



North Central Soybean Research Program

An integrated approach to enhance durability of SCN resistance for long term strategic SCN management

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Progress report October 2017

The soybean cyst nematode, *Heterodera glycines*, (SCN)) is the most damaging pathogen of soybeans in North America. Though SCN-resistant soybean varieties frequently are available to minimize yield loss, producers are faced with limited options for rotation once virulent SCN populations develop in their fields.

The widespread lack of genetic diversity in SCN resistance in soybean has significantly increased the prevalence of virulent SCN populations and reduced the effectiveness of current sources of resistance. Thus, we have two major research challenges that, when successfully achieved, will enable us to develop more efficient management practices for this pest in the future:

1. Plant breeders need to increase the genetic diversity of SCN resistance in commercially available SCN-resistant soybean cultivars and work with nematologists to determine the most effective rotation practices that preserve these sources,
2. Nematologists need to complete the SCN genome assembly (genetic blueprint of the nematode) to facilitate the identification of nematode genes required for the adaptation to reproduce on resistant cultivars, use these as markers to monitor nematode population shifts in the field, and exploit this knowledge to help plant breeders identify novel sources of resistance.

Project Objectives

1. Diversify the genetic base of SCN resistance in soybean
 - Develop and evaluate germplasm with new combinations of resistance genes in

high yielding backgrounds.

- Determine resistance gene copy number in the experimental lines for more effective breeding.

2. Identify SCN virulence factors and better understand how the nematode adapts to resistance

- Refine SCN genome assembly and its accessibility.
- Improve genome assembly.
- Genome curation and annotation.
- Conduct comparative population studies to identify genes associated with SCN virulence and evaluate utility as novel resistance targets.
- Determine unique resistance gene stacks that would be beneficial in rotations to enhance durability of SCN resistance.

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3. Translate the results of objectives 1 and 2 to increase the profitability of soybean for producers

- Educate growers on how SCN adapts to be able to grow on resistant soybeans.
- Inform growers on effective rotation schemes designed to protect our resistant sources.

Reporting Period Accomplishments

Objective 1 - *Diversify the genetic base of SCN resistance in soybean*

Experimental lines with alternative sources of resistance (PI 437654, PI 88788, PI 438489B, PI 567516C, PI 468916, and PI 90763) are being developed and advanced lines in yield tests show good agronomic promise. The University of Illinois released for seed increase by a private company a high yielding MG IV line that combines SCN resistance genes from PI 88788 and PI 468916.

During the summer of 2017, the University of Illinois conducted marker-assistant selection for SCN resistance genes. They tested 9,047 plants for resistance at Rhg1 and selected 1,141; tested 1,655 plants for both Rhg1 and Rhg4 and selected 286; tested 1,496 plants for Rhg1 and two SCN resistance genes from wild soybean (*Glycine soja*) and selected 121; and tested 641 plants for just the two genes from *G. soja* and selected 133.

The program grew yield tests during 2017 of breeding lines with resistance from PI 88788, PI 437654, Peking and *G. soja*. These tests are being harvested and as soon as

this is completed, data from the tests will be summarized and selections made. The Nguyen Lab developed ten BC2F2:5 experimental lines carrying up to three resistance genes using sources of resistance from PI 437654, PI 88788 and PI 567516C. To confirm gene stacking and establish contribution of each gene for SCN resistance, these lines are currently being phenotyped against six SCN races. The seeds will be sent to winter nursery to increase seed for use in rotational studies and progeny rows selections next year. Moreover, additional crosses were performed to produce BC3 and BC4 populations for ultimately combining up to five resistance genes.

In addition, 172 experimental lines from the 2016 SCN Regional Tests were tested using available diagnostic markers to detect types of resistance caused by rhg1 and presence of Rhg4. Among them 123 lines were detected with rhg1 PI 88788-type, 15 lines with rhg1 Peking-type and 13 lines with Rhg4.

Objective 2 - *Identify SCN virulence factors and better understand how the nematode adapts to resistance*

In this reporting period we utilized various state of the art methods to optimize genome sequencing and improve SCN genome assembly. A web interface has been created to house the SCN genome and its complementary annotation information.

Comparative analysis between virulent populations on resistant soybean continued with the identification of polymorphisms between populations. These polymorphisms are being pursued for validation and use as potential candidates for virulence markers. In addition, the functional impact of effector variants unique to virulent populations is being assessed to determine importance to virulence. The data generated by these two approaches will improve initial SCN population characterization and potential virulence mechanisms.

To determine the impact of SCN resistance on yield, a population of 95 experimental lines developed in 1.1 that segregates for rhg1 from PI 88788, two SCN resistance QTL alleles from *G. soja*, and a resistance QTL allele from PI 567516C was tested in two Illinois locations and one Missouri location during 2016, and repeated in 2017.

The HG type 1.2.5.7 field population from the Missouri location was chosen for use in a greenhouse study of selection in a series of rotation schemes in a greenhouse trial using a subset of the experimental lines with different gene combinations. Populations are being selected for eight generations with egg increases quantified after each

generation before they are re-typed. The eighth generation of selection was completed and HG typing of each selected population has been initiated.

Objective 3 - *Translate the results of objectives 1 and 2 to increase the profitability of soybean for producers*

A manuscript titled “Effects of Clariva Complete Beans seed treatment on *Heterodera glycines* reproduction and soybean yield in Iowa” was completed and accepted for publication in Plant Health Progress.