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1

OCCURRENCE OF COPPER AND STREPTOMYCIN RESISTANT XANTHOMONAS SPP. IN TOMATO IN NORTH CAROLINA

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Bacterial spot of tomato is a serious and complex disease caused by at least four species of *Xanthomonas- X. euvesicatoria*, *X. vesicatoria*, *X. perforans*, and *X. gardneri* including five physiological races (T1-T5). The disease affects all-above ground parts including leaves, stems and fruits and has a potential to cause up to 66% yield loss. The control of this disease is based on the chemicals such as copper, antibiotics (streptomycin), plant activators and cultural practices. However, the failure of these chemicals and antibiotics to control bacterial spot of tomato has been reported from different parts in North Carolina. Therefore, we were interested to assess the bacterial spot strains of North Carolina for sensitivity to copper and streptomycin. A total of 183 bacterial isolates were collected from symptomatic leaves of randomly sampled infected plants from 10 different fields in 5 different counties (Henderson, Madison, Haywood, Buncombe, Jackson, and Swain) covering the tomato growing regions of the Mountains of North Carolina. The bacterial isolates were collected from different varieties- Plum Regal, BHN784, Red Defender, Mountain Majesty, Biltmore, and various grafted genotypes. The streaked bacterial suspensions were cultured on Sucrose-Peptone Agar (SPA) media containing 100, 200, and 300 ppm of $CuSO_4$, and 20, 50, and 100 ppm of streptomycin. Strains capable to grow on the SPA media containing 200 ppm of CuSO4 and 100 ppm of streptomycin were considered as copper and streptomycin resistant, respectively. Out of 183 bacterial isolates, 172 were resistant to copper and 82 were resistant to streptomycin. Almost all bacterial isolates collected from these counties were resistant to copper, except the bacteria obtained from 'Mountain Majesty' cultivar from Haywood County. The bacteria collected from Jackson, Swain, and Buncombe counties were mostly susceptible to streptomycin, whereas, bacterial isolates from Henderson and Haywood showed variable reactions depending on the cultivars from which they were isolated, suggesting a cultivar and location interaction. The bacterial isolates collected from cultivars in Madison were mostly resistant to streptomycin. However, all fields sampled harbored bacteria that were copper or streptomycin resistant. These data indicate widespread existence of copper and streptomycin resistant strains of the bacterial spot pathogen in North Carolina and use of these chemical and antibiotic would be ineffective to control bacterial spot of tomato. Therefore, alternative strategies of controlling bacterial spot of tomato are desirable in North Carolina. These data will be complemented by race-typing and genetic diversity analysis and this information may be helpful for developing effective disease management strategies and breeding new bacterial spot resistant tomato cultivars.

2

DEVELOPMENT OF GENOMIC SELECTION MODELS FOR IMPROVING KEY MILLING AND NUTRITIONAL QUALITY TRAITS OF OATS

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Increasing the milling and nutritional quality of oat cultivars is important to the milling industry and to the consumers. To improve breeding efficiency, we developed genomic selection models for several key milling and nutritional quality traits. In 2015, a total of 227 oat genotypes were grown at four locations in South Dakota. Three traits were evaluated: groat percent, and beta glucan and fat content. Genotyping data were collected using genotyping-by-sequencing (Public Oat Genotyping Initiative, Jean-Luc Jannink). Genomic prediction models were developed using the R package rrBLUP. BLUP values were estimated using four different linear mixed models with or without accounting for field variations associated with row or column. Prediction accuracy ranged from 47 to 56 %, 35 to 41%, and 42 to 45% for groat percent, beta glucan content, and fat content, respectively, depending on the model used to calculate BLUPs. Prediction accuracy was increased for groat percent when heading date was used as covariate but not for the other two traits.

3

GENETIC MECHANISM THAT CONTROLS STAY GREEN IN AGS2000/NC06-19896 DOUBLED HAPLOID POPULATION UNDER HIGH TEMPERATURE STRESS CONDITIONS

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Damage caused by high temperature is a major limitation for wheat production in most of the wheat growing areas including USA. The annual occurrence of moderate heat stress, accompanied by periodic extreme heat stress events, prevents wheat from reaching its full potential yield in the USA. One of the major effects of high temperature is the alteration of various photosynthetic attributes which enhance accelerated senescence. The green area displayed by a crop is a good indicator of its photosynthetic capacity, while chlorophyll retention or 'stay-green' is regarded as one of the key indicator of heat tolerance as they show correlation with growth. The main goal of this study is to determine genetic mechanism for stay green in a doubled haploid population derived from AGS2000/NC06-19896, where NC06-19896 is the parent that is contributing stay green traits. The population was characterized for different stay green traits, normalized difference vegetation index (NDVI) and Chlorophyll fluorescence (Fv/Fm; an indicator of thylakoid membrane damage), under high temperature stress conditions in Plant Science Research and Education Unit, Citra, FL. NDVI data were collected throughout the developmental cycle, while Fv/Fm data were collected at flowering and grain filling stages. Our preliminary data analysis showed significant difference for NDVI and chlorophyll florescence among sister lines. Our major goal is to identify loci associated with stay green traits in this population. The final results will help us to identify genotypes with stay-green character which will be a valuable source for future genetic improvement for heat tolerance.

4

COOKING TIME AND SENSORY EVALUATION OF A DRY BEAN DIVERSITY PANEL

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Cooking time and flavor are two of the most important traits considered when selecting dry beans for production and consumption. Dry beans are a nutrient-rich food that often require long cooking times, particularly when cooked without prior soaking. They also display a range of sensory characteristics, with most consumers preferring beans that are sweet and soft when fully cooked. Consumer demand for faster cooking, good tasting beans and the increased interest in beans for processing to make gluten-free and other products necessitates studies assessing the diversity of flavor and texture attributes found in beans, which would allow suitable beans to be selected for specific end products. In this study, a panel of 387 dry edible bean (*Phaseolus v**ulgaris* L.) genotypes were assessed for cooking time, flavor characteristics, and texture. A Mattson Cooker was used to determine cooking time, defined as the time required for 80% of the seeds to be completely pierced by an 85g rod with a 2-mm pin. Cooking times ranged from approximately 15 to 90 minutes. A pre-screening panel determined flavor profiles of each genotype by specifying total flavor intensity, as well as beany, raw or cooked, vegetative, earthy, starchy, sweet, and bitter flavors on 5-point hedonic scales. The panel also rated seed coat perceptibility and bean texture on 5-point hedonic scales. A texture analysis using a 2mm cylindrical probe was used to determine work to bite for each genotype and to support the texture and seed coat perceptibility data obtained from the panel. The genome-wide association study (GWAS) of cooking time, flavor profiles, and texture will identify genomic regions influencing these traits. This information can enable breeders to target faster cooking times and specific flavor and texture profiles in their programs, as well as allow agronomic traits of dry bean varieties to be improved without sacrificing desirable cooking time and flavor. This study will also identify dry beans potentially suitable for new uses as ingredients.

5

POPULATION STRUCTURE AND GENETIC DIVERSITY ANALYSIS OF GERMPLASM FROM THE WINTER WHEAT EASTERN EUROPEAN REGIONAL YIELD TRIAL (WWEERYT)

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Characterization of population structure and genetic relatedness within wheat (*Triticum aestivum* L.) germplasm collections is critical for association mapping (AM) and training population development for genomic selection (GS). Cooperative regional or international nurseries are well suited for AM and GS studies due to the availability of multi-environment datasets that are often produced. In this study we analyzed population structure and genetic diversity of 283 genotypes from seven years of the Winter Wheat Eastern European Regional Yield Trial (WWEERYT). The collection was genotyped with 75,254 single nucleotide polymorphism (SNP) markers obtained via genotyping-by-sequencing (GBS). A subset of 548 highly polymorphic SNP markers was used for all analyses. Population structure was composed of seven subpopulations when using a correlated allele frequencies model (Model 1) and two subpopulations when using an independent allele frequencies model (Model 2) in STRUCTURE. The genotype's breeding program of origin, based on four major geographic regions, was closely related to, but not a perfect indicator of, subpopulation assignment. Under Model 1, genotypes of central and eastern European (CEE) origin were assigned to six of the seven populations indicating extensive diversity while genotypes from the United States (USA) were assigned to only two of the seven populations. The program STRUCTURE allowed for the inclusion of admixed individuals whose genetic composition is drawn from more than one of the subpopulations. With the potential for genotypes to have partial membership in up to seven subpopulations under Model 1, many individuals did not have the 50% membership threshold to be assigned to a single population and thus were classified as Mixed. Under Model 1, Mixed individuals (n=109) were composed of genotypes from all four regions with 45.0% of genotypes from CEE, 21.1% from central and western Asia (CWA), 17.4% from Turkey-CIMMYT-ICARDA (TCI), and 16.5% from USA. Under Model 1, the lowest F_{ST} value of 0.20 was between a population of predominately TCI genotypes and a population of predominately USA genotypes indicating a close relationship between material from these two regions. Under Model 2, population A was composed of genotypes from all four geographic regions with 72.9% from CEE and 20.0% from CWA. Under Model 2, population B was also composed of genotypes from all four regions with 42.2% from USA and 25.0% from TCI. Principal component analysis (PCA) was used to visualize the relationships among the 283 WWEERYT genotypes. Using PCA, separation of genotypes via principal component one (PC1) closely agreed with subpopulation assignment from Model 2 as well as breeding program origin. The subpopulation assignment based on Model 1 was not as readily inferred based on PC1 or PC2 and was due to the overlap of several subpopulations determined in STRUCTURE. The characterization of population structure and genetic diversity within these WWEERYT nurseries will help in the utilization and exchange of germplasm across important winter wheat breeding regions.

6

EVALUATING QUANTITATIVE TRAIT LOCI (QTL) SOURCES OF RESISTANCE IN TOMATO TO MULTIPLE *XANTHOMONAS SPP*.

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Bacterial Spot of tomato is a foliar disease caused by four species of *Xanthomonas*. Wild tomato species *S. pimpinellifolium* and *S. lycopersicum var. cerasiforme* provide quantitative trait loci (QTL) for partial resistance when introgressed into cultivated tomato. Three independent sources of resistance have been identified with QTL mapping to the same genetic region on chromosome 11. Genome resequencing and genetic analysis suggests that these loci are not alleles. To determine which QTL provides the greatest resistance to multiple species, we developed near isogenic lines using marker-assisted backcrossing. QTL-11a (H7998; *S. lycopersicum*), QTL-11b (PI11490; *S.lycopersicum var. cerasiforme*) and QTL-11c (LA2533; *S. pimpinellifolium*) were introduced into a uniform genetic background (OH88119). Genotypic selection for QTL11 and background genome selection were applied to 192 progeny of each backcross population. Heterozygous progeny containing approximately 95% of the recurrent parent were self-pollinated and homozygous families paired for resistant and susceptible QTL were assessed in field trails inoculated with the major species causing bacterial spot. Comparisons are based on a model to evaluate QTL11 allelic contributions. Results of this evaluation will provide a better understanding of quantitative resistance to multiple species of *Xanthomonas*.

7

ASSESSMENT OF GENOME CHANGES IN WHEAT (*Triticum aestivum* L.) POPULATIONS SUBJECTED TO GENOMIC SELECTION

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Plant breeding implies the incorporation of desirable traits into a single cultivar, changing allele frequency along the selection process and reducing genetic diversity. Plant breeders take advantage of the rapid advance of sequencing technologies such as genotyping-by-sequencing (GBS) to assisting in the screening process, as well as to selecting and accumulating favorable alleles. Genomic selection, which estimates genomic breeding values is the most recent application of genome-wide molecuar marker information. The same molecular marker information can be used to perform population genetics studies which are crucial for breeding process. Such studies are key to assess the within-program genetic diversity and the effects of selection methods on the genome. This assessments are useful to decide wheter new genetic diversity is needed, mainly because alleles selected are eventually fixed and genetic gain can reach a plateau. In this study, a soft red winter wheat training population (n = 470 F_4-derived) and individual from 4 cycles of genomic selection were genotyped for single nucleotide polymorphism discovery with GBS platform. By using these marker information, the genotyped populations were assessed for genetic characteristics, which included polymorphism information content, as well allelic diversity, linkage disequilibrium, Wright's index (F_{st}), Nei's fixation index (G_{st}) and effective population size (Ne). All indixes and attributes comparisons were made in a pair-wise manner among all the populations (e.g training population vs population with individuals from cycle one of genomic selection, cycle one vs cycle two etc). Preliminary results suggest reduction in genetic diversity as the genomic selection cycles advance, as well as changes in the pattern of linkage disequilibrium. Other results, incluiding the rate of genetic diversity decrease, effective population size and diveristy indexes, all relative to the training populaiton, will be presented and discussed.

8

SCREENING WHEAT PARENTS OF EIGHT PROSPECTIVE MAPPING POPULATIONS FOR NITROGEN USE EFFICIENCY

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In the Mid-Atlantic Basin, application of nitrogen fertilizers presents innumerable concerns for farmers due to cost, the potential for environmental degradation, and legislation aimed at protecting the Chesapeake Bay Watershed. Much of the gains in nitrogen use efficiency (NUE) to date can be attributed to more efficient agricultural practices (e.g. 4Rs of Nutrient Stewardship and Best Management Practices) while the utilization of genetic potential remains relatively untapped. Breeding soft red winter wheat (SRWW) cultivars for high NUE introduces a number of challenges due to the quantitative inheritance of NUE, field testing constraints, and the expensive of conventional phenotyping.

In an effort to overcome these challenges, Virginia Tech and The Ohio State University evaluated parents of eight prospective mapping populations to detect genetic variation in NUE. Populations with contrasting parents can then be used to map quantitative trait loci conferring increased NUE for use in SRWW breeding programs. During the 2015-16 growing season, a panel of 12 SRWW lines were grown as a replicated randomized complete block design in eight diverse environments. Each replication consisted of the 12 lines grown under a 'high' (134 kg N ha^{-1}) and 'low' (67 kg N ha^{-1}) nitrogen treatment. Lines were primarily evaluated for their ability to take up nitrogen and utilize applied nitrogen for the production of grain yield and protein. Additionally, stress indices and in-season phenotyping were used to further assess genotypic effects of NUE across SRWW lines. To date, significant differences ($P<0.05$) between lines and treatments have been detected for normalized difference vegetation index and canopy temperature depression at anthesis in all tested Virginia environments. At physiological maturity, one linear meter cuttings will be taken from each plot to assess grain and straw nitrogen yields and plots will be harvested to determine NUE, grain yield, and grain protein content.

9

GENOME-WIDE HAPLOTYPE ANALYSIS TO IDENTIFY GENOMIC REGIONS UNDER BREEDING SELECTION FORIMPROVING SOYBEAN YIELD

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Expanding genetic diversity in elite U.S. soybean breeding populations has become a necessity to improve genetic gain in seed yield. Woodruff, a high yielding soybean cultivar developed at Univ. of Georgia, has 25% of exotic germplasm (PI 416937) in its pedigree and yielded over checks in 2003-2005 USDA Southern Soybean Uniform Tests. Over 100 lines developed at eight public institutions derived from PI 416937 have been entered into USDA Southern Soybean Uniform Tests over the past 15 years. We are attempting to understand the contributions of the haplotype alleles from PI 416937 to these high yielding lines and compare them with the haplotypes in the North American gene pool. We have genotyped several of these lines with SoySNP 50k Infinium chips. By comparing genotypes of these lines, we have identified thirteen genomic regions from PI 416937 selected for in these high-yielding lines. We have also identified fifteen genomic regions from PI 416937 that have been selected against in these high yielding lines. Using clustering and principal component analysis approaches with the SoySNP 50k Infinium chip data, we have also accessed the genetic variation in relation to PI 416937, high-yielding PI 416937 derived lines and U.S. soybean ancestors at the whole genome level. The results showed distinct clustering of PI 416937 derived lines separately from soybean ancestral lines. We observed evidence of association of one of these peak regions (*Yld1*) with high yield in a population of 150 F5:6 RILs. A gene model for chitinase A was identified within this peak region.

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DEVELOPMENT OF 1KK - A NEW ANDROID APPLICATION FOR HIGH THROUGHPUT SEED PHENOTYPING

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Seed size and shape are important characteristics that affect the yield and many end uses of different crops. Accurately measuring these phenotypes and incorporating this information into breeding programs can potentially increase yield and quality. Previously, accurately measuring these seed shape phenotypes was time consuming, destructive or required expensive specialized machines. We have developed 1KK (one thousand kernel), an Android application designed to measure seed characteristics for a variety of crops using only an image taken with the phone or tablet camera. This makes it easily accessible, portable, and cost effective. To validate the accuracy of our application we measured 70 wheat lines, from a population with known seed size variation, were measured manually, with 1KK and with SmartGrain, a previously developed and validated software. The measurements from both 1KK and SmartGrain were highly correlated with each other (length R^2 = 0.89, width R^2 = 0.58) and with the manual measurements (1KK width R^2 = 0.771, SmartGrain width R^2 = 0.798, 1KK length R^2 = 0.582, SmartGrain length R^2 = 0.571). However, 1KK was significantly faster and simpler to use as it is only one procedure and requires less expensive equipment. To further demonstrate the utility of 1KK for genetic studies the doubled haploid synthetic hexaploid W7984 x Opata M85 wheat reference mapping population (SynOpDH) was utilized for QTL mapping of seed size and shape. The measurements taken using 1KK were successfully used to map a QTL for seed length using Composite Interval Mapping, thereby demonstrating the potential uses of the application for genomic analysis as well as a tool for plant breeding.

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IDENTIFICATION OF QUANTITATIVE RESISTANCE TO *PUCCINA STRIIFORMIS* AND *PUCCINA TRITICINA* IN THE SOFT RED WHEAT CULTIVAR JAMESTOWN

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Disease resistance is critical to soft red winter wheat (*Triticum aestivum* L.) cultivars. Leaf rust caused by *Puccinia triticina* and stripe rust caused by *Puccinia striiformis* are destructive pathogens of wheat. Phenotypic data was collected at diverse locations for resistance to leaf rust (NC, TX and VA) and stripe rust (AR, NC, GA, TX, and VA) in one primary mapping population Pioneer25R47 / Jamestown (P47/JT) comprised of 186 $F_{8:9}$ recombinant inbred lines (RIL). The P47/JT RILs RIL(s) were genotyped with public 90K iSelect SNP array. Analysis of the P47/JT population identified multiple putative resistance QTLs located on chromosomes 5B and 6A that are associated with leaf rust infection type and severity. Chromosome 5B contained two major and one minor QTLs for leaf rust resistance, while chromosome 6A contained two minor QTLs. Variation explained by the putative leaf rust resistance QTL of Jamestown on 5B was as high as 23.2%, while 6A was 17.7%. Initial results also identified multiple minor QTLs for resistance on chromosomes 2B, 5B, 6A associated with stripe rust infection type and severity in the P47/JT population. The variation explained by putative stripe rust resistance QTL of Jamestown on 2B, 5B, and 6A was as high as 18.3%. Use of these QTLs will lead to the introgression and pyramiding of leaf rust and stripe rust resistance by marker-assisted selection into soft red winter wheat cultivars.

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SNP GENOTYPING AS A TOOL FOR PEANUT BREEDING

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Genotyping of structured populations is an extremely useful tool for breeding. This research is crucial as an instrument for breeding in peanut since it can be contrasted with the phenotyping of biparental populations to identify QTLs and genes underlying agronomic traits. Therefore, a group of 23 genotypes from all the market classes including 10 parents such as Tifrunner, NC 3033, Florida 07, C76-16, SPT06-06 and New Mexico Valencia, etc., from a nested association mapping (NAM) population developed in Tifton, GA, and Raleigh, NC, were genotyped using an Affymetrix chip with 60k SNPs designed based on comparative analysis of tetraploid sequence with the two diploid ancestor reference genomes. The NAM population consists of 16 RIL populations with two common parents (Tifrunner and Florida 07) based on crosses of genotypes with different trait combinations such as disease resistance, drought tolerance, and pod morphologies. Thus, 11633 SNP markers were found to be polymorphic between the 23 genotypes and 8999 SNPs were found to be polymorphic between all the 10 CAP parents; 8965 for the crosses with Tifrunner and 8857 for the crosses with Florida 07. Additionally, one part of the RIL population from the cross of Tifrunner by NC 3033 was genotyped and the genetic map was generated based on 2288 polymorphic markers for the cross. The genetic position of the markers was compared with the chromosome sequences from the two diploid ancestor genomes to confirm the genetic positions and analyze potential rearrangements that could be present in the tetraploid genome as compared to the two ancestors. Seed and pod phenotypic traits have also been correlated with the genotyping data to identify QTLs. Studies will continue to confirm the applicability of this tool.

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IDENTIFICATION AND EVALUATION FOR QTL ASSOCIATED WITH FLOWERING AND BRANCHING TRAITS IN A PETUNIA RIL POPULATION

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Plant morphology can greatly influence the intensity of flower production by a plant. For example, plants producing more branches generally have a greater capacity to produce flower buds than single-stemmed plants. Plant architecture is influenced by both genetic and environmental factors, including irradiance, phytohormones, and plant nutrition. Understanding the genetic control of morphological traits underlying flowering intensity could support breeding efforts in developing cultivars that produce more flowers. The objective of the study was to identify quantitative trait loci (QTL) associated with flowering and branching traits using an interspecific *Petunia axillaris* × *P. exserta* F_7 recombinant inbred line (RIL) population. Total flower bud number, flower buds on the primary stem, total branch number and number of branches with flowers were evaluated for two seasons on 171 RILs and the parental species at 14, 17 and 20°C under a 16-hour photoperiod. A high-density single nucleotide polymorphism-based genetic linkage map for this population was generated using genotyping-by-sequencing. Results from the analysis of the first season's data identified 17 QTL accounting for 6.7-31.5% of the phenotypic variation for the four flowering and branching traits with 7 QTL at 14°C, 4 QTL at 17°C, and 6 QTL at 20°C. Three major QTL (explaining >25% phenotypic variation) were identified for total flower bud number, flower buds on the primary stem, and total branch number at 20 and 14°C. These results will be validated using the second season's data. Results from both analyses will be used for identifying candidate genes associated with traits contributing to flowering intensity.

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DISCOVERY OF *RPP7,* A NOVEL SOYBEAN RUST RESISTANCE GENE IN SOYBEAN ACCESSION PI 605823

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Soybean [*Glycine max* (L.) Merr.] is one of the world's most important crops, with over 315 million metric tons produced globally. One of the greatest disease threats to soybean production worldwide is Asian soybean rust (SBR), caused by the obligate biotrophic fungal pathogen *Phakopsora pachyrhizi* Syd. & P. Syd. SBR is a global threat to soybean production, as it can spread rapidly through windborne urediniospores and can cause premature leaf senescence and resultant yield losses of up to 80%. Host plant resistance to *P. pachyrhizi* conditioned by *Rpp* genes has been found in numerous soybean landraces and at least 12 *Rpp* genes or alleles have been mapped to six genetic loci. However, *P. pachyrhizi* strains can overcome *Rpp* gene resistance over time so new resistance genes are needed to stack into modern cultivars. We identified PI 605823 as being resistant to U.S. populations of soybean rust in both greenhouse and field trials. Using an $F_{2:3}$ population derived from 'Williams 82' × PI 605823 and an $F_{4:5}$ population derived from '5601T' × PI 605823, we have mapped a novel resistance gene, *Rpp7* (approved by the Soybean Genetics Committee), to a position on Chr 19 which is different from the genomic locations of previously reported *Rpp* genes. We hope this new gene will be incorporated into elite breeding lines to help provide durable resistance to SBR.

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GENETIC MAPPING OF QTL FOR FUSARIUM HEAD BLIGHT RESISTANCE IN WINTER WHEAT CULTIVARS ART AND EVEREST

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Fusarium head blight (FHB) is a fungal disease, mostly commonly associated with F. graminearum, which affects cereal crops such as wheat resulting in substantial yield losses and reductions in grain quality. The onset of the disease can occur rapidly when warm, wet or humid weather coincides with flowering in the spring. The pathogen also produces mycotoxins such as deoxynivalenol (DON) that accumulate in the grain and can be toxic to humans and animals. This results in additional economic losses as contaminated grain must be discarded or blended to reduce the amount of toxin in order to meet federal regulatory limits. Development and deployment of resistant cultivars has proved to be an effective method to combat the disease, and many resistant sources have been reported in the literature with the majority of major resistance coming from Chinese landraces. Transferring resistance from these sources into cultivars adapted to the U.S. has been a slow process due to linkage of FHB resistance genes with poor agronomic traits. Therefore, it is important for breeders to search for sources of resistance in native material adapted to their local conditions. In this study, we aimed to identify quantitative trait loci (QTL) for resistance to spread of FHB within the head (Type II resistance), accumulation of DON toxin in grain (Type III resistance), and resistance to kernel infection (Type IV resistance). Plant material consisted of 148 doubled haploid (DH) lines from a cross between the two moderately resistant hard red winter wheat (HRWW) cultivars Art and Everest. The study was conducted for two years using a point inoculation technique in a greenhouse in Manhattan, KS. Three QTL conferring resistance to FHB traits were detected on chromosomes 2D, 4B, and 4D. The QTL on chromosomes 4B and 4D overlapped with the major height genes Rht1 and Rht2, respectively. Plant height has shown previous associations with FHB, though the underlying cause of these associations is not well understood. The majority of results have reported increased susceptibility associated with shorter plant types; however, in this study, the haplotype analysis for the Rht-B1 and Rht-D1 loci showed an association between the dwarfing alleles and increased resistance to FHB. This suggests either pleiotropic effects of these loci or perhaps linkage with nearby genes for FHB resistance. Markers close to the peaks of the FHB resistance QTL have the potential for Kompetitive Allele Specific PCR (KASP) marker development and subsequent use in marker assisted selection (MAS) to help improve overall FHB resistance within breeding programs.

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UTILIZING DRY MATTER AND NEAR-INFRARED SPECTROSCOPY FOR SELECTION IN THE WSU APPLE BREEDING PROGRAM

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Washington state is the number one apple producer in the U.S. and grows at least 28 varieties commercially. Of those varieties, none have been bred for the Washington state growing region. The Washington State University Apple Breeding Program (WSUABP) aims to develop new and improved varieties with higher eating qualities that are better suited for the WA apple growing region. WSUABP uses a variety of analytical tests, such as firmness and titratable acidity (instrumental), as well as appearance and eating quality (sensory) traits, to evaluate selections throughout the season, both at harvest and after several months of refrigerated storage. Previous studies in New Zealand have found consumers prefer apples with high dry matter content (DM), however DM has yet to be assessed in the breeding program germplasm. Apple DM data was collected from the 2015 harvest using both traditional destructive methods and non-destructive near-infrared spectroscopy (NIR). The DM was compared to other sensory and instrumental fruit quality traits to predict correlation between traits. The instrumental and sensory traits were also compared to other wavelength ranges within the NIR region to determine if a correlation was present. The potential to incorporate DM ratings and/or NIR into the apple breeding selection process using either destructive or non-destructive methods is presented here.

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DIVERSITY AMONG LOWLAND SWITCHGRASS (*PANICUM VIRGATUM* L.) BASED ON MICROSATELLITE MARKERS (SSR)

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As an important crop for biofuel feedstock research, understanding the extent of genetic variation among and within different population of switchgrass is necessary to enhance efficiency in cultivar development. Twenty-three populations of lowland switchgrass including 13 Plant Introduction accessions obtained from USDA Germplasm Resource Information Network (USDA-GRIN) and 10 improved cultivars and breeding lines are being phenotyped at the University of Tennessee, East Tennessee Research and Education Center (ETREC) Plant Science Unit. Each population is represented by 15 genotypes. Upland 'Cave-in-rock' and 'Summer' were also included for comparison. Young leaves were collected from field-grown plants and DNA samples were extracted from each individual using the CTAB method. Touch down PCR was done using 384-well thermal cyclers. A total of 103 SSR markers and 4 chloroplast markers developed in Noble Foundation were used for PCR amplification. Samples were then genotyped using an ABI 3730 capillary sequencer at the Plant Biology Department of Noble Foundation. All genotypes were manually checked and cleaned using Genemapper. Base pair scores were converted to binary scores with the presence of a PCR product scored as 1 and 0 for its absence. Preliminary results using 27 SSR markers revealed a total of 50 alleles with an average of 2 alleles per marker per genotype. Hierarchical cluster analysis using Ward's minimum variance (R package) grouped the individual genotypes into four clusters representing different accession origins. Additional marker data will be included for further analysis.

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IMPROVING GENOMIC PREDICTION MODELS FOR WHEAT END-USE QUALITY

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Wheat breeding for quality is challenging because it entails many traits such as milling quality, grain hardness, protein and starch content, the dough mixing time, solvent retention capacity, gluten strength and extensibility, loaf volume and crumb texture. The complexity of phenotyping end-use quality requires a significant amount of labor and grain, thereby restricting quality selection to late in the breeding program. Additionally, selecting for end-use quality is difficult because the phenotyping procedures are time consuming and cannot occur until after harvest. To overcome these concerns, genomic prediction models for end-use quality in the International Maize and Wheat Improvement Center (CIMMYT) wheat breeding program are being developed. Currently, the models have forward prediction accuracies ranging from 0.32 for grain hardness and 0.62 for mixing time. However, twelve different phenotypic values for end-use quality are supplied to the breeders for each line, complicating selection. To streamline end-use quality selection, the prediction models will integrate the many end-use phenotypes into a single value, the CIMMYT end-use types. The end-use type categories were developed at CIMMYT to classify which market a wheat line's quality profile is best suited. The categories include Type 1 which is best suited for mechanized pan bread, Type 2 (flat bread and noodles), Type 3 (homemade bread), Type 4 (noodles and pastries), and Type 5 (feed quality). Subsequently, because CIMMYT develops wheat for many different markets, condensing the end-use quality data to end-use types will facilitate and simplify variety selection.

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GENOME WIDE ASSOCIATION ANALYSIS FOR DROUGHT TOLERANCE RESPONSES IN ANDEAN COMMON BEANS

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Drought is the most important abiotic stress limiting productivity of common bean (*Phaseolus vulugaris. L*.), especially under subsistence farming systems worldwide. Shoot traits are important in regulating physiological and biochemical processes associated with drought stress responses. In this study, we used a panel of 241 Andean common bean genotypes assembled as part of the global Andean diversity panel project (ADP) to perform genome-wide association (GWA) analysis to identify genomic regions associated with drought tolerance responses at seedling stage of common bean. The genotypes were evaluated in the greenhouse under drought conditions with four replications. Drought stress was applied by withholding watering 21 days after planting to all genotypes grown shallow pots. This limited root growth minimized root effects in order to provide unbiased assessment of shoot traits under drought stress. Photosynthetic traits such as photosystem II efficiency (Φ_{PSII}), non-photochemical quenching (NPQ), chlorophyll content (SPAD), and Liner electron flow (LEF) were measured using PhotosynQ instrument (PhotosynQ.org) every two for14 days.Single nucleotide polymorphism (SNP) markers from the BARCBean6K_3 Beadchip containing 5398 SNPs were filtered and used to perform SNP-trait associations for SPAD using a Mixed Linear Model (MLM) implemented in software program TASSEL. Significance threshold for SNPs was determined using the Bonferonni corrected $p=1.13x\ 10^{-5}$ (for $\alpha = 0.05$ and 4393 SNPs). Significant ($P<0.05$) differences were observed among the 241 genotypes for the photosynthetic traits measured. GWA analysis detected genomic regions for chlorophyll content on chromosome Pv01 with peaks at SNPs ss715647960, ss715650604, and ss715646884 and on Pv08 with a peak at SNP ss715647116 respectively. This study has demonstrated the effectiveness of GWA analysis for identifying genomic regions associated with a photosynthetic trait particularly chlorophyll content under drought stress, thus providing insights into the genetic architecture of drought stress responses at seedling stage in common bean.

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UTILIZATION OF MOLECULAR MARKERS TO SCREEN FOR CAROTENOID CONTENT WITHIN THE USDA CARROT GERMPLASM COLLECTION

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Cultivated carrot (*Daucus carota* subsp. *sativus*) is an important vegetable crop that is popular around world. Carrots are well known for their nutritional value due to the large amount of provitamin A carotenoids (alpha- and beta-carotene) found in their storage roots. To date, there are a limited number of reliable, predictive DNA tests to screen for economically important traits in carrot. Due to recent dedicated efforts to develop such tools, specifically the carrot genome project, the carrot breeding community is reaching a point at which molecular markers can begin to play a valuable role in the screening and improvement of germplasm. Recent research efforts have led to the identification of candidate genes for the *Y* and Y_2 traits in carrot, conditioning total carotenoid and beta-carotene accumulation, respectively. There are currently over 1,000 *D. carota* accessions at the North Central Regional Plant Introduction Station, including many that have yet to be characterized for root pigmentation. Utilizing recently discovered SNPs and InDels, several co-dominant markers for *Y* and Y_2 have been created to screen carrot Plant Introduction (PI) accessions for favorable combinations of alleles as well as to better characterize the collection. Furthermore, with markers for both *Y* and Y_2, it is now possible to select parents with the genetic potential to produce high-carotenoid accumulating progeny. In addition to root pigmentation markers, we hope to develop markers for valuable quality traits including flavor, texture and shape as well as for various abiotic and biotic-related traits. Moreover, molecular markers will be tested across several cultivated carrot subpopulations showing high levels of population structure, including Eastern (Central Asia, East Asia, and the Middle East) and Western (South America, North America, and Europe) groups, to better understand domestication events and to test whether the newly developed markers have utility across different geographic populations.

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GENOME-WIDE ASSOCIATION STUDIES OF YIELD COMPONENTS UNDER WATER LIMITATION FOR A WEST AFRICAN SORGHUM ASSOCIATION PANEL

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Water limitation stress is a major factor that limits grain sorghum (*Sorghum bicolor*) productivity in the semiarid regions. In a world affected by climate change, improving sorghum adaptation to drought through genomics is an important step forward to establish food security in semiarid areas of West Africa. Discovering the genomic region controlling water-limited stress may accelerate the process of developing new varieties of sorghum with high yield and tolerant to water stress. This study aims to assess the population structuration of 757 sorghum accessions from the West African countries of Senegal, Mali, Togo and Niger and identify markers associated with yield components- related traits under water-limited condition through Genome-Wide Association Studies (GWAS). Genotyping-by sequencing (GBS) was conducted using ApeKI restriction enzyme on the 757 accessions including landraces and improved breeding lines. In total, 106,887 SNP markers were obtained after aligning illumina HiSeq read sequences data to the latest version of the sorghum reference genome v3.1 and SNP calling using the TASSEL GBS pipeline. The Bayesian model-based clustering method, neighbor joining tree, and the principal components analysis revealed distinct groups with respect to the country of origin of the accessions. GWAS on the 2014 phenotypic data identified 9 SNP markers significantly associated with panicle weight, total grain weight per panicle, and canopy temperature. Another GWAS will be performed on 2015 phenotypic data collected in two different environments. The identified markers might be used as background and foreground markers in the West African breeding programs to make the selection process more efficient.

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ALTERNATIVE APPROACHES TO LOBLOLLY PINE BREEDING VALUE PREDICTIONS

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The goal of this study is to increase the selection intensity within Loblolly Pine breeding programs, by assessing the relationship between unique patterns of family gene expression and parental breeding values. We hypothesize that selection intensity can be increased in pine breeding programs under two conditions -first, that there are genetic differences among families in gene regulatory networks, and second, that those differences are correlated with family mean performance in field tests of progeny. Questions to be addressed include: (1) can we obtain reasonably reproducible results from triplicate samples of seedlings from OP, PMX, or CP families with respect to estimating family-mean levels of gene expression for a set of parents; (2) can we identify methods for combining those family-mean estimates of gene expression levels into covariance estimates for pairwise-combinations of parents that show utility in cross-validation studies for modeling phenotypic variation, and (3) do covariance matrices based on coding sequence SNP variation, gene expression level variation, or pedigree-based estimates of allele sharing have independent value for modeling phenotypic variation, or are they redundant so that one approach has the same information present in the other two? To answer these questions, we have chosen a total of 62 different parents, from a wide geographic distribution, with pre-existing progeny phenotype data available from field tests across multiple sites. Seeds (OP/PMX in 54 cases, CP in 8 cases) from each of these parents were grown in a greenhouse, and pooled seedlings were harvested at 3 months for RNA extraction/sequencing. Family-mean gene expression patterns are used with phenotypes from age 6 progeny tests to identify genes or clusters of genes having a relationship with the trait. This resulting analysis should provide insight into the capability of using RNA expression patterns as another screening effort in selecting individuals as parents for future breeding populations.

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COMPARISON OF POLLINATION BAGS FOR MASS PRODUCTION OF CONTROL CROSS SEED IN LOBLOLLY PINE

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Over the past 10 years, deployment of full-sib families has gained prominence relative to traditional open-pollinated loblolly pine (*Pinus taeda* L.) families. To produce control cross seed, a pollination bag must be used to isolate female strobili from outside pollen contamination. Bags from PBS International were compared to the industry-standard Lawson pollination bag to compare seed yields; open pollinated female strobili were also added as a control. The study was replicated in nine seed orchards in the southern US. Three clones per orchard site were used, and within the crown of each clone, 10 replications were installed. Replications consisted of the six different bag types: Lawson, Lawson with wire support, and PBS A, B, C, and D bags. As early predictors of seed yields, we assessed female strobili survival at time of bag removal and 3 months later following the "June drop". June drop is defined as the premature loss of first year female strobili and is caused by a variety of factors such as inadequate pollen, insect damage, cold injury, or mechanical injury.

Bags (PBS A, PBS B and Lawson wire) with more structural support had higher female strobili survival (p-value=<0.0001). Seed yields and seed efficiency per cone will be available in 2016 to compare bag types for seed yields. If the 2014 June drop survival corresponds with seed yield and seed efficiency per bag, PBS bags A, B, and Lawson with wire could produce about 25% more seed over the industry standard Lawson bags with no support wires. This could increase seed production by 25% and would have a large economic impact on the mass production of control cross seeds in loblolly pine, and potentially other forest trees.

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DIVERGENT SELECTION FOR FIBER LENGTH AND BUNDLE STRENGTH AND CORRELATED RESPONSES IN COTTON

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Cotton breeders must develop cultivars to meet the demand for longer, stronger, and more uniform fibers. In the current study, two cycles of divergent selection for fiber upper-half mean length (UHML) and bundle strength (Str) were conducted within five diverse parental combinations selected based on their potential for the genetic improvement of fiber quality. Realized heritability estimates for UHML and Str were calculated for each cycle, and correlated responses among fiber properties and lint percent (LP) were measured as they responded to selection for UHML and Str. The results suggest that early generation selection for UHML and Str is an effective strategy for the genetic improvement of fiber quality at College Station, TX. Although UHML and Str were consistently negatively correlated with LP, the results demonstrate that sufficient variation for fiber quality exists within the Texas A&M AgriLife Research upland cotton germplasm to improve UHML and Str without a concomitant reduction in LP. A negative phenotypic correlation between UHML and fiber elongation (Elon) was also observed and was independent of the association between Str and Elon in multiple populations. These findings suggest that further investigation into the relationship between UHML and Elon within the Texas A&M AgriLife Research germplasm is warranted.

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DEVELOPMENT OF THE FIRST CONSENSUS GENETIC MAP FOR INTERMEDIATE WHEATGRASS (THINOPYRUM INTERMEDIUM)

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Intermediate wheatgrass (*Thinopyrum intermedium*) has been identified as a candidate for domestication and improvement as a perennial grain, forage, and biofuel crop by several active breeding programs. To accelerate this process using genomics-assisted breeding, efficient genotyping methods and genetic marker reference maps are needed. Toward that goal, we present here the first consensus genetic map for intermediate wheatgrass (IWG), which confirms the species' allohexaploid nature with disomic inheritance (2n=6x=42) and homology to Triticeae genomes. As a first step, genotyping-by-sequencing was used to identify markers that fit expected segregation ratios and construct genetic recombination maps for 13 heterogeneous parents of seven full-sib families using a maximum likelihood procedure. These maps were then integrated using a linear programming method to produce a consensus map with 21 linkage groups containing 10,029 markers, 3,601 of which were present in at least two populations. Each of the 21 linkage groups contained between 237 and 683 markers, cumulatively covering 5,061 cM with an average distance of 0.5 cM between each pair of markers. Through mapping the sequence tags to the diploid ($2n=2x=14$) barley reference genome, we observed high colinearity and synteny between these genomes, with three homoeologous IWG chromosomes corresponding to each of the seven barley chromosomes, and mapped translocations that are known in the Triticeae. The consensuses map is a valuable tool for mapping loci associated with important agronomic traits and will be beneficial for wheat breeders attempting to locate important disease-resistance genes within intermediate wheatgrass. These genomic tools can help lead to rapid improvement of IWG and development of high-yielding cultivars of this perennial grain that would facilitate the sustainable intensification of agricultural systems, conserving natural resources while producing food for a growing global population.

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ASSESSMENT OF GENETIC DIVERSITY AND POPULATION STRUCTURE IN A SET OF *G. HIRSUTUM* LANDRACES

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Assessing genetic diversity, population structure, and identifying core sets in landraces can facilitate use of these sources of unexploited genetic diversity in breeding programs to improve cultivated germplasm. In this study, a set of 185 *G.hirsutum* landraces collected majorly from Central America during mid 1900s were genotyped using 122 genome-wide SSR markers to study the genetic diversity and population structure. A total of 819 alleles were identified across 143 markers loci and out of these 23.3% were unique alleles, observed only in one accession. Average genetic distance between accessions was 0.3570 suggesting higher levels of genetic variation present in wild germplasm. With Bayesian model based structure analysis, 5 major sub-groups were identified which roughly corresponded to regions of geographical origin of these accessions. Substantial degree of admixture was observed and accessions from different geographical locations were grouped together. Results from phylogenetic, PCA (Principal Component Analysis), and AMOVA (Analysis of Molecular Variance) analysis supported clustering from STRUCTURE software. Core sets representing various levels of allelic richness were also identified using POWERMARKER software.

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CHARACTERIZATION OF BASAL AND DISEASE RESISTANCES IN SORGHUM

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Early detection of pathogens is a critical component of plant immunity. Basal resistance, aka innate immunity, is the first line of defense to protect plants against a range of pathogens. Triggered by the recognition of microbe-associated molecular patterns (MAMPs) by pathogen recognition receptors (PRRs), the induction of basal resistance has been shown to vary quantitatively within and across species. In sorghum (Sorghum bicolor (L.) Moench), preliminary results support this hypothesis. The goal of this project is to investigate the genetic architecture and transcriptional response associated with the basal defense response in sorghum. Specific objectives in this project are to 1. Develop robust assays to measure disease resistance and the MAMP response in sorghum and screen a set of diverse sorghum germplasm for variation in these traits, 2. Examine the activity of fungal extracts of sorghum pathogens in inducing the MAMP response, 3. Identify genes differentially regulated during the MAMP response in high and low responding sorghum genotypes, 4. Measure the effect of the MAMP response on disease resistance in controlled assays, and 5. Determine whether control of variation in the MAMP response and variation in disease resistance is under shared genetic control.

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TOWARDS EFFECTIVE USE OF GOSSYPIUM A2 AND D1 GENOMES FOR IMPROVEMENT OF UPLAND COTTON

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Upland cotton (Gossypium hirsutum L.) contributes to over 90% of the globally produced cotton. Genetic improvement efforts must contend with relatively low levels of diversity due to reasons such as the self-fertilizing reproductive biology, low mutation rate and recent polyploidization; diversity among domesticated and modern elite types is even lower. With over 45 wild species within the Gossypium genus that have several agronomic traits of interest, cotton has abundant naturally occurring diversity that can be introgressed into the elite cultivars. However, introgression breeding into Upland cotton is time-consuming, labor intensive and complicated by reproductive physiology, differences in ploidy and meiotic affinity of genomes, chromosomal rearrangements, cytoplasmic male sterility, F1 sterility, hybrid lethality and other deleterious genetic interactions. We aim to study and facilitate diploid germplasm introgression breeding using a marker-assisted approach. Hybridization of G. arboreum (A2 genome, n=13) and G. thurberi (D1 genome, n=13), followed by chromosome doubling of the resulting F1 hybrid yielded a semi-fertile synthetic tetraploid, 2[A2D1]. More recently, we crossed the A2D1 synthetic to the inbred Upland line TM-1 and then backcrossed the F1 to TM-1 to develop a mapping population of 73 BC1F1 individuals. To develop SNP resources applicable to mapping and marker-assisted selection (MAS), we developed a diploid cluster file for the CottonSNP63K Array that includes Infinium II assays for over 63,000 potential SNPs. Using the Array and cluster file, we auto-genotyped 16,612 SNPs across all 73 BC1F1 hybrids. We then constructed a high-density genetic linkage map of SNP markers using the JoinMap 4.0 software. We grouped loci according to the maximum likelihood algorithm, and selected linkage groups (LGs) with LOD scores over 10, resulting in 26 linkage groups and a total of 5797 mapped loci. The LGs correspond to the 26 chromosomes and span 9143 cM. We analyzed map order by constructing and visually examining 2D Matrix Plots of the linkage groups constructed with CheckMatrix software. This information, along with comparisons to another recently published map of SNP markers based on the CottonSNP63K Array, was used to validate the map order. This linkage map provides us with positional information and a facile source of KASP markers for newly reported methods of cost-effective MAS of cotton seed or seedlings, e.g., for introgression and analysis of A2 and D1 germplasm via chromosome segment substitution line (CSSL) or “introgression line” (“IL”) development.

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COMPARISON OF GREENHOUSE AND FIELD RATING SYSTEMS FOR FUSARIUM CROWN ROT IN WINTER WHEAT

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Fusarium crown rot (*Fusarium culmorum*) is a common soil-born fungal pathogen causing 9.5% wheat yield losses and economic losses of nearly \$51.00 ha^{-1} in the Pacific Northwest United States (Smiley et al., 2005). Wheat breeders must screen for Fusarium crown rot severity in order to identify tolerant genotypes. Inconsistent results are often produced by environmental effects in field studies, so greenhouse screening methods have been developed to reduce this variation. The main purpose of this study was to determine if greenhouse screening produces results that are similar to results from the field. In this study, 48 soft white winter wheat varieties were selected from the 2015 Washington Statewide Winter Wheat Variety Trial. Each of these varieties were grown in both the field and greenhouse and were inoculated with a mix of 5 different isolates of *F. culmorum*. All of the varieties in both the greenhouse and field trials were then evaluated for disease severity on a 1 through 8 scale, with 1 being the most tolerant. Eyespot (*Tapesia yallundae*) was detected in addition to Fusarium crown rot in the field screening, which confounded the results. In 2016, we will screen for both Fusarium crown rot and Eyespot. If both infections continue to occur, it will emphasize the need to breed for resistance to both pathogens. Our results showed that there was a range in resistance among varieties in both the field and the greenhouse, but there was not a strong correlation between the two screening methods. Further data is also being collected in the greenhouse to improve the comparison between the field and greenhouse screening methods.

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FINE MAPPING OF GIBERELLIN-SENSITIVE DWARFISM QTL IN WINTER WHEAT

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The major dwarfing alleles of wheat, *Rht-B1b* and *Rht-D1b*, reduce internode length by disrupting gibberellic acid perception. The reduced sensitivity to GA results in a significantly shortened coleoptile, which causes reduced emergence and uneven stand establishment with deep sewing. Efforts were made to map dwarfism QTL that act through alternative pathways, which do not carry the negative pleiotropy associated with *Rht-B1b* and *Rht-D1b*. A genetic map comprised of GBS and KASP markers was used to map dwarfism QTL in the MPV57 x Massey mapping population. Two QTL were discovered on chromosomes 6A and 6D, which were detected over two years and in multiple field locations. SNP associated with the QTL were used for fine mapping in a second population, MPV57 x LA95135. Heterogenous Inbred Families (HIFs) were developed from F_4 plants heterozygous for the QTL regions on 6A or 6D. Individual F_5 plants which were heterozygous recombinant in the 6A or 6D QTL regions were selected, and plant height will be measured on replicated head-rows of F_7 HIFs. Comparisons will be made on highly replicated near-isogenic sister lines that contrast only for the QTL locus genotype, thereby controlling for genetic background effects and allowing for more precise estimates of the QTLs location.

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MAPPING OF FUSARIUM HEAD BLIGHT RESISTANCE AND DEOXYNIVALENOL ACCUMULATION IN KANSAS WHEAT

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Fusarium head blight (FHB) is a wheat disease caused by *Fusarium graminearum* that significantly reduces grain yield and produces mycotoxins that contaminate wheat grains and flour. Deoxynivalenol (DON) is the most prevalent mycotoxin and its advisory limit is 1 ppm in wheat products for human consumption. A large number of quantitative trait loci (QTL) for FHB resistance have been reported in the literature with effects varying according to the genetic backgrounds. The objective of this study was to map QTLs associated with FHB resistance to disease spread, DON accumulation, and perform a haplotype analysis to estimate the effect of stacking QTL within breeding lines. A doubled haploid (DH) population with 202 lines was developed from a cross between Everest and Cedar, which are moderately resistant and moderately susceptible to FHB, respectively. The experiment was conducted in the field at Rocky Ford FHB Nursery in Manhattan, KS in the 2014/2015 growing season in a randomized complete block design with 3 replications where each experimental unit was formed by a 1-meter long single row plot. The evaluation of percentage of symptomatic spikelets (PSS) started 21 days after heading and repeated every 3 days for a total of 5 evaluations. These evaluations were used to calculate the area under the disease progress curve (AUDPC). A sample of 100 grains from each plot was collected to measure DON accumulation and fusarium damaged kernel (FDK) using a single near-infrared spectroscopy instrument. DH lines and parents were genotyped using genotyping-by-sequencing (GBS). Then, a pipeline on TASSEL 4 was used to call and filter SNP markers. After that, a linkage map was created with MSTMap online software using the Kosambi mapping function. The GBS tags were blasted against the draft reference genome to assign linkage groups to chromosomes. The final linkage map contained 3,005 SNP markers covering 31 linkage groups. PROC GLM in SAS was used to estimate LSmeans for the phenotypic traits using plant height as a covariate. Composite interval mapping and multiple QTL mapping were performed using Haley–Knott regression with the package R/qtl in RStudio. Genome-wide LOD thresholds were set using 1000 permutations. Three QTL for type II resistance were found on chromosomes 3BS, 6AL and 6BL explaining 7.3 to 12.9% of the phenotypic variation of AUDPC. Another three QTL from Everest located on 1B, 5AL, and 5DS explained 9 to11.4% of the DON accumulation. The QTL on 1BL and 5AL for DON and FDK mapped to the same genomic region. The haplotype analysis showed that DH lines containing all QTL were significantly more resistant and presented lower values of FDK and DON than DH lines with no QTL. This study is being repeated to confirm the current findings. Later, diagnostic markers will be developed from the GBS tags flanking significant QTL to assist breeding for FHB resistance.

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IDENTIFYING GENETIC MARKERS FOR METABOLITE LEVELS IN POTATO

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The potato *Solanum tuberosum* is an important staple crop worldwide. Because of the significant role that potatoes play in the global diet, it is beneficial to focus potato breeding efforts on nutritional quality in addition to yield, disease resistance and agronomic traits. Potatoes can provide a wide range of nutrients such as vitamin C, folate, potassium, Vitamin B6, and selenium, as well as polyphenols, flavonoids, anthocyanins and carotenoids, all of which confer positive effects to human health. This project aims to facilitate the selection of potatoes with improved composition by developing genetic markers linked to individual, or groups of, important metabolites. Methanol extracts of cooked tubers from 229 diverse potato cultivars and breeding clones were analyzed by Ultra Performance Liquid Chromatography coupled with Mass Spectrometry (UPLC-MS). The same potatoes were genotyped with an Infinium SNP chip (8303 SNP markers). Nine-hundred and eighty one metabolic "features" were detected. Weighted Gene Correlation Network Analysis (WGCNA) was used to cluster individual features into groups. Eleven groups were formed. Step-wise regression was done on potato chip color, and group eigenvalues; two groups were correlated with chip color at $p < 0.05$.

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DISCOVERY AND ELUCIDATION OF RESISTANCE TO BACTERIAL SPOT IN AN ACCESSION OF THE WILD TOMATO SPECIES *SOLANUM PIMPINELLIFOLIUM*

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Bacterial spot of tomato is caused by four Xanthomonas species. Recently, *X. gardneri* emerged as a dominant component of epidemics in Brazil, the United States, and Canada. Few chemicals are effective against bacterial spot, thus the use of resistant varieties is an important component of the strategies to reduce disease. The objectives of this study were to identify sources of resistance to *X. gardneri*, detect regions of the genome associated with the trait, and breed for elite processing tomato lines carrying resistance. A total of 325 genotypes, including *S. lycopersicum* fresh market and processing lines, *S. lycopersicum var cerasiforme* and *S. pimpinellifolium* accessions were assessed for hypersensitive response (HR) and for field resistance. The proportion of variance explained by genetics for field resistance (34 to 81%) was higher than for the HR test (19 to 40%). Furthermore, HR reactions and field evaluations results were not correlated. Detection of quantitative trait loci (QTLs) underlying resistance was therefore based on field evaluations. The accession *Solanum pimpinellifolium* LA2533 was resistant under field conditions. A backcross (BC) population was developed with LA2533 as donor parent and an elite line from the Ohio breeding program as recurrent parent. The genetics of resistance was studied using a selective genotyping approach. One hundred and twenty seven BC_1 individuals were evaluated under inoculated field conditions. The seven most resistant and the eight most susceptible individuals were selected and self pollinated. Seventy-five BC_1S_1 individuals were genotyped with 204 SNP markers, and the BC_1S_2 families were evaluated under field conditions. A 44 Mb region in the chromosome 11 centromere was significantly associated with resistance from LA2533 and accounted for 38% of the phenotypic variation. Disease resistance and plant size were significantly correlated, with larger plants more resistant (p-value = $2.3x10^{-17}$, adj.R^2 = 0.59). A BC_1S_1 individual carrying the resistant allele on chromosome 11 was backcrossed twice to the elite parent, and self-pollinated. 3,019 segregating individuals were screened with six insertion-deletion markers on chromosome 11 to identify recombinants. Forty six plants carrying 12 different recombinant patterns were selected and self-pollinated. Divergent homozygotes for the QTL region were evaluated under inoculated field conditions. This third evaluation allowed us to confirm the presence of the QTL and to reduce the region associated with resistance to 15 Mb. The correlation between disease resistance and plant size was broken in these recombinants (p-value = 0.36, adj.R2 = 0.00). Lines with resistance to *X. gardneri* and reduced introgression size are currently being evaluated in test crosses with elite lines of our program. During this project, we successfully identified a wild accession resistant to *X. gardneri*, detected and confirmed a major QTL for resistance on chromosome 11, developed markers for selection, and broke linkage drag between plant size and resistance.

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TRANSCRIPTOME ANALYSIS OF *TARAXACUM KOK-SAGHYZ* USING RNA-SEQ AND IDENTIFICATION OF CANDIDATE GENES RELATED TO THE RUBBER BIOSYNTHESIS PATHWAY

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Taraxacum kok-saghyz (TK) is a potential alternative for natural rubber production due to its high molecular weight rubber, short life cycle, and diverse environmental adaptation. However, its inability to compete with weeds (e.g. *Taraxacum officinale*) results in low rubber production per acre. In order to improve rubber yield, breeding efforts are necessary. Until now, only limited breeding efforts have been carried out due to TK's self-incompatibility. The need to grow TK to maturity for accurate rubber yield estimation makes it an ideal crop for marker-assisted selection (MAS), a strategy integrating molecular genetics with traditional breeding efforts in attempt to select for desirable phenotypic traits, such as high rubber, in a short timeframe. Limited genomic resources currently available for this species make it difficult to implement MAS. Here, we present a comprehensive transcriptome dataset as well as identify putative markers tightly linked to quantitative trait loci (QTL) controlling rubber biosynthesis for further genomic studies and molecular breeding efforts (e.g. MAS) in this species.

In order to lay a foundation for MAS, RNA-Seq was used to detect sequence variants (e.g. single nucleotide polymorphisms, SNP). A total of 55,532 contigs with lengths over 200 bp were assembled using *de novo* assembly. When comparing our transcriptome sequence dataset with the publically available *Taraxacum kok-saghyz* root (TKR) EST database, 4,233 out of 6,966 (60.8%) unigenes in their database were covered by our transcriptome dataset (47,090 unigenes). All the enzymes in the terpenoid backbone biosynthesis pathway (potentially implicated in rubber biosynthesis pathway) were assigned by 102 contigs via KEGG pathway analysis in Blast2GO, while none of the enzymes in the MEP pathway (one branch) were assigned in the TKR EST database, suggesting an improvement and enrichment in relevant genes for TK. A total of 16,891 SNPs were detected between three high rubber and three low rubber plants. Of those 16,891 SNPs, 77 SNPs of 18 genes were involved in the terpenoid biosynthesis pathway. Forty-two SNPs were finally selected and converted to functional SNP markers using KASP (Kompetitive Allele Specific PCR) technology. These SNPs were then used for validation in an F1 population with 84 individuals. As a result, a total of 37 out of 42 SNP markers (88.1%) were polymorphic, 1 was monomorphic (2.38%) and 4 (9.52%) were counted as failed reactions. A marker-trait association analysis identified 2 SNP markers (SNP1113, SNP1245) that were significantly related to rubber content. Both of them were located in the gene encoding 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase in the MEP pathway, suggesting a potential linkage between SNP markers and quantitative trait loci (QTL) controlling rubber production.

To conclude, we have established significant genomic resource for TK, providing a comprehensive transcriptomic reference. The power of RNA-Seq to detect SNPs was validated. A large set of SNP markers, including the ones putatively related to rubber biosynthesis, were identified, providing a solid foundation for further MAS.

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IDENTIFICATION OF A *NLR* DISEASE RESISTANCE GENE INVOLVED IN *NICOTIANA* HYBRID LETHALITY

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Barriers involved in reproductive isolation are of interest to evolutionary biologists studying speciation, but their underlying mechanisms and architecture are poorly understood. These barriers are also of interest for plant breeding and genetic engineering, where lethality mechanisms can be applied as phenotypic markers. Hybrid lethality may also be a model for studying disease resistance. In cases where genes have been identified, many have involved immunity-associated nucleotide-binding site leucine-rich repeat (NLR) genes, a common form of *R* genes in plants. In *Nicotiana tabacum*, cultivated tobacco, haploids for doubled haploid (DH) production are typically produced using an interspecific cross with a distant relative, *N. africana*. The *N. tabacum* x *N. africana* cross produces abundant amounts of seed, but post-zygotic barriers result in a semi-lethal response, and few plants survive beyond the cotyledonary stage. The few plants that survive are a mixture of haploids and hybrids with the lethality factor missing due to aneuploidy or chromosome breakage. The hybrid lethality provides an efficient means for screening for haploids. In order to identify candidate genes involved in this *Nicotiana* interspecific lethality reaction, we used a *N. tabacum* line engineered with the maize *Ac*/*Ds* transposon system coupled with a combination of phenotypic and molecular markers. We identified a coiled-coil (CC) NLR gene as a candidate for the *N. tabacum* lethality factor. The candidate is a member of a gene cluster and shows homology to the *R1* gene of potato (*Solanum tuberosum*), which confers resistance to late blight (*Phytophthora infestans*). To confirm involvement of the candidate gene in interspecific lethality, we are pursuing reverse genetics approaches using agroinfiltration of the candidate gene into *N. africana* and gene knockouts using the CRISPR-Cas9 system.

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PLANT BREEDING E-LEARNING IN AFRICA – A COLLABORATIVE EFFORT TO DEVELOP AND DELIVER STATE-OF-THE ART CURRICULUM FOR THE NEXT GENERATION OF PLANT BREEDERS

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Africa needs a critical mass of well-rounded practical plant breeders to effectively and independently manage and scale up breeding programs. Breeders are also critical in advancing the emerging African seed industry through increased uptake of improved crop varieties to ensure food security. With funding from the Bill and Melinda Gates Foundation, an innovative educational partnership was formed between Iowa State University (ISU), and Kwame Nkrumah University of Science and Technology, University of KwaZulu-Natal, and Makerere University. Plant Breeding E-Learning in Africa (PBEA) is part of a larger project titled Improved Master of Science in Cultivar Development for Africa (IMCDA) managed by Alliance for a Green Revolution in Africa. The Integrated Breeding Platform of the CGIAR Generation Challenge Program is another collaborating organization affiliated with the project. The aim of PBEA is to develop state-of-the-art e-modules covering modern breeding approaches, data management, and technologies that will be freely available for use by any institution in the world. PBEA members bringing knowledge and expertise to the project include faculty from ISU Agronomy Department, an innovator in online and plant breeding education, ISU Departments of Agricultural Education & Studies, Industrial & Manufacturing Systems Engineering, Horticulture, and School of Education, as well as experts from educational technology centers (Brenton Center for Agricultural Instruction & Technology Transfer and the Agronomy Distance Programs Development Lab). Several e-modules and Applied Learning Activities delivered to partner universities in Africa are being used in teaching in the IMCDA program, and have been reported as a useful resource.

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GENOMIC STUDIES OF AN *EX-SITU* SORGHUM GERMPLASM COLLECTION FROM NIGER

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Sorghum *(Sorghum bicolor* L. Moench) is a staple crop for developing countries with its five racial groups distributed across diverse agroclimatic zones. Genomic studies of sorghum are important tools to enhance conventional breeding in Sub-Saharan Africa. In fact, molecular markers that have efficiently improved and hastened conventional breeding are needed in this region. The objectives of this study are to characterize the genetic diversity and the population structure of an ex-situ sorghum germplasm collection from Niger, and to understand its adaptation to different environments. We conducted Genotyping by Sequencing (GBS) method for 509 accessions from United States crop germplasm collection and identified 137,968 single nucleotide polymorphisms (SNPs). The SNP distribution across the chromosomes shows a high number of SNPs per bin in subtelomeric regions versus a low number of SNPs in pericentromeric regions. The genetic relatedness within the collection shows five main clusters grouped by botanical race (Durra, Caudatum, Guinea, and their intermediate races). A large cluster of intermediate races between Durra and Caudatum, which are frequent in semi-arid parts of Niger, was observed. The population structure reveals diverse subpopulations mainly influenced by racial group and geographic origin of the accessions. Our results validate the population structure of sorghum reported by previous studies. Genomic diversity, population structure and association mapping of sorghum may provide important resources underlying adaptive traits for marker-assisted breeding in Sub-Saharan Africa.

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GENOMIC PREDICTION FOR NITROGEN USE IMPROVEMENT IN MAIZE

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Nitrogen use efficiency (NUE) in maize (*Zea mays* L.) has received considerable attention in the scientific community. However, current breeding and biotechnological approaches have failed to develop a NUE maize hybrid. We hypothesize that genomic selection (GS) for N-use traits may speed up the breeding cycle of research programs targeting improved NUE in maize. The objectives of this research are to predict maize yield under different N fertilizer rates and predict different N-use traits using GS. An association panel of 86 ex-PVP inbreds (33 stiff stalk synthetic, SSS and 53 non-stiff stalk, NSS) was genotyped with 26,769 single-nucleotide polymorphism (SNPs), and 276 single-cross maize hybrids were grown and phenotyped in eight different environments during the years of 2011 and 2015 at two N fertilizer rates (0 and 252 kg N ha^{-1}) and three replications per environment. Different prediction methods (G-BLUP and BayesB) and training population compositions were compared across different N treatments and N-use traits. We concluded that training population size, composition, and genotype x environment interaction are important components for enhancing the prediction accuracy of GS. We anticipate that the N-use trait identified with the highest prediction accuracy could be integrated into marker-assisted breeding strategies to accelerate NUE improvement in maize.

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EFFECTS OF PLANTING DATE AND PHOTOPERIOD SENSITIVITY ON PERFORMANCE OF WINTER WHEAT IN A DOUBLE CROP ROTATION WITH SOYBEAN

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Of all the factors that can be controlled by farmers, planting date is one of the most important, due to the potential impact on crop productivity. Planting winter wheat (*Triticum aestivum*) earlier in the fall has the potential to increase wheat yields and allow for an earlier harvest. This provides an opportunity for an earlier soybean (*Glycine max*) planting date, which should also increase yields. The main objective of this study is to determine whether or not winter wheat in Virginia can be planted earlier than what is currently recommended, to increase yields in a double cropping with soybean. This study will allow us to better understand the obstacles growers would face when planting earlier (e.g. frost damage, Hessian fly, lodging). The other objective of this study is to evaluate the suitability of cultivars varying in heading and maturity dates, vernalization requirements, and photoperiod sensitivity for their potential performance in an earlier planted double cropping system.

Certain cultivars will perform better than others, therefore identifying these cultivars is crucial to optimizing an earlier planted double cropping system. This study also provides an opportunity to assess the genetic backgrounds of each cultivar, and whether or not genotypic data can predict a specific cultivar's likely success in an earlier planting system. Photoperiod sensitivity and vernalization requirements are controlled by genetic x environmental interactions, and affect developmental stages such as jointing, heading, and harvest dates. Understanding if and how genes in different wheat genotypes affect timing of the transition from vegetative to reproductive stage and ultimately their maturity will allow us to recommend cultivars that are better suited for an earlier planting date.

This study includes 4 locations across coastal Virginia and 15 commercially relevant winter wheat varieties (14 soft red and 1 hard red) that differ in maturity and photoperiod sensitivity. At each location we planted on 3 different dates, that are considered very early (week of Sept. 20th), early (week of Oct. 4th), and on time (week of Oct. 18th). The hypothesis is that planting winter wheat earlier will take advantage of the warm growing days and develop more fall tillers. Tillers produced in the fall contribute significantly more yield than spring produced tillers. Another benefit is that the wheat crop will reach heading and senescence dates earlier, resulting in the opportunity for an earlier harvest date. It is estimated that winter wheat can be harvested 1 to 2 days earlier for every week that it is planted earlier in the fall. This allows for an earlier soybean planting date, which it is estimated that for everyday that soybeans are planted earlier in the spring, growers could potentially capture a 0.5 to 1 bushel/acre increase in yield.

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A MULTI-LOCUS MIXED MODEL APPROACH TO ASSOCIATION MAPPING IN A GLOBAL PANEL OF WINTER WHEAT

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Genome-wide association studies are useful tools for genetically characterizing complex traits in structured populations. Statistical models for association mapping have seen major improvements in the last 15 years; most notably, utilizing population structure and kinship estimates led to a mixed linear model (MLM) that minimized confounding effects of population stratification. The MLM, which employs single-locus genome scans to identify marker-trait associations, remains one of the most commonly used methods. However, masking effects between causal loci can limit the power of single-locus models. Several methods have been proposed to mitigate this issue, including an empirical Bayes approach, Linear Mixed Model-LASSO, and a Multi-Locus Mixed Model (MLMM). The goal of this study was to evaluate the statistical power of multi-locus approaches using both simulated and real datasets. We examined the MLMM method by applying it to a dataset containing 1,411 hexaploid winter wheat accessions that were screened for resistance to stem rust (*Puccinia graminis* f. sp. *tritici*). Genome-wide marker coverage was obtained with the iSelect Infinium 9K Wheat SNP Array by Illumina, and each accession was evaluated for stem rust resistance using several *Pgt* isolates including the highly virulent race Ug99. We found that the MLMM method outperformed other common models such as MLM, compressed MLM, and a general linear model. Our analysis identified valuable SNP markers associated with eight previously identified *Pgt* resistance genes and revealed at least three putatively novel loci. Finally, multi-locus approaches applied to simulated datasets provided valuable insight into alternative interpretations of marker-trait association analysis.

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GREENHOUSE EVALUATION OF *MISCANTHUS* AND *ARUNDO* ACCESSIONS FOR USE IN A SWINE LAGOON WASTEWATER TREATMENT SYSTEM

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As interest in bioenergy crop production increases, so will demands on water for agricultural use. A possible solution to this problem will be the use of animal wastewater, such as swine manure effluent, not only as a nutrient source but also for irrigation. Recycling of swine manure wastewater could help mitigate the potential environmental impact of bioenergy crop production. Miscanthus (*Miscanthus* spp.) and giant reed (*Arundo donax*) have shown great potential as bioenergy crops for North Carolina because of their high yields and low input requirements. However, little is known about their potential to be part of a waste management plan for uptake of nutrients and water of swine lagoons. Moreover, as breeding efforts on development of new cultivars expand, it is important to understand the levels of genetic diversity present among and within these species for their ability to remove nutrients from swine effluent spray fields. This research aims at evaluating 38 accessions of these species in a greenhouse pilot study to determine which have the highest potential in order to further evaluate them under field conditions. Results from this study will provide a foundation for the incorporation of North Carolina bioenergy grasses as a waste management plan thereby increasing the positive environmental impact of the bioenergy initiative. Furthermore, our results will be useful for selection of breeding stocks for future cultivar development.

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GENOME-WIDE ASSOCIATION ANALYSIS FOR RESISTANCE TO SEPTORIA NODORUM BLOTCH IN A DIVERSE POPULATION OF EASTERN UNITED STATES WINTER WHEAT

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Stagonospora nodorum blotch (SNB; causal agent: *Parastagonospora nodorum*) is a common and potentially severe pathogen of wheat which reduces both yield and grain quality. The disease is characterized by lesions which can expand to consume much of the leaf canopy, as well as the glumes of developing heads. The objectives of this study were to (1) evaluate a collection of 382 soft winter wheat landraces, breeding lines, and cultivars from the eastern United States for resistance to SNB, and (2) perform a genome-wide association analysis using marker data from 3492 SNP markers developed previously using the Illumina iSelect HD Genotyping BeadChip for wheat. Lines were grown following a randomized complete block design with two repetitions at four locations over three years for a total of five environments. A two-digit scoring method was used to record both disease severity and progress up the height of the plant, and measurements were taken on three dates separated by 7-10 days starting at the time of head emergence. The PROC GLM program within Statistical Analysis Software v9.4 was used to analyze the phenotypic data and generate least square (LS) means of each line for disease progress and severity across measurement dates, and for an area under the disease progress curve. Significant differences ($p < 0.01$) were observed amongst lines and environments and their interaction. Genetic association analyses using the LS means from within and across environments were performed using a compressed mixed linear model implemented via the GAPIT package in R v3.1. Population structure was accounted for using a Q-matrix generated in JMP Genomics 6.0, and a kinship matrix calculated in GAPIT. Results are discussed.

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IDENTIFICATION OF HYBRIDS BETWEEN TETRAPLOID VACCINIUM CORYMBOSUM AND DIPLOID VACCINIUM ELLIOTTII

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Southern highbush blueberries (*Vaccinium corymbosum L.* hybrids) are cultivated tetraploids. Their closest wild relatives are native to eastern North America. The primary habitats of these wild ancestors include swamps, marshes and lakeshores with soils consisting of low-pH sand and peat. Elliott's Blueberry (*Vaccinium elliottii*) is an early ripening diploid blueberry, native to the Southeastern United States. It has small, yet high quality berries and a diverse habitat ranging from dry upland soils to wet swamps. Transferring traits across ploidy levels in *Vaccinium* involves chromosome doubling or unreduced gametes, because of the triploid block in *Vaccinium*. This project examined 40 putative hybrids between diploid *V. elliottii* and cultivated highbush blueberry cultivars. Seventy-eight seeds obtained by pollinating 4301 flowers of 19 highbush cultivars with pollen from 30 *V. elliottii* plants propagated from a forest in southwest Alabama were placed on pure peat in the greenhouse in November 2014 to germinate. The 45 seedlings that were obtained were transplanted to a high-density field nursery in Citra, FL, in May 2015. In early December 2015, the plants were phenotypically evaluated for hybridity. A nine-point scale was used to evaluate each seedling for characters in which the parent taxa differ strongly from each other. The characters evaluated were vigor, degree of evergreen leaf retention, leaf serration, leaf shape, leaf texture, and pubescence. Putative hybrid plants were dug, potted, and placed in a cooler at 5° C for 30 days to provide sufficient winter chilling. They were then placed in a bee-proof greenhouse to flower. The first open flowers from each hybrid that flowered, and from *V. elliottii* and *V. corymbosum* controls were used for pollen analysis. Pollen was shed onto a drop of 45% acetic acid on a microscope slide, and viewed at 250x. Flowers that did not readily shed pollen were emasculated and the anthers smashed to obtain pollen. Potential pollen viability and pollen tetrad size were recorded for all plants that flowered. The data indicated that there were 20 male-sterile hybrids, 4 *V. corymbosum* selfs, and 6 fertile hybrids that were probably tetraploid. The next ten flowers that opened on each potential hybrid, and on *V. elliottii* and *V. corymbosum* controls, were used for floral morphology measurement. Using a caliper, corolla length, corolla diameter, style length and the position of the stigmas and anthers relative to the tip of the corolla tube were measured. Using Comparisons were made between means of putative hybrids and *V. elliottii* and *V. corymbosum* controls. The results showed that all except 4 plants differed significantly from both *V. elliottii* and *V. corymbosum* in more than one floral feature. Based on pollen and flower data it was concluded that this flowering population consisted of 26 hybrids, and 4 *V. corymbosum* selfs. Of the 26 hybrids only 6 had the phenotypic features to be classified as F1 hybrids along with significant pollen fertility.

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COMPARING GROUND AND UAV REMOTE SENSING FOR VARIETY SELECTION IN WHEAT FOR NITROGEN USE EFFICIENCY

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One way to reduce the production costs with Nitrogen (N) fertilization in wheat (*Triticum aestivum* L.) is to improve the nitrogen use efficiency (NUE) of the cultivars themselves. But the selection tools currently available to breeding programs are slow and inefficient. The objective of this work was to determine if aerial measurements, taken in a matter of minutes, can be used instead of time-consuming ground measurements of the Normalized Difference Vegetation Index (NDVI) and canopy temperature for NUE estimation. Twelve wheat varieties were examined at two locations in Virginia, the Tidewater AREC in Suffolk and the Eastern Virginia AREC in Warsaw. Varieties were subjected to two N rates corresponding to a low spring application of 67 kg N ha^{-1} and a recommended normal rate of 134 kg N ha^{-1}. Measurements were taken at several growth stages with both ground and aerial sensors with an unmanned aerial vehicle (UAV). Ground taken measurements included NDVI, red-green-blue (RGB) images leaf area index, and canopy temperature depression. The UAV measurements were taken with three sensors individually mounted on the UAV: a RGB digital camera, a near-infrared (NIR) camera, and an infrared (IR) camera. Aerial images taken with the RGB camera were used to compute color space characteristics such as hue angle, intensity, saturation, and RGB-derived vegetation indices Green Area (GA) and Greener Area (GGA). The images from the NIR camera were used to derive aerial NDVI, while the IR images were used to obtain canopy temperature.

At each growth stage, ground and the aerial measurements were compared. Measurements taken with the UAV were more time effective than measurements taken from the ground. Both the GA and GGA were correlated ($R^2 = 0.7$) with the NDVI taken from the ground, and the IR camera was successful in discriminating varieties with high and low NUE. Using UAV platforms to collect data in a matter of minutes and under almost identical weather conditions has the potential to increase the power of the current selection tools and hasten the selection of wheat varieties with improved NUE.

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GENOMIC DISSECTION OF PANICLE ARCHITECTURE TRAITS IN SORGHUM USING NESTED ASSOCIATION MAPPING.

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Sorghum is an important crop in many agroclimatic regions worldwide, and has adapted to a wide range of conditions. This makes it an important crop for food security in the face of climate change for smallholder farmers in developing countries. Accordingly, global sorghum germplasm exhibits substantial variation in agroclimatic traits—traits that differ in germplasm from different agroclimatic zones—including many aspects of leaf and panicle architecture. Currently, our ability to improve sorghum adaptation and transfer useful alleles across different genetic backgrounds is constrained by our limited knowledge of the genomic regions that underlie agroclimatic traits. Nested Association Mapping (NAM), which uses multiple biparental families linked by a common parent, can improve dissection of agroclimatic traits by reducing the confounding effects of population structure and increasing the frequency of rare alleles. A sorghum NAM population comprised of 10 families and almost 2,500 recombinant inbred lines (RILs) has been developed and genotyped at approximately 100,000 SNPs with Genotyping-by-Sequencing (GBS). The population was phenotyped for panicle length and primary rachis branch length in two contrasting environments (locations) in Kansas, semi arid (Hays) and humid continental (Manhattan). Significant genotypic variation for these traits was observed. Association and joint linkage mapping confirmed several previously identified quantitative trait loci (QTL) and revealed many new QTL for the panicle architecture traits. QTLs were found for lower rachis branch length, we identified Sb07g023640 a Flavin Monooxgenase gene close to the *Dw3* region on chromosome 7. The QTL identified will be helpful in marker-assisted selection for better adaptation and yield.

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DEVELOPMENT OF MARKER ASSISTED BREEDING RESOURCES IN NAPIERGRASS AND INTERSPECIFIC HYBRIDIZATION WITH PEARL MILLET FOR HIGH BIOMASS PRODUCTION AND BIOSAFETY

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Napiergrass (*Pennisetum purpureum* Schumach), is one of the most promising candidates for lignocellulosic based biofuel production and forage in the Southern US, owing to its high biomass yield and persistence. However, due to the formation of wind dispersed seeds, napiergrass has potential for invasiveness and is listed as an invasive species by the Florida Exotic Pest Plant Council. Production of interspecific hybrids between diploid pearl millet and tetraploid napiergrass, called PMN hybrids, impart male and female sterility to the progenies due to triploidy. We have introgressed cytoplasmic male sterility into high biomass pearl millet lines and generated interspecific hybrids between pearl millet and napiergrass. The formation of large seeds following this interspecific hybridization, as compared to the small napiergrass seeds, also allow easy establishment of plots by using a seed drill. Alternatively, late flowering lines that flower after freeze events in Florida, thus compromising flowering, could be utilized as biosafe resources for future breeding programs in napiergrass. A mapping population from parents contrasting in flowering time response was developed and all the 185 progenies were confirmed as true hybrids using SSR markers. Genotyping by sequencing was used to genotype these progenies by mining the variants. Non reference based UNEAK, STACKS *de novo*, and GBS-SNP-CROP called 29,096; 26,406, and 15,631 SNPs respectively. Reference based TASSEL, STACKS, and GBS-SNP-CROP called 42,451; 68,784, and 6,696 SNPs respectively. An initial genetic linkage map for napiergrass has been constructed from these SNP markers in this F1 population of 185 progenies. Development of these resources helps in advancing and facilitating napiergrass breeding programs.

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QUANTITATIVE TRAIT LOCI (QTL) ANALYSIS OF FREEZING TOLERANCE IN ZOYSIAGRASS

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Zoysiagrasses (*Zoysia* spp.) are warm season turfgrasses with great potential as lower input grasses because of their low growth habit, reduced fertilizer demands, and general tolerance to abiotic stresses like drought, shade and salinity. However, one factor limiting the widespread use of zoysiagrasses is a relative lack of freezing tolerance, especially when compared to cool-season grasses. Limited progress has been made in the development of new cold-tolerant cultivars since the cultivar 'Meyer' was released in 1951. The identification of markers linked to genomic regions controlling cold tolerance in zoysiagrass would improve the accuracy and effectiveness of selection, which would ultimately lead to an increase in the availability of cold-tolerant cultivars. Genome mapping is a pre-requisite for identifying such associations.

A pseudo-F_2 mapping population was developed from the cross of cold-tolerant 'Meyer' with cold-susceptible 'Victoria'. For phenotypic evaluations of winter survival the 175 progeny of this cross and nine controls were planted in the spring of 2014 in a randomized complete block design (RCBD) with three replications at the Upper Mountain Research Station (Laurel Springs, NC) and the William H. Daniel Turfgrass Research and Diagnostic Center (West Lafayette, IN) based on the range of winter temperatures at these locations. Winter survival data was taken in spring 2015 with 59% survival in North Carolina and 21% in Indiana. This population was replanted at both locations in the summer of 2015 and will be evaluated with the 2014 populations for survival in the winter of 2015.

A total of 239 SSR primers were selected based on previous successful amplifications and mapping in zoysiagrass populations and were screened for polymorphism in this population. From these primers, 125 SSR polymorphic markers were used for genotyping in the mapping population on 12% polyacrylamide gel electrophoresis (PAGE) using LICOR sequencers. Genotyping by sequencing (GBS) is a high throughput, cost-effective sequencing technology that can be used for the development of genome-wide single nucleotide polymorphisms (SNPs). The mapping population was double-digested with restriction enzymes *PstI* and *MspI* and multiplexed with 177 Illumina adapter sequences for sequencing on a MiSeq 150 single read (SR) run. A total of 1,262 SNPs were successfully mapped to the *Zoysia japonica* 'Nagirizaki' reference genome using the GBS-SNP-CROP workflow. SNPs were mapped to all 20 chromosomes with an average read depth of 9.1 counts.

Winter survival data collection for this population will be completed in June 2016. The map of SNPs and SSRs will be used in conjunction with winter survival data in order to scan cultivar 'Meyer's' genome for quantitative trait loci (QTL). Markers showing the strongest association with winter survival will be used to aid in transferring cold tolerance from Meyer into elite zoysiagrass breeding materials through the implementation of a marker-assisted breeding program.

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A FIRST GENETIC MAP OF SWEET BASIL (*Ocimum basilicum*) FACILITATED BY DOUBLE DIGESTION RESTRICTION SITE ASSOCIATED DNA SEQUENCING (ddRADseq)

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Sweet basil (*Ocimum basilicum*, L., 2n=4x=48) is among the most widely cultivated specialty crops for use in fresh/dried culinary and potted plant US markets. Despite a relatively substantial economic importance, the tetraploid sweet basil genome has remained largely unexplored due to an intimidating size (2C=2.9-3.3 Gbp) and poorly understood chromosome behavior. The capacity to map complex genomes of non-model species has improved in recent years following the development of restriction site-associated DNA sequencing (RADseq). This technique provides a subset or reduced representation of large genomes by sampling loci using restriction enzymes appropriate to the genome of interest. A two-enzyme or double digestion RADseq (ddRADseq) approach was used to generate loci from 94 sweet basil F2 individuals resulting from the cross of inbred genotypes MRI (mother) and SB22 (father). The rare cutter *PstI* and common cutter *MspI* were used to digest genomic DNA samples for all genotypes. RADseq was performed on an Illumina HiSeq2000 and data were quality filtered using FastQC, resulting in 420.6 million high quality paired end reads. Stacks software was used for RADtag development and *de novo* SNP identification resulting in >25,000 polymorphic loci between the parents. RADtags containing more than 1 SNP per locus and deviation from the expected 1:2:1 segregation ratio for an F2 population ($p<0.10$) were omitted to generate a bi-allelic, homologous set of 1,798 polymorphic loci. Joinmap 4.1 was used to construct linkage groups using a minimum logarithm of odds (LOD) score of 3.0 and a maximum recombination frequency of 0.35. Strong evidence was provided for 24 linkage groups with LOD scores ≥8.0, corresponding to the expected haploid chromosome number set (2n=24) for sweet basil. The MRI x SB22 F2 mapping population demonstrates segregation for downy mildew (*Peronospora belbahrii*) response, Fusarium wilt (*Fusarium oxysporum* f.sp. *basilici*) response and content of major flavor/aroma volatile compounds. Development of the first sweet basil genetic map using the MRI x SB22 population provides the basis for quantitative trait loci (QTL) mapping of disease resistance and flavor/aroma.

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HEAT TOLERANT WHEAT BREEDING FOR CLIMATE CHANGE ADAPTATION AND FOOD SECURITY IN BANGLADESH

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Wheat, the second most important cereal crop in Bangladesh, is normally subjected to multiple environmental stresses including extreme heat. Terminal heat during grain fill is the most common abiotic stress and reduces wheat yield by 0.2 to 0.5 t ha^{-1} with each one degree Celsius increase in temperature. Most of the wheat in Bangladesh encounters heat stress at grain filling, and to sustain yield it is extremely important to develop heat tolerant varieties. With this objective, 16SABWGPYT nurseries were planted in Bangladesh to perform association mapping to identify heat tolerant QTLs, development of molecular markers, and selecting candidate genotypes for use in the development to heat tolerant varieties. Six hundred advanced breeding lines from CIMMYT and USAID Feed the Future Innovation Lab were evaluated and screened using augmented incomplete block design with two replications. Data were recorded for NDVI, canopy temperature, heading, maturity, grains per spike, thousand grain weight, and yield using handheld high throughput phenotyping platform. All 600 lines have been genotyped using genotyping-by-sequencing. The genotypic and phenotypic data will be used for association mapping for heat tolerance. Moreover, the data will be analyzed to calculate Genomic Estimated Breeding Values (GEBVs) that will accelerate the selection of candidate wheat lines. These candidate lines will be used in developing and released as superior varieties.

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DISTRIBUTION OF GENES CONTROLLING TOMATO SIZE AND SHAPE IN MODERN GERMPLASM

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Fruit shape and size are important selection criteria in vegetable breeding programs. Tracing the origin of the alleles in wild and cultivated germplasm provides insights into the history of the crop's domestication as well as providing information for crop improvement. Analyses of 1,008 tomato accessions, including members of the *Solanum lycopersicum var. lycopersicum* (SLL), *S. lycopersicum var. cerasiforme* (SLC), and S. *pimpinellifolium* (SP), showed the frequency of the derived alleles in 42 tomato subclasses[1] (Blanca et al, 2015). Subclasses were determined via PCA analysis using 7,720 SNP markers. Cultivated tomatoes (SLL) was classified into 5 groups and 12 subclasses[2] (Blanca et al, 2015). Our aim was to genetically compare the cultivated tomato subclasses. We investigated the allelic distributions of the major fruit weight loci (FW2.2, FW3.2 and FW11.3) and major fruit shape loci (LC, FAS, OVATE and SUN) for SLL. Subclasses SLL_1, SLL_early_breed, and SLL_processing_1_3 have the derived allele fixed for FW2.2, FW3.2 and FW11.3; and the wild allele fixed for FAS, OVATE and SUN. SLL_fresh_1 and SLL_fresh_2 have the derived allele fixed for FW3.2 and FW11.3, and the wild allele fixed for OVATE and SUN. In subclasses SLL_Mesoamerica, SLL_vintage/fresh and SLL_vintage_1 the derived allele for LC, FW2.2, FW3.2 and FW11.3 has higher frequency. For FAS, OVATE and SUN the wild allele has higher frequency in the vintage germplasm that was included in this study. The remaining subclasses show a combination of wild and derived alleles, fixed alleles for some loci, and heterozygote genotypes. The observed allele distributions suggest that tomato fruit was selected for larger size, as the derived fruit weight alleles are predominant across most of the subclasses. The allele distributions for the tomato fruit shape genes indicates that the wild alleles are predominant for most subclasses. This suggests that uniform rounder shapes have been the priority in general in tomato selection and breeding. Overall, it appears as tomato fruit was selected for larger and uniformly shaped fruit with few locules.

[1]Subclasses have at least 4 accessions

[2]Subclasses have at least 2 accessions

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BREEDING HIGH AMYLOSE RICE FOR THE US CANNING INDUSTRY AND EXPORT MARKETS

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Grain quality traits are important determinants of end-user acceptance and, therefore, the market success of new rice varieties. Acceptable grain quality, however, is perceived differently across geographical regions and amongst end-users. A major portion of the export market for US rice as well as the food processing and canning industry in the US, for example, favor high apparent amylose content, one of the key predictors of rice eating quality, as opposed to the intermediate and low amylose contents of most rice varieties originating from Asia and US breeding programs. To address this preference, we have dedicated a variety development pipeline for high amylose rice intended for both table use and as raw material in the rice processing industry, termed 'dual-purpose grain quality type'. Having both the high amylose content and intermediate gelatinization temperature traits, this varietal type satisfies both the cooked rice preferences of Central American markets, where most southern US rice is exported, and the improved canning stability and reduced washout losses preferred by the US food processing industry. To develop this grain quality type, parents with 'Newrex/Rexmont/Dixiebelle' cook type are used extensively in hybridization. The high amylose varieties Rexmont and Sabine, for example, have been utilized extensively as parents in crosses made since 2011. A dedicated variety development pipeline emphasizing high apparent amylose content, low chalkiness, and excellent milling traits during selection and/or yield testing stages, on the other hand, is used to identify breeding lines that outperform conventional long-grain and dual-purpose variety standards for both producer- and end-user-desired traits. In 2015, a high-amylose breeding line RU1104122 was identified for release as the first Clearfield® high-amylose rice variety that is now marketed by Horizon Ag as CL163. Also, a new conventional-type breeding line RU1104077, with high amylose content, low chalkiness, and milling traits acceptable to major rice millers in the US and Costa Rica will be released in 2016. These new rice releases provide additional options for US rice producers as well as the food processing industry. They also have good potential to capture added value via identity preservation in order to address the negative issues raised against the overall quality of US rice in recent years, thus increasing US rice competitiveness.

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IMPROVING SOYBEAN FOR INCREASED PRODUCTIVITY ON SPECIFIC SOIL TYPES

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Selection of soybean genotypes for release depends largely on the environment in which they will be grown. Many traits are tailored for the abiotic or biotic stresses present in specific environments, including drought & flood tolerance, soybean cyst nematode (*Heterodera glycines*) resistance, and resistance to Phytophthora root rot (*Phytophthora megasperma*). Also, many traits are suited for every environment. Breeders must determine those necessary traits when planning crosses for each environment. Often, material suited for one environment may be found when evaluating another. It is important to note how our selections may translate from one environment to the next. The objective of this study is to evaluate trait selection of lines planted on three diverse soil textures, to determine those traits necessary in each environment, and to determine whether any correlation can be made for selection regardless of soil type. In 2014, six F_5 nursery populations were planted in three different environments: a clay, loam, and sand soil type all located in the Missouri Bootheel. From these populations, selections were made to determine the ten best and ten poorest lines from each population and location combination. These lines were then replanted on each soil type in a replicated yield trial in 2015, along with the parents of each population and a competitive check. Tissue collection was conducted for genotyping, and field measurements were taken including yield, height, lodging, seed characteristics and maturity. Selections from each soil type were evaluated for their performance in all three soil environments. Statistical analysis was conducted using the general linear model procedure of the Statistical Analysis System (SAS) to determine if any difference could be found between our best and poorest selections both within and across soil types. Selections made on clay and sandy soils in 2014 were found to show significant differences when replanted on their respective soil type. However, when those selections were planted on other soils, no significant difference in yield could be found between selection categories. This indicates that our selections on clay and sand did not translate well to other environments. Selections made on loam soils in 2014 were found to be significantly different when planted on every soil type in 2015. In each occurrence, our best selections yielded significantly higher than our poorest. These data infer that when choosing one site to evaluate nursery populations, a loam soil type provides the best discrimination for all environments. Once genotyping has been completed on the superior and inferior lines, we hope to shed more light on the underlying traits associated with these differences. This will equip breeders with a better understanding on how to approach crosses for these environments in the future.

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PHENOAPPS: OPEN-SOURCE ANDROID APPS FOR PHENOTYPING

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Plant breeding and genetics research is an inherently data-driven enterprise. Typical experiments and breeding nurseries can contain thousands of unique entries and programs will often evaluate tens of thousands of plots each year. Due to temporal and economic limitations, many phenotypes that could prove useful for selection are neglected or collected only on a subset of lines. To operate a modern breeding program efficiently, electronic data capture and management is essential. Many research programs, however, continue to function by scribing and transcribing much, if not all, of their data. This places heavy burdens on human resources, decreases data integrity, and limits future utilization of data. We have developed several open-source apps to increase the speed and robustness of data collection in plant breeding programs. All of our apps run on consumer-grade Android phones and tablets, decreasing the cost to breeders and creating a viable solution for research programs in developing countries. By utilizing a modern mobile operating system makes, it becomes simple to receive feedback, add requested features, and publish updates. Field Book, an app for field and greenhouse data collection, has a simple and intuitive interface that allows adoption without a steep learning curve. Inventory pairs with a USB scale to simultaneously organize and weigh samples. Coordinate organizes data being collected in grids using customized templates. 1KK extracts seed morphological measurements from photos taken with the device camera. In creating these PhenoApps, we attempt to decrease both technological and cost barriers that hinder adoption of electronic data management in breeding programs. With our open-source, accessible solutions, the vision of one handheld per breeder can become a reality for plant breeding and genetics programs around the world and will enable the transformational capacity essential to achieve a contemporary green revolution.

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GENOME-WIDE FAMILY PREDICTION

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Genomic selection (GS) is used to compute genomic estimated breeding values (GEBV) of individuals. Implementation of GS in minor crops is limited by the high cost of genotyping each individual of the population. Furthermore, in some crops selection is performed at family, instead of the individual level. Here we studied the implementation of genome-wide family prediction (GWFP) in two loblolly pine (*Pinus taeda* L.) populations: i) a real breeding population composed of 63 families (5-20 individuals per family), phenotyped for four traits and genotyped using an Illumina Infinium assay with 4740 polymorphic SNPs, and ii) a simulated population, with a similar pedigree, 5000 polymorphic loci and two traits (oligogenic and polygenic). In both populations, phenotypic and genotypic data were pooled at the family level *in silico*. Phenotypes were averaged across all individuals and allele frequencies were computed for each SNP. Additionally, phenotypic data for each trait was divided into three classes: the smallest 10%, the largest 10%, and values between these extreme categories. Four validation populations were created: i) bottom: 10% families showing the smallest phenotypic values, ii) top: 10% families having the largest values, iii) middle: 10% families showing phenotypes between bottom and top, iv) combined: 3% from families in the bottom, 3% from top, and 5% of families from the middle. Marker effects were estimated at the individual (GEBV) and family (GWFP) levels with Bayes-B using BGLR, and validated using 10-fold cross validation. Predictive ability (correlating phenotypes with GEBV and GWFP) was higher for GWFP in both populations, even after standardizing GWFP to be comparable with traditional GS. In addition, prediction was always higher and more accurate for combined validations. Results revealed great potential for using GWFP in breeding programs that select families, such as outbreeding forage species, due to a significant reduction in genotyping and phenotyping cost.

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PARTIONING GENETIC VARIANCE TO QUANTIFY AND EXPLOIT HETEROSIS BETWEEN THE THREE SUB-GENOMES OF ALLOHEXAPLOID WHEAT

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The union of two complete suites of genes in a hybridization event that produces a new allopolyploid presents manifold possibilities for the resulting organism to adapt to new environments. The presence of multiple divergent homeoalleles, adapted to different environments in the founder species, allows immediate gene multi-functionality, and therefore environmental adaptability. With the availability of affordable genotyping and a reference genome to locate markers, breeders of allopolyploids now have the opportunity to manipulate sub-genomes independently. Additionally, this presents a unique opportunity to investigate additive effects and interactions of homeoalleles between sub-genomes as well as their interactions with the environment. We present theory and a statistical framework for partitioning genetic variance to individual sub-genomes of allopolyploids, predicting breeding values for each sub-genome, and determining the importance of inter-genomic heterosis using an allohexaploid wheat breeding population as an example. Due to the non-random mating typical of a breeding program, significant population structure causes a high correlation between the estimated additive genetic covariances for the three sub-genomes. Singular value decomposition of the genotype matrix was used to remove the largest sources of variance as a fixed population structure effect, and estimate covariance of sub-genomes based on the remaining dimensions. Predictive ability was equivalent to current genomic prediction methods and variance estimates from data sampling appeared relatively stable. Thus, we provide a new tool for breeders of allopolyploid crops to characterize the genetic architecture of existing populations, determine breeding goals, and develop new strategies for selection of additive effects and inter-genomic heterosis.

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THE EFFECTS OF *LYCOPENE B-CYCLASE* (*CYC-B*) ALLELE INTROGRESSION ON CHERRY TOMATO FRUIT QUALITY

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β-carotene is a carotenoid pigment from plants that supplies the most reliable source of pro-vitamin A in the diet. Tomato (*Solanum lycopersicum*), as one of the most frequently consumed vegetables, provides a model for improving dietary *β*-carotene. High *β*-carotene is imparted by alleles of the fruit specific *β*-cyclase gene, *Beta* (*B*). Alleles of *B* from three different sources were introgressed into a grape-cherry tomato, Tainan (PI 647556). These sources are Jaune Flamme and Purdue 89-28-1, both derived from *S. habrochaites*. The variety 97L97, a USDA release with *B* from *S. galapagense* was also used. Alleles were sequenced to develop molecular markers for seedling selection. BC_1 and BC_2 populations were genotyped for the *B* allele from each of the exotic sources. Background selection was applied on the BC1 plants using polymorphic insertion-deletion markers located on chromosome two and eleven. BC_2 populations were screened with 34 single nucleotide polymorphisms (SNPs) distributed across the genome. Evaluation of fruit quality in BC_1S_1 populations was based on a two-location replicated trial, with quantitative data collected for Brix, titratable acidity, and sensory attributes as measured by trained panelists. The source of the *B* allele contributed 16.1% of the variance for Brix. Location of the trial, Fremont or Wooster, explained only 1.2% of the variation for Brix. Plants with *BB* had significantly higher Brix than those with *bb*, suggesting that *B* allele or linked genes might affect sugar production. The sensory attributes measured were for fruit aroma, flavor, and texture. Panelists detected differences in flavor and texture attributes that depended on the source of the *B* allele. These analyses will help us determine which source of high *β*-carotene will be most useful in developing a quality grape-cherry tomato.

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TRAINING POPULATION AND ENVIRONMENT SELECTION FOR GENOMIC SELECTION OPTIMIZATION IN A HISTORICAL DATA SET OF SOUTHEASTERN US WINTER WHEAT

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Commercial breeding programs evaluate germplasm in the field every year and select the best individuals through years until obtain one or several new varieties at the end of each breeding cycle. A new tool, Genomic Selection (GS) is revolutionizing the way in which breeders can select new germplasm by reducing the amount of testing required with conventional approaches. GS is based in prediction of Genomic Estimated Breeding Values (GEBV) for new individuals with genome-wide marker information using a set of individuals with phenotypic and molecular marker data as training population (TP). Genotyping by sequencing (GBS) is used to generates high-density genome coverage at low cost. Accuracy of the GS model is evaluated by Pearson correlation between GEBV and BLUE. Random cross validation procedure yields different accuracies suggesting that the model can be improved by choosing the adequate set of individuals to be included in the training population in addition to selecting an adequate set of environment for which predictions will be make. The goals of this work are to determine the best accommodation of individuals in the TP and to evaluate the effect different subsets of environments on the accuracy of GS model. A set of 450 soft red winter wheat lines from GAWN over nine years were genotyped. The phenotypic data was unbalanced, with few varieties repeated across years and included yield, test weight, plant height, and heading date from 2008 to 2016. The GS model utilized in this study was Ridge Regression through the R-package RR-BLUP. Preliminary random cross validation results shown a mean accuracy of 0.60, 0.38, 0.48, and 0.56 for yield, test weight, plant height and heading date respectively, however maximum values were between 0.7 and 0.8 for each trait, which suggest potential to improve the GS model. Strategies to optimize GS models will be presented.

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UNLOCKING THE POTENTIAL OF TRANSCRIPTIONAL GENE SILENCING BASED RESISTANCE BULLETS AGAINST BEGOMOVIRUS LEAF CURL DISEASE COMPLEX

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Whitefly transmitted geminivirus are circular ssDNA viruses and known to be a major problem in the cotton and other crops in Pakistan particularly in the Punjab region. Crops infected with these viruses show a notable decrease in the yield which results in major losses for farmers in particular and for the nation's economy in general. Transcriptional gene silencing (TGS) is a novel intrinsic biochemical pathway in plant that blocks specific gene expression by promoter methylation. Transgenic cotton expressing the siRNA bullets homologous to the intergenic region of cotton leaf curl Burewala virus develops a wide spectrum resistance to an entire genus of whitefly transmitted geminiviruses. Here we discuss how small RNAs can be used to direct TGS in transgenic plant against virus infection.

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GENETIC CHARACTERIZATION AND MOLECULAR MAPPING OF HESSIAN FLY RESISTANCE QTL USING A WHEAT DOUBLE HAPLOID POPULATION

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Hessian fly (Hf), *Mayetiola destructor* (Say), is one of the most destructive pests in wheat worldwide. Its infestation at seedling stage results in low wheat seedling vigor and/or plant death. Application of pesticides is not effective and growing resistant cultivars is the preferred method to reduce fly damage. Although many Hf resistance genes have been identified, diagnostic markers are still not available for marker-assisted transfer of these genes to elite breeding lines. In this study, we developed a wheat double haploid (DH) population of 180 lines from the cross between a Hf resistant wheat cultivar Tiger and a susceptible cultivar Danby and used this population to construct a genetic linkage map with 1800 SNP markers generated by genotyping-by-sequencing (GBS). Meanwhile the DH population was screened for Hf resistance in the greenhouse in fall 2014 and spring 2015. Using the high-density SNP map, two QTLs were identified. One major QTL was mapped on the short arm of chromosome 1A, which explained 57% of the phenotypic variation. And the other QTL with a minor effect on chromosome 6D explained 8% of the phenotypic variation. These GBS-based SNP markers closely linked to the two QTLs will be converted into user-friendly KASP markers and validated in a diversity panel of cultivars and breeding lines. The markers linked to the two QTLs will be useful for pyramiding Hessian fly resistance genes in wheat breeding programs.

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GENETIC VARIATION IN POST-ANTHESIS HEAT STRESS TOLERANCE IN US SOFT WHEAT GERMPLASMS

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Global climate change effect especially stress due to high temperature at grain filling has emerged as a major constraint to achieve global food security. Post-anthesis heat stress is a common yield-limiting factor in US wheat growing areas. The annual occurrence of moderate heat stress, accompanied by periodic extreme heat stress events, prevents wheat from reaching its full potential yield. The huge yield reduction and quality loss of the wheat crop due to terminal heat stress, particularly at the time of grain filling, is a driving force for the development of thermotolerant wheat cultivars. Florida is an ideal location for screening post-anthesis heat stress in wheat germplasm due to more than optimum high temperature throughout the growing season, particularly during grain filling. A diversity panel, comprised of 246 southeastern soft wheat genotypes, was evaluated in two heat stressed locations, Citra and Quincy, FL for different stay-green (NDVI and SPAD chlorophyll content) and adaptation (canopy temperature, CT) traits. Our preliminary data analysis showed that there are significant genetic variations in CT, SPAD chlorophyll content and NDVI among genotypes. Our goal is to find unique alleles associated with those traits through genome-wide association analysis and utilize that information for genetic improvement for heat tolerance.

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PHENOTYPIC ASSESMENT OF CIMMYT WHEAT VARIETIES USING SMALL UNMANNED AERIAL SYSTEMS

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Next-generation phenotyping and genotyping tools promise to achieve desired genetic gains in breeding programs. The recent developments in the sensing and robotic technologies hold the potential to address the existing limitations in the High Throughput Phenotyping (HTP) systems. A Small Unmanned Aerial System or sUAS, fitted with lightweight spectral imaging sensors will enable high-throughput, precision analysis of a large number of breeding plots. Following the semi-automatic image processing and data analysis pipeline developed in our lab, we processed six datasets representing two years (2015 and 2016) and three agro-climatic zones across the wheat growing Indo-Gangetic Plains of India (Ludhiana, Jabalpur and PUSA). Two data extraction strategies to estimate the Digital Elevation Model (DEM)-derived plant height were evaluated. The first strategy was based on the quantile cutoffs of the crop canopy and ground surface pixels. Here, the plot-level absolute plant height was derived by subtracting the mean of the bottom 5% ground pixels from the top 85-95% pixels from the DEM. In the second approach, the ground Digital Terrain Model (DTM) was first inferred based on a nearest neighbor classification criterion. This ground DTM was then subtracted from the non-ground crop surface model to derive the absolute plant height. The quantile-based approach was highly correlated with the "ground-truth" plant height measurements (R^2=0.46, $p < 0.001$) compared to DTM based approach (R^2=0.32, $p < 0.001$). The within-site broad-sense heritability (H^2) ranged from 0.50 to 0.88 and 0.32 to 0.71 for the quantile and DTM approaches, respectively. The predictive ability of proximal measurements to target traits of biomass and grain yield is currently being analyzed. These initial results have improved the data management protocols, image processing pipelines and baseline validation of the phenotypic measurements from the sUAS. Finally, the sUAS aided precise analysis of plant height and other crop phenotypes would allow better dissection of complex plant traits and therefore help accelerate the crop improvement.

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EFFICIENT DONOR SELECTION FROM GENE BANKS

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Genebanks play a critical role to preserve and disseminate germplasm. However, it is a huge task to efficiently select and utilize donor accession(s) for crop improvement. Historically, breeders have relied on the phenotypic data or passport information to select best candidates for genetic introgression, but this approach is very limited since phenotypic information is often lacking or confounded by poor agronomic backgrounds of wild germplasm and passport data is often missing or incorrect. On the other hand, the selection based on genotypic data is expected to be more efficient. We applied genotyping-by-sequencing (GBS) to 565 *Aegilops tauschii* accessions held at Wheat Genetics Resource Center (WGRC) at Kansas State University. With ~145k single nucleotide polymorphic (SNP) markers, we were able to identify and remove ~30% duplicated accessions from the collection. Based on this analysis, a set of unique accessions was developed, which was further scrutinized to select a smaller core set to be used in wheat breeding and improvement. Combining already existing phenotypic data for leaf rust, Hessian fly and stem rust coupled with geographical data, forty *Ae. tauschii* accessions were selected that represent genetically diverse group of accessions. Because of the diversity bottleneck, capturing genetically diverse accessions in wild wheat is important for the wheat improvement. Population genomic analysis revealed that these forty accessions captures >90% allelic diversity present in the population. These accessions can be prioritized for introgressing genes into breeding programs for important traits including drought and heat tolerance.

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DEVELOPMENT AND APPLICATION OF A BIOINFORMATICS PIPELINE FOR GENOTYPING-BY-SEQUENCING (GBS) OF AUTOTETRAPLOID POTATO

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Genotyping-by-Sequencing (GBS) is being widely used in diploid crops as an efficient technology for identifying genome-wide markers to assist breeding. For autotetraploid crops, such as potato, the cost-effectiveness of GBS is less certain due to the higher read depth (50–60X) needed to differentiate the three heterozygous genotypes. Our objective was to develop a bioinformatics pipeline for variant and genotype calling in autotetraploids and apply it to a set of 91 elite breeding potato lines. Single-end 100 bp sequencing was done using two lanes of an Illumina HiSeq2000, which produced 4.6 Gb of quality reads aligned to 0.38% of the 674 Mb potato reference genome (version 4.03). Using the Genome-Analysis-Toolkit (GATK), we identified 62K single nucleotide polymorphisms (SNPs) at a genomic density of one SNP per 42 bp. The number of curated SNPs declined rapidly as the minimum average depth was raised, from 14K SNPs with at least 20X per sample (on average) to only 3300 SNPs with at least 50X. As expected, the number of variants called using both sequencing lanes (effectively 48-plex) was more than twice the number with only one lane (96-plex): the gain of variants with at least 50X per sample (on average) was six-fold. Cross-validation with 2601 Infinium array markers and 161 individuals was used to compare different imputation methods, including k-Nearest Neighbors (kNN), Random Forest (RF), and a polyploid Hidden Markov Model (HMM). For a validation set of 30 individuals, the error rates were 59% with kNN, 48% with RF, and 21% with the HMM. We conclude that GBS is a viable marker technology for autotetraploid potato; however, its cost-effectiveness compared to the potato Infinium array warrants further study.

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DISCOVERY OF GERMPLASM AND GENOMIC REGIONS TO IMPROVE DROUGHT TOLERANCE IN SOYBEAN

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Drought stress is a significant issue threatening the agricultural productivity of soybean (*Glycine max*). Slow canopy wilting and reduced transpiration rate have been used as traits to phenotype soybean plants for drought tolerance. However, the genetic mechanisms governing these strategies are poorly understood. In this study, we attempt to 1) identify soybean germplasm with drought tolerance by phenotyping for drought tolerance related traits in both the growth chamber and field; 2) elucidate genomic regions responsible for these traits using a genome-wide association study approach. A panel of 211 genetically diverse soybean lines genotyped with 50K SNPs was assembled and phenotyped. Field evaluation of canopy wilting was conducted at two locations (Athens, GA and Salina, KS) in 2015 after extended periods with little or no rainfall, and seven genotypes were identified in the top 15% for slow canopy wilting at both locations. Sensitivity of aquaporins can be correlated with the aforementioned traits and was evaluated in replicated walk-in growth chamber studies by calculating the difference in transpiration response of de-rooted soybean shoots to deionized water and a chemical inhibitor solution ($AgNO_3$). Genome-wide association scans have identified putative regions responsible for slow canopy wilting and response to the aquaporin inhibitor. Four of these regions matched QTL locations identified in previous studies for slow canopy wilting. Additional phenotyping of this panel and a RIL population will be conducted in 2016 using the previously mentioned techniques and a novel field-based approach to visualize canopy architecture.

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IMAGE-BASED PHENOTYPING AND BAYESIAN ANALYSIS OF A DIALLEL MATING DESIGN FOR TOP SIZE IN CARROT (*DAUCUS CAROTA*, L.)

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Crop establishment in carrot is limited by erratic germination, slow seedling growth, and delayed canopy closure, resulting in high management costs for weed control. Varieties with improved top size traits, such as higher shoot biomass and rapid canopy closure, may help mitigate weed control, but research on the genetics of these traits in carrot is limited. This project aims to estimate the genetic components of carrot top size using a diallel mating design and image-based phenotyping. Six diverse carrot inbred lines were crossed, including reciprocals, in Madison, WI in 2014 and 2015. F1 progenies and parents were grown out in a randomized complete block design (RCBD) with two blocks in El Centro, CA (2014, 2015) and in Hancock, WI (2015). Midseason and harvest measurements were taken for canopy height, canopy width, shoot biomass, and root biomass. Estimates of general combining ability (GCA), specific combining ability (SCA), and reciprocal effects were obtained using Griffing's Method I, Model I. In parallel, a general Bayesian approach was used to estimate additive, inbreeding, epistatic, and parent-of-origin effects and to avoid common challenges in traditional diallel analysis (e.g. missing data, outliers, model selection, and interpretation). Results from both analyses suggest that additive and dominance variation influence top size, with additive effects having a greater influence. The presence of additive genetic variation suggests top size phenotypes will respond to selection, while interactions due to non-additive genetic variation will be useful for the identification of superior hybrid combinations and heterotic groups. The Bayesian approach provided a more flexible means of analysis and more detailed estimates of genetic architecture for the traits measured. Image-based measurements of carrot morphology reduced the time needed to collect data, correlated well with hand measurements, and allowed quantification of previously unmeasured parameters such as root shape. The outcomes of this project will help facilitate breeding efforts and inform selection strategies for carrot improvement.

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EVALUATION OF TWO WINTER BARLEY MAPPING POPULATIONS FOR RESISTANCE TO FUSARIUM HEAD BLIGHT

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Fusarium head blight (FHB), caused by the pathogen *Fusarium graminearum* Schwabe, is a devastating fungal disease of barley (*Hordeum vulgare*) in the Mid-Atlantic region of the Unites States. Barley producers can experience severe quality and yield losses as a result of Fusarium damaged kernels and the production of mycotoxins. There has been a recent resurgence in winter barley production for its use as livestock feed, health foods, and malt. With the growing demand for barley, an emphasis on developing elite barley cultivars conferring greater resistance to relevant diseases is needed in order to meet the current and future demands of this grain crop. The objectives of this study are to identify FHB resistance quantitative trait loci (QTL) in the hulless winter barley cultivar Eve and to develop diagnostic markers for use in marker-assisted selection. Two mapping populations, comprised of recombinant inbred lines (RILs), were derived from crosses of resistant parent Eve to two FHB susceptible lines (Eve/'Doyce' and Eve/VA07H-35WS) in an effort to map resistance to FHB. In the 2015-16 growing season, 180 individuals from each RIL population were evaluated for FHB incidence and FHB severity with the assistance from cooperators in Lexington, KY, Blacksburg, VA and Mt. Holly, VA. In the 2014-2015 growing season, both populations were evaluated in Lexington, KY, Blacksburg, VA, Mt. Holly, VA, Kinston, NC, Raleigh, NC and China for severity and incidence. Genotype by location interactions was found to be significant for FHB incidence, but not for FHB severity between locations. In the Eve/Doyce (E/D) population a significant correlation for FHB incidence was observed in the data from KY and Mt. Holly, VA. Significant correlations were found for FHB severity in the E/D population between KY and Mt. Holly and between KY and Kinston, NC. A significant correction for FHB severity was found between KY and Mt. Holly in the Eve/VA07H-35WS (E/VA) population. The E/VA population was found to have a lower average for FHB severity (22.1%) and FDK (55%) than the E/D population (23.5%, 88%) across the Mt. Holly, KY, and Kinston locations. The E/D population was found to have a lower average for DON concentration (23.5%) than the E/VA population (30.6%) between Mt. Holly and Kinston locations. Each population will be genotyped with 9K SNP and screened for FHB resistance QTL. The FHB resistant QTL will be validated and diagnostic markers will be identified for use in marker-assisted selection in the VT breeding program.

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INFLUENCE OF GENOTYPE AND ENVIRONMENT ON WHEAT GRAIN FRUCTAN CONTENT

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Fructans are naturally occurring plant polymers composed of fructose molecules. Approximately 15% of flowering plant species contain fructans, including wheat. In plants, fructans serve as carbon stores and as a potential form of protection against water deficit. In addition to serving valuable roles in plant growth and development, the characteristics of fructans have potentially beneficial effects on human health. Genotypic variation for inulin content, a specific type of fructan, ranges from 0.4 to 2% in wheat seeds. The purpose of this study was to examine the factors that contribute to observed variation in winter wheat grain fructan content. Total grain fructan content was determined for 288 winter wheat genotypes grown over two years with three locations per year. The factors influencing the observed variation in wheat grain fructan content will be determined based on phenotypic and corresponding genotypic data. The results of this study will be useful for implementing recurrent genomic selection in winter wheat and guiding future decisions regarding breeding methodologies for total fructan content in wheat. A greater understanding of the effects of genotype and environment on fructan content will have implications for breeders, producers, and the food industry.

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CHARACTERIZATION OF A MAJOR QTL ON CHROMOSOME 18 ASSOCIATED WITH QUANTITATIVE RESISTANCE TO PHYTOPHTHORA ROOT AND STEM ROT IN SOYBEAN

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Host resistance is the main management practice for *Phytophthora sojae*, a soil-borne oomycete responsible for Phytophthora root and stem rot in soybean. However, the widespread deployment of race-specific *Rps* genes has led to a shift in physiological races of *P. sojae*. Partial resistance on the other hand, is quantitatively inherited and places less selection pressure on *P. sojae* populations. In a previous study, we identified a major quantitative trait locus (QTL) on chromosome 18 for quantitative resistance to *P. sojae*. As major QTL are uncommon in the soybean-*P. sojae* pathosystem, further investigation is warranted. The main goal of this study is to characterize and validate the QTL using near isogenic lines (NILs) derived from three RIL-F_7 individuals heterozygous at the target QTL. The specific objectives of this study are to determine the allelic effect on partial resistance to *P. sojae* and test for pleiotropic effects against other soybean root pathogens and pests. Three sets of NILs were phenotyped for quantitative resistance to *P. sojae* using greenhouse (layer test) and growth chamber (tray test) based assays in conjunction with field evaluation. NILs were phenotyped for resistance to *Fusarium graminearum* and soybean cyst nematode to evaluate pleiotropic effects of the QTL on resistance to these pathogens. NILs with the resistant allele at the QTL, in general, were significantly more resistant to *P. sojae* in the tray test and layer test, whereas, no effect on resistance to either *Fusarium graminearum* or soybean cyst nematode were observed. This characterization of the QTL will facilitate cloning of the gene(s) controlling this trait and use of the resistance allele in breeding programs.

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GENETIC VARIATION IN CARRYING CAPACITY IN LOBLOLLY PINE

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A site can support a finite number of individual plants of a given average size, which can be referred to as the *carrying capacity*. As plants grow and a stand becomes overcrowded, limitations for resources (light, nutrients, and water) will lead to competition and eventually induce mortality in a process called *self-thinning*. Plant species differ in their ability to withstand such competition, a concept known as *tolerance*. In forest tree species, tolerance and self-thinning patterns have been generally considered at the species level; however, tree breeders are increasingly interested in within-species variation for commercially important species. This research investigated differences in tolerance among ten open-pollinated families of loblolly pine (*Pinus taeda* L.) from two diverse provenances (Atlantic Coastal Plain and the Lost Pines of Texas) by evaluating their maximum size-density relationships. The maximum size-density relationship describes the upper boundary of average plant size and number of individuals per unit area on fully-occupied sites, a relationship that typically appears linear on the log-log scale. We modeled the maximum size-density relationship of permanent plots with repeated measurements from stand establishment through age 17 years. Seedlings were planted on a very infertile site in the Sandhills of Scotland County, NC with an optimal fertilization regime treatment and a control treatment (no fertilization) in a randomized complete block design with 9 blocks available for analysis. For fertilized plots, self-thinning started as early as age 10 and all fertilized plots appeared to be self-thinning by age 17. Very few of the control (non-fertilized) plots appeared to be self-thinning at the last measurement age (17 years). Atlantic Coastal Plain families grew much faster and began self-thinning at earlier ages than the Lost Pines Texas families. Differences in tolerance and the rate of self-thinning were found between provenances, with the Lost Pines of Texas displaying higher tolerance and slower rates of self-thinning. Differences in tolerance among open-pollinated families were found for the Atlantic Coastal Plain provenance, but not the Lost Pines Texas provenance. A statistical method for testing the hypothesis about the maximum size-density relationship that accounts for autocorrelation among repeated measurements on individual plots is described. These findings indicate that there may be the potential to select and breed for tolerance to competition among families of loblolly pine.

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PROGENY DERIVED FROM DISOMIC ALIEN ADDITION LINES FROM INTERSUBGENERIC CROSS BETWEEN *GLYCINE MAX* AND *G. TOMENTELLA*

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Disomic alien addition lines (DAALs, 2n=42) were obtained from an intersubgeneric cross between *Glycine max* [L.] Merr. cv. Dwight (2n=40) and *G. tomentella* Hayata (PI 441001, 2n=78). They are morphologically uniform but distinct from either of the parents. These DAALs were all derived from the same monosomic alien addition line (2n=41), and theoretically they should breed true because they had a pair of homologous chromosomes from *G. tomentella* and 40 soybean chromosomes. However, in some selfed progenies of DAALs the extra *G. tomentella* chromosomes were eliminated resulting in disomic progeny lines with 2n=40 chromosomes that had many phenotypic differences. The objectives of this research were to document the phenotypic variation among the progeny of these DAALs, and to understand the genetics behind these phenomena. In a replicated field study, variation was observed among the disomic progenies for the qualitative traits such as flower, seed coat, hilum, pod, and pubescence color, and stem termination that exist in neither parent. Differences were also observed for the quantitative traits protein and oil concentrations, plant height, lodging, and time of maturity. Among the disomic progeny population, we have documented lines with higher protein and oil concentration and lines that yield more than either the DAAL or Dwight. One line carries novel recessive allele at the pubescence color locus (*T*). Studying the plant transcriptome via RNA-sequencing documented that many genes that are critical to fundamental plant growth processes and related to stress and defense responses were differentially expressed between the DAAL (LG13-7552) and one of the disomic progeny (LG12-7063). Genetic studies have shown that the observed phenotypic changes are from DNA sequence changes.

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GENETIC DISSECTION OF YIELD-RELATED TRAITS IN A SOFT RED WINTER WHEAT PANEL GROWN IN VIRGINIA

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Despite the widespread adoption of genome-wide association (GWA) studies for examining quantitative traits in many different species, relatively few GWA studies have been conducted to study yield-related traits in wheat (*Triticum aestivum*), and even fewer in winter wheat specifically. Recently, genomic analyses in species lacking reference genomes have been facilitated by the adoption of genotyping-by-sequencing (GBS) technology, as well as various bioinformatics tools enabling the estimation of gene order on assembled chromosomal pseudomolecules. This study sought to assess the use of GBS-generated single-nucleotide polymorphism (SNP) marker data for performing GWA studies to identify yield-related quantitative trait loci (QTL) in winter wheat. Markers were aligned to the International Wheat Genome Sequencing Consortium's Chromosome Survey Sequence and assigned physical positions using population sequencing data. The germplasm used was included in an Allele-Based Breeding (ABB) panel as part of the USDA-NIFA *Triticeae* Coordinated Agricultural Project (TCAP), and consisted of 181 soft red winter (SRW) wheat lines from three regional breeding programs (Illinois, Kentucky and Virginia). Lines were evaluated in randomized complete block designs with 2 replications grown in Blacksburg and Warsaw, VA during the 2013-2014 and 2014-2015 winter wheat growing seasons. Data was collected on a total of eighteen yield-related phenotypic traits, including grain yield *per se*, test weight, plant height, harvest index, seeds per m^{-2}, seeds per head, and physiological development dates including heading date, physiological maturity date, and flag leaf senescence date. GWA analysis revealed a number of significant quantitative trait loci for the traits physiological maturity date, grain fill duration, normalized difference vegetation index (NDVI) at Zadok's growth stage 25, seeds per head, and grain starch content. The SNP significantly associated with grain fill duration is located on chromosome 5D, and is especially interesting as it is intronic within a gene containing a conserved DNA-binding ethylene response factor domain. Thus there is a plausible functional explanation for this SNP's effect on grain fill duration, though further work will be required to test this hypothesis.

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METABOLITE AND TRANSCRIPT PROFILING IN *ARABIDOPSIS THALIANA* TO INVESTIGATE THE INTERACTION BETWEEN RESPONSES TO COOL TEMPERATURE AND *PSEUDOMONAS SYRINGAE* INFECTION

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Salicylic acid (SA) is a critical phytohormone promoting plant defense responses against biotrophic pathogens. Interestingly, SA accumulates to a similar extent after pathogen infection as during multi-day exposure to cool temperatures, suggesting that plants acclimated to cool temperatures may mount faster and/or stronger pathogen defense responses. We chose to address this question with *Arabidopsis thaliana* and the Gram-negative bacteria *Pseudomonas syringae pv tomato* (*Pst*) because their interaction is one of the best studied in molecular plant physiology. Cold-acclimation treatments were performed using a 10°C day/8°C night temperature regime. Plants that experienced different durations of cool temperature exposure (0- 7 days) were syringe-infiltrated with *Pst* either at 10°C (simultaneous stress) or at 20°C after 10 hours of cold de-acclimation (sequential stress). Differential susceptibility to *Pst* was assessed by measuring bacterial growth in the leaf (colony forming units/leaf area) 3-5 days after infiltration. The simultaneous and sequential stress designs produced similar results: whether cold-acclimation increased or decreased susceptibility to *Pst* depended on the duration of cold-acclimation prior to infection. Short periods of cold-acclimation (1-4 days) resulted in increased susceptibility to *Pst*. This increased susceptibility was found to be absent in plants exposed to 10°/8°C for a longer period (7 days). Furthermore, the increased susceptibility effect found after relatively short exposure to 10°/8°C was dampened by 10 hours of de-acclimation at 20°C before infiltration (sequential stress design). In order to investigate the metabolic and gene-regulatory underpinnings of these results, we are using a combination of gas chromatography–mass spectrometry, microarray, and RNA-sequencing profiling platforms. Such approaches are allowing us to identify signatures of cold-acclimation-mediated suppression of induced plant defense responses. For example, we are interested in understanding what elements of short term cold-acclimation are antagonistic to SA-mediated pathogen defense responses. The outcome of combinatorial stress (whether simultaneous or sequential) is typically difficult to predict from knowledge of how plants respond to the stresses individually. However, not only are combinatorial stress studies more relevant to understanding the realities of plant life in agricultural and natural environments, but they also provide a potentially powerful approach to study synergistic and antagonistic interactions between regulatory processes at the systems level.

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MOLECULAR CHARACTERIZATION OF THREE NOVEL WHEAT *VRN-B1* GENES REVEAL STRUCTURAL VARIATION IN CODING REGIONS AFFECTING FLOWERING TIME

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Vernalization requirement has allowed winter wheat to grow successfully in temperate climates. Natural allelic variation of vernalization genes have conferred wheat populations the ability to adapt and persist in diverse geographical regions. Unpredictable temperature swings will affect temperate winter wheat growing regions in the United States. To develop climate resilient wheat varieties, unique vernalization genes could be stacked in different combinations to confer a range of flowering time response. To identify unique vernalization genes in diverse wheat populations, we employed a targeted next generation amplicon sequencing approach and identified three novel *VRN-B1* genes with mutations in exonic regions. The three *VRN-B1* variants detected led to a nonsynonymous mutation in exon 7, a three base pair deletion in exon 7 resulted in a frameshift mutation, and a two base pair deletion in exon 8 resulted in a premature stop codon. Lines carrying the respective mutations had late flowering phenotypes. Mutations within the *VRN-B1* coding regions are predicted to affect protein structure and function. Molecular marker analyses of the *VRN-B1* variants were predominantly present in Iranian wheat germplasm. The resources developed in this study will provide wheat breeders with additional sources of *VRN1* gene variants for breeding climate resilient cultivars.

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