National Association of Plant Breeders

NAPB

Improving Plants to Improve Lives

“Positioning Plant Breeding for the Future”

The Program for the 2013 Joint Annual Meeting
of the *National Association of Plant Breeders*
and the *Plant Breeding Coordinating Committee*

Hosted by the University of Florida,

Institute of Food and Agricultural Sciences

Tampa, Florida

June 2-5, 2013

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SUNDAY, JUNE 2

Mixer **7:00-9:00 pm** *(Student-organized)*

MONDAY, JUNE 3

NAPB and PBCC "BUSINESS" MEETINGS 8:00 - noon

GENERAL SESSION 8:00 - 9:30 - *Ballroom*

David Stelly (NAPB President), and Allen Van Deynze (PBCC Chair) presiding

8:00 **Opening remarks and logistics** – *D. Stelly, A. Van Deynze*

8:10 **PBCC and NAPB - importance, roles, needs and opportunities** – *Eric Young, Administrative Advisor to PBCC, Executive Director, SAAESD*

8:20 **Crop Science Society of America priorities** – *Mark Brick, President Crop Science Society of America*

8:30 **Election of officers –** *D. Stelly*

8:45 **Future annual meetings –** *Elizabeth Lee, Professor, U. Guelph and Dwight Bostwick, Head, NAFTA Corn Breeding Projects; James McFerson, Manager, Washington Tree Fruit Research Commission; Don Jones, Cotton Incorporated*

8:55 **NAPB general session** – *D. Stelly presiding*

9:15 **PBCC general session** – *A. Van Deynze presiding*

COMMITTEE REPORTS 9:25-9:55 *A. Van Deynze presiding*

- **Grand challenges**
- **Science, technology, and informatics**
- **Communications and outreach** – *M. Salas-Fernandez*
- **Education and training of plant breeders** – *D. Francis*
- **Graduate group –** *Sarah Potts*

9:55 **Instructions for break and breakout session** – *D. Stelly*

BREAK (exhibits; set up posters) 10:00-10:30 am - *Ballroom & Atrium*

COMMITTEE BREAKOUT SESSIONS *(concurrent)* 10:30-11:15 - *Multiple Rooms*

- **Advocacy–** *David Isenhour* - *Sarasota Rm*
- **Communications and outreach –** *Maria Salas-Fernandez*, Iowa State U. - *Orange Rm*
- **Education and training of plant breeders –** *David Francis* – The Ohio State U. *Manatee Rm*
- **Membership** – *Donn Cummings,* Monsanto Co. – *Pasco Rm*

COMMITTEE REPORTS 11:15-11:50 *E. Lee and Pat Byrne, Colorado State Univ. presiding* **-** *Ballroom*

- **Advocacy** – *D. Isenhour*
- **Communications and outreach** – *Wayne Smith*
- **Education and training of plant breeders** – *Shelby Ellison*
- **Membership** – *Donn Cummings*

11:50 **Announcement of Election Winners** *E. Lee & P. Byrne* presiding

LUNCH **Noon-1:00 pm:** On your own. Set up posters and sponsor displays.

EXCELLENCE IN PLANT BREEDING **1:00-2:45 pm,** *Jim Brewbaker, Univ of HI - Ballroom*

TALKS BY 2012 AWARD WINNERS 1:00 -2:20

1:00 **"From isozyme markers to GWAS" – 2012 Lifetime Achievement Awardee:** *Dr. Charles Stuber, North Carolina State Univ.*

1:30 **" A new era in plant breeding: the merger of tassel bags with modern technology"** – **2012 Impact Awardee:** *Dr. Marv Boerboom, Monsanto Co.*

1:55 **"Connecting genotype to phenotype: lessons from large-scale plant genetic studies", 2012 Early Career Awardee:** *Dr. Michael Gore, USDA-ARS (now Cornell Univ.)*

MINI-PRESENTATIONS: POSTERS & SPONSORS 2:20 - 2:50. *D. Stelly* presiding

2:20 **1-Minute Poster Introductions (Group A)**

Asjad Ali, Steve Becker, Kendra M. Blaker, Elizabeth Blissett, Megan Bowman, Mayo Natalia Castillo, Alan Chambers, Dario Chavez,

2:30 **Introductions - platinum & gold sponsors, 2-minutes each (10)**

SeedWorld, Dow AgroSciences, Monsanto, Pioneer, AgReliant Genetics, Birdsong Peanuts, Cotton, Inc., Dole Berry, Douglas Scientific, LGC Genomics, Nunhems/Bayer, Syngenta Seeds

POSTER AND SPONSOR SESSION 2:50-3:30 pm - *Ballroom &Atrium*

PLANT BREEDING EDUCATION **3:30-5:30 pm** *J. Sherman presiding* **-** *Ballroom*

3:30 **The Syngenta Breeding Academy** *– Heather Merk, Syngenta Breeding Academy Program Lead, Syngenta*

- **Inquiry-based learning and the Plant Breeding and Genomics community –** *Shawn Yarnes Content Coordinator for Plant Breeding and Genomics on eXtension.org*
- **Western Illinois University undergraduate education in plant breeding** – *Winthrop Phippen, Professor, Western Illinois University*
- **USDA/NIFA funding for plant breeding education present and future** *– Liang-Shiou Lin, National Program Leader, USDA-NIFA*
- **Monsanto fellowship program –** *Michael Lohuis, Director of IP and Collaborations, Global Breeding Monsanto Co.*
- **Dow AgroSciences Professional internship program –** *Don Blackburn, NA Seeds & Traits Field Breeding & Development Leader for Dow AgroSciences*,

4:30 **Plant Breeding Education Panel Discussion**

5:30 **ADJOURN for supper (on your own)**

TUESDAY, JUNE 4

TOUR (Breakfast & Lunch) **7:00 am-1:00 pm** *B.Tillman presiding* - ***BUSES***

Breeding Programs at the UF/IFAS Gulf Coast Research and Education Center (GCREC)

6:00 **a** **Box "Breakfast to Go"** available in the Lobby

7:00 !!! ***BUSES DEPART*** **for the GCREC**.

8:00 **Arrival at GCREC**

- **Welcome to GCREC**, *Dr. Jack Rechcigl, Director, GCREC*
- **Overview of IFAS plant breeding**, *Dr. John Hayes, Dean for Research and Director of the Florida Agricultural Experiment Station*
- **Introduction/Instructions for Tours**, *Dr. Vance Whitaker, Strawberry Breeder*

8:30 **Breeding Program Tours: (8:30-11:15)**

- **Strawberry breeding,** *V. Whitaker, Asst. Prof., Univ. of Florida*
- **Citrus breeding,** *Fred Gmitter, Professor, Univ. of Florida*
- **Tomato breeding,** *Jay Scott and Sam Hutton, Univ. of Florida*

BOX LUNCHES TO GO, LOAD BUSES for return to Hotel 11:15-11:45

GRADUATE STUDENT RESEARCH PRESENTATIONS **1:15-5:15 pm** *Duke Pauli presiding* **-** *Ballroom*

1:15 **Fine mapping of aphid resistance gene rag3 from soybean PI 567598b** *Carmille Bales, Michigan State Univ.*

1:30 **Inheritance of resistance to two strawberry crown diseases and their interactions** *Jozer Mangandi, Univ. of Florida*

1:45 **Effect of the hope variety *FT-B1* allele on heading time and agronomic traits under field conditions.** *Rebecca Nitcher, Univ. of California, Davis*

2:00 **1-Minute Poster Introductions- (Group B)**
Charlie Dowling, Justin Gifford, Jessica L. Gilbert, Sarah Grogan, Azize Homer, Colleen Kennedy, Jian Li , John MacKenzie, Matthew Mattia, Justin McKinney, Melaku Mekonnen , Gerardo H. Nunez, Joshua Parsons

POSTER AND SPONSOR SESSION 2:15-3:00 pm- *Ballroom & Atrium*

POPULATIONS AND PHENOTYPES **3:00-5:15 pm** *A. Van Deynze presiding* **-** *Ballroom*

3:00 **EUCARPIA in the century of plant breeding,** *Beat Boller, President, EUCARPIA, AgroscopeReckenholz-Tänikon, Research Station, Zürich, Switzerland*

3:25 **Utility of complementary populations structures for genome wide association studies in maize**, *Natalia de-Leon, Asst. Professor, University of Wisconsin*

3:50 **The cooperative forest genetics research program's southern pine breeding program**, *Gary Peter, Professor, Univ. of Florida*

4:15 **Prediction and beyond in breeding using genomic data**, *Patricio Munoz, Research Assoc., Univ. of Florida*

4:40 **Consumer-assisted selection in strawberry**, *Vance Whitaker, Asst. Professor, Univ. of Florida, GCREC*

5:05 **Discussion**

5:35 **Adjourn (until 6:30 Banquet)**

BANQUET / 2013 Awards / Plenary Talk

6:30 **Cash Bar**

7:00 **Dinner**

8:00 **2013 NAPB and PBCC Awards:**

Early Career Award- Seth Murray, Texas A& M

Impact Award - Roger Boerma, Georgia Seed Development Commission

Lifetime Achievement Award – Johnie Jenkins, USDA/ARS, Genetics and Precision Agriculture Research, MS.

8:15 **"Agricultural sustainability and the future of plant breeding",** *Molly Jahn, Professor in the Laboratory of Genetics and Department of Agronomy at the University of Madison-Wisconsin, and Special Advisor to the Chancellor and Provost for Sustainability Sciences, Univ. of Wisconsin - Madison.*

WEDNESDAY, JUNE 5

DATA COLLECTION, ARCHIVING, AND ANALYSIS **8:00-11:50** *David Francis presiding* **-** *Ballroom*

8:05 **"The iPlant Collaborative: Cyberinfrastructure for plant biology research and applications",** *Stephen Goff, Project Director, iPlant Collaborative, BIO5 Institute, Univ. of Arizona*

8:30 **"T3 database",** *Victoria Blake, Geneticist, USDA-ARS-WRRC*

8:55 **"The Integrated Breeding Platform: A new portal for modern breeding tools and services",** *Jean-Marcel Ribaut, Director, Generation Challenge Program, CGIAR*

9:20 **"The Virtual Lab in Plant Breeding (VLPB)",** *Rob Dirks, Adjunct Director for R&D, Rijk Zwaan Breeding B.V.*

9:45 **1-Minute Poster Introductions (Group C)**
Duke Pauli , Sarah Potts, Esteban Rios, Leah Ruff, Michael L. Schwieterman, Narinder Singh, Virginia R. Sykes, Nael Thaher , Steven Thornton, Yu-Chien Tseng, Kyle M. VandenLangenberg, Golam Rasul, Pheonah Nabukalu,

POSTER AND SPONSOR SESSION 10:00-11:00 am

11:00 **Discussion and Concluding Remarks** *E. Lee presiding* **-** *Ballroom*

11:50 **Poster Awards,** *J. Sherma, presiding* **-** *Ballroom*

LUNCH Noon-1:00 pm: *(On your own. Remove posters and sponsor displays.)*

CONCURRENT WORKSHOPS (2) and TOUR **1:00 – 4:00 pm**

1:00 **Data workshop,** *David Francis and Doreen Ware presiding* ***OR***

Life skills workshop, *Jamie Sherman and Kim Kidwell presiding*, ***OR***

TOUR: Dole-SunnyRidge blueberry and blackberry trial site, near Haines City, FL, contact Barry Tillman- btillman@ufl.edu for details

4:00 **Adjourn Meeting**

Poster Numbers and Abstracts

Abstracts for Invited Presentations

FINE MAPPING OF APHID RESISTANCE GENE *RAG3* FROM SOYBEAN PI 567598B

*Carmille Bales, Jiazheng Yuan, Cuihua Guo, and Dechun Wang, Michigan State University,
Department of Plant, Soil and Microbial Sciences; Qijian Song, David Hyten and Perry Cregan,
USDA-ARS Soybean Genomic Laboratory.

The soybean aphid (*Aphis glycines* Matsumura) has been a major pest of soybean [*Glycine max* (L.) Merr.] in North America since it was first discovered in 2000. The best approach to effectively control evolving biotypes of soybean aphids is to stack resistant genes from different sources using marker-assisted strategies. Plant introduction (PI) 567598B possesses strong antibiosis resistance to soybean aphids. Our previous study revealed that two recessive genes control the aphid resistance in PI 567598B. The QTLs were mapped on chromosomes 7 and 16. The objective of this study is to fine map the aphid resistance QTL on chromosome 16, designated as *rag3*, from soybean PI 567598B by selecting plants with recombination events within the QTL interval. Fine mapping was conducted by screening 4,041 BC_1F_2-derived lines using SNP markers that flank the interval of *rag3*. Fifty-five recombinants were tested with high-density molecular markers using the SoySNP50K genotyping array. Progenies of each recombinant were rated for damage by the soybean aphid and tested using custom-designed SNP assays. Results of fine mapping delimited *rag3* into a 152-kb interval between SNP markers on chromosome 16. The markers linked to *rag3* in PI 567598B are currently being used in marker-assisted breeding with PI 567598B as the aphid resistance source and in combination with other resistance sources. Potential candidate genes found within the interval and its role in soybean aphid resistance will be discussed.

THE TRITICEAE TOOLBOX:
SEPARATING THE GRAIN FROM THE CHAFF FOR SMALL GRAIN'S BREEDERS

Victoria Blake, USDA-ARS-WRRC, Genomics and Gene Discovery Unit, Albany, CA

The Triticeae Toolbox (triticeaetoolbox.org; T3) is the database suite for phenotype and genotype data generated by the NIFA-funded Triticeae Coordinated Agricultural Project (triticeaecap.org; T-CAP). The T-CAP merges two large communities of U.S. breeders: barley and wheat breeders, previously funded by the BarleyCAP and the WheatCAP programs respectively. As a result, researchers, breeders and educators across 21 states, from the USDA and 55 universities compose the T-CAP consortium. Data contribution to T3 is done as a community effort with the participants using test databases called ‘Sandboxes’ to assure data is loadable and accurate prior to submission to the production T3s. While some breeders use T3 solely for custom data delivery that is properly formatted for downstream data analysis packages (TASSEL, Flapjack, R), others use T3 tools for in situ data analysis, including genomic association and prediction. In May 2013, T3 barley held over 250K phenotype and 36M genotype data points and T3 wheat held over 185K phenotype and 25M genotype data points with more added every week. T3 is readily available and can be adapted to any crop.

A NEW ERA IN PLANT BREEDING:

THE MERGER OF TASSEL BAGS WITH MODERN TECHNOLOGY

Marvin Boerboom

Monsanto, Senior Fellow/ Line Development Breeder

Monsanto has steadily improved hybrid corn performance over the past 10 years. Plant breeder’s efforts provide the base genetic foundation of Monsanto’s pipeline. I will review where some of the genetic gains have come from. Industry breeders as a group, up until recently, have basically only increased the scale of their efforts but otherwise breeding has been somewhat stagnant. Breeders can now enter the technology world. The long term performance gains have come through conventional plant breeding but today it is no longer just about how many pollinations you make or the number of yield trials you grow. Breeders need to work smarter and utilize all the new tools to be most effective. I will cover how technology from other areas of science can be used to improve our ability to increase the odds of achieving success in our breeding programs. Breeders understand that they need to embrace the new opportunities provided to remain successful. How can a breeder best take advantage of the technologies given him? Knowing the germplasm ultimately means being in the field where you learn how to best exploit these new technologies.

EUCARPIA IN THE CENTURY OF PLANT BREEDING

Beat Boller

President, EUCARPIA, Agroscope Reckenholz-Tänikon Research Station, Zürich, Switzerland

How to provide sufficient food to an ever increasing and more demanding world population in a sustainable way is recognized as one of the major challenges of this century. There can be no doubt that plant breeding will significantly contribute to meeting this challenge. The FAO estimates that by 2050, global food production must be increased by 70 %, and that the great majority of this increase should be provided by an increase in productivity per unit area. Not surprisingly, sustainable intensification is one of the core objectives of European agricultural policy. The challenge to plant breeding inferred by the necessity to increase food productivity is tremendous. Peter Stamp, professor emeritus of ETH Zürich, Switzerland and Richard Visser from The Netherlands, currently president designate of EUCARPIA, have recently published a remarkable article on this topic (Stamp and Visser 2012). They state: “It is necessary to convince the public of this challenge, who are already dealing with concerns about climate change, a scarcity of good arable land, the demands placed on land with regard to biomass production, scarcity of water and phosphorous as well as increasing consumption of meat.” But they also spread optimism by saying: “This can be achieved by new technologies and genomics as well as the continuing development of more traditional breeding methodologies”. And they finish by declaring “The twenty-first century, the century of plant breeding” in the title of their paper.

EUCARPIA, the European Association for Research on Plant Breeding, wants to play an important role in that century of plant breeding. We want to help the European community of plant scientists and breeders prepare for their great and honorable task to the benefit of mankind. We do this by providing a platform of collaboration and exchange of ideas across the disciplines, from basic hard core molecular genetics to cultivar registration and multiplication. Quite clearly, the boost of new possibilities in plant breeding opened up by the speedy development of molecular biology has given this type of exchange a new dimension. The gap between the latest discoveries and their practical application seemingly widened in the last years, and ideas such as genomic selection have made it merely impossible for a single institution to combine development, verification and application of the method in one hand.

EUCARPIA currently has 1506 members from 51 European and 35 non-European countries, 41 members are from the U.S. We are organized in 8 crop specific and 3 thematic sections. The sections meet every two to four years and a general congress of all sections is held every four years, next time 2016 in Switzerland.

Stamp P. and Visser R. 2012. The twenty-first century, the century of plant breeding. Euphytica 186, 585-591.

CONNECTING GENOTYPE TO PHENOTYPE: LESSONS FROM LARGE-SCALE PLANT GENETICS STUDIES

Michael Gore

Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY

The plant breeding and genetics community is faced with both a tremendous opportunity and challenge to combine emerging molecular, statistical, and engineering approaches to rapidly connect genotype to phenotype within and between populations. We used high-throughput genotyping and phenotyping tools to study the genetic basis of nutritional content in maize grain and the developmental and physiological responses of cotton to heat and drought stress. In a multi-institutional effort, we conducted more than 12,000 high-pressure liquid chromatography runs to quantify carotenoid (pro-vitamin A) and tocochromanol (vitamin E) compounds in grain from the maize nested association mapping (NAM) population. Through a genome-wide association study of the maize NAM population, we identified some of the key genes and revealed distinct genetic architectures for these two pathways. In cotton, we developed a tractor-based, phenotyping system to simultaneous measure canopy height, spectral reflectance, temperature, and geometry on field-grown plants. The system was used to phenotype a cotton recombinant inbred line (RIL) population grown under well-watered and water-limited conditions, with measurements taken at multiple sampling time points over the growing season. Through a time-related QTL analysis of the cotton RIL population, we revealed the expression dynamics of QTLs controlling phenotypic variation for canopy temperature and a wilting index. We conclude that the continued development and integration of novel approaches that cross numerous disciplines is needed to improve the effectiveness to which plant breeders can develop nutritionally dense, stress tolerant germplasm.

NIFA SUPPORT OF PLANT BREEDING EDUCATION

Liang-Shiou Lin

National Institute of Food and Agriculture, U. S. Department of Agriculture

The National Institute of Food and Agriculture (NIFA) has supported plant breeding education primarily through its main competitive grant program Agriculture and Food Research Initiative (AFRI) and its predecessor National Research Initiative (NRI). In 2007, plant breeding education was supported through two program areas in the NRI Plant Biology program cluster. In 2008 a new program called Plant Breeding and Education was created solely to support projects integrating plant breeding research and education. In 2010, after NIFA underwent major programmatic reorganization, this program ceased to exist. However, plant breeding education has also been supported as a component of the Coordinated Agricultural Projects (CAP) grants and the non-AFRI Farm Bill Programs: Organic Research and Extension Initiative (OREI) and the Specialty Crop Research Initiative (SCRI). To a lesser extent, the NIFA Higher Education Programs and the Fellowship Program have also provided support. Since 2007, NIFA has supported training of more than 300 undergraduate students and more than 140 graduate students in plant breeding and/or genomics. Other resources, such as new germplasm releases, curricula and courses developed, Web sites created, workshops and webinars given, have also been made possible by these grants. With the disappearance of the Plant Breeding and Education Program, NIFA no longer has a program dedicated to the education and training of plant breeders, although there was a Plant Breeding research priority in the 2013 Foundational RFA for Plant Health, Production and Plant Products.

INHERITANCE OF RESISTANCE TO TWO STRAWBERRY CROWN DISEASES AND THEIR INTERACTIONS

*Jozer Mangandi, Luis Osorio and Vance Whitaker, Gulf Coast Research and Education Center,
University of Florida, Wimauma, FL

Crown rot diseases in Florida are caused by a variety of fungal species including those in the genus *Colletotrichum* and *Phytophthora.* Resistance to these diseases among cultivars developed at the University of Florida is variable, and there is no single cultivar with high levels of resistance to more than one pathogen. The purpose of the study was to generate genetic parameters for resistance to crown rot caused by *Colletotrichum gloeosporioides* and *Phytophthora cactorum*, and to examine their interactions with each other and with production traits. Approximately 900 seedlings were obtained by crossing 27 strawberry cultivars and advanced selections in a circular diallel mating design, with a maximum of 13 seedlings/full-sib family. Seedlings were clonally propagated by runners in a summer nursery and planted in six blocks at the Gulf Coast Research and Education Center in Balm, FL. Plants in two blocks were inoculated by dipping the roots in an oospore suspension of *P. cactorum* prior to planting. Plants in another set of two blocks were inoculated with *C. gloeosporioides* spore suspension directly into the crown. Plant collapse was recorded weekly during the 2012-2013 season for both diseases using a binomial scale (0=plant alive, 1=≥75% crown collapsed). Plants in the final set of two blocks were not inoculated but were harvested weekly to obtain multiple yield traits. General mixed models were used to analyze yield traits at total harvest, point at which incidence of plant collapsing was 29% for *P. cactorum* and 66% for *C. gloeosporioides.* Heritabilities for resistance to *C. gloeosporioides* were estimated as $H^2=0.38\pm0.05$ and $h^2=0.49\pm0.12$ and were higher than those for resistance to *P. cactorum* ($H^2=0.23\pm0.05$ and $h^2=0.25\pm0.09$). Estimates of h^2 were higher due to negative epistatic variance. These estimates indicate little non-additive genetic variance controlling these resistances and suggest that genetic progress can be made via recurrent selection by choosing superior parents for crossing. The genetic correlations among the two disease traits was low ($r_a=-0.10$, $P=0.39$), indicating that different genes control the two traits. *C. gloeosporioides* disease ratings positively associated with marketable yield ($r_a=0.63$, $P \leq 0.0001$), whereas no significant correlations of disease scores were found with cull rate ($r_a=0.08$, $P=0.46$) and fruit size ($r_a=-0.04$, $P=0.70$). This raises the possibility that increased fruit load on the plant could result in an increased rate of plant collapse due to plant stress. Susceptibility to *P. cactorum* exhibited a moderate positive correlation with fruit size ($r_a=0.44$, $P \leq 0.0001$), whereas associations with soluble solids content ($r_a=0.03$, $P=0.74$), cull rate ($r_a=0.10$, $P=0.37$) and marketable yield ($r_a=-0.11$, $P=0.32$) were low and non-significant. These results suggest that improvement for resistance to both diseases should be done independently. However, it is evident that resistance to these crown diseases can be achieved by recurrent selection techniques at the University of Florida strawberry breeding program.

THE SYNGENTA BREEDING ACADEMY

Heather L Merk

Syngenta

Meeting our world's expanding needs for food security in an environmentally sustainable way challenges agricultural professionals, such as plant breeders, to develop and deliver ever more efficient offers to growers. The current rapid evolution of technology and exponential increases in data provide breeding professionals with opportunities for innovation in developing and delivering more productive varieties. To fully leverage these opportunities, breeding professionals must continue to enhance their capabilities. The Syngenta Breeding Academy is a first-of-its kind global learning initiative that is designed to accelerate innovation in breeding and help bring integrated crop solutions to market more quickly. Programs offered by the Syngenta Breeding Academy range from increasing foundation knowledge, to updating and upgrading skills, to sharing best practices across crops and functions. In addition to further developing capabilities of Syngenta employees, Syngenta is collaborating with world re-known universities to help them prepare students for careers in breeding-related disciplines.

EFFECT OF THE HOPE VARIETY *FT-B1* ALLELE ON HEADING TIME AND AGRONOMIC TRAITS UNDER FIELD CONDITIONS

*Rebecca Nitcher, University of California, Davis Department of Plant Sciences; Jorge Dubcovsky, University of California, Davis Department of Plant Sciences,
Howard Hughes Medical Institute.

A precise regulation of flowering time is critical for a plant's reproductive success, and in grain crops to maximize yield. The *FLOWERING LOCUS T* (*FT*) is a central integrator of seasonal signals perceived by the leaves. The mobile protein encoded by this gene (part of the florigen) is transported to the shoot apical meristem where it induces flowering. In wheat, the dominant *FT-B1* allele from the wheat variety Hope carries a retroelement insertion in the promoter and has been previously associated with earlier flowering. To study the effect of this allele and its epistatic interactions with the main meristem identity gene, *VRN-1,* we developed six sets of BC_4F_3 sister lines with and without the Hope allele in different *VRN-1* genetic backgrounds. Results from two years of field experiments showed that the Hope allele had a significant effect on accelerating heading time (*P*=0.0044), but smaller effects were detected in the earlier *VRN-1* alleles. Some of the sister line pairs showed additional significant differences in yield components. These backcross lines will be publicly available to aid breeders to test the effect of this allele in their particular environments.

WESTERN ILLINOIS UNIVERSITY UNDERGRADUATE EDUCATION IN PLANT BREEDING

Winthrop B. Phippen

Western Illinois University, School of Agriculture

The overall goal of our program is to increase the number of students pursuing graduate degrees in plant breeding while increasing the science-based knowledge of a new bio-energy crop, field pennycress (*Thlaspi arvense* L.). The educational objective of this project focuses on recruiting students to the field of plant breeding from high schools and community colleges by creating a new plant breeding minor program at Western Illinois University (WIU). The minor offers new courses in traditional and contemporary approaches to plant breeding along with providing hands-on laboratories and field trip experiences to active breeding programs and germplasm banks. Competitive research awards and employment opportunities were also provided to students. A highlight of this program is the summer internship programs with Pioneer Hi-Bred Int., University of Illinois, USDA-North Central Region Plant Introduction Station, and the USDA-National Center for Agricultural Utilization Research. Direct outcomes from this project include undergraduate summer internships, undergraduate research projects, creation of new courses and planting breeding minor at WIU, and the creation of a Pennycress Resource Network website. In addition, literature and career information has been distributed to academic advisors at high schools and community colleges to further encourage students to participate in a plant breeding career.

FROM ISOZYME MARKERS TO GWAS

Charles W. Stuber

North Carolina State University, Center for Plant Breeding and Applied Plant Genomics

This discussion will highlight the major activities and accomplishments in the plant breeding and genetics research career of Charles W. Stuber. It will begin with a brief discussion of field experiments on estimation of genetic variances and gene action with a primary focus on epistasis. It will then move to the pioneering developments of molecular marker technology, beginning in 1970 with the modification and enhancement of laboratory techniques for using isozymes as markers. The first marker studies focused on the evalution of associations of markers with phenotypic responses by correlating changes in frequencies of isozyme alleles with changes of grain yield in long term maize selection studies. The next studies focused on the use of isozyme markers as selection tools in maize populations and then moved to predictions of single-cross hybrid responses. The following studies focused on the use of markers to identify and locate quantitative trait loci (QTLs) in two large F_2 populations using marker loci. For each of the 82 phenotypic traits evaluated, QTLs were detected and located to genomic sites. A publication in 1992 reported the results of a very large study conducted using 76 isozyme and RFLP markers to identify and characterize factors affecting heterosis in the B73 x Mo17 hybrid and evaluate QTL by environmental interaction. This study involved 3168 plots grown at 4 locations in NC, one in IA, and one in IL. QTLs were detected on most chromosomes, and the heterozygote class had the higher phenotype. The gene action appeared to be largely dominance or overdominance (possibly pseudo-overdominance). A later study in which the a major QTL on chromosome 5 was dissected (“fine-mapped”) showed two dominant genes in repulsion phase linkage and that overdominance was probably not the type of gene action being expressed. There was little evidence for QTL by environment interaction in the “heterosis” study. A major follow-up study (in which different levels of moisture stress, nitrogen stress, and planting density stress were imposed on a population generated from the B73 x Mo17 single cross) showed little evidence for QTL by environment interaction. Further studies were conducted in which the goal was to enhance the B73 x Mo17 single cross by introgressing QTLS from Tx303 into B73 and from Oh43 into Mo17. Tests conducted over three years showed that the grain yields of the best “enhanced hybrids” were significantly better than the non-enhanced single cross. Another procedure for the development of enhanced lines was developed and tested in which a series of NILs are generated by sequentially replacing segments of an elite line (to be improved) with corresponding segments from a donor genome. This requires no prior identification of QTLs in the donor. Although the studies in my career were accomplished with a very limited number of markers, the efficacy of using marker technology for plant breeding programs was established. With rapid advancements in the tools for using marker technology in plant breeding, e.g., genome wide association studies coupled with genomic selection, plant breeders should be well on their way to meet the challenges to feed the world’s greatly expanding population.

IDENTIFICATION OF QUANTITATIVE TRAIT LOCI (QTL) RELATED TO HEAT STRESS TOLERANCE IN CHINESE CABBAGE

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A genetic linkage map of Chinese cabbage (*Brassica rapa* L.) ssp. *Pekinensis was* constructed with 142 RAPD (random amplified polymorphic DNA) and 24 SSR (simple sequence repeat) markers using F_2 population comprising of 91 individuals. The F_2 individuals were obtained from F_1 that was derived by crossing heat tolerant line 92 and a heat sensitive line 93. To investigate the heat stress response twenty day old seedlings of F_3 population were exposed to 43^oC for seven days under 80% relative humidity (RH) followed by three days of recovery under normal controlled growth conditions (15 to 22^oC). Heat stress response was based on visual ratings (0=survived and 1=dead) after the heat treatment. The segregation of linkage with each marker was examined by using JoinMap version 4.0. Fourteen linkage groups were generated with 101 mapped markers covering 963.7 cM with an average marker interval 9.5 cM. Quantitative trait loci (QTL) were mapped for heat stress tolerance by using MAPQTL 5.0 package. Three QTLs were discovered explaining 17.6%, 18.5% and 41.1% of the total phenotypic variation of heat tolerance. These QTLs linked to heat stress tolerance would be useful in marker assisted selection program for heat stress tolerance breeding of Chinese cabbage.

SYNTHETIC HEXAPLOID WHEAT IMPROVES THE DIVERSITY AND YIELD POTENTIAL OF BREAD WHEAT GERMPLASM

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Crop domestication and selection have created a bottleneck effect in the diversity found within modern bread wheat (*Triticum aestivum* L.) varieties. The objectives of this research include: (i) reducing this bottleneck through the introgression of diversity from synthetic hexaploid wheat lines (SHW), (ii) identifying genomic regions associated with improved performance by genotyping-by-sequencing a synthetic-derived backcross population, and (iii) improving the diversity and yield potential of adapted germplasm available to plant breeders. Six selected SHW lines were used as donor parents for backcrossing with U.S. High Plains adapted, winter wheat cultivars 'Hatcher' and 'Goodstreak'. Pre-breeding efforts included testing the segregating SHW-derived populations for yield and yield components in eight environments in Colorado and Nebraska in 2010 and 2011. Significant differences ($P<0.05$) among genotypes were found within each location for yield and test weight. Both high yield potential and yield stability were found in a SHW-derived line which outranked the recurrent parent 'Hatcher' in all but one environment, resulting in a 4% increase in overall yield. Significant ($P<0.05$) correlations with grain yield under moisture stress conditions were found for biomass, average seed weight, and spikes per unit area. Single-plant derived headrow plots were selected in 2012 and advanced for evaluation in yield trials in 2013. Genotyping-by-sequencing has identified molecular markers in these advanced lines which will be used to identify any selective advantage of genomic regions of synthetic origin. These regions may be useful for targeted candidate gene identification or for marker-assisted selection. The 2013 yield trials will identify SHW-derived lines adapted to the U.S. High Plains region, which can be integrated into local breeding populations for improvement in yield potential and stability through novel genetic diversity.

UNIVERSITY OF ARKANSAS RICE BREEDING

*Gregory Berger, Karen A.K. Moldenhauer, Xueyan Sha, Debra Ahrent, Zongbu Yan, and
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Arkansas ranks 1st in U.S. rice (*Oryza sativa* L.) production, which accounts for nearly 50% of total U.S. rice acreage. The University of Arkansas has invested in breeding programs to meet the demands of rice producers, millers and consumers. Concomitantly, the programs conduct research which contributes to the rice scientific community. Breeding efforts at the University of Arkansas Rice Research and Extension Center (RREC) located in Stuttgart, AR currently focus on the development of conventional and Clearfield® (CL) long-grain cultivars under the direction of Dr. Karen Moldenhauer, conventional semi-dwarf long-grain, and medium-grain and CL long- and medium-grain cultivars under the direction of Dr. Xueyan Sha, aromatic rice cultivars under the direction of Debbie Ahrent and conventional long- and medium-grain hybrids under the direction of Dr. Gregory Berger. Diversity of the programs contributes to differences in breeding objectives and methodologies. Both traditional breeding and marker-assisted selection (MAS) have contributed to improvement of rice germplasm over time. Although the breeders work on cultivar development, many scientists contribute to the breeding and testing process. Working closely with agronomists, pathologists and entomologists, potential cultivars are tested over multiple years and environments to access agronomic performance, milling quality, grain quality and resistance to pathogens. Over 40 rice cultivars have been released by the University of Arkansas since 1936, 25 since 1982. Current efforts look to continue this trend and to provide the next generation of rice cultivars to both Arkansas and U.S. producers, millers and consumers.

SENSORY AND INSTRUMENTAL MEASUREMENTS OF FRUIT TEXTURE IN AN F_1 SOUTHERN HIGHBUSH BLUEBERRY POPULATION

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Increased fruit firmness is critical for selection of improved southern highbush blueberry cultivars. A unique crisp texture was identified in the University of Florida southern highbush blueberry germplasm, and several cultivars and selections considered to be crisp (‘Sweetcrisp’, Fl 97-136, FL 98-325, FL 02-22, and FL 03-161) were crossed to develop five F_1 populations segregating for fruit texture. Subjective sensory evaluations of texture were measured three times during the spring 2011 harvest season using a nine-point rating scale. Four of the five populations fit expected segregation ratios single gene inheritance with incomplete dominance in an autotetraploid. A single population (FL 98-325 x ‘Sweetcrisp’) having the greatest representation of crisp-textured seedlings was selected for evaluation the following year. A texture analyzer was used to measure the force required to puncture a berry with a 4 mm probe (bioyield). The population demonstrated a normal distribution with a bioyield force ranging from 333 to 617 g and a mean force of 450 g. While this distribution is descriptive of quantitative inheritance, it is unclear whether the genetic basis of crisp texture is regulated by one or several genes due to the polyploid nature of blueberry and the high level of background noise from other quantitative traits and environmental interactions that contribute to overall fruit texture. Progress has been made in constructing a genetic linkage map in tetraploid blueberry that could be used to anchor markers segregating in this population and identify QTL associated with crisp texture in southern highbush blueberry.

HOW DOES ROOT COMPLEXITY DETERMINE THE RESPONSE OF MAIZE (*ZEA MAYS* L.) TO ABIOTIC STRESSES?

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Maize (*Zea mays* L.) cultivars exhibit significant genetic variation for complexity of root systems. However, there is little known about how the complexity of root systems determines plant response to abiotic stresses, specifically drought stress and low nitrogen fertility. The main purpose of this study is to identify the relationship between maize root complexity and biomass partitioning when maize plants are subjected to low nitrogen fertilization and drought stress. Six elite hybrids comprising two contrasting root complexity phenotypes will be evaluated in both field and greenhouse experiments under well-watered and water-stressed conditions, as well as in field conditions under low and adequate nitrogen fertilization. Traits will be observed at biologically significant developmental stages spanning vegetative and reproductive growth. Traits observed will include root, stem and leaf mass, diameter at each node with a fully collared leaf, internode length, and the length and width of each fully collared leaf during the vegetative growth. During reproductive growth the previously described characteristics will be observed, as well as tassel mass, ear location, and ear mass. At all stages soil moisture and chlorophyll content will be monitored. A control trial was conducted in the greenhouse to establish a point of reference prior to execution of the stress trials. Fractal geometry was used to phenotype the root structures of the six hybrids prior to selection for use in the study. Non-linear mixed models will be used to detect significant differences in biomass partitioning between hybrids. We expect our findings to be critical in understanding the relationship between root complexity and key abiotic stresses and to guide breeding efforts to develop maize cultivars with improved stress tolerance.

DROUGHT STRESS RELATED GENE EXPRESSION PATTERNS AND SUB-GENOME LOCALIZATION OF FIVE AQUAPORIN GENES IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM*)

*Megan Bowman, Wonkeun Park, Philip Bauer, and B. Todd Campbell, USDA-ARS, Florence, SC; Justin Page and Joshua Udall, Brigham Young University; Brian Scheffler USDA-ARS, Stoneville, MS.

As water resources become more and more limited, it is essential to understand how these changes in climate impact crop production. These environmental stresses are of particular concern for cotton, the world’s most important natural fiber and a significant crop economically for the Southeast US. One approach to gain insight on the influence of water deficit on cotton is to study aquaporins, a large family of conserved proteins responsible for the regulation of cellular water uptake. Towards that end, using real time quantitative PCR (RT-qPCR), we have evaluated the level of transcript abundance of several genes from three sub families of aquaporins in the leaf and root tissues of tetraploid upland cotton cultivar Siokra-L23 during drought stress. Transcript amounts varied for each of the selected genes studied. Additionally, aquaporin sequence analysis from a wide range of diploid and tetraploid *Gossypium* germplasm and the use of a newly published PolyCat annotation pipeline have increased our knowledge of sub-genome localization and potential gene duplication of these important proteins in tetraploid cultivated upland cotton.

BREEDING RESISTANCE TO MCMV (MAIZE CHLOROTIC MOTTLE VIRUS) IN MAIZE

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A maize virus disease of increasing severity worldwide is MCMV (Maize Chlorotic Mottle Virus). It is referred to as CLN or MLN ("Corn Lethal Necrosis" or "Maize Lethal Necrosis") when infection is accompanied by complementary potyviruses like MDMV (Maize Dwarf Mosaic Virus), first observed in W. USA 40 years ago. Yield losses have been severe in recent years in E. Africa and S. China. However, we believe that MCMV can alone inflict death in corn, e.g., following major nutritional stresses. MCMV was first observed in Hawaii 20 years ago. Upon its arrival Nov. 2010 at our Waimanalo Research Station on Oahu, Hawaii, we've nurtured it as an epibiotic by bi-weekly plantings of susceptible stocks. ELISA tests by Dr. John Hu show that all sampled plants in our fields test positive and often have similar virus titer irrespective of symptoms. MCMV and other potyviruses do not occur at this station, although they are known in Hawaii. Accompanying research on MCMV has sought to determine (1) extent of genetic tolerance to MCMV in maize, (2) heritability of tolerance, and (3) ease of conversions to resistance. MCMV is transmitted by thrips in Hawaii and is easily kept epidemic by planting susceptible check-plots. Respected inbreds B73 and Mo17 are among our standard susceptible checks. A replicated survey of >100 tropical and temperate inbreds revealed 46% to be highly tolerant (1-2.5 on a 1-9 scale), 23% highly susceptible (5-9 on the scale) and 31% intermediate. Yield loss appears common on all except highly tolerant inbreds. MCMV was first recorded on grasses in Peru a century ago, and many of >200 Latin American races and tropical varieties of maize we've studied are tolerant or segregate high tolerance. Recurrent mass selection is ongoing for 18 of Hawaii's open-pollinated synthetics of field, sweet, and waxy corns (www.ctahr.hawaii.edu/hfs). Genetic advance has been excellent after three or four cycles. Tolerance is correlated with vigor and generation-mean analyses have thus offered little clarity to genetic control. Genetic studies have been most revealing from sets of recombinant inbreds and from conversions of susceptible inbreds to tolerance. At least two major gene loci are inferred, one of evident dominance and the other co-dominant and apparently linked to the A2 locus on Chrom. 7, as revealed by our 150 NILs of resistant tropical inbred Hi27 (cf. Maize Genetics Newsletter, 2012). Genetic conversions to tolerance have been generally successful with five backcrosses followed by inbreeding. Major conversions focus on previously-susceptible inbreds Hi26 (field corn), Hi36 (supersweet), and Hi60 (a Mo17 NIL) that are among those favored in Hawaii's tropically-adapted commercial hybrids.

VALIDATING THE USE OF A SINGLE KERNEL NIR SORTER TO SELECT FOR PROTEIN CONTENT IN SEGREGATING WHEAT POPULATIONS

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Wheat grain protein content is an important characteristic for end-use quality. Environmental factors significantly affect grain protein content, which can make it difficult for breeders to select for this trait, especially using traditional bulk grain analyses of protein content. The high protein content gene (*Gpc-B1*) derived from *Triticum turgidum ssp. dicoccoides* has been shown to increase protein content in hexaploid wheat. Although molecular markers are available for this gene, screening thousands of segregating lines is time consuming and still relatively expensive. A low-cost, non-destructive method to sort individual kernels at high speed would be beneficial to wheat breeding programs. A single kernel NIR system has been developed to successfully sort individual kernels based on their protein content. The objective of this research was to determine if this system could effectively sort and select kernels with high protein and putatively with *Gpc-B1* from among F_2 populations segregating for the gene. The 10% of kernels with higher grain protein content were sorted and saved from seven spring wheat F_2 populations in which *Gpc-B1* originated by pedigree from the cultivar 'Glupro'. The high protein content sorts were on average 4.7 percentage points higher than the seed samples from which they were separated. For each population, 50 individuals from the higher protein content sort were genotyped with the molecular marker, *Xuhw89*. The protein content of the original population samples and their higher protein sorts ranged from 12.5 to 15.7 and from 15.8 to 22.4, respectively. For two populations as determined by genotyping, the segregation ratios in the high protein content sort were significantly different than the segregation ratios expected in an unselected F_2 population. The number of individuals homozygous for *Gpc-B1* was higher than the number of heterozygous individuals and individuals without *Gpc-B1*. This suggests that for two populations the singe kernel NIR system was successful in selecting individuals with *Gpc-B1*. For the other populations, the segregation ratio was not significantly different than is expected in a F_2 population without selection. To successfully apply the single kernel NIR system to any segregating population may require adjusting the calibration of the sorter and tailoring it to a specific population.

PHENOTYPIC EVALUATION OF WILD COTTON ACCESSIONS FOR THE DEVELOPMENT OF SALT TOLERANT CULTIVARS

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Concerns have increased in regards to the negative infliction of saline sediment depositions and saline water that limit irrigation practices and crop efficiency. Novel agronomic models are being implemented today to address the salinity challenge. The primary objective of this study was to screen and evaluate the effects of salinity among wild cotton varieties using a hydroponic technique. Phenotypic responses were recorded from 2007 through 2011 to identify salt tolerant germplasm. Preliminary results showed one wild accession to be more tolerant than others when plants were treated with NaCl. Focus of this research is to compare the effect of salinity stress among a wild cotton accession, three commercial lines and two enhanced lines using the Arabidopsis genes to determine if differences in root biomass can be attributed to salinity tolerance. The study was conducted under greenhouse conditions at the Texas A&M AgriLife Research and Extension Center in Lubbock, Texas. The experimental design was a randomized split block with four replications, four treatments, and ten plants/treatment sampling error. Differences ($p < 0.05$) were observed for dry-root biomass in the dose response screening study among the six different genotypes: two commercial cultivars, two genetically transformed lines and their corresponding wild type cultivar, and one accession from the collection deemed to be salt tolerant from preliminary screening results. The hydroponic system was an effective screening method to evaluate responses and to isolate individual plants with respect to morphological and physiological responses to salinity stress and can be used as an assessment tool to identify contrasting phenotypes at high salt concentrations early in plant development and to assist in the development of salt tolerant germplasm.

IDENTIFYING FUNCTIONAL FLAVOR GENE CANDIDATES IN STRAWBERRY USING RNA-SEQ IN A SEGREGATING POPULATION

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Human health and nutrition can be positively impacted by increased consumption of fresh fruits and vegetables, but the organoleptic quality of these products has deteriorated over time. Flavor is now increasingly important when combined with advances in post harvest quality, disease resistance, and yield. The focus on fruit flavor is especially increasing for many Rosaceae breeding programs including strawberry (*Fragaria* x *ananassa*). Still, efficient methods for improving flavor are lacking. Here we present the development of a functional, candidate gene identification method that combines RNA-seq and volatile profiling from a segregating population in strawberry. Cultivars “Mara des Bois” and “Elyana” were crossed and the progeny were evaluated for volatile composition over three years. Ripe fruit from fourteen progeny and both parents were included in an RNA-seq experiment coupled to GC/MS volatile analysis. Within season volatile variation and the complexity of an octoploid genome were leveraged to identify and validate functional flavor gene candidates from this data set. Candidate genes for two flavor-active organoleptic volatiles (γ-decalactone and methyl anthranilate) were identified in the segregating population. These volatiles impart “peach” and “grape” sweet flavor notes, respectively. Approximately 25% of progeny showed detectable levels of methyl anthranilate and 50% of progeny showed detectable levels of γ-decalactone. These results are evidence of how quickly beneficial volatiles can be lost from a breeding program if not carefully maintained. Candidate genes for both volatiles were validated by qRT-PCR using tissues from multiple environments and developmental stages. The ultimate goal of this research is to provide simple PCR-based markers to track favorable alleles in a breeding program thus enabling seedling selection.

GENETIC DIVERSITY, POPULATION STRUCTURE AND LOCI UNDER SELECTION IN THE UNIVERSITY OF FLORIDA PEACH (*PRUNUS* SPP.) GERMPLASM

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The University of Florida Stone Fruit Breeding and Genetics Program was created in 1952 to breed early ripening stone fruit cultivars with high quality, adaptation to summer rainfall climates, low chilling requirements, and the ability to withstand high disease pressure. Different germplasm sources were used as sources of desirable traits in UF's breeding pool. The main objective of this research was to determine the genetic diversity and population structure of the breeding germplasm, and to search for loci under selection in the breeding germplasm, using cultivars and selections from throughout the program's history. A total of 195 peach genotypes representative of five major breeding pools were used: UF varieties and advanced selections (n=168), varieties and selections from the UF-UGA-USDA joint breeding effort (n=13), landrace cultivars (n=4), high-chill cultivars released by NCSU (n=5), and related *Prunus* (n=5) species. A total of 36 SSR markers distributed across the peach genome, amplified 423 alleles. An average of 18 genotypes were detected per marker, *A* (number of observed alleles) of 11.43, *Ae* (effective number of alleles) of 2.58, *Ho* (observed heterozygosity) of 0.4, *He* (expected heterozygosity) of 0.52, *F* (Wright's fixation index) of 0.25 and *PIC* (polymorphism information content) of 0.48. UPGMA cluster analysis based on Nei's genetic distance represented best the known pedigree information for the germplasm pools. Two major groups were observed across the germplasm corresponding to melting and non-melting flesh varieties. Population structure results supported major subgroups: melting and non-melting flesh varieties/selections. No clear structure separation was observed between peach and nectarine selections. Several loci closely located to genome regions where different phenotypic traits have been previously mapped were detected to be under selection. This study constitutes the baseline for genetic diversity studies of low chill breeding programs around the world as the UF's germplasm pool has been used as their founder material.

SELECTION PROGRESS FOR REDUCED IRIS YELLOW SPOT SYMPTOM EXPRESSION IN ONION GERMPLASM AFTER ONE SELECTION CYCLE

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Onion thrips and *Iris yellow spot virus* (IYSV) cause qualitative and quantitative losses to onion bulb and seed production throughout the world. An increased resistance to insecticides by onion thrips and the high cost of pesticide applications, restrict onion grower's options to effectively control thrips population and IYSV. Currently, resistant cultivars to thrips and IYSV do not exist. In the summer of 2009, plants with fewer Iris yellow spot (IYS) disease symptoms were selected from a field screening and self-pollinated in the following year to produce seed. The objective of this study was to measure the progress made from this selection for reduced IYS symptom and any other related traits. In October of 2011, IYSV-infected bulbs were placed on the first and last bed of the study and at the front and back borders to obtain maximum exposure from thrips and IYSV to the test plots. Seed of an IYSV-susceptible cultivar, NuMex Dulce, was sown in autumn of 2011 between every two rows of the test plots to act as disease spreader rows. The original and selected onion germplasm lines were evaluated in 2012. Data were collected on number of onion thrips per plant from ten plants per plot at three times 4 weeks apart, starting at 17 weeks after sowing. Plants were rated for IYS severity based on a rating scale of 0 to 4 at three intervals, starting at 17 weeks after sowing and 4 weeks apart. At 25 weeks after sowing, plants of NMSU 10-807 had fewer thrips than plants from its original population of NMSU 07-53-1 and of the susceptible check, 'Vaquero'. At 21 weeks, plants of NMSU 10-785, NMSU 10-799, and NMSU 10-813 exhibited lower disease severity than plants of their original populations, NMSU 07-32-2, NMSU 07-52-1, and NMSU 07-53-1, respectively, in addition to plants of the susceptible checks, 'Rumba' and 'Vaquero'. At 17 weeks, plants of NMSU 10-785 had a lower disease incidence from than plants of its original population, NMSU 07-32-2, and of the susceptible check, 'Rumba'. No differences were observed among entries for thrips count, IYS disease severity and incidence at other observation times. Based on this study, a limited amount of progress was observed for better resistance for thrips and IYS in improved populations after one selection cycle.

INFLUENCE OF PLANT AGE ON HAPLOID EMBRYO FORMATION IN WHEAT

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Doubled-haploid (DH) technology has been increasingly employed in wheat breeding programs over the past few years. Improvements of protocols to produce DH wheat lines are necessary to derive the maximum benefit from this technology. Examples of such improvements have increased haploid production efficiency and reduced costs in applying the technology to wheat; however, continual improvements are necessary to best implement the technology in breeding programs. The developmental stage of a wheat plant may affect its ability to respond to haploid embryo induction, and thus, identifying the optimal stage of producing haploid embryos may help programs plan for ideal times to pollinate when producing haploids by wide-hybridization. Our objective was to identify the optimal spike development time at which to produce DH wheat lines using wide-hybridization. For this, the F_1 progenies of twenty-two crosses, including winter and spring wheat genotypes, were used as females to pollinate with maize. Spikes produced at various stages of plant development were evaluated for production of haploid embryos. Regardless of the cross, a significant decrease in embryo formation was observed for the tenth formed and later plant spikes. Conversely, the first to eighth spike formed on the plant produced significantly more embryos after pollination with maize. We suggest that breeding programs should focus on optimizing pollinations of the first to the eighth spike produced in order to maximize the number of DH lines derived from wide-hybridization.

CHARACTERIZATION AND INTROGRESSION OF COLD TOLERANCE IN NAPIERGRASS: TOWARDS EXPANSION OF FEEDSTOCK PRODUCTION POTENTIAL

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Perennial C_4 grasses, such as napier grass (*Pennisetum purpureum* Schumach.**; 2n=4x=28**), are vital in the recurrent rise in the demand for more energy output from renewable energy sources. The advancements occurring in the area of biomass feedstock processing and conversion technology makes the lignocellulosic energy platform provided by biomass feedstocks like napiergrass more feasible in the long term. In comparison to other high yielding dedicated and dual-use energy crops, napiergrass' production region is limited to areas of the Southern United States. Wild species within *Pennisetum* harbor enhanced cold tolerance in comparison to the cultivated *Pennisetum* species, pearl millet and napiergrass, which allows for the opportunity to incorporate cold tolerance into the napiergrass genome by way of interspecific hybridization. Wide interspecific crosses utilizing the wild species Oriental grass [*P. orientale* (2n=4x=36)] and flaccid grass [*P. flaccidum* (2n=4x=36)] as pollinators with napiergrass as the female parent are being analyzed for viable hybrid production. Embryo rescue techniques in the instance of zygotic termination in the napiergrass ovule are being investigated while the production of natural hybrids may be a possibility. The characterization of genetic diversity for cold tolerance within the napiergrass species is also being investigated with genotypes that exhibit superior adaptation for winter hardiness and cold tolerance already present in the napiergrass germplasm collection from the Perennial Grass Breeding Program at Texas A&M University. The development of species-specific microsatellite markers for napiergrass, Oriental grass, and flaccid grass are currently underway for rapid hybrid verification. Preliminary data to be discussed and presented.

UTILIZING GENOTYPING BY SEQUENCING TO IDENTIFY CANDIDATE GENES UNDERLYING DOMESTICATION TRAITS IN CARROT (*DAUCUS CAROTA* L.)

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Domestication of carrots as a root crop (*Daucus carota* L.) began in Central Asia over 1,000 years ago. Several traits associated with the domestication syndrome of carrot include increased pigment (carotenoid and anthocyanin) and sugar accumulation, decreased lateral root formation and reduced bolting. With the exception of the *Rs* locus controlling sugar accumulation and type, very little is known about the genetic loci controlling these aforementioned traits. The focus of this work was to use a Genotyping by Sequencing (GBS) approach to identify the location of candidate genes underlying two domestication traits: 1) carotenoid accumulation and 2) reduced lateral root formation. Previously an advanced inbred (F_4) population, segregating for both traits, was developed from a cross between a white-branched wild carrot (Queen Anne's lace - QAL) and a smooth-orange USDA inbred line (B493). The population, comprising 174 carrot roots, was grown in Hancock, WI over the summer of 2012 and later phenotyped for carotenoid content using visual assessment and High Performance Liquid Chromatography (HPLC). Additionally, a novel scale and procedure was developed for scoring lateral root prominence. DNA from the carrot roots was extracted and used to genotype the population using the GBS platform. 2688 non-overlapping SNPs were aligned to the draft carrot genome assembly and used to identify genome-wide associations for the traits of interest. A 450 kb region of the genome, containing the Y_2 locus, was flanked by two of the most significant markers for carotenoid accumulation whereas two regions of the genome were identified to contain significant marker associations for lateral root development. We are currently analyzing the data of an RNA-Sequencing experiment to identify genes that are differentially expressed within these regions as well as throughout the genome. Together these experiments will be used to locate candidate genes for two agronomically important domestication traits. Further, the molecular markers developed in this project will facilitate rapid genotypic screening for carrot population improvement within the breeding program.

QUANTITATIVE TRAIT LOCUS ANALYSIS FOR BIOMASS TRAITS IN *MISCANTHUS SINENSIS*

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In light of rising energy costs, lignocellulosic ethanol has been identified as a renewable alternative to the petroleum based transportation fuels. In an attempt to reach government mandated ethanol production levels, potential plant biofeedstock candidates have been investigated and perennial accessions within the C_4 grass genus *Miscanthus* have been identified as leading contenders in the Midwestern United States due to their high yield and cold tolerance. With this in mind, a QTL study was conducted in a pseudo testcross mapping population segregating for flowering time, height, leaf width, and yield from a cross between two *M. sinensis* accessions. A three year study investigating the genetic architecture underlying traits important to biomass production in a population of 221 progeny from the cross of *M. sinensis* accession 'Grosse Fountaine' with *M. sinensis* 'Undine' established in the spring of 2010 revealed 69 high-confidence QTLs across 14 traits. Of the 38 QTLs identified in 2011, 24 were confirmed in 2012. The drastic difference in growing conditions between 2011 and 2012 in Champaign-Urbana as well as the transition between the establishment and the mature phase (two-three years) of this perennial crop may explain the 14 QTLs not detected in 2012. The use of spring emergence as a covariate to account for variation related to differences in establishment increased the power to detect QTLs in the establishment period; its utility was confirmed in 2012. The marked increase in the ability to explain the phenotypic variation by genotype from the second to third year for certain traits further illustrates the establishment effect. The lack of an increase in ability to explain variation between the two years, on the other hand, suggests certain traits are less influenced by the establishment effect and may be reliably phenotyped during the establishment phase. Leaf morphology, flowering time, and tiller diameter appear to be candidates for early selection while height, the number of tillers, compressed circumference, basal circumference, and yield appear to be heavily influenced by differences in plant establishment. In addition to QTL, we report high correlations between compressed circumference, basal circumference, height, and the number of tillers with yield: 0.86, 0.68, 0.56, and 0.79, respectively. This analysis sets the foundation for fine mapping, positional cloning, and the development of a marker assisted selection program in the ongoing effort to improve *Miscanthus* as a biofuel crop.

CONSUMER-ASSISTED SELECTION IN BREEDING FOR SOUTHERN HIGHBUSH BLUEBERRY FLAVOR

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When selecting for flavor in the University of Florida southern highbush blueberry (SHB, *Vaccinium corymbosum* L. hybrids) breeding program, sugar:acid ratios and subjective breeder preference have been the primary factors taken into consideration. The implementation of a more precise method for evaluating flavor was supported by a study conducted to identify consumer blueberry preferences which indicated that aspects of blueberry flavor outrank berry texture, firmness, size, color, and human nutrition for consumer interest, and may affect consumer-purchasing behavior more than any other fruit trait. To identify potential breeding targets for flavor and assess potential environmental variation, we surveyed biochemical flavor components of six SHB genotypes (FL 06-377, 'Emerald', 'Farthing', 'Meadowlark', 'Primadonna', and 'Scintilla'), grown at three locations at three different time points in harvest season. Total soluble solids (SS) and titratable acidity (TA) were measured, and individual sugars were quantified using Sucrose/D-Glucose/D-Fructose enzymatic reaction kits. Volatile profiles were analyzed using gas chromatography-mass spectrometry (GC-MS). Sensory panels were conducted on the same genotypes to measure perceived sweetness, sourness, flavor intensity, and overall liking of the six SHB genotypes from the nine separate harvests. The biochemical and sensory data were pooled to discover correlations between biochemical compounds and the panelists' hedonic measurements. Significant relationships were found between overall liking and sweetness, sourness, bitterness, flavor intensity, as well as with measures of SS and TA. Similarly, significant relationships were found between perceived sweetness and SS, and between perceived sourness and TA. Although total volatiles did not exhibit a significant relationship with any of the hedonic measures, certain individual volatiles did show significant relationships with measures overall liking, sweetness, sourness, and flavor intensity, underscoring the importance of taking volatiles into consideration when breeding for blueberry flavor.

EFFECTS OF WATER STRESS SEVERITY AND TIMING ON FERTILITY AND YIELD IN 300 WINTER WHEAT VARIETIES

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Drought stress is expected to increase in frequency and severity in the U.S. Great Plains. A better understanding of the relationships among phenology, yield components, and water stress will aid the development of more drought tolerant cultivars. Three hundred entries belonging to the scho (TCAP) Hard Winter Wheat Association Mapping Panel (HWWAMP) were grown under water stressed and non-stressed treatments in Greeley, CO during the 2011-2012 field season. 2012 was a very hot, dry spring and summer with 28 days above 30 °C (86 °F) and only 8.2 cm of precipitation between January 1 and July 1. Water was managed in both treatments using drip irrigation. Water stress contributed to significant phenotypic differences between treatments and among genotypes. Pairwise comparisons between treatments illustrate that under stress genotypes reached booting, heading, anthesis, and physiological maturity an average of 3.60, 2.34, 4.25, and 7.72 days sooner than under well-watered conditions. This reduced the duration of grain-filling by an average of 3.47 days (10.77%) under stress, a reduction from 32.21 to 28.74 days. Genotypic differences also affected the timing and duration of key phenological stages. On average genotypes received 6.79 cm (40.70%) less water by booting under water stress, 10.38 cm (48.99%) less by heading, and 13.16 cm (51.52%) less by anthesis. Water during grain-filling was reduced by an average of 8.90 cm (57.12%), but ranged from a 2.24 and 14.10 cm reduction under stress. The treatment effect contributed to a mean yield reduction of 47.8% under stress, from 4808 kg/ha to 2507 kg/ha. We dissect yield into fertility and fecundity traits including proportion of fertile spikelets, number of kernels per spikelet, number of spikelets per spike, and number of spikes per square meter. Knowledge of the sensitivity of yield components to drought stress in current Great Plains wheat germplasm will help guide future crop improvement efforts.

EVALUATION OF WYOMING-BRED WINTERHARDY FEED PEA LINES FOR MULTIPLE USE WITH AN "INDEX OF MERIT"

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Winter feed pea (*Pisum sativum* ssp. *arvense*) is a nitrogen-fixing cool season annual legume that might serve as a partial or complete replacement for fallow in the winter wheat-summer fallow (WW-SF) system in the Central Great Plains (CGP), thus making farming and ranching in the region more economically and environmentally sustainable, with all the benefits of a legume in the rotation and the potential to integrate cereal and livestock production. Benefits resulting from rotation with legumes include nitrogen credit, increased soil organic matter, reduced soil erosion, pest and pathogen control, increased soil water storage efficiency, economic diversity and, perhaps, sequestration of carbon via more intensive cropping in an age of climate change. Winter feed pea has successfully integrated cereal and livestock production elsewhere (e.g., Europe, southern Australia and the Palouse region of the U.S. states of Washington and Idaho).

The goal of this long-term project was to breed winter feed pea for adaptation to the CGP. The specific objective of the present study was to evaluate our advanced breeding lines in comparison with existing winter feed pea cultivars that were bred elsewhere. In 2000, diverse winter feed pea genetic lines/cultivars were hybridized in the greenhouse at the University of Wyoming (UW) Laramie Research and Extension (R&E) Center. F_1 hybrid plants were grown to produce F_2 seed. Natural and artificial selection began with an F_2 spaced plant breeding nursery at the UW Archer R&E Center. Further selection continued at the UW Archer and Torrington R&E Centers, and on to the UW Sustainable Agriculture R&E Center at Lingle WY. Throughout this process, natural and artificial selection began among single plants, and then among single plants within superior segregating families, and finally among bulked progenies of advanced lines. As breeding populations were advanced from the F_2 through F_9 generations, the number of lines retained was reduced, as seed of elite, advanced lines was increased. All selection was in the WW-SF system in the CGP. In the 2010-2011 and 2011-2012 winter annual growing seasons, and at two locations (Lingle WY and Laramie WY), seven elite Wyoming breeding lines were tested together with the three most available U.S. winter pea cultivars ('Common', 'Specter', and 'Windham'). We evaluated yield of lines/cultivars for forage and seed yield under both dryland and irrigated conditions. Results demonstrate that breeding for the Wyoming environment can produce superior locally adapted lines for the CGP.

An "index of merit" that integrates yield potential for Forage Dryland, Forage Irrigated, Seed Dryland, and Seed Irrigated systems demonstrated that five Wyoming bred lines are the top five lines of ten tested in this evaluation. The three check cultivars were in the bottom five lines tested, along with two Wyoming lines that were lines that were retained because they exhibited morphological diversity, but not high yield potential, in early generation testing. We conclude that our elite lines, especially Wyo#11 and Wyo#13, proposed for release as 'Archer' and 'Arrow', respectively, are well-adapted to Wyoming and yield well under different conditions. We also discuss alternative "indices of merit," related to "selection indices," as ways of evaluating and graphically illustrating the value of lines/cultivars tested for multiple use (e.g., in our case, forage vs. seed, and dryland vs. irrigated) in sustainable agroecosystems.

EXAMINING A POTENTIAL SHARED RATE-LIMITING RESISTANCE MECHANISM TO TWO MAJOR ANTHRACNOSE DISEASES OF STRAWBERRY

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Anthracnose is one of the major fungal diseases of strawberry occurring worldwide and causes substantial yield loss to the strawberry industry in the southeastern United States. Two major species predominate in this region, causing anthracnose crown rot (ACR) and fruit rot (AFR) and are incited by *Colletotrichum gloeosporioides* and *Colletotrichum acutatum*, respectively. Previously, it was shown that the genetic parameters of resistance to these diseases varied with respect to the additive and dominance genetic variation which suggests different genes and gene actions may control resistance to these two plant pathogens in strawberry. However, both pathogens share a biphasic life style and are capable of producing asymptomatic, hemibiotrophic infections with sporulation capacity in vegetative tissues (mainly leaves). This symptomless, latent infection serves as a site for proliferation and secondary sporulation which is visually undetectable and allows for the widespread distribution of disease in nursery and fruiting fields. Although each species' necrotrophic phase targets different plant tissues (crown versus fruit), we hypothesize that resistance mechanisms to hemibiotrophic foliar infections are shared and could be used to simultaneously breed for effective rate-limiting resistance to both anthracnose diseases. The goals of this research are to (i) identify reliable methods of inducing and quantifying latent foliar infections of *C. gloeosporioides* and *C. acutatum*, (ii) screen selected strawberry germplasm to identify variation within the germplasm across anthracnose species for foliar resistance, and (iii) develop segregating populations to estimate genetic parameters and determine appropriate breeding strategies. In 2012, advanced selections from the NCSU strawberry breeding program were evaluated for foliar resistance to *C. gloeosporioides*. Latent infection severity was measured by quantifying the percent leaf area with visible sporulation. Sporulation was visualized by treating detached, inoculated leaves with herbicide (paraquat) and incubating in a humid chamber. Percent sporulating leaf area was estimated using a modified Horsfall-Barratt scale. Strawberry genotypes were found to significantly differ in their resistance to latent infections of *C. gloeosporioides*. A current methods study seeks to refine the inoculation procedure and is utilizing the imaging software 'ImageJ' to increase the precision of our estimate of the percentage leaf surface area affected. These refined methods will be implemented to screen additional genotypes for varying degrees of resistance to latent infections by each pathogen.

ESTIMATION OF GENETIC PARAMETERS FOR RESISTANCE TO FOLIAR POWDERY MILDEW IN STRAWBERRY USING DIVERGENT SELECTION

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The Florida strawberry industry supplies the eastern United States and Canada with strawberries from November through March. An annual, highly intensified growing system gives rise to cultural challenges including fungal disease control. One such ubiquitous, wind-spread disease is powdery mildew (PM) caused by the obligate parasite *Podosphera aphanis*. To control PM, multiple applications of fungicides are necessary each season. There are no commercial cultivars with high PM resistance for Florida, and to date there have been no published reports on powdery mildew resistance in the Florida strawberry breeding population. Therefore, the objective of this study was to perform a divergent selection experiment to observe response to selection and estimate genetic parameters for PM and related traits. In 2010, clonally replicated individuals from seven bi-parental crosses arising from 11 parents were included in a field trial designed as a modified Latin square with four replications. Seedlings were evaluated visually for percent coverage of PM mycelium on the abaxail leaf surface using a modified Horsfall-Barratt scale of 0 to 6. Two rounds of divergent selection ensued. For the first round of selection and crossing, one resistant and one susceptible genotype were selected as parents from within the top and bottom 10% of each full-sib family and mated in circular half diallels within resistant and susceptible classes. Genetic parameters were estimated using the “animal model” in ASReml statistical software utilizing a 13-generation pedigree. The base population mean PM score was 2.8 with full-sib family means ranging from 1.8 to 4.0. The means for the resistant and susceptible seedling populations arising from the first round of divergent selection were 1.8 and 3.7 respectively and for the second round were 0.3 and 4.5, respectively. Heritabilities for PM score were H^2=0.49±0.09 and h^2=0.41±0.39, for the base population. For the resistant population in the first round of divergent selection, heritabilities for PM score were H^2=0.64±0.07 and h^2=0.60±0.22, but by the second round there was no additive variance detected. For the first round in the susceptible population, heritabilities for PM score were H^2=0.68±0.03 and h^2=0.65±0.03. In contrast to the resistant population, after two rounds of divergent selection in the susceptible population, there remained considerable additive variance (h^2=0.56±0.05). This indicates that alleles for PM resistance have become fixed in the resistant population and that further rounds of divergent selection would not result in additional selection response. Considering the overall moderate to high heritability estimates and clear response to selection for two generations, we conclude that resistance to PM is genetically controlled through mostly additive effects. Through field selection based on natural infection and traditional breeding techniques, good progress can be made toward developing strawberry cultivars with resistance to PM for Florida.

DEVELOPING IMPROVED NATIVE PLANT VARIETIES FOR COASTAL RESTORATION

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Numerous wetland restoration projects are completed each year to reduce coastal erosion in Louisiana. Plants such as smooth cordgrass (*Spartina alterniflora* Loisel.) and sea oats (*Uniola paniculata* L.) reduce coastal erosion by stabilizing soil in brackish and saline marshes and beaches, respectively. Smooth cordgrass and sea oats are perennial grasses native to the Gulf of Mexico and Atlantic coasts and are incorporated into Louisiana's coastal restoration projects. Most projects specify the use of a single smooth cordgrass variety, 'Vermilion', and a single sea oats germplasm source, 'Caminada'. However, use of a single cultivar in restored sites eliminates the genetic variation necessary for a population to adapt to environmental changes. To increase the genetic diversity of smooth cordgrass and sea oats varieties, breeding programs for both species were initiated. In 1998, smooth cordgrass seeds from 126 populations were collected throughout Louisiana and portions of Texas. Smooth cordgrass genotypes were evaluated for plant performance in replicated field trials for 9 years in 11 environments. Plant performance was determined by measuring plant vigor, spread, height, and rust resistance (caused by *Puccinia sparganioides* Ellis & Tracy). Six selected smooth cordgrass genotypes had high plant vigor and spread and acceptable plant height and rust resistance and were selected as potential varieties. The genetic similarity, as determined by Jaccard similarity coefficients, was determined for the selected genotypes. Based upon performance and Jaccard similarity data, six improved smooth cordgrass varieties were released in 2012: 'Cameron', 'Terrebonne', 'Jefferson', 'St. Bernard', 'Las Palomas', and 'Lafourche'. To develop sea oats varieties, seeds were collected in 2001 from 113 populations throughout the Atlantic and northern Gulf of Mexico coasts. Sea oats genotypes were evaluated in beach trials for 3 years; in 1 year beach trials were subjected to a major hurricane event, Hurricane Gustav. Plant performance was evaluated as plant vigor, stem density, and plant height. Three genotypes had excellent performance before and after a major hurricane. Jaccard similarity coefficients, using 534 amplified fragment length polymorphism (AFLP) markers, were high for the three genotypes but were within acceptable ranges based upon previous findings that sea oats are very similar when AFLP markers are utilized. In 2012, three improved sea oats varieties were released: 'Lizette', 'Rosa', and 'Henderson'. The six improved smooth cordgrass varieties are recommended for brackish to saline marsh restoration in the northern Gulf of Mexico coast, while the three improved sea oats varieties are recommended for beach restoration in the northern Gulf of Mexico coast.

CHARACTERIZATION OF STEM RUST RESISTANCE IN WHEAT CV. GAGE

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Hard red winter wheat cultivar Gage is preferred and highly recommended as a source of resistance to stem rust caused by the fungus *Puccinia graminis* f.s. *tritici* (*Pgt*) due to its superiority in field resistance. However, its resistance have not been characterized which is needed for it to be use efficiently in breeding programs. We created 237 $F_{2:3}$ families from crosses between Gage and highly susceptible cultivar “Bill Brown”. Inheritance of seedling and adult plant resistance to stem rust race QFCSC indicated that additional gene to *Sr2* is working in Gage. Seedling and adult plant phenotype from F_2 generation confirmed that one dominant and one recessive gene are involved in Gage’s resistance. Microsatellite SSR marker gwm533 segregated on F_2 generation and $F_{4:5}$ families clearly classified individuals in the population for *Sr2*. Genotyping-by-sequencing on $F_{2:3}$ families identified molecular markers associated to stem rust resistance in Gage but not linked to *Sr2* marker.

FINE MAPPING OF QTL AFFECTING BACTERIAL SPOT OF TOMATO: RESISTANCE ON CHROMOSOME 11 AND SUSCEPTIBILITY AT OR NEAR THE FUSARIUM WILT RESISTANCE GENE *I-3* ON CHROMOSOME 7

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Tomato (*Solanum lycopersicum* L.) is one of the most economically important vegetable crops in Florida, with an annual value of approximately $500 million. Bacterial spot, caused by at least four different *Xanthomonas* spp., is a serious disease of field-grown tomatoes produced in humid environments. The disease causes defoliation and reduction in both total and marketable yields and is a particular problem in Florida's subtropical climate. Host resistance remains an attractive strategy for disease control, but breeding efforts have been hampered due to limited availability of effective resistance sources, emergence of new pathogen races (and species) and quantitative inheritance of resistance. *X. perforans* race T4 is currently the most prevalent strain in Florida. Previous research determined that a quantitative trait locus (QTL) on chromosome 11 is highly associated with race T4 resistance, while the *I-3* locus on chromosome 7 is associated with race T4 sensitivity. In this study, a map-based cloning approach is being used to fine map the chromosome 11 QTL and identify candidate genes controlling resistance. Results will allow improved selection efficiency for this QTL by marker assisted selection (MAS) in breeding programs; and identification of the underlying gene(s) will be useful in understanding the mechanism of resistance. A similar approach is being employed to determine whether the *I-3* association with bacterial spot susceptibility is the result of pleiotropy or tight linkage with deleterious alleles. If the problem is due to linkage, the dissociation of *I-3* from bacterial spot sensitivity should greatly benefit breeding efforts, which utilize the *I-3* resistance gene.

IDENTIFICATION AND EVALUATION OF QTL ASSOCIATED WITH DEVELOPMENT RATE IN PETUNIA

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High heating costs for petunia greenhouse production during the late winter and early spring greatly reduces growers' profits. Developing new cultivars with faster development rates (leaf-unfolding rate) could be a strategy to reduce the production time at lower temperatures to reduce heating fuel usage. However, little is known about the genetics of development rate in petunia. We previously utilized a *Petunia integrifolia* × *P. axillaris* F_2 population to generate an SSR and CAPS marker-based genetic linkage map and identified three quantitative trait loci (QTL) associated with development rate, two on linkage group one and one on linkage group five. Collectively, these QTL explained 49% of the variation for development rate. In order to evaluate the utility of the markers flanking the previously identified QTL for breeding petunia with increased development rate, we evaluated crop timing traits in an F_7 recombinant inbred line (RIL) population derived from the *P. integrifolia* ×*P. axillaris* F_2 population. One hundred fifteen RILs were phenotyped during summer 2012 under a long-day photoperiod at 24 ºC. The number of nodes that had formed on the primary shoot was recorded at two-week intervals and used to calculate plant development rate. Among the RILs, development rate ranged from 0.17 to 0.94 leaves per day, with a population mean of 0.65 leaves per day. The twenty fastest and twenty slowest developing RILs were identified and genotyped for the QTL-flanking markers. From these data, we generated a series of test crosses among RILs with varying numbers of positive and negative alleles associated with development rate. We are currently evaluating F_2 populations derived from these crosses to assess the utility of the flanking markers in selecting for fast development rate in petunia.

GENETIC IMPROVEMENT IN MAIZE EAR DEVELOPMENT

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Since the widely-adopted introduction of maize hybrids in the late 1930's, the beginning of the hybrid era, grain yield of maize has steadily increased by roughly 1 kg ha^{-1} yr^{-1}. Density tolerance is primarily responsible for the yield improvement achieved during the hybrid era. Some progress has been made toward identifying the physiological mechanisms that confer density tolerance such as improved dry matter accumulation and growth rate around silking. However taken together, neither mechanism completely explains the density tolerance of modern hybrids. Recent studies demonstrate that distal spikelets which form late in ear development exhibit atypical morphology and do not contribute to the final kernel number. We hypothesize that genetic improvement of increased density tolerance is due to changes in spikelet development. To examine this hypothesis we are using five Canadian ERA hybrids that reflect genetic improvement over five decades. Comparison of the number of atypical spikelets per ear and the density tolerance for each hybrid will reveal whether spikelet development underlies the genetic improvement to kernel number per ear. Using three plant population densities, potential and actual yield will be evaluated at one location for two years. Preliminary observations indicate that grain yield loss as a result of increased plant density is primarily due to a reduction in number of kernels per row rather than a decrease in kernel weight or number of kernel rows. Furthermore, removal of light competition during the grain filling period does not restore final kernel number per ear to levels attained in plots with minimal light competition throughout their lifecycle. Taken together, these observations suggest that density-induced pre-flowering stress reduces yield potential, possibly by decreasing the number of spikelets per ear with normal morphology. Further examination of the factors that influence final kernel number will provide novel insight into maize yield potential and will identify the next "biological weakness" for maize breeders to target.

EFFECT OF IMMATURE TOMATO SHOULDER COLOR ON YELLOW SHOULDER DISORDER AND SOLUBLE SOLIDS CONTENT OF RIPE TOMATOES

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A recent publication in Science found that a tomato (*Solanum lycopersicum* L.) cultivar with green shoulders had significantly more soluble solids than an isogenic cultivar with uniform light green shoulders (*u* gene). The authors concluded that when tomato breeders selected for uniform light green shoulders they were inadvertently "compromising traits that are valuable for processed products and the flavor of fresh fruit." Tomato breeders have selected for uniform light green shoulders to reduce the amount of tomato yellow shoulder disorder (YSD) which causes tomato shoulder pericarp tissue to remain hard and turn yellow rather than red when fruit ripen in the sun. To test the effects of shoulder color on soluble solids and YSD parental lines with green, uniform green (*u*), uniform gray-green (*ug*), "apple green", "medium green", and "uniform pale green" shoulder colors were crossed in all combinations to produce an F_1 and F_2 generations. Parents, F_1, and F_2 populations were planted in the field and mature green fruit of plants were evaluated on a per plant basis both phenotypically and with a colorimeter. Two table ripe tomatoes per plant were harvested, and measured for soluble solids with a digital refractometer. All ripe fruit were then harvested, counted, weighed, and the incidence of YSD was determined from bulked parental lines and from eight randomly selected plants within each of the F_2s. The F_2 plants were partitioned by immature fruit phenotype. Data analysis is currently underway and the results will be presented.

INFLUENCE OF PLANTING DATE, PLANT POPULATION, AND CULTIVAR SELECTION ON MANAGEMENT OF SPOTTED WILT IN PEANUT (*ARACHIS HYPOGAEA* L.)

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Spotted wilt, caused by *Tomato spotted wilt virus* (TSWV), is a major disease that has impacted peanut production for growers in the southeastern United States since the mid-late 1990s. Currently, there is no single control measure that manages spotted wilt in peanut sufficiently; however, collaborative research has identified several management factors that, when used together, can minimize losses due to the disease. Three of the essential cultural practices used to reduce incidence and severity of spotted wilt in peanut are date of planting, seeding density, and cultivar selection. New peanut cultivars with improved resistance to spotted wilt have been developed in the Southeast peanut production areas, but even the most resistant cultivars are at risk for spotted wilt when planted in April at lower seeding densities. The effects of planting date, plant population and cultivar in management of spotted wilt were assessed in a field experiment over three consecutive years (2010-2012) near Marianna, Florida. Data collection included three measures of visual disease symptoms (two foliar and one seed), ImmunoStrip (ELISA) testing of root crowns for presence or absence of TSWV, pod yield, and grade. There was no effect of planting date on spotted wilt symptoms or TSWV infection. However, viral infection varied among genotypes. Assessment of spotted wilt just prior to harvest indicated traces of the disease in all peanut cultivars with little variation among cultivars. However, ImmunoStrip results revealed that viral infection differed widely among cultivars. Viral infection was lower in cultivars Florida EP^{TM} '113' and UFT312 compared to Georgia Green and Florida-07. Foliar assessed spotted wilt symptoms were highly correlated with each other (r=0.73), however, only symptoms on the seed were highly correlated with TSWV infection (r=0.77). This result indicates that foliar symptomology is not as reliable in assessing genotype resistance as is TSWV infection, especially in seasons when disease pressure is low. However, the strong correlation between seed coat symptomology and virus infection indicates that seed inspection may be a good predictor in identifying resistant cultivars, and is much less expensive than ImmunoStrip testing. New genotypes demonstrated a higher level of TSMK than Florida-07, suggesting major improvements have been achieved in this very important agronomic trait. Results from this experiment illustrate that in years when less severe epidemics of spotted wilt occur, the impact of planting date and seeding rate effects on spotted wilt are minimal. Cultivar resistance is the primary means of control. The cultivars Florida EP^{TM} '113' and UFT312 display a new level of resistance that could possibly override other factors such as planting date and seeding density.

RELATIONSHIP BETWEEN ROOT PULLING FORCE AND AGRONOMIC TRAITS IN CANOLA (*BRASSICA NAPUS* L.) UNDER IRRIGATED AND RAINFED CONDITIONS

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Root traits have been used in breeding to select genotypes with better adaptation to drought and moisture stress. Root Pulling Force (RPF), the vertical force required to pull plants out of the ground, is an integrated measure of root system development and architecture in plants, and is known to be highly correlated with yield-related traits in field crops such as corn and rice. One hundred and forty-eight canola (*Brassica napus* L.) doubled haploid lines from the DHYB mapping population along with the population’s parents, DH12075 and YN01-429, were grown under two moisture levels, irrigated and rainfed, in 2011 and 2012 in Fort Collins, CO. Lines showed significant differences and transgressive segregation for RPF in both these treatments in 2011, but only in the irrigated treatment in 2012. RPF was significantly correlated with plant height (r=0.542, P<0.001), fresh above-ground biomass (r=0.47, P<0.001) and lateral root numbers (r=0.482, P<0.001) in both years and for both moisture treatments. The strong positive correlation of RPF with the yield component and above-ground biomass suggests that it can be used to detect genotypes with higher yield potential in moisture stressed environments. We propose that RPF can be a reliable variable to select genotypes with better root numbers and establishment, facilitating better water utilization and enhanced drought adaptation.

IS THE YEAR EFFECT ON MAIZE GRAIN YIELD RELATED TO PROPER FEMALE FLORET DEVELOPMENT?

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In maize, grain yield is highly related to kernel number. There are numerous factors, including pollination and kernel abortion that influence final kernel number. However, work in our lab suggests that the total number of florets initiated does not vary from year to year in the same manner as kernel number. This work and work done by others suggests that differences in kernel number and floret number variation are due to the improper development of these florets. Under less favorable environments, such as high plant density, a higher proportion of florets in the distal portion of the ears do not appear to be fully developed and are therefore not capable of being fertilized. When underdeveloped florets are controlled for, the number of normally developed florets is statistically equivalent to the number of kernels on an ear. We hypothesize that proper floret development is one of the underlying causes of the year effects that we have observed in kernel number. To test this hypothesis we are using a set of 4 inbred lines and 5 hybrids grown at 3 plant population densities (40,000 plants ha^{-1}, 80,000 plants ha^{-1} and 160,000 plants ha^{-1}) over 3 years (2011-2013). Initial results indicate that both kernel number and floret number vary across years and plant population densities. Floret number varies with respect to the total number of florets and the proportion that are normally developed. These preliminary findings suggest that a portion of the year effect on grain yield (i.e., kernel number) is likely due to environmental influences on floret development.

DEVELOPMENT OF AN EFFICIENT SEA OATS BREEDING PROGRAM FOR COASTAL RESTORATION

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Uniola paniculata (sea oats) is a dominant coastal dune grass of the southern Atlantic and Gulf of Mexico coasts of United States. This native perennial grass has been used extensively to build artificial dunes as well as stabilize existing dunes. A breeding program could enhance coastal restoration by developing improved plants for beach restoration. Our goal was to initiate a successful breeding program for sea oats adapted to shallow dune profiles, with high seed yield and germination, and superior vegetative biomass essential for reducing coastal erosion. The specific objectives were to: 1) examine effect of storage environment on seed germination; 2) determine time necessary for seeds to germinate; 3) determine seed moisture content; 4) determine pathogen incidence during germination; 5) determine survival and performance of vegetative plants and seedlings at beach environments with shallow dune profiles; 6) develop efficient methods to identify saturation tolerant lines; 7) determine seed yield in natural and artificial environments and 8) identify fungal and bacterial pathogens of seed. To examine seed storage environment, length of time for sea oats to germinate, seed moisture content, and seed pathogen incidence, mature panicles were harvested, threshed and seed placed into six storage environments in 2009. Seeds were removed from each storage environment every 28 days, seed moisture determined and germination initiated. Seed germination and pathogen incidence were measured every 7 days for 35 days. Sea oats seed stored in hermetically sealed jars at room temperature had highest average germination and seed germination was highest 21 days after germination. Seed moisture content, ranged from 6 to 16 %, and was negatively correlated with germination. To determine minimal sea oats size needed for restoration, vegetative plants, large seedlings, and small seedlings were evaluated from 2008 to 2010. Small seedlings had highest mortality however, seedling cost significantly less than vegetative plants. Increasing seedling densities could reduce production costs and result in acceptable survival rates accompanied with genetic diversity. To develop saturation tolerant lines, seedlings were evaluated for saturation tolerance in greenhouse, beach, and field environments from 2010 to 2012. We found that small seedlings flooded continuously to 14 cm depth in greenhouse for 3 months could predict sea oats survival in saturated beach conditions after 6 months. In 2007, 2009, 2010, and 2011 we determined sea oats seed yield in natural and artificial environments. Consistent seed yields were not obtained for either environment; however, sea oats seed were produced in artificial production nurseries. Finally, to determine seed pathogens colonizing sea oats seed, bacteria and fungi were isolated from sea oats seed harvested in 2011 and identified using both morphological and molecular techniques. The dominant bacterial genera colonizing sea oats seed were *Bacillus* and *Enterobacter*; while the dominant fungal genera were *Fusarium* and *Curvularia.* Through these investigations, the sea oats breeding program has identified a selection environment for saturation tolerance that allows for multiple selection cycles to occur each year, identified sea oats seed storage environments that prolong seed viability, identified planting designs that minimize restoration costs and also identified seed production environments to support development of genetically diverse sea oats populations for coastal restoration.

BREEDING FOR ROOT TRAITS IN *VACCINIUM* SPP.

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In *Vaccinium* spp., published information about root traits is scarce and the measurement of these traits can be challenging. Here we describe some of the methods we are employing to identify and breed for root traits in the *Vaccinium corymbosum* L. hybrids (southern highbush blueberry). *Vaccinium* spp. differ in their soil adaptation responses, including optimum organic matter content, soil pH, nutrient uptake capacity and drought tolerance. These differences suggest that there may be divergent root-level physiological or morphological events between these species. Our work has focused on the contrasting iron and nitrate uptake and root architecture between *Vaccinium corymbosum* L. hybrids and *Vaccinium arboreum* Marsh. (a wild species native to the Southeastern U.S.). Two approaches have been utilized to assess the breeding potential of *V. arboreum*. Our first approach consists of growing rooted cuttings of the *Vaccinium* genotypes of interest in a hydroponic growth system where we have full control of the pH and nutrient concentrations that plants are exposed to and can produce roots for enzymatic and proteomic work. Our second approach consists of growing seedling families in bench-top rhizotrons where we are able to control the soil characteristics that plants are exposed to and produce roots for morphological research. We have used gel-based and biochemical methods to visualize, quantify and compare the activity of the relevant enzymes in the nitrate and iron uptake pathways in hydroponically-grown *Vaccinium* roots. Meanwhile, we have used neutral staining, high-definition scanning and image analysis to describe the root architecture and morphology of rhizotron-grown *Vaccinium* roots. Using bromocresol purple as an indicator of pH change, we found that neither *V. corymbosum* hybrids nor *V. arboreum* are capable of acidifying their rhizosphere, a process commonly associated with soil iron mobilization. Additionally, we have learned that greater than 75% of all root length in *Vaccinium* spp. has diameters smaller than 0.9 mm. *V. corymbosum* hybrids, *V. arboreum* and interspecific crosses between the two exhibit similar average root diameter and root branching when grown under similar conditions. Conversely, genotypes with *V. arboreum* in their pedigree exhibit greater maximum root depth than genotypes that do not have *V. arboreum* in their pedigree. Moreover, genotypes with more recent *V. arboreum* introgressions (F_1 or BC generations) exhibit greater root dry weight, total root length and volume than other genotypes. Results from both lines of research have been useful in identifying root traits in *V. arboreum* that could broaden the soil adaptation of southern highbush blueberry cultivars.

DEVELOPMENT OF A RANDOM MATING POPULATION FOR RECURRENT SELECTION IN PEACH

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The genetic variation in commercial peach germplasm is low. Closely related species such as *Prunus dulcis* (almond), *P. kansuensis* (kansu peach) and *P. davidiana* (davids peach) represent valuable sources of genetic variation. These species have been used to a limited extent in rootstock breeding but have been largely ignored in scion breeding. The reluctance to use related species in peach scion breeding results from the high penalty in fruit quality of early generation crosses and the number of generations required to produce selections with commercial fruit size and quality. Large population sizes are needed to sample numerous recombination events and reduce linkage drag. The generation of large populations from controlled crosses is very laborious in peach due to the low seed content of fruit and the low fruit set of hand pollinations. In this work we present a breeding scheme that uses male sterility to enhance outcrossing in peach, facilitating the generation of large segregating populations for recurrent selection.

IDENTIFYING NEW GENES FOR *MELOIDOGYNE INCOGNITA* NEMATODE RESISTANCE IN CARROT

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Root knot nematodes (*Meloidogyne* spp.) are a major pest attacking carrots (*Daucus carota*) worldwide, causing galling and forking of the carrot root, and rendering them unacceptable for market. The current management practices of applying broad spectrum nematicides is effective, but is coming under more restrictive regulations, is costly for growers, and is considered damaging to the environment. Genetic resistance to nematodes could eliminate or strongly reduce the use of broad spectrum soil fumigants in carrot production. Resistance to *M. javanica* has already been discovered and mapped to the *Mj-1* locus on chromosome 8 in a 'Brasilia' cultivar. Genetic resistance to *M. incognita* has been observed but previously unmapped. Three diverse sources of resistance, from Syria (HM), Europe (SFF) and South America (B1091) have been identified. Two F_2 mapping populations were developed using these parents, (B1091 x HM1) and (SFF x HM2), as well as a segregating population developed by self-pollinating a single carrot from an open pollinated cultivar of HM (HM3). Plants of all three populations were grown individually in pots in a greenhouse, inoculated with *M. incognita*, and evaluated for their resistance to infection. DNA samples were collected and evaluated with AFLP fingerprinting, SSRs, and SNPs. QTL analysis using r/qtl revealed 5 QTL for B1091 x HM1, 6 for SFF x HM2, and 3 for HM3 (using a significance threshold of 0.1 on 1,000 permutations for each population individually). A consensus map was developed using JoinMap and the QTL regions were compared between populations. One QTL was present in all 3 populations, in the same region on chromosome 8 as *Mj-1*. There were also 2 other QTL regions shared between B1091 x HM1 and SFF x HM2. F_3 progeny from the F_2 mapping populations have been phenotyped and are being genotyped to confirm and refine mapping of the QTL regions.

LARGE, MULTI-YEAR FIELD TRIALS IDENTIFY NOVEL BARLEY MARKER-TRAIT ASSOCIATIONS

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Barley (*Hordeum vulgare* L.) represents one of the earliest domesticated crops of man and today is the fourth largest crop in terms of area and biomass harvested. The ever-changing climate of agricultural production areas has led to the need for development of new cultivars that are able to cope with this environmental variation. In conjunction with this, the time for cultivar development must be reduced so that new challenges to our agricultural production system can be met at a more rapid pace. In order to achieve these goals, the identification of novel, beneficial alleles in current advanced generation breeding material remains the most promising approach to meeting these challenges. In order to identify these novel alleles, a genome wide panel of 3,072 SNPs representing the current allelic variation of US spring barley breeding programs was genotyped on approximately 3,000 advanced generation lines as part of the US BarleyCAP. The trials were grown over a period of four years in a randomized complete block design replicated in rain fed and irrigated conditions in Bozeman, MT. 778 lines were evaluated each year with equal representation among the participants of the BarleyCAP. The data were used to conduct genome wide association studies in order to elucidate the alleles responsible for variation in six agronomic traits: yield, plant height, heading date, test weight, kernel plumpness, and grain protein content. The data were analyzed by year and environment to increase scope of the study. Mixed linear models were applied to the data using a Q + K approach in order to find single marker associations with the above phenotypic traits. Two programs, TASSEL and GAPIT were used with the implementation of FDR p-values to identify significant associations. The results of our study give a comprehensive overview of the salient regions of the barley genome impacting the agronomic performance of this crop. Although a large number of identified associations were previously documented in biparental populations, a majority of those found were novel. In addition, there exists a large amount of genetic diversity that can readily be employed using traditional breeding methods. These results were also used to construct a 384 SNP chip specific to the Montana production region for further analysis of our germplasm and for the implementation of genomic selection.

DISSECTING THE GENETIC BASIS OF PLANT DENSITY TOLERANCE

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Despite the growing demand for corn grain, the economic and ecological factors involved in the developing of new agricultural land make significant enlargement of agricultural land unlikely. This suggests that yield will need to increase by means of producing more grain in the same land area, which can be accomplished by increasing plant density while maintaining ‘per-plant’ yield. The initial survey phase of this project investigated hybrids derived from 12 diverse corn inbreds that recently lost their plant variety protection (exPVP). The hybrids were grown at six plant densities (19,000 to 54,000) and measured for 48 phenotypic traits. This survey identified six parental inbreds that were high yielders at high density and 20 traits that were associated with high plant density tolerance. Populations of recombinant inbred lines (RILs) were derived from crosses between these parental inbreds. These populations were connected due to common parentage. The RILs were testcrossed and evaluated for 20 traits at two locations in 2012. All RILs were genotyped using genotype-by-sequencing technology, which is a marker discovery genotyping system with the ability to produce an enormous output of genotypic data. This high density marker set can lend accuracy to analyses, but is accompanied by challenges due to high-dimensionality and multicollinearity. Specialized statistics will be needed for overcoming such challenges. By combining phenotypic and genotypic information, QTL will be mapped and their effects estimated. This will be the first step towards identifying candidate genes involved in plant density tolerance.

A SEMI-MICRO ASSAY AND GENETIC EVALUATION FOR LATE-MATURITY ALPHA-AMYLASE ACTIVITY IN SPRING WHEAT

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Alpha-amylase is one of the enzymes that occurs naturally in all wheat and is found mainly in the aleurone layer. This enzyme is activated during the germination or sprouting process and its activity can quickly break down starch and convert it into free sugar molecules, resulting in a loss of flour viscosity. Elevated levels of α-amylase are a concern in bread making because this enzyme breaks down starch granules in wheat flour when mixed with water causing the dough wet, sticky and hard to handle. Pre-harvest sprouting is generally associated with high levels of late-maturity α-amylase activity (LMAA), one of the four modes of α-amylase enzyme accumulation. Late-maturity α-amylase activity appears to be a genetic defect as it is limited to certain genotypes that are subjected to be influenced by environmental factors, and therefore, it is a big challenge to wheat breeders and understanding the genetic control of LMAA in spring wheat is highly desirable. A variety of analytical methods to measure specific α-amylase activity are available. Ceralpha method (American Association of Cereal Chemists Method 22-02.01) is one of the most commonly used assay procedures for the measurement of plant α-amylases and the assay kits are commercially available from Megazyme International (Ireland). This assay kit is designed for small scale cereal quality lab and it costs about $300 USD for 100 assays per kit ($3 USD/dataset). Therefore, an alternate procedure was imperative for high-throughput wheat breeding program to screen for LMAA in spring wheat germplasm.

A semi-micro assay procedure has been developed to quantify LMAA in spring wheat that can be used in high-throughput breeding program which allows screening at least 96 samples per day per person. This alternate assay procedure reduces the usage of reagents up to one third and thus enables to lower the cost down to $1 USD/data point. A collection of 18 spring wheat germplasm from USA, Canada, Australia, UK and CIMMYT were used to validate this semi-micro assay procedure and were evaluated for LMAA over 3 environments (site-year combinations) for genetic analysis. Another set of 14 germplasm from advanced yield trials of a spring wheat breeding program were also evaluated for LMAA over 9 environments to validate the results from genetic evaluation. The datasets will be analysed using a GGE (genotype and genotype-by-environment interaction) model with mixed linear model approach (minimum norm quadratic unbiased estimation) and principle components analysis will be presented using AMMI (additive main and multiplicative interaction) bi-plot on R platform.

EVALUATING TEOSINTE INTROGRESSIONS IN A B73 BACKGROUND FOR GRAY LEAF SPOT AND SOUTHERN LEAF BLIGHT RESISTANCE

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Gray Leaf Spot [(GLS), causal agent *Cercospora zeae-maydis*] and Southern Leaf Blight [(SLB), casual agent *Cochliobolus heterostrophus*] are two important maize diseases in the United States. Current control methods for SLB and GLS include using resistant cultivars, crop rotation, and conventional tillage. Geneticists and breeders are constantly mining for novel resistance alleles to these two diseases with many useful studies published identifying chromosome regions of interest. Teosinte (*Zea mays* ssp. *Parviglumis)* offers a good source of potential resistance alleles as it is a wild progenitor of maize and easily forms hybrids with current maize inbreds. The aims of this research are to identify alleles from teosinte conferring resistance to each disease. 775 teosinte near isogenic lines (NILs) from ten populations were developed by Sherry Flint-Garcia, USDA-ARS; Columbia, MO. The NILs were developed by crossing ten different teosinte accessions to the maize inbred B73 followed by four backcrosses to the recurrent parent, B73, and then selfed twice to form BC_4S_2. The BC_4S_2 populations were genotyped on a GoldenGate (Illumina) assay using 728 informative single nucleotide polymorphism (SNP) markers at USDA-ARS, Columbia, MO. SLB disease evaluations were conduction on eight of the ten NIL populations in 2009 and all ten NIL populations in 2010 in Clayton, NC. GLS disease evaluations were conduction on eight of the ten populations in 2009 and nine NIL populations in 2010 in Andrews, NC. Significant markers were identified from QTL analysis and individual NILs that carried introgressions from teosinte that encompassed these markers were selected within each family. For SLB, selections were made in bins 2.04, 3.04, 3.05, and 8.05, yielding 38 NIL lines. For GLS, selections were made in bins 2.04, 3.06, 4.07, 5.03, 8.06, and 9.03, yielding 41 NIL lines. $F_{2:3}$ families were developed by crossing each selected NIL to B73 followed by self pollinating the progeny twice. The $F_{2:3}$ families will be and have been evaluated for each respective disease. Further fine-mapping within each QTL region using the KASPar SNP genotyping assay will be conducted once the QTL and markers have been validated to associate with diseases resistance.

MODE OF REPRODUCTION AND REPRODUCTIVE EFFICIENCY IN BAHIAGRASS

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Bahiagrass (*Paspalum notatum* Flügge) is widely used for forage and low maintenance turf applications in Florida. Both diploid and tetraploid races are primarily established from seed. Diploid races produce ovules having only a single meiotic embryo sac (SES), and reproduce sexually. In contrast, tetraploid races reproduce by apomixis and are pseudogamous. Obligate apomictic plants produce ovules having a single or multiple aposporous embryo sacs (AES). However, facultative apomictic plants produce ovules having a SES together with one or more AES (AES+SES).The objective of this study was to determine the mode of reproduction of 17 bahiagrass genotypes and their reproductive efficiency (RE). Different ploidy levels constituted the selected genotypes: 1) diploids: the cultivar 'Pensacola' and two breeding lines MR2 and DDD2; 2) tetraploids: five wild genotypes (3Fpen5, 3Fpen8, 3Fpen9, Fldw 6-3 and Fldw 6-5); the cultivars 'Argentine' and 'Wilmington', the breeding line M8mar, and six mutant genotypes obtained after exposing Argentine (A4%EMS, AEMS03 and A60GY101) and Wilmington (W80GY02, WEMS12 and WXR02) to mutagenic treatments. Reproductive pathways were determined by cytoembryological analysis of ovules at anthesis. Plants were classified as sexual, facultative apomictic and obligate apomictic based on the embryo sacs produced. Mature seed heads were harvested in mid-summer, dried, threshed, and cleaned. Empty spikelets were removed and the percent seed set was calculated for each sample along with percent germination from three replicates. All diploid genotypes produced only SES and were classified as sexual. At the tetraploid level, four dwarf wild genotypes (3Fpen5, 3Fpen9, Fldw 6-3 and Fldw 6-5) were classified as facultative apomictic since all of them produced either AES, SES or both AES+SES in the same ovule. The proportion of AES varied between 57-80% among the dwarf plants. They also produced a high number of ovules bearing AES+SES. The production of aborted embryo sacs (AbES) among the dwarf lines varied between 5-20%. The cultivars Argentine and Wilmington, the breeding lines 3Fpen8 and M8mar, and all the mutant genotypes produced only AES. Among these obligate apomictic plants, the proportion of AbES varied greatly (5-80%), with two mutant plants WXR02 (45%) and A4%EMS (80%) showing the higher number of AbES. Seed set varied among all genotypes (11-54%). The higher seed set values corresponded to two highly apomictic plants, and the lower values to two facultative apomictic lines and WXR02. Interestingly, the seed set for A4%EMS was 20% (the same as the proportion of AES produced). Great variability was observed for germination (2-98%). The lowest germination corresponded to A4%EMS. All facultative apomictic plants had a germination value lower than 54%. Highly apomictic or highly sexual plants produced the highest germination percentages. Values of RE were also highly variable (0.4-33%). In general, facultative apomictic plants were less prolific than sexual or obligate apomicts, except for the genotypes A4%EMS (0.4%) and WXR02 (9%). Commercial cultivars ranged between 16-23% for RE. There are both sexual and obligate apomictic genotypes that showed a greater RE than commercial cultivars. In conclusion, sexual and highly apomictic genotypes had higher RE than facultative apomictic genotypes; although seed production may be compensated with more numerous seed heads produced per unit area. In addition, the mutant genotypes retained the apomictic characteristic, and in general produced viable seeds.

PHENOTYPIC AND GENETIC ANALYSIS OF THE FIRST BACKCROSS GENERATION BETWEEN SOUTHERN HIGHBUSH BLUEBERRY AND SPARKLEBERRY

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Wide crosses between sparkleberry (VA, *Vaccinium arboreum* Marsh.) and southern highbush blueberry (VC, *Vaccinium corymbosum* L. hybrids) were made with the primary objective to develop hybrids more suitable for machine harvest. Due to ploidy differences, crosses between VA and VC do not occur naturally, and colchicine doubling of the VA genome was necessary for direct hybridization between the two species. Two half-sib populations resulting from a backcross between two VC cultivars and a VC x VA hybrid (FL 08-467) were selected to evaluate vegetative and reproductive growth characteristics with the goal of developing a linkage and QTL map. Survival rate in population A (Southern Belle x FL 08-467) was 100% during the first year, 80% in the second, and 71% in the third; while population B (Abundance x FL 08-467) decreased dramatically, with only 19% of the original progeny surviving by year three. Pollen germination percentage, an indication of fertility, averaged 76% in population A compared to 28% for the hybrid FL 08-467. In comparison, a panel of cultivars of southern highbush blueberry averaged 86% pollen germination. Population B averaged 70% pollen germination, although plants from this population had a higher incidence of abnormal pollen tetrads. Phenotypic traits important for mechanical harvest, such as bush architecture, pedicel length, as well as typical fruit quality measurements showed significant variation in both populations. These initial evaluations resulted in the selection of Population A for further genetic analyses. At present, more than 70 microsatellite markers present on the reference VC linkage map have been used to genotype the entire population. Unique alleles from VA have been used to confirm introgression of the VA genome in a VC background and identify selfed individuals in the population. Linkage map development is ongoing, and will greatly aid in tracking of VA alleles for key machine harvest traits during backcross breeding efforts.

HETEROSIS AS EVIDENCE OF YIELD ALLELES FROM WILD SOYBEAN

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To guarantee future global food security and sustainable crop production, there is strong need for broadening the relatively narrow genetic base of the soybean (*Glycine max* [L. Merr.]) germplasm and looking for new resources to develop soybean cultivars. Wild soybean (*Glycine soja* [Sieb. and Zucc.]) may be an excellent source of new agronomic alleles for this purpose. Heterosis for yield is proposed as a signal for detecting yield alleles in wild soybean. The objectives of this study were to 1) examine heterosis in F_2 bulks derived from the cross of *G. max* parental cultivar N7103 and 19 breeding lines, which were developed from a cross between *G. max* cultivar N7103 and *G. soja* accession PI 366122, 2) assess whether heterosis could detect the presence of yield alleles derived from wild soybean, and 3) ascertain the possibility of predicting heterosis using genetic markers and agronomic traits. The individual F_2 bulked seed were yield tested in replicated bordered row plots at four locations in 2012. Two cross combinations showed significant ($P \leq 0.05$) percent midparent heterosis for yield (+9% and +10%). One cross showed significant heterosis over a theoretical maximum that could be expected based on dominance effects coming from only the *G. max* parent. Thus, these results suggest that yield alleles reside in wild soybean. The percent of *G. soja* alleles present in each breeding line, based on 558 single nucleotide polymorphic markers, positively and significantly associated ($r = 0.60$) with midparent heterosis. Genetic distance may be used as a guide for plant breeders when incorporating diverse germplasm into breeding programs and help predict future agronomic performance.

LINKAGE MAP AND QTL ANALYSIS OF NUTRITIONAL AND HORTICULTURAL TRAITS IN TETRAPLOID POTATOES

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Decreasing cost of high throughput next generation sequencing technologies have led to the published sequence of the potato genome and development of the Infinium 8303 potato array. This new array provides 8,303 high confidence SNPs that have been shown to cover 650 Mb of the 727Mb potato genome. This array has been shown to possess many dosage sensitive markers making it ideal for analyzing tetraploid potato populations. Utilizing this new technology we will build a linkage map and perform QTL analysis on two different populations. The first population is B2721, a cross between Atlantic x B1829-5. Atlantic is an Internal Heat Necrosis (IHN) susceptible clone and B1829-5 is an IHN resistant clone. IHN is non-pathogenic necrosis found in potatoes that causes extensive economic losses in the mid-Atlantic and southeastern United States. This population has been mapped and analyzed for QTL in the past, which will allow us to compare and contrast the data we will obtain using the new SNP platform. The second population will be one of four crosses we are currently developing to detect variation in anthocyanin pigments. An increasing interest in anthocyanins has been developing do to their health benefits, and anthocyanins found in potatoes have been reported to stand out as potential alternatives for synthetic food dyes. Pigment will be extracted using the procedures described by Giusti and Wrolstad. Monomeric anthocyanin content will be determined using the pH-differential method. Linkage map and QTL analysis for both populations will be performed using TetraploidMap software.

STRAWBERRY FLAVOR: DIVERSE CHEMICAL COMPOSITIONS, A SEASONAL INFLUENCE, AND THEIR EFFECT ON SENSORY PERCEPTION

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Fresh strawberries are valued for their characteristic red color, juicy texture, distinct aroma, and sweet fruity flavor. In this study, genetic and environmentally induced variation is exploited to generate a diversity of strawberry fruit, which are simultaneously assayed for: biochemical inventories of volatile compounds, sugars, and organic acids; physical measures of titratable acidity, soluble solids content, and firmness; and consumer hedonic and sensory responses. Analyses identify seasonal effects and fruit attributes influencing hedonics and sensory perception of strawberry fruit using a psychophysical approach. Progression of harvest season exerts a negative influence on soluble solids content, which is attributed to decreasing sucrose, leading to less volatile content. These effects are perceivable as sweetness intensity, flavor intensity, and texture liking have significant influence on overall liking through variations in sugars, specific volatiles, and firmness. Other volatiles potentially contribute to perceived sweetness of fruit independent of sugar concentration, helping to better define distinct, perceptually impactful compounds from the larger mixture. The importance of sucrose to sweetness intensity is evident, and the correlation of total volatiles to sucrose highlights the dependence of secondary metabolism to primary metabolism. Overall liking is most greatly influenced by sweetness and strawberry flavor intensity, which is undermined by environmental pressures that reduce sucrose and total volatile content. This is potentially countered with greater concentrations of individual volatiles contributing to flavor or sweetness, *i.e.* consumer defined traits for future breeding. This approach garners insights into fruit metabolomics, flavor chemistry, and a paradigm for enhancing liking of natural or processed products.

GENETIC PARAMETERS AND CORRELATION IN EARLY MEASUREMENT CYCLES IN RUBBER TREES

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To improve rubber plantation productivity, breeding programs need to exploit their populations genetically to obtain superior clones. The quantitative genetic information helps to determine the best selection strategy by overcoming problems and difficulties in superior genotype selection and by widening knowledge of rubber tree genetics and reproductive performance. The objectives of the present study is to estimate, in early measurement cycles, genetic parameters and genetic and phenotypic correlations for the variables rubber yield (RY), annual girth growth (AGG), number of latex vessel rings (NLR) and virgin bark thickness (BT). In this study 22 open pollination progenies, obtained from 22 parental clones selected phenotypically in Asian (*Hevea brasiliensis*) clone population from Malaysia introduced at Agronomic Institute of Campinas, Brazil in 1952, were assessed. The progeny trials were installed in three different rubber cropping regions in the state of Sao Paulo, Brazil (Jau, Pindorama and Votuporanga). The progeny trials were set out as a randomized complete block design with six replications and plots formed of a row of 10 plant, spaced at 3 m x 3 m. Three early measurement cycles were carried out for the traits rubber yield and annual girth growth. To bark thickness and number of latex vessel rings a single measurement was performed during the first measurement of rubber yield and annual girth growth. The variance components were estimated using REML (Restricted Maximum Likelihood) and total genetic individual hereditability in each location was calculated together with plot additive hereditability, progeny mean based hereditability (assuming complete survival), additive genetic and phenotype correlations and genetic gains based on a 20% selection intensity. Statistical significance was evaluated using an approximate F-test. The estimates of genetic correlation for bark thickness among its three early measurement cycles in the location of Jau (r_g = 0.53*, 0.46* and 0.52*) were similar to the ones obtained for Pindorama (r_g = 0.69**, 0.62** and 0.55**) and for Votuporanga (in the first and second measurement, r_g = 0.71* and 0.52*). In the Jau location, the third yield measurement correlated genetically with the three AGG (r_g = 0.57**, 0.61**, 0.43*). In Pindorama, the first AGG measurement was correlated genotypically with the three yield measurements (r_g = 0.55**, 0.56** and 0.63**) along with the number of latex vessel rings (r_g = 0.60*, 0.54**, 0.45*). The progeny mean based joint hereditability, presented mean values greater than individual plants and within progeny plants of 0.85, 0.29 and 0.24, respectively. The genetic gain in the combined analysis for the three locations was 19.01 The AGG and BT are variables that are positive genetically correlated. They remained correlated in the different locations through the three measurement cycles. Simultaneous selection for AGG and BT can be used to raise rubber tree productivity. The progeny mean based hereditability for the RY trait and AGG were superior to individual and within progeny plants. This can be an adequate strategy to increase the genetic gain in rubber. The early measurement cycles were efficient to detect significant genetic variability and to select the best genotypes.

SELECTION PROGRESS FOR REDUCED IRIS YELLOW SPOT SYMPTOM EXPRESSION IN ONION

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Onion thrips and *Iris yellow spot virus* (IYSV) are two major pests of onions worldwide for which host plant resistance is absent. In the summer of 2009, plants with fewer Iris yellow spot (IYS) disease symptoms were selected from plant introduction accessions and the resulting progeny were evaluated in the summer of 2012. These selected lines were compared with their respective original population and 'Rumba' to see if any progress had been made for reduced thrips number and IYS symptom expression. In order to ensure that every plant in the field screening had the potential to be infected with IYSV, the experiment was design with the spread of thrips and IYSV in mind. In Oct. 2011, border rows were planted with thrips-containing onion bulbs selected from the previous year's IYSV study. Spreader rows were sown at the same time with a known IYS susceptible cultivar. Plants of the test entries were transplanted in Mar. 2012. As bulbs of the border rows flowered, thrips and IYSV moved to the plants of the spreader rows. When those plants matured, thrips moved to the test plants and moved the virus from the periphery of the field to the interior. The number of thrips per plant was determined from 10 plants/plot at 9, 12, and 15 weeks after transplanting (WAT). An increase in thrips number was observed with every date. Since thrips exhibit feeding differences based upon leaf color and epicuticular wax amounts, plants were rated for leaf color and waxiness at 9 WAT. At 12, 14, 16, and 18 WAT, plants were rated on a scale of 0 to 4 for disease severity, where 0 indicated no symptoms and 4 represented more than 50% of leaf tissue was necrotic. Consistent increase in severity was also observed with every rating date. NMSU 10-575-1, which possessed waxy, bluish green leaves, exhibited significantly fewer thrips at 15 weeks when compared to its original population. NMSU 10-577-1 and NMSU 10-582-1 did not exhibit any reduction in thrips number, but showed significant less IYS severity when compared to their original populations. NMSU 10-575-1 and NMSU 10-577-1 exhibited less severe symptoms when compared to 'Rumba'. The results from this evaluation suggest that the progress can be made towards the development of cultivars with reduced IYS symptoms.

DIALLEL ANALYSIS OF TRAITS ASSOCIATED WITH BIOMASS YIELD IN SWITCHGRASS

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Switchgrass (*Panicum virgatum* L.) is a perennial, warm season grass, native to North America. It is important as a forage crop and, more recently, has received considerable attention as a potential biofuel crop. An ideal biofuel switchgrass plant can be defined as a plant with high biomass yield and high ethanol yield; however, the morphological traits associated with these two types of yield have not yet been fully examined. The objectives of this research are to determine: i) general and specific combining abilities (GCA and SCA) among eight switchgrass parents for biomass yield and component traits, ii) correlations between biomass yield and component traits, and iii.) heritability and heterosis of the above traits. Eight parents with divergent phenotypic characteristics were crossed in a complete diallel design. Parents included two Kanlow selections (K2, K3), five Alamo selections (A1, A10, AS, T1, T4), and Miami (M). The resulting F_1 full-sib progeny were planted at two locations, the East TN Research and Education Center in Knoxville, TN and the Plateau Research and Education Center in Crossville, TN. Seedlings were started in a greenhouse, divided into two clonal propagules, one per location, and planted in single plant plots on 1 m centers in a randomized complete block design with four blocks. Each location contained twenty replications of each cross and eight clonal replications of each parent. Plants were evaluated in the fall for rust, height, tiller number, and biomass yield. GCA was significant for all traits except biomass yield while SCA was significant for all traits. Results for GCA indicated significant best linear unbiased predictor (BLUP) values for lower rust (A1, M), higher tiller number (A10), and higher height (A1) and for higher rust (K3), lower tiller number (K2), and lower height (AS). Within GCA, only A1 was significant for more than one trait, with significantly lower rust and higher height. Significant SCA BLUPs were observed for higher biomass yield (A10-AS, A10-M, T1-M), lower rust (K3-A10, M-T1, T1-M), and higher tiller number (T1-M), and for lower yield (K3-M), higher rust (AS-A1, AS-M, K3-M), and lower tiller number (AS-T1, K3-M). Within SCA, T1-M and K3-M were significant for three out of four traits, with T1-M exhibiting significantly higher yield and tiller number and significantly lower rust and K3-M exhibiting significantly lower yield and tiller number and significantly higher rust. Correlation results showed a strong positive correlation between yield and tiller number (r=0.85), a moderate positive correlation between yield and height (r=0.43), and a weak negative correlation between yield and rust (r=-0.22). Yield, tiller number, and height exhibited similar genetic parameters, with additive variation accounting for 7%-10% of total variation, dominance variation accounting for 3%-5% of total variation, and narrow-sense heritability estimates between 0.07 and 0.10. Rust was an exception with additive variation accounting for 41% of total variation, dominance variation accounting for 7% of total variation, and narrow-sense heritability of 0.41. Out of 56 crosses, significant mid-parent heterosis for yield was observed in 27 crosses, including 10 Alamo-Alamo, 12 Alamo-Kanlow, and five Alamo-Miami. High-parent heterosis for yield was observed in eight crosses, including five Alamo-Alamo, two Alamo-Miami, and one Kanlow-Miami. Future work will include evaluations of spring traits, ethanol yield, and second year evaluations for all traits. Results obtained from this study should provide breeders with information necessary to make more effective and efficient crosses and selections when breeding biofuels switchgrass.

INTELLECTUAL PROPERTY MANAGEMENT FOR AGRI-FOOD INNOVATION

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Plant breeding, like most areas of agricultural research and development (R&D), is increasingly exposed to demands to make knowledge accessible and available for the purpose of commercialization. Knowledge Translation and Transfer (KTT), especially as practiced within the Ontario Ministry of Agriculture and Food (OMAF)-University of Guelph Partnership relies to a great extent on access to information in order to transfer and generate more knowledge. In today's world, significant creative and economic potential is believed to lie in making information produced by public R&D institutions more accessible to a wide range of stakeholders. It is also widely recognized that this implicates improved intellectual property (IP) management in agricultural R&D, including clear and strategic decision-making on a range of copyright-related issues, has also led to the development of new open innovation strategies. The University of Guelph Ridgetown Campus produces reports on a variety of topics for local agri-food industries funded by the OMAF alongside producers groups, seed companies and other commercial interests. The example of the Ontario Vegetable Crop Research Electronic Repository is a pilot collection designed to support the ongoing dialogue with evidence based practice. This collection is a systematic review of all available written or electronic reports that study Ontario vegetable crops which are licensed for public use. We established a model called the OPEN scorecard for policy development to support IP management by public R&D institutions. The project is designed to deepen the relationship by determining policy for licensing research reports and placing them in the public domain for online access. It also seeks to assist KTT managers with awareness raising and decision making by examining information access and IP management in relation to their KTT activities in the OMAF-U of G Partnership. The case study addresses how to institutionalize something as common as information dissemination and to identify decisions made as material is collected and digitized, and possibly, moved into open access for agricultural R&D stakeholders.

DETERMINING THE RELATIONSHIP BETWEEN SEED CALCIUM UPTAKE, FIELD EMERGENCE, AND DISEASE RESISTANCE IN PEANUT

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Late leaf spot is a fungal disease of peanut that occurs world-wide, and can result in severe yield loss. Highly resistant cultivars have been developed; however problems with emergence during seed production lead to the removal of these cultivars from production. While the exact causes of this poor emergence are not fully understood, poor calcium uptake by the seed of resistant cultivars is believed to be an important factor. Recent research showed that the cultivars have lower average seed calcium concentration than susceptible cultivars when grown on soils with adequate calcium. In addition, low seed calcium has previously been correlated with poor emergence. This suggests that seed of resistant cultivars do not absorb sufficient calcium for emergence. The relationship between leaf spot resistance, calcium uptake, and emergence are not well understood. In order to study this relationship the leaf spot resistance, seed calcium concentration, and field emergence of a group of about 175 breeding lines was evaluated in Marianna, FL from 2009 to 2012. These lines were derived from crosses between York (a resistant cultivar with poor emergence) and several unrelated, susceptible genotypes. Phenotypic and genotypic correlations between traits were determined. Field emergence showed genetic and phenotypic correlation with leaf spot resistance and seed calcium (ρ~0.6-4.0). Also, seed calcium and leaf spot resistance were correlated (ρ~0.4-1.2). These correlations indicate that there is a genetic relationship between leaf spot resistance, seed calcium concentration, and field emergence, which must be considered when breeding for leaf spot resistance. In addition, lines were identified that had good resistance ratings, high seed calcium concentrations, and good field emergence, which indicates the potential for developing commercially viable cultivars with resistance to late leaf spot that do not have the problems with emergence that have hindered the success of previous resistant cultivars

TOWARDS IDENTIFICATION OF SSR MARKERS LINKED TO TSWV RESISTANCE IN PEANUT (*ARACHIS HYPOGAEA* L.)

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Spotted wilt caused by tomato spotted wilt virus (TSWV) is one of the major diseases affecting peanut (*Arachis hypogaea* L.) production in the Southeastern USA. Occurrence, severity, and symptoms of spotted wilt disease are highly variable from season to season making it difficult to efficiently evaluate breeding populations for resistant line selection. Molecular markers linked to spotted wilt resistance could overcome this problem and allow selection of resistant lines regardless of seasonal conditions. The objective of this study is to identify the simple sequence repeat (SSR) markers linked to TSWV resistance in peanut through 1) evaluating the TSWV reaction of the F_2 and $F_{2:3}$ populations; 2) screening polymorphic SSR markers between the two parental lines of the F_2 population, and mapping the TSWV resistance loci using SSR genotyping of the F_2 population.

A total of 199 F_2 progeny derived from the cross between Florida-EP^{TM}'113', a TSWV resistant variety and Georgia Valencia, a highly susceptible cultivar were evaluated by ELISA (enzyme-linked immunosorbent assay) for the presence of TSWV. The $F_{2:3}$ population were further phenotyped using a visual 1 to 10 scaling method on both canopy and seed coat and ELISA Immunostrip. The ELISA and Immunostrip results confirmed that most of the symptomatic plants were infected by TSWV with some exceptions, which didn't display visual symptoms but exhibited positive ELISA reactions. This result indicates that ELISA and Immunostrip may be a better method for phenotyping TSWV infection in peanut. For genotyping, a total of 2000 SSR markers with high polymorphic information content or mapped on peanut linkage groups were screened against the two parental lines of the F_2 segregating population. Totally, 186 polymorphic SSR markers were screened, which will be used to map the TSWV resistance conferred by Florida-EP^{TM}'113' and to identify the flanking markers linked to spotted wilt resistance.

DEVELOPMENT OF MOLECULAR MARKERS USING NEXT-GENERATION SEQUENCING OF RNA IN *STEVIA REBAUDIANA*

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Stevia rebaudiana (stevia), a member of the Asteraceae family, is a small perennial shrub that has been used for centuries as a bio-sweetener and for its medicinal properties. Stevia accumulates high concentrations of diterpene steviol glycosides which contribute to its high-potency sweetening with no calorific value. These natural high-potency sweeteners are of great interest in stevia production and breeding. Until now, breeding efforts have focused on phenotypic selection for specific glycoside concentrations which can be heavily influenced by the environment. Most importantly, these measurements, which are made on adult plants, are expensive and tedious to perform using highly specialized equipment. The development of molecular markers linked to important agronomic traits will facilitate early selection for these critical traits. Microsatellite repeats in expressed genes are useful for the development of molecular markers because of their abundance, level of polymorphism and functionality. In this study we used next-generation sequencing of RNA to develop a reference transcriptome. This *de novo* assembly was then mined for simple-sequence repeat (SSR) markers. Using the Illumina HiSeq 2000 sequencing system, a total of 194,965,048 paired-end reads of 100bp length were obtained from a bulked RNA sample of diverse tissue types. After quality trimming and removal of low complexity reads, 171,503,922 were used to construct a reference transcriptome using Velvet and Oases assembly methods. A single isoform of each locus was selected using the Oases-to-CSV script and the remaining 48,238 transcripts were used to identify SSRs using the MISA software package. A total of 5,876 SSR were identified in 4,879 transcripts. Approximately 10% of transcripts have at least 1 SSR with 1.6% of SSR found in compound formation. Primers were designed for 4,193 SSR. *In silico* PCR was performed on these primers using the ipcress module of Exonerate to remove primer pairs that may produce multiple amplicons. The remaining 3,396 SSR primers were then compared to 2 other *de novo* assemblies to identify those present in all three assemblies and considered the most robust (1,063). These markers are currently being verified in a segregating bi-parental breeding population and will be used for QTL analysis of agronomic traits of interest.

BREEDING FOR DOWNY MILDEW RESISTANCE IN CUCUMBER

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Cucumber (*Cucumis sativus* L.) is the fourth most widely grown vegetable in the world behind tomato, cabbage, and onion. It is eaten fresh, pickled, or fried and has various uses in the cosmetics industry. Currently, the oomycete pathogen *Pseudoperonospora cubensis* (downy mildew) represents a significant challenge to production throughout the world. Downy mildew infects over 50 species of cucurbits, with important hosts including melon, watermelon, and squash. For nearly half a century in the United States, planting resistant cultivars developed in the mid-20th century has controlled epidemics of downy mildew in cucumber. However, in 2004 the downy mildew pathogen population underwent a significant change and the single-gene resistance deployed in most commercial cultivars no longer provides high levels of resistance. Without genetic sources of resistance, frequent and heavy fungicide applications are now required for high yield and quality under disease pressure. New sources of resistance were identified in a multiyear germplasm screening and retest conducted at North Carolina State University by Criswell (2008) and Call (2010). Currently, multiple studies are being conducted in order to both understand the genetics and mechanism of the new form of resistance as well as develop material with high resistance and good horticultural traits. Preliminary results suggest the new source of resistance is quantitative and under the control of at least three recessive genes. Additional results indicate that resistance is more strongly expressed in adult plants, though further testing is needed. Studies being conducted include: inheritance pattern, adult versus juvenile stage resistance, recurrent selection, backcross development, and an $F_{2:3}$ and recombinant inbred line quantitative trait loci identification program.

BREEDING FOR RESISTANCE TO POTYVIRUSES IN TROPICAL PUMPKIN

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Zucchini yellow mosaic virus (ZYMV) and *Papaya ringspot virus* (PRSV) are *Potyvirus* that cause serious yield loss in cucurbits around the world. In Puerto Rico they are the most important viruses affecting production of tropical pumpkin (*Cucurbita moschata*). One objective in our breeding program is to produce tropical pumpkin lines with horticultural attributes similar to the OP cultivars currently used on the island, but with improved potyvirus resistance. We used the African landrace 'Nigerian Local' as a source of genes for resistance to both viruses in a backcrossing program. Susceptible Puerto Rican OP cultivars 'Soler', 'Taína Dorada' and 'Verde Luz' were used as recurrent parents. Plants were mechanically inoculated with ZYMV or PRSV and susceptible plants culled in the greenhouse and/or field. Decisions to cull were made on the basis of both disease severity and ELISA tests. BC:F_2 populations were selected for either ZYMV or PRSV resistance and for good horticultural traits (large fruit size, thick flesh, orange flesh color). BC:F_3 or F_4 lines were evaluated in the field in Isabela or Mayaguez, Puerto Rico for virus severity and horticultural traits (the traits mentioned above plus percent dry matter and °Brix). One or two generations of backcrossing resulted in BC:F_3 or F_4 lines with significantly more resistance to ZYMV or PRSV compared to the susceptible parents. However, even the best lines showed mild virus symptoms and/or had high ELISA readings, unlike resistant Nigerian Local. Both symptom severity and ELISA tests should be used to evaluate for resistance since asymptomatic plants can have high virus titer. No lines combined all the desired horticultural attributes along with ZYMV or PRSV resistance, but some lines may be valuable for release as improved germplasm for further breeding. In tropical pumpkin, evaluation of individual plants requires a minimum area of 7 m^2, thus greatly limiting the number of plants that can be screened given limited field space and resources. Small population sizes likely contributed to the difficulty in combining potyvirus resistance with good horticultural traits.

DEREGULATING CYSTEINE AND METHIONINE BIOSYNTHESIS IN MAIZE

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It has previously been shown that constitutive expression of bacterial sulfonucleotide reductases in maize chloroplasts resulted in significant increases in the rate of sulfur assimilation and cysteine/methionine accumulation in kernels, but with growth inhibition resulting from the accumulation of toxic intermediates. The evidence suggests that cell-specific gene expression and removal of metabolic intermediates through adjustment of other metabolic steps might alleviate growth inhibition and further enhance methionine accumulation. Towards this goal we examined the effect of expressing *Pseudomonas aeruginosa* 5'-adenylylsulfate reductase or *Escherichia coli* 3'-phospho-5'-adenylylsulfate reductase (EcPAPR) in combination with *Arabidopsis* serine acetyltransferase (AtSAT1) in either bundle sheath under control of the RbcS promoter, mesophyll cells under control of the PepC promoter, or general expression under control of the Ubi promoter. Transgenic lines of maize Hi-II B x A were isolated for all constructs with a range of expression levels of each transgene. In general, it was found that bundle sheath expression of PaAPR alone or in combination with AtSAT1 does not alleviate the toxic effect of deregulating sulfur assimilation. However, bundle sheath expression of EcPAPR and AtSAT1 results in the deregulation of sulfur assimilation with reduced impact on plant growth. By generating plants that overexpress EcPAPR or PaAPR in a tissue-specific or constitutive manner, we are also trying to determine which of these combinations is able to decouple increased sulfur assimilation from phenotypic aberrations. Currently, cell-specific expression of EcPAPR in the mesophyll or bundle sheath cells shows plant phenotypes that range from normal to severe (e.g., presence of white sectors). Analysis of protein expression levels and localization are in progress. Additional results concern the effects of transgenic expression of sulfur assimilation enzymes in mesophyll cells and general expression in all cell types.