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| Project Number: | 1820-172-0118-A |
| Project Title: | Utilizing genes from the soybean germplasm collection to mitigate drought stress. |
| Organization: | University of Arkansas |
| Principal Investigator Name: | Larry C. Purcell, Ph.D. |

**What key activities were undertaken and what were the key accomplishments during the life of this project? Please use this field to clearly and concisely report on project progress. The information included should reflect quantifiable results (expand upon the KPIs) that can be used to evaluate and measure project success. Technical reports, no longer than 4 pages, may be included in this section.**

**Objective 1, Experiment 1 (GWAS evaluation of plasticity) and Objective 2, Experiment 3 (Confirmation of drought tolerant traits using GWAS data):**

In Fayetteville in 2017, we planted 200 accessions for seed increase including 100 accessions that were selected based on the breeding values of canopy temperature (CT), canopy wilting (CW), water use efficiency (WUE, measured using C13 ratio), and nitrogen derived from the atmosphere (NDFA, as a measure of nitrogen fixation), and 100 accessions were selected from the original GWAS panel based on genetic diversity.

In 2018, we planted the 200 MG 4 accessions along with six checks in an augmented incomplete experimental design with three replications at four locations: 1) Rohwer, AR; 2) Pine Tree, AR; 3) Maricopa, AZ; and 4) Columbia, MO. Four checks, including PI416937 (slow wilting), PI471938 (slow wilting), A5959 (fast wilting), and 08705\_16 (fast wilting), were planted once per replication, and two checks, LG11-8169-007F (a public adapted, high-yielding MG 4 line) and Lee non-nodulating, were planted in each of 12 incomplete blocks under irrigated and non-irrigated conditions.

We collected phenotypic data of drought-related traits, including canopy wilting (CW), canopy temperature (CT), nitrogen derived from atmosphere (NDFA), and water use efficiency (WUE). Preliminary results of the CW data indicate that there was broad phenotypic variation at all locations. Many genotypes wilted less as compared to the two slow wilting checks (PI416937 and PI471938), and there were a few genotypes that wilted more severely than the two fast wilting checks (A5959 and 08705\_16). Analysis of variance on the CW data indicate that there were significant effects of genotype, location, treatment (irrigated and non-irrigated conditions), and all two-way and the three-way interactions (P < 0.05). We found significant positive correlations for canopy wilting under both irrigated and non-irrigated conditions for all locations.

Association mapping analysis of CW using 34,680 polymorphic markers identified 40 loci under irrigated conditions and 32 loci under non-irrigated conditions associated with CW at the level of -Log10 (*P*) ≥ 3.5; *P* ≤ 0.0003. There were 18 SNPs associated with average CW across all locations under irrigated conditions and 23 associated with average CW across all locations under non-irrigated conditions. We confirmed 18 genomic regions that were coincident with previously identified loci for CW.

In this study, 100 new USDA-GRIN lines were selected based on the genomic predicted breeding values. Therefore, we compared the actual CW phenotype observed in this study with true breeding values (TBVs) and genomic estimated breeding values (GEBVs) using BayesB genomic prediction model in a previous study. There was a positive correlation between predicted values and observed values at different locations that ranged from *r* = 0.32 to *r* = 0.42 for TBVs and that ranged from *r* = 0.19 to *r* = 0.61 for GEBVs.

At three locations (Rohwer, AR, Pine Tree, AR, and Columbia, MO) aerial CT measurements were made using a thermal-infrared camera from a drone. At Maricopa, AZ, CT were measured using Apogee SI-131 infrared thermometers mounted on a LeeAgra AvengerPro customized hydrostatic spray vehicle. We are now in the process of extracting CT data for the four locations.

To measure C13 ratio (WUE) and NDFA, three-plant biomass samples were harvested from all plots at Columbia, MO and Maricopa, AZ. However, at the two Arkansas locations, plant samples were taken from irrigated treatments only because there was no irrigation differential on plant growth associated with water treatment. We are currently grinding and processing these samples for stable isotope analysis.

After obtaining all phenotypic data, we will perform association mapping for plasticity and stability loci.

**Objective 1, Experiment 2 (Physiological mechanisms of drought tolerance):**

Ten extreme genotypes (best and worst) for WUE, CT, CW, NDFA, or a combination of all four of these traits, along with four checks including PI416937 (slow wilting), A5959 (fast wilting), KS4895 (MG 4 cultivar), and Lee non-nodulating were planted at Fayetteville, AR and Columbia, MO. We collected phenotypic data for physiological traits(WUE, CT, CW, and NDFA), gas exchange measurements, and leaf and shoot samples. Our preliminary results indicate that there were significant effects of genotype, water availability treatment, and genotype and treatment interactions for CT and CW. Two genotypes that were selected as coolest and warmest for canopy temperature (based on the breeding values), performed as expected. Under non-irrigated conditions, the genotype expected to have the coolest temperature (based on breeding values), PI495017B, had a lower relative temperature (relative temp. = 0.76) than the genotype predicted to have the warmest temperature, PI423890C (relative temp. = 0.85). But under irrigated conditions, the genotype predicted to have the warmest temperature, PI423890C, actually had a lower relative temperature (relative temp. = 0.80) compared to the genotype predicted to have the coolest temperature, PI495017B (relative temperature =0.86). As expected, the slowest wilting genotype (based on GEBV), PI407735, had lower wilting scores (IR=17, NR= 21) compared to the fastest wilting genotype, PI507407 (IR=28, NR= 34). These responses are consistent with the hypothesis that slow wilting genotypes conserve soil moisture when soil moisture is plentiful and that the conserved soil moisture is then used when soil moisture in other genotypes is depleted. We collected three plant samples from all plots at both locations, and are now in process of preparing these samples for CID and NDFA analysis.

**Objective 2, Confirmation of drought tolerance traits using bi-parental populations**

**Experiment 4**

**WUE and CT population: KS4895 × Jackson**

A population consisting of 168 recombinant inbred lines (RILs) derived from a cross between KS4895 × Jackson was planted at Pine Tree, AR and Rohwer, AR. There was a broad range of CT at Pine Tree and Rohwer, respectively. Overall analysis of variance indicated that there was a significant genotype × environment interaction effect on CT. We identified two QTLs, one on chromosome Gm02 and one on chromosome Gm20 that were associated with CT under well-watered conditions at Pine Tree. These QTLs collectively accounted for 19% of the phenotypic variation for CT. At Rohwer, one QTL on chromosome Gm15 and one on chromosome Gm19 were associated with CT under mild drought conditions, which collectively explained 16% of the phenotypic variations. The favorable alleles for QTLs on Gm19 and Gm02 were from Jackson, and the favorable alleles for QTLs on Gm15 Gm 20 were from KS4895. The QTL on chromosome Gm02 was previously associated with slow canopy wilting in the 93705 KS4895 x Jackson population (Hwang et al., 2015). The QTL on chromosome Gm19 was previously associated with low shoot ureide and slow canopy wilting (Hwang et al., 2013; 2015, Kaler et al., 2017). The QTL on chromosome Gm20 co-segregated with a QTL associated with biological nitrogen fixation (Geraldi et al., 2013).

**Experiment 5**:

**WUE population: PI 416997 x 567201D**

This population, consisting of 196 RILs, was grown in 2016 at Stoneville, MS, and in 2017 at Fayetteville, AR, Columbia, MO, and Stoneville, MS. Parents of this population were selected from previous USB-funded research as extremes for WUE (i.e., C13 ratio). ANOVA of plant samples collected in 2016 and 2017 for C13 ratio indicated a significant genotype by environment interaction. Combined over all locations, narrow-sense heritability was 0.84. As part of previous USB-funded research, the population was genotyped by GBS (genotype by sequencing), however there were gaps on some chromosomes. Analysis of parental 50KSNP Chip data identified an additional 75 polymorphic SNPs in the gap regions. KASP primers were manufactured for these 75 SNPs and are now being applied to the RIL population.

In 2018, this population was planted near Columbia, MO to conduct pilot studies aimed at further characterization of the physiology of contrasting RILs in more detail. A new protocol for photosynthesis measurements was tested and executed on the entire population two times during the growing season. Initial examination of net photosynthesis, stomatal conductance, and intercellular CO2 concentration data from the first measurement date showed normal or close to normal distributions and preliminary single marker analyses indicated that it may be possible to identify QTL based on the new phenotyping protocol.

**Experiment 6:**

**NDFA population: PI442012A x PI404199**

Plant biomass samples collected from the NDFA population PI442012A (high NDFA) x PI404199 (low NDFA) grown in Mississippi and in Missouri in 2017 have been course ground. Further processing with a ball mill and weighing of samples is ongoing. This NDFA population was planted again in Mississippi and in Missouri in 2018. Plant tissue samples were harvested and are now being processed for NDFA analysis.

**N concentration population: PI361103 x PI567572B**

The RIL population derived from the cross between PI361103 and PI567572B was grown in 2017 at the Bradford Research Center near Columbia, MO. In 2018, this 262 RIL population was planted at three locations (Rollins Bottom, Novelty, and Bradford farms) in Missouri. Whole-plant biomass samples were collected for 2,358 plots, which are now being processed to determine N concentration. Seed samples are also now being collected for future N concentration determination. DNA is currently being isolated from each RIL for genotyping using an Illumina 50KSNP array in the near future. When phenotypic and genotypic data have been completed, QTL mapping will commence.

**N concentration population: PI567572B x PI361103 (reciprocal):**

This population is a reciprocal cross of the above N concentration population, and was planted in the same field as the PI361103 x PI567572B RIL population at Bradford farm near Columbia, MO. Whole-plant samples were collected and are now being prepared to determine N concentration, with seed collection also underway. We observed significant differences in above-ground mean nitrogen levels across the populations between directions of this cross in previous years, which suggested maternal factors in the parents could play a role. This year, the two reciprocal populations were grown in the same field to remove confounding factors associated with different growing environments and test the hypothesis that maternal factors (mitochondria, plastids) do in fact play a role in the regulation of tissue N concentrations in soybean.

**Objective 3, Germplasm and population development**

**Experiment 7 (WUE Breeding Line Test):**

The WUE efficiency breeding yield study was planted at Stoneville, MS. Stem and leaf tissue of 28 F6-derived breeding lines derived from PI 567201D x DS25-4 and checks (Lee Non-Nod and AG51X8) were harvested from replicated yield plots in Stoneville. Plots were sub-sampled for a total of 216 samples. Samples were course ground and are now being prepared for isotope analysis. Maturities ranged from early IV to V. All plots have been harvested and analysis of yield data is ongoing. The seed quality and quantity harvested in 2018 should be sufficient for the experiments planned for 2019.

**Objective 3, Experiment 8 (Genomic selection and stacking traits related to drought tolerance):**

We selected 20 genotypes for crossing with an agronomically sound [AS], high-yielding MG 4 common parent. Among these 20 genotypes there were four genotypes that had the most favorable values for each of our traits (CW, CT, WUE, NDFA) plus four genotypes with a favorable combination of all four of these traits. Crosses were made at DeWitt, AR, Columbia, MO, and Stoneville, MS. At DeWitt, a total of 731 attempts were made this summer with a total of 302 sets. For all 20 crosses, we have between 31 and 38 potential hybrid seeds. At Columbia, MO, we experienced high heat and drought which negatively impacted our ability to make pollinations. However, approximately 250 pollinations were attempted (~15-20 per cross combination). At Columbia, harvest of F1 seed is in progress. At Stoneville, harvest of F1 seed has been completed and an inventory of F1 seed per combination is in progress. F1 seed will be used for later multi-parent (F1xF1) trait stacking crosses in the summer of 2019.

Tissue was collected from all parents and DNA extracted at the Stoneville, MS location. The sequence information of 231 SNPs, which were identified in a previous study for these drought traits, was used to generate high-throughput PlexSeq genotyping primers. These primer sets are being evaluated on a set of 94 DNA’s (including the 21 parental genotypes). They will be used to test progeny of the crosses described above as well as in future genomic selection procedures. The adapted parental line, LG11-8169-007F, will also be genotyped with the 50KSNP Illumina array. All parents used successfully for crosses will be whole genotype re-sequenced in 2019.

**Did this project meet the intended Key Performance Indicators (KPIs)? List each KPI and describe progress made (or not made) toward addressing it, including metrics where appropriate.**

**Objective 1: Physiological Mechanisms of drought tolerance.**

* *Functional relationships among physiological tolerant traits (CW, CT, WUE, and NDFA) and the implications for improving drought tolerance are established through field experiments in 2019-2020.*

Significant progress was made toward the development of a better understanding of the physiological traits. We collected the phenotypic data of physiological traits(WUE, CT, CW, and NDFA), gas exchange measurements, and leaf and shoot samples in the physiological experiments at Fayetteville, AR and Columbia, MO. We have started to process and analyze these data, and have some preliminary results of a subset of traits. Preliminary analyses revealed significant differences among genotypes and treatments for some of the measurements that were conducted. Once complete data are in hand, the responses of the genotypes to differences in water availability can be examined for each of the phenotypes obtained in 2018.

* *Tradeoffs associated with stability or plasticity of targeted physiological mechanisms associated with yield under drought are determined through field experiments in 2018 and 2019.*

We collected data associated with drought stress and are now analyzing these data to understand the tradeoffs associated with stability or plasticity of targeted physiological mechanisms associated with yield under drought. Data from the Columbia, MO location where severe drought occurred, and the Maricopa, AZ location where water availability can be readily managed to obtain repeatable drought stress will provide useful insights about plasticity. However, since the two Arkansas locations did not have water limitations that affected crop growth, plasticity experiments will need to be repeated in 2019.

**Objective 2: Identification and confirmation of putative drought tolerance loci.**

* *Candidate genes and genomic locations of markers* *associated with CW, CT, WUE, NDFA are identified and made available for use by private or public breeding programs beginning in 2019.*

In previous research, we identified the genes and genomic locations of markers associated with CW, CT, WUE, NDFA. This year, we collected phenotypic data of these traits using a diverse panel of 200 accessions grown in four different environments under irrigated and non-irrigated conditions. Preliminary analysis of the CW data confirmed 18 previously-identified loci associated with CW and identified some novel genomic locations. Currently, we are preparing a manuscript of these results and are processing samples and/or analyzing results for other traits.

* *Report the performance of estimated gains in drought tolerance using predicted breeding values from GWAS, in comparison with the estimated gains from phenotypic selection using narrow-sense heritability estimates determined from bi-parental RILs to soybean breeders through publications and seminars (2020-2021).*

The 2018 field experiments allowed the collection of a large amount of data across the different experiments. These and continued collection of data provide the foundation to meet this KPI. As such, we are on track to meet this KPI.

**Objective 3: Germplasm and population development.**

* *Establish Material Transfer Agreements with private and/or public breeding programs to facilitate public and private introgression of the high germinability/high WUE lines in cultivar improvement programs (2019-2020).*

We are on track to meet this future KPI.

* *New germplasm sources with predicted greater drought tolerance than existing sources are identified in 2018-2019 and that knowledge will be disseminated to the soybean community in the form of presentations and publications (2019).*

Preliminary analyses of data collected in 2018, identified genotypes with more extreme phenotypic values than those of our checks. We are on track to meet this KPI.

* *The value of WUE as a drought tolerance trait as observed in high WUE lines and low WUE lines is determined through 2 years of yield testing in irrigated/non-irrigated trials across multiple states (AR, AZ, MO, and MS) by 2020.*

A preliminary yield test on 28 CID advanced breeding lines and checks was conducted in the summer of 2018 at Stoneville, MS. Data are being analyzed. Sufficient seed was harvested for the next round of tests in multiple locations scheduled for the 2019 season.

We are on track to meet this KPI.

**Expected Outputs/Deliverables - List each deliverable identified in the project, indicate whether or not it was supplied and if not supplied, please provide an explanation as to why.**

We have published nine peer-reviewed manuscripts and contributed 12 presentations at various meetings.

**Objective 1: Physiological Mechanisms of drought tolerance. Experiments encompassed under Objective 1 will:**

* *Publish peer-reviewed manuscripts on novel insights into the plasticity of the primary physiological traits (WUE, CT, CW, and NDFA), and the implications associated with differences in plasticity relative to performance in different environmental conditions.*

We collected the phenotypic data of physiological traits(WUE, CT, CW, and NDFA) in different environments in 2018. We are in now process analyzing these data.

* *Establish the extent and types of interrelationships that exist among the primary drought-tolerance stress traits.*

We found positive correlations among CT, CW, and WUE. NDFA was negatively correlated with CT, CW, and WUE. We will confirm these correlations after obtaining all phenotypic data from experiments this year.

* *Publish manuscripts documenting underlying physiological mechanisms that confer genotypic differences in CW, CT, WUE, and NDFA.*

We published three manuscripts for genotypic differences in CW, CT, WUE and made four presentations.

**Peer-reviewed Manuscripts:**

Bai, H. and L.C. Purcell. 2018. Aerial canopy temperature differences between fast- and slow-wilting soybean genotypes. J. Agron. Crop Sci. DOI: 10.1111/jac.12259.

Bai, H., and L.C. Purcell. 2017. Response of carbon isotope discrimination and oxygen isotope composition to mild drought in slow- and fast-wilting soybean genotypes. J. Crop Improvement 32:239-253.

Kaler, A.S., S.K. Bazzer, A. Sanz-Saez, J.D. Ray, F.B. Fritschi, and L.C. Purcell. 2018. Carbon isotope ratio fractionation among plant tissues of soybean. Plant Phenome. Plant Phenome J. 1:180002. doi:10.2135/tppj2018.04.0002.

**Presentations:**

Sanz-Saez, A., H. Zakeri, A. Scaboo, and F.B. Fritschi. 2017. Using carbon isotope discrimination to estimate WUE in soybean and its relation with physiological traits. ASA, CSSA, and SSSA International Annual Meetings Oct. 22-25, 2017, Tampa, FL.

Almtarfi, H. and F.B. Fritschi. 2017. Top-soil root architecture characteristics of obsolete and modern soybean cultivars and their shoot and seed nutrient contents. ASA, CSSA, and SSSA International Annual Meetings Oct. 22-25, 2017, Tampa, FL.

Fritschi, F.B. 2018. Exploring soybean root architecture – genetic diversity, markers, and improvement. Soybean Breeders Workshop, St. Louis, MO, Feb 12th, 2018.

Fritschi, F.B. 2018. Physiological mechanisms and genetic markers associated with water use efficiency in soybean. Symposium on Improving Agricultural Water Use Efficiency, Center for Agricultural Water Research in China, China Agricultural University, August 20-21, 2018.

* *Identify putative new mechanisms for soybean drought tolerance including hydraulic conductivity and leaf anatomical differences.*

We collected gas exchange measurements, and leaf and shoot samples in the physiological experiment at Fayetteville, AR and Columbia, MO. Tissue samples will be processed during the winter months and data will be analyzed.

**Objective 2: Identification and confirmation of putative drought tolerance loci.**

* *Communicate results of QTL mapping of WUE, CT, CW, and NDFA to the soybean research community through presentations at meetings, reports, and publications.*

We published five manuscripts and made seven presentations concerning QTL mapping of drought-related traits.

**Peer-reviewed Manuscripts:**

Kaler, A.S., A.P. Dhanapal, J.D. Ray, C.A. King, F.B. Fritschi, and L.C. Purcell. 2017. Genome-wide association mapping of carbon isotope and oxygen isotope ratios in diverse soybean genotypes. Crop Sci. 57:3085-3100.

Kaler, A.S., J.D. Ray, W.T. Schapaugh, C.A. King, and L.C. Purcell. 2017. Genome-wide association mapping of canopy wilting in diverse soybean genotypes. Theor. Appl. Genet. 130:2203-2217.

Kaler, A.S., J.D. Ray, W.T. Schapaugh, A.R. Asebedo, C.A. King, E.E. Gbur, and L.C. Purcell. 2018. Association mapping identifies loci for canopy temperature under drought in diverse soybean genotypes. Euphytica. 214: 135. https://doi.org/10.1007/s10681-018-2215-2.

Herritt, M., A.P. Dhanapal, L.C. Purcell, and F.B. Fritschi. 2018. Identification of genomic loci associated with 21 chlorophyll fluorescence phenotypes by genome-wide association study in soybean. BMC Plant Biol. (in review).

Kaler, A.S., J.D. Ray, W.T. Schapaugh, M.K. Davies, C.A. King, and L.C. Purcell. 2018. Association mapping identifies loci for canopy coverage in diverse soybean genotypes. 2017. Mol. Breeding. 38:50 doi.org/10.1007/s11032-018-0810-5.

**Presentations:**

Kaler A.S., and L.C. Purcell L.C. 2017. Utilizing true breeding values to explore soybean germplasm for drought and agronomic-related traits. Oct-2017, ASA, CSSA, SSSA International Conference, Tampa, FL.

Kaler A.S., and L.C. Purcell. 2017. Comparison of models for genome-wide association mapping in plants. Oct-2017, ASA, CSSA, SSSA International Conference, Tampa, FL.

Kaler A.S., and L.C. Purcell L.C. 2017. Evaluation of genomic prediction models for different heritable traits in soybean. Oct-2017, ASA, CSSA, SSSA International Conference, Tampa, FL.

Bazzer, S.K., L.C. Purcell, A.S. Kaler, C.A. King, J.D. Ray, and S. Hwang. 2017. Mapping of QTLs associated with carbon isotope discrimination in soybean using a recombinant inbred population. Oct-2017, ASA, CSSA, SSSA International Conference, Tampa, FL.

Gillman, J.D., Fritschi F.B. and Smith, J.R. 2017. Some like It Hot; QTL and RNAseq Investigation into the Basis of a Unique Form Resistance to Heat-Induced Seed Degradation. ASA, CSSA, and SSSA International Annual Meetings Oct. 22-25, 2017, Tampa, FL.

Kaler A.S., and L.C. Purcell L.C. 2018. Utilizing true breeding values to explore soybean germplasm for drought and agronomic-related traits. Plant and Animal Genome Conference, San Diego, CA, Jan 13-17, 2018.

Kaler A.S., and L.C. Purcell L.C. 2018. Utilizing true breeding values to explore soybean germplasm for drought and agronomic-related traits. Soybean Breeders Workshop, St. Louis, MO, Feb 12-14, 2018.

Kaler A.S., and L.C. Purcell L.C. 2018. Allele mining of drought-related traits in soybean. The 17th Biennial Conference of the Molecular and Cellular Biology of the Soybean, Athens, GA, August 26-29, 2018.

* *Identify* *novel loci putatively associated with plasticity of each primary physiological trait and communicate that information through presentations and publications.*

We collected the phenotypic data of physiological traits(WUE, CT, CW, and NDFA) using a diverse panel of accessions grown in four different environments in irrigated and non-irrigated conditions. In two of the environments, drought stress was not significant this year. This will limit our ability to identify plasticity loci and will require additional experiments in 2019. Nonetheless, we are able to conduct initial analysis and expect to identify novel loci putatively associated with plasticity for each primary physiological trait based on the 2018 data. These efforts will lead to publications in peer-reviewed journals and presentations at different meetings in future years of the project.

* *Share identity and locations of confirmed genes (QTLs) for CW, CT, WUE, and NDFA to the soybean community through meetings, reports, and publications.*

We shared locations of identified QTL and gene candidates for CW, CT, and WUE in SoyBase for the soybean community. We are working to confirm and extend these results using data collected this year, and will publish the confirmation data and present results in meetings as appropriate in future years of the project.

**Objective 3: Germplasm and population development.**

**For current F6-derived WUE lines (PI 567201D x DS25-4):**

* *Document results of 2018 irrigated yield trials comparing high WUE lines versus low WUE lines through scientific presentations, reports, and publications by 2019.*
* *Identify the best WUE lines based on irrigated and non-irrigated trials in 2019/2020 and enter those lines for Regional Uniform testing by 2020.*
* *Determine the “realized heritability” of the WUE trait based on 5 years of pedigree selection for WUE and 3 years of replicated testing of the resulting lines in multiple states (AR, AZ, MO, and MS) by 2020. 2018 yield trial data is currently being analyzed*

We are on target to meet these deliverables.

**Describe any unforeseen events or circumstances that may have affected project timeline, costs, or deliverables (if applicable.)**

Excessive rainfall in Arkansas this summer limited phenotypic measurements of canopy temperature and wilting to just a few days. Similarly, there was no irrigation differential on plant growth associated with water treatment at the two Arkansas sites, and plant samples for C13 analysis were collected only from the ‘irrigated’ treatment. This limits the analysis of plasticity and will necessitate repeating the GWAS experiment in 2019.

**What, if any, follow-up steps are required to capture benefits for all US soybean farmers?Describe in a few sentences how the results of this project will be or should be used.**

The 100 accessions out of 200 were selected based on the predicted breeding values. Our preliminary results indicated a positive correlation between predicted breeding values and observed phenotype (CW) in this study. Our initial results corroborated that these predicted breeding values may be used to select genotypes from the USDA soybean germplasm collections that will be useful to breed for improved drought tolerance.

We are identifying and confirming genes and genomic locations for these drought tolerance-related traits, which can be used to improve soybean germplasm.

We began crossing 20 genotypes contrasting for CW, CT, WUE, and NDFA with an agronomically sound, high yielding MG 4 common parent for stacking these drought tolerance-related traits and to develop drought tolerant cultivars in the future. The above crosses, also are the initial steps of the development of a Multi-parent Advanced Generation Inter-Cross (MAGIC) mapping population. We will follow the crossing scheme needed to complete this MAGIC population over the next years, which will provide us with an unparalleled resource to understand the genetics of the four traits and potential tradeoffs, and thus, novel information that will be used to accelerate breeding for greater drought tolerance in soybean.

**List any relevant performance metrics not captured in KPI’s.**

Education and training of the next generation of soybean researchers is critical for the competitiveness of US soybean farmers. Our team is providing training at every level required for a successful research enterprise, including part-time workers, undergraduate and graduate students as well as postdoctoral research associates that are distributed across the different sites.