**Objective 1.**Search for the best germplasm lines with novel SCN resistance for studying genetics and breeding soybean cultivars.  
**Goal 1:**  All soybean germplasm lines in the USDA germplasm collection were screened first with the SNPs (Single Nucleotide Polymorphism) developed in the previous studies. A total of 371 soybean lines were positive of the SNP markers, and among them 317 lines were not tested in the previous study.   
**Goal 2:** These 317 soybean lines plus 32 lines of wild soybean (*Glycine soja*) were included in this test.  The lines were first screened by testing one plant per line with SCN HG Type 2.5.7.  Soybean lines were grown in cone-tainers in the greenhouse.  After 30 days, the females formed on the soybean roots of individual plants were extracted and counted. Female Index (FI) were calculated: FI = females formed on a soybean line × 100/females formed on control Williams82.  During this period, the lines (175 lines) with FI less than 40 were tested again with two plants per line to confirm their resistance to the SCN population.  Soil samples of the greenhouse test with SCN HG Type 2.5.7 for these 175 lines have been collected, and they are being processed.  
We will test all 349 lines for their resistance to HG Type 0.  
**Goal 3**: The top 23 soybean lines were selected for further test of their resistance to multiple populations of SCN HG Type 2.5.7.  The 23 lines have been tested with three SCN populations.  The tests for another two SCN populations have been set up in the greenhouse.   
   
**Objective 2.**Conduct genome-wide association study (GWAS) to validate the novel SCN resistance QTL and associated SNP markers.  
   
A Total of 130 soybean lines positive “HG Type 2.5.7 resistance” SNP markers as determined in Objective 1, and 145 lines negative of the markers were randomly selected from the USDA germplasm collection for this study. The soybean lines were grown in cone-tianers in the greenhouse inoculated with SCN HG Type 2.5.7, six plants per line (Figure 1). After 30 days, the cysts formed on the soybean were collected and counted.  Female Index (FI) were calculated: FI = females formed on a soybean line × 100/females formed on control Williams82. Genetic data of individual soybean lines were obtained from the SoyBase (<http://soybase.org/>). The genetic data contain approximately 50,000 SNP markers across the 20 chromosomes in the soybean genome. Genome-Wide Association Study (GWAS) were conducted to identify the SNP markers associated with the SCN resistance.  The same major QTL found in the previous study was also found with this set of data (Figure 1).  The results validated the QTL and SNP markers founded in the previous study.  
   
**Objective 3.**Determine the effect of sequences of SCN-resistance sources on SCN population densities and virulence phenotypes.  
A field experiment was initiated in 2008 in Lamberton to study how the rotations of different resistance sources affect the dynamics of SCN population densities and their virulence phenotype. The initial population was race 1 (HG Type 2.5.7), which is virulent to cultivars carrying the PI 88788 resistance.  The main aim of the experiment is to determine whether any cultivar sequence can change the population from virulent to avirulent or change to other HG Types so that the PI 88788-source and/or Peking-source cultivars can be used.  We will determine if there is any fitness cost for SCN virulence and if rotation with SCN-susceptible cultivars can select avirulent phenotypes and be helpful in managing problematic HG Types.  
The treatments include different combinations of the four cultivars Pioneer 92B13 (susceptible), Latham EX547 RR N (PI 88788 resistance), Pioneer 91M90 (Peking resistance), and Latham AR5084 (PI 437654 resistance) (Table 1). This is a long-term study and the data from the site will serve as a model to predict trend of race shift.  In 2019, soil samples were collected from each plot to determine the SCN population densities at planting and harvest, and soybean yield was measured.  The SCN soil samples have been processed for the SCN egg counts. The soil samples taken at harvest are being cultured in the greenhouse to increase SCN population density and will be tested in the greenhouse for virulence phenotypes (reproductive ability) of SCN on the source of resistance PI 88788, Peking, and PI 437654 with Lee74 as control.

**Achievements:**

A previsional patent application has been filed.

**Challenges:**

We have short of supporting workers in the summer of 2019, so this project is a little behind. We hired an additional technician to work on this project.  However, our lab is under reduced operation mode during the covid-19 pandemic, and our progress of the experiment and sample processing has been affected.