MISSISSIPPI SOYBEAN PROMOTION BOARD
PROJECT NO. 32-2015 (YEAR 3)
2015 Annual Report

Title: Phenotyping F_2 populations segregating for frogeye resistance.

Investigators:
PI: Jeffery D. Ray (jeff.ray@ars.usda.gov), Phone: (662) 686-3036
Dr. Alemu Mengistu
Dr. James R. Smith
Dr. Renée S. Arias

BACKGROUND AND OBJECTIVES

Frogeye Leaf Spot, caused by *Cercospora sojina*, is common in the southern and southeastern soybean production region of the USA, including Alabama, Mississippi, Louisiana, Arkansas, Tennessee, Kentucky, North Carolina, and Virginia. Recently, FLS has spread further north into Midwestern soybean growing states, including Ohio, Indiana, Wisconsin, Michigan, Illinois, Iowa, and Missouri.

Under favorable environments, reported yield reductions due to FLS range from 10 to 60%. Fungicides of the strobilurin class are widely used to control foliar diseases including FLS. So far, strobilurin resistant isolates of *C. sojina* have been detected in Tennessee, Illinois, Kentucky, Alabama, Arkansas, Mississippi, Missouri, Indiana, North Carolina, Virginia and Louisiana since 2010, thus reducing the effectiveness of this input as an FLS disease control option.

Reliance on fungicides could be reduced with the development and use of FLS-resistant cultivars. Several soybean genes conferring resistance to FLS have been identified, among which the *Rcs3* gene from cultivar Davis has provided the most durable resistance against all known isolates of FLS in the USA. However, this single gene resistance presents a risk as it is only a matter of time before it is defeated by *C. sojina*. Additionally, *C. sojina* is a highly prolific fungus with more than 44 known races.

The future development of *C. sojina*-resistant cultivars may be dependent on developing race-specific resistance. Molecularly mapping soybean resistance genes will allow the ability to differentiate and identify germplasm with new genes. The research reported here provides the foundation for that process.

The objectives of this research project are to: (1) Apply molecular markers to F_2 DNA from a previous F_2 phenotypic screen; (2) Phenotype a confirming F_2 soybean population segregating for *C. sojina* resistance; (3) Collect tissue and isolate DNA from confirming population; and (4) Where possible and appropriate, advance F_2 lines in the breeding program.

REPORT OF PROGRESS/ACTIVITY

Pathogen grouping of *C. sojina* isolates is needed to differentiate and identify germplasm with new genes. Frogeye isolates were collected from a wide geographic area in the United States. Over 83 isolates of *C. sojina* were screened on a set of 12 soybean differential cultivars. Host reactions were assessed at 14, 21 and 28 days after inoculation. A rating score from 0 to 9 was used for disease assessment. Cluster analysis was able to separate isolate x differential responses into multiple groups. Additionally, the number of lesions, lesion size, how far the lesion moved from the infection site, and the total number of nodes the infection has moved to on the plant were recorded. This approach allowed classification of the most virulent pathotype that may infect all genotypes, pathotypes with moderate infection, the least virulent pathotype that infects only some but not all cultivars, and pathotypes with no infection on all genotypes. The degree of infection on the 12 differentials provided data that showed various levels of aggressiveness of isolates within pathotypes. This is a tool that can be used by breeders and others to screen useful resistant genes against the various *C. sojina* pathotypes.

Objective 1. Apply molecular markers to F_2 DNA from a previous F_2 phenotypic screen.

Efforts in this quarter have focused on working out the protocols for the new growth chambers. Parental lines have been successfully screened with six different isolates. We are now ready to begin screening one of the new F_2 populations.

Objective 2. Phenotype a confirming F_2 soybean population segregating for *C. sojina* resistance.

Currently the seed of the following crosses is being grown in Puerto Rico:

List of Crosses:	No. of F1 Plants
Blackhawk x PI 424595	6
Blackhawk x PI 458175B	6
PI 458175B x Blackhawk	8
Blackhawk x PI 507470	1
Blackhawk x PI 509098	4

The seed of these populations have not been harvested (or harvest is underway). We expect the seed to arrive back in Stoneville sometime in May 2016.

Objective 3. Collect tissue and isolate DNA from confirming population.

We will collect tissue and DNA from the new F2 populations currently being phenotyped at Jackson, TN.

Objective 4. Where possible and appropriate advance F_2 lines in the breeding program.

We expect to advance lines in the summer of 2016.

Presentations

In March 2015, Dr. Mengistu presented some of the results of our FrogEye research at the Southern Soybean Disease Workers meeting in Pensacola. The presentation was titled “Phenotypic Characterization of *Cercospora sojina* Isolates Collected from Wide Geographical Areas” by Alemu Mengistu, J. D. Ray, J. R. Smith and H. M. Kelly