Project Update - April 1st, 2020

I. **Project Title:** An integrated approach to enhance durability of SCN resistance for long-term, strategic SCN management (Phase II)

II. **Principle and Co-Principle Investigators:** Dr. Andrew Scaboo, Dr. Melissa Mitchum, Dr. Brian Diers, Dr. Thomas Baum, Dr. Gregory Tylka, Dr. Matthew Hudson, and Dr. Andrew Severin

III. **Brief Description of Accomplishments as of April 1st, 2020:**

A description of relevant progress for principle and co-principle investigators is below for each objective and sub objective in our proposal. Our team has made tremendous progress in accomplishing our research goals, publishing refereed journal articles, and communicating our results to scientists and soybean producers. Also of note, we had our last group research meeting in person in November of 2019 in St. Louis, MO, and our next group meeting is scheduled for April of 2020 for research planning and proposal preparation.

Objective 1: Diversify the genetic base of SCN resistance in soybean.

Although a large number of sources of resistance to SCN are available to soybean breeders, PI 88788 is the resistance source for over 90% of the varieties available to growers in the North Central US. The effectiveness of PI 88788 resistance has decreased over time as the nematodes have adapted to this resistance source. Research over the past 20 years has resulted in the identification of resistance genes from several other sources of resistance. However, the resistance genes from novel sources largely have not been transferred into elite soybean varieties. Research is needed to overcome the bottlenecks that have slowed the incorporation of these new genes into commercial varieties.

1.1: Develop and evaluate germplasm with new combinations of resistance genes in high-yielding backgrounds (*Diers, Scaboo*)

Diers – Our research is continuing to develop new varieties with non-PI88788 sources of resistance. New, high yielding lines with SCN resistance from non-PI 88788 sources were selected in 2019. Five new high yielding lines that have *rhg1-b* from PI 88788 combined with two resistance genes from *G. soja* were selected for testing in uniform or regional test this summer.

Scaboo – We are developing germplasm and varieties in the relative maturities 3.5 to 4.2 with resistance to SCN HG 1.2.5.7 (Race 2), which is currently the predominate HG type in Missouri. We are using novel SCN resistant sources including PI 437654, PI 90763 and PI 468916, with most support from USB and MSMC for these efforts. We will continue population development by forward and backcrossing, using phenotypic screening and molecular markers for SCN resistance selection, and by yield testing elite germplasm in both state and regional tests (run by Diers). Our first yield tests of novel soybean material with Race 2 resistance was during the summer of 2019, and we plan on having this material in various stages of yield testing every year thereafter.

Objective 2: Identify SCN virulence genes to better understand how the nematode adapts to reproduce on resistant varieties.

Past research efforts to determine the inheritance of SCN virulence (i.e., the ability of the nematode to reproduce on resistant varieties) led to the identification of the reproduction on resistant varieties or *ror* genes, which were shown to be inherited in both dominant and recessive manners. However, since the

initial discovery of these genes there has been no further information published concerning their sequence identity or mechanism in conferring SCN virulence. Genome and transcriptome comparisons of SCN populations that differ in virulence on resistant soybean have the potential to identify genes underlying virulence, determine the mechanism/s of virulence, and lead to the development of molecular diagnostic tools to assess for virulence in field populations.

2.1: Sequence, curate and annotate SCN reference genomes for each common HG type (*Severin, Hudson, Baum*)

Baum/Severin – One of the major milestones in SCN biology is developing a completely annotated SCN reference genome, which we have recently accomplished (Masonbrink *et al*., 2019). Using NCSRP funds we continue to refine this resource further. We have made considerable progress in that direction and now have a chromosome level genome assembly ready and annotated. Currently, we are preparing a manuscript describing these results to be submitted shortly. Simultaneously, we have developed a centralized, web-based repository called SCNBase (SCNBase.org). We have developed this web portal de novo and published it in November 2019 (https://doi.org/10.1093/database/baz111). This web portal now is the home to all bioinformatic, genetic, genomic, and molecular data generated for SCN, most of it through soybean check-off funding. Using this web portal, researchers and breeders from all over the world can access and analyze all public bioinformatic data generated in this proposal and curated from previous research at the nucleotide level. We are already seeing significant "web traffic" to this web portal suggesting that it is generating considerable interest in the SCN community from all over the world. For example, since SCNBase has been open to the public earlier in 2019 it has been accessed by 1,792 unique users. During the period of January 1 to March 26, 2020 alone, this web portal had 307 unique users, almost half of which were located outside of USA. As such, SCNBase provides prime visibility and impact of the collective data procured through farmer investments in research, which and will enable others in a coordinated fight against this pathogen. This current NCSRP project is already generating and will continue to generate thousands of gigabytes of data, which will be incorporated into SCNBase as we continue to develop this web portal.

Hudson – Our project has now generated high quality genome sequences for five SCN isolates: OP50, TN 7, 8, 20, and 22. These sequences are all more complete than the TN10 sequence published by our consortium last year. The TN10 reference has now been improved to comparable or better quality by the Iowa group. We thus have six complete genomes of different SCN strains with assemblies each with N50 > 10MB, plus the Chinese group's assembly of the X1 strain, which is less reliable than those from our own project. The five completed sequences have been annotated and effector sequences have been identified using sequence similarity to a set of 80 curated plant parasitic nematode effectors. So far, the variability of size in the seven different assemblies, and the sequencing and assembly methods used, seem to be affecting the overall number of genes and effector genes more than the likely biological differences. We are in the process of curating the assemblies to make them more comparable. However, we are able to identify the presence of between 63 and 69 of the 80 effector families in each genome, giving each isolate a substantial arsenal of effector proteins. The correlation between effector families in the genome and virulence on specific hosts is an ongoing analysis expected to generate preliminary data by September 2020. We are in the process of repeating and enhancing these methods on two more isolates, MM26 and PA3. We are using the new PacBio sequencer which should produce even better data than the nanopore sequencing used previously. Sequencing is completed for PA3 and in progress for MM26. Assembly for PA3 has begun. Both genomes are expected to be completed by September 2020, giving us high quality whole-genome sequences of all the key HG types.

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Mitchum – Continuously maintained live cultures, prepped and provided all of the genetic material for each common HG type in sufficient quantities for various sequencing platforms used to generate the reference genomes described above.

2.2: Generate sufficient genetic material of virulent SCN populations selected on different types of resistance (*Mitchum, Baum*)

Mitchum – In Phase I of this project (under Obj 2.3 of the previous project) we identified a HG type 1.2.5.7 field population and continuously selected this population in the greenhouse on either a susceptible soybean line (SCN inbred population MM-BD1), a soybean line containing the *rhg1* resistance gene from PI 88788 (SCN inbred population MM-BD2), a soybean line containing the *rhg1* and *Rhg4* resistance genes from PI 437654 (Hartwig) (SCN inbred population MM-BD3), and a soybean line containing resistance genes on chromosomes 15 and 18 from wild soybean *G. soja* (inbred population MM-BD4) for more than 12 generations. The original SCN field population and this series of SCN populations selected for virulence on each set of resistance genes has been continuously reared to generate sufficient genetic material for sequencing. The populations were subjected to another 6 months of selection in this project period, HG typed, and frozen.

2.3: Resequence the genomes and transcriptomes of virulent SCN populations described in 2.2 and conduct comparative analyses (*Severin*, *Hudson, Mitchum, Baum*)

Baum/Severin – Our group is actively involved in developing, analyzing and comparing gene expression in from virulent (i.e., ab le to infect resistant soybean cultivars) and avirulent (i.e., unable to infect resistant soybean cultivars) SCN populations with the goal to identify the genetic determinants of virulence. For that purpose, we are focusing on three individual gland cells, in which the nematode produces the effectors/tools required for infection and defense suppression, using a method we previously had developed. Toward that end, we have completed three independent biological replications of mRNA purification, library construction and sequencing (which is essentially an identification of all genes expressed in the gland cells at a given time) from each of the virulent (MM10) and avirulent (PA3) SCN populations. Furthermore, gene identities from all sequencing experiments have been generated utilizing the SCN TN10 genome produced by us (Masonbrink *et al*., 2019). We identified 13,617 unique transcripts from the PA3 population and 8,820 unique transcripts from the MM10 population, which represent a snapshot of gene activity during the early parasitic stage of SCN infection (parasitic J2). As a point of validation, we have identified all previously discovered SCN effectors expressed during this early parasitic stage within our gland cell-specific sequence data. Initial analysis of these sequence data has revealed intriguing gene expression differences between these virulent and avirulent SCN populations. Specifically, there are 32 genes upregulated in the SCN PA3 libraries versus the MM10 libraries. Protein products of 13 of these genes are predicted to be nuclear localized and likely have gene regulatory functions. This includes a diverse group of proteins involved in functions such as structural maintenance of chromosomes, splicing factors, a glycosyltransferase involved in increased virulence in other parasitic nematodes, DNA-binding proteins, and a ‘ran’-binding protein, among others. Conversely, we discovered 17 genes that are upregulated in SCN MM10 versus PA3. Protein products of eight of these genes are predicted to be nuclear localized. Among this group are previously reported effectors, a microtubule binding protein homolog from an animal-parasitic nematode, signal transduction proteins, and several unknown proteins. We are still at the initial stages of analysis but it is already clear that we have generated a rich source of critical data needed to understand SCN virulence.

Mitchum – The MM26 parental population for the adapted populations outline in 2.2 above was prepared and sent for genome sequencing; the others will follow. RNA-seq data generated from early parasitic life stages of a virulent and avirulent population of SCN were used to conduct a reference-based transcriptomic analysis with the aid of the SCN genome. We identified 207 genes unique to the virulent SCN that could be turned on to overcome resistance mechanisms; conversely, 92 genes that could be turned off to evade triggering resistance mechanisms. Interviewed and hired an excellent new postdoctoral research associate with expertise in advanced bioinformatics, population genetics, and genomics who is an ideal fit for the project. He will focus on extending our work on the molecular genetic and comparative genomics analysis of soybean cyst nematode population structure as it relates to virulence on resistant host plants. Unfortunately, we are now faced with a significant delay in his joining our team due to COVID-19. We continued our collaborative effort with the Baum lab to generate nematode gland-specific RNA-seq datasets of a virulent and avirulent population of SCN; several joint meetings were held to discuss comparative analyses which are underway to identify differentially expressed gene candidates with a potential role in virulence using the newly annotated pseudomolecule SCN genome assembly

2.4: Validate and characterize genes associated with SCN virulence and evaluate their utility as novel resistance targets (*Mitchum, Baum*)

Mitchum – As candidate SCN virulence genes are identified, gene function will be confirmed through biochemical and/or genetic analysis to not only better understand the mechanisms of virulence, but to also evaluate these gene targets as vulnerable points of disruption in the SCN life cycle as a means to enhance resistance in soybean. We focused our efforts on validating the genes identified in 2.3 above to prioritize candidate virulence genes for further molecular functional studies.

Baum – Being a sedentary endoparasite that relies exclusively on its host for survival, SCN has to suppress host defense responses for a significant duration in order to survive. The SCN achieves this by producing a large number of effector molecules and delivering them into the soybean cells via its mouth spear. These effectors specifically target host factors and modulate their functions, thereby also altering soybean defense responses. Generating an in-depth understanding of how individual effectors help SCN establish and maintain infection is a very difficult but necessary task that will reveal vulnerable “nodes” in host defense pathways that can be strengthened via either breeding or molecular approaches.
As a part of this project, we are actively involved in conducting in-depth molecular characterization of SCN effectors specifically involved in host defense suppression. For this reporting period, we specifically focused on the effector named 28B03. We have identified that this particular effector is a robust host defense suppressor. We have observed that due to its function, plants become more susceptible to cyst nematodes. We have also identified that this effector specifically targets a previously uncharacterized plant protein kinase. By physically interacting with this novel protein kinase, the 28B03 effector suppresses phosphorylation of its substrate protein and completely alters the associated signal transduction pathway. This discovery and an in-depth molecular characterization of a novel defense response related kinase cascade in plants are breakthrough discoveries of this study. We are currently writing a manuscript describing these results. Simultaneously, we are gearing up to conduct another high-impact protein interaction experiment in order to identify the complete ‘interactome’ of the proteins associated with this kinase cascade.

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Objective 3. Determine what combinations of resistance genes would be beneficial in variety rotations to enhance the durability of SCN resistance in soybean.

As described above, experimental lines with resistance gene combinations developed in Objective 1 during Phase I of this project were tested in four different rotation schemes with experimental lines containing various resistance gene combinations in a greenhouse study. SCN population increase was measured after each generation for 8 generations. Following the eighth generation of selection, the HG type of each population was determined. From this, we identified alternative resistance gene combinations that when used in rotation reduce the selection pressure on the SCN population thereby slowing nematode adaptation to resistant varieties.

3.1 Evaluate how rotations of various resistance gene combinations impact SCN field population densities and virulence profiles (*Diers*, *Scaboo*, *Tylka*, *Mitchum*)

Diers – The Illinois location of the rotation trial was harvested and fall soil samples were taken to evaluate SCN population changes over the summer. Samples from susceptible checks show that the SCN population was an HG type 2 (Race 5) in two plots and a HG type 1.2 (Race 2) in one plot. The analysis of the change in egg number between the spring to the fall show that there was a 5 X increase in eggs through the growing season for the susceptible check, a 3.8 X increase for lines with only *Rhg1b*, a 1.6 X increase for lines with *Rhg1b* plus two QTL from *G. soja*, a 3 X increase for *Rhg1b* plus two QTL from *G. soja* and a fourth QTL on chromosome 10, a 2 X increase for lines with *Rhg1a* + *Rhg4* from Peking, and finally only a 0.3 X change for PI 90763. These results are close to what we expected and show that the different sources influenced SCN reproduction in the field. Preparations are being made to plant the second year of the test in the field.

Scaboo/Mitchum – Microplot field experiments were established to evaluate how rotations of SCN resistance gene combinations impact SCN field population densities and virulence profiles. Treatments with resistance genes: rhg1-a, rhg1-b, Rhg4, cqSCN-006/cqSCN-007, and the chromosome 10 QTL, along with susceptible and resistant checks were designed to form 12 treatments with 3 replications in a randomized complete block design. The virulent SCN HG type 1.2.5.7 was selected for microplot inoculation and had a female index of approximately 20% on Peking and approximately 40% on PI 88788. Hand planting and inoculation were done on May 31st, 2019. Soil samples from all 36 plots were obtained directly after inoculation to determine the baseline of SCN egg density. A moderate level of infestation was achieved. At 60 days post-inoculation (DPI), soil samples from the three susceptible plots and one field sample collected between the microplots were collected to determine the initial HG type. SCN HG type at 60 DPI was the same for all three susceptible plots. The HG type for these plots was HG type 2.5.7, which was similar to the SCN population present in the field location between plots.
At the end of the growing season, soil samples from all plots were obtained to determine egg density and SCN HG type at harvest. All resistance genotypes had a reduction in egg densities and the susceptible treatment had an significant increase in SCN egg density, while PI 90763 had the greatest percentage of egg count reduction followed by genotypes with resistance genes, *Rhg1-a + Rhg4*. SCN HG type results at the end of the first growing season show no specific trend.

Tylka – At the conclusion of the 2019 growing season, two separate soil samples were taken from each microplot in both experiments conducted in Iowa. The first set of soil samples were used to obtain an end-of-season population density of SCN in each plot, and the second set of samples were sent to the University of Missouri for HG Type testing to determine if and how the soybean genotypes grown in the microplots in 2019 might have shifted the virulence phenotypes (HG types) of the SCN populations

added to the microplots in the spring of 2019. Preliminary data analysis was completed for each of the experiments in Iowa, and some trends in SCN population density were observed. In both experiments, the highest SCN population densities were found in microplots in which the susceptible soybean variety was grown. The second highest SCN population densities were found in microplots in which soybeans with only *rhg1-b* resistance were grown. The lowest population densities were found in plots where PI 90763 and *rhg1b*+soja+ch10 resistance were grown. The results of the HG Type test results on the SCN populations in the soil samples collected from the microplots at harvest in 2019 are not yet available. Preparation and planning for the 2nd growing season has begun with the arrival of seed.

Objective 4. Translate the results of objectives 1-3 to the SCN Coalition to increase the profitability of soybean for producers.

In Phase I of the project, an extension and outreach coordinator, advised by project Co-PI Dr. Tylka, was hired to provide farmer education and outreach for the project. A survey of extension and outreach educational materials about SCN biology and management in the NCSRP states was conducted by the coordinator. Materials from land-grant universities and private seed and chemical companies were gathered, analyzed, and compared.

4.1: Inform growers on effective rotation schemes designed to protect our resistant sources (*Tylka, Mitchum*)

Tylka/Mitchum – A news release about stacking SCN genetic resistance and rotation strategies was created and disseminated in 2019 and it led to interviews of Melissa Mitchum on Brownfield Ag Network and Brian Diers on Adams on Agriculture radio programs and an interview by Melissa Mitchum with Successful Farming/Agriculture.com (print/digital media). Also, the February 2020 issue of Progressive Farming magazine had a special section titled “Crop Invaders”, and it contained four pages devoted to SCN resistance (see Appendix) and an article titled “A New Movement: The Push for SCN Varietal Resistance Broadens” in which Brian Diers discusses novel SCN resistance genes and rotating their use to preserve their effectiveness. Also, our NCSRP-funded research was mentioned in radio and print interviews with Greg Tylka by the following media at the Commodity Classic meeting in San Antonio February 27-28, 2020: Emily Unglesbee, DTN; Gil Gullickson, Successful Farming; Mike Perrine, MP Ag Radio; Michelle Rook, WNAX; Mike Adams, Adams on Ag; Anna Hastert, Iowa Agribusiness Radio; DeLoss Janke, Illinois FB radio; Clinton Griffiths, Farm Journal; George Bower, KICD radio, Spencer; Ashley Davenport, Michigan Ag Today radio; and Mick Kjar, AgNews 890.

Objective 5. Coordinate the testing of publicly developed SCN resistant experimental lines.

During 2018, the testing of SCN resistant experimental lines developed by breeders in 11 north central US states and Ontario was coordinated. The tests include 182 SCN resistant experimental lines and varieties that are being grown in 104 maturity group specific trials across 39 locations. These lines are also being tested for SCN resistance and the soil samples from the environments will be evaluated for SCN population density and HG type.

5.1: Organize tests of experimental lines developed by public breeders in the north central US states and Ontario *(Diers)*

Diers – The report from the 2019 SCN Regional Test was completed and the first version of the results was sent to all test collaborators on 19 December 2019. This version included the agronomic,

composition and resistance test results. This version was followed by the distribution of the final version on 6 January 2019 which included the results of testing the egg number and HG type of nematode populations in field environments. This quick reporting of the 2019 results is important for breeders so this information can be used in release and crossing decisions. Planning has taken place for the 2020 tests and entry lists for the trials have been made and seed has been distributed to cooperators. The 2020 tests will include 194 entries that range from maturity group 00 to IV. The test will be grown in 32 environments in 10 states and one Canadian province. Because of the Covid 19 outbreak, it is not known how many locations will be planted.

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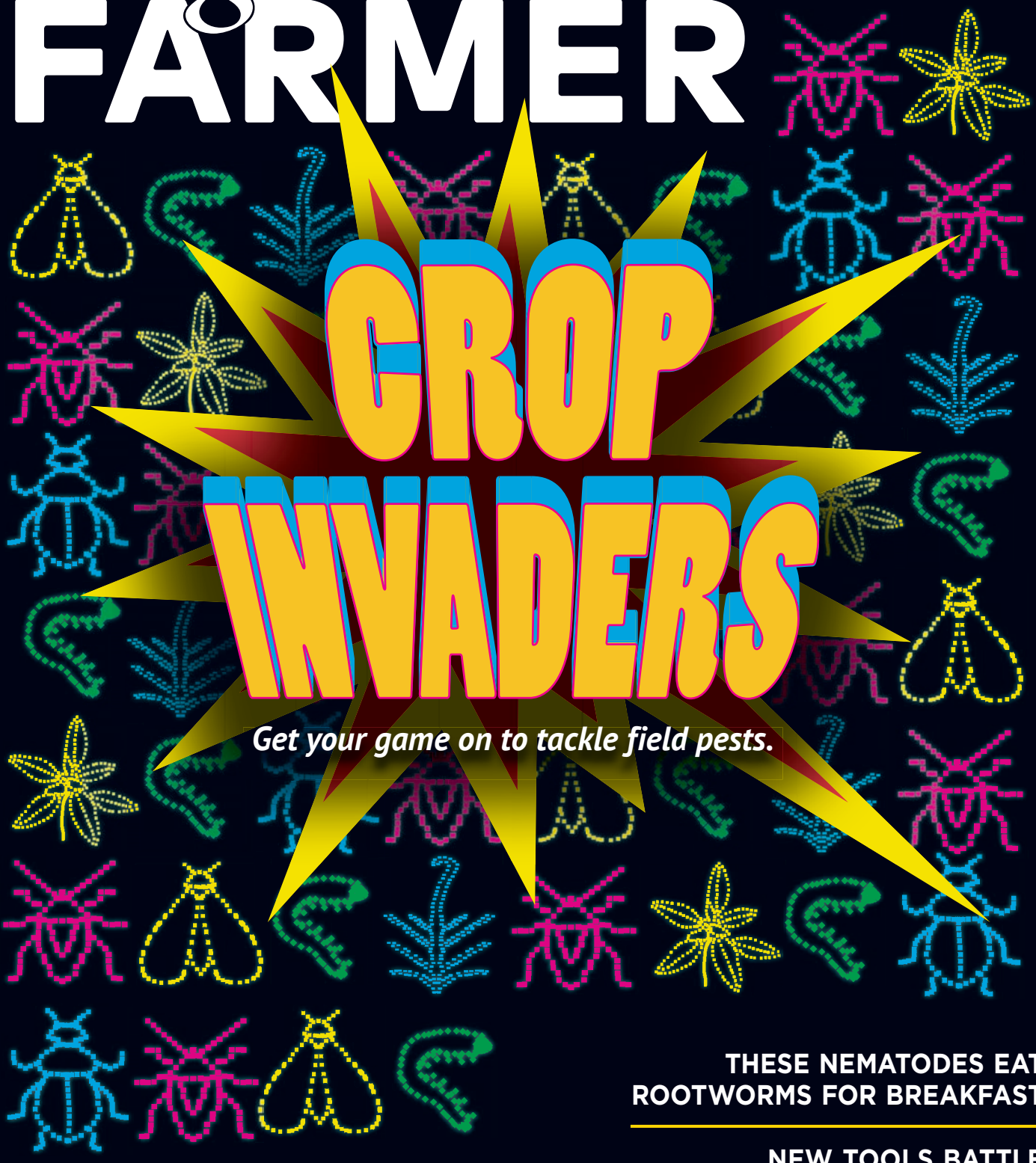
Progressive FARMER



CROP INVADERS

Get your game on to tackle field pests.

THESE NEMATODES EAT ROOTWORMS FOR BREAKFAST

NEW TOOLS BATTLE WHITE MOLD

SCN RESISTANCE REMINDERS

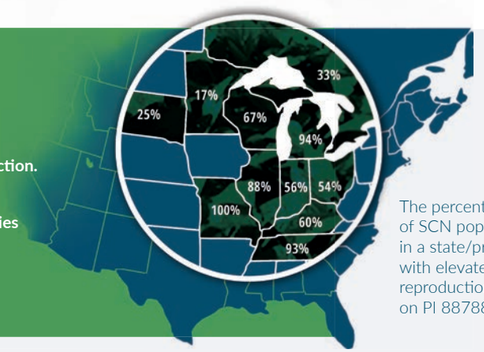
SCN REPRODUCTION PUTS RABBITS TO SHAME

WHY YOU NEED to test your fields for SCN.

For more than 20 years, greater than 95 percent of all SCN-resistant soybean varieties have included resistance from the PI 88788 breeding line.

Nematodes are becoming "resistant to the resistance."

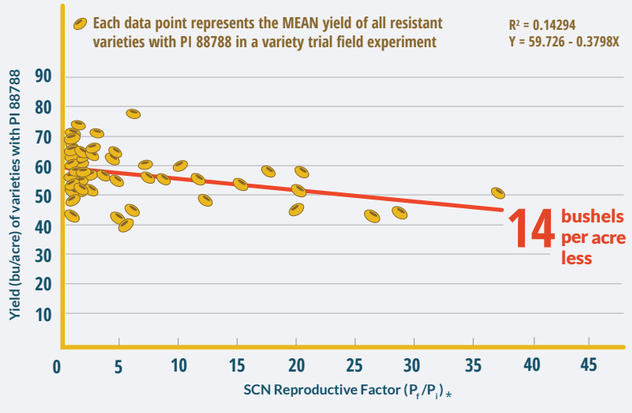
A resistant variety should allow less than 10 percent reproduction. In other words, a resistant variety should stop 90 percent of the SCN in a field from reproducing. Across the region, varieties with PI 88788 resistance aren't hitting the mark. On some farms, one out of every two nematodes can reproduce.



The percentage of SCN populations in a state/province with elevated reproduction (>10%) on PI 88788

AS SCN REPRODUCTION INCREASES,

yields decrease by as much as 14 bushels per acre.



Research shows yield loss as SCN populations increase on varieties with the PI 88788 resistance source. This data is from 25 years of variety trial experiments in farmers' fields in Iowa.

The Reproductive Factor (RF) is the end-of-season number of SCN eggs divided by the beginning-season number of eggs. An RF of 2 means SCN egg numbers doubled from spring to fall. An RF of 4 means egg numbers quadrupled. The last data point on the far right in the graph has an RF of almost 40 (a fortyfold increase).

*McCarville, M.C. et al. 2017. PHP dx.doi.org/10.1094/PHP-RS-16-0062.

SOURCE:THESCNCOALITION.COM

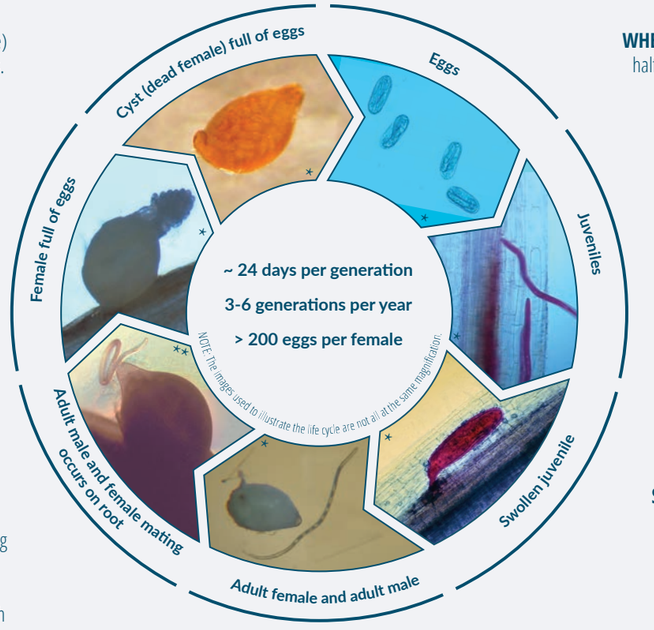
THE SOYBEAN CYST NEMATODE life cycle.

The SCN life cycle can be completed in as few as 24 days during the growing season. There can be from three to six generations per year. Even with an attrition rate of 99 percent (meaning only 1 percent of eggs survive each generation), 200 eggs from one cyst can become 48,828 eggs after four generations.

EACH CYST (dead female) contains 200 or more eggs.

AFTER MATING, she makes about 50 eggs outside her body and fills up with another 200+ internally. Then she dies and her body wall hardens to form the cyst.

THE FEMALE GETS SO LARGE that she ruptures out of the root onto the root surface and sends out a chemical signal to attract mates. There's no such thing as nematode monogamy. Females mate with many males, and males mate with many females. There's a lot of genetic mixing.



WHEN THE CYST BREAKS, half of the eggs will become male and half will become female.

JUVENILE WORMS hatch from eggs and burrow into soybean roots to feed and develop. There's no way to tell whether a juvenile is male or female at this stage.

THIS JUVENILE IS SWOLLEN from feeding in the root for several days. If this juvenile is female, she'll stay in the soybean root and keep feeding.

IF THE JUVENILE IS MALE, it will revert back to a worm shape and leave the root.

* Tylka, Iowa State University
** Chitwood, USDA

SOURCE:THESCNCOALITION.COM

Visit ***TheSCNcoalition.com*** for more information.

STORY AND PHOTO BY *Matthew Wilde*

SCN Sleuth

Meet the Iowa farmer who refused to be beat by an unseen pest.

Ron Heck isn't known to wear an ascot, but maybe he should after helping solve one of the Midwest's great agricultural mysteries.

The Perry, Iowa, farmer has a lot in common with Freddy of "Scooby-Doo, Where Are You?" fame. Both have the drive to decipher whodunits—but in different ways.

The teenage sleuth would devise a kooky trap to catch the fake ghost to solve a crime. Heck simply used an inquisitive nature, a little persuasion and, most importantly, yield maps in 1994 to eventually "unmask" once-mysterious villains, soybean cyst nematodes (SCNs). It was and continues to be the No. 1 soybean yield robber responsible for an estimated $1 billion in losses annually, experts say.

But, it used to be much worse. Industry officials and farmers agree Heck played a pivotal role in increasing awareness of SCN and its devastating effects in the Midwest. That led to more intensive management of the pest, Heck's prominent role fighting SCN, significant yield increases that put billions of dollars in growers' pockets and a shift in agricultural research.

"Ron is a visionary and insightful enough to recognize how this new tool in the early 1990s (yield mapping) could so powerfully be used," says Kirk Leeds, Iowa Soybean Association (ISA) CEO. "He made a difference ... and set the stage for what was to come."

Farragut, Iowa, farmer Steve Lorimor adds, "Ron's the guy with an answer to a question that nobody else could answer."

UNRAVELING A MYSTERY

Heck suspected great yield variability in his soybean fields prior to the mid-1990s, but he didn't know for sure. It wasn't until he installed a yield monitor in his combine 26 years ago and embraced precision agriculture, including yield mapping, that it was confirmed.

In those days, yields fluctuated from 20 to 60 bushels per acre (bpa) within many fields, even those with few visual symptoms. Why? Initial guesses were iron deficiency chlorosis or problems with pH, fertilizer or drainage.

"I didn't know anything about SCN. It was a Southern problem, so we thought," Heck says.

He showed the maps to Iowa State University (ISU) researchers and fellow Iowa Soybean Promotion Board (ISPB) and ISA directors.

Heck surmised if his fields succumbed to mysterious yield variations, it wasn't an isolated case. He suggested to colleagues to use soybean checkoff money to fund an on-farm research project to find out why.

"It was not a hard sell," recalls Lorimor, then chairman of the ISPB Research Committee. "If Ron hadn't (suggested the project), we might not have ever got started."

ON-FARM RESEARCH

The study, which started in 1996, consisted of two 50-acre sections of the middle of two fields in a corn/soybean rotation on Heck's farm. Each section was divided into half-acre grids. Two other sites were added in years two and three.

Researchers studied everything that could cause soybean yield variations—compaction, weed control, seed population, soil type, etc.

"Soil tests were taken along with an SCN count not expecting to find anything," Heck remembers. "We were all surprised that not only did I have nematodes but a lot of them. Some counts exceeded 30,000 (eggs per 100 cc [cubic centimeter] of soil)."

"I thought a 45-bpa average was good, but I could have had 55 or better with the right soybean varieties and had I known what to do," Heck says.

HECK'S ROTATION FOR SCN SUCCESS

Managing SCN is a lengthy process. It took Ron Heck years to reduce and keep SCN populations low. Yields jumped 10 bpa or more as a result.

Here's Heck's six-year strategy to reduce SCN yield loss and egg count:

- **Season 1:** Plant a PI 88788-resistant soybean variety.
- **Season 2:** Plant corn.
- **Season 3:** Plant a different PI 88788-resistant soybean variety.
- **Season 4:** Plant corn.
- **Season 5:** Plant a Peking resistant soybean variety.
- **Season 6:** Plant corn.

CATALYST FOR CHANGE

The study's data proving SCN is the primary soybean-yield-stealing culprit has changed the industry, officials contend.

The North Central Soybean Research Program started the SCN Coalition in 1997. The group's iconic campaign, "Take the Test, Beat the Pest," pushed awareness and soil testing for SCN. University researchers worked together more than ever to offer management recommendations.

SCN-resistant soybean varieties weren't available in large quantities or bred with northern soil and climates in mind. Soybean associations, with tens of thousands of members each, convinced seed companies and public breeders to change that.

Yield losses attributed to the parasite were reduced 5 to 10 bpa or more, depending on the severity, Heck says. But, they weren't eliminated.

SCN is no longer a mysterious yield robber thanks to Heck's actions. Though still a problem, it's not as costly as it once was.

"You get a big smile out of me for that," Heck says. "We changed the industry for the better. We made soybeans a better crop." ///

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FOR MORE INFORMATION

SCN Coalition: **www.thescncoalition.com**

BY *Pamela Smith*

A New Movement

The push for SCN varietal resistance broadens.

If you owned one pair of blue jeans and wore them every day for two decades, you'd expect some wear and tear.

In much the same way, the genetic resistance you depend on to protect against soybean cyst nematode (SCN) is fraying. Some 95% of the commercially available SCN-resistant varieties depend on a single source of resistance called PI 88788.

"In the last decade, we've seen a reduction in the effectiveness of PI 88788 in the prime soybean-growing areas," says Kaitlyn Bissonnette, a University of Missouri plant pathologist. "Soybean farmers need to be clamoring for increased access to new sources of varietal resistance."

UNIVERSITY OF ILLINOIS

Some SCN-resistant genes are easier to work with than others when it comes to inserting into high-yielding lines, but plant breeders are making breakthroughs, says Brian Diers, University of Illinois.

THE CHALLENGE

Soybean breeders have been working for years to insert other types of genetic resistance into elite soybean varieties. PI 548402 (Peking), PI 90763 and PI 437654 (Hartwig) are the most promising, but they are much more difficult to work with than the PI 88788 variety.

Brian Diers, a University of Illinois plant breeder, explains that PI 88788 involves one major gene: Rhg1. Peking, on the other hand, involves two genes: Rhg1 and Rhg4. It's simply harder for breeders to work with two genes, and it takes time to achieve yield parity.

"But, as you continue cycles of breeding, you are able to incorporate these genes more readily into elite, high-yielding lines," Diers says. Better genetic markers also help breeders select the genes needed and speed varietal development.

VARIETY ACCESS GROWS

Soybean growers, particularly in the Midwest, are seeing more soybean varieties enter the market with the Peking source of resistance, offering farmers more opportunities to rotate sources of varietal resistance. "We have a large amount of evidence showing that this reduces selection pressure on SCN populations to continually adapt," Diers says.

PAMELA SMITH

Varieties containing Peking as a source of SCN resistance are increasingly available through commercial companies.

More cultivars with PI 437654 (Hartwig) are coming, too. Diers says his Illinois program released two high-yielding lines, which were commercialized by companies through licenses from the university.

Diers' team also recently released a variety with a three-gene stack. "We combined the two resistance genes from wild soybean with Rhg1 from PI 88788 and have shown that this combination gives greater resistance than Rhg1 alone," he says.

He's also developed a four-gene stack—two new resistance genes from wild soybean stacked with Rhg1 from PI 88788, plus another resistance gene from PI 567516C. "If you look in the literature, there are many SCN-resistance genes that have been mapped," he says. "We worked on the gene from PI 567516C because it can give a greater increase in resistance than most other genes identified."

ANOTHER TYPE OF ROTATION

Farmers battling aggressive nematode populations should note that not all varieties containing PI 88788 are created equal. Simply rotating between soybean varieties may be helpful, Diers notes.

"Varieties derived from PI 88788 resistance do not all have the same level of resistance, and this may be related to the number of copies of the Rhg1 gene. There are normally 10 copies of the Rhg1 gene in varieties with PI 88788 resistance, but some may have fewer copies. With PI 88788, the higher the copy number, the higher the resistance," he explains. ///

FOR MORE INFORMATION

The SCN Coalition: **www.thescncoalition.com**