40 research articles in Nature, EMBO Journal, EMBO Reports, Plant Cell, PNAS and other journals with a total citation count of over 4,900. His main research focus is on plant stress responses, particularly on redox sensing and epigenetic and transcriptional regulation in response to biotic and abiotic stress.

yxia@hkbu.edu.hk

Notes:

Rakesh K Srivastava, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Translating advances in pearl millet genomics to farmer preferred cultivars

Rakesh K Srivastava
International Crops Research Institute for the Semi-Arid Tropics, India

Pearl millet is one of the most climate resilient cereals. It is grown in marginal and dry areas of the world with poor soil fertility, low moisture holding capacity in subsistence agriculture. It forms critical food, nutrition and livelihood support for the millions of poor living in Africa, Asia and other parts of the world. Pearl millet is one of the cereals which received poor attention towards generation of genetic and genomic resources in the past. However, lately a lot of efforts have been made in trait discovery, mapping and deployment of some key traits. One successful example is HHB 67 Improved, which is the first marker-assisted breeding product in India and is gown in more than 750,000 ha every year. In pearl millet more than 20 pairs of mapping population have been generated, segregating for an array of traits of economic interest. In addition, a world association mapping panel called PMiGAP, chromosome segment substitution lines (CSSLs), TILLING population have been developed. Recently, at ICRISAT the whole genome sequencing of a pearl millet reference line Tift23D2B1P1-P5 has been completed, along with re-sequencing of about 1,000 accessions consisting of wild and cultivated germplasm and breeding lines. By virtue of available genetic maps, QTL locations and effects, the pearl millet community is strongly placed for mining genes and gene networks for an array of traits. The genome sequence will help us utilize various reverse genetics tools, carry our genome-wide association studies (GWAS), genomic selection (GS) leading to efficient cultivar development.

Biography

Rakesh K Srivastava has obtained his PhD from the Indian Agricultural Research Institute (IARI) New Delhi, India. He currently leads the pearl millet genomics team at ICRISAT, India. He is extensively involved in generation of various genetic and genomic resources, mining, mapping and deployment of QTLs/genes for various biotic, abiotic, grain and fodder quality traits in collaboration with the National Agricultural Research System (NARS) in pearl millet. He has contributed significantly towards the international whole genome sequencing for pearl millet involving world reference germplasm and entire association mapping panel. He is actively involved in various capacity building programs for NARS.

r.k.srivastava@cgiar.org

Notes:

Zhi Min Yang et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

New insights into genome-wide change of DNA methylation and its association with gene expression in cadmium-exposed rice (*Oryza sativa*)

Zhi Min Yang[1], **Sheng Jun Feng**[1], **Xue Song Liu**[1], **Shang Kun Tan**[1], **Shan Shan Chu**[1], **Hua Tao**[1], **Tao Liu**[1] and **Youko Oono**[2]
[1]Nanjing Agricultural University, China
[2]National Institute of Agrobiological Sciences, Japan

Plant exposure to cadmium (Cd) affects transcriptional responses. Whether Cd modified DNA methylation marks are associated with transcription and functional consequences in plants remain unknown. We present the genome-wide single base resolution maps of methylated cytosines in Cd exposed rice, along with global transcriptional change in mRNA. Widespread differences were identified in the composition and patterning of CG and non-CG methylation marks between Cd exposed and control rice genomes. There are 2393 non-redundant differentially methylated regions (DMRs). RNA sequencing revealed that most of DNA methyltransferases, histone methyltransferases and DNA demethylases differentially changed in transcription under Cd exposure. By profiling global DNA methylation and gene transcription, we found more genes hypermethylated than those hypomethylated in CG, CHH and CHG (where H is A, C or T) contexts in the regions of upstream, gene body and downstream under Cd stress. Seventy-nine genes ($p<0.05$, two-fold change) with a strong preference of differential expression in Cd exposed rice plants was identified. Many of them were involved in stress response, metal transport and transcription factors. A subset of loss of function mutants defective in DNA methylation/demethylation and histone modification activities were used to identify transcript abundance of selected genes. In most cases, genes in the mutants were repressed by Cd treatment. Provision of azacitidine (a global DNA methylation inhibitor) attenuated root growth inhibition but promoted biomass and Cd accumulation under Cd exposure. Finally, we identified 108 transposons and 254 retrotransposons that were modified by methylation, where transcriptional expressions of 30 neighboring genes were changed under Cd exposure.

Biography

Zhi Min Yang is a Professor of Plant Physiology and Molecular Biology in Nanjing Agricultural University (NAU). He has earned his PhD degree at NAU in 1999 and received his Postdoctoral training at the University of Kagawa, Japan and Justus-Liebig University, Germany. He is working on physiological and molecular mechanisms for plant abiotic stress responses (salt, drought or heavy metals). His major interest is in epigenetic regulation of stress tolerance, toxic metal uptake and accumulation in plants through small/long non-coding RNAs (e.g. microRNAs) and DNA methylation. He has published 80 peer-reviewed papers and serves as Associate/Academic Editor of *Gene, Plant Gene and PloS One*.

zmyang@njau.edu.cn

Notes:

Frank-Holm Roegner, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Electron treatment of seed

Frank-Holm Roegner
Fraunhofer Institute for Organic Electronics, Electron Beam and Plasma Technology, Germany

Providing the world´s growing population with nutritious food is an enormous challenge, that solution starts very early in food production. Beside the known chemical seed dressing there is another way for killing pathogens. This environmental friendly, purely physical disinfection of seed, bases on the biocidal effect of accelerated electrons. The Fraunhofer Institute for Organic Electronics, Electron Beam and Plasma Technology (FEP) developed the basics for this technology years ago. Electrons are a versatile tool for numerous applications in all fields of industry. Beside the known and well established processes in medicine and pharma, the electron treatment of seed became more and more important. Accelerated electrons are characterized by their kinetic energy. When these electrons penetrate matter, they are acting by losing their energy through collision processes. Once the energy is spent, they do not penetrate further into the material. This fact is used to control the sphere of action of electron treatment precisely. This method can be used to apply an even dose on all sides of the individual seed grains. Electrons only penetrate into the seed coat far from the embryo and the endosperm to avoid genetic changes. Harmful organisms hit by a sufficient dose of accelerated electrons will be killed or inactivated. In testing series the chemical seed dressing, as the state of the art process for winter wheat treatment, is used as 100% standard. There is a slight increase of grain yield and a significant increase of emergence for electron treated seed on average over long period. The reason for this behavior is a non-selective effect of physical treatment methods. Thereby the treatment is able to eliminate all pathogens on and inside the seed coat. Due to the advantages for farmers, producers and the environment the companies CERAVIS and BayWa could sell more than 15.000 tons of electron-treated cereal seeds within 2015 with upward tendency.

Biography

Frank-Holm Roegner is a German Physicist. He is graduated in Physics in the year 1988. He is working as a Head of the Department for e-processing in Fraunhofer Institute Electron Beam and Plasma Technology. He is working as a Member of iiA and RADTech-Europe, Founder member of Fraunhofer Cleaning Technology Alliance since 2002, and leading referent for an annual course, "Cleaning Technology for industrial Production".

frank-holm.roegner@fep.fraunhofer.de

Notes:

Soumitra Paul et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Molecular analysis of bioengineered rice: A proteomic and transcriptomic approach

Soumitra Paul[1], **Dipak Gayen**[2], **Swapan K Datta**[2] and **Karabi Datta**[2]
[1]University of Calcutta, India

Food security is a major challenging issue in developing countries like India where rice is the staple crop. Abiotic stress like drought affects most of the rice production in India. The generation of drought tolerant rice cultivar by overexpression *AtDREB1A* is an important breakthrough in biotechnology research. In addition, rice contains very little amount of iron and zinc in the edible endosperm. Therefore, biofortification of these two micronutrients in rice grains is believed to be the most promising strategy for enhancing mineral nutrition in diets. The bioengineered high iron rice grain has already been developed by overexpression of soybean and rice endogenous ferritin genes. Low phytate rice grain by RNAi mediated silencing of phytic acid biosynthesis also facilitates iron accumulation in milled rice grain. However, the molecular signaling network operating in transgenic crops still remains unclear. In our current study, we performed the proteomic analysis of *DREB1A* over expressing drought tolerant rice cultivars. The proteome profile of rice roots revealed metabolic alteration in energy and carbohydrate metabolism. A novel r40c1 protein species has been identified which play a crucial role in *DREB1A* mediated drought tolerance. Recently, the role of miRNAs in iron transport has been deciphered in transgenic ferritin over expressing rice plants which unravel the molecular mechanism of iron loading in high iron rice grains. Four novel miRNAs targeting NRAMP4 has been considered for enhancement of iron loading in transgenic rice plants.

Biography

Soumitra Paul is an Assistant Professor of Botany at Kaliganj Government College, Kaliganj, Nadia, West Bengal, India. He is a Doctorate in Botany (PhD) from University of Calcutta, India. He has 8 years of research experience on Crop Molecular Biology and Biotechnology and has published several papers in renowned international peer-reviewed journals. He is an Editorial Board Member and Reviewer of different journals such as *Frontiers in Plant Science, Rice and African Journal of Biotechnology* etc.

psoumitra@ymail.com

Notes:

Riddhi Datta et al., Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

An insight into the molecular mechanism of glutathione-ethylene interplay in plant defense

Riddhi Datta and **Sharmila Chattopadhyay**
Dr. A P J Abdul Kalam Govt. College, Newtown, India

Plant defense is regulated by a network of signaling pathways where salicylate, jasmonate and ethylene (ET) function as key signaling molecules. Glutathione (GSH) is gradually gaining importance as a dynamic player in this network playing critical roles during stress. We have earlier reported that enhanced GSH level can provide resistance against *Botrytis cinerea* infection presumably through its crosstalk with ET. In this study, we demonstrate that GSH induces ET biosynthesis by modulating the transcriptional and post-trancriptional regulations of its key enzymes, ACC synthase (ACS) and ACC oxidase (ACO). Transgenic *Arabidopsis* plants with enhanced GSH content exhibited remarkable up-regulation of ACS2, ACS6 and ACO1 at transcript as well as protein levels while they were down-regulated in the GSH depleted *pad2-1* mutant. We further observed that GSH induced ACS2 and ACS6 transcription in a WRKY33 dependent manner while ACO1 transcription remained unaffected. On the other hand, the mRNA stability for ACO1 was found to be increased by GSH which explains our above observations. In addition, we also identified the ACO1 protein to be a subject for S-glutathionylation which is consistent. However, S-glutathionylation of ACS2 and ACS6 proteins was not detected. Further, the transgenic plants exhibited resistance to necrotrophic infection and salt stress while the *pad2-1* mutant was sensitive. Exogenous GSH improved stress tolerance in wild-type plants but not in the ET signaling mutant, *ein2-1*, indicating that GSH mediated resistance to these stresses occurs via an ET mediated pathway. Together, our investigation reveals a dual-level regulation of ET biosynthesis by GSH during stress.

Biography

Riddhi Datta is a Gold-medallist in Botany in Under-graduate as well as Post-graduate courses from University of Calcutta, India. She has been working in the field of Glutathione and its role in plant defense since 2011 and has recently submitted her PhD thesis from CSIR-Indian Institute of Chemical Biology, India. She has published 14 papers in reputed international journals. At present, she is an Assistant Professor in Botany, Govt. General Degree College, New Town, India and a Visiting faculty in the Post-graduate Department of Botany, Barasat Govt. College, India.

riddhi.bot@gmail.com

Notes:

Alka Vasan, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Selection of barley genotypes for nutritional composition vis-à-vis malting trait for improvement

Alka Vasan
CCS Haryana Agricultural University, India

Barley (*Hordeum vulgare vulgare L.*) is an important cereal grain of semiarid regions globally due to its nutritional value. The present investigation was carried out to evaluate the nutrient composition and effect of processing on four new barley genotypes viz. BH- 942, BH- 952, BH-933 and BH-946. The results revealed that BH-94 had higher crude fiber (4.25%) and crude protein (12.39%) content. The total soluble sugars, reducing sugars, non-reducing sugars, starch and dietary fiber content of barley genotypes ranged from 3.29 to 3.48, 0.55 to 0.62, 2.67 to 2.91, 57.27 to 58.57, 12.45 to 13.48 per cent, respectively. The availability of minerals and in-vitro digestibilities were also higher in barley genotype BH-942, but had lower antinutrients. Malting not only increased the protein and crude fiber content, but also sugars, minerals and in-vitro digestibilities for protein and starch, with the highest increase in BH-942 and BH-946, whereas it reduced the crude fat, ash, starch and antinutrients content in all genotypes. Genetic variability among four barley genotypes can be enhanced through recombination to enhance accumulation of essential minerals; synthesis of precursors of vitamins; modified quantities and qualities of starch, proteins and fats in improving human health and nutrition through efficient phenotypic screens and genotypic markers. QTLs and genes for above stated traits have been identified and mapped on various barley chromosomes for incorporation into breeding programs using molecular marker based selection for further improvement and development of new barley varieties combing useful traits for the benefit of farmers, processors and human health.

Biography

Alka Vasan has completed her PhD in Foods and Nutrition from CCS Haryana Agricultural University, Hisar, India with her research focus on study of processing of barley (*Hordeum vulgareL.*) genotypes and its effect on Barley's nutritional composition. Having worked with researchers of such high repute, she is now set to work towards development of innovation in value addition of the crop and her experiences learnt during her research have made her get her work published both nationally and internationally. Her publications include eleven papers, four book chapters and a couple of paper & poster presentations in India and abroad.

alkavasan@yahoo.com

Notes:

conferenceseries.com
549th Conference

4th International Conference on

Plant Genomics

July 14-15, 2016 Brisbane, Australia

Workshop

John Salmeron, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

John Salmeron

Precision BioSciences Inc., USA

Precision genome engineering for a bright food future

Genome editing promises to drive a new generation of crop trait products with reduced development times, low regulatory hurdles and broad applications. The ARCUS technology platform at Precision BioSciences delivers custom meganuclease editing agents with extremely high levels of specificity. Delivered through a rapid cell-based screening process, ARCUS nucleases have been proven effective across a wide range of target sites for gene mutation, deletion and insertion in a variety of crops.

Biography

John Salmeron is the Director of Plant Sciences at Precision BioSciences, Inc., in Durham NC, USA and has worked in the field of Plant Biotechnology for over 20 years. Prior to joining Precision, he has held positions in Business Development and led the agricultural R&D team at Intrexon Corporation, a Leader in Synthetic Biology. He was a Research Portfolio Manager at Syngenta Biotechnology Inc., and held leadership roles directing teams in trait development and genomics. He is the Founder of eiiConsulting, an early-stage biotechnology consulting firm. He has an AB degree from Washington University in St. Louis and a PhD from Duke University.

John.salmeron@precisionbiosciences.com

Notes:

Ana Cláudia de Macêdo Vieira, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Ana Cláudia de Macêdo Vieira

Faculdade de Farmácia, Universidade Federal do Rio de Janeiro, Brazil

Parasitic castration entomógena in neotropical species : Models malpighiaceae of salt marshes

Plant reproductive organs are considered very sensitive to the action of midges and depending on the induced change level, leads to parasitic castration phenomenon causing the prevention of sexual reproduction of plants. Few models of floral galls have been described for neotropical regions, however, the salt marshes of Marica and Grumari, State of Rio de Janeiro, were recorded and described floral galls on Byrsonima sericea DC. and Niedenzuella acutifolia (Cav.) W.R.Anderson (Malpighiaceae). In B. sericea has identified the occurrence of three floral galls. induced by insects. In the gall-induced Diptera larvae developed in the pocket by inhibiting the development of pollen and ovules. In galls induced Lepidoptera, the larva settles on pedicel, excavating the central bud, preventing the formation of the pistil. In the third gall, the larval chamber is formed at the apex of the floral button receptacle, leading to no training in their reproductive structures. In all, the cup and the corolla form ,, with varying degrees of atrophy in each type of gall. N. acutifolia occur two floral galls. In galls induced by Diptera, the pistil hypertrophy, forming sheetlike structures where there are the larval chambers. In other galls, only the cup develops and sepals are welded, forming a chamber and no other whorl forms. In the five galls analyzed, changes in varying degrees in the differentiation of floral structures led to parasitic castration, because none of the flower buds affected by midges are able to complete its development, affecting the reproductive success.

Biography

Ana Cláudia de Macêdo Vieira has completed his PhD at the age of 36 years from University of São Paulo, Brazil. She is associate professor at the School of Pharmacy of the Federal University of Rio de Janeiro and coordinates the pharmacobotany Laboratory, where she develops research with galls on sandbank environment, control of drugs and medicinal plants. Develops university extension projects with rational use of medicinal plants and unconventional food plants to farmers.

anavieira@gmail.com

Notes:

Andre Luis de Alcantara Guimaraes, Adv Crop Sci Tech 2016, 4:3 (Suppl)
http://dx.doi.org/10.4172/2329-8863.C1.002

Andre Luis de Alcantara Guimaraes
Federal University of Rio de Janeiro, Brazil

Gall inducers and host plants: What changes may these organisms induce on plant metabolism?

Galls are anomalies in plant development of parasitic origin that affect the cellular differentiation or growth and represent a remarkable plant-parasite interaction. The galls may occur in all organs of the host plant from roots to fruits. However, the existence of galls in reproductive organs and their effects on host plants are seldom described in the literature. In the past decades, many studies aimed to analyze not only the morphological changes induced by these parasites but also the metabolic changes. Nevertheless, the mechanisms involved and how these organisms regulate these intricate changes still remain unclear. In our research, we present a novel study of galls in plants of the Neotropical region: The 'witches' broom' galls developed in floral structures of Byrsonima sericea (Malpichiaceae). The affected inflorescences and flower buds showed several morphological and anatomical changes. The sepals, petals and carpels converted into leaf-like structures after differentiation and the gynoecium followed new destinations. In this work, we discuss the changes in the development of reproductive structures caused by witches' broom galls and their effects on the reproductive success of the host plants. These results, combined with patterns in galls in different Neotropical plant species, suggest that gall inducers may alter gene expression, plant hormones and chemical compounds of host plants on their behalf.

Biography

Andre Luis de Alcantara Guimaraes has completed his PhD in Botany from Federal University of Rio de Janeiro (UFRJ) and Postdoctoral studies at the Faculty of Pharmacy from UFRJ. He is an Associate Professor of Faculty of Pharmacy from Federal University of Rio de Janeiro. He has published papers in reputed journals of Plant Science, especially with galls and their metabolical changes on host plants and research with medicinal plants.

andreluis.guimaraes@gmail.com

Notes: