

Nebraska Soybean Board
FINAL Research Report Form



1/13/2020

Note: Submit this report no later than 90 days after the NSB-funded project officially terminates.

This post-project 90-day time-frame will allow the Lead PI time to complete any final data analysis and a final technical report, plus the drafting of any articles for submission to scientific journals. Note that this completed report will be provided to the National Soybean Checkoff Research Database, (soybeanresearchdata.com).

Project # and Title: Genetic Mapping of Yield Stability Genes

Principal Investigator: Dr. David Hyten

Co-PI's & Institutions: Dr. George Graef

Project Date (Including Extension): 10/01/2016 **to** 09/30/2019 **(For example: mm/dd/yyyy to mm/dd/yyyy)**

Total Budget for Project: \$ 229,139.00

1. Briefly State the Rational for the Research:

A key factor to releasing a new cultivar is that the experimental variety has consistent high yields across a large geographical region. Many experimental varieties are eliminated in advanced yield trials because they may yield at the top of some yield tests but near the bottom of other tests. This ability to consistently yield across diverse environments is likely under genetic control. This research will take the first steps to find genetic markers associated with yield stability across Nebraska soybean production areas, in order to better understand the underlying genetics controlling this trait. With these markers we will be able to incorporate selection for consistent yield earlier into soybean breeding programs at the University of Nebraska and elsewhere.

2. Research Objectives: (copy from project, but keep in a brief bullet format)

- This research project's main objective is to map genes that are responsible for increasing soybean yield stability.
 - o It will provide molecular markers for yield stability genes that can be utilized in a breeding program.
 - o It will provide a better understanding of the genetic basis of yield stability
- This research project will determine which methods for early selection of yield stability genes is most effective in a soybean breeding program.

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3. General Approach Used and (if applicable) the Nebraska Test Locations:

We set up an association analysis panel of elite Nebraska soybean cultivars and experimental lines that vary for the amount of yield stability across diverse environments. These environments with the years they were used as testing locations were as follows: Lincoln (2017-19), Mead (2017-19), Phillips (2017-19), Cotesfield (2018-19), Wymore (2017-18), and Holdrege (2019). Locations were scouted weekly during the growing season to control biotic stressors as well as collect notes on various agronomic qualities.

Leaf tissue was collected on these lines to have the DNA extracted for genotyping. Lines were genotyped using a sequencing with imputation approach to generate a high density SNP panel of ~10,000,000 markers. These markers were used to refine and perform several association analyses to detect yield stability QTL, termed 'vQTL'. In addition, we began working with current breeding populations within the Nebraska soybean population to develop methods to enrich selected lines with positive vQTL and increase yield stability.

4. Describe Deliverables & Significance Attained for Each Research Objective:

The project's main objective was to map genes responsible for increasing yield stability in order to provide molecular markers (SNPs) for yield stability and garner a better understanding of the genetic basis controlling this trait. In order to obtain a high density marker panel for these analyses, a low coverage sequencing with imputation approach was tested. Initially, a 1X sequence was started as a baseline for whole genome sequencing of the Nebraska lines. However, analysis from the first round of sequencing enabled us to test how low we could sequence and still have good imputation results. This analysis determined that a 0.3X coverage level gave the same accuracy of calling SNPs as sequencing at the 1X level. This approach was found to have a 94.4% accuracy rate. The reference panel for imputation was constructed from 99 lines with publicly available high depth sequence data resulting in a dataset of ~10,000,000 SNP markers. The yield stability panel of 213 Nebraskan lines were sequenced at a 0.3X+ coverage covering 300,000+ SNPs, and the reference panel then used to infer the remaining 9,000,000+ SNPs. Leveraging this imputation approach allowed an over 10-fold increase in genetic information from the whole genome sequencing data, at the cost of a few hours of computational time. This result is significant in that it effectively decreases per line genotyping costs, allowing researchers to expand their projects to encompass more lines and/or generate more genotype information with less funds.

This SNP panel was implemented in the exploration of yield stability GWAS models. Both traditional modeling and direct GxE modeling has been explored and refined over the duration of this project. Direct GxE modeling has revealed that interactions of genotypes with the environment, which are responsible for the level of stability a line has across locations, is incredibly unique to the year and location combination in which it is grown.

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4. Describe Deliverables & Significance Attained for Each Research Objective (continued)

Nearly all of the QTL discovered in this manner fell under the 'genotype by year by location' category, as opposed to 'genotype by year' or 'genotype by location'. This approach also revealed several dozen QTL. As a result we now have a better understanding of the high level of sensitivity a genotype has to environmental conditions that results in adjustments to yield, and ultimately differences in yield stability. More traditional analyses were also performed, with 29 different yield stability measures generated from raw yield numbers. Twenty-three stability measures each resulted in one or more stability QTL being discovered. Across these GWAS, three QTL were conserved in several of the analyses that will be promising targets for future study to further dissect the genetic basis of yield stability.

The broad GWAS analysis described above informs us on which methods of early selection of yield stability might be effective. As the direct GxE modeling approach resulted in dozens of small effect QTL which is typical of a quantitative trait. These results imply that genomic selection would be a good choice for implementation for concurrently selecting on a large number of genes. The traditional analyses produced stronger, large effect association signals, but much less in number. Marker assisted selection would be the best pathway for incorporation of these stability genes as it is generally applied to traits that have few, but large effect QTL.

5. List where the Project Research Results/Findings were Publicized:

Imputation analysis was published July 2019 in G3: Genes, Genomes, Genetics. Poster presentations were/will be given at the University of Wisconsin-Madison (Fall 2018), University of Missouri (Winter 2018-19), Nebraska Plant Science Retreat (Spring 2019), and Plant and Animal Genome XXVIII Conference (Jan 2020). Oral presentations were/will be given at the University of Missouri (Winter 2018-19) and Plant and Animal Genome XXVIII Conference (Jan 2020). GWAS analysis manuscripts will be written and submitted for publication in 2020.

Note: The above boxes will automatically accommodate for your text inputs; HOWEVER, the Final Report comprised of the above listed items must be kept to THREE PAGES. A Technical Report of no more than TEN PAGES (preferably fewer) can be appended to this report.

Submit both reports as a single PDF with this file name format: [#XXX > FINAL > Project Title > PI last name](#)

Please email this completed form to the Agriculture Research Division (jmonaghan2@unl.edu) based on the reporting schedule given to you. If you have any questions, please call the ARD at 2-2045 or Victor Bohuslavsky at the Nebraska Soybean Board Office at (402) 432-5720.