North Central Soybean Research Program

Characterization of *Phytophthora sojae* and *Phytophthora sansomeana* populations in the North Central Region and an Assessment of Management Strategies

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Project Objectives

1) Recover *Phytophthora sojae* from fields within each state and characterize for pathotype and genetic diversity.

2) Evaluate the new sources of resistance to these regional populations.

3) Recover *Phytophthora sansomeana* from fields within each state and characterize for host range and genetic diversity.

4) Establish sensitivities (EC50) values for *P. sojae* and *P. sansomeana* isolates recovered from fields towards the new active ingredients ethaboxam, strobilurin, and oxathiapiprolin fungicides.

5) Compare new seed treatments on varieties with different resistance packages (Rps gene(s) and partial resistance) in field trials.

6) Evaluation of potential herbicide interactions with the development of seed rot and stand loss.

7) Develop outreach publications on the management of Phytophthora spp. that infect soybean in the North Central U.S. and Ontario regions.

Project Description

Phytophthora sojae is present in many soybean fields across the north-central region of the U.S. and Ontario, Canada and had been managed very successfully with the deployment of single resistance Rps genes (Rps1a, Rps1c, Rps1k, Rps3a, and Rps6) as well as partial resistance (field resistance or tolerance). However, there are an increasing number of reports where varieties are sold that have Rps genes that are no longer effective towards the regional population or lack sufficient levels of partial resistance. The consequence is stand loss from damping-off or the development of stem rot throughout the season which results in lower yields

and added weed pressure.

The most recent survey of *P. sojae* pathotypes (races) was completed during 2012/2013. In that study, 213 unique pathotypes were identified among 873 isolates collected from 202 fields in eleven states. Two key findings from this sampling indicate that the ability to recycle Rps genes is highly unlikely:

1) a greater number of regions have a higher proportion of isolates with virulence to key Rps genes, such that the resistance gene will no longer be effective
2) Phytophthota isolates across the region continue to increase in complexity.

In another study (2010-2013) funded by soybean checkoff dollars, the genotypic diversity among *P. sojae p*opulations was examined. With new markers, and in-depth sampling of populations recovered in the 2000s, regional populations of *P. sojae* in the Midwest were identified. Because P. sojae is a soil-borne organism, it was believed that *P. sojae* should be clonal (every individual is the same within a field and between neighboring fields) – but the findings from this study clearly indicated that the *P. sojae* populations in the Midwest are not clonal.

These findings indicate that a more thorough assessment of the *P. sojae* populations in the North Central region is needed. In addition, new Rps genes have been identified but their effectiveness is still highly questionable. Among the 15 Rps genes that were identified prior to 2001, only 5 were effective and incorporated into varieties.

A second Phytophthora, *P. sansomeana*, also appears to be contributing to seed and seedling damping-off of soybean at greater incidence than previously thought, both from surveys previously reported in Illinois (Malvick), Ohio (2003 and 2015 data), and region wide (Chilvers USDA-AFRI project data). This is intriguing as *P. sansomeana* has a larger host range (corn, douglas fir, soybean). As part of this proposed study, populations of *P. sansomeana* in each state will also be examined for host range, resistance in current soybean cultivars, and efficacy of seed treatment fungicides.

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1. Recover *P. sojae* from fields within each state and characterize for pathotype and genetic diversity.

Soil collection and baiting of 25 to 50 locations is mostly complete for those states that were going to participate. In addition, we have 17 locations from Kentucky. The plan is to complete the baiting, isolation and pathotyping of most of these isolates soon.

Before the ground froze – More than 292 fields were sampled across IA, IN, IL, OH, MI, MN, SD, & KY. The winter has been spent baiting and isolating from these soil collections as well as pathotyping.

2. Evaluate the new sources of resistance to these regional populations.

Seed was increased during fall 2017 to develop differentials with these putatively novel Rps genes. Seed will be increased again in 2018 as the quality due to weather conditions and total

amount was low for some lines. An agreement to share this germplasm is currently being evaluated. Once this is agreed to then we can share these lines for additional testing.

3. **Recover *P. sansomeana* from fields within each state and characterize for host range, genetic diversity.**
These will be collected along with the *P. sojae* through the baiting process as well as in season diagnostic samples.

4. Establish sensitivities (EC_{50}) values for *P. sojae* and *P. sansomeana* isolates recovered from fields towards the new active ingredients ethaboxam, strobilurin, and oxathiapiprolin fungicides.

- EC_{50} values for oxathiapiprolin were completed from isolates collected in Ohio during 2015-2016
- Two manuscripts are in development for long term studies of ethaboxam and oxathiopiprolin in Ohio
- One set of isolates is complete, published from Minnesota – Radmer et al., 2017, Plant Disease 101:62-72.

5. Comparison of new seed treatments on varieties with different resistance packages (*Rps* gene(s)/partial resistance) in field trials.

Santiago Mideros Mora evaluated a number of lines from Brian Diers program to include in this study. Both Rps gene and partial resistance were characterized to evaluate which set of varieties would work best.

Data to be collected of the seed treatment will be stand and canopy closure. We did identify a need in establishing these field protocols as well as situations where inoculations maybe necessary.

6. Evaluation of potential herbicide interactions with the development seed rot and stand loss.
Loren Giesler has modified the protocol for this trial for 2018 field season. A minimum of 5 herbicides will be applied at or within 2 days of planting. Seedling injury will be measured and seedlings will be collected to evaluate the incidence of those seedlings colonized by pathogens. Plans for at least 5 locations in 2018.