

Markers for resistance-breaking SCN populations (Primary Investigators: Terry Niblack, Kris Lambert, Greg Noel)

The team of Terry Niblack, Kris Lambert, and Greg Noel has conducted research to understand the mechanism of sex determination in SCN. Traditionally, the analysis of the population dynamics of SCN has almost exclusively focused on female parasitism. Female nematodes, due to their enlarged bodies that obstruct normal root function and to their heavy feeding demands, are believed to be the main agent of the disease. Typical symptoms of yield loss, stunting and chlorosis are associated with SCN-infested fields. When making recommendations on the use of resistant soybean to control SCN, observations of changes in female parasitism over time in fields planted to resistant soybean are used as the criteria. Soil samples are analyzed to detect the presence of SCN eggs and approximate the parasitic ability of SCN females in field populations. However, on susceptible plants, adult males and females generally occur in equal numbers. Unlike some species of nematodes, like the root-knot nematodes for example, males are required for reproduction. This predominately female focus results in exclusion of 50% of populations, and ignores the genetic contribution of males.

The identification of the mechanism of sex determination in SCN would not only provide answers to important population biology questions regarding the soybean cyst nematode, but could potentially improve recommendations given to soybean producers. If sex determination is in fact influenced by the environment, this would provide a control point to alter SCN development; if it is not, then this is important to know. Although the mechanism of sex determination in SCN, and in the family Heteroderidae, is as yet unknown, recent molecular tools could help find genomic differences between males and females. AFLP (amplified fragment length polymorphism) is an excellent technique for this purpose. Another way to ascertain the mechanism of sex determination in SCN is to search for nematode genes already known to be involved in sex determination. The knowledge of how SCN determines its sexual fate should allow the manipulation of the pathway to help control this damaging pathogen.

As with SCN, the most efficient and economic method for reduction of damage to soybeans from sudden death syndrome (SDS) is the use of resistant varieties. In collaboration with USDA-ARS scientists, we are studying the SDS pathogen interaction with soybean hairy and normal roots using partially resistant and sensitive genotypes. (Lozovaya et.al., in preparation) We measure the effect on induction of enzymes involved in phenylpropanoid biosynthesis and the compounds themselves including isoflavones and the phytoalexin glyceollin. The root resistance correlates with the induction of this pathway that indicates that a genetic engineering approach that would stimulate flow through this pathway could be effective for obtaining fungal disease resistance.

The goal of this project is to develop a rapid, reliable test that can be used to assess the “virulence profile” of a SCN population. The test would significantly improve cultivar recommendations for soybean producers. A virulence profile would consist of a list of the HG Type indicator lines that the nematode is able to parasitize, much like the information provided by greenhouse bioassays, but DNA-based. We have already developed many of the tools needed to pursue this goal: SCN inbred lines by single-cyst-descent and mass selection on the four major sources of SCN resistance; AFLP markers associated with virulence on each of these sources of resistance; and optimized real-time PCR protocols to allow quantification of virulence markers within a SCN population. The next steps required to achieve the goal are to develop the

AFLP markers into reliable probes, and to verify that SCN virulence profiles can be used in lieu of race or HG Type tests to make cultivar recommendations for soybean producers.

Heterodera glycines, the soybean cyst nematode (SCN), is the most economically important pathogen of soybean in the North Central Region. Worldwide, SCN is responsible for yield losses valued at over \$2 billion. SCN can be managed effectively – that is, yield losses can be limited and SCN populations kept low – through the use of such tactics as rotations with nonhosts and resistant soybean cultivars. One important limitation to the use of resistant cultivars is that resistance is not complete. SCN can reduce yields of resistant cultivars if nematode numbers are high enough. In addition, some populations of SCN can adapt to resistant cultivars, rendering the resistance ineffective. No soybean PI or cultivar has complete resistance, as shown by our ability to select SCN populations with virulence to every source of resistance in use today. The current push to incorporate new sources of resistance in cultivars, along with the demonstrated ability of the nematode to adapt to these sources, highlights our need for new diagnostic tools with which to counter future problems posed by SCN.

The specific planned accomplishments include the following: clone and sequence the AFLP markers for virulence on PI 548402 (Peking), PI 88788, PI 90763, and PI 437654 (these four lines account for 99% of all SCN-resistant cultivars available in the North Central region); conduct a DNA gel blot analysis to confirm marker polymorphism; design TaqMan assays to specifically detect virulent markers and a conserved reference gene; identify, with collaborators in six North Central states, at least 25 fields with SCN populations high enough to damage resistant cultivars and plant the fields with sets of the four PI lines and cultivars derived there from; develop pre-plant and post-harvest virulence profiles of the SCN populations in each field by means of HG Type tests and real-time PCR test results; compare results from the bioassays (HG Type tests) and PCR tests to determine whether the PCR-based test is usable on a practical basis. Cooperating institutions will include Iowa State University, Kansas State University, Purdue University, University of Minnesota, University of Wisconsin, and USDA-ARS, Jackson, Tennessee.