



**Joint International Sweet
Corn Development
Association (ISCDA)
and
Corn Breeding Research
(CBR – NCCC167) Annual
Meeting**

December 9-10, 2019

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Monday, December 9, 2019

8:00 am Opening remarks

Larry Darrah Student Presentations Session 1

8:15am *Genetic dissection of resistance to corn stunt disease complex using a tropical maize diversity panel*
Fernando Espolador - University of São Paulo/University of Wisconsin

8:30am *Sugarcane mosaic virus resistance in the Wisconsin sweet maize diversity panel*
Lillian Hislop - University of Wisconsin

8:45am *Sweet corn production in the Columbia Basin of Washington: Screening for cold tolerance and resistance to seedling blights*
Ryan Solemslie - Washington State University

9:00am *Nitrogen stress affects the determination of heterotic groups in tropical maize*
Júlia Morosini - University of São Paulo/University of Wisconsin

9:15am *Going with the flow: predicting water-use efficiency in maize*
Lucas Roberts - University of Illinois

9:30am *Comparing controlled environmental conditions to simulate field trial emergence in sweet corn*
Linda Dao - University of Florida

9:45 Break

Larry Darrah Student Presentations Session 2

10:25am *Finding patterns of inbreeding in some ex-PVP lines members of the stiff stalk heterotic group*
Fernando Aguilar - Iowa State University

10:40am *Population genomic analyses of sweet corn*
Vincent Colantonio - University of Florida

10:55am *Influence of selection on performance stability in the maize BSSS population*

Bridget McFarland - University of Wisconsin

- 11:10am *Predicting sugar and starch in mature sweet corn kernels*
Hope Hersh - University of Florida
- 11:25am *Crop growth model calibration of 15 publicly available corn hybrids in North America*
Cassandra Winn - Iowa State University
- 11:40am *Utilizing doubled haploids in sweet corn breeding: haploid induction and selection*
Nicholas Boerman - Iowa State University
- 11:55pm Lunch
- 1:30pm *Recent developments tweaking starch biosynthesis and creating new products in fresh corn*
Bill Tracy, Ph.D. - University of Wisconsin
- 2:00pm *GEM- Germplasm Enhancement of Maize Project: increasing genetic diversity in public and private sector maize breeding*
Walter Trevisan, MS.c. - GEM steering committee chair
- 2:30pm *overexpression of a maize transcription factor in maize increases grain yield in the field*
Jeff Habben, Ph.D. - Corteva Agriscience
- 3:00pm Break
- 3:30pm *High-throughput phenotyping*
Addie Thompson, Ph.D. - Michigan State University
- 4:00pm *Ionomics and nutritional quality of sweet corn*
Matt Baseggio, Ph.D. - Seneca Foods
- 4:30pm *From Genomes to Fields: Exploring genotype-by-environment interactions and environment specific prediction in maize hybrids*
Anna Rogers, NCSU
- 5:00pm ISCDA Business Meeting

Tuesday, December 10, 2019

- 8:00am *Putting the G in GxE*
Cinta Romay, Ph.D.- Cornell University
- 8:30am *Expanding the vision of near-infrared spectroscopy to create novel breeding tools for Sweet Corn.*
Jeff Gustin, Ph.D. - University of Florida
- 9:00am *Diversity breeding and technology deployment*
Emily Combs, Ph.D. - Corteva Agriscience
- 9:30am Break
- 10:00am *Influence of sweet corn quality traits on willingness to pay for fresh sweet corn*
Paul Mitchell, Ph.D. - University of Wisconsin
- 10:30am *Methods to identify multiple disease resistance in maize*
Peter Balint-Kurti, Ph.D - USDA
- 11:00am *Maize volatiles that guide the behavior of the insect pest fall armyworm*
Anna Block, Ph.D - USDA
- 11:30am NCCC167 Business Meeting

Genetic Dissection of Resistance to the Corn Stunt Disease Complex Using a Tropical Maize Diversity Panel

Espolador, Fernando Garcia^{1,2*}; Morosini, Júlia Silva^{1,2}; Gevartosky, Raysa¹; Gotardi, Leonardo Fioravante¹; Borsato Junior; Ronaldo¹; de Leon, Natalia¹; Fritsche-Neto, Roberto²

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Abstract

The Corn Stunt Disease and the Maize Bushy Stunt Phytoplasma are severe maize diseases transmitted by the vector *Dalbulus maidis*, and are commonly identified as Corn Stunt Disease Complex. Recently, they have gained emphasis due to the significant productivity losses that they have inflicted in tropical areas. Despite their severity, there is limited information about the genes control of resistance for this disease complex. In this context, we performed a genomic wide association study (GWAS) to identify areas of the genome associated with resistance to the Corn Stunt Disease Complex. For that, 13,854 SNPs were assessed on 360 maize inbred lines of a tropical diversity panel. The 360 lines were evaluated in two sites (Piracicaba and Anhumas, Brazil), with two replicates of 20 blocks each. The evaluation included three resistance indices: a) proportion of survivor plants (PSP), b) sanity score in survivor plants (SSSP), and c) whole sanity score (PSP*SSSP = WSS). The GWAS was performed using the R-package FarmCPU with three genomic main principal components, Bonferroni’s multiple tests with alpha equal to 0.01, and a 100kb sliding window to investigate potential genes. In total, we identified seven SNPs to be significantly associated with the resistance indices, which referred to 12 potential resistance-related genes. One of the markers was associated with SSSP and WSS. Each marker explained between 12% to 35% the respective trait. Among the main functions, candidate genes were found to be associated with the gibberellic acid and DNA repair mechanisms, which are tightly connected to symptoms of the disease complex, such as internode short elongation, prolificacy, and leaf chlorosis/necrosis. In addition, defense genes and metabolic routes are also involved, such as terpenoid and salicylic acid. Our findings reveal useful potential candidate genes associated with the Corn Stunt Disease Complex and provide a promising resource for breeding programs.

Funding acknowledgment: This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001, National Council for Scientific and Technological Development (CNPq), São Paulo Research Foundation – FAPESP (Process 2017/24327-0), and University of Wisconsin-Madison.

Sugarcane Mosaic Virus Resistance in the Wisconsin Sweet Maize Diversity Panel

Lillian Hislop, Elizabeth Stephanie, Pat Flannery, William F. Tracy

Abstract

Sugarcane Mosaic Virus (SCMV) is a viral disease that negatively impacts yield in *Zea mays*. The goal of this experiment was to identify sweet maize varieties that show signs of resistance to SCMV and confirm genomic regions of resistance previously identified in field maize (*the Scmv1 and Scmv2 loci*) or characterize regions unique to sweet maize. 8 replicates of 563 sweet maize accessions were tested for SCMV resistance. Plants were inoculated 14 days after planting and observed for signs of infection 28 days after planting. Forty seven of the lines were found to be completely resistant. GWAS was conducted to identify loci corresponding to resistance. We used an Illumina NextSeq500 to genotype 67126 sites using Genotyping By Sequencing for 446 of the tested accessions. This research will aid sweet corn breeders in selecting for SCMV resistance and recognize publicly available germplasm that will be useful to future breeding projects.

Sweet corn production in the Columbia Basin of Washington: Screening for cold tolerance and resistance to seedling blights

Solemslie, Ryan*¹ and du Toit, Lindsey¹

¹ Washington State University Mount Vernon Northwestern Research and Extension Center

Abstract

Washington State is a major producer of sweet corn in the USA with roughly 36,400 ha planted in the semi-arid Columbia Basin annually. However, cold spring soil conditions and soilborne pathogens can cause significant stand and yield losses. In 2018, conventional (n = 31) and organic (n = 16) sweet corn fields were surveyed in the Columbia Basin to assess the prevalence of stand losses and seedling blights. Isolations from stunted seedlings primarily yielded species of *Fusarium*, *Pythium*, and *Rhizoctonia*. Of 63 *Pythium* isolates representing four species, 95.2% were *P. ultimum* based on sequencing the internal transcribed spacer (ITS) region of ribosomal DNA (rDNA). Of 66 *Rhizoctonia* isolates representing five species/anastomosis groups, 69.7% were *R. solani* AG 4 based on ITS rDNA sequences. Of 350 *Fusarium* isolates identified by sequencing the *translation elongation factor 1-alpha* gene, *F. equiseti*, *F. oxysporum*, *F. solani*, and *F. verticillioides* were most prevalent among 14 species identified. Ten isolates of each of *Pythium* and *Rhizoctonia*, and 40 isolates of *Fusarium* were tested for pathogenicity on the sweet corn cv. SuperSweet Jubilee Plus. Isolates of *P. irregulare*, *P. ultimum* and *P. sulcatum* were highly virulent, as were isolates of *R. solani* AG 4 and AG 2. For *Fusarium*, isolates of *F. acuminatum*, *F. graminearum*, *F. fujikuroi*, *F. oxysporum*, *F. proliferatum*, *F. solani*, and *F. verticillioides* were the most virulent. Virulent isolates will be used to screen a sweet corn diversity panel of >600 lines for resistance to seedling blights. In early spring 2019, 182 sweet corn lines from this diversity panel were planted in the Columbia Basin to screen for cold tolerance. Twenty-four breeding lines had better vigor and emergence in the cold spring conditions than a standard processing hybrid, GSS 3071. A similar field trial in the Columbia Basin in 2020 will be used to evaluate the full sweet corn association mapping panel for cold tolerance.

Nitrogen stress affects the determination of heterotic groups in tropical maize

Morosini, Júlia S.^{1,4*}; Espolador, Fernando G.^{1,4}; Vidotti, Miriam S.²; Alves, Filipe C.³; Gevartosky, Raysa¹; Santos, Anna Rita M.¹; de Leon, Natalia⁴; Fritsche-Neto, Roberto¹

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² Plant Breeding Department, Federal University of Goiás, Goiás, Brazil

³ Department of Epidemiology and Biostatistics, Michigan State University, East Lansing, MI

⁴ Department of Agronomy, University of Wisconsin, Madison, WI

Abstract

Nitrogen (N) deficiency is a major constraint for maize productivity, especially in tropical regions. This stress can significantly confound inferences from genetic studies, with negative impact on breeding programs. Thus, we investigated the effect of N deficiency on the determination of two heterotic patterns in tropical maize. For that, 906 maize hybrids obtained from a diallel scheme of 49 inbred lines were genotyped *in silico* using 34,571 SNP and evaluated for grain yield (GY) in four environments in São Paulo, Brazil, each with two N regimes: optimal (OP) and stress (LN). Genotypic estimates were obtained considering an additive+dominance model, in which the general (GCA) and specific (SCA) combining abilities were assessed using an additive and a dominance incidence matrix for lines and hybrids, respectively. From the SCA estimates, we calculated a distance matrix for the 49 lines and performed a hierarchical clustering. The genetic estimates were lower for LN compared to OP (significant at the 0.01 level). For instance, broad-sense heritability increased from 0.25 in LN to 0.32 in OP. The composition of heterotic groups changed considerably between OP and LN (43% and 73% of coincidence for groups 1 and 2, respectively), and the proportion of lines in each cluster remained similar (28x21 for OP and 30x19 for LN). For OP, the best lines concerning GCA were designated to different groups, while for LN they were clustered in the same set. Furthermore, the genetic distance between groups was higher for OP. Our findings indicate that N stress hinders resolution in determining heterotic patterns. Since the environmental effects tend to be higher in stressful conditions, the genetic effects can be underestimated. Therefore, the N stress condition seems to compromise the exploration of heterosis, the main goal in hybrid breeding, and must be appropriately addressed for studies involving N use efficiency.

Funding acknowledgment: São Paulo Research Foundation – FAPESP (Process 2017/25549-6 and 2019/06532-0), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001, University of Wisconsin-Madison.

Going With the Flow: Predicting Water-Use Efficiency in Maize

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Abstract

Water limitation is an increasing threat to crop production across the globe, and in the US, drought is the leading cause of yield loss in maize. Given that commercial hybrids specifically marketed as being drought tolerant have only become available within the last decade, large improvements are likely still attainable for this trait. Selecting for increased abiotic stress tolerance has been one successful approach to enhance plant performance under water limiting conditions. However, a more proactive approach is to select for increased water-use efficiency (WUE) by reducing the amount of water required per unit of grain. This strategy has the potential to prevent or lessen the need for stress tolerance, but could also be complementary as stacked traits. In this study we evaluate the leaf stable carbon isotope ratio, $\delta^{13}\text{C}$, which has been shown to be a proxy trait for WUE in maize. To achieve our goal of developing $\delta^{13}\text{C}$ into a useful trait for breeders, we looked at $\delta^{13}\text{C}$ in a set of 394 off patent lines (ExpVPP) in three locations over two years. With this data we first compared $\delta^{13}\text{C}$ to plant morphological and agronomic phenotypes. No correlations were observed between $\delta^{13}\text{C}$ and other phenotypes, which signifies the value of collecting $\delta^{13}\text{C}$ as an independent data point to represent WUE at the physiological level. Because of the complex genetic architecture of $\delta^{13}\text{C}$, Genotyping-By-Sequencing was performed on our ExpVPP panel in order to run GBLUP models to predict $\delta^{13}\text{C}$. Initial prediction accuracies were low which lead us to implement heterotic group specific models. A next step is to measure whole plant water-use efficiency and test a model that combines $\delta^{13}\text{C}$, morphological traits, and genomic data to assess the predictive advantage of including $\delta^{13}\text{C}$. This type of model would allow breeders to efficiently select for whole plant WUE.

Comparing Controlled Environmental Conditions to Simulate Field Trial Emergence in Sweet Corn

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¹University of Florida

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Abstract

Environmental conditions are important in determining seedling emergence. For early spring plantings, unpredictable weather conditions necessitate cold tolerant varieties. This is particularly important for sweet corn, which have a recommended minimum planting temperature of 5.5°C greater than field corn. We evaluated soil-based growth chamber assays to estimate genetic effects on cold tolerance. Our rationale was to reduce extraneous environmental factors from field trials, while maintaining a soil-based assay. Two cold environments were analyzed: an acute and chronic cold test. The acute test imbibes kernels at 4°C for 5 days with emergence assayed over 7 days at 24°C. The acute test uses a machine vision platform known as VIGOR, which automatically scores emergence with high accuracy. For the chronic cold test, seeds were sown and maintained in 14°C day and 10°C night, 14/10 h cycle to more closely simulate likely field conditions. Emergence was scored by visual counts on a daily basis from 14 to 30 days after sowing. An initial trial was conducted with 6 *sugary1* and *shrunk2* genotypes to compare the two cold conditions along with a 24°C control. The two cold treatments revealed similar trends in cold sensitivity for emergence percentage but had different scales of emergence time. For a second trial, we selected 14 *sugary1* genotypes that had previously been shown to vary in emergence time and percentage in a field study in Central Washington. Comparisons between the field study and the growth chamber data are in progress. We anticipate that these experiments will help define a controlled temperature regime that can be used to find field-relevant alleles associated with sweet corn cold tolerance in a genome wide association study.

Finding patterns of inbreeding in some ex-PVP lines members of the stiff stalk heterotic group

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Abstract

The stiff stalk heterotic group has a narrow germplasm base, increasing the probability to have chromosomal segments that are identical by descent (IBD segments). Identification of these segments can contribute to the understanding of inbreeding depression by detecting long regions harboring mild/small-effect deleterious mutations. The objective of this experiment was to map IBD segments in a set of four inbred lines (B14, B37, B73, and B84) and 11 founders (A3G-3-1-3, AH83, CI187-2, CI540, I159, Hy, Os420, Tr, WD456, B2, and FE) of the BSSS synthetic population. Imputed genotypic data, aligned to B73 AGPv4, was obtained from the Genomes to Fields initiative, season 2017, and from Panzea ZeaGBSv2.7. SNP filtering was performed by keeping biallelic markers and by a calling rate of 95%. After data-cleaning, 313803 SNP loci remained. Regions in the genome that have been inherited from common ancestors (IBD) were identified within and among inbred lines using GERMLINE's algorithm. The coefficient of coancestry (f), was calculated as the ratio of the sum of the length of the shared IBD segments and the total genome length covered by the SNPs (L). Estimates of coancestry between the founder lines ranges between 0.19 to 0.34, suggesting that some regions in the genome have been conserved from several generations. For the four inbred lines, estimates of kinship ranges from 0.35 to 0.59, with more resemblance between B73 and B84 ($f=0.59$), and B14 and B73 ($f=0.54$). Inbred lines B37 and B84 were more closely related to the founder I159, B14 to WD456, while both Hy and I159 were closely related to B73. For all inbred lines, between 50 and 62% of the shared IBD segments were between 0.5 and 1.0 Mb. More in depth analysis to these IBD regions is required to identify deleterious recessive mutations harbored in long homozygote regions with no recombination.

Population Genomic Analyses of Sweet Corn

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Abstract

Sweet corn is predominantly defined by mutations within genes that affect the sugar content of the endosperm, such as *sugary1* and *shrunk2*. Due to these mutations and the importance of a few founder sweet corn varieties to modern germplasm, sweet corn is known to have undergone a major selection bottleneck. To better understand the genomic differences between modern sweet corn and other types of maize, we performed population genomic analyses using publicly available genotype by sequencing data across ~5,000 maize accessions, 590 of which are sweet corn. We performed population structure and phylogenetic analyses and found sweet corn lines to be clustered similarly and next to flint varieties. By comparing populations of *sugary1* and *shrunk2* genotypes against populations of other types of maize, we looked for regions of the genome that are being constrained by selection. Calculations of F_{st} , Tajima's D, and XP-CLR were used to define regions of the genome undergoing selection sweeps. As expected, we discovered genomic regions around the *sugary1* and *shrunk2* genes that were under strong selection. Interestingly, we also discovered areas of strong selection around genes which are known to play roles in flowering time, starch biosynthesis, and sugar transport. Overall, by looking at modern sweet corn germplasm through the eyes of population genetics we can further understand what areas of the genome are being selected for in sweet corn, which can help provide targets for the further genetic improvement of sweet corn.

Influence of selection on performance stability in the maize BSSS population

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¹ Department of Agronomy, University of Wisconsin – Madison

Abstract

To ensure dependable plant growth and productivity in farmers' fields, plant breeders evaluate the stability, or consistency of plant performance across a range of environments, and then select stable hybrids that maximize productivity. The goals of this study were 1) identify environmental stability of hybrids generated by unselected, less selected, and more recently released inbreds derived from the Iowa Stiff Stalk Synthetic (BSSS) population and 2) evaluate how estimates of stability can be refined using climatic data. A set of hybrids was generated by crossing 102 inbred lines derived from BSSS (which varied in release date and selection level) by tester DK311H6. Hybrids were evaluated in 31 environments as part of the GenomesToFields Initiative across two years. Stability was estimated using two environmental indices with Finlay-Wilkinson linear regressions; (1) performance-based, using the average hybrid performance in each environment; and (2) environmentally-based, using average hybrid photothermal time at flowering in each environment. Slope and mean squared error (MSE) estimates were extracted. Estimates from both indices suggest that selecting for improved plant performance is associated with improved stability. The average pairwise population differentiation index (F_{ST}) indicates that selecting for productivity has reduced genetic similarities of the founding BSSS inbred lines as represented on the more selected lines. When comparing values' significant difference from ideal stability, the environmentally-based index identified more hybrids as stable compared to the performance-based index. Future work will focus on identifying key environmental factors to optimize performance stability estimation and ultimately assist breeders with evaluations across environments.

Predicting Sugar and Starch in Mature Sweet Corn Kernels

Hersh, Hope^{1*}; Boehlein, Susan¹; Gustin, Jeff¹; Resende, Marcio¹; Settles, A. Mark¹

¹University of Florida

Abstract

Sweet corn quality is dependent on sugar and starch content in the kernel at eating stage. Sweet corn lines with higher sugar levels at eating stage have a tendency for poor germination and emergence suggesting a trade-off between eating and seed quality. However, the relationship between eating stage constituents and mature kernel composition is not well understood. Quantifying sugar and starch levels analytically is time-consuming and expensive. To enable lower cost phenotyping, we developed a calibration for single kernel near infrared reflectance (skNIR) spectroscopy to predict sugar and starch in mature sweet corn kernels. A panel of 100 sweet corn varieties was assembled consisting of equal parts sugary1 (su1) and shrunken2 (sh2) mutant backgrounds. Single-kernel NIR spectra from 910 nm to 1670 nm were collected for 300 kernels. The individual kernels were milled into a fine powder and sugar and starch were quantified using enzymatic analytical chemistry. Surprisingly, mature su1 and sh2 kernels have extensive overlap of sugar and starch levels suggesting other genetic factors contribute to the final accumulation of these constituents in mature kernels. Predictive models were developed with Partial Least-Squares (PLS) regression of 67 genotypes. The models were then validated with the remaining 33 genotypes. Predictions for preliminary data using skNIR have a standard error of prediction for sugar of 33.2 mg g⁻¹ fw and standard deviation of 49 mg g⁻¹ for su1 and sh2 types. This error was substantially below the standard deviation of the populations suggesting that the PLS model can be used to bin kernels into high, moderate, and low sugar groups. Starch modeling is awaiting finalization of the analytical measurements. These results suggest that skNIR could be a rapid way of assessing sweet corn sugar content, which can help better define the relationships between eating quality, post-harvest shelf life, and mature seed germination.

Crop Growth Model Calibration of 15 Publicly Available Corn Hybrids in North America

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²USDA-ARS Corn Insects and Crop Genetics Research Unit, Ames, IA 50011, USA

Abstract:

Crop modeling approaches that combine environmental parameters, management, and maize hybrid properties have been described to predict genotype by environment interactions. Plant breeders have the potential to be greatly supported by crop growth models. However, large-scale application of crop modeling in plant breeding is limited by labor and cost required to measure cultivar-specific crop model parameters. The use of crop models in plant breeding has primarily been for identifying and improving physiological traits. Typically, calibrations in these studies are based on only a subset of genetic coefficients needed to fully parameterize a crop model. Our objectives were to determine which parameters differentiate 15 publicly available ex-PVP central corn belt hybrids, determine if differences in traits of interest can be accurately simulated from a limited set of parameters, and evaluate the amount and type of observed phenotypic data that is required to make an adequate hybrid calibration. In this experiment, the APSIM (Agricultural Production Systems sIMulator) maize model was calibrated for 15 hybrids grown widely throughout the Genomes To Fields Initiative. Model calibrations revealed differences among hybrids for 12 genetic coefficients and substantial differences in traits including yield, biomass accumulation, partitioning, and nitrogen uptake. Sensitivity analyses for traits of interest were performed by running 20-year simulations and varying 23 maize crop parameters one factor at a time. In terms of yield, crop development parameters accounted for 52% of the sensitivity, while 28% was attributed to crop growth parameters and 20% to grain component parameters. Our results demonstrate that hybrid performance differences can be simulated using crop growth models and that a large portion of performance variation can be simulated with a subset of parameters. However, our results also demonstrate that phenology parameters alone could only account for just over half of the variation in yield performance differences among these hybrids.

Utilizing Doubled Haploids in Sweet Corn Breeding: Haploid Induction and Selection

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* Presenting author

Abstract:

In recent years, doubled haploid (DH) lines have seen a marked increase in use within field corn breeding programs. However, usage of DH lines in sweet corn breeding programs is less prevalent. This is likely due in part to presence of pigment inhibitors that prevent the expression of *R1-nj* which confers red pigmentation of the aleurone and scutellum and is used as a phenotypic marker for haploid kernel discrimination. Additionally, haploid induction rates in sweet corn tends to be lower than field corn. As a part of the SweetCAP initiative, 482 lines have been randomly selected from a diversity panel representing the genetic diversity of sweet corn. These lines were induced in Ames, Iowa during Summer 2019. During the haploid kernel selection process, pigment expression was visually scored for both the aleurone and scutellum. Also, the number of kernels with aborted embryos, putative haploid and putative hybrid kernels were recorded and used to calculate the abortion and induction rates, respectively. Preliminary results and future steps will be discussed.

Recent developments tweaking starch biosynthesis and creating new products in fresh corn.

William F. Tracy, Department of Agronomy, University of Wisconsin-Madison

Abstract:

Much of what plant biochemists know about starch synthesis in the endosperm of grasses is due to the morphology of the maize ear, the frequency of mutation, and the elegant work of a few maize geneticists. The naked kernels, clinging tightly to the cob, which is a rare, if not unique, combination allows the easy visual identification of allelic variants and associated genetic ratios. We now have an excellent schematic of the pathway, and while there is still much to learn, we know enough to create and test hypothesis. In my short time today, I hope to highlight some significant historical events and discuss more recent developments and potential products. Alleles to be discussed include, *su1*, *se1*, *sh2*, *sh2-i*, *isa2*, *wx1*.

GEM- Germplasm Enhancement of Maize Project:- Increasing Genetic Diversity in Public and Private Sector Maize Breeding

Walter Trevisan* ; Candice Gardner** David Peters*** and Matt Krakowsky****,

*GEM TSG Chair-Retired Industry Maize Research Lead and Breeder; **USDA-ARS and Iowa State University, Ames, IA ; ***USDA-ARS, Ames, IA; ****USDA-ARS, Raleigh, NC.

The importance of access and utilization of genetic plant resources for improvement of modern cultivars is widely recognized. The maize seed industry has struggled to maintain long term germplasm introgression efforts to incorporate genetic diversity into their elite breeding pools because of lack of adaptation and undesirable agronomic traits associated with exotic maize germplasm, the time required to extract valuable material, and the rapid nature of breeding cycles in commercial programs. Today, use of unadapted germplasm for crop improvement is more feasible than ever before because of advances in application of genetic and genomic technologies. In the early nineties, at the conclusion of the Latin American Maize Project (LAMP) project, US participants pursued discussions of how materials identified with good potential could actually be utilized to broaden the diversity of U.S. maize. The Germplasm Enhancement of Maize (GEM) Project resulted from these discussions and recognition by the U.S. Congress of the urgent need to broaden and enhance the maize germplasm base. After 25 years, 60 entities representing the private, public, and non-governmental organizations in the US and 12 other countries now collaborate to achieve GEM objectives.

More than 310 inbreds have been released from programs based in Ames, IA, Raleigh, NC, and from university researchers, from about 40 maize races, tropical hybrids and inbreds. Also, about 220 doubled haploid lines from nearly 60 exotic landraces have been jointly released with Iowa State University to serve as rich resources for exploration of allelic diversity and novel traits, and to provide valuable germplasm for maize research and graduate students in plant breeding and genetics. New germplasm and knowledge derived will support efforts to meet ever increasing challenges to sustainable maize production. Aiming to keep pace with a constantly changing environment in the seed industry, recently the GEM program reviewed its entire breeding methodology to decrease cycle time, access germplasm not previously available, and increase the quality of the germplasm to be released. Public-Private-Partnership efforts are essential to provide useful germplasm for introgression, to perform breeding and testing activities, to evaluate germplasm for abiotic and biotic stress resistance (especially for diseases and pests not yet endemic to the U.S.), for yield, agronomic and grain quality traits, and to conduct research to identify useful haplotypes from exotic donor genomes.

Overexpression of a Maize Transcription Factor in Maize Increases Grain Yield in the Field

Jeff Habben, Corteva Agriscience

Abstract:

Increasing maize grain yield has been a major focus of both plant breeding and genetic engineering to meet the global demand for food, feed, and industrial uses. MADS-box transcription factors have been shown to regulate genes involved in controlling numerous plant growth and development characteristics. We have increased and extended the expression of a maize MADS-box transcription factor gene, *zmm28*, under the control of a moderate-constitutive maize promoter. The resultant transgenic maize plants have increased plant growth, photosynthesis capacity, and nitrogen utilization. Overall, these positive attributes are associated with a significant increase in grain yield relative to wild-type controls that is consistent across years, environments, and elite germplasm backgrounds. We conclude that alteration in expression of a single native maize gene in maize can improve both resource capture and resource utilization, resulting in a significant improvement in grain yield, the ultimate complex quantitative trait.

Ionomics and nutritional quality of sweet corn

Matt Baseggio, Ph.D. - Seneca Foods

Abstract:

Nutritional deficiencies are a worldwide problem and affect mainly children, women, and adults over 65 years. Although these deficiencies are far less prevalent in the developed nations, surprisingly large proportions of the US population still do not obtain the daily recommended amount of several nutrients, particularly iron and zinc. Given that sweet corn is the third most commonly consumed vegetable in the US and previous work has shown it to possess high variability for these compounds, we assessed the natural accumulation of minerals in fresh kernels of a sweet corn association panel. Genome-wide association studies on the kernel ionome identified candidate genes associated with accumulation of iron and zinc (*nas5*, nicotianamine synthase), as well as cadmium (*hma3*, heavy metal ATPase). Within-location analysis showed associations for nickel and molybdenum in NY and for calcium in WI, and candidate genes include *ras2* (Ras-like GTPase) for calcium and *ptr2* (peptide transporter) for nickel. We also developed whole-genome prediction models with moderate predictive abilities that may now be used in a genomic-assisted breeding program for developing sweet corn lines with improved kernel element composition.

From Genomes to Fields: Exploring genotype-by-environment interactions and environment specific prediction in maize hybrids

Anna R. Rogers and James B. Holland

Abstract:

Plant breeding programs are often faced with challenges in making initial selections among breeding materials based on evaluation in a single environment, with the ultimate goal of creating new varieties that will later be planted across multiple, more diverse conditions. In some cases, genotypes that initially seemed very promising are observed to vary dramatically for important agronomic traits across diverse environments. Genotype-by-Environment interactions (G×E) underlie relative differences in performance across environments but are difficult to predict without understanding how genotypes respond to specific environmental covariates. Recent advances in genomics and prediction modeling have accelerated the ability to perform selections using genomic data, but little has been done to incorporate environmental data into such modeling. Including environmental variables in G×E analysis often results in issues with multicollinearity, caused by presence of large numbers of predictors that are often highly correlated, each of which only explains a small amount of variance. Development of methods to incorporate both genomic and environmental data into genomic prediction models should provide ability to predict environment specific performance of individual genotypes.

Using publicly available data for 1,919 maize hybrids spread across multiple locations over three years in North America, we explore G×E modeling using a mixed models approach incorporating high density DNA marker data and weather covariates. Using these data, we gain a clearer insight of what G×E means in context of plant development and response to fluctuating environmental conditions, and explore the possibility of predicting hybrid phenotypes in previously untested environments.

Putting the G in GxE

Joseph L. Gage^{1,4}, J. Arcadio Valdes², Evan R. Reese², GxE Research Coordinators³, Natalia de Leon³, Edward S. Buckler^{1,2,4}, M. Cinta Romay⁴

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Abstract:

The revolution in sequencing technologies during the last few years have allowed us to provide researchers in the G2F Initiative with increasingly more complete genotypic data for the germplasm grown in the GxE fields. Since the first fields were planted in 2014 about 2,000 entries have been genotyped: initially using genotyping by sequencing (2014-2017 germplasm), and more recently by random skim sequencing with an average coverage of 5x (2018-2019 germplasm). In addition, 25 inbred lines have been selected to be sequenced using long read technology at approximately 40x depth to provide draft assemblies. These lines include parents of the “common hybrids”, parents of the populations evaluated in the last cycle, and the testers from the last cycle. In order to combine the draft assemblies and skim sequencing, a computational framework called the Practical Haplotype Graph (PHG) has been implemented and used to call SNPs. A summary of the sequencing that has been done thus far, and preliminary results checking the quality of the assemblies and SNP calls, will be presented. Future directions for genotyping within the Initiative will be discussed with the community.

Expanding the Vision of Near-Infrared Spectroscopy to Create Novel Breeding Tools for Sweet Corn.

Jeff Gustin¹, John Williams¹, John Baier¹, Paul Armstrong², Marcio Resende¹, William Tracy², Mark Settles¹

¹ Horticultural Sciences Department, University of Florida, Gainesville, FL

² USDA-ARS Grain Marketing & Production Research Center, Manhattan, KS

³ Department of Agronomy, University of Wisconsin, Madison, WI

Abstract:

Successful sweet corn hybrids possess numerous characteristics that optimize producer profit and satisfy consumer tastes. Breeders incorporate these numerous traits into their selection criterion when developing new inbred and hybrid lines. Phenotypic characterization can limit the number of evaluated lines if the trait is difficult or time-consuming to measure, particularly if the data is collected at fresh eating stage. Therefore, tools that reduce data collection time can increase the number of lines evaluated and lead to faster genetic gain. Near-infrared spectroscopy (NIRS) is widely used for estimating the chemical composition of mature seeds and grains. We developed a custom NIRS platform that collects spectra from individual kernels. These near infrared (NIR) reflectance data can be translated into accurate predictions of chemical composition such as oil and protein content as well as physical characteristics such as mass and density. We will show recent advances for predicting relevant sweet corn kernel traits using single-kernel NIR. Specifically, we developed a prediction model for kernel pericarp thickness, an important trait contributing to consumer likability and pathogen resistance during imbibition and seedling emergence.

Diversity breeding and technology deployment

Emily Ziemke (Combs), Corteva Agriscience

Abstract:

Genomic prediction is key to the success of a modern corn breeding program. This presentation will explore the key factors underlying successful use of genomic prediction. The presentation will close with a discussion of enhancing genetic diversity in a corn breeding program.

Influence of Sweet Corn Quality Traits on Willingness to Pay for Fresh Sweet Corn

Fengxia Dong and Paul Mitchell, Agricultural and Applied Economics, University of Wisconsin-Madison

Abstract:

As part of the USDA SCRI Sweet CAP Project, we have been conducting consumer panels in Florida and Wisconsin. Panelists taste 4 to 5 different varieties of fresh sweet corn and evaluate them in terms of specific quality traits: sweetness, juiciness, flavor, texture and tenderness, and rank them in terms of overall likeness. In addition, the panel includes an experimental auction in which the consumer panelists bid on each variety. The auction uses a Becker-DeGroot-Marschak auction mechanism, and if a panelist's bid is a winning bid, they "buy" a package of the specific sweet corn variety. This auction allows incentive compatible measurement of consumer willingness to pay (WTP) for each sweet corn variety. Regression of consumer WTP on measured and assessed quality traits are used to estimate the impact of the different quality traits on the value consumers assign to each variety. Conceptually, results allow derivation of the average value of each quality trait to consumers. Preliminary results will be presented from the three initial panels and lessons learned will be summarized.

Methods to identify multiple disease resistance in maize

Peter Balint-Kurti, USDA-ARS Raleigh, NC and NC State University

Abstract:

As with other agronomic traits, breeding for disease resistance in maize is largely conducted using a combination of empirical data and genomic selection and does not necessarily require knowledge of specific loci or underlying mechanisms. However, unlike other agronomic traits, requirements for disease resistance are uniquely unpredictable due to the random emergence of new pathogen races and species. We are exploring methods that may be used to complement and enhance resistance breeding. I will discuss approaches we are using to identify and characterize loci and germplasm conferring multiple disease resistance.

Maize Volatiles That Guide the Behavior of the Insect Pest Fall Armyworm

Anna Block, USDA-ARS Gainesville, FL

Abstract:

Fall armyworm, an important pest of corn, uses host derived volatile compounds (semiochemicals) to locate suitable hosts on which to lay its eggs. Identifying which volatiles are used as positive or negative cues for oviposition can inform both maize breeding programs and integrated pest management strategies to improve fall armyworm control. In this study electroantennogram-gas chromatography was used to assess the ability of fall armyworm to perceive volatiles from 3 maize inbred lines. Quantification of the volatiles by gas chromatography-mass spectrometry coupled with oviposition choice assays led to the identification of one compound that is attractive to fall armyworm moths and three that are potentially repellent.

Student Presentations Judging Criteria

PRESENTER:

- Pace of delivery
- Projection, articulation, and presence (posture, eye contact, etc...)

SLIDES:

- Logical presentation of material
- Organization of material on slides
- Audience friendly color schemes
- Readable font size

RESEARCH:

- Knowledge of material
- Ability to convey significance
- Explanation of the experimental design, results and conclusions
- Ability to answer questions

NOTES:

My vote:

1.