



## North Central Soybean Research Program

### **Accelerating soybean yield improvement by utilizing yield genes from soybean wild relatives**

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Neither soybean breeders nor soybean producers are satisfied with the rate of progress that is being made in improving soybean yield. In order to achieve yield gains in soybean closer to those that have been made by corn breeders, increasing the diversity available to soybean breeders is a strategy that has much promise.

We have preliminary data that indicate that very useful yield genes exist in both annual (*Glycine soja*) and perennial (*Glycine tomentella*) wild relatives of soybean (*Glycine max*) that are not being used in commercial soybean breeding today.

Commercial soybean breeding companies are making major investments in producing new transgenic varieties and commercial soybean breeders are efficient and effective in producing new varieties using the limited genetic diversity available in the commercially used gene pool. However, these companies are doing no research with perennial *Glycine* and very little research with wild soybean (*G. soja*) to exploit the important variation in these wild relatives and are dependent on the public sector to make these very important genetic resources available for commercial use.

### **Project Objectives:**

- Map genomic regions from *G. tomentella* associated with significant yield increases in the soybean variety Dwight;
- Genetically map chromosomal regions that differentiate the soybean from the wild soybean; and
- Use the information from Objective 2 to select high yielding experimental lines from soybean by wild soybean crosses that have DNA markers in these regions but do not have the undesirable wild soybean traits.

### **Results**

We previously created two mapping populations using as parents *G. tomentella*-derived lines that yielded 3.6 bu/a and 7.3 bu/a more than Dwight, the soybean parent. In 2016, we are yield testing 225 random inbred lines from each population, plus the parent lines and high yielding checks. Because of delays in

seed coming from the winter nursery in 2015, we were only able to plant 1 location with 2 replications in 2016. All lines have been genotyped by sequencing. We continue to develop additional high yielding G. tomentella-derived lines. We selected 39 lines that had G. tomentella as the female parent and thus G. tomentella cytoplasm and 28 lines with soybean as the female parent and soybean cytoplasm. Averaged over 3 locations that best line with G. tomentella cytoplasm yielded 11.0 bu/a more than Dwight and the best line soybean cytoplasm yielded 8.2 bu/a more than Dwight. With the help of many cooperators, these lines are being grown in at least 7 locations this summer.

Using the genetic marker data from the wild soybean mapping population, we performed QTL mapping for six traits related to soybean domestication (height, lodging, stem diameter, shattering, seed weight, and growth habit). Because of the large number of lines included in the mapping study, we were able to detect more QTL than previously reported. We found a total of 51 significant QTL and at least seven QTL were detected for each trait. For some traits, such as height and stem diameter, we found a mixture of both positive and negative effects for the wild parent allele. The identification of beneficial alleles from wild soybean could imply that there are favorable alleles or genes in the wild soybean that may not be found in the domesticated gene pool. The domestication QTL were distributed across the majority of the genome, with 18 out of 20 chromosomes containing at least one locus for one of the traits. This mapping study presents numerous targets for introgression of new genes from wild soybean into the commercially used soybean gene pool.

To identify introgressions from wild soybean that are beneficial to yield, we are evaluating experimental lines derived from crosses with wild soybean. In 2015, 416 lines derived from 12 different wild soybean parents were evaluated at two locations. We observed a wide range in yield from 30.1 to 84.7 bu/ac. The highest yielding lines were derived by backcrossing three times to different soybean parents. Out of 165 lines that could be directly compared to their soybean parent, 44 were not significantly different in yield, which is a significant accomplishment for wild soybean-derived lines. LG14-3378 (Williams 82 x PI 468916) yielded 3.8 bu/a more than Williams 82 but that difference was not statistically significant. Using the data from 2015, 300 lines derived from 11 wild soybean parents were selected for testing in 2016 at five locations. All experimental lines are currently being prepared for sequencing to obtain genetic markers and identify introgressed chromosomal segments.

During the next 6 months, data collection will be completed on all of the yield plots and plots will be harvested. Seeds from the two mapping populations will be prepared and distributed to cooperators in the new NCSRP yield project. Data from yield tests of the G. tomentella-derived lines will be summarized and distributed to the cooperators. The best lines will be made available for use as parents. The QTL mapping of domestication traits will be completed and the results prepared for publication. The field data for the wild soybean-derived lines will be summarized from all locations. Genotyping by sequencing will be completed for all experimental lines and SNPs will be identified that can be used for tracking

introgressions from the wild soybean parent to the experimental lines. DNA introgression from wild soybean will be identified for each line with special attention to those genomic regions near the domestication QTL that we identified. These are regions from which wild soybean genes are most likely to have been excluded during the domestication process. We will also complete genotypic and phenotypic comparisons of lines with the same pedigree. Based on 2015 data, we included lines in the 2016 test that are full sibs and differed by 10 to 20 bu/a depending on the pedigree. Our objective is to identify genetic differences between the high and low yielding lines and determine if any of alleles associated with high yield were derived from the wild soybean parent.