

University of Florida PLANT SCIENCE SYMPOSIUM

April 13-14, 2017

Harnessing Plant Diversity to Cope with a Changing Climate

University of Florida, Gainesville, FL

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University of Florida Plant Science Symposium



University of Florida

Plant Science Symposium

A DuPont Plant Sciences Symposia series

April 13-14, 2017

HARNESSING PLANT DIVERSITY TO COPE WITH A CHANGING CLIMATE

VENUE: CANCER & GENETICS RESEARCH COMPLEX University of Florida 2033 Mowry Road, Gainesville, FL 32610

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UF IFAS Research UNIVERSITY of FLORIDA UNIVERSITY of FLORIDA

UF/IFAS Plant Breeders Workgroup UF/IFAS Agronomy Department UF/IFAS Horticultural Sciences Department UF/IFAS Environmental Horticulture UF/IFAS Plant Pathology



Schedule : April 13th 2017

7:30 - 8:30 AM	Check-in, Breakfast, Poster Set-up					
8:30 - 8:40 AM	Opening Remarks - Dev Paudel, UF Plant Science Council					
8:40-8:50 AM	Dr. Tabare Abadie - DuPont Pioneer					
8:50 - 9:00 AM	Dr. John Davis - UF/IFAS					
9:00 - 9:50 AM	Dr. Senthold Asseng: Food security and climate change.					
9:50 - 10:40 AM	Dr. Stephanie Greene: Wading deeper into the gene pool: using					
	crop wild relatives to breed climate resilient crops.					
10:40 - 10:50 AM	COFFEE BREAK					
10:50 - 11:40 AM	Dr. P.V. Vara Prasad: Impact of Climate Change and Climate					
	Variability on Productivity of Food Grain Crops.					
11:40 - 11:55 AM	Craig Beil: Fixed vernalization 1 alleles increase genomic selection					
	prediction accuracy of winter injury in the genetically diverse					
	facultative and winter wheat observation nursery					
11:55 - 12:10 PM	Regina Enninful: Characterization of parents of sorghum mapping					
	populations exposed to water-deficit stress					
12:10 - 12:25 PM	Uttam Bhattarai: Identification of root and shoot QTLs in rice during					
	drought stress using SNP based highly saturated genetic map					
12:25 - 12:40 PM	Waltram Ravelombola: Association mapping for salt tolerance in					
	cowpea using a genotyping-by-sequencing approach					
12:40 PM - 3:00 PM	Lunch / Poster session [Evaluation from 1-3 PM]					
3:00 - 3:10 PM	COFFEE BREAK					
3:10 - 4:00 PM	PM Dr. Jim Hancock: Breeding strawberries and blueberries in a					
	changing global environment.					
4:00 - 4:40 PM	Dr. Charlie Messina: Improving phenotypic prediction through crop					
	model-whole genome prediction integration.					
4:40 - 4:50 PM	Student Travel Awards - DuPont Pioneer					
4:50 - 4:55 PM	Student Poster Awards - IFAS					
4:55 - 5:00 PM	Closing Remarks: Dr. Esteban Rios					

Schedule: April 14th, 2017

7:30 AM - 8:00 AM	Assemble at Fifield Hall and coffee			
8:00 AM - 8:30 AM	Travel to Citra			
8:30 AM - 8:45 AM	Welcome Remarks (Jim Boyer)			
8:45 AM - 9:45 AM	Tour 1: Dr. Kevin Kenworthy (Turfgrass)			
9:45 AM - 10:45 AM	Tour 2: Dr. Ali Babar (Wheat)			
10:45AM- 11:45AM	Tour 3: Dr. Patricio Munoz (Blueberry)			
11:45 AM - 1:00 PM	Lunch			
1:00 PM - 1:30 PM	Arrive in Gainesville			

Live stream: Morning Session https://goo.gl/Xvj4iV Live stream: Afternoon Session https://goo.gl/IXe7el





Dr. Senthold Asseng University of Florida, Department of Agricultural and Biological Engineering

FOOD SECURITY AND CLIMATE CHANGE

Dr. Asseng's research interests are in systems analysis to understand, compare and improve the productivity and sustainability of atmosphere-crop-soil systems changing over time and space and at different scales. He specializes in impact and adaptation of climate variability and climate change on cropping systems. Dr. Asseng joined the faculty of the agricultural and biological engineering department in late 2010. Asseng is well known for his modeling expertise, organizational ability, and program leadership.





Dr. Stephanie L. Greene USDA-ARS, Fort Collins, CO

WADING DEEPER INTO THE GENE POOL: USING CROP WILD RELATIVES TO BREED CLIMATE RESILIENT CROPS.

Dr. Stephanie L. Greene is a Supervisory Plant Physiologist and the lead scientist of the Seed Preservation Program at the Plant and Animal Genetic Resources Preservation Unit. Dr. Greene's main research focus is the conservation of crop wild relative species that are native to the United States. These wild species are important genetic resources that can be used to develop productive and climateresilient crops and many are vulnerable. She is also leading a team assessing the dispersal of genetically-engineered genes from alfalfa into the environment to determine avenues of escape and strategies to minimize adverse impacts on alfalfa hay and seed growers producing for export and organic markets.





Dr. P. V. Vara Prasad Kansas State University Department of Agronomy

IMPACT OF CLIMATE CHANGE AND CLIMATE VARIABILITY ON PRODUCTIVITY OF FOOD GRAIN CROPS

Dr. Prasad is currently a Professor of Crop Ecophysiology and Director of Center for Sorghum Improvement in the Department of Agronomy at Kansas State University. His research mainly focuses on understanding responses of food grains crop to changing environments (temperature, water and climate change factors) and developing crop management strategies for efficient use of inputs.He is passionate about international research and education. He has several on-going international research programs in Africa (Ghana, Mali, Burkina Faso, Niger and Kenya) and Asia (India, Philippines) focusing on soil, water, nutrient and crop management practices, and stress tolerance for improving crop productivity. Dr. Prasad has published more than 100 peer reviewed journal articles and book chapters, and served as a peer reviewer for more 35 different international journals. He currently serves on editorial boards of international journals including Crop Science, Agronomy Journal and Journal of Crop Improvement.





Dr. Jim Hancock Michigan State University

BREEDING STRAWBERRIES AND BLUEBERRIES IN A CHANGING GLOBAL ENVIRONMENT.

Dr. James Hancock is a professor of horticulture in the College of Agriculture and Natural Resources and MSU AgBioResearch expert blueberry breeder. He has released four of the most popular Northern Highbush blueberry varieties in the world: Draper, Liberty, Aurora and Huron. Hancock's innovations regarding these varieties of Northern Highbush blueberries represent highly productive means of generating flavorful and long-lasting blueberries. Approximately 20 million plants of these four varieties have been sold. Michigan has been the No. 1 blueberry-producing state for the last 70 years, partly due to the Hancock varieties.





Craig Beil PhD Candidate Colorado State University

FIXED VERNALIZATION 1 ALLELES INCREASE GENOMIC SELECTION PREDICTION ACCURACY OF WINTER INJURY IN THE GENETICALLY DIVERSE FACULTATIVE AND WINTER WHEAT OBSERVATION NURSERY.

My name is Craig Beil and I'm a Ph.D. candidate studying wheat breeding and genetics in the Soil and Crop Sciences Department at Colorado State University. I received my Bachelor's degree in Agronomy from Truman State University in Kirksville, MO in 2010 where I was also a four year varsity soccer player. My undergraduate studies focused on vegetable production as I was interested in growing food for local foods dinners. I then received my Master's degree in Bioagricultural Sciences and Pest Management from Colorado State University in 2013. My Master's researcher focused on field and greenhouse trials evaluating a new organic herbicide molecule. In addition, I worked on screening mutagenized wheat populations for novel herbicide resistance while also measuring the potential for gene flow between wheat and jointed goatgrass as part of a biotech risk assessment grant. It was during this time that I became interested in global food production and began to understand the important role that plant breeders can have in adapting crops and mitigating global hunger. My doctoral studies in plant breeding and genetics are focused on population structure and genetic diversity analysis, genomic selection, and highthroughput phenotyping in international facultative and winter wheat nursery collections. I hope for my project to facilitate more effective and efficient germplasm exchange between the U.S. Great Plains wheat breeding programs and wheat breeding programs in Eastern Europe and Western Asia. This will help to increase genetic diversity across several important wheat producing regions and allow breeders to be better able to adapt to changing consumer and environmental demands.





Regina Enninful PhD Student Kansas State University

CHARACTERIZATION OF PARENTS OF SORGHUM MAPPING POPULATIONS EXPOSED TO WATER-DEFICIT STRESS

Ms. Regina Enninful is a PhD student of the crop physiology laboratory at the Department of Agronomy, Kansas State University. Her research work is on looking into different dimensions of water-deficit stress tolerance in Sorghum. Her major objective involves in depth physiological and biochemical characterization of Nested Association Mapping founder lines with an overall goal of mapping genomic regions that can further enhance tolerance to water-deficit stress among sorghum lines. After pursuing a Natural Resources Management program at the undergraduate Level at KNUST in Ghana, she realized the many environmental problems in the world that have arisen from improper management of the Natural Resources. Thus she undertook studies at the University of Greenwich-UK which led MSc. Natural to the award of Resources-Sustainable Environmental Management. Regina's previous studies included investigations on climate change adaptation and generating an up-to-date information crucial for monitoring a GSBA (Globally Significant Biodiversity Area) in Ghana. She has also worked on determining optimal conditions to propagate Moringa oleifera which is critical for supporting livelihoods and addressing nutritional needs.

As a lecturer and a researcher, Regina looks forward to spearheading research and imparting knowledge and skills acquired over the years. She is dedicated in contributing to solving challenges in the agricultural and environmental sciences as well as in the management of natural resources.





Waltram Second Ravelombola MS Student University of Arkansas, Fayetteville

ASSOCIATION MAPPING FOR SALT TOLERANCE IN COWPEA USING A GENOTYPING-BY-SEQUENCING APPROACH.

Waltram Second Ravelombola is originally from Madagascar. He is a current Master's student in the interdisciplinary Cell and Molecular Biology Program at the University of Arkansas, Favetteville. He is working for Drs.Ainong Shi and Yuejin Weng from the Vegetable Breeding and Genetics Program of the Horticulture Department. His current research deals with the association mapping for cowpea salt tolerance using a genotyping-by-sequencing approach. His research project aims at finding some significant SNPs associated with salt tolerance in cowpea. In addition, he has an Agronomist Engineering degree from the University of Antananarivo, Madagascar back in 2013. He has been focusing on plant breeding, genetics, and pathology. Waltram has strong interests in understanding the genetic architecture underlying crop tolerance to abiotic stresses along with the epigenetic regulations that crop undergo under drought conditions. He is looking forward to actively participating in the Consultative Group for International Agricultural Research (CGIAR) such as IITA, CIAT, CYMMIT were he can positively impact smallholder farmers' life through his findings.





Uttam Bhattarai PhD student Louisiana State University

IDENTIFICATION OF ROOT AND SHOOT QTLS IN RICE DURING DROUGHT STRESS USING SNP BASED HIGHLY SATURATED GENETIC MAP.

I am Uttam Bhattarai, a Ph.D. Student at Louisiana State University, Baton Rouge, Louisiana. I am working on the molecular genetics of rice resistance to drought. My study aims in finding the QTLs related to drought tolerance, Identifying the candidate genes responsible for drought tolerance and incorporating the drought tolerance characteristics in USA rice genotypes. I like to visit different places, making friends and enjoy the local tradition and culture.



1. GENETICALLY ENGINEERED SALT TOLERANCE IN POTATO WITH ATRIPLEX CANESCENS BADH GENE DRIVEN BY 3 COPIES OF CAMV35S PROMOTER Institute of Molecular Biology and Biotechnology,The

University of Lahore, punjab, Pakistan

Potato (Solanum tuberosum L.) is ranked among the top leading staple foods in the world. Salinity adversely affects potato crop vield and quality. Therefore, increased level of salt tolerance is a key factor to ensure high yield. The present study focused on the agrobacterium-mediated transformation of Atriplex canescens betaine aldehyde dehydrogenase (BADH) gene, using single, double and triple CAMV35s promoter to improve salt tolerance in potato. Detection of seven potato lines harboring BADH gene, followed by identification of T-DNA insertions, determination of transgenes copies no through Southern Hybridization and quantification of BADH protein through Enzyme Linked Immunosorbent Assay were considered in this study. The results clearly depict that the salt tolerance of potato was found to be promoter-dependent, as the potato transgenic lines with triple promoter showed 4.4 times more glycine betaine production which consequently leads towards high resistance to salt stress as compared to transgenic potato lines with single and double promoters having least production of glycine betaine. Moreover, triple promoter transgenic potato lines have also shown lower levels of H2O2, malondialdehyde (MDA), relative electrical conductivity, high proline and chlorophyll content as compared other two lines having a single and double promoter. Insilco analysis also confirmed that Atriplex canescens BADH has the tendency to interact with sodium ions and water molecules. Taken together these facts it can be concluded that overexpression of BADH under triple CAMV35s promoter with more glycine betaine, chlorophyll & MDA contents, high relative quantities of other metabolites results in an enhanced level of salt tolerance in potato.



2. GENETIC CONTROL OF ALFALFA FALL DORMANCY AND COLD TOLERANCE

Laxman Adhikari¹, Orville Lindstrom¹, Dev Paudel² and Ali M. Missaoui¹ ¹ University of Georgia ² University of Florida

Fall dormancy (FD) and winter hardiness (WH) in alfalfa (Medicago sativa L.) have been reported as yield limiting traits. Therefore, understating the genetic basis of these two traits through quantitative trait loci (QTL) mapping is crucial for alfalfa improvement. The objective of this study was to identify QTLs associated with FD and WH of alfalfa. A bi-parental F1 mapping population was developed by crossing two cultivars contrasting in FD trait: 3010 (FD= 2) and CW1010 (FD=10). One hundred ninety F1 hybrids were confirmed using five SSR markers. The mapping population along with the two parents, and standard checks were planted using RCBD design with three replications at two locations: Athens and Blairsville in GA. FD was measured as canopy height after 28 days of an autumn clipping on 21st September and in mid-winter to confirm the dormancy level of the segregated genotypes. Chlorophyll content was also noted for FD phenotyping. An indoor screening of the mapping population in a cold chamber was also optimized using standard checks to score freeze sensitivity of the genotypes in a greenhouse. Regrowth height and biomass of indoor cold temperature treated and control samples were compared. FD levels of parents and mapping progenies were estimated using regression equation derived via check cultivars, which displayed segregation of mapping population into various FD levels. Similarly, frost damage visual scoring data also showed a distinct segregation of the mapping population from cold sensitive (score 1) to cold susceptible (score 5). Preliminary results showed a positive but weak correlation between FD and frost damage. The mapping population was genotyped by using Genotyping-by-sequencing (GBS) after a single digestion of DNA using ApeKI enzyme followed by annealing of adapters and amplification. We received 2032 million raw reads from Illumina NextSeq PE75 High Output Flow Cell out of which 1008 million paired reads were usable. We utilized GBS-SNP-CROP pipeline to analyze the genotyping data. The raw reads were trimmed and demultiplexed followed by alignment to a mock reference genome, which was designed by using only the parental reads. Identification of potential SNPs and further analysis to construct linkage map is underway.



3. CITROPSIS FOR CITRUS CULTIVAR DEVELOPMENT AND GERMPLASM ENHANCEMENT

Ethan Nielsen, Jude Grosser University of Florida, Citrus Research and Education Center, Lake Alfred, Florida

African cherry-oranges (Citropsis species) are near Citrus relatives that are a source of novel traits that could be used for improvement of Citrus, especially in light of changing climactic conditions, but until recently conventional breeding methods have failed. Citropsis sp. are graft compatible with Citrus, but are only marginally sexually compatible (resulting hybrids have been sterile). Somatic hybridization has been useful for making hybrids between Citropsis and Citrus. All Citropsis species are from tropical Africa, and recent publications suggest Africa as the source of the Liberobacter family responsible for Huang Long Bing (HLB) disease. Genes for resistance to this disease and possibly other tropical diseases and afflictions may be present in this gene pool. Using biotechnology methods and traditional breeding, hybrids were created between Citrus and Citropsis gilletiana Swingle & M. Kellerm, in an attempt to exploit traits for improving Citrus germplasm. The first sexual hybrid using a tetraploid somatic hybrid (*Nova mandarin* hybrid + *C. gilletiana*) when it flowered for the first time in December 2014, over 20 years since this hybrid was created. This is the first and only documented flowering of an intergeneric Citrus somatic hybrid. A single seedling was obtained using ovule rescue techniques, as fruit failed to develop naturally past 30 days. Somatic hybrids were also obtained using W. Murcott mandarin callus and Red Cooper grapefruit callus and C. gilletiana leaves. Hybrids have been identified phenotypically and confirmed using flow cytometry to identify tetraploids. Nematode inoculation was performed to assess nematode tolerance or resistance.



4. FIXED VERNALIZATION 1 ALLELES INCREASE GENOMIC SELECTION PREDICTION ACCURACY OF WINTER INJURY IN THE GENETICALLY DIVERSE FACULTATIVE AND WINTER WHEAT OBSERVATION NURSERY (FAWWON)

Craig Beil¹, Victoria Anderson¹, Scott Haley¹, Alexey Morgounov²

¹Dep. of Soil and Crop Sciences, Colorado State Univ., 1170 Campus Delivery Fort Collins, CO 80523 ²ICARDA-CIMMYT, P.K. 39 Emek, 06511 Ankara, Turkey.

International exchange of germplasm is important in addressing existing and emerging constraints to global wheat (Triticum aestivum L.) production. Elite breeding lines tested in international and regional performance nurseries best showcase a pool of genotypes for cultivar release or as parents in future crosses. In this study we analyzed genetic diversity and low temperature (LT) tolerance of genotypes from the international Facultative and Winter Wheat Observation Nursery (FAWWON) in relation to genotypes currently being grown in the Southern Great Plains. The collection was genotyped with single nucleotide polymorphism (SNP) markers obtained via genotyping-bysequencing (GBS). The germplasm was also genotyped at important vernalization and photoperiod loci using Kompetitive Allele Specific PCR (KASP). Population structure was composed of four subpopulations when using a correlated allele frequencies model in the program STRUCTURE. Three subpopulations were characterized as having a high percentage of genotypes from the FAWWON while the fourth subpopulation had a high percentage of genotypes from the Southern Regional Performance Nursery. The Wright's fixation index (FST) values ranged from 0.16 to 0.32 between subpopulations. The FAWWON genotypes showed considerable variation in LT tolerance across six environments in Colorado, Genomic selection (GS) prediction accuracies using only GBS SNPs on LT tolerance ranged from 0.22 to 0.74. A GS model with Vrn-A1, Vrn-B1a, Vrn-B1b, and Vrn-D1 alleles as fixed effects and GBS SNPs as random effects provided the highest prediction accuracy across locations and years and ranged from 0.35 to 0.78. Population structure and GS models predicting LT tolerance will help foster the utilization and exchange of FAWWON germplasm across diverse global winter wheat production regions.



5. EVALUATION AND COMPARISON OF FLAVOR IN ROASTED VIRGINIA TYPE HIGH-OLEIC PEANUT (*Arachis Hypogaea* L.) BREEDING LINES TO NORMAL-OLEIC CULTIVAR BAILEY GROWN IN THE VIRGINIA-CAROLINA AREA.

F.R. Cantor Barreiro¹, T.G. Isleib¹, S.C. Copeland¹, H.E. Pattee¹, W.G. Hancock¹, M.A. Drake² and M.D. Yates² ¹Dept. of Crop and Soil Sciences, N.C. State Univ., Raleigh, NC 27695-7629

²Dept. of Food, Bioprocessing, and Nutrition Sciences N.C. State University, Raleigh, NC 27695-7624.

Flavor was measured for the popular normal-oleic cultivar 'Bailey' and seven back-cross derived high-oleic lines (N12006ol, N12007ol, N12008olCLSmT, N12009olCLT, N12010ol, N12014ol, and N12015ol). A trained descriptive sensory panel at NC State Univ. was used. The samples came from 9 tests during 2012-2015 conducted in N.C., then processed and submitted to the panel from 2013-2016. The data were examined for a difference between the high-oleics and Bailey, and variation among them. Four lines scored significantly higher than Bailey for roasted peanut (N12014ol 4.94 vs 4.40 flavor-intensity-units "fiu" P=.001, N12015ol 4.81vs4.40, P=.006, N12007ol 4.79vs4.40, P=.013 and N12010ol 4.70vs4.40, P=.035) and sweet (N12014ol 4.47vs3.99, P=.000, N12009olCLT 4.40vs3.99, P=.001, N12015ol 4.34vs3.99, P=.005, and N12007ol 4.31vs3.99, P=.012), and two lines for nutty (N12014ol 3.98vs3.58, P=.002 and N12015ol 3.88vs3.58, P=.020) considered an improvement. Among high-oleics, N12008olCLSmT scored significantly lower than N12014ol for roasted peanut (4.57vs4.94, P=.026) and N12006ol for sweet (4.09vs4.97, P=.008). N12014ol scored higher for nutty attribute than N12008olCLSmT (3.98vs3.66, P=.019), N12006ol (3.98vs3.65, P=.027), and N12010ol (3.98vs3.61, P=.011). N12014ol scored lower than Bailey in some attributes generally thought to be negative including under-roast, fruity, bitter-aftertaste and cardboard. Intensity of off flavors of the high-oleics was less than Bailey's, N12014ol scored lower on moldy and N12015ol on the attribute tongue/throatburn. The high-oleic Bailey derivatives represent an improvement of roasted-peanut flavor. These results could be used to identify a suitable replacement of 'Bailey' for a high-oleic derivative on the basis of Flavor.



6. ASSOCIATION MAPPING FOR SALT TOLERANCE IN COWPEA [Vigna Unguiculata (L.) Walp] USING A GENOTYPING-BY-SEQUENCING APPROACH

Waltram Ravelombola¹, Ainong Shi¹, Yuejin Weng¹, Beiquan Mou², Wei Yang¹, Dennis Motes³, Gehendra Bhattarai¹.

¹Department of Horticulture, University of Arkansas, Fayetteville, AR 72701, USA

²Crop Improvement and Protection Research Unit, US Department of Agriculture, Agricultural Research Service (USDA-ARS), 1636 E. Alisal Street, Salinas, CA 93905, USA

³Vegetable Research Center, University of Arkansas, Alma, AR 72921, USA.

Cowpea is one of the most important cultivated legumes in Africa. The worldwide annual production in cowpea dry seed is 5.4 metric tons. However, cowpea is unfavorably affected by salinity stress at germination and seedling stages, which is exacerbated by the effects of climate change. The lack of knowledge on the genetic underlying salt tolerance in cowpea limits the establishment of a breeding strategy for developing salt tolerant cowpea cultivars. The objectives of this study were to conduct association mapping for salt tolerance at germination and seedling stages and to identify SNP markers associated with salt tolerance in cowpea. We analyzed the salt tolerance index of 116 and 155 cowpea accessions at germination and seedling stages respectively. A total of 1,049 SNPs postulated from genotyping-by-sequencing were used for association analysis. Population structure was inferred using Structure 2.3.4; K optimal was determined using Structure Harvester. TASSEL 5, GAPIT, and FarmCPU involving three models such as single marker regression (SMR), general linear model (GLM), and mixed linear model (MLM) were used for the association study. A large variability of salt tolerance index in germination rate, plant height reduction, fresh and dry shoot biomass reduction, foliar leaf injury, and inhibition of the first trifoliate leaf was observed. The cowpea panel accessions were structured into two subpopulations. Three SNPs, Scaffold87490_622, Scaffold87490_630, and C35017374_128 were highly associated with salt tolerance at germination stage. Seven SNPs Scaffold93827_270, Scaffold68489_600, Scaffold87490_640, Scaffold87490 633, Scaffold82042 3387, C35069468 1916. Scaffold93942 1089 were found to be associated with salt tolerance at seedling stage. The SNP markers were consistent across the three models and could be used as a tool to select salt tolerant lines and plants in molecular breeding for improving cowpea tolerance to salinity.



7. CHARACTERIZATION OF PARENTS OF SORGHUM MAPPING POPULATIONS EXPOSED TO WATER-DEFICIT STRESS

Regina Enninful, John V. S. Sunoj, Impa Somayanda, Vara P. V. Prasad, and Krishna S.V. Jagadish. Department of Agronomy-Kansas State University, Manhattan, Kansas.

Changing climate presents new challenges to agricultural production and global climate models project increased intensity and magnitude in water-deficit stress conditions in the future. This is especially challenging for the arid and semi-arid regions of the world, where sorghum forms an important component of the cropping system. The research objective was to characterize 11 genetically and geographically diverse sorghum genotypes for shoot related physiological parameters and changes in the leaf lipidome under water-deficit stress. A lysimetric based experiment was set up in the greenhouse and water-deficit stress (55% to 60% water-holding capacity) was imposed for 15-days, starting from 35-days after emergence. Gravimetric pot weighing was followed daily to determine transpiration efficiency during this period. Roots were carefully removed and washed at the end of stress period. Morphological root features were determined by analyzing scanned images with WinRHIZO. On average, the LSmeans for the cumulative water transpired was 1.77 liters for stressed plants and 7.87 liters for the well-watered plants. Almost all parameters varied significantly between stressed and well-watered plants regardless of genotypic variances. With respect to photosynthetic assimilation, stomatal conductance, stem height, leaf and tiller numbers, total root length and total root surface area, effects of the stress was genotype specific. Results from electrospray ionization-tandem mass spectrometry analysis showed significant effects of water-deficit stress on the regulation of leaf membrane lipid composition. Findings were validated using contrasting lines and differential physiological and rooting morphological characteristics identified will help complement efforts currently ongoing to enhance drought resilience sorghum. in



8. MORPHOLOGICAL COMPONENTS OF RESISTANCE TO SORGHUM SHOOT FLY, ATHERIGONA SOCCATA

Satyanarayana Taddi¹, Riyazaddin Mohammed², Polavarapu B. Kavi Kishor², Santosh P. Deshpande¹, Hari C. Sharma^{1*}

¹Entomology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru 502 324, Telangana, India.

²Department of Genetics, Osmania University, Hyderabad 500 007, Telangana, India.

Sorghum shoot fly, Atherigona soccata is a major constraint in sorghum production, and host plant resistance is an effective, economical, and environment friendly method of managing shoot fly damage in sorghum. Therefore, we evaluated 102 sorghum lines for shoot fly resistance to understand the underlying mechanisms of resistance. Data were recorded on shoot fly damage and morphological traits across three seasons. Thirtyone sorghum genotypes exhibited resistance to shoot fly (<37.0%) plants with deadhearts as compared to 92.7% in the susceptible check, Swarna), of which 25 genotypes showed non-preference for oviposition and antibiosis against A. soccata. Genotypes x environment interactions were significant, which had a considerable bearing on expression of resistance to A. soccata. Leaf glossiness, seedling vigor, leaf sheath pigmentation and trichome density were associated with expression of resistance/susceptibility to A. soccata, and these traits were used to select shoot fly resistant sorghums. Similarity matrix and principle coordinate analyses placed the shoot fly-resistant genotypes into different groups, which can be utilized to enhance the levels and broaden the basis of resistance to A. soccata.

Keywords: Sorghum; shoot fly; Atherigona soccata; resistance mechanisms; antixenosis; antibiosis.



9. ANTIMICROBIAL ACTIVITES ON EIGHT EXTRACTED SAMPLES OF OLIVE LEAVES EXTRACTS

Muhammad Tayyab Gul, Department Of Botany Islamia College Peshawar, Kp Pakistan.

Dr. Samin jan. Department of botany islamia college peshawar, kp Pakistan

Antimicrobil activites on olive leaves extract from 8 solvents on 6bacterialstrainsandonefungalstrain.



10. TIME-RESOLVED METABOLOMICS REVEALS GUARD CELL PHYTOHORMONE FUNCTIONS UNDER ELEVATED CO2

Sisi Geng¹, Ning Zhu¹, Evaldo de Armas², David Huhman³, Hans T. Alborn⁴, Lloyd W. Sumner³, Sixue Chen^{1,5}

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 ⁴Chemistry Research Unit, Center of Medical, Agricultural, and Veterinary Entomology, ARS, United States
 Department of Agriculture, Gainesville, FL, 32610, USA
 ⁵Proteomics and Mass Spectrometry, Interdisciplinary
 Center for Biotechnology Research, University of Florida, Gainesville, FL 32610, USA.

Foliar stomatal movement regulates plant water status and gas exchange. Global climate change is associated with elevated atmospheric carbon dioxide (CO2), which is known to induce stomatal closure. However, current knowledge on CO2 signal transduction in stomatal guard cells is limited. Here we report metabolomic responses of Brassica napus guard cells to elevated CO2 using a hyphenated metabolomics approach. During the onehour CO2 treatment, the metabolome showed a general increasing trend under elevated CO2. This may be explained by the availability of carbon source. Interestingly, jasmonic acid (JA) biosynthesis was significantly increased under elevated CO2 treatment. Interestingly, under low CO2, a branching pathway of JA biosynthesis leading to traumatic acid production was induced. Together with results obtained from JA biosynthesis and signaling mutants as well as CO2 signaling mutants, we discovered that jasmonic acids partially mediates high CO2 induced stomatal closure, but not low CO2 induced stomatal opening. This study also showed the utility of single cell-type metabolomics in discovering and testing new nodes and edges in cellular molecular networks.



11. ENRICH PLANT METABOLIC PATHWAY DATABASES: METABOLIC PATHWAY EXTRACTION FROM TEXT

Cacile Pereira, Ana Conesa University of Florida, Gainesville, FL

The metabolism is defined as the chemical processes that occur within a living organism in order to maintain life. It exist, at least 35 databases listing metabolic pathways or reactions. These databases differ by the organisms and processes represented. It was shown that even for the same organism, the recovery between these databases is smaller than 16%. Furthermore, some processes like the plant response to stress are still not well integrated in databases, even if a large number of publications are available.

We propose to automatically extract metabolic and signaling reactions involved in a list of processes given by the user. Our method combines abstract selection method (medline ranker) with text mining methods (Banner, tmChem, TEES), databases of metabolic reactions (Brenda) and ortholog detection methods (MARIO) to provide a complete and accurate set of compounds, genes and reactions involved in the processes of interest.

We tested the methodology on two well described pathways in plants and bacteria. We shown that this methodology allow to recover more than 90% of the genes and compounds described in metacyc. Moreover, even for these well known pathways, it propose new entities and reactions possibly involved in the process and actually described in the literature.



12. ASSESSING THE EFFECT OF ROOT HAIR GROWTH OF PHOSPHOROUS STRESSED BARLEY (HORDEUM VULGARE) ON PHYSIOLOGICAL CHARACTERISTICS USING A SPLIT-ROOT SYSTEM

Yucong Xie¹, Guodong David Liu², Bala Rathinasabapathi², Bruce Schaffer³ and Rao Mylavarapu¹ ¹University of Florida, Gainesville ²University of Florida, Gainesville, FL ³University of Florida, Homestead, FL

(P) deficiency global Phosphorus is а problem. То comprehensively investigate the contribution of root hairs induced under low-P stress to plant growth and P uptake efficiency, a split-root experiment in a hydroponic medium was conducted with a root-hairless mutant barley genotype (brb) and its corresponding wild type (WT-Pallas). A Pi source with limited solubility (tri-calcium phosphate; TCP) was applied to one-half of the root system and a nutrient solution without Pi (CNS-P) to the other half to create a soil solution with a buffered low-P condition. The control treatment consisted of plants with nonsplit roots in CNS-P. Root hair variables (length and density), P uptake efficiency, plant biomass and tissue P concentration were determined for both barley genotypes. The WT-Pallas in a medium with TCP developed significantly longer and denser root hairs than in a solution with CNS-P. The mutant was defective in root hair formation. Short-term P uptake efficiency, root dry weight and shoot P concentration in half of the root system of the WT-Pallas in TCP were significantly higher than in the brb, but not different from the CNS-P control. Additionally, there were no significant genotypic or treatments differences in shoot biomass and root P concentration. In summary, the differences in P uptake efficiency and shoot P concentration between WT-Pallas and brb genotypes were attributed to the root hair development. However, even though TCP can stimulate production and length increase of root hairs, it did not make a difference in increasing P uptake efficiency.



13. CHANGE IN CLIMATIC PARAMETERS ACROSS AGRO-ECOLOGICAL ZONES DURING CROPPING SEASONS IN PAKISTAN

Muhammad Haroon Abdullah, Adeel Ahmad

Pakistan is a low income country, getting highly vulnerable to climate change. Its vulnerability comes from high dependence of agriculture, weaken economv on economy and poor infrastructure. This study argued that variation in climatic parameters is a mighty blow, threats food security by effecting agricultural productivity. Variation in climatic parameters during both cropping season is highly dependent on the type of agroecological zones in Pakistan. For keen insight each season is further disintegrated in three growth stages. Meteorological data for the period of 1961-2013 is utilized to evaluate climatic parameters by taking 30 years moving averages. In results, study revealed that three agro-ecological zones having rugged topography are highly vulnerable during Rabbi, while smooth and plane topography is much susceptible during Kharif. Variability in climatic parameters is almost doubled since last two decades. There is an immediate need of adaptation strategies to ensure food security for growing population of Pakistan.



14. TOWARDS FINE-MAPPING A MAJOR LOCUS CONTROLLING TOMATO SPOTTED WILT DISEASE RESISTANCE IN CULTIVATED PEANUT

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Previously a major quantitative trait locus (QTL) controlling tomato spotted wilt disease resistance was mapped into an interval with genetic distance of 4.4 cM and physical distance of 28.8 Mb on chromosome A01. To realize marker assisted selection (MAS) of tomato spotted wilt resistance in peanut breeding programs, fine-mapping strategies were applied to further validate and narrow down the interval of this major QTL. A fine mapping population of 2200 individuals was developed from 24 heterozygous F5 lines genotyped at the two flanking markers harboring the major QTL. Based on visual evaluation of the fine mapping population in the field a total of 194 susceptible lines were selected and planted into 194 plots in the field for both visual evaluation of the disease severity and ELISA examination of viral presence and abundance. Nine SSR markers flanking the OTL were used to genotype the 194 lines, which revealed a OTL region shifted from the previously reported position. Amplicon-seq were applied for marker enrichment in the interval. The refined position of this major QTL will provide critical information for developing markers to realize MAS of resistance to tomato spotted wilt in peanut breeding programs.



15. NITROGEN ACCUMULATION AND PARTITIONING BY NON-DEHISCENT SESAME CULTIVARS IN THE HUMID SOUTHEASTERN US

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Sesame (Sesamum indicum L.) yield response to nitrogen (N) fertilization has been well-documented, but the temporal dynamics of sesame N uptake and partitioning are poorly understood. Such information is needed to better inform fertilization decisions and improve N use efficiency. The objective of this study was to characterize N uptake and partitioning by diverse non-dehiscent sesame cultivars in North Florida. A twoyear field study was conducted in Jay, Florida and data from 2015 are presented. Three cultivars (S34, S35, and S39) with variable maturity and branching characteristics were sampled at two week intervals beginning three weeks after planting (WAP) and divided into stem/branch, leaf, flower/capsule, and grain components to determine N accumulation and partitioning. Sampling date significantly affected nitrogen uptake, but there were no cultivar or cultivar x sampling date effects on N uptake. Nitrogen accumulation was minimal through the first month of growth, but increased rapidly from late-vegetative (5 WAP) through early-bloom (7 WAP) stages during which time cultivars accumulated 11 kg N/ha/day. A relatively large proportion of total N (53%) was accumulated during reproductive growth. Nitrogen content in the flower/capsule component increased by 50 - 70% during the reproductive phase which was likely due to the indeterminate nature of sesame. Harvested grain removed approximately 56 kg N/ha, which amounted to N harvest index of 0.34. Plant available N during late-vegetative and earlyreproductive growth may improve nutrient use efficiency by sesame.



16. STUDY OF GENETIC VARIATIONS FOR FRUITING EFFICIENCY, GRAIN NUMBER, AND YIELD IN BREAD WHEAT ASSOCIATION PANEL UNDER DROUGHT AND HEAT CONDITIONS

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Wheat yields need to increase 1.6% per year to meet anticipated food demands in 2050. To achieve that goal, we need to explore available genetic resources to find new genes associated with sink strength and partitioning of spike photo assimilates to growing grains, and exploit those genes for increasing yield potential of wheat. An association mapping panel was assembled after screening 60,000 CIMMYT high yielding spring wheat germplasm, alien introgression lines and land races for finding genes related to grain number and associated traits, and fruiting efficiency. Objectives of the present study were to characterize an association panel for those traits under heat and drought stress conditions. Four hundred diverse wheat genotypes were characterized in CIMMYT-IWYP phenotyping hub located in Ciudad Obregon, Mexico in 2015 under heat and drought conditions, while 370 lines were characterized under heat stress conditions in the same location in 2016. All traits (days to anthesis, days to maturity, plant height, spikelets spike-1, spikes m-2, grains m-2, grains spike-1, grains spikelet-1, 1000-grain weight, grain filling rate, fruiting efficiency and yield) showed strong genetic variations. High broad-sense heritabilities were recorded for yield, grain filling rate, 1000-grain weight, grain m-Â², grain spike-1, grain spikelet-1, days to anthesis, maturity days, plant height, and spikelet spike-1 under drought and heat stress conditions in 2015; whereas, fruiting efficiency, 1000 grain weight, days to anthesis, days to maturity, and spikelet spike-1 under heat in 2016 showed high Correlation analysis showed very strong associations heritability. between yield and grain m-Â², grain spike-1, grain spikelet-1, grain filling rate in all three environments. 1000-grain weight showed moderate to low correlation with yield. The grain number m-2 and related traits were predominant trait for yield in this panel. Fruiting efficiency showed significant positive correlations with grains m-2 (0.310***), grains spike-1 (0.202***) and grains spikelet-1 (0.263***). Path coefficient analysis revealed that grains m-2, grains spike-1, 1000-grain weight, grain filling rate, maturity days had positive direct effect on grain yield under irrigated, drought and heat conditions. All grain related traits showed strong positive indirect effect on yield through grain filling rate and days to anthesis. Our results demonstrate that the germplasm in this panel could be a potential source of finding new loci for genetic improvement of sink strength which is resulted from increased partitioning of photo assimilates from different parts of spikes to growing florets.



17. EFFECTS OF ROOT ARCHITECTURAL DIVERSITY ON GRAIN SORGHUM YIELDS UNDER VARIABLE RAINFALL CONDITIONS

Jackson Nielsen, UF, Gainesville, FL

The homogenous rooting system of a genetically uniform cropping system may be inherently inefficient at exploiting the nutrient and water resources present in the soil profile. By limiting the area explored by the root system in time and space, a uniform root system may increase interplant competition and the likelihood that water and nutrients will escape below the rooting system. This study was performed to determine the effects of grain sorghum [Sorghum bicolor (L.) Moench] root architectural diversity on nutrient and water uptake under irrigated and rainfed conditions. The effects of root architectural diversity and irrigation level on grain and biomass yield of grain sorghum were tested using a split plot design with five replicates on Arredondo fine sand soil at The University of Florida Plant Science Research and Education Unit near Citra, FL. Under irrigated conditions the high diversity treatment (five shallow and five deep rooting genotypes) produced more grain and more forage biomass than either the deep rooting or shallow rooting monocultures. The shallow rooting monoculture plots tended to produce more grain (4.65 Mg ha-1) than the deep rooting plots (4.12 Mg ha-1), but the deep rooting monocultures produced more forage biomass (5.89 Mg ha-1) than the shallow monocultures (5.17 Mg ha-1). It is interesting then, that under irrigated conditions the diversity treatment produced both most grain (4.70 Mg ha-1) and the most forage biomass (6.33 Mg ha-1) considering it is an equal mix of shallow and deep rooting genotypes. However under rain-fed conditions, the diversity treatment had the worst performance in terms of both grain and biomass yields. Increased root architectural diversity does not appear to convey a yield advantage under variable rainfall conditions, and may even have a negative impact.



18. AN INTEGRATED GENOMICS-MODELING APPROACH TO PREDICT COMPLEX PHENOTYPES UNDER CHANGING CLIMATES

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Combining tools for genome analysis with those provided by dynamic crop simulation models (CSMs) can produce gene-based models to simulate crop performance under defined environmental conditions, including those that are expected to be brought about by climate change. Currently, dynamic CSMs can capture site-specific information and predict the adaptability potential of crop germplasm to specific environments. These models require two types of input: environmental data comprising soil characteristics, weather, and management practices throughout the growing season, and quantitative intrinsic characteristics of genotypes in a particular crop. The latter are obtained by calibrating the model with each genotype, a process that generates a set of genotypespecific model parameters using simple regression or sophisticated Bayesian methodologies. Estimated parameters contain intrinsic developmental information of the genotype, and its programmed environmental responses. We attempted to extract the genetic information from model parameters using data from a large segregating population grown in a multi environment experiment, but very little genetic information was obtained. This could be explained by the fact that the CSM was not constructed with genetics in mind, and the fact that parameterization is optimized to generate parameter values that confer the best predictive ability to the model, regardless of the genetic mechanisms involved. To address this problem, we are now using statistical mixed effects models to capture the genetic, environmental, and genotype-by-environment interaction components of variation to predict the phenotype with almost the same degree of accuracy as the crop simulation model. As an alternative approach, we are now developing modular crop-growth model, where each module represents a physiological function dictated by the genotype, the environment and their interactions as described by a function derived from a mixed-effects models. The new generation of gene-based models could help plant breeders select in silico genotypes adapted to specific environments.



19. PREDATION OF SILVERLEAF WHITEFLY (*Bemisia tabaci*) BY DICYPHUS HESPERUS ON GREENHOUSE TOMATO

Pritika Pandey, University of Florida, Gainesville, Florida

Florida produces about 34% of tomatoes grown in the US. *Bemisia tabaci* Gennadius is one of the most devastating pests of tomato globally. *Dicyphus hesperus* Knight has been evaluated for control of greenhouse whitefly *Trialeurodes vaporariorum* in temperate environments and has potential as a biocontrol agent for B. tabaci. The major objectives of this research are to assess the predatory capacity of *D. hesperus* on *B. tabaci*. An experiment was designed to evaluate the average number of whitefly eggs and nymphs consumed by mated and unmated female *D. hesperus* per day and during her adulthood on tomato plants. *Dicyphus hesperus* consumed more no. of *B. tabaci* nymphs than eggs. The predation increases with increase in number of food source. This research contributes to the potential use of *D. hesperus* as a biological control agent of *B. tabaci*.

Keywords- Bemisia tabaci, Dicyphus hesperus, Biological control



20. POTENTIAL FUNGAL PATHOGENS OF Melissa officinalis AND Hibiscus acetosella

Nichole Barber and Emily Tharp, University of Florida

Two horticulturally interesting plants were studied from the standpoint of pathogenic fungi that may be associated with them. *Melissa officinalis* (Lemon Balm) is of great economic value due to its medicinal and edible qualities. There is growing interest in Hibiscus acetosella (Cranberry Hibiscus, Panama Red) as an economically valuable crop. Both M. officinalis and H. acetosella were observed for disease symptoms at a home garden of 10 acres. Symptoms of possible fungal infection were found on both plant species in several areas of the property. Several samples were collected to begin Koch's Postulates. After pure cultures were isolated, PCR and sequencing were conducted on the ITS Pestalotiopsis was region of the nuclear ribosomal DNA. identified from *M. officinalis* and *Cvathus lignilantanae* was identified from *H. acetosella*. Pestalotiaopsis is a common pathogen, but thorough research revealed no reported instances of Pestalotiopsis as a pathogen or endophyte of *M. officinalis*. The species of Cyathus found, Cyathus lignilantanae, has yet to be found in the United States. Typically, Cyathus is a saprobic fungus, however there were symptoms of fungal disease present on the plant and Cyathus was the only fungus isolated from several samples. Currently both M. officinalis and H. acetosella are being grown under controlled conditions, as part of our efforts to fulfill Koch's Postulates with inoculations of spores of mvcelium Pestalotiaopsis and of Cvathus.



21. HERITABILITY OF PHOTOSYNTHESIS AND STOMATAL CONDUCTANCE IN AMBIENT AND ELEVATED OZONE CONCENTRATIONS

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Exposure to ozone, an air pollutant, is known to reduce crop yield. Ozone is expected to increase with climate change. Maize is one of the most important economic crops in the world and is used for food and nonfood products. Increases in the rate of photosynthesis and stomatal conductance results in increased vield. Yet, the degree that additive genetic variation contributes to photosynthetic and conductance traits in maize is not well studied. In particular the influence that ozone stress has on the heritability of photosynthesis and stomatal conductance is unknown. Identifying the genetic and non-genetic components of variation in photosynthetic traits and stomatal conductance is critical to determine whether the impacts of elevated ozone on maize can be easily addressed through breeding efforts. In this study, we used a diallel mating design to estimate heritability of stomatal conductance, photosynthetic rate, specific leaf area and chlorophyll content of plants grown in ambient and elevated ozone concentrations. Parents of the diallel had been previously assessed for response to ozone, and there was variation in ozone response that differed among the parental lines.

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