



North Central Soybean Research Program

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

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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 (genetic blueprint of the nematode) assembly 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
2. Identify SCN virulence factors and better understand how the nematode adapts to resistance
3. Translate the results of objectives 1 and 2 to increase the profitability of soybean for producers

Reporting Period Accomplishments

- We have made a significant progress in diversifying the sources of soybean cyst

nematode (SCN) resistance, which will offer growers viable choices to control this pest.

- We have developed and commercialized a soybean variety that has Rhg1 combined with the two resistance genes from *G. soja* providing additional management tools.
- This project has shown that SCN resistance levels of soybean lines can be predicted by combining the copy number results with the identification of alleles present at Rhg1 and Rhg4. This advance will significantly speed up breeding progress.
- Different SCN resistance gene stacks are being tested in different field locations to gauge their influence on the nematodes' ability to overcome soybean resistance genes. Data from these experiments will be critical in developing stewardship guidelines for available soybean resistance genetics to ensure longevity of varieties.
- This project coordinated the regional multi-site testing of publicly developed SCN resistant soybean lines. These data will tremendously improve breeding efforts and will critically inform farmers' cultivar decisions.
- This project invested considerable resources into the advancements of the SCN genomics and transcriptomics data.
- One of the major hurdles for SCN researchers was the lack of a properly annotated SCN reference genome. In the past three years, we have extensively improved our initial SCN genome assembly and have finished multiple analyses.
- Our work has identified a whole suite of previously undiscovered effectors, the nematode secreted proteins that play critical roles in establishing infection. Now scientists can begin to conduct in-depth functional characterization of the roles played by these effectors as such knowledge can pave way to develop novel nematode resistance resources in future.
- Simultaneously, we developed and published the first completely annotated genome of an endosymbiont directly sequenced from the plant-parasitic nematode. This will help future SCN sequencing efforts as it ensures that the endosymbiont sequence does not contaminate SCN-specific sequences.
- Additionally, we have made significant progress in sequencing genomes from multiple, distinct SCN populations. It is impossible to raise truly homogenous SCN nematode culture. Thus, one always ends up with sequences from multiple heterologous individual nematodes, which makes developing high quality genome assemblies of SCN populations a challenging and time-consuming task. However, NCSRP funds have allowed significant progress in this regard and sequencing of multiple populations is now complete and a high quality research manuscripts describing these results is in preparation.
- Sequencing multiple populations with distinct Hg types can eventually lead to development of a simple molecular test to identify distinct SCN populations in fields so that farmers can make informed decisions about the most suitable soybean cultivars they can grow.
- It is an intriguing question how certain SCN populations are able to overcome the available SCN resistances in fields. We hypothesize that inherent differences in either effector populations or the levels of expression of one or more effector families within the SCN populations could be the reason behind the differential virulence displayed by these populations. To address this question, we have sequenced RNA from the salivary glands

from a virulent and a non-virulent SCN population and these data will be analyzed in the next funding period.

- This project has generated large amounts of sequencing data and has yielded multiple analyses. It is essential to have a proper online portal to distribute all these data so that scientists and end-users worldwide can have access and use. To this end, we have developed the online portal “SCNBase.org”, which displays all the relevant information in a user-friendly manner. A research manuscript describing this online tool will be published soon.