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 glycine*s, (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,
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> (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
   - 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 grow on resistant soybeans.
- Inform growers on effective rotation schemes designed to protect our resistant sources.

Reporting Period Accomplishments
Objective 1
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 is releasing for seed increase by a private company a high yielding MG IV line that combines SCN resistance genes from PI 88788 and PI 468916.

129 experimental lines from the Southern MO breeding program are being tested in the Nguyen lab with available diagnostic markers to detect CNV for Rhg1, Rhg4, qSCN11, qSCN10, and qSCN18. The same set is being phenotyped in Mitchum lab.

Objective 2
We have completed PacBio sequencing of the original nematode DNA used for the JGI assembly, using a new chemistry. Kim Walden is now leading this project. Kim has extensive experience of whole genome sequencing and assembly. Automated shotgun assembly of the data has produced an unfiltered first pass N50 (minimum size of 50% of the genome) of 43KB, with strong gene completeness (BUSCO) scores and a total size of 169MB. Kim has developed a new method for isolating extremely high molecular weight DNA. We are currently using this to produce contigs using the 10x genomics method. We have also produced an assembly of the endosymbiont bacterium of SCN.

An initial GMOD instance of Tripal, a web content manager for genomic datasets has been set up to host the SCN data. This web resource currently hosts the genome assembly and annotation. We continue to focus on designing an intuitive and useful website interface. This includes tools to analyze the data, to explore potential collaborations and projects, to learn about the website/protocols and a page to download all data. This web resource will integrate with Soybase.

The Mitchum lab continued computational comparative analysis between virulent populations on resistant soybean at the transcriptome level. Effector analysis is underway, examining effector variation and differential expression between populations. Effector variants unique to virulent populations will be further

characterized to identify their role in virulence. This effector analysis will build off of the previous large scale analysis to identify 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.

Across environments, when the lines with resistance alleles were compared to lines with the alleles for susceptibility, lines carrying the resistance allele at the *G. soja* QTL cqSCN-007 yielded 3.25 bu/acre better than those that did not, and lines with the PI 567516C resistance allele yielded 1.75 bu/acre better. However, lines with resistance at rhg1 yielded 2 bu/acre less than those without that allele. These results show that depending on the environment, different resistance genes can have a positive impact on yield.

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.

To determine the impact of SCN genes stacks, lines with combinations of three, two and one resistance gene were developed in 1.1 by the Nguyen Lab. These lines segregate for Rhg1 from PI 88788, Rhg4 and qSCN11 from PI 437654, and qSCN10 and qSCN18 from PI 567516C. Line with different gene combinations will be phenotyped and planted in spring 2017.

Objective 3
Following a review of SCN information available on the internet, Dr. Bissonnette presented the results in a poster titled "Survey of internet resources on the soybean cyst nematode" and was invited to present a talk titled "Grower perceptions of SCN: the 1990s versus 2015" about grower perceptions of SCN and its management at the 2016 SCN Conference (December, 2016).

Analyses of the seed treatment nematicides Ilevo and Clariva were completed and are being developed into two manuscripts. Results were presented at the MVTL agronomist meeting and as an invited talk at NCERA 137 (March, 2017). An update on the current status of SCN was also presented at the SSDW meeting in March of 2017 titled "Soybean Cyst Nematode: Current status, challenges, and opportunities for sustained, profitable soybean production." Finally, Dr. Bissonnette has met with and been updated by the researchers working on Objective 2.