



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) Phytophthora isolates across the region continue to increase in complexity.

In another recent study (2010-2013) funded by soybean checkoff dollars, the genotypic diversity among *P. sojae* populations 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.

Progress Report April 2017

We are very excited to report that we are quickly reaching our first goal of sampling fields for baiting and have reached 92 fields sampled in 6 states for 920 soil

samples (10 per field). Fields have already been identified to complete the sampling this spring and baiting has begun on some of the fall samples. Lines to develop into differentials carrying putative new sources of resistance will be the focus of the next few weeks. With the goal for seed increase this summer. The team will have a conference call on April 3 to finalize field studies for the summer. Our first goal is to evaluate the interaction of herbicides and the development of *Phytophthora* seedling blight.