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Nebraska Soybean Board
FINAL Research Report Form

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: Screening for stem borer resistance

Principal Investigator: Dr. David Hyten

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

Project Date (Including Extension): 10/01/2019 ***to*** 09/30/2021 ***(For example: mm/dd/yyyy to mm/dd/yyyy)***

Total Budget for Project: $ 112,011.00

1. Briefly State the Rational for the Research:

The stem borer, Dectes texanus, LeConte (Coleoptera: Cerambycidae) has quickly expanded into Nebraska as a soybean pest. This pest causes yield loss due to increasing the plants susceptibility for the stems to break from external forces such as high wind or heavy rain. It is now commonly found in Southeastern and South Central Nebraska and even north of I-80 (Wright and McMechan, 2018). Insecticidal control has been demonstrated to be ineffective because the insecticides cannot penetrate the stems to contact the larva. Host resistance is a potential way to control this pest. Currently very few accessions have been identified as potential sources of resistance. The resistance from these accessions only provide partial resistance. New sources of resistance need to be discovered that can be used to help control this pest effectively. This project provided an initial screening of diverse germplasm for resistance to stem borer found in Nebraska.

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

This research project's main objective is to understand the potential of genetic resistance to soybean stem borer.

Objective 1: Screen diverse germplasm for resistance to stem breakage and girdling due to soybean stem borer infestation

Objective 2: Assess antixenosis and antibiosis resistance in diverse soybean lines

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

Seven hundred and twenty diverse accessions were seelcted to screen for stem borer resistance. This germplasm encompass a wide sampling of the genetic diversity found in the USDA soybean germplasm collection. The general approach was a short row, randomized complete block design with two replications. A subset of University of Nebraska elite lines were also included in the screen. Test locations were at Havelock Farm of UNL in Lincoln, NE and at a Kansas location as part of a collaboration with Dr. Bill Schapaugh of Kansas State University. At both locations ten plants per short row were screened for stem borer infestation at least three weeks after the R8 stage by breaking the base of the stem and visualizing the overwintering stem borer larvae. Girdled stems were recored in the Kansas location. Previously these 720 lines were genotyped with 50,000 SNPs. We performed a genome-wide association study (GWAS) with the phenotypic data collected to find genomic regions contributing to lower infestation rates.

In NE, we also tested an alternative phenotyping method. The stem borer adult was known to lay more than once in a plant, but the larvae cannibalize each other once they reach the stem. Because of this cannibalistic behavior only 1 reaches the base to over winter. We hypothesized that we could test for possible antibiosis or antixenosis characteristics if we knew the total amount of larvae laid. Based on previous stem borer presence data in NE, coupled with the development timeline, we hypothesized that the most larvae can be found in the petioles by the first two weeks of August. To test the alternative phenotyping method in the first year, 20 genotypes were chosen to have high stem borer susceptibility. Each genotype was planted in short row, randomized, four replications. The second year, six genotypes were chosen that had highest susceptibility scores from year one antixenosis/antibiosis study and six other genotypes that had had scores of low infestation and low stem breakage (possible resistance) from the 720 genotype screening. Oviposition punctures and the number of live larvae were recorded for three to five plants from each replication.

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

This project provided preliminary data that is essential for setting up future studies to identify resistant germplasm that can be used to breed for stem borer resistance. We also identified potential QTL that if verified can be integrated into elite soybean lines to increase resistance to soybean stem borer. We were able to successfully screen the 720 accessions over two years in two locations. We screened the lines for infestation rate of the stem borer larvae and for stem breakage. Plants infested with stem borer are more susceptible to stem breakage which is the main factor causing yield loss. Both locations over both years had good infestation of stem borer. In Nebraska 86% of the genotypes scored had at least one larvae found in the reps scored. Kansas, where stem borer has a much higher infestation, had 99% of the genotypes infested with at least one larvae in 2020 and 100% in 2021. Overall, no soybean accession had complete resistance to larvae infestation over the two years and across the two locations. Stem breakage was scored in Kansas which saw 83% of the accessions have at least one stem broken in 2020 and 93% of the accessions with at least one stem broken in 2021. From the 720 accessions we did identify the ones that demonstrated the highest resistance to larvae infestation and to stem breakage. These lines can now be used to verify their resistance and their mode of resistance. These accessions can also begin to be used as parents to create germplasm lines with increased resistance to stem borer and to potentially stack resistant genes from multiple germplasm lines.

We were able to perform a genome-wide association study (GWAS) for larvae infestation and for stem breakage. In total there were 12 unique marker-trait associations for larvae infestation indicating potential QTL for resistance. For stem breakage we discovered 16 unique marker-trait associations. We are still analyzing the GWAS to determine if any of these QTL are major QTL that could potentially be used in marker-assisted selection.

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

Another objective was to assess antixenosis and antibiosis resistance in a subset of accessions. This objective gave us the opportunity to understand the labor and time involved in this method of phenotyping for stem borer resistance. In year two, we selected six lines that were found to be highly resistance to larvae infestation and stem breakage in the year one data. From the 240 plants screened with this method, we found a total of 270 larvae. The number of larvae ranged from 2-39 with only one genotype having ten or fewer ovipostion marks with only one larvae found inside. The genotype with the ten or fewer oviposition marks and one larva suggests possible antixenosis and antibiosis resistance.

As expected this method of phenotyping is really time intensive. It takes a week for one person to phenotype 12 genotypes. We have concluded that this method of phenotyping is best used when when we can identify potential sources of resistance from the phenotyping methods performed in objective one. Then screen that smaller subset with this method to determine the mode of resistance.

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

A poster presentation was planned to be given at the Plant and Animal Genome Conference (Jan 2022) but that conference was canceled. We plan to present this data in a poster or as a talk at a scientific conference when the opportunity arises. A manuscript with the screening results and QTL mapping results will be written and submitted for publication in 2022.

Note: The above boxes will automatically accomodate 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 (jmcmahon10@unl.edu) based on the reporting schedule given to you. If you have any questions, please call Jen McMahon at the ARD at 2-7082.