A MULTI-STATE EFFORT TO CONTAIN AND MANAGE MELOIDOGYNE ENTEROLOBII IN VEGETABLE CROPS. Agudelo, Paula1, J. Corbin1, J. Desaeger2, A. Gorny3, Z. Grabau4, Z. Guan5, A. Hajihassani6, J. Mueller6, L. Quesada-Ocampo6, W. Rutter6, and P. Wadl7. 1Clemson University, Dept. of Plant and Environmental Sciences, Clemson, SC 29634, 2University of Florida Gulf Coast Research and Education Center, Dept. of Entomology and Nematology, Wimauma, FL 33598, 3North Carolina State University, Dept. of Entomology and Plant Pathology, Raleigh, NC 27695, 4University of Florida, Dept. of Entomology and Plant Pathology, Gainesville, FL 32611, 5University of Georgia, Dept. of Entomology and Plant Pathology, Tifton, GA 31793, 6USDA-ARS, Charleston, SC 29414.

FINDMe (Focused Investigations on the Distribution and Management of Meloidogyne enterolobii) is a project sponsored by the USDA National Institute of Food and Agriculture's Specialty Crop Research Initiative. The program's research partners include Clemson University, North Carolina State University, the University of Georgia, USDA-ARS and the University of Florida. The spread of Meloidogyne enterolobii (Me.) into vegetable production in the southeastern United States is a high risk that can cause significant losses in yield and quality and its quarantine status jeopardizes both interstate and international trade. A major concern is the ability of Me. to infect and damage crop genotypes that are resistant to the other major species of RKN, including sweetpotato, cucumber, watermelon and tomato. New resources and information are urgently needed to help farmers manage this aggressive and polyphagous pest. The goal of this project is to reduce the vulnerability of growers to the emerging agricultural threat posed by Me. Our interdisciplinary team is working to achieve this goal by using a systems-based approach involving five interconnected research and extension objectives: 1) Study the prevalence and distribution of Me. in vegetable crops in the Southeast, and characterize the genetic variability encountered; 2) Evaluate and develop vegetable germplasm with resistance to Me.; 3) Evaluate the efficacy of nematicides, cover crops, and rotations as management strategies for Me.; 4) Assess the costs and returns of management tactics such as rotations, cover crops, and nematicides for the mitigation of Me. on sweetpotato, cucumber, watermelon and tomato crops; 5) Develop print and web-based educational materials on management and containment strategies for Me. It is critical for commercial growers and home gardeners to learn about Me. so that they can both prevent and manage the infestation.

50 YEARS OF NEMATOLOGY RESEARCH: CHANGING RESEARCH THEMES AND IMPLICATIONS FOR THE FUTURE. Alake, Gideon1, and N. Musa2. 1Department of Entomology and Nematology, University of Florida, 1881 Natural Area Dr., Gainesville FL 32611. 2Department of Crop Protection, Ahmadu Bello University, Samaru, 810001, Zaria, Nigeria.

Scholarly literature in nematology is an invaluable source of data that is concealed as texts. Several papers have been published addressing various areas of basic and applied nematology research, such as describing new nematode species, unraveling novel metabolic pathways and processes, and developing more efficient nematode management options. Abstracts from scientific papers and conferences efficiently convey important study findings and offer insights into past, present, and future research paths. We performed a comprehensive textual analysis of abstracts from academic nematology papers and abstracts from Society of Nematology conferences spanning 50 years (1970–2020). We applied text mining analytical techniques to over 50,000 abstracts retrieved from the Journal of Nematology archive, PubMed (MEDLINE), Microsoft Academic, and Web of Science databases. We utilized several specialized R packages in RStudio to extract, analyze and visualize data from pdf files containing conference abstracts and retrieved search results from online databases. This study aims to highlight global research priorities and trends, demonstrate the evolution of research themes, identify nematodes that have posed persistent challenges to global agriculture, and show how nematode management has evolved over the last five decades. We focused on Meloidogyne spp., Pratylenchus spp., Heterodera spp., Globodera spp., and Rotylenchulus spp. in this analysis due to their economic significance and research commitments. We noted some nematode pests that have lately garnered nematologists’ attention and a few significant nematode species that continue to pose a threat to agriculture. We reviewed several plant-parasitic nematode management methods that have been used throughout the years, including the use of resistant plants, nematicides, biological control, and cover crops. Also, we identified the impact of government policies on nematode management and the quest to find alternative solutions to the nematode problems. This study shows a considerable increase in nematode research productivity over the last five decades and a shift in foci to align with innovations in sustainable management for current and emerging nematode pests. Nematode resistance and the utilization of more eco-friendly chemistries for nematode management have both increased recently, with the root-knot nematodes, M. incognita, ranking highest in research impact. In addition, we provide information on the top-cited nematology publications. This study is crucial to academics, grant-funding organizations, extension agents, agrochemical and agribiotech companies and because it highlights growing nematode risks to worldwide agriculture and suggests future nematology research hot spots.

MANIPULATING LIPID METABOLISM IN PLANTS TO CONTROL PLANT PARASITIC NEMATODES. Anderson, Scott1 and C. Gleason1. 1Washington State University, Dept. of Plant Pathology, Pullman, WA 99164.

Plant parasitic nematodes (PPNs) cause upwards of $180 billion in crop loss worldwide annually. Of these agricultural pests, the root-knot nematodes (Meloidogyne spp.) are the most economically destructive. Unfortunately, many chemical nematicides are now banned due to health and environmental concerns. In addition, the relative dearth of resistant crop plants has left growers at a disadvantage when it comes to combatting these destructive animals. Our research explores an alternative form of PPN control based on manipulating plant lipid
metabolism to deliver toxic chemicals to PPNs. This research is based on data from Caenorhabditis elegans, a free-living bacteriophagous nematode. When C. elegans is fed a specific dietary fatty acid, dihomo-γ-linolenic acid (DGLA), the nematodes become sterile. The sterility is due to a form of programmed cell death called ferroptosis in developing germ line cells. A bioinformatics analysis of the genome of Meloidogyne incognita showed that the nematode contains genes homologous to C. elegans that are involved in the modulation of ferroptosis as well as de novo lipid biosynthesis and desaturation. Using gas chromatography/mass spectrometry (GC/MS) analysis of fatty acid methyl esters, we found the most abundant 20-carbon polysaturated fatty acid in C. elegans was also present in M. incognita. Based on this data, and the highly conserved nature of the ferroptosis pathway in animals, we hypothesize that root-knot nematodes would be susceptible to germ-line cell death when exposed to DGLA or its 18-carbon precursor γ-linolenic acid (GLA). Root-knot nematodes only feed on plants, but plants do not make GLA or DGLA. Therefore, our goal has been to generate plants that produce these fatty acids by introducing into them two genes, a desaturase gene from a picoalga and an elongase gene from moss. We have generated stable transformed Arabidopsis and tomato plants to express these genes, and GC/MS analysis of the roots of the transformed plants indicate that they can make GLA and DGLA. Initial infection assays on transgenic tomato and Arabidopsis producing these fatty acids indicate that they may affect nematode fecundity. Overall, our data on nematode fatty acids and ferroptosis will provide for a better understanding of the core lipid biosynthesis pathways in parasitic nematodes and provide a novel method for nematode control.

METAGENOMIC APPROACH TO DECIPHER HOST-MICROBE INTERACTION AMONG NATIVE ENTOMOPATHOGENIC NEMATODES. Baniya, Anil1, and P. DiGennaro1. 1University of Florida, Dept. of Entomology and Nematology, FL 32611.

Entomopathogenic nematodes (EPN) are used as biological control agents against different insects and help to reduce the harmful effect of chemical pesticides on the environment and human health. For some time, EPN and its symbiotic bacteria were considered to have a “monoxenic” association and the combination of these two partners was solely considered to kill the insects. However, recent finding suggests that the biology of EPN is more complex than previously considered. In this study, we investigated the genetic diversity and microbial associates of two native EPN of Florida: Steinernema diairepesi and S. khuongi that are dominant among different geographical regions: central ridge and flatwood region respectively. These two species are effective in controlling Citrus root weevil (Diaprepesi abbreviati), one of the devastating pests responsible for considerable yield loss in citrus and other ornamental crops in Florida and the southwestern parts of the United States. Our objectives were to observe the genetic diversity of these two nematodes, identify the symbiotic associates of S. khuongi, characterize other microbial associates of these two nematodes and reveal the functional attributes of the associated microbes in nematode health and pathogenesis. A whole genome metagenomic approach was used to simultaneously sequence and assemble the genome. The final genome of S. diairepesi contains 35,545 contigs with a total length of ∼118 Mb, contigs N50s of 11,474 bp, GC 45.01%, with the longest contigs of 1,706,490 bp. Similarly, the S. khuongi genome has 8,794 contigs with a total length of ∼82 Mb, the largest contig of 428,226 bp, and N50 of 46 kb. BUSCO scores indicate that nematode genomes are >85% and >86% complete, respectively, for S. diairepesi and S. khuongi. The symbiont of S. khuongi has a total length of ∼3.5 Mb, the largest contig of 116,532 bp, and N50 of 17,487 bp. Annotation of a bacterial genome and in silico genome-genome hybridization identified the symbiotic bacteria of S. khuongi as Xenorhabdus poinarii. Analysis of associated microorganisms indicated that these two EPN are associated with different genera of microbes namely: Stenotrophomonas spp., Acinetobacter spp, Delftia spp, Pseudomonas spp., Achromobacter spp., Caulobacter spp., Variovorax spp., Chryseobacterium spp., Sphingomonas spp., Sphondobacter spp., Alcaligenes spp., Pseudochrobactrum spp., etc. Function-based analysis of the associated microbes indicated that these bacterial populations harbor the genes that produce secondary metabolites similar to that of endosymbionts and also provide essential nutrients like biotin and riboflavin to the nematode. Our data indicated that the success of the EPN may be shaped by the microbial associates of the nematode as these microbes plays important role in nematode fitness and eventually improve the effectiveness of EPN as a sustainable biological control agent.

UNDERSTANDING THE CONDITION OF THE SOIL FOOD WEB USING THE INDICES OF NEMATODE COMMUNITIES IN MEDITERRANEAN FRUIT SYSTEMS. Bastidas, Brynelly2, E. Arellano1, A. Gaxiola4, E. Aballay4, and S. Sánchez-Moreno6. 1Facultad de Agronomía e Ingeniería Forestal, Pontificia Universidad Católica de Chile, Santiago, Chile, 2Center of Applied Ecology and Sustainability (CAPES), Santiago, Chile, 3Departamento de Ecología, Facultad de Ciencias Biológicas, PUC, 4Instituto de Ecología y Biodiversidad, 5Departamento de Sanidad Vegetal, Universidad de Chile, 6Departamento de Medio Ambiente y Agronomía, Centro Nacional Instituto de Investigación y Tecnología Agraria y Alimentaria (INIA, CSIC) Ctra. Coruña km. 7.5. Madrid 28040 (España).

Indices based on the functional guilds of the nematode community serve as descriptors of ecosystems functionality. These indices have been used to evaluate the structure and function of the soil food web under environmental disturbances, such as those caused by intensified agriculture systems (IAS) that extensively use agrochemicals, which has seriously affected soil biodiversity. However, there are still no clear patterns of the effects of IAS on the soil food web in some biomes, as in Mediterranean type climates in Central Chile. This region contains the largest fertilized fruit production in the country, most of it under intensive management to exporting markets. IAS in this area must be causing severe damage to the structure soil food web. Therefore, the objective of this study was to determine the condition of the soil food web in representative fruit systems, such as table grape and cherry, using nematode community indices (Maturity, Sigma, Plant Parasitic, Channel, Basal, Enrichment and Structure index). We also compared whether there were differences in the soil food web in the irrigation line (row) and the areas had cherry and grape crops, cultivated and non-cultivated areas were sampled to be used as reference. Additionally, the physicochemical properties of each soil were analyzed. We found that the maturity index was between 1.61 and 2.58, which shows the degree of alteration in the evaluated fruit systems. These results are possibly associated with the agricultural management intensity of each farmer and the differences in soil physicochemical parameters. On the other hand, the soil food web was more complex in the rows than in the non-cultivated areas, which could be linked to the effect of tillage and fertigation in this area. Despite this complexity, the enrichment index showed that decomposition was mediated by bacteriovorous nematodes, which indicates that the soil could have a higher percentage of labile organic matter, which triggers direct dependency to the functionality of the soil in fruit systems.
VERTICAL DISTRIBUTION OF NEMATODES AT A CONSTRUCTION SITE IN EAST TENNESSEE. Bernard, Ernest C.1, G. Phillips1, D. Sain1 and L. S. Taylor2. 1Entomology & Plant Pathology Department and 2Biosystems Engineering & Soil Science Department, University of Tennessee, Knoxville, TN 37996.

Free-living soil nematodes typically are most dense in the root zone and upper soil layers with higher proportions of organic matter but can occur at depths much greater than 2 m, especially in deep, uniformly sandy or silty soils. The demolition of Ellington Hall on the University of Tennessee campus provided a window of opportunity to sample soils that were not uniform but instead contained distinct horizons and differences in textural classes by depth. Three near-vertical soil faces at the demolition site were selected for sampling. Soil faces were cleaned of concrete dust and loose substrate to provide a pristine surface, and each of the faces was marked at 30-cm increments from the surface to the bottom of the excavation. The three faces were designated as North face (grass/clover surface,10 samples to 270-cm depth), West face (grass/clover surface, 4 samples to 90 cm) and SW face (magnolia root zone, 3 samples to 60 cm). Peripheral surface samples also were collected: grassy landscape within 2 m of the excavation (SE surface) and bare soil under conifers (South surface). From newly exposed soil under parts of the old building, samples were collected from under the old auditorium and from under the basement location of the elevator shafts. Surface samples were collected with a soil sampling tube and the others were removed with pickaxes. Nematodes were extracted by means of sugar flotation–centrifugation, counted and identified to genus. Soil texture was evaluated qualitatively. Shannon diversity indices, ΣMI, Enrichment Index and Structure Index were calculated for samples that contained at least five taxa. Nematode richness and density were highest in the five surface samples, with 15–21 taxa and 188–3,448 nematodes/100 cm³ soil. Surface-sample Shannon diversity indices ranged from 2.08 to 2.64 but were below 1.00 for all subsurface samples. Densities dropped precipitously at greater depths; only three subsurface samples had more than 10 nematodes. Surface ΣMI values ranged from 1.61 (North face) to 2.36 (SE sample). The Maturity Index for the North face surface was strongly influenced by a high proportion of Mesorhabditis sp. (one-third of sample abundance). The few North-face nematodes at depths below 30 cm were rhabditid J2 and J3, Acrroboloeules J2 and both adult and juvenile Prismatolaimus sp. One deteriorated rhabditid J2 was below the auditorium. Surface sample textures were silt loam (SW face silty clay). Subsurface samples typically were silty clay loams, but the 150 and 180-cm North-face samples were sandy loam. Downward nematode movement in the North face may have been severely restricted due to a thick layer of clay at the 30-cm depth. Building demolition sites, when fully excavated to reveal deep intact soil profiles, offer a unique opportunity to assess the depths at which many commonly-studied free-living nematodes live.

GENOME SEQUENCE OF THE ENTOMOPATHOGENIC NEMATODE HETERORHABDITIS INDICA. Bhat, Chaitra G.1, V. S. Somvanshi1, R. Budhwar1, R. Shukla3, A. R. Dillman1 and U. Rao1. 1Division of Nematology, ICAR-Indian Agricultural Research Institute, New Delhi, India, 110012, 2Bionivid Technology Private Limited, Bangalore, India, 560043, 3Department of Nematology, University of California, Riverside, CA 92521.

Entomopathogenic nematodes (EPNs) in the genera Heterorhabditis and Steinernema are used as biological control agents for insect pests worldwide. They are an excellent genetically tractable model to study biological phenomena such as mutualism and parasitism. Sixteen Heterorhabditis and one hundred Steinernema species have been described from various parts of the world. However, their full potential as bio-control agents and as a model system remains mostly unexplored. Omics information such as genomics data combined with other molecular techniques are a powerful tool to explore EPN biology and lays the groundwork for the improvement of their bio-control traits. Presently, whole-genome information is available for one heterorhabditid and five steinernematids. Here we present the draft genome of H. indica, the most prevalent EPN species in India and tropical countries. An inbred line of H. indica, strain H-V, was derived by inbreeding for 20 generations. Three high-quality genomic libraries with insert sizes 300 bp, 600 bp, and 5 Kb were prepared for Illumina paired-end sequencing with approximately 50x coverage to generate 5 GB data per library. The final H. indica genome assembly was 91.26 Mb, arranged in 3,538 scaffolds with an N50 of 587 Kb. The GC content of the assembled genome was 35.31%. The genome completeness assessment by Benchmarking Universal Single-Copy Orthologs (BUSCO) method showed that out of 303 conserved eukaryote genes, 266 (87.78%) were fully present, 4.95% were partially mapped and 7.26% were missing, indicating the high quality of the draft genome. A total of 10,974 protein-coding genes were predicted in the H. indica genome. Identification of orthologous groups of genes present in H. indica genome as compared to four other nematode genomes by OrthoMCL detected 2,917 orthologous groups. The Zinc finger C2H2 type domain, WD domain, G-beta repeat, ABC transporter, Immunoglobulin I-set domain, and Protein kinase domain were the five most abundant protein domains in H. indica. The raw sequence data has been deposited in GenBank under BioSample No. SAMN18671197, BioProject No. PRJNA720543 and SRA IDs SRR14181568, SRR14181569 and SRR14181570. Additional analyses of the genome assembly are underway. This resource will facilitate functional and comparative genomic studies in Heterorhabditis nematodes.

25 YEARS OF ANNOTATION. Bird, David McKenzie. Bioinformatics Research Center, North Carolina State University, Raleigh NC 27695.

The advent of whole genome sequencing (WGS) has permitted the prediction of many genes in plant parasitic nematodes. However, as is the case for most organisms, ascribing specific function remains elusive for up to half of the deduced genes. Very few genes act independently to execute any given biological function. Rather, genes encode sets of proteins that function in concert to produce “physiology.” Understanding how nematode physiology gives rise to parasitism is a current challenge emerging from the WGS projects. Using root-knot nematode (Meloidogyne spp.) as a platform, I will discuss an approach based on deducing physiology, in contrast to the “candidate gene” approach.

THERMAL STABILITY, SOIL HEALTH, POTATO TUBER YIELD AND NEMATODES. Bird, George1, B. Basso1, R. Price1 and M. Otto2. 1Michigan State University, 2Agri-Business Consultants Inc.

Two Michigan commercial fields were evaluated in 2017, 2018 and 2019 for thermal stability, soil health indicators, potato tuber yields and at-harvest population densities of selected nematodes. Thermo stability is a concept developed by the Basso Laboratory. The thermal
stability process captures spatial and temporal variation of plant canopy temperatures throughout a growing season or over multiple years as measured by thermal sensors mounted on drones, fixed-wing aircraft or satellites. An area within a potato field identified as hot and stable describes a site where plant canopy temperatures are higher than sites described as cold and stable. Hot indicates higher temperatures, while stable indicates the constant response of high temperature through time compared to cold and stable. In areas depicted as unstable, some plants have high temperatures, whereas others are significantly cooler than the mean temperature of the field. Results from the thermal stability process correlate with crop yield stability (Maestrini and Basso, 2019). Hot and stable areas are indications of plants signaling inadequate soil water availability or poor shoot system development caused by abiotic or biotic factors such as root-lesion nematodes or soil-borne fungi. The process generates maps that capture within-field spatial variability of temperature. For this project, geopositioned reference sites with specific thermal properties were selected for hand-dug potato tuber yields and soil samples for soil health indicator and nematode analyses. The soil health analyses were conducted by the Cornell University Soil Health Laboratory using four physical, four chemical and four indicators. Both soil and root tissue were analyzed for at-harvest nematode occurrence and population densities. In general, marketable potato tuber yields were higher in cold and stable sites compared to lower yields associated with hot and stable sites. At-harvest population densities of *Pratylenchus penetrans* were higher in the cold and stable sites, compared to hot and stable areas. In one field in 2017, very high population densities of a Dorylaimoid species occurred in hot and stable areas compared to the cold and stable locations in the same field. In addition to having utility as a new soil health indicator, thermal stability analysis appears to have potential for use in designing nematode sampling protocols.

THE SCN COALITION: A PUBLIC PRIVATE PARTNERSHIP. Bird, George1, S. Markell2, K. Bissonnette2, C. Bradley3, J. Johnston4, M. G. Mitchum4, A. Tenuta5, G. Tyll6 and M. Wenck7. 1Michigan State University, 2North Dakota State University, 3University of Missouri, 4University of Kentucky, 5MorganMyers, 6University of Georgia, 7Ontario Ministry of Agriculture, Food and Rural Affairs and 8Iowa State University.

*Heterodera glycines* (soybean cyst nematode) is a highly significant pest of soybeans in the U.S., Canada and other soybean-producing areas of the world. The soybean cyst nematode (SCN) is currently managed by growing nonhost crops and resistant cultivars and using soybean nematicide seed treatments. The vast majority of the SCN-resistant cultivars used in the U.S. and Canada in the last thirty years, however, were developed from a single source of resistance named PI 88788. Continual and prolonged use of these resistant cultivars has resulted in development of aggressive populations of SCN that reproduce well on these cultivars and cause yield losses. The SCN Coalition, which includes university scientists from twenty-eight states, the Ontario Ministry of Agriculture, Food and Rural Affairs and eight corporations, was launched in 2018 to combat this problem. This Public Private Partnership (PPP) uses a multimedia approach to promote active SCN resistance management in an effort to change soybean grower practices to reduce yield loss and slow the development of nematode populations that are aggressive on PI 88788. A unique aspect of the coalition is its engagement of a professional communications and marketing firm, MorganMyers, to craft the SCN active management messages and implement a communications strategy. The marketing consists of a modern/dynamic multi-media approach and robust assessment of impacts. From 2018-2020, the coalition was mentioned in 429 online articles resulting in 21.4 million impressions in the agricultural media. In late 2020, a six-week *Let's Talk Todes* media campaign promoting six new SCN active management videos generated more than 913,070 video views and 1.2 million impressions in the targeted agricultural media. Results of national market research conducted in 2015 and 2020, demonstrated The SCN Coalition has been associated with statistically significant (95% confidence level) increases in utilization of active management of SCN among growers, conservatively saving them millions of dollars. This PPP provides a novel roadmap for future marketing of the science of nematology in an era of dynamic multimedia technologies.

MONOCLONAL ANTIBODIES FOR THE IDENTIFICATION OF PLANT-PATHOGENIC NEMATODES. Bogale, Mesfin1, E. Sampson4, W. Hu1, A. Baniya1, S. Mishra1, A. Doty1, Y. Zhang2, D. A. Moraga Amador2, O. Guryanova2, M. Mathieu2, D. Shabashvili3, M. Miranda2, L. Xoi2, and P. DiGennaro1. 1University of Florida, Dept. of Entomology and Nematology, Gainesville, FL 32611. 2Interdisciplinary Center for Biotechnology Research, University of Florida, Gainesville, FL 32610.

Identifying soybean cyst nematode (SCN; *Heterodera glycines*) and root-knot nematode (RKN; *Meloidogyne* spp.) in the field is paramount to inform crop rotations and resistance breeding programs but currently relies on time-consuming plant resistance screening. SCN and hyper-virulent RKN continually erode crop resistance which has led to a substantial decrease in yield. Due to the complex nature of nematode genomes, identification of genetic markers linked to differences in virulence remain largely elusive. Placement of these pathogens into subspecies groups that inform host range, (HG types for SCN and races for RKN), requires pathogenicity tests, which are cumbersome and not always conclusive. To our knowledge, there are no current molecular tools that may be used to circumvent these limitations. Here we describe a novel, high-throughput approach involving the comparative transcriptomics of individual memory B cells from nematode-immunized mice to identify unique monoclonal antibodies (mAb) that differentiate RKN races and SCN HG types. This robust method produces a maximum of 10,000 viable mAb sequences per nematode immunized mouse. Downstream production of mAb antigen binding sites from sequences is accomplished by cell-free in vitro protein synthesis and validation by ELISA. The high-throughput capture of nematode-antigen reactive mAb sequences also has implications in defining race/HG type specific biology.

NUANCE OR NUMBERS: TAXONOMIC BIAS IN APPROACHES TO MEASURE NEMATODE BIODIVERSITY. Borgmeier, Abigail1, K. Gattoni1, T. Harris5, P. Mullin1, D. Porazinska1, K. Powers1, D. Wedin1, and T. Powers1. 1Department of Plant Pathology, 406 Plant Science, University of Nebraska-Lincoln, Lincoln NE, 68583, 2Department of Entomology and Nematology, University of Florida, FL 32611.

The North American tallgrass prairie has been considered one of the most diverse grasslands, however over 95% has been converted to agriculture in the past 150 years. The remaining prairie supports a wide variety of plants, insects, mammals, and soil-dwelling microorganisms, creating an incredibly complex ecosystem. The earliest attempt to measure nematode diversity in prairie soils was by Orr and Dickerson (1966) in which 228 species in 80 genera were recorded from 61 soil samples from Kansas. Today, their morphological
approach would be considered daunting and untenable given the time and taxonomic expertise required for analysis. The advent of next generation sequencing has introduced metabarcoding, where DNA sequences from an extracted nematode community can be analyzed simultaneously, resulting in measurements of taxonomic diversity that are generated via a computational pipeline linked to a reference database. The aim of our study was to compare three approaches for the analysis of nematode diversity within a 10-mile long habitat corridor of protected prairie remnants near Lincoln, Nebraska. The methods are 1) a traditional morphological analysis of 150 nematodes per study site, 2) a metabarcoding analysis of the nematode community from 100 cc of soil collected at each site using the 18S-V9 genetic marker, and 3) a Sanger Sequencing DNA barcode analysis of selected nematodes from each site using COI and 18S genetic markers. Fifteen 40x40 m² plots, each in the middle of a one-hectare site, were sampled during the summer of 2019. Each site has been variously managed; either burned, hayed, grazed, but none have been plowed or used for agriculture. A vegetation survey and soil analysis were conducted for each site. The three approaches produced different estimates of nematode diversity. Nematode genus richness based on morphology produced a range of 19 to 38 genera per site, and 80 total genera across all 15 sites. The metabarcoding analysis resulted in 171 unique Molecular Operational Taxonomic Units (MOTUs). However, only 45 genera of the 80 genera identified via morphology were specifically represented in the taxonomic assignments of the metabarcoding MOTUs. The identification of MOTUs was limited by the existing taxonomic resolution and content of the reference database. The DNA barcode approach using the COI genetic marker revealed greater taxonomic resolution and more diversity within certain genera. Only 34 genera of the 80 genera identified via morphology were represented by COI, as non-amplification events with some taxa reduced overall assessment of taxonomic diversity. By combining COI and 18S analyses from the same individual, we were able to build species-level phylogenetic trees and link morphological characters to the DNA sequences. This combination of analyses when added to the reference database will improve the discriminatory power of the metabarcoding approach and accelerate studies of nematode diversity.

RATES OF MOLECULAR EVOLUTION IN ANTARCTIC AND TEMPERATE NEMATODES. Brim, Jinna and Byron Adams. Department of Biology, Brigham Young University, Salt Lake City, Utah.

Relative to nematodes from temperate climates, Antarctic nematodes have very short windows of time for growth and reproduction each year. This allows little opportunity for mutations to accumulate in the population. Thus, we expect the rates of molecular evolution to be slower than related sister taxa, since nematodes in warmer regions complete more generations in the same period of time. We used time calibrated molecular clocks generated from previous studies on phylogenetic divergence times in Panagrolaimidae to estimate rates of evolution of Antarctic nematodes more accurately and estimate dates of divergence. We also explored patterns of ice sheet advancement and retreat to test hypotheses of species divergence in response to glacial dynamics. We discuss our results in the context of mechanisms by which the Antarctic nematodes generate and maintain genetic variation and the implications of these mechanisms on their ability to respond to climate-driven changes.

STRATEGIES TO ENHANCE THE EFFICACY OF ENTOMOPATHOGENIC NEMATODES FOR THE MANAGEMENT OF DIAMONDBACK MOTH AND IMPORTED CABBAGEWORM. Budhathoki, Sabina, and K.-H. Wang. Department of Plant and Environmental Protection Sciences, University of Hawaii, Honolulu, HI 96822.

The success of foliar application of entomopathogenic nematodes (EPNs) to manage diamondback moth (DBM) and imported cabbageworm (ICW) in the field had not been promising due to its susceptibility to environmental stress. Greenhouse trials were conducted to test the efficacy of adjuvants in protecting Steinernema feltiae. Adjuvants 1) Oroboost®, 2) Kinetic® and 3) Exit® mixed at 390.6 ml/L, and 4) no adjuvant in 9-cm diameter plates containing 500 IJs freshly harvested infective juveniles (IJ) were exposed to 49°C in the greenhouse for 0, 30, 60, 120 and 180 min. Oroboost® enhanced the survival rates of S. feltiae for 2 hours compared to no adjuvants, whereas Kinetic® and Exit® showed a sign of EPN toxicity with lower survival rates than the control. In another greenhouse trial where 10 DBM 4th instar were introduced on cabbage seedlings in pots, Oroboost® outperformed the other adjuvants in reducing DBM number survived 2 days after EPN application. A laboratory and a greenhouse experiment were conducted to test the dosages of S. feltiae at 0, 0.625, 1.25, and 2.5 IJ/cm² mixed with Oroboost®. Both experiments showed that 0.625 IJ/cm² was as effective as the commercial (1.25 IJ/cm²) and higher dosage (2.5 IJ/cm²) in killing and infecting DBM larvae. Two field trials were conducted by integrating trap cropping (kai choi) with EPN sprays (1.25 IJ/cm² of S. feltiae + Oroboost®) to manage DBM as well as ICW, one trial was on head cabbage and the second trial was on kale. Both experiments were arranged in 2 × 2 (trap crop × EPN) factorial design with 4 replicated plots. It was hypothesized that trap crop would lure DBM away from cash crops and reduce the pest pressure for EPN to be effective. DBM numbers on the plants were monitored weekly over 6 weeks. Planting trap crop suppressed the abundance of ICW (73%), DBM (47%), and their damage on head cabbage (P ≤ 0.05). On the other hand, EPN suppressed the abundance of ICW larvae by 43.4% compared to no EPN but had no effect on DBM. In kale experiment, trap cropping did not affect DBM abundance and damage but did reduce ICW damage by 12.6%. However, EPN significantly suppressed DBM numbers on kale by 87.5% (P ≤ 0.05) probably due to low numbers of DBM in the kale (<0.2 DBM/ plant) than in the cabbage (>0.3 DBM/plant). No interaction between trap crop and EPN was observed indicating that trap cropping could not improve efficacy of EPN against DBM and ICW. This study concluded that while Oroboost® at 390 ml/L could extend persistency of EPN against DBM and ICW. This study concluded that while Oroboost® at 390 ml/L could extend persistency
management information. A nematode survey was conducted on seven Asian vegetable farms in Wimauma, FL. Thai basil, luffa, sweet potato, bitter gourd, water spinach, Malabar spinach, galangal, ginger, and Indian tare were the most grown vegetables. None of the growers in our survey had knowledge of plant-parasitic nematodes, nor were familiar with nematicides or other nematode management options. Root-knot nematode (RKN, *Meloidogyne* sp.) were very common and found on all farms. Other nematodes found were sting, stubby root, lesion and spiral nematodes. Species-specific primers and restriction fragment length polymorphism methods were applied to identify RKN species. *M. enterolobii* was found in five out of seven farms, and *M. incognita*, *M. arenaria* and *M. haplanaria* were found more sporadically. Our survey indicated that *M. enterolobii* was widely distributed in surveyed farms. The prevalence of *M. enterolobii*, is especially of concern, as this species is an emerging threat for vegetable production in the southeastern U.S, with limited management options available. To educate Asian vegetable growers about nematodes and *M. enterolobii*, on-farm nematode management trials are ongoing and nematode fact sheets in Vietnamese have been distributed among growers.

**CONTROL OF GLOBODERA PALLIDA USING TRAP CROP, SOLANUM SISYMBRIIFOLIUM COMBINED WITH SINAPIS ALBA SEED MEAL EXTRACT OR 4-HYDROXYBENZYL ALCOHOL.** Chhetri, Prativa¹, L. M. Dandurand, and I. Popova.¹ ¹Department of Entomology, Plant Pathology and Nematology, University of Idaho, Moscow, ID 83844-2329, ¹Department of Soil and Water Systems, University of Idaho, Moscow, ID 83844-2340.

The pale cyst nematode, *Globodera pallida*, is a highly specialized, economically important pest for potato production. The control of this endo-parasitic nematode is challenging because of its ability to remain dormant in the soil for up to 20 years in the absence of its host. The specificity of *G. pallida* hatching makes this life stage a potential target for designing efficient integrated control strategies. We have previously demonstrated that *Sinapis alba* seed meal extract (SME) which contains 4-hydroxybenzyl alcohol (HBA), enhances *G. pallida* egg hatch when combined with the hatching stimulus found in potato root diffusate. The increase in the hatch in the presence of potato root diffusate is speculated to be due to an increase in egg permeability. Similar to potato, the trap crop, *Solanum sisymbriifolium*, is known to promote *G. pallida* hatch, however, subsequent reproduction in infected plants is arrested. This study aims to determine the efficacy of *S. sisymbriifolium* to control *G. pallida* when combined with the hatch enhancement properties of HBA or *Sinapis alba* seed meal extract. The impact of 0 and 4.48 t/ha SME or HBA (equivalent to 464 μmol/g sinabin) combined with 4-week-old *S. sisymbriifolium* on egg density, hatch, and viability were determined under greenhouse condition. *Solanum sisymbriifolium* alone reduced the number of encysted eggs compared to non-treated control by up to 67% indicating that this trap crop induced hatch of *G. pallida*. When combined with HBA or SME, *S. sisymbriifolium* further significantly reduced egg density, along with viability compared to the trap crop only. Fewer encysted eggs found with the combination suggest that more egg hatch was stimulated in the presence of trap crop after the treatment with HBA or SME. Moreover, further experiment to assess the impact of the combination on *G. pallida* reproduction, determined by bioassay with susceptible potato cultivar, is underway.

**CAN NEMATODES AID IN SPOTTED WING DROSOPHILA CONTROL (DROSOPHILA SUZUKII)?** Cole, Emilie¹, J. Perkins¹, R. Isaacs¹, and M. Quintanilla.¹ Michigan State University, Dept. of Entomology, East Lansing, MI 48823.

The invasive pest, spotted wing Drosophila (*Drosophila suzuki* [SWD]), causes significant yield damage to small fruit cropping systems including blueberries and raspberries. SWD are unique in that they are equipped with a serrated ovipositor that allows them to infest unripened berries, thus rendering fruit unmarketable. This, in combination with their rapid life cycle, makes management difficult, causing many growers to abandon traditional IPM practices and to turn to calendar spray programs. To reduce the need for frequent pesticide spray regimes, we completed a study investigating the potential for entomopathogenic nematodes (EPNs) to control SWD. The objectives of this study were to 1) evaluate three EPN species (*Heterorhabditis bacteriophora, Steinernema carpocapsae*, and *Steinernema feltiae*) in their ability to reduce SWD survivorship when applied during 3rd instar, pupal and infested fruit life stages under laboratory conditions and 2) determine EPN efficacy in reducing SWD populations under field conditions in blueberries. Laboratory assays were completed by creating arenas in 30 mL deli cups filled with 10g of sand. For each EPN species, 10 arenas were created that included either 5, 3rd instar SWD larvae, 5 SWD pupae, or 1-2 SWD infested berries with an average of 10 eggs per arena. Within each arena, approximately 250 individuals of the appropriate EPN species were inoculated. Distilled water served as a control. After 15 days, the number of emerged adults was counted. Laboratory assays indicated that when exposed to 3rd instar larvae, *H. bacteriophora*, best reduced adult emergence resulting in 64% survivorship compared to 90% in the control. Alternatively, *S. feltiae*, significantly reduced adult emergence when applied to the pupal stages, resulting in 10% survivorship compared to 44% in the control. Adult survivorship in infested berry arenas was most reduced with *S. feltiae* with 21% survivorship compared to 40% in the control. Based on these results, *S. feltiae* and *H. bacteriophora* were selected for further testing against an untreated control in the field. Plots consisted of 7 ’Bluecrop’ bushes and were organized in a CRBD. EPNs were applied every two weeks starting in July at labeled rates. Over the course of the fruiting season SWD populations were monitored via traps and salt testing of collected fruits. The trial is still ongoing and final results are forthcoming. Though EPNs may not be able to provide 100% control of SWD populations, they may be a valuable addition to the IPM toolbox, however another season of field work is needed to determine the impact of EPNs on SWD population dynamics.

**WINTER WHEAT BREEDING FOR RESISTANCE TO THE ROOT LESION NEMATODE, PRATYLENCHUS NEGLECTUS.** Consoli, Erika¹ and A. Dyer.¹ ¹Montana State University, Department of Plant Sciences and Plant Pathology, Bozeman, MT 59717.

The root lesion nematodes, *Pratylenchus neglectus* and *P. thornei* present a challenge to dryland wheat production worldwide. Montana, a leading US wheat producing state, has ideal climatic conditions for these nematodes. A statewide survey conducted in 2006 and 2007 detected damaging populations of *P. neglectus* in poorly performing winter wheat fields. Among these fields, average *P. neglectus* densities were 3390 nematodes/kg soil and 4045 nematodes/kg for 2006 and 2007, respectively. *P. thornei* was not detected. Statewide, winter wheat yield losses due to root lesion nematode infestations were estimated at 12% to 15%, representing an estimated US$60 million to US$70 million in economic losses annually. Subsequent rotational studies revealed that peas, lentil, and barley significantly reduced nematode populations
when used in rotation with winter wheat (P-value <.001). Nearly ten years after the initial survey and the deployment of resistant crop rotations, a 2-year reassessment of root lesion nematode populations revealed *P. neglectus* densities of 268 nematodes/kg soil and 377 nematodes/kg soil (2015 and 2016, respectively). Despite the overall decrease of nematode densities, intransigent *P. neglectus* populations were found in nine fields. Populations tested from eight of these fields revealed four populations of *P. neglectus* that were able to multiply on barley and two that were able to multiply on lentil, and one of these populations was able to simultaneously multiply in both barley and lentils. Rare male specimens of *P. neglectus* were also observed. The detection of these virulent populations has only heightened the need for resistant wheat cultivars, a core priority of our research program. To address this priority and introgress *P. neglectus* resistance into Montana adapted winter wheat lines, the land race Persia-20 with reported resistance to both *P. neglectus* and *P. thornei* was backcrossed into winter wheat cultivar Yellowstone. From the >600 resulting progeny lines, seven BC,F, winter wheat lines were identified with good agronomic performance and good partial resistance to *P. neglectus*. Unfortunately, these lines were too tall for large-scale production systems. Therefore, two of these lines (RLN I 145 and RLN I 184) were forward crossed with solid stem cultivar Warhorse to produce shorter RLN resistant lines. F1 seed produced from these crosses were then used to produce double haploid lines (DHLs). Initially, 58 lines were screened in greenhouse assays for resistance to root lesion nematodes. Ten lines displayed significant resistance to root lesion nematodes (PF<1). An additional 49 double haploid lines are currently being evaluated for resistance with the hope of identifying additional resistant lines. This fall the nematode resistant lines will begin their agronomic evaluation in nematode-infested fields across the state. In addition to the development of resistance cultivars, the nematode resistant lines along with susceptible lines will be used to examine their overall impact on plant root health and sustainable pest management.

**EFFECTS OF PESTICIDE AND ROOT HEALTH PROGRAMS ON A GOLF PUTTING GREEN INFESTED BY MULTIPLE PLANT-PARASITIC NEMATODES.** Crow, William T1, R. Snyder1 and J. Frank1, 1Entomology and Nematology Department, University of Florida, Gainesville FL USA, 2Harrell’s, Lakeland FL, USA.

The three most damaging nematodes to golf course turf in Florida USA are the sting nematode (*Belonolaimus longicaudatus*), grass root-knot nematode (*Meloidogyne graminis*), and lance nematode (*Hoplolaimus galeatus*). Due to the warm climate and sandy soil in Florida, nematodes, fungi, and insects are all common problems on golf greens and if left unchecked can cause severe decline and even death of the turf. To combat these pests, nematicides, fungicides and insecticides are commonly applied. To help promote root growth, reliance on programs including multiple root health products is a common practice on Florida golf courses. The objective of this trial was to evaluate the impacts of a pesticide program and a root health program individually, and in combination, on turf health in a nematode-infested putting green. The test site was a bermudagrass putting green naturally infested with sting, grass root-knot, and lance nematodes. Treatments were: i) untreated control, ii) pesticide program including turfgrass nematicides, fungicide, and insecticide, iii) root health program including a combination of humic acid, fulvic acid and seaweed extract, and iv) a combination program including both pesticide and root health programs. The 2-year experiment used a randomized block design with 5 replication of each treatment. Effects on population density of each kind of nematode, on visual turf health, percentage green cover, and on root length were quantified throughout the trial. Treatment impacts were greatest on sting and lance nematodes; the pesticide program alone and in combination virtually eliminated sting nematode, but numbers of lance nematode increased over the course of the experiment with those same treatments. Turf quality, percentage green cover, and root lengths were generally higher in the pesticide and combination treatments than the untreated and root health treatments throughout the experiment, although cumulative root length was greatest in the combination treatment. These results indicate that i) turfgrass nematicides are more effective on some kinds of plant-parasitic nematodes than others, ii) for turf under nematode pressure the benefits from root health programs is likely minimal, and iii) when turf pests, including nematodes, are effectively managed root health products may enhance root growth.

**REKLELEM™ ACTIVE AS A NEMATICIDE FOR WARM-SEASON TURFGRASSES.** Crow, William T1, T. C. Thoden2, A. Agi1, and A. Habteweld1. 1University of Florida, Gainesville, FL 32611, 2Corteva Agriscience, Germany.

Plant-parasitic nematodes are major pests of warm-season golf course and athletic turf in the southeastern United States. In Florida, sting (*Belonolaimus longicaudatus*), grass root-knot (*Meloidogyne graminis*), and lance (*Hoplolaimus galeatus*) nematodes are the species that cause the most damage, and often occur concomitantly with each other and with other plant-parasitic nematodes. Because current nematicide options are more efficacious on some nematodes than others, and none work well against all three of these species, there is great need for additional effective turfgrass nematicides. Reklemel active (fluazindolizine) is a novel nematicide in a separate chemical class (sulfonamide) than the other turfgrass nematicides currently in use. The Landscape Nematology Lab at University of Florida has been conducting turfgrass field trials with Reklemel targeting sting, grass root-knot, and lance nematode management for several years. These trials evaluated treatment effects on turf and root health, and on nematode population densities compared to untreated control and standard nematicide treatments. In a separate trial we compared treatment effects of Reklemel and fluopyram on non-target nematodes in the field. Our results indicate that multiple applications of Reklemel at rates of ≥2.27 kg a.i./ha consistently improved turf health. These rates also reduced population densities of the target nematodes, but not as consistently as results on turf health benefits. Impacts on non-target nematodes were much greater from fluopyram than from Reklemel, particularly on bacteriovores and omnivores. Reklemel had no effect (P > 0.01) on bacteriovores and omnivores, whereas fluopyram reduced population densities of bacteriovores and omnivores by 66% and 96%, respectively. Our results indicate that Reklemel is an effective treatment for the three nematode species of primary concern to turfgrass in the southeastern United States, has minimal impact on non-target nematodes, and is an excellent complement to existing nematode management programs.

**DEVELOPMENT OF A RAPID SCREENING METHOD FOR GUAVA ROOT-KNOT NEMATODE IN SWEETPOTATO.** Culbreath, Julianna1, W. Rutter3, P. Wadl2 and C. Khanal1. 1Department of Plant and Environment Science, Clemson University, Clemson, SC 29634, 2USDA, ARS, Charleston, SC 29414.
Meloidogyne enterolobii is an aggressive root-knot nematode species that has emerged as a significant pathogen of sweetpotato (*Ipomoea batatas*) in the southeastern U.S. This nematode can be spread through the movement of infected 'seed' sweetpotatoes used for propagation, which has prompted regulatory agencies to impose quarantines on regions infected with *M. enterolobii*. Detecting storage roots infected with *M. enterolobii* is a challenging task that requires a trained eye, as it is relatively easy to overlook this nematode unless an intensive and informed effort is made on behalf of regulators. Here, a sweetpotato storage root survey method has been developed, tested, and implemented to detect and identify *M. enterolobii* and assist in monitoring the spread of infected storage roots. The sweetpotato skins are removed using an industrial vegetable peeler, and 10 ml samples are collected and processed for DNA analysis to detect the presence of *M. enterolobii*. As a post hoc test, *M. enterolobii* eggs are extracted from the extra skins, to be used for inoculation of susceptible and RKN resistant solanaceous crops. The sensitivity of the survey method is confirmed by adding varying amounts of *M. enterolobii* eggs into collected 10 ml skinning samples and performing DNA analyses. *M. enterolobii* was successfully detected and recovered in all the symptomatic fresh market storage roots and nematode inoculated controls. Using a *M. enterolobii* specific primer set, as little as 2 eggs/10 ml were able to be detected in the sensitivity check. Further experiments need to be conducted, but this sweetpotato storage survey method presents a promising and novel approach at screening, monitoring and ultimately managing *M. enterolobii* for the multimillion-dollar sweetpotato production industry in the U.S. and abroad.

DEVELOPMENT OF RESISTANCE TO POTATO CYST NEMATODES. **Dandurand, Louise-Marie**, 1 J.C. Kuhl, 1 and A. Caplan, 1 F. Xiao, 1 R. Novy, 2 J. Whitworth, 1 I. Zasada, 1 W. De Dong, 1 and X. Wang. 1 University of Idaho, Moscow ID 83844, 2USDA-ARS, Aberdeen, ID, 3USDA-ARS, Corvallis, OR 97330, 4Cornell University, Ithaca, NY 14853, and 5USDA-ARS, Ithaca, NY 14853.

Potato cyst nematodes, *Globodera pallida* and *G. rostochiensis*, are internationally recognized plant quarantine pests of potato because of their ease of dispersal as cysts in contaminated soil through international trade, ability to survive for 30 years or more in the absence of a host crop, and economic impact. Invasive worldwide, discovery of an infestation has severe trade implications and may lead to sanctions on potato and other soil bearing commodities. The unexpected appearance of the pale cyst nematode, *G. pallida*, in Idaho in 2006, the emergence of a new pathotype (Ro2) of *G. rostochiensis* in New York, and the continued presence of *G. rostochiensis* in New York, are evidence of the threat that this group of nematodes poses to the multi-billion-dollar U.S. potato industry. The enforcement of quarantine regulations in the U.S. has greatly contributed to restricting *G. pallida* infested fields to a small area in Idaho of 1,267 ha and *G. rostochiensis* in New York to 2,305 ha. Host resistance is an efficient way to control invasive nematodes such as PCN, prevent economic losses, and reduce nematode populations. Resistance to PCN has been characterized from close relatives of potato including *S. tuberosum* ssp. andigena, *S. spagazzinii*, and *S. vernei*. The dominant gene, *H1*, provides high levels of resistance to *G. rostochiensis* pathotypes Ro1 and Ro4, but not Ro2. Since no single gene such as *H1* confers resistance to *G. pallida*, developing resistance to *G. pallida* has proven to be more challenging. Efforts to breed for resistance to *G. rostochiensis* Ro2 and *G. pallida* are ongoing, and include development of marker assisted selection, integrating PCN resistance genes, in particular *GpaIV* and *Gpa5* into suitable market types, pyramiding resistance genes from multiple sources, and screening for resistance in wild potato species. We have also demonstrated that the trap crop *Solanum sisymbriifolium* significantly reduces *G. pallida* populations to below damage or detection thresholds. To understand the plant defenses of this trap crop, we have developed genomic resources to use for transfer into potato, which has led to identification of candidate resistance genes. Our team has identified defense-signaling pathways and putative resistance (R) genes from *S. sisymbriifolium* which may be associated with decreased PCN infection. A wide range of these genes include genes encoding protease inhibitors, peroxidases, receptor kinases, and several genes encoding nucleotide-binding, leucine-rich repeat (NLR) receptors. Our progress in developing resistance, and the role of genes and pathways from *S. sisymbriifolium* that may contribute to host defense will be discussed.

DIFFERENCES IN ROOT PENETRATION AND FEEDING BY PRATYLENCHUS PENETRANS, P. NEGLECTUS, AND P. CRENATUS ON CARROT. **Darling, Elisabeth**, 1 S. Thapa, 1 H. Chung 1 and M. Quintanilla. 1 Michigan State University, Department of Entomology, East Lansing, MI 48824.

Severe infestations by root lesion nematodes (*Pratylenchus* spp.) in young carrot seedlings can hinder production by causing early seasonal damage (field patchiness, seedling death) or late seasonal damage (root forking, stunting). This damage is primarily associated with the species *Pratylenchus penetrans*. However, recent findings within our team’s field trials, together with existing literature, has documented that two other species, *P. neglectus* and *P. crenatus*, are also present in carrot systems in the northern states of the U.S. Our preliminary findings suggest *P. crenatus* do not cause forked carrots but do significantly reduce carrot seedling survivorship by 59.1% (*P* < 0.05). It is currently unknown if these species pose the same damage and threat to the industry that *P. penetrans* does. To investigate this, we conducted observational trials and a greenhouse trial to document potential differences in biological and pathogenic factors between the three species. First, we conducted an observational trial to document potential penetration and feeding habits of *P. penetrans*, *P. neglectus*, and *P. crenatus*, to carrot taproots. This was repeated twice to ensure observational habits were consistent. Second, a greenhouse trial was established to document reproductive rates and corresponding damage by the three species. If there are differences in aggressiveness between species, new action triggers should be established, and plant diagnostic laboratories should prioritize utilizing molecular species identification tools to give species-specific recommendations and avoid over- or under- use of nematicides.

CHLOROPICRIN FUMIGATION ON THE FIRST CROP INCREASES ROOT-KNOT NEMATODE DAMAGE ON CUCURBIT DOUBLE CROPS. **Desaeger J. and Hung X. Bui.** Department of Entomology and Nematology, University of Florida Gulf Coast Research and Education Center (GCREC), Wimauma, FL 33598, United States.

Most vegetable production in Florida and the southeastern US occurs in open field and on plastic-mulch raised beds in combination with drip irrigation. Cucurbits are often planted as double crops in these systems following tomatoes, peppers or strawberries. While new beds are almost always fumigated, this is not the case for double crops who often do not receive any nematicide treatment. Root-knot nematodes (*Meloidogyne spp.*) are one of the major soilborne constraints in plasticulture and cause significant yield loss. This is
especially true for double-cropped vegetables due to the increased nematode population accumulated from the first crop. The following study evaluated the effect of fumigant and non-fumigant nematicide treatments applied on the first crop, on nematode infection and yield of the second crop. Nine field trials were conducted at the GCREC between 2017 and 2020. Fumigants were chloropicrin (Pic100), and chloropicrin + 1,3-D (PicClor60), and non-fumigant nematicides were oxamyl (Vydate), fluensulfone (Nimitz), flupyrad锌 (Velum), fluazaindolizine (Salibro), Burkholderia rinojensis toxins (Majestene), Purpureocillium lilic anus (Melcon) or combinations thereof. First crops were tomato or cucumber, and double crops were cucumber, squash, zucchini, and watermelon. Fumigation with chloropicrin on the first crop increased root-knot damage on the cucumber double crop in all trials except one, while chloropicrin+1,3-D resulted in root-knot damage less than chloropicrin but more than non-fumigated plots. Cucumber yield was greater in non-fumigated beds in four of the trials, and in chloropicrin-treated beds in two of the trials. Non-fumigant nematicides applied on the first crop had no significant impact on nematode infection and yield of the double crop, except for Nimitz which reduced root-knot damage on the second crop in half of the trials. With the disappearance of methyl bromide, chloropicrin has become the leading fumigant in Florida. Our results indicate that while chloropicrin may reduce nematode damage on the first crop, it may lead to increased root-knot nematode pressure on subsequent crops. More research is needed to understand the processes behind this, but it is possibly related to the broad-spectrum fungicidal activity of chloropicrin.

BASAL PLANT BIOLOGY AND ITS ROLES IN HOST RESPONSES TO ROOT-KNOT NEMATODE. DiGennaro, Peter1, S. Mishra1 and W. Hu2. 1Department of Entomology and Nematology, University of Florida, Gainesville, FL 32611.

Manifestation of plant disease requires the interactions between a host, a pathogen, and a suitable environment. Disruption in the quality or composition of any one of these constituents results in an incompatible interaction. With a cosmopolitan pest, such as Root-Knot Nematode (RKN; Meloidogyne spp.), basal host biology and environment arguably play larger roles in defining the success and severity of disease than pathogens with limited host ranges. The complexity of this interacting triad is compounded by recognizing the myriad of potential factors represented within basal plant biology such as genotype and circadian rhythms, and those clustered within suitable environments such as associated microbes and temperature fluctuations. Here I present an overview of multiple high-throughput ‘omics’ approaches and datasets that attempt to define RKN resistance and acknowledge the complexity of these interactions by underscoring the importance of biotic and abiotic factors influencing disease success. The goal of this work is to better characterize plant responses by identifying pathways that play specific, significant, and yet universal roles, in responses to RKN parasitism. Development of novel resistance- or tolerance-based management strategies across a broad range of host may be defined within the fundamental roles of basal plant biology and environment in the RKN interaction.

ARTHROPOD COMMUNITY RESPONSES REVEAL POTENTIAL PREDATORS AND PREY OF ENTOMOPATHOGENIC NEMATODES IN A CITRUS ORCHARD. Dritsoulas, Alexandros1,2, S-Y. Wu1, and L. W. Duncan1. 1Citrus Research and Education Center, UF-IFAS, Lake Alfred FL 33850, 2Agricultural University of Athens, Athens, Greece, 3College of Plant Protection, Fujian Agriculture and Forestry University, Fujian, China.

The contributions of soil arthropods to entomopathogenic nematode (EPN) food webs are mainly studied in highly artificial conditions. We investigated changes in arthropod and nematode communities in a citrus orchard following inundation of soil with Steinernema feltiae or Heterorhabditis bacteriophora. We hypothesized that arthropod taxa which decline or increase in EPN-treated compared to untreated plots represent potential key prey or predators of EPN, respectively. Soil samples were taken 3, 7, 14 and 28 days after nematodes were applied to eight, three-tree plots per treatment. DNA was extracted from the organisms that were separated from soil by sucrose centrifugation, libraries prepared, and the ITS2 and CO1 gene regions were sequenced according to Illumina protocol. Augmentation of S. feltiae and H. bacteriophora reduced the numbers of Heterorhabditis indica, an abundant indigenous EPN, by 70% (p = 0.02) and 51% (NS), respectively, compared to numbers in untreated plots. Arthropod species from 108 microarthropod (mites and collembola) families and 121 insect families were identified. EPN applications reduced the insect species richness from 32.6 molecular operational taxonomic units (MOTU) in untreated plots to 26.8 in plots with S. feltiae (P = 0.02) and 30.4 in those with H. bacteriophora (NS). Most insect taxa were rare, but several were encountered frequently and their responses to EPN treatments as well as correlations with endemic H. indica suggests an important role for an ant (Formicidae) and a non-biting midge (Chironomidae) in maintaining EPN in this orchard. Between days 3 and 28, the numbers of H. bacteriophora declined by 80%, which was more than twice the rate for S. feltiae (46%). Consistent with the different EPN disappearance rates, there were 44% fewer micoarthropod amplified sequence variants (ASV) in plots treated with S. feltiae than with H. bacteriophora (P = 0.001). Microarthropod species richness also tended to be higher (P = 0.051) in plots treated with H. bacteriophora than with S. feltiae. The responses over time of the individual microarthropod species (MOTU) suggest that regulation of EPN resulted from a cumulative response by many species, rather than by a few key species.

WORKSHOP ON CONTRIBUTING TO THE NEMATOLOGY 101 SUPER COURSE. Eisenback, Jonathan. Virginia Tech, School of Plant and Environmental Sciences, Blacksburg, VA 24061.

Nematology 101 Super Course is composed of three main components: 1) PowerPoint presentations covering the whole of nematology, 2) Screen recorded videos of the lectures, and 3) Textbook chapters expanding ideas and concepts that are presented in the lessons. The Super Course is divided into several sections with more than 125 lectures. Sections include Introduction, History, Morphology, Biology, Taxonomy, Development, Physiology, Plant Pathogens, Disease Complexes, Nematodes, Vertebrate Parasites, Invertebrate Parasites, Free-living Nematodes, Ecology, Behavior, Management, and Plants. Each presentation is limited to 20 minutes; however, topics that require more time can be broken down into smaller units. Additional sections may also be included. The PowerPoint presentations will be made available to all members of the SON through a Creative Commons with Attribution copyright. The videos will be made available worldwide and housed by the library at Virginia Tech in perpetuity, and the textbook chapters will be as a print-on-demand resource. All resources will be available for translation into additional languages. The workshop will explain the structure of the course, demonstrate the
steps required for contributing to the course, and make resources available so that each contribution is cohesive and similar in structure. This project was supported by a SON Capacity Building Grant.

PROJECT NEMATODA – A COLLECTION OF EVERY SPECIES DESCRIPTION OF EVERY NEMATODE. Eisenback, Jonathan. Virginia Tech, School of Plant and Environment Sciences, Blacksburg, VA 24061.

A collection of the original description of every species of nematode, valid or not, has made much progress in a database organized and stored online in Zotero. Thus far the database has more than 30,000 entries, but the letters “S” and “T” have not been completed. Upon completion of the of the descriptions of these last two letters, the data entries will start over with the letter “A” adding all the new species that have been collected since the beginning. Volunteers with descriptions that are not in the collection are welcomed to submit them to the Project or to enter them directly into the Zotero database. Contact the database manager at jon@vt.edu, and to gain access as a contributor. Any member of the SON can request to use the database or ask for copies of the original descriptions. In the future, perhaps the Taxonomy Committee of the SON will be agreeable to maintain this resource for members of the Society and perhaps even members of the nematology community. This project was supported by a SON Capacity Building Grant.

REPRODUCTION POTENTIAL AND SURVIVAL OF *MELOIDOGYNE INCOGNITA* IN FURROW-IRRIGATED HYBRID RICE IN ARKANSAS. Faske, Travis R.¹, J. Kelly¹, and N. Bateman². ¹University of Arkansas System Division of Agriculture, Department of Entomology and Plant Pathology, Lonoke Extension Center, Lonoke, AR 72086. ²University of Arkansas System Division of Agriculture, Department of Entomology and Plant Pathology, Rice Research and Extension Center, Stuttgart, AR 72160.

Over the past five years the annual production of furrow-irrigated rice or upland rice has increased from a few 1,000 to over 100,000 ac in Arkansas. Currently, there is limited information on the host suitability of hybrid rice to the southern root-knot nematode, *Meloidogyne incognita*, and no information on the survival of root-knot nematodes in this new production system in Arkansas. Eight hybrids were evaluated for host suitability to *M. incognita* in two greenhouse pot experiments. All hybrids were suitable hosts for the southern root-knot nematode with a reproduction factor (RF = Pf/Pi) that ranged from 7.5 to 13.5 and averaged 9.7. In a second greenhouse pot experiment, *M. incognita* reproduction was similar with three isolates on four hybrids. Soil samples (3/field) were collected at harvest from ten furrow-irrigated rice fields. Root-knot nematode J2 were recovered in one sample at a very low population density (3 J2/100 cm² soil), but this recovery does indicate nematode survival in furrow-irrigated rice in Arkansas. The soil texture in these fields were loam or silt loam. Hybrid rice is a suitable host for *M. incognita* and could sustain root-knot nematodes in furrow-irrigated rice production in Arkansas and the Mid-Southern U.S.

POTENTIAL ROLE OF THE FILTERING FRAMEWORK IN NEMATODE COMMUNITY ASSEMBLY. Gattoni, Kaitlin¹, A. Borgmeier², E. Gendron¹, J. P. McQueen¹, P. Mullin², K. Powers², T. O. Powers², and D. L. Porazinska¹. ¹Department of Entomology and Nematology, University of Florida, FL 32611. ²Department of Plant Pathology, 406 Plant Science, University of Nebraska-Lincoln, Lincoln NE 68583.

Although the patterns and mechanisms driving the assembly of aboveground macroorganisms have been well documented, how communities of belowground microscopic organisms assemble is still largely unknown. The filtering framework, in which abiotic drivers and species interactions play a role in the community composition, has been widely used for plants and here we applied this framework to examine the potential role of biotic and abiotic factors in the assembly of nematode communities in the Western Nebraska Sandhills. In October of 2019, we collected 45 samples from 5 lake basins spanning an alkalinity gradient ranging from neutral to highly alkaline (pH 7 – 10). Within each lake basin, samples were taken along a habitat gradient including aquatic (lake and shoreline sediments) and terrestrial (prairie soils) environments. Each sample was a mix of 12-16 cores representing an area ~ 20 m². Samples were processed and analyzed for: 1. nematode communities using microscopy and 18S rDNA metabarcoding, 2. microbial communities using 16S and 18S rDNA metabarcoding, and 3. biogeochemistry. We hypothesized that: H1. nematode communities from the three habitats would be distinct, and H2. the relative importance of biotic vs. abiotic factors in shaping these distinct communities would vary. To address H1, we used general linear models (GLM) and PERMANOVA to examine the patterns of alpha and beta diversity. Alpha diversity (Shannon index) indicated prairies supported the most diverse nematode communities, followed by shorelines, and lakes (P < 0.05). In addition, communities became less diverse with increasing alkalinity but only in the lakes (P < 0.05). Computationally, prairie communities were most distinct from both the shoreline and lake communities (P < 0.05). Although generally, shoreline and sediment communities differed from each other, the communities from the most alkaline lakes and shorelines were indistinct. To address H2, we used general dissimilarity models (GDM) with abiotic (i.e., biogeochemistry) and biotic (i.e., microbial diversity and biomass) variables to explain the degree of nematode community dissimilarity in lakes, shorelines, and prairies. In the lakes, >50% of community dissimilarity was explained by the model, in which biotic variables were overwhelmingly dominant despite the harshness of the alkalinity gradient in this habitat. In contrast, community dissimilarity was explained by only ~30% and ~20% in the shorelines and prairies, respectively. In the shorelines, dissimilarity was explained by similar roles of abiotic and biotic variables, while in the prairies abiotic variables were more dominant. Overall, results suggest a strong role of biotic factors in nematode community assembly despite the harshness of the alkalinity gradient. In future work we will expand the models to include the role of nematode-nematode interactions with *in vitro* assays.

UTILIZING SHOTGUN MITOCHONDRIAL METAGENOMICS FOR IMPROVED DATA COLLECTION AND IDENTIFICATION OF NEMATODES. Gendron, Eli MS¹, J. L. Sevigny², T. O. Powers³, W. K. Thomas³, I. Byiringiro³, and D. L. Porazinska¹. ¹Department of Entomology and Nematology, University of Florida, Gainesville, FL 32611. ²Hubbard Center for Genome Studies, University of New Hampshire, Durham, NH 03824. ³Department of Molecular, Cellular, and Biomedical Sciences, University of New Hampshire, Durham, NH 03824.

The use of DNA barcoding and metabarcoding has greatly increased our understanding of biodiversity on the planet. Currently, the 18S and 28S rRNA genes are among the most common markers used to identify and classify members of the phylum Nematoda [1],
however, these loci often lack species-level taxonomic resolution. Over the last decade loci from mitochondrial DNA (mtDNA), primarily from the cox1 gene, has been increasingly used to distinguish nematode species [2]. However, due to the hypervariability of the priming region of the cox1 gene, targeted marker gene approaches require the expensive and time-consuming process of the development of taxon-specific primer pairs to successfully amplify mtDNA from divergent species [2,3]. In contrast to these PCR-based methods, metagenomic approaches can overcome these limitations through multiplex sequencing of pooled whole mitochondrial genomes and genome assembly pipelines [4]. Although reference-based metagenomic assemblies can recover the true diversity of highly complex communities akin to targeted marker gene approaches, they require a large and diverse database of well-annotated reference genomes [5]. By extracting sequences from multiple databases (NCBI, Midori, EPPD-bank), we identified several gaps in the available mitochondrial genome data. For example, cox1 sequences are dominated by species from the order Rhabditida, accounting for over half of all sequenced species. Furthermore, these sequences primarily represent animal and plant parasites, thus limiting the ability to identify and classify nematodes from complex environmental communities. While progress has been made in developing more robust methods for the assembly and annotation of metazoan mitochondrial genomes [6], nematode specific tools and comprehensive databases are still missing. Here, we detail the use of shallow shotgun sequencing (also known as skim-sequencing) as a method for: 1) the development of a publicly available database of nematode mitochondrial genomes that fill in the missing phylogenetic gaps and facilitate the accurate and rapid identification of nematode diversity from environmental samples, 2) the discovery of novel taxa, and 3) the testing of our pipeline for the rapid identification of complex nematode communities without the need for targeted sequencing, using in-situ mock communities.

EVALUATION OF HOT WATER TREATMENT FOR THE MANAGEMENT OF GUAVA ROOT-KNOT NEMATODE. Giles, Celeste, and C. Khanal. Clemson University, Department of Plant and Environmental Sciences, 105 Collings St., Clemson, SC 29634.

Guava root-knot nematode (Meloidogyne enterolobii) is distributed worldwide, attacks a wide variety of economically important crops, and cannot be managed with currently available management options. Therefore, hot water treatment was developed and evaluated as an alternative management method for M. enterolobii. Freshly hatched second-stage juveniles of M. enterolobii were exposed to 1 mL of hot water in 1.5 mL Eppendorf microcentrifuge tubes in Thermomixer-C at 42, 44, 46, 48, and 50°C for 0, 30, 60, 120, and 240 minutes. Nematode viability was assessed based on movement of nematodes when 1% ethanol was added to tubes 24 hours after hot water treatment. Exposure to temperature of 44°C for 120 minutes resulted in 100% nematode mortality. Similarly, 100% mortality occurred when nematodes were exposed to temperatures higher than 46°C for at least 30 minutes. These results suggest that thermotherapy has potential to be employed as exclusion and eradication strategies for the management of M. enterolobii.

EFFICACY OF CERTIFIED BIONEMATICIDES FOR CONTROL OF MELOIDOGYNE INCOGNITA IN THE GREENHOUSE CONDITIONS. Gitonga, Denis1, N. Hamidi1, and A. Hajihassani1. 1Department of Plant Pathology, University of Georgia, Tifton, GA 31793.

Root-knot nematodes (RKN: Meloidogyne spp.) are considered as one of the major limiting factors in the global crop production system. Management of these nematode pests has been attempted using various approaches, including biorational products as an alternative to chemical nematicides whose use has been largely criticized due to the adverse effects on the environment and human health. Two independent greenhouse experiments were conducted to evaluate the nematicidal efficacy of eight commercially available products (Majestene, TerraNeem, AzaGuard, Molt-X, NemOmex, EcoWorks, Monterey, and Promax) against M. incognita. The experiments were established in 10-cm diameter plastic pots and laid out in a completely randomized design with seven replicates per treatment. Each pot was filled with sterile field soil, inoculated with 2,500 second-stage juveniles, and mixed well to distribute the nematodes in the soil evenly. The treatments were applied based on the recommended rates on the label and tomato (cv. Rutgers) seedlings planted in each pot. The bioematicides were soil drenched three times; at planting and 10 and 28 days after planting. Tomato plants with (positive control) and without (negative control) the nematode inoculation was used for comparison. After eight weeks, shoot length, shoot dry weight, fresh root weight, root gall severity using a scale of 0 to 5, and eggs per gram of root were evaluated. There was no significant difference in the shoot dry weight and shoot length among all the treatments. AzaGuard and Majestene had the highest (P < 0.05) root weight, while Monterey had the lowest root weight compared to both control checks. Monterey had the lowest (P < 0.05) galling index followed by AzaGuard and Molt-X compared to the positive control. However, Monterey had undesirable effects on the root system resulting in low galling severity and egg counts. The number of eggs per gram of root at the end of the experiments varied greatly and ranged from 1806 to 4815. AzaGuard had the lowest (P < 0.05), while TerraNeem had the highest eggs per gram of roots compared to the positive control. AzaGuard outperformed all the other bioematicides and will be selected for the field trials to manage Meloidogyne spp. in organic vegetables.

SCREENING FOR A SOLUTION: EVALUATING DIVERSE CROP GENOTYPES FOR RESISTANCE TO MELOIDOGYNE ENTEROLOBII. Gorny, Adrienne M.1, T. Schwarz2, and E. Davis2. 1North Carolina State University, Dept. of Entomology and Plant Pathology, Raleigh, NC 27695.

Meloidogyne enterolobii (syn. M. mayaguensis, colloquially known as the pacara earpod tree or guava root-knot nematode) is hypothesized to be an introduced plant-parasitic nematode species to North Carolina and has limited distribution within the United States. This species has been observed to produce severe root galling symptoms, frequently resulting in crop stunting and yield losses. As a quarantine regulated species, M. enterolobii poses a particular challenge for domestic and international shipment of crops in which the marketed portion of the plant is produced underground, such as carrot, white potato, and sweetpotato, or transport of planting material such as plugs or slips. Management of M. enterolobii in the field is difficult, as the species can overcome known root-knot nematode resistance genes, including the Mi-1 (tomato), Mh (Irish potato), N and Me1 (bell pepper), and Mr1 (soybean) genes. Further, the species reproduces on sweetpotato cultivars resistant to M. incognita, including ‘Covington’. Chemical management of M. enterolobii is economically and environmentally costly and may not provide sufficient season-long suppression to highly sensitive crops. Therefore, host resistance remains the most desired management method for M. enterolobii and other root-knot nematodes. Through greenhouse trials, resistance to M. enterolobii in a diverse array of crop genotypes is being screened for in breeding lines, experimental material,
and wild relatives with the objective of identifying moderate to high resistance, defined through galling and egg production. Current research efforts are heavily focused in evaluating sweetpotato and soybean, with additional screening trials in cotton, eggplant, tomato, hemp, and several cover crops. Young plants are challenged with nematode egg inoculum from North Carolina isolates of *M. enterolobii*. Plants are then evaluated for severity of root galling symptoms, total root mass, and eggs produced per gram of root tissue. A molecular quantification method using quantitative real-time PCR was developed to calculate nematode eggs extracted from test plants, providing a reliable alternative to manual counting of eggs and increasing trial throughput.

**EVALUATION OF FLUENSULFONE IN COMBINATION WITH METAM POTASSIUM AS A BROAD-SPECTRUM SOLUTION TO CONTROL PLANT PARASITIC NEMATODES, SOIL- FUMIGATION CHEMISTRIES AND METHODS FOR *MELOIDOGYNE INCognITA* MANAGEMENT IN SWEETPOTATO.** Grabau, Zane J.,¹ and R. Sandoval-Ruiz.¹ University of Florida, Entomology and Nematology Department, Gainesville, FL 32611.

*M. incognita* (southern root-knot nematode) is an important pest in sweetpotato production. Some common cultivars, such as ‘Covington’, have moderate resistance to this nematode, and nematicides are often applied in conjunction with resistance cultivars. If fumigation is used, applications are often targeted only in the zone where beds will be formed, commonly using one application shank per bed to save costs. Metam potassium is a common fumigant, but it has limited horizontal movement in soil, so modifying in-bed application methods to increase distribution may increase efficacy for managing nematodes. Impacts on non-target, free-living nematodes are another consideration when applying nematicides. In this study, efficacy of metam applied using one (M-1S) or two shanks per bed (M-2S) was compared with 1,3-dichloropropene (1,3-D) with one shank per bed and untreated control for *M. incognita* management and non-target effects in sweetpotato production. Efficacy was assessed in a replicated small plot field trial in North-Central Florida in 2020 using ‘Covington’. *M. incognita* soil abundances were low and unaffected by fumigation at midseason. At harvest, soil abundances were substantial, and less for 1,3-D or M-2S than M-1S. There was minimal tuber galling at harvest, but yield was affected by *M. incognita* management. Total yield was greater for 1,3-D than other treatment. Marketable yield was greater for 1,3-D than control or M-1S and intermediate for M-2S. Fumigation also had negative impacts on non-target, free-living nematodes as fumigation decreased free-living nematode soil abundances relative to untreated control. Increasing soil coverage by increasing from one to two in-bed shanks improved *M. incognita* management by metam, but 1,3-D still provided a greater yield response. All fumigation chemistries and methods had negative impacts on free-living nematodes, so none of them were a good option for minimizing non-target impacts.

**FLUENSULFONE AND FUMIGATION FOR STING NEMATODE MANAGEMENT IN POTATO PRODUCTION.** Grabau, Zane J.,¹ C. Liu,¹ and P. A. Navia Ginec.¹ University of Florida, Entomology and Nematology Department, Gainesville, FL 32611, ADAMA Agricultural Solutions Ltd., Raleigh, NC 27604.

Florida is an important producer of potatoes during the winter season. Sting nematode causes substantial damage in Florida potato production and fumigation with 1,3-dichloropropene (1,3-D) is the primary means of management. Prior research trials from 2016 to 2019 have shown that fluensulfone can be an effective alternative to 1,3-D as fluensulfone at 2.1 kg a.i./ha decreased final sting nematode soil abundances by 71% and increased marketable yield by 41%. In the same trials, 1,3-D decreased final sting nematode abundances by 83% and increased marketable yield by 49%. The purpose of this study was to determine if metam potassium fumigation improves sting nematode management alone or in combination with fluensulfone. Nematicides were tested in replicated, small plot fields in Northeast Florida in 2020 and 2021. In 2020, treatments included untreated control, metam at 292 kg a.i./ha, 1,3-D at 66 kg a.i./ha, fluensulfone at 2.1 kg a.i./ha, metam mixed with fluensulfone, and metam followed by in-furrow fluensulfone at 2.1 kg a.i./ha. In 2021, the same treatments were applied except the final treatment was replaced with in-furrow fluensulfone at 1.6 kg a.i./ha. Except for in-furrow applications, nematicides were applied at 25 and 26 days before planting in 2020 and 2021, respectively. In both years, any treatment with metam exhibited early season phytotoxicity based on visual observations, stand counts, and vigor ratings. Nematicide efficacy at managing sting nematode and increasing yield varied by year. In 2020, any treatment, except preplant fluensulfone, was effective at managing sting nematode based on midseason abundances. Yield was greatest for 1,3-D, least for metam alone and intermediate for the other treatments in 2020. In 2021, treatments with metam or 1,3-D were effective for managing sting nematode, but fluensulfone-only treatments were not, based on midseason and final nematode soil abundances. Marketable yield was greater for metam alone or 1,3-D than any other treatment in 2021. Treatments with better sting nematode management generally had greater yield and treatments with early season symptoms of phytotoxicity generally had lower yield, but this was not a consistent relationship, likely due, in part, to interaction of these two factors. Fumigation with 1,3-D was the most effective nematode management option in this study. Fluensulfone had efficacy but was less consistent than 1,3-D. To make an accurate assessment of efficacy of metam alone or in combination with fluensulfone for managing sting nematode in this system, phytotoxicity issues need to be resolved, potentially by adjusting application rate.

**EVALUATION OF SEED-APPLIED NEMATICIDES AND INSECTICIDES TO PRESERVE COTTON SEEDLING PLANT HEALTH AND YIELD.** Graham, Scott H.,¹ K. S. Lawrence¹ and C. T. Graham.¹ Auburn University, Dept. of Entomology and Plant Pathology, Auburn, AL 36849, Bayer CropScience, Grenada, MS 38901.

Management of early season pests, including plant parasitic nematodes, seedling diseases, and thrips is critical for optimizing cotton management. In Alabama, two key plant parasitic nematodes, *Meloidogyne incognita* (root-knot nematode) and *Rotylenchulus reniformis* (reniform nematode), are important in various locations across the state. The tobacco thrips, *Frankliniella fusca*, is the dominate insect pest of seedling cotton statewide. Due to the ease of application and relative efficacy, this early season pest spectrum is often managed using seed-applied products. The objective of this study was to evaluate the effects of early season cotton health in nematode infested fields with various insecticide/nematicide seed-applied treatments. Field trials arranged as a RCBD with four or five replications were established in central (root-knot) and north (reniform) Alabama. At both locations, a nematode susceptible variety, DP 1646 B2XF was planted at a seeding rate of four seeds per foot. Treatments included: 1) Fungicide Only check 2) Gaucho (imidacloprid) insecticide seed treatment
(IST) 3) Aeris Seed Applied System (imidacloprid + thiodicarb) 4) Gaucho IST + Poncho/Votivo (clothianidin + Bacillus firmus I-1582) 5) Gaucho IST + COPEO Prime (fluopyram). Regardless of location, cotton treated with an IST show less thrps injury than the fungicide only control. Similarly, cotton treated with an IST tended to have better vigor and greater above and below ground biomass than the fungicide only control. In central Alabama, where the root-knot nematode was the primary species, there were no differences in nematode population levels at 36 days after planting (DAP). In north Alabama, where reniform nematode was the primary species, all treatments except Gaucho IST + Poncho/Votivo resulted in significantly lower populations of nematodes at 40 DAP. Other data to be collected include white bloom counts at first flower to measure cotton maturity and yield.

UNDERSTANDING THE ROLE OF α-SNAP GENE IN SOYBEAN RESISTANCE TO THE SOYBEAN CYST NEMATODE. Haarith, Deepak, E Nelson, R Zapotocny and A F Bent. 1Plant Pathology, University of Wisconsin, Madison, Wisconsin, USA.

Soybean cyst nematode (SCN, Heterodera glycines) is the most economically consequential pathogen of one of the world's major food crops, soybean. Managing this evolving nematode has been a challenge and despite best efforts, almost all counties that grow soybeans in the US are increasingly infested with SCN. Although host resistance is the most effective tool in managing SCN, the resistance is mostly derived from a single source, PI 88788. This resistance is conferred by a 3-gene quantitative trait locus (QTL) called rhg1-b, but many field populations of SCN are gradually overcoming this resistance. The most prominent alternative source of resistance, from the soybean line Peking is a multi-QTL resistance involving the rhg1-a haplotype and the Rhg4 QTL as well. However, the mechanism(s) of resistance conferred by the genes within these QTLs are not fully understood. The different sources of resistance are effective against different HG types of nematodes in the field. In my current work we have learned that introduction of an extra copy of the α-SNAP (alpha-Synaptosomal-Associated-Protein) gene from rhg1-b or rhg1-a into a variety with the Peking background bolstered the resistance provided by the Peking variety, both in growth-chamber and greenhouse yield assay. However, an extra copy of α-SNAP in a variety with the PI 88788 background did not significantly improve the resistance of the variety to SCN. We are currently investigating the molecular basis of this enhanced resistance by investigating the expression of the three genes in rhg1 and the GmSHMT (serine hydroxymethyltransferase) gene in Rhg4 loci.

PHYLOGENETIC RELATIONSHIPS OF SOME BELONOLAIMUS LONGICAUDATUS POPULATIONS ASSOCIATED WITH TURFGRASSES IN THE SOUTHEASTERN USA. Habteweld, Alemayehu, M. L. Mendes, R. N. Inserra, and W. T. Crow. 1University of Florida, Entomology and Nematology Department, Gainesville, FL32611-0620, 2Florida Department of Agriculture and Consumer Services, Division of Plant Industry, Gainesville, FL 32614.

Belonolaimus longicaudatus is among the most destructive plant-parasitic nematodes to a wide range of plants including turfgrasses, ornamentals, forages, vegetables, agronomic crops, and trees. There is no information on the morphological and genetic variability of B. longicaudatus populations from turfgrasses. Hence, a study was conducted to assess inter- and intra-population variation of morphological and molecular characters of different populations associated with turfgrasses from different locations in the southeastern USA. The D2D3 and ITS regions of rDNA from 31 populations of B. longicaudatus associated with turfgrasses in different locations of southeastern USA were sequenced and subjected to phylogenetic analysis. The result showed that there were variations in DNA sequences among populations, and morphology and morphometric characters as well. The phylogenetic analysis using D2D3 LSU and ITS1-5.8S-ITS2 rDNA sequences grouped the south Florida populations together at 91 and 85% support, separated from other B. longicaudatus populations from other localities that clustered in another subclade. The south Florida populations as a group tended to have smaller mean stylet knob width, stylet/tail and tail integument thickness, shorter mean lip length, stylet length, and distance of excretory pore from anterior end and esophagus length. Principal components analysis of seven selected morphometric characters also showed correlations among populations related to the subclade they belong. Overall results suggest that the populations from turfgrasses in south Florida fit morphologically the paratypes of B. longicaudatus described by Rau (1958) from central Florida, which have a S/T ratio value ≤ 1. On the contrary, the populations from other localities grouping in a different subclade in the phylogenetic tree have the highest range of S/T values > 1. The intra- and inter-population variations and differences in DNA sequences observed in the present study confirm that B. longicaudatus is a species complex as previously noted by other authors. Although the parasitism to turfgrasses by the B. longicaudatus populations grouping in the two different subclades results in serious damage, more studies are needed to define many biological, ecological, and genetic aspects of these populations from turfgrasses.

ENTOMOPATHOGENIC NEMATODE BIOCONTROL OF STRIPED FLEA BEETLE LARVAE: A NOVEL METHODOLOGY FOR EFFICACY TESTING. Haines, Stephanie A., A. C. Green, D. K. Londoño, and S. D. Berry. BASF, Research Triangle Park, NC 27709.

Striped flea beetle (Phyllotreta striolata) is a major worldwide pest, particularly for canola and other cruciferous crops. These insects provide a challenge for laboratory testing due to maintaining a colony in captivity. However, laboratory assays are crucial to evaluate new methods of flea beetle control. Control methods currently available to growers include chemical seed treatments and foliar sprays, but these methods, if used alone, can lead to insecticide-resistant populations. Biocontrol methods include natural enemies like parasitic wasps and other beetles, but these provide minimal control. However, entomopathogenic nematodes (EPNs) show promising results when used to control flea beetle larvae. Adult flea beetles can cause devastating damage to young plants, while larvae cause little damage to plants, so larval control measures can be used to reduce the population of new generations in a field before they begin to cause crop damage. For this study, new methodologies were developed for testing flea beetle larvae in a laboratory. Results showed that Steinernema carpocapsae, when applied at rates of 250 million, 500 million, and 750 million nematodes per acre, to radish plants infested with striped flea beetle larvae, led to a reduction in subsequent leaf damage after a month by 71%, 81%, and 95%, respectively.

IDENTIFICATION OF RESISTANCE BREAKING POPULATIONS OF MELOIDOGYNE INCognITA IN GEORGIA, USA. Hajihassani, Abolfazl, J. Marquez, and N. Hamidi. Department of Plant Pathology, University of Georgia, Tifton, GA 31793.
Root-knot nematodes (RKN; *Meloidogyne* spp.) are primary pathogens of vegetable crops. In a recent study conducted in southern Georgia, USA, more than 67% of vegetable-growing fields had at least one RKN species. The occurrence of virulent populations of *Meloidogyne* spp. has limited the effectiveness of resistance conferred by *Mi*-1 gene in tomato. In this study, two hundred and seventy-nine isolates (populations) of *Meloidogyne* spp. from vegetable fields in southern Georgia were used to evaluate their potential to reproduce on a tomato cultivar, Red Bounty, with the *Mi*-1 gene, which confers resistance to *M. javanica, M. arenaria,* and *M. incognita.* We found four naturally occurring virulent RKN populations (Cr2, Lo13, G16, and S10) in vegetable fields from four counties in Georgia with no history of tomato cultivation of the *Mi* gene. The identity of these populations was confirmed as *M. incognita* with duplex PCR analysis using species-specific primers. PCR with Mi2F4/Mi1R1 primers produced a 300 bp DNA fragment for the S10 population, while the PCR with SEC-1F/SEC-1R primers produced approximately 400 to 450 bp DNA fragments for three populations of Cr2, Lo13, and G16. Two consecutive greenhouse experiments were also conducted to compare the reproduction of virulent and avirulent (*M. incognita race 3*) populations in susceptible (cv. Rutgers) and resistant (Amelia, Skyway, and Myrtle) tomato cultivars. Results showed that all four virulent *M. incognita* populations reproduced on resistant cultivars with the *Mi*-1 gene, while *M. incognita race 3* was unable to overcome host resistance. In addition, various levels of parasitism were observed among four virulent populations on the resistant cultivars, with the Cr2 population having a higher reproductive potential than the other populations (*P* < 0.05). To our knowledge, this is the second report of RKN populations that evade the *Mi*-1 gene in the United States after California.

ANALYSIS OF QUANTITATIVE TRAIT LOCI ASSOCIATED WITH RESISTANCE TO *MELOIDOGYNE INCOGNITA* IN GLYCINE LATIFOLIA. Han, Jae Yong1, L. L. Domier3, K. N. Mc Coppin2, S. L. Lim2, N. E. Schroeder4, and G. L. Hartman1. 1University of Illinois, Dept. of Crop Sciences, Urbana, IL 61801, 2USDA-ARS, Urbana, IL 61801; 3Chungnam National University, Dept. of Applied Biology, Daejon, South Korea.

Perennial Glycine species are potentially valuable genetic resources that can improve disease resistance in soybean by hybridization or gene transfer techniques. The goal of this research is to discover novel *M. incognita* resistance quantitative trait loci (QTL) from perennial Glycine spp. that can be further characterized for potential use in soybean. From our initial screening of 18 accesses of 10 perennial Glycine species for resistance to *Meloidogyne incognita,* we discovered that *G. latifolia* plant introduction (PI) 559300 has a higher level of resistance to *M. incognita* than the resistant soybean check Forrest. To identify QTL associated with resistance to *M. incognita* in *G. latifolia,* we have conducted a QTL analysis using recombinant inbred lines derived from resistant (PI 559300) and susceptible (PI 559298) *G. latifolia* accessions and single nucleotide polymorphism markers generated through genotyping by sequencing. The initial analysis identified a single QTL on *G. latifolia* chromosome 13. The QTL interval spans a region from about 7.8 to 11.2 Mb, explaining 34% of the phenotypic variation. This QTL contains at least 73 genes, including at least three putative disease resistance genes that have not been examined for their functions against *M. incognita.* We expect that the QTL on *G. latifolia* chromosome 13 is a major QTL responsible for resistance to *M. incognita* and contains novel genes that confer this resistance. We also anticipate that *G. latifolia* PI 559300 is a good candidate for utilizing genes that are effective against *M. incognita* and could be used to improve soybean resistance to *M. incognita.*

MOLECULAR AND MORPHOLOGICAL CHARACTERIZATION OF *TRICHODORUS N. SP.* (NEMATODA: TRICHODORIDAE) FROM MARYLAND, UNITED STATES. Handoo, Zafar A1, M. Kantor1, W. Decraemer3, and S. Subbotin4. 1Mycology and Nematology Genetic Diversity and Biology Laboratory, USDA, ARS, Northeast Area, Beltsville, MD 20705, USA, 2Nematology Research Unit, Department of Biology, Ghent University, K.L. Ledeganckstraat 35, B9000 Ghent, Belgium, 3Plant Pest Diagnostic Center, California Department of Food and Agriculture, Sacramento, CA 95832, USA, 4Center of Parasitology of A.N. Severtsov Institute of Ecology and Evolution of the Russian Academy of Sciences; Leninskii Prospect 33, Moscow 117071, Russia.

Specimens of *Trichodorus* n.sp. were recovered during a nematode survey of natural vegetation along the bank of Western Branch Patuxent River from Upper Marlboro, Maryland. The length of the new species is about 1 mm, with a medium-sized onchoistylet. Males have a 42 µm long spicule on average, gubernaculum typical keel-like thickening posteriorly and 17 µm long. When relaxed, females have a largely straight or slightly ventrally curved body and possess a short barrel-shaped vagina. Specimens of *Trichodorus* n.sp. were recovered during a nematode survey of natural vegetation along the bank of Western Branch Patuxent River from Upper Marlboro, Maryland. The length of the new species is about 1 mm, with a medium-sized onchoistylet. Males have a 42 µm long spicule on average, gubernaculum typical keel-like thickening posteriorly and 17 µm long. When relaxed, females have a largely straight or slightly ventrally curved body and possess a short barrel-shaped vagina. *Trichodorus* n. sp. is close to *Trichodorus eburneus* and *Trichodorus obtusus* (syn. *T. proximus*). To better differentiate between *Trichodorus obtusus* and *Trichodorus* n.s., phylogenetic relationships and statistical parsimony were used. Both morphological observations and molecular analysis indicated that these specimens represent a new nematode species of *Trichodorus* which is discussed here.

TRAP CROPS FOR THE ERADICATION OF *GLOBODERA PALLIDA,* THE PALE CYST NEMATODE IN INFESTED IDAHO FIELDS. Hickman, Paige1, and L. M. Danduran2. 1University of Idaho, Dept. of Entomology, Plant Pathology, and Nematology, Moscow, ID 83844.

*Globodera pallida,* the pale cyst nematode (PCN) is a quarantined pest of potato in Idaho. USDA-AFPHIS regulates this pest. Growers with infested acreage cannot plant potato until their fields have undergone an extensive deregulation process that demonstrates that PCN is no longer present. With potential to cause up to 80% yield loss and remain dormant but viable in the soil for 20 to 30 years in the absence of a host, PCN presents a serious threat to the Idaho potato industry. The primary method of PCN eradication has been soil fumigation; however, use of soil fumigants, such as methyl bromide, is becoming more and more restricted or banned altogether due to environmental concerns. Alternative more sustainable control of PCN is a necessity. Trap crops can be a feasible option for PCN control. A trap crop for PCN must be a nonhost that stimulates egg hatch. Litchi tomato (*Solanum sitymbriifolium*) has proven to be a successful PCN trap crop because it has been shown to cause 90 to 100% PCN reduction in rotation with potato. Growers are hesitant to plant litchi tomato in their fields as it has potential to become an invasive noxious weed and does not provide an economic return. This research seeks to investigate trap crop potential of several other species of interest through host and hatch assays, and to compare them to the effect of litchi tomato in greenhouse and field trials. Solanaceous trap crops of interest shown to be nonhosts that cause hatch include naranjilla (*Solanum quitoense*), wonderberry (*Solanum retroflexum*), African eggplant (*Solanum macrocarpon*), Ethiopian eggplant (*Solanum aethiopicum*), and *Solanum douglasii.* The hatching effect of these species was evaluated and showed that naranjilla and wonderberry cause the greatest
PCN hatch. *Chenopodium quinoa* has also been found to cause PCN hatch. Several varieties of quinoa adapted for the Pacific Northwest were evaluated for PCN hatching stimulus. The impact of quinoa on PCN was also compared to that of litchi tomato in a field trial under Idaho growing conditions. While quinoa does not have impact equivalent to that of litchi tomato, it does appear to cause PCN reduction over time and has the added benefit of producing a valuable crop in rotation in infested fields. Ultimately, this research will ideally provide growers with infested fields an alternative strategy that can be used in PCN eradication.

EVALUATING WINTER PENNYCRESS AND CAMELINA AS ALTERNATIVE HOSTS TO SOYBEAN CYST NEMATODE UNDER FIELD CONDITIONS. **Hoerning, C.**, **S. Chen**, **K. Frels**, **D. Wyse**, and **M. S. Wells**. 1Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN 55108, 2Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108.

Winter oilseed crops, pennywort (*Thlaspi arvense* L.) and winter camelina (*Camelina sativa* (L.) Crantz), are being developed for incorporation into corn (*Zea mays* L.) and soybean (*Glycine max* (L.) Merr.) cropping rotations. The incorporation of the winter oilseed crops into the cropping system offers ecosystem and productivity benefits during the fall and spring when the ground is fallow. Exposed soil in the Midwest during. Adding a new crop into an established cropping system enhances risk. One identified risk, observed in controlled greenhouse conditions, is that pennywort is an alternative host of soybean cyst nematode (SCN, *Heterodera glycines*). Similar greenhouse studies indicated camelina is a non-host or a potential trap crop. Greenhouse studies have environmental limitations as these controlled environments do not accurately represent field growing conditions for the winter annual oilseeds. The winter oilseeds are planted in the fall and harvested in early summer; this is a temporal period when soil temperatures are low. Low soil temperatures, especially those below 10°C, are known to inhibit SCN development. The objective for this experiment was to investigate whether adding pennywort and camelina oilseed to a soybean-oilseed-corn rotation affected SCN population density. Three sites were used across Minnesota to evaluate SCN population density in cropping rotations including the winter oilseeds. SCN population density in treatments containing the winter oilseed treatments were not significantly different from the SCN population density of treatments without the winter oilseed treatments.

NEW MANAGEMENT PRACTICES PROVIDE PROMISING CONTROL FOR THE NORTHERN ROOT-KNOT NEMATODE (*MELOIDOGYNE HAPLA*) IN DAYLILY (*HEMEROCALLIS* SPP) FIELD PRODUCTION. **Howland, Amanda D.**, **E. Cole**1, and **M. Quintanilla**1. 1Michigan State University, Department of Entomology, East Lansing, MI.

The northern root-knot nematode, *Meloidogyne hapla*, is one of the main pathogens in the floriculture industry in the north-eastern United States and Canada. Michigan is the third largest producer in the floriculture industry and a major component of that industry is the production of bare-rooted daylilies, *Hemerocallis* spp. with a value of $1.1 million in 2018. Daylilies are one of the most popular and important ornamental perennial plants and are grown in the field for three years. High populations of nematodes can result in severe root decay and plant death, and *M. hapla* is responsible for over 20% yield loss in the daylily industry. Additionally, their visible symptoms on the roots further reduce marketability and can inhibit plant shipments from being sold and distributed. Previous field trials testing different management strategies to control *M. hapla* throughout daylily’s entire production cycle showed several treatments with promising nematode management that also increased plant growth. Therefore, a three-year field trial was established in 2020 in Zeeland, MI with the objective to test these top treatments in combination with a prescriptive blend compost employed by the nursery to determine which treatment most effectively manages *M. hapla*. The treatments included in the trial are 1) Compost + Indemnify Dip, 2) Compost + Indemnify Dip + TerraClean 5.0, 3) Compost + Indemnify Dip + AzaGuard, 4) Compost + Indemnify Dip only, 5) Compost + Indemnify Drench only, 6) a compost control, and 7) a negative control of no treatments. In the field, the seven treatments were arranged in a randomized block design with five replications. Compost was raked into the plots before planting; Indemnify dipped daylilies were dipped in Indemnify and immediately planted. Drench treatments were then applied to each respective plot. To monitor *M. hapla* population levels, soil samples are taken yearly in the spring, mid-season, and end-season. At the mid-season sampling period, plant height, eye calculations, and root samples are also taken; root samples are stained with acid fuchsin to determine presence of *M. hapla* inside the roots. Preliminary results show that TerraClean 5.0 had the lowest *M. hapla* g of root with the Compost + Indemnify Dip having the most. The Compost + Indemnify Dip treatment significantly had the smallest plant heights while the Compost + Indemnify Drench had the highest. TerraClean 5.0 had the greatest number of eyes while the Compost Control had the lowest. This trial will be concluded in October of 2022; final nematode population levels and plant measurements (plant height, crown width, shoot and root weights, and grade of each plant) will be taken. Results will provide daylily producers the best management strategy to reduce *M. hapla* populations in their production fields while increasing plant yield.

QUANTIFYING PLANT PARASITIC NEMATODE NITROGEN ASSIMILATION WITH ISOTOPE ENRICHED PROTEOMICS. **Hughes, Kody**, **S. Mishra** and **P. M. DiGennaro**. Department of Entomology and Nematology, University of Florida, Gainesville, FL 32611.

C-terminally encoded peptides (CEP) are common to all vascular land plants and play important roles in root architecture and adaptive responses to nitrogen stress conditions. Specifically, one of the nitrogen pathways regulated by plant CEP is that of nitrogen transporter genes. Genes encoding CEP like peptides are also present in the sedentary endosymbiont *Meloidogyne hapla* and the sedentary semi endoparasite *Rotylenchus reniformis* genomes. The presence and activity of CEP in sedentary plant parasitic nematodes may reveal exploitable pathways to impede nematode parasitism by modulating nitrogen transportation. We hypothesize that nematode encoded CEP are involved in commandeering nitrogen allocation pathways in parasitized plants, redirecting nitrogen to feeding sites. We demonstrate that exogenous application of plant and *M. hapla* CEP increases plant nitrogen transporter gene expression. Further, we incorporated a heavy labeled isotope of nitrogen in plant fertilizer and quantified nematode nitrogen assimilation through high-throughput proteomics with and without the presence of exogenous CEP. Proteomes of *M. hapla* extracted from infected root tissues and galls were examined at 7-, 21- and 40-days post inoculation. Comparisons of heavy labeled nitrogen isotopes incorporated into nematode encoded proteins reveal the timing of feeding, role of CEP in nematode nitrogen assimilation from plants as well as specific pathways responsible for nitrogen

Abstracts from the Society of Nematologists Annual Meeting 2021 15
acquisition. Targeted characterization of nitrogen metabolic pathways in nematode genomes and modification of essential nutrient transportation in plants may present novel control methods for these significant agricultural pests.

TRACING GLACIAL PATTERNS AND REFUGIA WITH SCOTTNEMA LINDSAYAE NEMATODE. Jackson, Abigail1, T. Powers2, K. Powers3, T. Harris4, D. H. Wall5, and B. J. Adams1. 1Brigham Young University, Provo, UT 84062, 2University of Nebraska, Lincoln, NE 68588, 3Colorado State University, Fort Collins, CO 80523.

Climate-driven glacial expansions and retreats drastically alter terrestrial biota’s survival and geographic distribution. This is especially true in polar regions, like the Antarctic Dry Valleys. During the Last Glacial Maximum (LGM; about 20,000 years ago), much of the Antarctic continent was blanketed by ice, yet nearly all of Antarctica’s extant species are endemic and so must have survived glaciation events in situ. The Dry Valleys are infamously harsh environments that foster neither high terrestrial biodiversity nor species recruitment. Freezing temperatures and saline soils limit terrestrial life to simple, dispersed microbial communities and microscopic soil invertebrates. This provides a simplified ecosystem to study the impacts of glacial history and refugia. Refugia are habitable, high elevation soil ecosystems that avoided inundation by expanding glaciers and have continually experienced periodic wetting, reducing inhospitable saline conditions of the Dry Valleys. Terrestrial biota could have survived large-scale glacial expansion in refugia areas. The objective of this study is to test hypotheses regarding areas that could serve as refugia within Antarctica’s McMurdo Dry Valleys. We test putative refugia on a fine-scale utilizing the mitochondrial COI gene of the most ubiquitous terrestrial animal in Antarctica – Scottnema lindsayae – by determining phylogeographic patterns left by historical glaciations. We sequenced 250 bp COI haplotypes from 16 sites across the Dry Valleys. These sites represent high and low elevations corresponding to glaciated sites and recolonized forefields respectively. We analyzed phylogeographic patterns of haplotype diversity in the context of hypothesis testing consistent with persistent refugia. We anticipate that putative refugia populations will have signatures of high genetic diversity, while subsequent glacial retreats allowing range expansion will create phylogeographic patterns from refugia to recolonized glacial forefields. Utilizing phylogeographic approaches on the most ubiquitous microfauna species, S. lindsayae, refugia hypothesis testing can be applied on a fine, universally applicable scale. This study demonstrates characteristics of refugia that enable terrestrial biota to survive periods of extreme climate-driven environmental changes. Looking forward, refugia sites contain unique haplotypes therein and are important habitats for conservation in the face of climate change. Thus, identifying historical refugia areas is the first step in preserving this rapidly changing environment.

EFFICACY OF ORGANIC NEMATICIDES AGAINST MELOIDOGYNE INCognITA INFeCTING CUCUMBERS UNDER GREENHOUSE CONDITIONS. Jagdale, Ganpati1, A. Hajihassani2, and D. Shapiro-Ilan1. 1Department of Plant Pathology, University of Georgia, Athens, GA, USA 30602, 2Department of Plant Pathology, University of Georgia, Tifton, GA, USA, 31794, 3USDA-ARS, Byron, GA 31008, USA.

Cucumber (Cucumis sativus) is one of the major market vegetable crops grown in the U.S., including Georgia. Root-knot nematode (Meloidogyne incognita) is considered an important pest of vegetables including cucumber. Pre-plant soil fumigation with chemicals is commonly used to manage plant-parasitic nematodes (PPNs), especially root-knot nematodes in many vegetable production systems. Due to environmental or regulatory concerns, alternative control methods are needed, especially nematicidal products that can be effective against PPNs, safe for humans and the environment. Two independent experiments were conducted in 2019 to compare the efficacies of metabolites of two entomopathogenic bacteria (Xenorhabdus szentirmaii and X. bovienii), Majestene™ (a.i.- Heat-killed Burkholderia sp. strain A396), MeloCon WG (a.i.- Paecilomyces lilacinus strain 251), compost topdressing, and Vydate (a.i. oxamyl) against M. incognita in cucumber under greenhouse conditions. Three-week-old seedlings of cucumber were transplanted individually into clay pots (15 cm2 surface area) filled with 1.3 kg steamed field soil and washed sand (1:1 v/v). Plants were inoculated with 1000 infective juveniles of M. incognita by pipetting one ml of nematode suspension into three holes around the plant in each pot. Then the nematodes were allowed to acclimatize for one day in each pot. Based on the labeled per acre rates, low and high concentrations of each nematicide were prepared in water and drench applied in each pot. Only water was applied in untreated control pots. The experiment was arranged in a randomized-complete block design with seven replications. Population densities of M. incognita, root-galling indices using a 0-5 scale (0=no galls seen, 5=roots completely covered in galls), plant growth parameters and cucumber yields were determined 60 days after treatment (DAT). The population densities of M. incognita and root gall indices were significantly reduced in the treatments with Vydate, low concentrations of Majestene and high concentrations of metabolites of both bacteria, X. szentirmaii and X. bovienii compared to the other treatments. Also, dry shoot weights were significantly higher in only a treatment with the high concentration of metabolite of X. szentirmaii than the other treatments and untreated control. This suggests that the bacterial metabolite played a significant role in providing some nutrients to plants. Furthermore, fruit weight was significantly higher in planted treated with Vydate than other treatments. Bacterial metabolites demonstrated potential efficacy to control M. incognita in the current study; however, future studies will include field evaluations of these metabolites to assess the biological control ability on root-knot nematodes.

COMPARATIVE EFFICACY OF FLUENSULFONE AND STEINERNEMA CARPOCAPSÆ AGAINST PEACH NEMATODES. Jagdale, Ganpati1, C. Oliveira-Hofman3, D. Chavez3, B. R. Blauw4, L. Duncan3, G. Colson4, C. H., Bock1, and D. Shapiro-Ilan2. 1Department of Plant Pathology, University of Georgia, Athens, GA, 30602, USA, 2USDA-ARS, Byron, GA 31008, USA, 3Department of Horticulture, University of Georgia, Griffin, GA, 30223, USA, 4Department of Entomology, University of Georgia, Athens, GA, 30602, USA, 5IFAS, University of Florida, Lake Alfred, FL, 33850, USA, 6Agricultural and Applied Economics, University of Georgia, Athens, GA, 30602, USA.

Root- knot (Meloidogyne incognita) and ring (Mesocriconema xenoplax) nematodes are two economically important pests of peach in the U.S. Pre-plant soil fumigation with 1, 3-dichloropropene is commonly used to manage PPNs, mainly root- knot and ring nematodes in peach orchards in the Southeast. Due to environmental or regulatory concerns, alternative control methods are needed, especially nematicidal products that can be applied post-plant to extend the productive life of peach. Fluensulfone, a non-fumigant nematicide
and, entomopathogenic nematodes, *Steinernema carpocapsae* may have potential for post-plant application to suppress the nematode populations. Comparative efficacy of fluenosulfone and *S. carpocapsae* was evaluated in two greenhouse studies during 2019. Lovel peach seedlings were planted in 15 cm-diam-pots containing a greenhouse soil mix and inoculated with 2,000 ring nematodes plus 20,000 root-knot nematode eggs. Five treatments included fluenosulfone (at a lower rate of 4 liters/ha), *S. carpocapsae* (1 million nematodes/pot), *S. carpocapsae* plus galleria larva (1 million nematodes plus 2 galleria/pot), and non-treated controls with or without root-knot and ring nematodes. All the treatments were applied 7 days after nematode inoculation, and the experiment was arranged in a randomized design with six replications. Population densities of root-knot and ring nematodes were determined 30 and 60 days after treatment (DAT). Data from both greenhouse trials were then pooled and percentage reductions in nematode populations relative to the control (with no PPNs) was calculated by using formula: \((A-B)/A\times(100))\). Where \(A=\) mean number of nematodes from no-PPN control treatment and \(B=\) mean number of nematodes from each treatment. Since root-knot nematodes did not survive in this experiment, only ring nematode data were presented. We found that the application of *S. carpocapsae* nematodes plus galleria larvae caused comparatively higher percent reduction in populations of ring nematodes (33%) than the application of fluenosulfone (19%) and Sc nematodes alone (17%) at 30 DAT. However, at 60 DAT, fluenosulfone (50%) was comparatively more effective than *S. carpocapsae* nematodes alone (33%) and *S. carpocapsae* nematodes with galleria larvae (29%) in reducing ring nematodes. Although, fluenosulfone demonstrated potential as a post-plant nematicide to control ring nematodes, more studies are needed to confirm these results and therefore, we are currently repeating this trial in the greenhouse.

**METABARCoding INVENTORY OF CAMBRIDGE BAY Tundra System Reveals Highly Endemic Nematode Communities.** Jorna, Jesse¹, B. Vandenbrink², B. Adams²³, I. Hogg⁴, and D. Wall⁵. ¹Brigham Young University, Provo, UT, ²Canadian High Arctic Research Station, Cambridge Bay, Nunavut, ³Monte L. Bean Museum, Provo, UT, ⁴Colorado State University, Fort Collins, CO.

Biodiversity assays of High Arctic tundra systems are rare in the current literature, though these systems harbor significant amounts of the worlds micro-invertebrate diversity and biomass which is important for ecosystem functioning. Increasing human exploitation of these regions could have significant consequences for the ecology of these regions, but current diversity and function is often undescribed. Indigenous knowledge of these ecosystems provides a baseline to inform landscape management, but taxonomic knowledge of soil biota is limited. This study provides the first genetic inventory of micro-invertebrate diversity in the Canadian High Arctic tundra near Cambridge Bay, Nunavut. Six soils of two broadly defined ecotypes (mineral and humic) were inventoried by DNA extraction and subsequent metabarcoding sequencing using 18S primers. A total of 361 ASVs were identified and were assigned to closest matching order, mostly comprising of members of the *Nematoda* and *Arthropoda* phyla. Humic soils showed higher overall richness and diversity and had a larger proportion of ASVs exclusively assigned to this soil type. Most nematode taxa were highly endemic to a single location or exclusive to one soil type, and generally more abundant in mineral soils than in the humic soils which were arthropod-dominated. This study provides a first inventory of the highly endemic communities at a High Arctic tundra site, with important suggestions for future genetic studies of this ecosystem.

**DIFFERENTIAL EFFECTS OF FLUOPYRAM AND ABAMECTIN ON BELONOLAIMUS LONGICAUDATUS AND MELOIDOGYNE GRAMINIS IN VITRO.** Kammerer, Christian¹, G. Alake¹, and W. T. Crow⁴. ¹Entomology and Nematology Dept., University of Florida, Gainesville, FL 32611.

*Meloidogyne graminis* and *Belonolaimus longicaudatus*, grass root-knot nematode and sting nematode respectively, are two of the most important nematodes that damage warm season turfgrasses on golf courses and athletic fields in the southeastern U.S. Turfgrass managers commonly use nematicides for managing these nematodes; abamectin and fluopyram are currently the most often used turfgrass nematicides. The objective of this study was to determine the relative short-term (72 hours and less) effects of these two nematicides on the motility and mortality of *M. graminis* and *B. longicaudatus in vitro*. For the experiment, nematodes were placed in cell culture wells and exposed to different concentrations of abamectin and fluopyram that bracketed the estimated highest rate the nematodes would be exposed to from field applications of the highest labeled rate for either 1 hr, 24 hr or 72 hr. At each time interval nematode motility and mortality were evaluated. Motility was the percentage of the nematodes that were expressing movement. After evaluating motility, sodium hydroxide was added to each well to stimulate movement in nematodes that were lethargic but not dead. The percentage of nematodes not exhibiting movement after exposure to sodium hydroxide was used to evaluate mortality. Abamectin had rapid effects on *M. graminis*, 72% reduction in percent motility after 1 hr exposure at 1 ppm; fluopyram effects on *M. graminis* motility were only observed at rates >2 ppm at 1 hr exposure time. Motility effects of either nematicide, based on either ppm or time of exposure, were greater on *M. graminis* than on *B. longicaudatus*. Mortality effects from either nematicide were more influenced by time of exposure than by rate of exposure for both nematodes and were greater on *M. graminis* than *B. longicaudatus*. Fluopyram had greater effect on percent mortality (98% and 91% mortality at 72-hr exposure of 16 ppm to *M. graminis* and *B. longicaudatus*, respectively) than abamectin (54% and 27% mortality at 72-hr exposure of 16 ppm to *M. graminis* and *B. longicaudatus*, respectively). Knowledge of the responses of the different nematicides to the nematodes in *M. graminis* and *B. longicaudatus* respectively) promotes further understanding of nematicide responses in the field, and in selecting optimum nematicide programs for the major nematodes present in each field.

**FIRST REPORT OF SEVILLE ROOT-KNOT NEMATODE, MELOIDOGYNE HISPANICA (NEMATODA: MELOIDOGYNIDAE) FROM NORTH AMERICA.** Kantor, Mihail¹, Z. Handoo¹, S. Subbotin²³, A. Skantar⁴ and P. Vieira⁴. ¹Mycology and Nematology Genetic Diversity and Biology Laboratory, USDA, ARS, Northeast Area, Beltsville, MD 20705, USA, ²Plant Pest Diagnostic Center, California Department of Food and Agriculture, Sacramento, CA 95832, USA, ³Center of Parasitology of A.N. Severtsov Institute of Ecology and Evolution of the Russian Academy of Sciences, Moscow 117071, Russia, ⁴USDA-ARS, Molecular Plant Pathology Laboratory, Beltsville, MD, 20705-2350, USA, ⁵School of Plant and Environmental Science, Virginia Tech, Blacksburg, VA, 24061, USA.

*Meloidogyne hispanica* Hirschmann, 1986 specimens were recovered in 2019 from soil samples collected from a corn field located in Pickens County, South Carolina, USA. A high number of *M. hispanica* juveniles were recovered through sieving and sugar centrifugal
flotation method from rhizospheres of corn plants. Extracted nematodes were examined morphologically and molecularly for species identification which included sequence alignments and phylogenetic estimation using statistical parsimony of ITS rDNA, D2-D3 of 28S rRNA and intergeneric COII-16S gene region of mtDNA. The molecular analysis separated the South Carolina M. hispanica population from other related species and clustered with sequences of M. hispanica from Portugal and Australia. The morphological examination and the morphometric details of the specimens were consistent with the original description of the type material specimens and indicated that the specimens of root knot juveniles were M. hispanica.

**DISTRIBUTION AND MANAGEMENT OF PLANT PARASITIC NEMATODES IN MID-ATLANTIC SOYBEAN PRODUCTION. Kessler, Alexandra C. and A.M. Koehler.** University of Delaware Department of Plant and Soil Sciences, Georgetown, DE 19947.

Plant parasitic nematodes are persistent but often undiagnosed, pests of soybeans in the Mid-Atlantic. Sandy soils throughout the region favor numerous nematodes including Soybean Cyst Nematode (SCN, *Heterodera glycines*) and Root Knot Nematode (RKN, *Meloidogyne incognita*). For decades, genetic resistance from the P188788 resistance gene has been the primary SCN management strategy; but surveys conducted across Delaware and Maryland in 1993 and 2009 indicated elevated reproduction on this resistance source. To improve understanding of current distributions and populations, a new set of surveys was initiated across Delaware and Maryland in 60 locations in 2019 and 35 locations in 2020. Within sites sampled in 2019, SCN was recovered from 27% of fields, RKN from 17%, Lesion nematode from 60%, and Dagger nematode from 17%. In 2020, SCN was recovered from 54% of fields, Lesion nematode from 80%, and RKN from 29%. In addition to the surveys, two seed treatment efficacy trials were conducted in 2020 in a field with confirmed SCN. The first trial evaluated two soybean nematicide seed treatments, ILEVO (fluopyram) and Saltro (pydiflumetofen), compared to non-treated plain seed, for stand emergence, control of SCN, and yield differences. A second trial that was part of a multi-state coordinated seed treatment trial assessed six nematicidal seed treatments compared to plain seed and seed with only fungicide and insecticide base treatments. In both trials, soil samples were collected prior to planting and at harvest. Soil samples from the first trial were assessed for second stage SCN juveniles (J2s), while SCN eggs were counted for the second trial. Forty days after emergence, SCN females were evaluated by destructively sampling five plants per plot and conducting a root-blasting protocol to collect females for visual enumeration. Yield data was collected by harvesting the center two rows of each plot. In the first trial, baseline SCN populations ranged from 820-1,000 J2s per 500 cc soil. At the 40 days after emergence interval, Saltro treated plants had significantly lower (p=0.03) cysts recovered than ILEVO or non-treated seed. Yield differences were not observed. Initial egg counts across treatments in the second trial ranged from 28,292-41,500 per 250 cc of soil. Significant differences in cyst recovery, percent egg reduction, or yield were observed. The most notable effect in both trials was increased percent emergence in treated seed. Nematode distributions are inherently patchy, and these trials will be replicated in future years to continue to assess seed treatment performance. Surveys have confirmed widespread nematode distribution across the Mid-Atlantic and management strategies are needed to mitigate yield losses.

UNDERSTANDING THE MECHANISMS OF SOIL-FUNGUS-SOYBEAN CYST NEMATODE EGG INTERACTIONS. Kim, Donggyu1, S. Chen1, and K. Bushley2. 1Plant Pathology, University of Minnesota, Saint Paul 55108, 2Plant and Microbial Biology, University of Minnesota, Saint Paul 55108.

A diverse community of soil fungi antagonize the soybean cyst nematode (SCN; *Heterodera glycines*) through direct parasitism, secretion of nematostatic and/or nematotoxic secondary metabolites, or a combination of both. Characterizing the dynamics of fungal antagonism towards SCN, and conversely the molecular responses of SCN to fungal antagonism, may help better understand the involved mechanisms and targeted molecular processes, and lead to the formulation of more effective fungal biocontrol agents or biopesticides. As established bioassays quantify the antagonistic properties of fungal isolates only at an arbitrary endpoint of an otherwise dynamic interaction, inspecting fungus-SCN interactions at multiple time points using complementary approaches is critical in painting a fuller picture of the roles of direct parasitism and secondary metabolites during the process. To this end, a combined microscopic and transcriptomic approach was employed to understanding the dynamics of fungus-SCN egg interaction during a time-course of infection. Clean SCN eggs were placed on fungal colonies and harvested at 1-, 3- and 5-days post-inoculation for RNA extraction. Fluorescent labeling at the same time points was conducted with the non-specific cellulose and chitin stain Calcofluor White M2R and DNA-intercalating cell death stain propidium iodide. Fluorescent labeling of fungal structures and nematode cell death within SCN eggs, in combination with transcriptomic analysis of unhatched SCN juveniles, was used to compare the infection process and mechanism of antagonism between two representative fungal isolates (*Pochonia chlamydosporia* and *Ilyonectria sp.*) towards SCN eggs. Fluorescence microscopic observations and quantification revealed distinct rates of SCN egg infiltration and nematode cell death induced by the fungal isolates. Analyses of differentially expressed nematode transcripts indicated drastic changes in cellular and metabolic processes resulting from these interactions. Pairwise comparisons between fungal treatment groups further uncovered unique transcripts that support known fungal antagonism mechanisms, as well as isolate-specific nematode stress responses. This research will further our understanding of fungus-nematode interactions and help identify potential targets of fungal antagonism in SCN.

**THE HOST-SPECIFIC IMPACT OF ROOT EXUDATES ON POTATO CYST NEMATODE, GLOBODERA PALLIDA. Kud, Joanna1, S. S. Pillai1, A. Caplan1, J. Kuhl2, F. Xiao3, and L. M. Dandurand4. 1Entomology, Plant Pathology & Nematology, University of Idaho, Moscow, ID, 83844, USA. 2Department of Plant Sciences, University of Idaho, Moscow, ID 83844, USA.**

The potato cyst nematode (PCN), *Globodera pallida*, is an important soil-borne pathogen that threatens the $4 billion US potato industry. The life cycle of this plant parasitic nematode begins with dormant eggs in the soil that hatch only once on exposure to cues released by host roots. A sophisticated synchronization of hatching with the presence of signals from the host roots may be an adaptive survival mechanism for this hyperspecialized parasite which has a narrow host range. Because of its ability to remain dormant in the absence of its host, PCN can persist in infested fields for decades; making management of this nematode challenging. Besides hatching factors, root exudates are a rich source of other biologically active components that plants use to shape their local rhizosphere. The composition of
EFFECTS OF PLANTING DENSITY ON LITCHI TOMATO (Solanum sisymbriifolium) TRAP CROP EFFICACY AGAINST THE TOBACCO CYST NEMATODE, Globodera tabacum. LaMondia, James A., and L. M. Dandurand. The Connecticut Agricultural Experiment Station Valley Laboratory, Windsor, CT 06095, University of Idaho, Moscow, ID 83844.

The effects of Litchi tomato (Solanum sisymbriifolium) on reproduction of the tobacco cyst nematode, Globodera tabacum (TCN), were compared at two different planting densities to nematode-resistant or -susceptible cigar wrapper tobacco (Nicotiana tabacum) and a nonhost oat crop. Field plots 5-m x 10-m, naturally infested with various densities of TCN, were transplanted with nematode-susceptible shade tobacco (cv. ‘8212’), nematode-resistant broadleaf tobacco (cv. ‘B2’), litchi tomato or drilled with a non-host oat crop. High- or low-density litchi tomato plots consisted of three rows 0.9 m apart with plants spaced every 0.6 m within rows or two rows per plot 1.8 m apart with plants at 1.2 m spacing within rows, respectively. Tobacco was transplanted at the same spacing as the high-density litchi tomato plots. Plots were transplanted on 4 June 2020. Tobacco plants were harvested after 10 weeks, and litchi tomato plants were mowed to 15 cm in height after 8 weeks and tilled after 12 weeks. TCN densities were determined before planting and again after harvest and rototilling soil by soil determined at 40× magnification. Nematode reproduction as determined by the ratio of the final (Pi) to initial (Pi) populations differed significantly between treatments (P < 0.003). Pi/Pi ratios were 1.39, 0.31 and 0.53 for susceptible tobacco, resistant tobacco, and oats, respectively. Litchi tomato Pi/Pi ratios were 0.11 and 0.12 for the high-density and low-density plantings, respectively. Litchi tomato resulted in the greatest reduction in nematode populations regardless of planting density. These results are consistent with previous research that litchi tomato stimulates tobacco cyst nematode hatch better than resistant or susceptible tobacco but does not allow significant nematode reproduction in roots, indicating that it may be an effective trap crop for management of cyst nematodes such as G. tabacum or G. pallida. The efficacy of even lower density plantings or shorter cropping periods remains to be determined.
Jasmonates (JA; jasmonic acid and its derivatives) are responsible for regulating diverse defense and developmental processes in plants. Studies have demonstrated that exogenous application of JA in plants can induce systemic resistance against various plant pathogens. Thus this study was planned to investigate the effects of different concentrations (0, 10, 50, 100, 1000, and 5000 µM) of a JA derivative, methyl jasmonate (MeJA), by seed priming (S) for 24 hours, foliar spray (F), and their combination effect (S + F) on Meloidogyne incognita parasitism in Glycine max (Pioneer P25T09E). The MeJA primed and unprimed (for foliar application) soybean seeds were planted in 500 cm³ styrofoam cups in a randomized block design with five replications in the greenhouse. Methyl jasmonate foliar spray was applied at the two trifoliate stage until runoff 24 hours prior to nematode inoculation. All plants were inoculated with 3,000 M. incognita eggs near the root systems. Root and leaf samples from the plants were collected pre-inoculation (0 day post inoculation i.e., 0 dpi), 1 dpi, 3 dpi, and 6 dpi for RT-qPCR analysis of the genes associated with the JA signaling pathway. Plant growth parameters, nematodes root penetration, and galling were assessed by destructive sampling at 15 dpi. Data were analyzed with SAS 9.4 using PROC GLIMMIX and LS-means were compared using Tukey-Kramer's method (P ≤ 0.05). In the study, the variation among different MeJA concentrations were not statistically significant thus, MeJA concentrations were combined for data presentation. Seed priming with MeJA had negative effect on seed germination, growth, and development of the seedlings. The growth and development of the seedlings were significantly lowered compared to the untreated control. The height of the plants were reduced by 46% and 42%, shoot fresh weight by 55% and 49%, and root fresh weight by 43% and 38% by seed priming (S) and combination treatment (S + F) respectively compared to the control. In the RT-qPCR analysis, GhLOX1 and GhOPR3 genes correlating to JA signaling pathway were observed to be upregulated (>1.5 fold) at 3 dpi and 6 dpi compared to the control. Numerically, all the MeJA applications (S, F, and S + F) reduced M. incognita nematode root penetration and development at 15 dpi; however, only the foliar application significantly reduced nematode density (55 M. incognita /gram root) compared to the control (87 M. incognita /gram root). At 15 dpi, M. incognita nematode population density in the roots was reduced by 29%, 32%, and 37% in plants treated with combined (S + F), seed priming (S), and foliar (F) treatment, respectively compared to the control. Greenhouse trials are ongoing to determine the effect of the MeJA treatments on nematode population and plant growth at 35 dpi. The overall results to date indicated that exogenous application of MeJA can induce JA signaling pathway impairing M. incognita infection in G. max.

NEMATODE MANAGEMENT IN FLORIDA SWEET POTATO USING NON-FUMIGANT NEMATICIDES. Liu, Chang¹, and Z. J. Grabau.¹ Entomology and Nematology Department, University of Florida, Gainesville, FL 32611.

Southern root-knot nematode (Meloidogyne incognita) is the most important nematode species affecting sweet potatoes in Florida. In 2018, 2019 and 2020, field trials were conducted at Live Oak, Florida to test the efficacy of fluazaindolizine (Salibro), fluopyram (Velum), oxamyl (Vydate L), and 1,3-Dichloropropene (Telone II) for managing root-knot nematode on sweet potato. Six treatments were applied: 1) Salibro 30.7 oz/A, 2) Salibro 61.4 oz/A, 3) Salibro 30.7 oz/A + Vydate L 128 oz/A, 4) Telone II 8 gal/A, 5) Velum 6.8 oz/A, and 6) Vydate L 128 oz/A. Telone II was applied as a broadcast shank application 3-4 weeks before planting. The other treatments were soil-directed broadcast applications approximately 1 week before planting, except that Velum was applied as a drench in 2020. Moderately resistant cultivar ‘Covington’ was used in 2018, and susceptible cultivars ‘Bearegard’ and ‘Orleans’ were used in 2019 and 2020, respectively. Tubers were dug, sorted into marketable and unmarketable categories, and weighed to assess yield. Soil samples were taken at midseason (approximately 2 months after planting) and at harvest, and nematodes were extracted and assessed under microscope. In 2018, initial nematode pressure was moderate with 180 juveniles/100 cm³ soil. No treatment effects were observed on root-knot nematode abundance at mid-season. Treatments with Salibro significantly reduced (P < 0.05) root-knot nematodes at harvest. Only Telone II increased (P < 0.05) total yield, and both Telone II and Salibro at 61 oz/A increased (P < 0.05) marketable yield. There was low initial nematode abundance in both 2019 and 2020, with 4 and 14 juveniles/100 cm³ soil respectively. In 2019, treatments with Vydate L, Telone II, and Salibro at 61.4 oz/A reduced (P < 0.05) root-knot nematode populations at midseason, but there were no differences at harvest. Treatments had no effect on total yield, but treatments with Vydate L increased (P < 0.05) marketable yield. In 2020, only Telone II decreased (P < 0.05) root-knot nematode abundance at mid-season, and only Telone II increased (P < 0.05) total yield and marketable yield. Results suggested that Telone II is the most consistent option for root-knot nematode control on sweet potatoes, but that Salibro, Vydate L or combinations of the two products can also be effective.

COTTON TOLERANCE AGAINST ROTYLENCHULUS RENIFORMIS EMPLOYS JASMONATE SIGNALING IN ROOT HAIR DEVELOPMENT. Liu, Wenshan, K. Gattoni, A. Adhikari, and SW. Park. Department of Entomology and Plant Pathology, Auburn University, Auburn, AL 36849, USA.

Plant parasitic nematodes (PPN) are microscopic soil herbivores that cause damages to many economic crops. Plants in turn activate R-gene mediated disease resistance and reactive oxygen species (ROS) bursts that subsequently trigger hypersensitive response (HR), a rapid programmed cell death at the sites of infection. However, molecular mechanisms underlying PPN-dependent HR activations is mostly unknown. To investigate if and/or how host plants develop HR against PPN infections, we employed a confocal microscope analysis and monitored real-time interactions between Rotylenchulus reniformis and three cotton germplasms: Lonren-1 (known to confer HR), Barbre-713 (tolerant line) and SureGrow-747 (susceptible line). However, none of those cotton plants appeared to develop HR upon R. reniformis infections. In fact, Lonren-1 did not accumulate H₂O₂, which is often used as a cellular marker of HR. Interestingly, we observed that Barbre-713, a tolerant line, develop a larger number of root hairs, comparing to SureGrow-747 and Lonren-1, allowing us to alternatively hypothesize that root hair growth and/or development are critical in plant tolerance/resistance against PPN. In this context, mutant plants disrupting salicylic acid defense responses (npr1) grow rather longer and more numbers of root hairs, whereas a jasmonate signaling mutant (cpp20-3) suppresses root hair growth, as PPN infections upregulate jasmonate biosynthesis pathway especially LIPOXYGENASES but not OXOPHYTODIENOATE-REDUCTASE 3. Together, these findings underpin potential, important roles of OPDA (12-oxo-phytodienoic acid) signaling in plant defense responses against PPN. Though, further study will be needed to assess if heightened jasmonate signaling confers increased plant protection against PPN and herbivory attacks.
EFFECTS OF SEASONAL FLUCTUATIONS OF EDAPHIC FACTORS ON VERTICAL DISTRIBUTION OF PLANT-PARASITIC NEMATODES IN VEGETABLE FIELDS OF SOUTH GEORGIA. Marquez, Josiah1, P. M. Severns2, and A. Hajihassani2. 1Department of Plant Pathology, University of Georgia, Tifton, GA 31794. 2Department of Plant Pathology, University of Georgia, Athens, GA 30602.

Plant-parasitic nematodes (PPNs) can migrate vertically to cope with extreme winter and summer conditions. This study aimed to understand how seasonal fluctuation in edaphic factors associates with the vertical distribution of PPN communities in different vegetable cropping systems of South Georgia. Composite soil samples were taken from 3 random locations in 6 different vegetable fields representing 4 cropping systems (plastic-bed vegetable rotation; bare-ground cucumber and row crop rotation; and plastic-bed watermelon and row crop rotation) at monthly intervals from 5 different soil depths (0-15, 15-30, 30-45, 45-60, and 60-75 cm) from March 2020 to February 2021. The incidence (%), mean, and maximum relative abundance (nematodes per 100 cm³ of soil) of PPNs detected consisted of Meloidogyne spp. (41.9, 9, 5520), Mesocriconema spp. (45.1, 24, 744), Nanidorus spp. (26.2, 2, 64), Helicotylenchus spp. (16.2, 2, 236), Hoplolaimus spp. (7.1, 1, 144), Pratylenchus spp. (4.4, <1, 44), Tylenchorynchus spp. (0.9, <1, 4), Xiphinema spp. (0.2, <1, 3), and Belonolaimus spp. (0.3, <1, 16). Principal component analysis suggested minimal seasonal variation among most edaphic factors (sand, clay, gravimetric soil moisture, volumetric soil moisture, bulk density, total porosity, water-filled porosity, and air-filled porosity). However, soil temperatures at 5, 10, and 20 cm depths did vary seasonally with the first 0-5 cm depth showing the greatest seasonal fluctuation. A generalized linear mixed model found interaction between region, month, and soil depth (P < 0.001) regimes among Meloidogyne spp., Nanidorus spp., and Helicotylenchus spp. Non-metric Multidimensional Scaling analysis suggested that latitude and soil temperature were associated with nematode community differences between fields in the north (Crisp and Sumpter counties) and south (Grady, Brooks, and Lowndes counties) regions. Indicator Species Analysis found Meloidogyne spp. as an indicator of the south region (P < 0.001), while all other PPNs were indicators of the north region (P < 0.05). Meloidogyne spp., Helicotylenchus spp., and Hoplolaimus spp. were indicators of the 15 cm depth, while Nanidorus spp. and Mesocriconema spp. were indicators of the 30 and 45 cm depth (P < 0.05), respectively. Patterns of vertical migration were limited to the cold months of February and April within the 0-45 cm depth for Meloidogyne spp. and Nanidorus spp. in the south region and 0-30 cm in the north region for Nanidorus spp. These results suggest that vertical migration is not a concern in the summer but should be considered by growers in the early spring when sampling or applying fumigants/nematicides.

SPECIES IDENTITY AS A DOMINANT DRIVER FOR THE ASSEMBLY OF NEMATODE GUT MICROBIOMES IN THE DRY VALLEYS OF ANTARCTICA. McQueen, J. Parr1, K. Gattoni1, E. Gendron1, P. Sommers2, J. Darling2, S. Schmidt1, and D. L. Porazinska1. 1Department of Entomology and Nematology, University of Florida, FL 32611, 2Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, CO 80303.

The knowledge of nematode gut microbiomes holds the potential to better understand basic nematode ecology, including nematode feeding habits. Recent work examining the gut microbiome of C. elegans has indicated the presence of a species-specific microbiome that is conserved among individuals collected from a wide range of habitats. However, the knowledge of how these microbiomes assemble and how they differ from other nematode species is extremely limited. Microbial mats within Antarctic Dry Valleys provide a simple and tractable natural ecosystem with exactly two morphologically and phylogenetically distinct nematode species (bacterivorous Plectus murrayi and omnivorous Eudorylaimus antarcticus). The main objectives of this study were to: 1. characterize gut microbiomes of the two nematode species, and 2. examine potential factors that could play a role in the assembly of these gut microbiomes. We collected three replicate samples of two types of coexisting cyanobacterial mats (Black and Orange) residing within four streams (Canada, Bowles Creek, Delta, and Von Guerard) across a biogeochemical and geographical gradient in Taylor Valley, Antarctica. For all 24 mat samples, 10-12 individual hand-picked nematodes of each species and the mats they inhabited were processed for 16S rDNA metabarcoding to characterize bacterial communities. We hypothesized that: 1. Microbial communities of mats would be distinct from the guts of both nematode species, 2. Gut microbiomes of the two nematode species would be distinct from each other, and 3. Gut microbiomes would be more explained by nematode identity than by environmental characteristics. To test these hypotheses, we used generalized linear models to test for differences in alpha diversity (e.g., richness and Shannon index) and PERMANOVAs for community composition (e.g., Bray-Curtis). Sequencing data confirmed that Black and Orange microbial mats represent two dissimilar food sources that can be distinguished by different characteristic cyanobacteria (Black by Nostoc and Orange by Phormidium). Gut microbiomes of P. murrayi were less diverse than the mat they were collected from (p < 0.05), and E. antarcticus guts were less diverse than both P. murrayi and mat communities (p < 0.05). No variation of alpha diversity was observed in nematode guts between mat type or stream (p > 0.17). Community composition showed that gut microbiomes were more similar to each other than to mats (p < 0.05). In contrast to mats, cyanobacteria comprised a minor component of both nematode species’ guts (p < 0.05), while other bacterial phyla were enriched in only one nematode species (e.g., Bacteroidetes in P. murrayi, p < 0.05 and Proteobacteria in E. antarcticus p < 0.05), but there was no effect of mat type or stream. Overall, results from this simplified ecosystem indicate the possibility that nematode species identity, and therefore host ecology, is the dominant driver of the gut microbiome assembly.

PLANT AND ROOT-KNOT NEMATODE CO-EXPRESSION NETWORKS OF DIURNALLY REGULATED GENES IMPLICATE METABOLIC PATHWAY. Mishra, Shova1, O. Salichs1, and P. M. DiGennaro1. 1Department of Entomology and Nematology, University of Florida, Gainesville, FL 32611.

Obligate parasites like root-knot nematode (RKN; Meloidogyne spp.) communicate intimately with their host to establish and maintain specialized feeding cells. They likely regulate this interaction by monitoring host biology and behavior. As plant gene expression and biology vary temporally, RKN gene transcription and interactions are likely to follow similar patterns. Here, we aim to interrogate such interactions of the root-knot nematode feeding site within a period of 24 hours to better define gene sets and metabolic pathways regulated during the interaction in the context of plant diurnal rhythms. We profiled RKN and plant transcripts over a period of 24 hours and identified approximately 1,000 differentially expressed genes (DEG) in nematode and model host Medicago truncatula with majority of DEG occurring at the middle of the dark period. Differentially expressed genes of both nematode and plant are of interest.
to identify potential pathways that are central to compatible RKN-host interactions. Therefore, to redefine the genes and characterize the most interacting pathways we developed co-expression patterns between nematode and plant DEG. This analysis revealed *M. hapla* genes encompassing a broad range of biological functions including endopeptidase inhibitory activity, oxidation-reduction process and *M. truncatula* genes involved in defense responses. Interestingly, 5 of 33 plant genes linked to nematode genes are associated with the phenylpropanoid metabolic pathway. The phenylpropanoid pathway produces secondary metabolites including phenolics, flavonoids that act as a defense response to biotic stress. We further examined if this pathway interacts in a similar pattern in another compatible host, tomato, by quantifying phenolics and flavonoid compounds. Both compounds showed temporal variation in production with higher production during day compared to night in uninoculated but not in inoculated plants. However, during the dark period, there was an increase in flavonoid content in infected plants indicating that plants responding to increased nematode activity at night. This study elucidated pathways that are involved in nematode-host interaction and implicated some potential plant pathways via co-expression gene network analyses that could be targeted to develop a management strategy via tolerance or resistance.

**DECIPHERING THE MECHANISMS OF SOYBEAN CYST NEMATODE ADAPTATION TO THE NON-HOST CROP PLANT TOMATO.** Mitchell, Makayla1, B. Averitt1, M. Kantor2, T. L. Niblack1, Z. Handoo3, and M. G. Mitchum1. 1University of Georgia, Dept. of Plant Pathology and Institute of Plant Breeding, Genetics, and Genomics, Athens, GA 30602, 2USDA-ARS, Mycology and Nematology Genetic Diversity and Biology Laboratory, Beltsville, MD 20705, 3Ohio State University, Dept. of Plant Pathology, Columbus, OH 43210.

Soybean is the major host crop for soybean cyst nematode (SCN) *Heterodera glycines*, a billion-dollar yield robber widespread throughout soybean-producing areas of the United States. SCN has a host-range that extends to 23 plant families, mostly legumes in the plant family Fabaceae, including at least 116 weed species. Non-hosts or poor hosts for SCN include corn, wheat, rice, cotton, peanuts, tomato, among others. Little is known about nonhost resistance to SCN or how readily SCN can adapt and reproduce on non-related crop species. A lemon cyst nematode isolated from a field in southeastern Missouri in 1991 by Drs. Allen Wrather and Terry Niblack was determined to reproduce on tomato and soybean. Since then, this population has been independently maintained on soybean (TN2-S) and tomato (TN2-T) for twelve generations per year in the greenhouse to develop highly inbred populations. In this study we first confirmed this lemon cyst nematode species is *H. glycines* by morphometric analysis and molecular identification. Next, we explored the ability of TN2-T to evade or overcome nonhost resistance mechanisms in tomato by comparing rates of hatch, penetration, development, and reproduction on soybean and tomato with that of PA3, a known *H. glycines* population unadapted to tomato. Our results confirmed that tomato is a poor host for PA3; however, several egg-laying females were recovered. In contrast, the tomato-adapted TN2-T population reproduced well on both soybean and tomato. Hatch assays were then conducted to determine if PA3 and TN2-T hatch rate differs in response to tomato and soybean root diffusate. Interestingly, TN2-T, but not PA3 eggs were stimulated to hatch in response to tomato root diffusate whereas both populations were responsive to soybean root diffusate at some level. Tomato penetration assays showed that both TN2-T and PA3 second-stage juveniles can penetrate tomato roots; however, PA3 exhibited a higher percentage of male development and visible necrosis at feeding sites, whereas TN2-T development progressed unimpeded. Taken together, these results reveal potential non-host resistance mechanisms of tomato to SCN and opens the door for future work to determine the underlying molecular basis for SCN adaptation to non-related crop species.

**PROBING THE TRANSCRIPTIONAL AND METABOLIC BASIS OF SHMT8-MEDIATED RESISTANCE TO THE SOYBEAN CYST NEMATODE HETERODERA GLYCINES MITCHUM, Melissa1, V. Lakshman1, A. Poudel1, P. Kandoth1, and S. Roje1.** 1Dept. of Plant Pathology and Institute of Plant Breeding, Genetics, and Genomics, Athens, GA 30602, 2University of Missouri, Division of Plant Sciences and Bond Life Sciences Center, Columbia, MO 65211, 3National Agri-Food Biotechnology Institute, Mohali, Punjab, India, 4Washington State University, Institute of Biological Chemistry, Pullman, WA 99164.

Resistance to soybean cyst nematode (SCN) *Heterodera glycines* in the soybean cultivar Forrest is mediated by *rhg1-a* (SNAP18) and *Rhg4* (SHMT8). SHMT8 is a cytosolic isomerase of the enzyme serine hydroxymethyltransferase that is central to L- folate metabolism. To obtain insight into the gain in function of SHMT8 in SCN resistance, we analyzed the ways SCN affects soybean biochemical pathways in cv. Forrest and how these pathways are altered in SHMT8 mutant plants, including the SHMT8 E61K (F6266) mutant, which retains partial resistance, and the SHMT8 Q226* (F234) null mutant, which exhibits a complete loss of resistance to SCN. Synchronous nematode infection assays of soybean seedlings enriched for feeding sites were used to prepare the biological material for transcriptomic and metabolomic profiling studies at the earliest stages of infection when the resistance response is active. The major category of differentially expressed genes fall into cellular metabolism, including changes in expression of genes encoding enzymes that regulate metabolic processes related to folate metabolism, production of secondary metabolites, followed by the categories of stress- and defense-related signaling. Interestingly, several key enzymes leading to the production of plant compounds where folates act as substrates, such as amino acids and ethylene, are differentially expressed, as well as key enzymes involved in methylation. The transcriptional changes are clearly reporting perturbations to folate homeostasis. Due to their low abundance, rapid turnover, and the highly localized response in nematode feeding cells in soybean roots we were unable to detect meaningful differences in the pools of folates; however, we did measure a significant SHMT8-dependent increase in the expression of downstream pathway genes and enzymes, and metabolites including S-adenosylmethionine (AdoMet) upon SCN infection of the resistant cv. Forrest. We coupled this with Metabolon's global metabolite profiling platform to identify differentially abundant metabolites, including amino acid, lipid, nucleotide, and secondary metabolites that represent SHMT8-dependent changes in abundance with possible roles in SCN resistance. By coupling next-generation sequencing with global and targeted metabolite profiling, we now have a library of SHMT8-dependent SCN resistance-associated genes and metabolites to begin to unravel the molecular and cellular basis of resistance to SCN.

**EFFECT OF NEW NON-FUMIGANT NEMATICIDES ON THE MOTILITY AND MORTALITY OF DIFFERENT TROPHIC GROUPS OF NEMATODES.** Moreira, David, and J. Desaeger. Department of Entomology and Nematology, University of Florida Gulf Coast Research and Education Center (GCREC), Wimauma, FL 33598, United States.
Plant-parasitic nematodes cause more than $100 billion dollars per year in damage to crops (>14% global crop production). Non-parasitic, free-living nematodes are critical components of the soil food web playing important roles in nutrient cycling and retention, regulating microbial populations, decomposition and improving soil structure. Traditionally nematode management has relied on the use of soil fumigants and broad-spectrum insecticide/ nematicides, all of which are detrimental to human health and the environment. Recently, new selective contact nematicides have emerged offering safer alternatives, but little is known about their specific activity against different types of nematodes. Our main objective was evaluating the intrinsic activity of new and older nematicides in a series of laboratory-based \textit{in-vitro} assays and greenhouse-based pot assays. Different feeding groups of nematodes (bacteriophage, fungivore, entomopathogenic and plant-parasitic) were directly exposed to varying concentrations of three new non-fumigant nematicides (Nimitz®, Salibo® and Velum® Prime), a biological nematicide (Majestene®) and carbamate nematicide (Vydane® 1 L) to evaluate their effect on mortality and motility. Direct exposure to the different nematicides was conducted using 48-well tissue culture plates, at five different time points (24h, 48h, 72h, 96h, and 168h). After exposure to the different nematicides nematodes were first evaluated visually and categorized into groups: active, affected, and immobile. Living and dead nematodes were later determined by adding 1 N NaOH to each well and counting the nematodes that reacted (alive) and the nematodes that were not able to respond (dead). Plant-parasitic nematodes (PPN) evaluated were different species of root-knot nematodes (\textit{Meloidogyne arenaria}, \textit{Meloidogyne enterolobii}, and \textit{Meloidogyne floridensis}) and sting nematode (\textit{Belonolaimus longicaudatus}). Free-living nematodes (FLN) were \textit{Cephalobus sp.}, \textit{Aphelenchus sp.}, and \textit{Steinernema carpocapsae}. Results indicate an overall greater effect \textit{in-vitro} of all the nematicides on the mortality of PPN in comparison to FLN, suggesting greater selectivity of the products towards plant-parasitic nematodes. All the chemical nematicides were more effective than the biological nematicide which required much higher concentrations. Among PPN, RKN were more affected than sting nematodes and only minor differences were seen among RKN species. Velum® and Nimitz® were more effective than Salibo®, especially towards sting nematode.

INVESTIGATING THE ROLE OF ROOT LESION NEMATODES IN GINSENG. Munawar, Asifa¹, K. Jordan¹, and V. Adam¹. ¹University of Guelph, Dept. of Plant Agriculture, Simcoe, ON N3Y 4N5.

Plant parasitic nematodes (PPNs) have a major direct and indirect impact on ginseng yield and quality. PPN damage can render ginseng roots unmarketable leading to estimated yield losses of 10% and an estimated industry-wide loss of $37 million in revenue annually. Additionally, due to the damage of PPN, an estimated 36% of the total marketable roots are sold at a lower value. Among PPNs, root knot nematodes have been previously reported to cause damage on ginseng roots. Some studies from other countries have indicated the damage due to root lesion nematodes (RLNs) but there is limited information available for the role of this nematode in Ontario-grown ginseng. To determine the presence and population level of RLNs, 248 soil and root samples were collected from six year-1, and nine year-2-5 ginseng gardens across Norfolk and Middlesex County, Ontario from 2019-2020. The soil samples were processed using both Baermann Pan (BP) and centrifugal flotation method and root samples were only processed through the BP method. Low numbers of RLNs were observed in some soil (0-60/kg of soil) and root (0-18/g of root) samples of year-1 gardens. The RLNs were not observed either in soil or root samples of year-2-5 gardens. Symptoms such as rusty appearance and constrictions were observed on some year-1 root samples regardless of the presence of nematodes. To test the pathogenicity of RLN (\textit{Pratylenchus penetrans}) against ginseng, the nematodes were cultured and maintained on corn roots in Petri dishes containing B5 agar media. Ginseng plants were grown from seeds in a growth cabinet in 3.5-inch pots (3-5 seeds/pot). A set of five pots were inoculated with \textit{P. penetrans} and another set was treated with water as a negative control. Corn plants were also inoculated as a positive control. Plants were treated 30-days after seeding with approximately 230 RLNs/50 g of soil. All plants were kept at 22°C and a shade cloth was erected over ginseng plants in the growth cabinet. Plants were watered and fertilized during the experiment as needed. Nematodes were extracted from soil and root samples of all treated pots 89 days post-inoculation using the BP method. The symptoms were also recorded on the ginseng roots. All inoculated roots (100%) were found with various symptoms such as stunted tap roots, rusty, constriction, or both rusty and constriction. 85% of the control roots were found healthy and 15% of the control roots showed symptoms mentioned above. \textit{Pratylenchus penetrans} did not multiply on ginseng roots but did multiply on corn roots with a reproduction factor of 2.5 or higher. In summary, RLNs were found in low numbers in year-1 gardens. The results of the inoculation study suggested that \textit{P. penetrans}, although not parasitic to ginseng, can cause damage to ginseng roots possibly through their attempted feeding.

EVALUATION OF FLUENSULFONE IN COMBINATION WITH METAM POTASSIUM AS A BROAD-SPECTRUM SOLUTION TO CONTROL PLANT PARASITIC NEMATODES, SOIL-BORNE DISEASES AND WEEDS IN FRUITING VEGETABLES. Navia Gine, P. A.¹, and A. Hajihassani². ¹ADAMA Agricultural Solutions Ltd., Raleigh NC 27604, ²University of Georgia, Plant Pathology Department, Tifton, GA 31793.

Combinations of fumigants such as chloropicrin, 1,3-dichloropropene (1,3-D) and metam potassium/sodium have been used as a replacement of Methyl Bromide in the past 20 years in the United States as pre-plant treatments to control several pests such as nematodes, soil-borne diseases, and weeds in the production of fruiting vegetables in plastic mulch. The objective of this study is to evaluate the efficacy of fluensulfone in combination with metam potassium as a pre-plant treatment to control nematodes, soil-borne diseases, and weeds. The grower standard fumigant combination used in this study was 1,3-dichloropropene and chloropicrin 60% (Pic-Clor 60 EC) and it was shanked in the soil 12 inches deep at 21 days before planting. The combination of fluensulfone and metam potassium was tested as a tank mix and injected with drip irrigation 15 days prior planting. Trials were conducted in Thonotosassa Florida in 2018, 2019, 2020 and Tifton Georgia in 2020. Crops involved in the study were tomato, peppers, and strawberries. The most dominant nematode in tomato and peppers was \textit{Meloidogyne incognita}, and the most dominant nematode in strawberries was \textit{Belonolaimus longicaudatus}. Treatments included untreated control, metam potassium at 420 l/ha, 1,3-dichloropropene and chloropicrin 60% (Pic-Clor 60 EC) at 336 kg/ha, fluensulfone (NIMITZ) at 6 kg/ha, combinations of fluensulfone at 4 kg/ha, 6 kg/ha and 8 kg/ha mixed with metam potassium at 280 l/ha, 420 l/ha and 561 l/ha respectively. Nematode control was effective with all treatments except for the untreated control, all trials show significant differences in nematode control. In three trials nematode control of metam potassium by itself was not significantly different than the untreated control. In soil-borne diseases all treatments were effective except for untreated control and fluensulfone by itself.
In most of the trials the combinations of fluensulfone plus metam potassium were significantly better in disease control than metam potassium and fluensulfone by themselves. Combinations of fluensulfone and metam potassium had a rate effect in soil-borne disease control and in all cases showed similar level of control compared with Pic-Clor 60. Weed control was superior in all treatments that had metam potassium as a component or solo. In all trials yield data was significantly better for all treatments compared with the untreated control. In all the trials the combinations of fluensulfone and metam potassium are not significantly different in terms of yield than Pic-Clor 60. Also, in all trials, treatments with mixtures have numerically better yield than solo treatments. The combination of fluensulfone and metam potassium seems to be a very effective tool for broad-spectrum pest control as a pre-plant treatment for fruiting vegetables. This combination adds flexibility in application methods, rate combinations and pre-plant timing when compared to chloropicrin and 1,3-dichloropropene combinations.

**EVALUATION OF UREA AMENDMENTS IN MEDIA FOR QUANTIFICATION OF NEMATODE TRAPPING FUNGI. Neilsen, Lily, B. Edgar, and J. B. Kotcon.** Division of Plant and Soil Sciences, West Virginia University, 1194 Evansdale Drive, PO Box 6108, Morgantown, WV 26506.

Agar media amended with urea has been reported to improve isolation of nematode-trapping fungi, but results are inconsistent. We compared recovery of trapping fungi using several media and bait nematodes in five experiments, each with five replicate plates of each treatment examined for presence of traps after 4, 7, 10, and 14 days. In Experiment 1, trapping fungi were isolated from six soils using water agar and cornmeal agar amended with 0 and 300 mg urea/L. Experiment 2 evaluated rate of trap formation in water agar plates amended with 0, 75, 150, 300 and 600 mg urea/L and inoculated with Arthrobotrys oligospora and a Dactylaria sp., with, versus without, nematode baits (100-200 eggs of Meloidogyne incognita per plate). In Experiment 3, plates with water agar amended with 0 or 300 mg urea/L were inoculated with A. oligospora spores, and five plates of each were inoculated with bait nematodes, 0.25 g of sterile soil, or 0.25 g of nonsterile soil. Experiment 4 compared trapping rates of A. oligospora and Dactylaria sp. on water agar alone with M. incognita J2 as bait. In Experiment 5, plates with 0, 300, and 600 mg urea/L were inoculated with A. oligospora and Dactylaria sp. and inoculated or uninoculated with M. incognita eggs or raw soil. Results from Experiment 1 showed that urea increased incidence of recovery of trapping fungi from soil with water agar, but not corn meal agar. In Experiment 2, traps formed on 44 and 52 % of plates inoculated with A. oligospora and Dactylaria spp., respectively. All concentrations of urea increased incidence of trap formation compared to the unamended plates, with the maximum occurring at 300 mg/L. Addition of bait nematodes also increased incidence of trap formation. Trap formation by Dactylaria sp. was increased more by bait nematodes than for A. oligospora. In Experiment 3, urea did not significantly increase trap formation, but bait nematodes did. Traps were observed in plates amended with non-sterile soil, but not with sterile soil. The first traps of A. oligospora were observed 4 days after inoculation, whereas traps with Dactylaria sp. were not observed until 10 days after inoculation. Various nematode species were observed in most plates inoculated with nonsterile soil, but not in plates with sterile soil. In Experiment 4, Dactylaria trapped a mean of 5.8 of 10 M. incognita J2 added per plate, while A. oligospora trapped only 2.8 of 10 M. incognita J2 added. In Experiment 5, trap formation was greater with M. incognita eggs than without, and was greater with 300 mg urea/L than without, but was intermediate at 600 mg urea/L. We conclude that trap formation is stimulated by nematodes and by urea, and their effects on trap formation were additive. Additional experiments to compare trap formation with other bait nematodes are underway.

**SUPPRESSION OF SOYBEAN CYST NEMATODE (HETERODERA GLYCINES) BY COVER CROPS AND THEIR ASSESSMENT AS POTENTIAL TRAP CROPS. Neupane, Kamal and G. P. Yan.** Department of Plant Pathology, North Dakota State University, Fargo, ND 58108.

Ten cover crops species and cultivars, including alfalfa (cv. Bullseye), chickling vetch (Pulse), daikon radish (Eco-till), faba bean (Petite), flax (Carter), oilseed radish (Concorde, Control, and Image), sunn hemp, and white mustard (Master) were evaluated for their effect on a soybean cyst nematode (SCN) population (SCN103; HG type 0) from North Dakota in an outdoor microplot. Plants were grown in large pots each with 5 kg of naturally infested soil for seven weeks. Trials were conducted in 2019 and 2020, and treatments were arranged in randomized complete block design each with five replications. A local SCN susceptible soybean cultivar (Barnes) and an unplanted infested soil (fallow) were used as controls. Soil samples were collected from each pot to extract SCN juveniles and eggs to determine final population density (FPD) and population reduction (PR) for each of the treatments. All tested cover crops and fallow had significantly lower FPD than soybean in both trials. When compared to the fallow treatment, all cover crops significantly reduced the initial population density in the first trial, having higher PR values. In the second trial, all the cover crops except oilseed radish cv. Image and chickling vetch significantly reduced the nematode in the soil as compared to the fallow. The average population reductions by the cover crops ranged from 37.5% to 82.3% throughout the experiments. These experiments suggested possible impacts of cover crops on SCN biology thus reducing the population from the infested soil. Cover crops may reduce nematode population through trapping mechanism that may start with stimulating hatching and allowing juveniles to penetrate their roots without supporting reproduction. Six cover crops, including alfalfa, daikon radish, faba bean, oilseed radish (Concorde and Control), and white mustard, were further evaluated for their possible trapping mechanism using the same SCN population and controls. Cover crops along with controls were planted in two sets each using cone-containers with four replications for each treatment in a growth chamber. Plants were harvested 15 and 30 days after planting (DAP) and their roots were stained with food coloring dye to visualize the presence of nematodes inside the roots. Soil from each cone-container was also processed to quantify SCN eggs and juveniles. Faba bean had a significantly higher number of juveniles in soil and inside the roots combined than other cover crops and fallow 15 DAP, suggesting greater SCN hatching than all the other cover crops and fallow. Moreover, significantly more SCN juveniles penetrated the roots of faba bean than all other crops in the first 15 days and subsequently, those juveniles were significantly reduced 30 DAP inside the roots of faba bean without forming white females. These results indicated that faba bean cv. Petite has a great potential to serve as a trap crop for SCN management. Further evaluations will be performed to validate the obtained results.
EFFICACY OF FUMIGANT AND NON-FUMIGANT NEMATICIDES IN MANAGING ROOT-KNOT NEMATODES IN A PEPPERSQUASH PLASTICULTURE SYSTEM. N. Namdi, Ch. Chana, and A. Hajihassani. 1Department of Plant Pathology, University of Georgia, Tifton, GA 31794.

Plasticulture systems boost crop yield by enhancing temperature absorption and retaining soil moisture, fertilizers, and chemical fumigants. Vegetable growers in the southeastern USA usually utilize plasticulture over several cropping seasons to save on the cost of installation and removal of the plastic mulch. This practice, however, builds up the population of the root-knot nematodes (RKN), which can infest the crop and lead to poor growth and yield reduction. Due to this fact, fumigants are applied to the first crop, while drip-applications of non-fumigant nematicides are used in subsequent crops grown on the same plastic beds. This research was conducted in the spring and summer of 2019 and 2020 to investigate the best chemical control practice for RKN in a pepper-squash plasticulture system.

Spring treatments were soil fumigants (1,3-dichloropropene, allyl isothiocyanate, and 39%, 1,3-dichloropropene + 59.6% chloropicrin [Pic-Clor 60]), a M. incognita-resistant pepper cultivar (Carolina Wonder) and an untreated check. Fluopyram, flusulfuron, fluazindolizine, oxamyl, Burkholderia spp. strain A396 and an untreated check were the non-fumigant treatments in the summer trial. All spring treatments except allyl isothiocyanate reduced ($P < 0.05$) root galling compared to the untreated check at pepper harvest. However, the post-harvest number of second-stage juveniles of M. incognita in the soil was only lower ($P < 0.05$) for Carolina Wonder treatment than the untreated check. Though the resistant variety treatment had the lowest soil population density of M. incognita and significantly reduced root galling, it had the lowest pepper fruit yield. On the other hand, Pic-Clor 60 treatment had the highest fruit yield. All the nematicides suppressed ($P < 0.05$) root galling for the summer trial than the untreated check plots. Squash fruit yield was only significantly greater in Burkholderia spp. strain A396, fluensulfone, oxamyl, and fluopyram treatments than the untreated check. This study suggests that in a pepper-squash plasticulture system, Pic-Clor 60 is likely an ideal fumigant to apply when laying the plastic, and any of the non-fumigant treatments may be used in RKN control for the next crop.

BETTER BED WETTING VIA ASSESSMENT OF THE RADIAL SPATIAL PATTERN OF A CHEMICAL TRACER MOVING THROUGH SOIL. Noling, Joseph W, 1University of Florida, IFAS, CREC, Lake Alfred, FL, 2University of Florida, IFAS, GCREC, Balm, FL 33598.

The effects of chemical injection schedules and subsequent irrigation cycles on soil movement and spatial patterns of recently developed, nonfumigant nematicides needs to be measured to formulate recommendations that optimize nematode management in raised bed, plasticulture-based production systems. We evaluated the suitability of a water soluble, nonadsorptive chemical tracer, sodium bromide, to serve as a proxy for pesticide transport in the water content within a Florida fine sandy soil. All studies were conducted at the UF Gulf Coast Research and Education Center in Balm, FL, where raised beds were formed, covered with plastic mulch, and installed with Netafim® Streamline drip tape with 30 cm emitter spacing delivering 0.91 LPH @10 psi to stream irrigation water to both strawberry planted and unplanted rows. Distribution of drip irrigation water for the different irrigation treatments (application periods, split applications, prewetting conditions) were evaluated using sodium bromide, which was metered into the irrigation stream (7000 ppm) through one or two drip tubes per bed at various, seasonally determined irrigation schedules, water volumes, prewetting practices, and split run times. For all trials, with either single or twin drip tubes per bed, measurements of drip water dispersion was temporally measured at 11 different locations along and across the bed at points on the emitters and equidistant between emitters. At each sampling date (1, 3, and 7 DAA), soil cores were taken for bromide residue determinations using the Probinator, a tractor mounted hydraulically operated deep soil coring probe, which removed and encapsulated soil cores into a 5 cm diam x 1.2 m long acetate sleeve. Each acetate sleeve was cut into 15 cm increments and a 45cc soil subsample removed and assessed for bromide ion residue. Bromide ion concentrations in soil water solution were measured with a Thermo Fisher Scientific Orion Star+ A214 pH/ISE Benchtop ISE Meter using an Orion Star+ bromide ion electrode Model 9635BNWP and a reference electrode (Orion, Model No. 900200). The results from these studies will be presented to demonstrate whether limited outward radial expansion of the tracer from the drip emitter might identify a component cause of treatment inconsistency. The method also provides a new tool to redefine irrigation injection schedules to maximize pest exposure, and efficacy.

PRELIMINARY SCREENING OF THE EMERGING ROOT-KNOT NEMATODE MELOIDOGYNE ENTEROLOBII FOR GEORGIA, USA. Nugraha, Gema, and A. Hajihassani. University of Georgia, Dept. of Plant Pathology, Tifton, GA 31793.

Root-knot nematodes (RKNs, Meloidogyne spp.) are the most important plant-parasitic nematodes of agronomic crops in Georgia, USA. A newly emerging RKN species, previously known as the ‘guava’ root-knot nematode, M. enterolobii, has been reported in the southeastern US, including Louisiana, Florida, South Carolina, and North Carolina, yet not found in Georgia. As a part of the Focused Investigations on the Distribution and Management of M. enterolobii (FINDMe) project, the aim of this study was to investigate the presence of this species in Georgia. Between October 2019 and April 2021, 187 soil samples were received from University of Georgia Extension agents from cotton, peanut, tobacco, and several vegetable crops in 35 counties. Nematodes were extracted from soil samples using the standard flotation-sieving technique to detect RKN second-stage juveniles and then cultured by potting with tomato (Solanum lycopersicum) cv. Rutgers. After 8 to 10 weeks, female nematodes (n=3) were isolated from galled roots for genomic DNA extraction by smashing females in a 1.5 ml microcentrifuge tube followed by a freeze-thaw (95°C, 1 min). Each DNA sample was initially screened with duplex PCR method using RKN species-specific primer sets (Mi2F4/Mi1R1 for M. incognita and Far/Rar for M. arenaria or SEC-1F/SEC-1R for M. incognita and Fjav/Rjav for M. javanica). Negative samples were also subjected to DNA sequence-by-type identification for M. enterolobii detection. Out of 157 RKN-infested soil samples, 111 were successfully cultured. Most fields were infested with only M. incognita (82%) followed by a mixed population of M. incognita and M. arenaria (9%); only M. arenaria (5%); only M. javanica (1%); M. incognita and M. javanica (1%); M. arenaria and M. javanica (1%), and a mixed population of the three species (1%). Meloidogyne incognita was found in all counties sampled. With the current and past (2018) survey conducted in Georgia, a total of 623 soil samples have been analyzed, and no M. enterolobii was detected. However, further investigation will consist of sampling from other counties and host crops throughout the state.
UNDERSTANDING THE HOST-PARASITE RELATIONSHIP OF PARATYLENCHUS NANUS WITH FIELD PEA CULTIVARS. Ojha, Ekta and G. P. Yan. Department of Plant Pathology, North Dakota State University, Fargo, ND 58108.

Pin nematodes, Paratylenchus nanus, are among the most frequently occurring plant-parasitic nematodes (PPNs) in North Dakota, and previous studies showed that they negatively impact the yield of field pea cultivars. These nematodes are ectoparasitic and exist in different life stages (eggs, juveniles, and adults). They utilize their stylet to extract nutrients from root tissues and cause damage to host plants. Previous studies indicated that several species of Paratylenchus have a persistent survival stage (primarily fourth-stage juvenile) that is devoid of or has a reduced stylet which helps them maintain their population in adverse environmental conditions. It is unclear what factors are responsible for their survival in the soil without physically extracting nutrients from the host plants. Our preliminary experiments demonstrated that the fourth-stage juveniles underwent molting to develop stylet in the presence of field pea root exudates. We performed this study to understand the host-parasite relationship between P. nanus and field pea under controlled greenhouse and laboratory conditions. Soil naturally infested with P. nanus was collected to conduct greenhouse trials to evaluate the host response of 31 field pea cultivars to P. nanus. The initial population densities for the first and second trials were 600 and 1,080 nematodes/kg of soil, respectively. Plants were harvested after 11 weeks of growth, and then nematodes were extracted from soil and roots to determine the final population density. Host response was determined based on the reproductive factor (RF), which is the final nematode population density divided by the initial population density. Greenhouse trials demonstrated that cultivar Columbia showed the highest nematode reproduction with RF of 13.0, while the least nematode reproduction (RF = 1.3) was observed in cultivar Aragorn. None of the tested cultivars showed resistance (RF < 1) to P. nanus. Among all the cultivars tested, 10, 13, and 8 cultivars were classified as susceptible (RF > 4), moderately susceptible (RF = 2 to 4), and moderately resistant (RF = 1 to 2), respectively. To determine the effect of root exudates of moderately resistant and susceptible cultivars on P. nanus molting from fourth-stage juveniles to the adult stage, twenty juveniles (fourth-stage) were hand-picked and kept on glass microscope slides containing root exudates. Experiments were maintained in an incubator (22°C), and the nematodes were observed for molting in 2-day intervals for 30 days. A relatively high number of nematodes molted when kept in the root exudates of susceptible cultivars, similar to that in distilled water which was used as a control. However, retarded molting was observed in root exudates of moderately resistant cultivars, suggesting that certain compounds might have restricted the stylet development in the juveniles. These experiments, for the first time, provided us with insights into molting in pin nematodes possibly influenced by field pea root exudates. Further validation would be necessary and chemical analysis of root exudates can be promising to study this unique phenomenon in pin nematodes.

AN UPDATE OF SOME FOLIAR NEMATODES IN FLORIDA, LOUISIANA, AND NORTH CAROLINA: SPECIES DELIMITATION AND NOTES ON THEIR PHYTOPARASITIC STATUS. Oliveira, Clemens,1 S. A. Subbotin2, R. N. Inserra3, J. A. Brito4, and J. Desaeger1. 1Entomology and Nematology Department, University of Florida, Gulf Coast Research and Education Center, Wimauma, FL, 33568, USA, 2Plant Pest Diagnostic Center, California Department of Food and Agriculture, 3294 Meadowview Road, Sacramento, CA 95832-1448, USA and Center of Parasitology of A.N. Severtsov Institute of Ecology and Evolution of the Russian Academy of Sciences, Leninskii prospect 33, Moscow 117071, Russia; 3Florida Department of Agriculture and Consumer Services, DPI, Nematology Section, P.O. Box 147100, Gainesville, FL 32614-7100, USA.

In 2017-2020, nematode populations previously identified as Aphelenchoides besseyi and A. fujianensis were studied in a cooperative project. Using an integrated approach, the A. besseyi species complex contains several cryptic species: A. besseyi sensu stricto, A. oryzae, A. pseudobesseyi. A population from Florida strawberry morphologically fits the A. besseyi of both Christie and Allen and is considered the only representative of this species. A Louisiana rice population fitted the descriptions of A. oryzae of both Yokoo and Fortuner; PUS length was consistently less than one-third of vulva and anus distance (VA). Aphelenchoides oryzae, parasitising rice and other monocots, was re-established based on morphological and molecular datasets. Three populations from Florida ornamental plants (Dryopteris erythrosora, Echinacea sp, and Farfugium japonicum) differed from those of the two above-mentioned species and were described as A. pseudobesseyi. Populations previously identified as A. besseyi sensu latre from several countries were considered representatives of this new species, which usually had a large and conspicuous PUS, 8–14 μm wide and with a length greater than one-third of VA in 40-70% of studied specimens. Morphological variability made separation of A. pseudobesseyi from A. oryzae and A. besseyi unreliable without the examination of numerous specimens and molecular analysis. Aphelenchoides pseudogoodoyi, which was initially misidentified as A. fujianensis, differed from the type population of the latter species from China because it was without males, and females lacked a functional spermatheca, whereas type A. fujianensis is an amphimictic species. The Florida A. besseyi sensu stricto infected strawberry and gerbera daisy, but not soybean and alfalfa. Aphelenchoides pseudogoodoyi is mainly mycetophagous. However, localized inoculation of 300 specimens applied with filter paper adhering to the blade of the soybean leaves resulted in nematode penetration into the mesophyll with subsequent development of lesions limited to the inoculated area of the blade. Our research confirms the difficulty in the morphological separation of species previously considered as ‘A. besseyi’ detected on rice, ornamental plants, and strawberry in the Southeastern United States, which has implications for farmers, scientists, and global regulatory agencies.

POTATO EARLY DIE: RESEARCH ON MANAGEMENT ALTERNATIVES AND FUTURE INSIGHTS. Parrado, Luisa M.1, E. Cole1, and M. Quintanilla1. 1Applied Nematology Lab, Michigan State University. East Lansing, MI, United States.

The association of the root-lesion nematode Pratylenchus penetrans and the soil-borne fungus Verticillium dahliae is known as the Potato Early Die complex (PED), a disease that greatly affects potato productivity. Potato yields can be reduced up to 50% causing growers to rely heavily on chemical-based products, but the arising economic and environmental pressures are leading to the critical development of sustainable strategies to manage PED. In 2020, we evaluated two different PED management approaches: manure-based and chemical. The objective of the studies was to determine if a manure-based approach is as effective as a chemical-based approach. In the “manure-based” trial we evaluated 10 different manure-based amendments and biological antagonistic microorganisms, and in the “chemical” trial we evaluated 8 different nematicides, fungicides and bio stimulants. Each treatment had 6 replicates which were
planted in a complete randomized block design. Throughout the season, measurements regarding P. penetrans and V. dahliae density in soil, root-lesion nematode incidence in roots, Verticillium incidence in stems, plant height, PED incidence and severity, and yield were collected. In the “manure-based” trial, no significant differences were found between treatments at any point in the season regarding P. penetrans density in soil. However, poultry manure, Blend A+ MeloCon, poultry manure+ MeloCon, and poultry manure+ Vydate did keep P. penetrans populations at levels similar to the positive controls (Cruiser Maxx and Vydate). Root-lesion nematode incidence in roots was significantly lower in the poultry manure + Vydate treatment (p = 0.023). As for V. dahliae, propagule density in soil significantly decreased overtime (p < 0.0001); however, V. dahliae incidence in stems significantly increased along with the severity of the disease over time (p-value < 0.0001). Overall, treatment effectiveness remained lower than 40%. Lastly, there was an increase of 41 CWT/A with Blend A compared to the untreated control and the lowest vascular discoloration was observed in tubers treated with Blend A+ MeloCon (p-value < 0.0001). In the “chemical” trial, we found that the greatest reduction of P. penetrans in soil was with Plen-T Sweet (a carbon biostimulant) and interestingly, P. penetrans in soil increased with Vydate. As for V. dahliae, propagule density in soil significantly decreased over time whereas incidence in stems significantly increased (p-value < 0.0001) and overall, treatment effectiveness remained lower than 50%. Lastly, the highest yield was with Vydate but with only an increase of 4 CWT/A when compared to the untreated control and vascular discoloration was lowest with a combination of chemical-based products. These results allow us to conclude that a sustainable management for PED is available, but deeper research needs to be done to improve the effectiveness of such approach.

SCREENING SORGHUM/SORGHUM-SUDANGRASS HYBRIDS FOR ALLELOPATHIC EFFECTS AGAINST ROOT-KNOT NEMATODES AND THEIR POTENTIAL FOR SOIL HEALTH MANAGEMENT IN A NO-TILL AGROECOSYSTEM. Pandel, Roshan, K.-H Wang, and P. Waisen. Plant and Environmental Protection Sciences, University of Hawaii at Manoa, Honolulu, HI 96822.

Sorghum and Sorghum-sudangrass hybrids (SSgH) are used as a cover crop to improve soil health by adding soil organic matter, enhancing water conservation, and suppressing soil-borne pathogens in various cropping systems. A wide range of SSgH varieties that include forage sorghum, energy sorghum, sudangrass, and sorghum-sudangrass hybrids were examined to identify the most efficient varieties in tropical climate for 1) plant-parasitic nematode suppression, 2) soil water conservation, and 3) soil microbe enhancement. The allelopathic potential of SSgH against plant-parasitic nematodes is hypothesized to vary by variety and age. Two greenhouse tube bioassays were conducted to compare the amendments of 13 SSgH varieties to sunn hemp (Crotalaria juncea) and an unamended control against Meloidogyne incognita infection on mustard green ‘Hirayama’ (Brassica juncea) using sterile sand: soil mix. Soil was amended with shredded tissues at 1% (w/w, dry weight basis) collected from 1-, 2-, and 3-month-old SSgH tissues grown in open field. Each dibble tube was inoculated with 220 second-stage juveniles (J2) of M. incognita on the same day of soil amendment and mustard planting. In both trials, energy sorghum ‘NX-D-61’ and SSgH ‘Latte’ were most suppressive to M. incognita with lowest female per g roots 1 month later. The allelopathic effect of most varieties was not different from the non-amended control as the plant aged, except for ‘NX-D-61’ (NX2) and ‘Latte’ (LA) where 3-month-old tissue materials were still suppressive to M. incognita. A field trial was conducted at the Poamoho Experiment Station where 7 SSgH varieties were grown for 2.5 months, terminated using flail mower and eggplant were planted in a no-till system. Energy sorghum ‘NX2’ had the highest plant biomass, soil moisture, and soil microbial respiration (using Solvita CO₂-burst reader) throughout the cover crop and eggplant growing cycle. At the termination of the cover crop, NX2 also increased soil carbon and total microbial biomass (using Total Phospholipid Fatty Acids, TPLFA), although these effects dissipated at the end of the eggplant growing cycle, and the most improvement in microbial biomass was shown by LA at 3 months after growing eggplant. Canonical correspondence analysis (CCA) showed most of the soil health indicators including total PLFA, soil microbial respiration rates, soil moisture, soil carbon, nematode enrichment index, maturity index, structure index, and abundance of omnivorous nematodes were negatively related to abundance of plant-parasitic nematodes at termination of the SSgH cover cropping period. Negative relationship between root-gall index on eggplant with the above-mentioned soil health indicators was observed at 3 months after eggplant planting. These results suggested improvement of soil health by SSgH led to suppression of root-knot nematode infection on the cash crop in a no-till system. In conclusion, NX2 and LA were most effective SSgH cover crop varieties for root-knot nematode suppression and soil health management using a no-till system in Hawaii.

A METHOD FOR CONDUCTING HATCHING STUDIES WITH PRATYLENCHUS SPP. Pennewitt, Monica and G. L. Tylka. Department of Plant Pathology and Microbiology, Iowa State University, Ames, IA 50011.

Root-lesion nematodes (Pratylenchus spp.) cause yield loss in many crops. Compounds that reduce hatching may be useful for managing these nematodes by lessening nematode reproduction, lowering population densities, and decreasing damage potential. Studying hatching of migratory endoparasitic nematodes, such as Pratylenchus, is more difficult than conducting experiments with sedentary endoparasites, such as Meloidogyne and Heterodera. Swollen adult females of sedentary endoparasites produce hundreds of eggs each that can be used in experiments whereas verminiform adult females of migratory endoparasites such as root-lesion nematode produce only 1 to 2 eggs per day and fewer than 70 per female in total. The objectives of our study were to develop a method to collect large numbers of Pratylenchus eggs and to assess effects of compounds on hatching of those eggs. Cultures of Pratylenchus scribneri were maintained on root explants of sweet corn (Zea mays) growing in Pluronic gel containing Gamborg’s-B5 with vitamins. Nematodes were grown for 2 months, then the Pluronic gel was liquified by cooling to 4°C. The life stages of the nematode were separated by passing the liquified medium containing the nematodes through stacked sieves. The sieves used, from top to bottom, had porosities of 150 µm, 75 µm, 45 µm, 38 µm, 25 µm, and 20 µm. The bottom, 20-µm-pore sieve captured both second-stage juveniles (J2) and eggs. To separate the J2s from the eggs, contents of the 20-µm-pore sieve were transferred to 23-µm-pore sieves and incubated in deionized water in glass beakers on a platform shaker rotating at 50 rpm for 2 hours. The majority of J2s passed through the sieves during this time, leaving mostly eggs remaining on the sieves. Approximately 250µl of egg suspension were placed in individual wells of a 24-well plate, and the J2s present were counted using a microscope. This method reduced the number of J2s among the eggs from >500 per well to <50. The contents of the wells were transferred via pipette onto 23-µm-pore micro-sieves which were placed into individual wells of 6-well tissue culture plates containing test solutions. The plates were
incubated at 25°C for 14 days. Test solutions included deionized water, 100 ppm abamectin, 1 percent acetic acid, and 5.6 mM ZnSO₄, a hatch stimulant of H. glycines. Hatching percentages were determined by subtracting the number of J2s present among the eggs when the experiment was initiated from the number of hatched juveniles present on day 14, then dividing this number by the total number of eggs and juveniles at the end of the 14-day period. Hatching was variable (38 to 80 percent) in deionized water in preliminary experiments. Hatching was inhibited with 100 ppm abamectin and 1 percent acetic acid and was not affected by 5.6 mM ZnSO₄. This method could be used to evaluate the effects of compounds, such as active ingredients of nematode-protectant seed treatments, on hatching of Pratylenchus spp.

EXTREME PHENOTYPIC VARIABILITY IN Thelastoma spp. (NEMATODA: THELASTOMATIDAE). Phillips, Gary; E.C. Bernard, J.K. Moulton and C.T. McAllister. 1Entomology & Plant Pathology Department, University of Tennessee, Knoxville, TN 37996 and 2Science and Mathematics Division, Eastern Oklahoma State College, Ida, OK 74745.

The arthropod-symbiotic nematode genus Thelastoma contains about 91 described species, some of them not well described or described from only a few specimens. The major characteristics used to separate females are overall length, the relative locations of the secretory-excretory pore (SEP) and vulva, and the length and shape of the tail; males are distinguished by the genital papilla pattern and the presence or absence of lateral alae and spicules. We investigated the Thelastoma populations that inhabit the intestines of four spirobolid millipedes of the indigenous Florida genus Floridobolus: F. floydi, F. orini, F. penneri and Floridobolus sp. (undescribed); and Thelastoma in specimens of the spirobolid Narceus americanus from Hochotaham, Oklahoma. All known Floridobolus spp. live in restricted areas of the Florida sandhills while N. americanus is distributed throughout the eastern half of the United States. Approximately 1,540 Thelastoma individuals were extracted from 313 specimens of Floridobolus spp. and 163 Thelastoma were collected from 42 N. americanus. A total of 23 characteristics (including several ratios) were used to compare measurements of 156 individual Thelastoma nematodes from Floridobolus spp. and 59 nematodes from N. americanus (26 dagger-like tails v. 33 filiform tails). Glycerin-mounted specimens were measured exhaustively for dimensions and morphometrics, which were subjected to statistical analysis. DNA was extracted, amplified and compared for Thelastoma within each millipede genus. Body lengths, location of SEP and vulva location (V) of Thelastoma populations from Floridobolus spp. were all significantly different (p < 0.05) except for F. floydi v. F. sp. Tail shape varied widely from filiform to short conoid or clubbed within nematode populations. Although several key characters were morphometrically different, DNA analysis of the 28S D2-D3 region showed that all sequenced females from the four host Floridobolus spp. were identical. Two distinctly different male types, one large and with prominent lateral wings, the other small and without wings, were molecularly identical to each other and to the females. Thelastoma females dissected from N. americanus featured either a dagger-like tail or filiform tail; all females within a particular millipede had the same tail type. Although key characters such as nematode length, SEP location, V and tail length all differed significantly between females of the two tail types, DNA analysis using 28S D2-D3 generated identical sequences. The extreme variability in tail shape and/or size suggests more than one nematode species in each millipede genus, even though 28S D2-D3 profiles were identical within each Thelastoma group. The complete genome of Thelastoma from F. penneri has recently been sequenced and will be used to aid in the search for more discriminating molecular markers.

MI-RESISTANT TOMATOES FOLLOWED BY CONTACT NEMATICIDES OR MUSTARD SEED MEAL MITIGATED ROOT-KNOT NEMATODE DAMAGE IN CARROTS. Ploeg, Antoon and J. O. Becker. University of California, Dept. of Nematology, Riverside, CA 92521.

Root-knot nematodes (rkn) are the primary cause of plant disease problems in California’s carrot production, which accounts for nearly 90% of the US fresh market production. In 2017 about 44% of the carrot area was treated with soil fumigants. Currently, several novel nematicides are in late-stage development. The project’s objective was to evaluate a two-step method to lower the rkn population with Mi-resistant processing tomatoes, followed by applying novel non-fumigant nematicides or a botanical amendment before seeding carrots. A Meloidogyne incognita-infested sandy loam field site at the UC South Coast Research and Extension Center, Irvine, CA, was planted in spring of 2018 with processing tomato cultivars. The trial was arranged in a randomized split-plot design with 5 replications. The main treatment plots consisted of 20-ft long sections of 40-inch wide beds. Each one-half of the beds was planted with an rkn-resistant tomato, the other half with a genetically similar but susceptible cultivar. The pre-season nematode levels were 150 rkn J2/100 g soil. After harvest, the beds were disked and re-bedded in the same location as sub-treatment plots for the following carrot crop. The treatments included product-ready formulations of fluensulfone, fluopyram, fluaazindolizine, as well as oxamyl and metam sodium as standards, mustard seed meal, and an untreated control. Metam sodium (chemigation) and mustard seed meal (mechanically incorporated) were applied three weeks before seeding. All nematicides were used at the manufacturers’ recommended times and rates, suspended in 2 gal water per replicate. They were applied with a sprinkler can and roto-tilled into the bed’s top 4 inches. Untreated carrot seed cultivar Imperator 58 was seeded in single row. At harvest after 3 months, one linear meter of carrot row was removed from each plot, the roots were counted and weighted. Ten mature roots were randomly selected for root gall disease rating (scale 0-10, 0-3 marketable). The rkn population had increased at the resistant and susceptible tomatoes to 231 and 884 J2/100 g soil, respectively. However, the yield did not differ between the cultivars. All contact nematicides and mustard meal lowered galling in carrots following resistant tomato. Especially the novel compounds increased the yield by 40-50% compared to the non-treated control. The carrot root galling was very severe after susceptible tomatoes. Consequently, the marketable product was extremely meager. Even the most effective nematicide treatment yielded only 25% of commercially acceptable carrots. In conclusion, with a combination of rkn-resistant tomato and application of contact nematicides or mustard seed meal before seeding carrots, a significant reduction in galling was achieved and a substantial increase in marketable yield. Overall, the novel fluorinated nematicides fluensulfone, fluopyram, and fluaazindolizine were at least as effective as the older standards. Rkn-resistant tomatoes in combination with mustard seed meal before seeding carrots might provide an alternative to organic growers.

RESPONSE OF NEMATODE COMMUNITIES TO CLIMATE-DRIVEN PLANT COLONIZATION OF A HIGH ALPINE LANDSCAPE. Porazinska, Dorota L, C. P. Bueno de Mequita, E. C. Farrer, M. J. Spasojevic, K. N. Suding and S. K. Schmidt. 1Department of...
Entomology and Nematology, University of Florida, Gainesville, FL 32611, 2Ecology and Evolutionary Biology, University of Colorado, Boulder, CO 80309, 3Institute of Arctic & Alpine Research, University of Colorado, Boulder, CO 80309, 4Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, LA 70118, 5Department of Evolution, Ecology, and Organismal Biology, University of California Riverside, Riverside, CA 92521.

Climate warming is a key factor driving species range shifts. While previous work has focused on shifts of aboveground plant communities, changes in climate and vegetation should affect soil communities and hence ecosystem-level nutrient cycling and ecosystem functioning. High alpine ecosystems are particularly sensitive to climate warming because snow is among the main drivers of ecosystem structure and function. Climate-warming snow cover changes at Niwot Ridge in the Colorado Rocky Mountains have resulted in a consistent plant colonization of previously unvegetated soils generating a natural gradient of soil habitats ranging from unvegetated to increasingly vegetated. We used this gradient of plant communities at different successional stages to determine if nematodes respond to climate-driven changes in this high-alpine landscape and if they play a role in changes in soil C and N. We hypothesized that there would be clear shifts in nematode communities along the gradient as a function of snow cover, plant richness and density, and water holding capacity but that these shifts would be dependent on nematode feeding habits and their positioning in the soil foodweb and, the shifts would be associated with accumulating soil C and N. To test these hypotheses, we measured nematodes, plants, and soil microbes, snow cover, pH, soil water holding capacity, and different forms of soil C and N in 98 plots across the plant successional gradient. As predicted, nematode communities exhibited extensive shifts from a few individuals of a single species in unvegetated soils to hundreds of individuals and tens of species within every feeding group under complex plant communities. Representatives of omnivorous and bacterivorous K-strategists preceded plants and plant parasites and root associates dependent on plants most. Linear regression models indicated that plants, microbial communities and soil water holding capacity, but not snow cover, were the most predictive factors of nematode diversity and density across all trophic levels and that all nematode groups were positively related to all measures of soil C and N. Structural equation models confirmed these results, but also indicated that effects of climate warming on nematodes were indirect primarily through shifts in plant and microbial communities and changes of soil water holding capacity. Moreover, nematode trophic group densities, but not their diversity, played a potential role in the accumulation of soil N, and to a lesser degree of soil C. Because nematode communities at Niwot Ridge are largely at their early phases of assembly, with continuing climate warming, we predict their increasing abundance and diversity will likely continue, as will their impact soil C and N processes.

INTERACTION STUDIES BETWEEN MELOIDOGYNE JAVANICA AND FUSARIUM OXYSPORUM F. SP. LYCOPERSICI (FOL) RACE 3 ON DIFFERENT ISOLINES OF TOMATO CV. TASTI LEE. Regmi, Homan1, G. E. Vallad2, S. F. Hutton3, and J. Desaeger4.

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The Mi gene in tomato confers resistance to the most common tropical root-knot nematodes (RKN, Meloidogyne javanica, M. incognita and M. arenaria), one of the major problems in Florida tomato fields. However, root-knot juveniles may still puncture and penetrate Mi-resistant tomato roots, causing damage and creating points of entry for soilborne pathogens such as Fusarium wilt (Fol), another major problem in Florida. To study the interactions between root-knot, Fusarium and Mi in tomato, two greenhouse experiments were conducted using four isolines (with and without I-3 and Mi genes) of the cultivar Tasti Lee* (TL). In the first experiment all isolines were subjected to two levels of RKN (~10000 eggs/pot and no eggs) and two levels of Fol (1000 cc soil with 1000cfu/g and no Fol), both applied at planting. In the second experiment, the two isolines without I-3 were exposed to two levels of RKN as described above and three levels of Fol (50 ml Fol with 1 x 10^6 cfu/ml applied at planting, applied after 10 days, and no Fol). Fol reduced root-knot infection and reproduction when both Fol and RKN were inoculated at planting, but not when Fol was inoculated ten days later. Fol damage was more severe in experiment 1 when inoculum was premixed in soil than in experiment 2 where Fol was drenched. Plant damage from Fol was exacerbated in the presence of RKN, especially when both pathogens were present at planting. Isolines with I-3 grew better in Fol-inoculated soil but had no effect when Fol and RKN were both present. Isolines with Mi gene reduced RKN infection and reproduction, but did not affect plant damage caused by Fol. In summary, while RKN reproduction was reduced in the presence of Fol, the overall plant damage was more severe when both pathogens were present.

SURVEY AND SENSITIVE DETECTION OF NEMATODE TRANSMITTED VIRUSES AND VECTORS OF SMALL FRUIT CROPS IN THE PACIFIC NORTHWEST (USA). Reinhold, Lauri1, M. Sudarshana1, and I. Zasada1.

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The Pacific Northwest (PNW) maintains a $840 million small fruit industry susceptible to nematode-transmitted nepoviruses. Washington has reported nepoviruses on small fruit crops, including grapevine fanleaf virus (GFLV) on juice and wine grapes, tobacco ringspot virus (TRSV) on blueberry and grape, and tomato ringspot virus (ToRSV) on blueberry and raspberry. Tomato ringspot virus has been detected on wine grapes in Oregon. The known dagger nematode vectors of these viruses, Xiphinema americanum sensu strico, X. californicum, and X. rivesi, have been reported in the PNW, increasing the risk of virus transmission among and between plant hosts. The first objective of this research is to assess the risk of nepoviruses to small fruit production in the PNW by conducting a survey of nematode-transmitted viruses and vectors of grape, raspberry, blueberry, blackberry, and strawberry. In May to June 2021, plant and soil samples were collected from sites with and without known nepovirus infections for virus and vector screening. Plant samples will be tested for: Arabis mosaic virus (ArMV), cherry leaf roll virus (CLRv), GFLV, peach rosette mosaic virus (PMV), strawberry latent ringspot virus (SLRSV), ToRSV, and TRSV. Nematodes will be extracted from soil and identified to species. Presence of nepoviruses and dagger nematodes will be reported, and potential impact will be discussed. The second objective of this research is to develop quantitative (qPCR) and digital droplet PCR (ddPCR) assays to detect naturally occurring titers of plant virus in individual nematodes. Conventional methods of virus detection (ELISA and PCR) are limited in sensitivity and unable to detect low virus titers found in nematodes. In fall 2020, plant and soil samples were collected from five and eight nepovirus-positive field sites, respectively. Thirteen nepovirus-positive plant samples...
were obtained from greenhouse collections. RNA and dagger nematodes were extracted from plant and soil samples, respectively, for use in assay validation and optimization. Specificity and sensitivity of ToRSV and TRSV qPCR and ddPCR assays will be compared and discussed. The comprehensive survey and virus detection in nematodes allows for virus transmission and virus-vector relationships to be studied and will ultimately inform risk and management practices for PNW small fruit growers.

DISTRIBUTION OF ROOT-KNOT NEMATODES IN FLORIDA WITH THE FOCUS ON MELOIDOGYNE ENTEROLOBI. Riva, Gabrieli1, H. X. Bui1, M. Gu1, and J. A. Desaeager1. 1Department of Entomology and Nematology, University of Florida Gulf Coast Research and Education Center, Wimauma, FL 33598, United States, 2FMC Stine Research Center, Newark, DE 19711.

Root-knot nematodes (RKNs; Meloidogyne spp.) are ubiquitous in Florida, but little is known about the distribution of different RKN species throughout the state. M. enterolobii is a highly virulent RKN species that is becoming increasingly important in the southeastern United States. A survey of RKN distribution in Central and South Florida was started in 2020-2021 and so far, a total of 233 soil and root samples were collected from 46 different crops. Samples were collected from commercial vegetable farms, as well as small community gardens and included tomato, pepper, cucurbits, and several Asian vegetables. Molecular identification using Restriction Fragment Length Polymorphism (RFLP) and RKN species-specific primers were employed. As a result, we identified several RKN species including Meloidogyne arenaria, M. enterolobii, M. hapla, M. haplanaria, M. incognita, and M. javanica. Preliminary results from this survey revealed that M. enterolobii was the most prevalent RKN species and was found in 66 samples from various crops belonging to Amaranthaceae, Araceae, Basellaceae, Brassicaceae, Convolvulaceae, Cucurbitaceae, Fabaceae, Lamiaceae, Malvaceae and Solanaceae family. The survey work is part of the FNDMe project (Focused Investigations on the Distribution and management of Meloidogyne enterolobii) project with the goal to study the distribution and the host plants of M. enterolobii in the southeastern US and provide recommendations for integrated nematode management of this emerging pest.

ANTARCTIC NEMATODE MICROBIOME’S RESPONSE TO TEMPERATURE Robinson, Colin1. 1Brigham Young University, Dept. of Microbiology and Molecular Biology, Provo, UT 84602.

Recent studies have shown that Plectus murrayi, a mesophilic Antarctic nematode in the McMurdo Dry Valleys (MCM), reaches peak metabolic activity at 40°C. However, when monitoring population dynamics of P. murrayi, researchers have found that population sizes decline steadily at temperatures higher than 22°C. Although metabolic enzymes continue to function at 40°C, other pathways, such as cellular repair mechanisms, likely begin to fail at temperatures higher than 22°C, which could account for increased mortality in P. murrayi populations that are held at those temperatures. Another potential explanation is that the composition of the P. murrayi microbiome changes at temperatures above 22°C, resulting in a less diverse microbiome. Low diversity microbiomes are known to cause decreased fitness in Caenorhabditis elegans and may have a similar impact on the health of individual P. murrayi individuals. To determine how the composition of the P. murrayi microbiome changes with temperature, nematode populations were held at various temperatures for 2 weeks. Every day, worms were taken from each sample and their microbiomes were analyzed using 16S DNA sequencing. The results of this study can inform predictions of future trends of P. murrayi population dynamics and the impact of future climate-driven changes on soil ecosystems.

WHEAT PRODUCTION ALTERS SOIL MICROBIAL PROFILES AND ENHANCES BENEFICIAL MICROBES IN DOUBLE-CROPPING SOYBEAN. Rocha, Leonardo 1, J. P. Bond1, and A. M. Fakhoury1. 1School of Agricultural Sciences, Southern Illinois University – Carbondale, IL 62901.

Plant-parasitic nematodes represent a substantial constraint on global food security by reducing the yield potential of all major crops. The soybean cyst nematode (SCN) (Heterodera glycines I.) is widely distributed across all soybean production areas of the US, being the major yield-limiting factor, especially in the Midwestern US. Double cropped soybean (DC) is commonly planted following winter wheat. We previously reported double-cropping soybean fields with reduced SCN counts compared to fallow at both R1 soybean growth stage (beginning of flowering) (-31.8%) and after soybean harvest (-32.7%). Literature suggests that enriched microbial communities could be correlated with the suppression of SCN in fields previously planted with wheat. Recent progress in several sequencing-based techniques brought a new perspective vis-à-vis the broadness of microbial diversity and powerful tools to elucidate some of the ecological principles driving these communities, their functions, and implications on plant health. In many instances, these new techniques can be implemented to interpret patterns in microbial diversity and how they correspond with disease suppression in production soils.

Considering that growing wheat contributes to reduced SCN populations in the succeeding growing season and that research suggests microbial community composition as a potential factor in suppressing nematode populations, the objectives of this research are to: 1) describe microbial community profiles from DC fields previously described to have SCN suppression; 2) identify differentially abundant taxonomic groups across treatments; 3) pinpoint potential microbial groups related to the suppression of SCN; 4) provide further evidence in support of the adoption of wheat in DC systems to manage SCN populations in soybean production fields. To explore these hypotheses, three field locations with noted SCN suppression were selected for a metagenomics study. Ten subplots were elected (5 wheat and 5 fallow) from each location. A total of 90 soil samples were selected: 3 fields x 2 treatments x 3 timepoints x 5 replications. Three DNA markers targeted distinct microbial groups: bacteria (16S V4-V5), fungi (ITS2), and Fusarium (tef1). Amplicons were sequenced using an Illumina MiSeq platform (300-300 bp paired-end). Sequencing datasets were processed in R using the DADA2 pipeline. After taxonomy and abundance tables were generated, data was uploaded to the Microbiome Analyst (https://www.microbiomeanalyst.ca/), a web-based platform providing comprehensive statistical, visual, and meta-analysis of microbiome datasets. Alpha and beta-diversity were estimated using Shannon’s diversity index and Bray-Curtis similarity index, respectively. Subsequently, enriched taxa were using LEfSe (Linear Discriminant Analysis Effect Size). Fungal communities were significantly different between DC and fallow plots at soybean planting and after harvest (P < 0.001). Fungal populations were affected by location in all sampling times and by treatments before planting and after soybean harvest. Several enriched fungal and bacterial taxa in wheat plots were previously reported to parasitize SCN cysts and eggs, suggesting a potential role of beneficial microbes in suppression of SCN in soybean fields double-cropped with wheat.
NOVEL DORSAL GLAND EFFECTOR CANDIDATES IDENTIFIED FROM ROOT-KNOT NEMATODE ADULT FEMALES. **Rocha, Raquel**, R. S. Hussey, and M. G. Mitchum. University of Georgia, Dept. of Plant Pathology and Institute of Plant Breeding, Genetics, and Genomics, Athens, GA 30602.

The root-knot nematode, *Meloidogyne incognita*, represents one of the most damaging species of plant-parasitic nematodes, with a world-wide distribution and the ability to infect virtually any cultivated crop species. Through a hollow, protrusable stylet, these nematodes secrete effectors to manipulate host cell structures and function for their own benefit. These effectors are produced by highly specialized secretory esophageal gland cells, one dorsal and two subventral, whose roles differ throughout the nematode life cycle. Elucidating the transcriptomic profile of these gland cells has proven to be a promising approach for identifying new effectors involved in nematode parasitism during its motile and sessile phases. Prior gland isolation studies have focused on juvenile stages of the nematode. In this study, we developed a protocol to enrich the highly active dorsal glands from *M. incognita* adult females for RNA extraction and identification of novel effector candidates. Female heads were manually cut from the body and a combination of sonication and vortexing was used to dislodge the contents inside the heads. Dorsal glands fractions were collected by filtering using cell strainers. The validity of this method was confirmed by RT-qPCR analyses of three known *M. incognita* putative dorsal gland secretory proteins (msp) – msp1 (2E07), msp6 (7A01), and msp12 (11A01) – which showed a relative expression enrichment of 45, 54, and 47 times in comparison to whole females, respectively. Comparative transcriptome profiling of pre-parasitic second-stage juveniles 2 (pp2), female heads, and dorsal glands was conducted using RNA sequencing. When mapped to the *M. incognita* v3 reference genome, 37,160 unique genes were identified across the three experimental samples. Pair-wise comparison of dorsal glands with pp2 and female heads identified 17,089 and 2,286 differentially expressed genes (DEG), respectively. Out of the two sets of DEG, 1,788 genes were common in both comparisons, with 458 genes upregulated in dorsal glands samples and, thus, of interest to this study. A total of 83 genes in the dorsal gland sample contained a predicted signal peptide, lacked transmembrane domains, and showed no homology to proteins in the free-living nematode *Caenorhabditis elegans*. Of these genes, 59 were previously unidentified to be expressed in dorsal glands. Additional analyses of these dorsal gland effector candidates showed that 36 had a DOG box promoter motif, 22 contained a nuclear localization signal (NLS), and 63 contained a predicted MERCI effector motif within their encoded protein sequences. Taken together, we have identified potential novel candidate *Meloidogyne* effector genes that may have important roles during later stages of parasitism.

EXPLORING YIELD LOSSES ON COTTON DUE TO *ROTYLENCHULUS RENIFORMIS* OVER SIX YEARS IN THE SOUTHEAST UNITED STATES. **Rondon, Marina N., B. R. Lawaju, and K. S. Lawrence.** Auburn University, Department of Entomology and Plant Pathology, Auburn, AL 36849

The reniform nematode (*Rotylenchulus reniformis*) is among the major problems of cotton in the United States. Reniform infested cotton fields exhibit reduced growth, dwarving, interveinal chlorosis, reduction of root biomass with the presence of egg masses covered with soil particles, and finally yield losses. Six years of trials have been conducted in the southeast United States located in north Alabama to understand yield losses caused by reniform nematode on cotton. Each year the trials were arranged in a randomized complete block design with five replications. Plots consisted of four rows, in which two rows were treated at planting with a nematicide and two rows untreated. The same design was conducted in a non-reniform infested field. Reniform infested and non-reniform fields were less than 500 meters from each other. Different cultivars were planted among the six years, 2014-2019. Plant parameters and nematode populations were evaluated between 30 and 45 days after planting. Cotton bolls were mechanically harvested, and yield determined. Data were subjected to mixed-model analysis of variance using PROC GLIMMIX in SAS 9.4 to test for fixed effects and interactions (nematode|nematicide), and random effects (year|cultivar). LS-means were separated with Tukey-Kramer (*P* < 0.05). Our results from six year indicated that cotton yield in the reniform infested field was statistically reduced by 2077 kg/ha or 55% (*P* < 0.001) when compared with the non-reniform infested field. Over the six years, cotton yield in the reniform infested field ranged from 2153 to 2969 kg/ha, while in the non-reniform field ranged from 4230 to 5045 kg/ha. Statistically higher cotton yield was observed when the nematicide was added for crop protection (*P* < 0.001). In the absence of reniform nematode, the yield of cotton treated with the nematicide and untreated were equivalent (*P* = 0.001). However, in the presence of reniform nematode, the cotton yield statistically increased compared with untreated cotton (*P* < 0.001). This study provided insight into cotton yield losses caused by *R. reniformis* in the southeast United States and the full benefit of nematicide application when reniform nematode is present.

REINIFORM NEMATODE MANAGEMENT WITH *BRASSICA CARINATA* A. BRAUN IN THE SOUTHEAST UNITED STATES. **Sandoval-Ruiz, Rebeca**, Z. Grabau, R. Seepaul, D. Wright, and I. M. Small. Entomology and Nematology Department, University of Florida. Gainesville, FL 32611, North Florida Research and Education Center-Quincy, University of Florida. Quincy, FL 32351.

*Rotylenchulus reniformis* (reniform nematode, RN) can reduce cotton (Ct) yield. Management options are limited, and mostly rely on chemical nematicides. In this research, we focused on the use of cultural practices that include a new crop in the Southeast United States, *Brassica carinata* (carinata, Ca), to manage RN. The first objective was to determine if Ca affects RN when included as part of a winter rotation system. This field rotation consisted of 2-year rotation of Ca-fallow, oats-Ca, and fallow-cauliflower with 4-year summer rotation of corn, Ct, soybean, and peanut, with each crop present each year. The results suggested that Ca could help manage RN populations. This led to the second objective, to determine if Ca could be defined as a non-host crop for RN. For that, a host suitability test was established under greenhouse conditions. Crops with known host status for RN (canola, oats, peanut, hairy vetch, and Ct) were used to compare RN reproduction on Ca. The reproduction factor (RF) of Ca was <1 and was separated from the RF of Ct and hairy vetch, crops known as good hosts of RN. This helped to define that Ca is a non-host crop of RN and could be included as a winter crop to manage RN. Furthermore, Ca, like most brassicas, has glucosinolates, substances that can be toxic to soil pathogens as a biofumigant. However, actual management of nematodes by brassicas under growing conditions through biofumigation may vary. Therefore, a third objective
was to assess biofumigation on RN by Ca and other winter crops (canola, oats, and hairy vetch) under greenhouse conditions. Soil was inoculated with 6000 nematodes/pot and winter crop shoot and root residues were applied at 2% dry or fresh tissue by weight relative to soil weight. Cotton was planted in each pot one week after organic matter (OM) incorporation. A positive control (Ctrl+, Ct plants inoculated with nematodes but without OM), and a negative control (Ctrl-, Ct plants without nematodes or OM) were included. After 2.5 months, nematodes were counted, and growth variables were measured from the Ct plants. The number of nematodes in the roots and in the soil were lower in the treatments with dry OM, than in the treatments with fresh OM or the Ctrl+. In general, the growth of the plants was greater in the dry OM treatments, intermediate with fresh OM and least with the controls. This indicate that the application of OM, regardless of crop, positively influenced plant growth and helped manage RN compared to the Ctrl+

DEVELOPMENT OF AN ANATOMICAL DATABASE FOR NEMATODES. Schroeder, Nathan1. 1University of Illinois at Urbana-Champaign, Dept. of Crop Sciences, Urbana, IL 61873.

Detailed maps of nematode anatomy provide insight into the function of individual tissues. For example, the complete reconstruction, annotation, and availability of original data for the Caenorhabditis elegans nervous system has allowed researchers to study behavior at the level of a single neuron. While the anatomy of several nematode species has been examined in detail, only a subset of the original data are published and available to researchers. The goal of the SON Capacity Building Grant awarded to myself and Dr. Jim Baldwin was to digitize his electron microscopy (EM) archives. We planned to transfer these digitized data to the University of Illinois where they will be made available to the public. Unfortunately, the COVID-19 pandemic delayed our plans. Despite this, my lab has made progress on another archived data collection—the digitization of the EM data set from Dr. Burton Endo. These data are from seven species, including both plant and animal parasites and with emphasis on the anterior neurosensory and esophageal tissues. The largest representative species of these data is the soybean cyst nematode, Heterodera glycines. We have digitized approximately 15,000 of the estimated 40,000 images from glass plate negatives and prints. Approximately 1,000 images of Meloidogyne incognita and Heterodera glycines have been annotated and deposited in the open-access Illinois Data Bank (https://databank.illinois.edu/). In the future, these data will also be deposited in the WormImage database (https://www.wormimage.org/). WormImage and the associated WormAtlas websites were originally developed to focus on C. elegans anatomy. I joined the WormAtlas team to focus on expanding its anatomical offerings beyond C. elegans.

VERTICAL DISTRIBUTION OF NEMATODES IN PEANUT-COTTON CROPPING SYSTEMS. Schumacher, Lesley1 and Z. Grabau2.
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Cotton (Gossypium hirsutum) and peanut (Arachis hypogaea) are important field crops grown in the southeastern United States. The plant-parasitic reniform nematode (Rotylenchulus reniformis) is a pathogen of cotton capable of reducing lint yields, so crop rotation is commonly used for its management. One specific rotation system, sod-based rotation, uses two years of bahiagrass (Paspalum notatum) followed by one year each of peanut and cotton compared with a conventional crop rotation (peanut-cotton-cotton). Peanut and bahiagrass are poor hosts of reniform nematode. Agronomic benefits of a sod-based rotation like improved cotton root growth are well-known, but information about its effects on free-living, non-parasitic nematodes (fungivores, bacterivores, omnivores, predators) is limited. These nematodes contribute to soil nutrient cycling and may be beneficial in crop production. Additionally, reniform nematode is present deep in the soil profile, but not much is known about free-living nematodes at deeper depths. By surveying a long-term experimental site in Quincy, FL, our study aimed to investigate both plant-parasitic and free-living nematodes at different soil depths in sod-based and conventional rotation with or without irrigation. Soil samples were collected to a depth of 120 cm before planting (March 2017, March 2018), after harvest (October 2017, October 2018), and in the winter (January 2018, January 2019) using a hydraulic probe. Free-living and reniform nematode abundances were analyzed in 30 cm-sections. No irrigation effects were observed in any of the sampling dates (P > 0.05). There was significant crop by depth interactions (P < 0.05) for free-living nematode abundances for all sampling dates, but only in harvest sampling dates for reniform nematode abundances. For these interactions, effects varied by sampling date for free-living nematode abundances. Yet, sod-based rotation reduced reniform nematode abundances at all depths compared with conventional rotation for post-harvest sampling dates. Overall, both free-living and plant-parasitic nematodes were present up to 120 cm deep in the soil profile and cropping system affected nematode abundances.

SIZE AND DOSE DEPENDENCY ON THE LETHALITY OF THREE US PHASMARHABDITIS SPECIES (P. HERMAPHRODITA, P. CALIFORNICA, AND P. PAPILLOSA) AGAINST THE INVASIVE ITALIAN WHITE GARDEN SNAIL (THEBA PISANA). Schurkman, Jacob, I. De Ley, and A. Dillman. University of California Riverside, Dept. of Nematology, Riverside, CA 92521

The invasive Italian White Garden Snail (Theba pisana) has recently expanded its geographical range and is potentially an emerging gastropod nuisance in Southern California. The snails are found in highest density in San Diego County, CA, spread to Los Angeles County and recently detected for the first time in San Mateo County. In San Diego, they have been found in extremely large numbers in various fields, on the sides of houses, various other city infrastructure, and commercial buildings, to the point where in the latter, their presence had become more than a nuisance to customers. Mitigating this invasive pest should be a priority to Southern California. Phasmarhabditis hermaphrodita is a gastropod specific parasite, commercially sold as Nemaslug®. It is only available throughout Europe (Nemaslug®) and Sub-Saharan Africa (Slugtech®SP) as an effective method of biological control against pestiferous gastropods. Recently discovered isolates of Phasmarhabditis (P. hermaphrodita, P. californica, and P. papillosa) may be effective for biocontrol against these pestiferous invasive gastropods in the United States. Past assays proved that the recently discovered isolates can effectively kill T. pisana, ranging in size between 4-6mm and 20-100mg in weight at five times the recommended dose of Nemaslug® (150DJs/cm²). The isolates caused similar mortality in the smaller T. pisana compared to the chemical molluscsid Sluggo Plus® used at the higher recommended dosage of 4.88kg/m². Here we assessed size-and dose-dependency in the lethality of three Phasmarhabditis species compared with Sluggo Plus® at the same recommended dose against bigger and heavier T. pisana (> 6mm in length and heavier than 100mg on average). We found that at this snail
size and weight range, all three *Phasmarhabditis* species when used at five-fold the recommended dose (150DJs/cm$^2$) can kill *T. pisana* at a more effective rate than Sluggo Plus*. *Phasmarhabditis californica* is the most widely distributed species in California, so this species was chosen in subsequent trials to determine its lethality on bigger specimens but at lower doses. Preliminary trial shows that the use of this nematode at the recommended dose (30DJs/cm$^2$) and three times the dose (90DJs/cm$^2$) did not cause effective mortality. However, additional trials are needed to confirm this, and to further determine if a lower dose of 30DJs/cm$^2$ or 90DJs/cm$^2$ can kill *T. pisana* smaller-sized snails (4-6mm in length).

**Superior Fitness in Entomopathogenic Nematodes Applied in Infected Hosts.** Shapiro-Ilan, David$^1$, S. Gulzar$^2$, M. Usman$^1$, W. Wakil$^3$, B. Gulcu$^4$, C. Hazir$^5$, M. Karagoz$^6$ and S. Hazir$^7$. $^1$USDA-ARS, Byron, GA 31008, USA, $^2$University of Agriculture, Faisalabad 38040, Punjab, Pakistan, $^3$Duzce University, Duzce-Turkey, $^4$Adnan Menderes University, 09100, Aydin, Turkey.

Entomopathogenic nematodes in the genera *Steinernema* and *Heterorhabditis* are biocontrol agents that are used to control a wide variety of economically important insect pests. Generally, the nematodes are applied in aqueous suspension using standard agricultural equipment (e.g., sprayers and irrigation systems). However, the nematodes can also be applied in their infected hosts. In this approach, the infected cadavers are applied to the target site and pest suppression is subsequently achieved by the emerging progeny nematodes. In prior studies, the infected host application approach was reported to be superior to aqueous application in terms of nematode dispersal, infectivity, and biocontrol efficacy. In the current study, we explored the impact of application approach on environmental tolerance. Prior to our research, differential stress tolerance among nematodes that emerged from infected host cadavers versus those applied in aqueous suspension had not been investigated. Specifically, we explored the fitness of nematodes applied by cadaver versus aqueous following exposure to temperature extremes (heat and cold) and desiccation. The nematodes, *Heterorhabditis bacteriophora* and *Steinernema glaseri* were assessed for viability, virulence, and reproductive capacity. Following exposure to 30°C, 35°C and 37.5°C, nematodes of both species exhibited higher survival and reproductive capacity in the cadaver treatment compared with aqueous application. No differences were observed between the cadaver and aqueous treatments in cold tolerance, i.e., after a sequence of exposures from 10°C to -2°C. For desiccation tolerance, following exposure to 85% relative humidity both nematode species exhibited higher survival and reproduction in the cadaver treatment than in the aqueous treatment, whereas no differences were observed in virulence. Our findings indicate additional advantages when using the cadaver approach for biocontrol applications and suggest EPNs existing in natural populations may have broader environmental tolerance than those applied via aqueous suspension.

**Long-Term Nitrogen Deposition in Alpine Tundra Affects Nematode Communities.** Shepherd, Rachel$^1$, L.M. Brigham$^2$, C.P. Bueno de Mesquita$^{3,4}$, J.G. Smith$^1$, S.K. Schmidt$^5$, K.N. Suding$^1$, and D.L. Porazinska$^1$. $^1$Entomology and Nematology Dept., University of Florida, Gainesville, FL 32611, $^2$Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, CO 80309, $^3$Institute of Arctic and Alpine Research, University of Colorado, Boulder, CO 80301.

Human-driven nitrogen (N) deposition can result in shifts of plant communities and soil biogeochemistry. Because plants and abiotic characteristics of the soil environment are known drivers of soil microbial communities, N deposition can also influence soil communities (e.g., indirectly via changes in plants and directly via changes in soil biogeochemistry). As high elevation ecosystems are typically N limited, N deposition can have pronounced effects on their functioning. Alpine tundra at Niwot Ridge in the Colorado Rocky Mountains is co-dominated by two plant species differing in their response to N deposition: *nitrphilic Deschampsia cespitosa* (bunchgrass) expands its range and biomass and nitrogen-sensitive *Geum rossii* (forb) declines. We hypothesized that the response of nematode communities to N deposition would be modified by the identity of these co-dominant plants. We examined plant-nematode relationships in response to N deposition by capitalizing on a long-term (20 yr) experiment at Niwot Ridge involving two types of manipulations: 1. N addition (control, N added) and 2. removal of co-dominant plant species (control, removal of *G. rossii*, removal of *D. cespitosa*). The experiment consisted of 7 blocks each with 6 treatments for a total of 42 plots spanning an area of 5 km$^2$. In August 2018, we collected 10 composite soil cores per each plot and took 5 g and 20 g subsamples to characterize soil biogeochemistry (soil moisture, pH, ammonium, nitrate, and total dissolved nitrogen) and nematode communities, respectively. Nematodes were first extracted, counted, and identified using microscopy, then processed for DNA extraction and 18S rDNA metabarcoding using standard protocols. Plant community richness and productivity were evaluated using point intercept method and clipping of aboveground biomass. Differences in alpha and beta diversity in nematode communities among the different treatments were tested using ANOVA and PERMANOVA, respectively. Potential relationships with plant and soil variables were tested using dbRDA. Neither removal of co-dominant plants nor N addition affected the measures of nematode alpha diversity. In contrast, there were significant shifts in nematode community composition but only in response to N addition ($P < 0.001$). The trophic groups most affected by N addition included bacterivores, plant parasites, and root associates ($P < 0.001$). Although the influence of the identity of the removed plant was limited, dbRDA analysis indicated that the biomass of *G. rossii* as well as pH and soil moisture could also play a role in shifts of nematode communities. Overall, our data suggests that nematode communities are highly sensitive to N deposition. Whether compositional shifts are linked to plants is unclear as effects of plants could be obscured by the dominant effect of nitrogen. Detailed analysis of nematode and plant community relationships will help to resolve this question.

**Emergence of *Steinernema Felthiae* Infective Juveniles from “Living Bombs” of *Tenebrio Molitor*.** Sipes, Brent, K.-H. Wang, and L. Wong. University of Hawaii, Honolulu, HI 96822.

Entomopathogenic nematodes (EPN) are generally applied as aqueous solutions that subject the nematodes to ultraviolet light and desiccation. Application of living bombs of EPN overcomes these issues and may improve EPN performance. *Galleria mellonella* (wax moth) larvae infected with *Steinernema carpocapsae* successfully controlled *Cossus cossus* burrowed in chestnut trees by acting as a “living bomb” transporting the EPNs into areas spray application could not access. However, *Tenebrio molitor* (mealworm) larvae infected with *S. felthiae* applied to control *Plutella xylostella* (diamondback moth) were less successful perhaps because of insufficient rates or timing of Infective Juvenile (IJ) emergence. The objective of a series of laboratory experiments was to determine the rate and level of EPN...
emergence from living bombs. In the first experiment, ten 0.16 g mealworm larvae were exposed to 2000 IJs of S. feltiae in a petri dish. This was repeated in 5 dishes. Mealworm cadavers were collected after 48 hours and transferred into individual White traps. Newly emerged IJs were collected and counted every 48 hours. In a second experiment, the insect cadavers were placed in individual White traps and IJ collected every 24-48 hours. In a third experiment, two sizes of mealworms of 0.14 and 0.18 g, respectively were exposed to S. feltiae as described above and cadavers transferred to individual White traps. IJ were collected and counted every 24 hours. In the first experiment, IJ were observed 7 days after infection. IJ were observed at each collection with peaks at day 15 and 21. In the second and third experiments, a peak of IJ emergence was recorded at 6, 15, and 21 days. Mealworm larval weight did not affect emergence nor total IJ per larva. IJ emergence from a mealworm did not have a single peak, but multiple peaks. The peaks occurred every 5-6 days, parallel to completion of a nematode life cycle. Cadavers released 20,980 IJ per mealworm over 22 days of observation. The release of IJ from living bombs occurs over a period of time and this release needs to be timed to the life cycle of the target insect pest. It will also be necessary to quantify the population density of living bombs needed per treated area. Additional research should quantify IJ emergence by EPN species and species of the insect living bomb.

INCIDENCE AND MOLECULAR DIVERSITY OF CACTODERA SPP. DETECTED IN THE UNITED STATES. Skantar, Andrea M.,1 Z. A. Handoo,1 S. Hafez,2 M. R. Kantor,1 M. Grabowski,3 and M. N. Hult4. 1USDA ARS Northeast Area, Mycology and Nematology Genetic Diversity and Biology Laboratory, Beltsville, MD, 2University of Idaho, Parma Research and Extension Center, Parma, ID. Minnesota Department of Agriculture, Plant Protection Division, St. Paul, MN.

The genus Cactodera (Kral and Kral, 1977) currently includes 16 species. Cyst nematodes were received for identification after detection in Cooperative Agricultural Pest Surveys (CAPS), during surveillance for potato cyst nematode (PCN) or from concerned growers. Morphological examination and morphometrics of cysts (when available) and juveniles were taken, followed by molecular phylogenetic analysis including ITS and 28S rDNA, mitochondrial cytochrome oxidase I (COI), and heat shock protein 90 (Hsp90). Comparison of available sequences in GenBank was used to construct DNA sequence alignments. Phylogenetic trees were made for populations and species of Cactodera using Bayesian Inference (BI). These approaches have been used to identify new populations of Cactodera cacti from a cactus garden in Idaho, C. milleri from potato fields in Minnesota and Colorado, and C. weissi from potato in New York.

ROOT-KNOT NOT LIKE WE THOUGHT! – IDENTIFYING A NEED FOR GEOGRAPHICALLY SPECIFIC SEQUENCES TO AID IN THE DEVELOPMENT OF MOLECULAR TOOLS FOR NEMATODE DIAGNOSTICS. Soule, Michelle1, C. Gleason2, S. Chovashi3, A. Peetz4, and I. Zasada4. 1Oregon State University, Dept. of Botany and Plant Pathology, Corvallis, OR 97331, 2Washington State University, Dept. of Plant Pathology, Pullman, WA 99163, 3AGNEMA, Pasco, WA 99301, 4USDA-ARS Horticulture Crops Research Unit, Corvallis, OR 97330.

In the Pacific Northwest the two most common root-knot nematodes are Meloidogyne hapla and Meloidogyne chitwoodi. Of these, M. chitwoodi poses a significant threat to the $1.8$ billion potato industry in the region as it can proliferate rapidly and continue destruction while tubers are in storage. Currently, diagnostic clinics use labor-intensive microscopy to identify nematodes based on morphology. There is a need for molecular techniques such as quantitative PCR (qPCR) for faster and reliable Meloidogyne spp. identification and quantification. Two separate hydrolysis probe qPCR assays targeting the ITS-2 region of M. chitwoodi and M. hapla have been validated and published. However, these assays failed to detect PNW Meloidogyne spp. populations. There was also difficulty with designing a new assay for PNW Meloidogyne spp. due to the limited number of distinctly PNW accessions in the NCBI Genbank repository. Additionally, some sequences commonly used to genetically distinguish plant-parasitic nematodes lacked the diversity needed to create a highly specific and robust assay or had characteristics that are not ideal for qPCR, such as having a GC content that is too low. For the reasons outlined above, Hsp90 was chosen as the assay target because it is conserved among most living organisms but has highly variable functionality conferring enough sequence variation for primer and probe design. At the time of designing the Hsp90 primers, whole genome sequences (WGS) became available for two M. chitwoodi races (race 1 and race 2) and a third M. chitwoodi "Roza" isolate. The primers were tested in silico against the WGS, and amplicons were verified using BLAST. The M. hapla amplicon returned 98 to 100% coverage for M. hapla with E-value <0.01 and the M. chitwoodi amplicon returned 100% coverage for M. fallax (not found on potato in the Pacific Northwest) and M. chitwoodi with E-value <0.01. In conventional PCR, the primers amplified one target at the expected size of ~150 bp in both races of M. chitwoodi and M. hapla. Preliminary multiplex results are promising as assay optimization and validation are underway.

COTTON INFECTION BY ROTYLENCHULUS RENIFORMIS AS DETERMINED FROM FOUR ROOT SYSTEM PORTIONS. Stetina, Salliana R., and J. Erpelding. USDA ARS, Crop Genetics Research Unit, Stoneville, MS 38776, USA. Rapid screening based on the number of females infecting the cotton root system is typically destructive to the plant, although recovery of resistant plants is desired by breeders. The objective of this work was to determine whether resistance designations could be determined reliably if only a portion of the root system was examined. In a repeated growth chamber test, three susceptible cotton lines (Deltapine 16 and MD 25 and G. arboreum A2-101) and three resistant cotton lines (G. hirsutum LONREN 2, G. arboreum A2-190, and G. barbadense TX 110) were inoculated 5 to 7 days after planting with 1,000 vermiciform reniform nematodes (Rotylenchulus reniformis) suspended in water. Four weeks later, the plants were removed from the pots and the roots were gently rinsed free of soil. Four root retention treatments were examined. The root system was cut off at either 0, 1, 2.5, or 5 cm below the soil line and used for counting the number of females that had infected the roots. The test was a completely randomized design with a factorial treatment arrangement (genotype x root retention) and 5 replications. Data from both trials were combined and transformed $[\log_{x}(x + 1)]$ prior to analysis of variance. Significant differences were found between genotypes ($F = 113.55, P < 0.0001$) with respect to number of females, with each genotype displaying resistance or susceptibility as expected: Deltapine 16 = 113.5, A2-101 = 58.4, MD 25 = 57.4, TX 110 = 19.2, A2-190 = 8.4, and LONREN 2 = 7.9. The number of females did not differ significantly based on the amount of root tissue retained with the stem ($F = 2.50, P = 0.0609$), and no significant interactions between genotype and root retention ($F = 1.40, P = 0.1504$) were found.
Thus, resistance or susceptibility could be determined reliably across a range of cotton genotypes while keeping some root tissue with the plant to facilitate recovery of desirable individuals.

REKLEMEL™ ACTIVE (FLUAZAINDOLIZINE, SALIBRO™) A NEW NEMATICIDE FOR THE MANAGEMENT OF KEY PLANT-PARASITIC NEMATODES IN TREE NUTS. **Tewari, Sunil, S. Colbert, T. Thoden, and B. Braxton**. Corteva Agriscience, 9330 Zionsville Rd., Indianapolis, IN 46268, USA.

Reklemel™ active (fluazaindolizine, Salibro™) is a novel, non-fumigant, chemical nematicide discovered and being developed by Corteva Agriscience for the control of key plant-parasitic nematodes infesting a wide range of annual and perennial crop groups in North America including tree nuts and tree fruits as well as fruiting vegetables, cucurbits, root and tuber vegetables, stone fruits, and grapes, among others. Reklemel is the first sulfonylamide nematicide, has a unique mode of action (MoA), a favorable environmental and toxicological profile and can be applied in a variety of methods and timings. It has demonstrated selective and effective control of key nematode pests including a wide range of root-knot species (*Meloidogyne* spp.) as well as some root-lesion nematodes (*Pratylenchus* spp.), among others. Tree nuts, including almonds and walnuts, are key crops in California with more than a million acres and economic value in excess of $7 billion. Plant-parasitic nematodes pose serious challenge to tree nut growers, especially during early establishment of orchards. Reklemel will be an excellent tool for post-plant management of key nematode pests in tree nuts, promoting early plant growth and establishment in heavily infested orchards. Information on the chemical and biological attributes of Reklemel™ and results from comparative efficacy trials against key plant-parasitic nematode species in tree nuts will be presented.

SOYBEAN CYST NEMATODE (*HETERODERA GLYCINES*) RESISTANT VARIETY ROTATION SYSTEM IMPACTS NEMATODE POPULATION DENSITY, VIRULENCE AND YIELD. **Thapa, Sita¹, E. Cole¹, A. D. Howland², B. Levene³, G. Bird¹ and M. Quintanilla¹**.

¹Michigan State University, Department of Entomology, East Lansing, MI 48824, ²Bayer Crop Science, Dewitt, MI.

Soybean cyst nematode (SCN) is the most economically devastating pathogen of soybeans in the United States and most soybean growing countries worldwide. The most effective SCN management practice is the use of resistant cultivars. SCN, however, still causes significant yield loss due to the continuous use of cultivars derived from a single line of resistance, resulting in selection for virulent populations. A four-year field study (2017–2020) was conducted to evaluate the impact of six rotation systems with varieties derived from Peking/P1 548402 (PDV) and P1 88788 (8DV) on SCN population development, virulence and yield. The rotation systems were: 1) 8DV/PDV/8DV/PDV, 2) PDV/PDV/PDV/PDV, 3) 8DV/Susceptible cultivar (S)/PDV/8DV, 4) PDV/S/8DV/PDV, 5) BV/8DV/8DV/8DV, and 6) PDV/S/S/S. The trial was conducted on a grower-operated farm in St. Charles, MI. SCN population levels were significantly lower in the PDV/8DV cultivar rotation in 2018 compared to the PDV/S cultivar rotation. In 2020, SCN population levels were the lowest in the 8DV/PDV/8DV/PDV cultivar rotation system and highest in PDV/PDV/PDV system. In 2017, there were no substantial soybean yield differences among the system, but for the remainder of the trial, the PDV/8DV rotations had the highest yields. The HG type test showed that rotation of resistance sources can alter the virulence of the SCN population. The initial 2017 SCN population was HG type 1.2. The final 2020 populations for three of the rotation systems (8DV/PDV/8DV/PDV, PDV/PDV/PDV/PDV, and 8DV/S/8DV/PDV) was HG type 1.2.5.7 and HG type 1.2.3.5.6.7 for the other three systems (PDV/S/8DV/PDV, 8DV/8DV/8DV/8DV, and PDV/S/S/S). In a greenhouse trial, we found that a Michigan SCN population from continuous PI88788 from Monroe can also reproduce on Peking. These findings indicate rotating Peking and PI88788 derived cultivars can reduce SCN density and maintain high soybean yield, thus rotating these two sources of resistance with non-host rotations might delay the aggressiveness of SCN populations further, reducing soybean yield loss.

REKLEMEL™² active - KEY ATTRIBUTES AND LEARNINGS FROM A GLOBAL NEMATICIDE DEVELOPMENT PROJECT. **Thoden, Tim¹, J. A. Wiles², M. Garcia³, A. Agi³ and B. Braxton¹**. ¹Corteva Agriscience, Germany, ²Corteva Agriscience, United Kingdom, ³Corteva Agriscience, Indianapolis, US.

Reklemel™ active (fluazaindolizine) is a proprietary novel nematicide developed by Corteva Agriscience for commercialization in various geographies including North America. The development of this chemistry started more than 10 years ago and during its global development, more than 3000 field studies were initiated to test it under different edaphic and climatic conditions in numerous crop-nematode combinations. In addition to that, hundreds of laboratory studies were done to thoroughly characterize this molecule and evaluate key performance drivers of a nematicide. During our talk, we will present key biological attributes (Spectrum, effective concentration ranges, soil health compatibility) of this novel chemistry as well as key learnings on its soil behavior (soil concentrations, soil mobility & soil residuality) that we made throughout the development process.

EFFICACY OF NEMATICIDES AT MANAGING PLANT PARASITIC NEMATODES IN FIELD CORN. **Tsegay, Mussie, and Z. J. Grabau**. Department of Entomology and Nematology, University of Florida, Gainesville, FL 32611.

Corn is an important food and fuel field crop in the United States. Plant-parasitic nematodes can be a serious problem in field crops like corn and can cause significant yield reduction. While nematicides are commonly applied to reduce densities of plant-parasitic nematode populations, there are still relatively few studies that compare efficacy of current products in field corn. To determine which nematicide chemistries are most effective for specific plant-parasitic nematodes, field experiments were conducted in 2019, 2020, and 2021 in Hastings, FL. The main objective was to compare the nematicides 1,3-dichloropropene (1,3-D, Telone II) at rates of 28 and 56 l/ha, terbufos (Counter 20G) at 5.49 kg/ha and fluopyram (Propulse in 2019 and Velum Prime in 2020) at 0.59 and 1.01 l/ha, with untreated control for plant-parasitic nematode management. The study was constructed in complete randomized design with five replicates. Terbufos and fluopyram were applied in-furrow at planting, whereas 1,3-D was applied as a broadcast shank fumigation at least two weeks before planting. Soil populations of plant-parasitic and free-living nematodes were assessed at midseason (approximately 6 weeks after planting) and at harvest. Due to a mechanical issue, grain yield was assessed for fluopyram and terbufos only in 2019, but for all treatments in 2020. Data was
analyzed separately for each sample date using analysis of variance and means were separated using Fisher’s protected least significant difference \((P < 0.05)\). Nematicides did not significantly affect soil nematode abundances of any nematodes at harvest in either year. At midseason, and 1,3-D at either rate significantly reduced stunt nematode \((Tylenchorhynchus\) spp.) soil abundances compared with control in 2019 and 2020 whereas terbufos was effective in 2019 only. Terbufos significantly reduced stubby-root nematode \((Paratylenchus\) spp.) abundances compared to control at mid-season of 2019 but showed no significant difference in 2020. In 2019, all nematicide treatments significantly reduced lesion nematode populations \((Pratylenchus\) spp.) at midseason compared to control but there was no significant difference in reduction in 2020. Sting nematodes \((Belonolaimus longicaudatus)\) were not significantly reduced relative to control by any treatments in 2019 or 2020. The population of free-living nematodes was highly reduced by any nematicide treatment at midseason in 2019, but not affected in 2020. Terbufos significantly increased yield compared to control in 2019 and 2020. The results of this study could better assist growers to make informed nematicide application choices in corn production.

EVALUATING SOIL CORE INTEGRITY ON THE EFFICIENCY OF PLANT-PARASITIC NEMATODE EXTRACTION FOR GOLF COURSE GREENS. Tucker, Matthew\(^1\), D. McCall\(^1\), and J. Eisenback\(^1\). \(^1\)Virginia Tech, Dept. of Soil Plant and Environmental Sciences, Blacksburg, VA 24061.

Sampling for nematodes on golf courses consists of multiple soil cores ranging from 1.7 to 2.5cm in diameter. Cores typically remain intact during elutriation, potentially trapping plant-parasitic nematodes (PPN) within the core. The goal of this study was to determine if manipulating soil core integrity affects the efficiency of extraction from samples. Soil cores were collected from a ‘007’ bentgrass putting green in Blacksburg, VA at a depth of 15cm. Collected cores and soil material were mixed in a bucket to produce one homogenous sample. Each subsample contained five soil cores and additional soil totaling 250 mL. The integrity of the soil cores in each subsample was altered by the following treatments: 1) cores intact, 2) cut with scissors into 4–8 pieces perpendicular to the length of the core, 3) shredded by hand into 4–8 pieces, and 4) blended for two minutes on high. Four subsamples, one from each treatment, were randomly assigned and elutriated simultaneously in a four-day semi-automatic elutriator. This extraction was repeated five times for a total of 24 subsamples. Extracted nematodes were counted with a microscope and identified to genus. Nematode counts were analyzed with JMP Pro 15 (Cary, NC) to determine differences in treatments. An ANOVA of means showed no significant differences in the total number of PPN extracted by treatment. There were also no significant differences of treatment by genus. These results indicate that soil core integrity does not affect extraction of PPN from golf greens. Repetition of this study with samples from other locations, with differing turfgrass canopy health levels, and from different turfgrass cultivars/species is necessary to validate the implications of this study.

AUGMENTATION OF MELOIDOGYNE INC boat M AND R OTYLENCHUS R ENIFORMIS RESISTANT COTTON CULTIVARS WITH CORTEVA AGRI SCIENCE NEMATICIDES FOR YIELD ENHANCEMENT. Turner, A. Kate\(^1\), K. S. Lawrence\(^1\), S. Graham\(^1\), N. Potnis\(^1\), S. Brown\(^1\), and J. Richburg\(^1\). \(^1\)Auburn University, Dept. of Entomology and Plant Pathology, Auburn, AL 36849, \(^2\)Auburn University, Crop Soils and Environmental Science, Auburn, AL 36849, \(^3\)Corteva Agriscience, Headland, AL 36345.

Meloidogyne incognita (root-knot nematode) and Rotylenchulus reniformis (reniform nematode) accounted for an estimated 7% of the cotton lost in Alabama in 2020. New nematode resistant cotton cultivars and new nematicicides are becoming available to help manage nematode yield reductions. The objectives of this study were: 1) to determine the yield potential of the new \(M.\) incognita resistance variety PHY 360 W3FE and the \(R.\) reniformis resistant variety PHY 332 W3FE in nematode infested fields and 2) to determine the additional benefit of adding the new nematicide fluazaindolizine, with Vydate C-LV (oxamyl), and the seed treatment TRIO™ with genetic resistance to further enhance yields. TRIO™ is an on-seed application of products including fungicides, insecticides, and biological nematicides. In 2020, four field trials were established in nematode infested fields and arranged as a RCBD with five replications. A Vydate C-LV and fluazaindolizine mixture was applied at planting as an in-furrow spray across two resistant cultivars, PHY 360 W3FE and PHY 332 W3FE, and a susceptible cultivar, PHY 340 W3FE to further reduce nematode population levels. Field trials indicated that both \(M.\) incognita and \(R.\) reniformis eggs per gram of root were significantly \((P \leq 0.05)\) lower on the resistant cotton cultivars, PHY 360 W3FE and PHY 332 W3FE, at 45 days after planting compared to the control PHY 340 W3FE without nematicides. Meloidogyne incognita population levels were 84% lower on PHY 360 W3FE compared to PHY 340 W3FE and \(R.\) reniformis populations were 78% lower on the PHY 332 W3FE variety compared to PHY 340 W3FE. Nematode eggs per gram of root were further reduced after addition of Vydate C-LV and fluazaindolizole to both susceptible and resistant varieties. In the \(M.\) incognita tests, PHY 360 W3FE with TRIO™ + Vydate C-LV + fluazaindolizole at the high nematicide rate supported the greatest lint yield \((1571\) kg/ha), which was increased by \(419\) kg/ha over the lowest yielding treatment, PHY 340 W3FE + TRIO™ \((1152\) kg/ha). The addition of the nematicides improved yield by 34 and \(15\) kg/ha for PHY 340 W3FE and PHY 360 W3FE, respectively. In the \(R.\) reniformis tests, PHY 332 W3FE with TRIO™ + Vydate C-LV + fluazaindolizole at the medium nematicide rate, supported the greatest yields \((2137\) kg/ha) which was increased by \(1288\) kg/ha over the lowest yielding treatment, PHY 340 W3FE. The addition of the nematicides improved yield by \(572\) and \(293\) kg/ha for PHY 340 W3FE and PHY 332 W3FE, respectively. Overall, the use of the resistant varieties significantly increase yield while limiting nematode population density; the addition of the nematicides also further enhanced yields of the PHY 360 W3FE and PHY 332 W3FE, nematode resistant varieties.

EFFECTS OF TEMPERATURE ON PLECTUS MURRAYI LIFE CYCLES. Velez, Brandon\(^1\), and C. Robinson\(^2\). \(^1\)Brigham Young University, Dept. of Biology, Provo, UT 84602, \(^2\)Brigham Young University, Dept. of Microbiology and Molecular Biology, Provo, UT 84602.

The effects of global warming on Antarctic ecosystems can be more clearly understood as we study how temperature changes affect soil fauna within these ecosystems. Found in the lower elevation levels of the McMurdo dry valleys, the mesophilic animal \(Plectus murrayi) has been observed to be resistant to an extreme range of temperatures. Our preliminary experiment studying \(P.\) murrayi thermal viability expressed a continual decrease in populations reared at temperatures above \(22°C\) and below \(10°C\), with homeostatic populations at temperatures in between. The observed patterns of these populations prompt further analysis of the life cycles of these nematodes at this range of temperatures. We hypothesize that the cause of this population decline is related to the life cycles of these nematodes and their
abilities to mature and reproduce dependent upon the temperatures they are reared in. To observe the effects of temperature on *P. murrayi* life cycles, we placed a singular, mature worm on 21 agar plates and held them at 10°C, 15°C, 20°C, 22°C, and 25°C over an extended period of time. Counts were made each day to identify the number of reproductive events which were then used to gauge the life cycles of these worms. By observing the birth, growth, and death of *P. murrayi* at these temperatures, the effects of global warming on their ability to reproduce would be more greatly understood and applied to the context of Antarctic faunal community health and persistence amidst rising global temperatures.

A CYST NEMATODE EFFECTOR TARGETS THE ARABIDOPSIS HAESA LEUCINE-RICH REPEAT RECEPTOR-LIKE KINASE. **Verma, Anju**, M. Liu, J. C. Walker, T. Hewezi, T. J. Baum, and M. G. Mitchell. 1University of Georgia, Dept. of Plant Pathology and Institute of Plant Breeding, Genetics, and Genomics, Athens, GA 30602, 2University of Missouri, Division of Plant Sciences and Bond Life Sciences Center, Columbia, MO 65211, 3University of Missouri, Division of Biological Sciences, Columbia, MO 65211, 4University of Tennessee, Dept. of Plant Sciences, Knoxville, TN 37996, 5Iowa State University, Dept. of Plant Pathology and Microbiology, Ames, IA 50011.

Cyst nematodes are a major threat to agriculture and represent a significant constraint to global food security. These phytomnematodes secrete effector proteins via a styllet into root cells to suppress plant defenses and modulate developmental programs that give rise to a specialized feeding site called a syncytium. The syncytium arises from a single initial cell which expands along the vasculature by fusion of neighboring cells through local cell wall dissolution. The extensive cell wall remodeling during syncytium formation is likely under the control of multiple nematode effectors, but the precise mechanisms remain largely unknown. The novel 2D01 effector protein belongs to a highly expanded superfamily of effectors with multiple variants present in the genomes of cyst nematodes. The soybean cyst nematode *Heterodera glycines* 2D01 and sugar beet cyst nematode *H. schachtii* (Hs) 2D01 sequences are highly conserved. 2D01 expression is highly upregulated in the dorsal esophageal gland cell of parasitic life stages implicating this effector in feeding cell establishment. The subcellular localization of Hs2D01 was determined by transient expression in *Nicotiana benthamiana* leaves. When Hs2D01 was expressed without a secretion signal peptide (SP) and fused to green fluorescent protein (GFP), Hs2D01 localized in the cytoplasm. To identify potential host protein targets of 2D01, we used Hs2D01ΔSP as a bait to screen a prey library generated from *Arabidopsis thaliana* roots infected with *H. schachtii* and identified HAESA (HAE), a plasma membrane-associated receptor-like kinase (formerly named RLK5) that harbors an extracellular LRR domain and an intracellular kinase domain. The 2D01 effector protein was found to interact with the intracellular kinase domain of this receptor. Bimolecular fluorescence complementation (BiFC) experiments provided further validation of HAE as a host target of Hs2D01. Histochemical analysis of nematode-infected transgenic plants harboring a HAE promoter::β-glucuronidase reporter gene showed increased activity of the HAE promoter at nematode feeding sites where HAE, thus, could serve as a viable target for Hs2D01. Consistent with a role in syncytium formation, a HAE and HAESA-LIKE2 (HSL2) double mutant showed a significant decrease in the number of female nematodes developing on the roots of the mutant plants compared with wild-type Col-0. HAE is involved in a signaling pathway that activates several cell wall-modifying enzymes important for cell separation during abscission and lateral root emergence. More recently, HAE has also been implicated to play a role in plant defense. Taken together, our results suggest that the 2D01-HAE interaction may manipulate the HAE signaling pathway to promote cyst nematode parasitism.

**FAGUSTAT: INVESTIGATING THE THREAT OF BEECH LEAF DISEASE IN EUROPE.** Viena, Nicole, N. Ebrahimi, A. Haegeman, A. van Bruggen, N. Ogris, S. Sirc, B. Gerić Stare, T. Prior, A. Pérez Sierra, M. Groza, M. Coman, M. J. Hurley, D. Lanterbecq, S. Van Kerkhove, and Q. Léory. 1Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Belgium, 2Netherlands Food and Consumer Products Safety Authority (NVWA), the Netherlands, 3Slovenian Forestry Institute (SFI), Slovenia, 4Agricultural Institute of Slovenia (KIS), Slovenia, 5Fera Science, UK, 6Forest Research (FR), UK, 7National Phyto sanitary Authority (NPA), Romania, 8Department of Agriculture, Food and the Marine (DAFM), Ireland, 9Research Center for agronomy and agro-industry HEPH–Condorcet (CARAH), Belgium, 10Ornamental Plant Research (PCS), Belgium, 11Observatoire Wallon de la Santé des Forêts (OWSF), Belgium.

Beech Leaf Disease (BLD) has been reported from several northeastern states of the USA, as well as from Canada (Ontario). The cause of this emerging disease is still not fully understood. It was demonstrated that a nematode species is involved in BLD: *Litylenchus crenatae* subsp. *mc Cannii*. The nematode was isolated from leaves and buds of *F. grandifolia* (American beech) but was also found on *F. sylvatica* (European beech). In Japan, *L. crenatae* was isolated from leaves of *F. crenata*, but has not been associated with damage. Pathways of transmission are still unknown. The European beech is one of the most popular forest and ornamental trees in Western and Central Europe. It is not known if BLD or *Litylenchus* spp. occur in Europe. In FAGUSTAT, a Euphresco project, we want to increase awareness of BLD in Europe and make a first assessment of its status in the region. This will be done through surveys on *Fagus* spp. for symptoms of BLD in forests, parks, botanical gardens, and nurseries in the six participating countries (Belgium, the Netherlands, Romania, Slovenia, United Kingdom and Ireland). Beech leaves, buds, but also nuts, will be analysed for the presence of nematodes. Nuts might play a role in nematode transmission and have not been fully investigated to date. We will also investigate possible ways of entry and spread and plan to study the biology of the nematode and the epidemiology of BLD in European beech cultivars under local climatic conditions. This will be carried out in growth chambers (under biosafety conditions) as well as on trees if the nematode is found. In addition, we intend to investigate the microbial community of leaves and buds using high-throughput sequencing (HTS) technology. This will enable comparison of the associated microbiomes between regions and between healthy and infected leaves. For the latter, we count on information obtained in infested regions, and possibly in Europe. The main purpose of this poster presentation is to elaborate the outline of the project and search for networking possibilities, especially non-European nematologists who are confronted with BLD. In this project, where each partner finances its own contribution, we want to share findings and experiences to urge measures to curtail BLD in an international context.

IDENTIFICATION OF NEW NEMATODE EFFECTOR TARGET GENES OF ECONOMICALLY IMPORTANT MIGRATORY NEMATODES. **Vieira, Paulo.** Virginia Tech, School of Plant and Environmental Sciences, Blacksburg, VA 24061.
Infection. The variations) for both trials revealed that disease incidence and nematode community analysis. Root pieces of asparagus were plated on Komada medium to estimate the percentage of roots colonized by the migratory nematodes Pratylenchus penetrans and Radopholus similis. Analyses of gene contents for these species revealed a diverse and emergent repertoire of effectors, which has been shaped by various evolutionary events including neofunctionalization, lateral gene transfer and possibly by de novo gene birth and have been largely overlooked from a historically sedentary endoparasite-centric stance. Considering the damage caused by these migratory nematodes, the expanded and novel effector repertoires identified for P. penetrans and R. similis represent a series of new targets for the development of biotechnological alternatives for nematode control.

Metatranscriptomics for the discovery of novel RNA viruses in nematodes and other soil-inhabiting organisms. Vieira, Paulo1, S. A. Subботин1, N. Alkhароф2, J. D. Eisenback3, and L. G. Nemchinov4. 1Virginia Tech, School of Plant and Environmental Sciences, Blacksburg, VA 24061, 2USDA-ARS, Beltsville Agricultural Research Center, Molecular Plant Pathology Laboratory, Beltsville, MD 20705, 3California Department of Food and Agriculture, Plant Pest Diagnostic Centre, Sacramento, CA 95833, 4Towson University, Department of Computer and Information Sciences, Towson, MD 21204.

In recent years, several new viruses infecting free-living, plant- and animal-parasitic nematodes have been described. The previous characterization of nematode-associated viruses was specific to single nematode species. The advent of next-generation sequencing allowed the detection and identification of new viruses associated with a myriad of soil and aquatic micro-organisms. Thus far, no comprehensive research focusing on metagenomic analysis of the nematode virome has been carried out. In this work, we have attempted to fill the gap in our knowledge by investigating viral communities associated with soil-inhabiting nematodes which included the full range of nematode trophic groups. Soil samples were collected from four different states in the US (Maryland, Virginia, Florida, and California), and processed for extraction of nematodes and soil-inhabiting microorganisms. This research explored the feasibility of using pooled soil samples for study of viral metagenomics and provided an overall view of the virome associated with soil-inhabiting nematodes. A remarkable diversity of RNA viruses infecting soil-inhabiting nematodes and associated microorganisms in natural environment was unveiled, including a significant number of novel viral species.

Watermelon (Citrullus spp.) transcriptome analysis in response to southern root-knot nematode (Meloidogyne incognita) infection. Waldo, Benjamin1, W. B. Rutter1, W.P. Wechter4, and A. Levi4. 1US Vegetable Lab, USDA-ARS, 2700 Savannah Hwy, Charleston, SC 29414

Watermelon (Citrullus spp.) is an important crop grown in the US with a farm gate value at $575 million. The southern root-knot nematode (Meloidogyne incognita) is an important pathogen of watermelon in the southeastern US that can significantly reduce watermelon yield. Genetic resistance is a fundamental tool used to manage root-knot nematodes in several crops, lessening dependency on nematicides. While no M. incognita resistance is currently available in cultivated watermelon (Citrullus lanatus), moderate resistance has been documented in some wild watermelon (Citrullus amarus) lines, suggesting these lines could be used source for breeding M. incognita resistance into commercial watermelon. In our study, we used an RNAseq approach to two investigated the transcriptional changes in two C. amarus lines USVL114 (M.i. susceptible), USVL246 (M.i. resistant), and the commercial C. lanatus cultivar ‘Charleston Grey’ (M.i. susceptible) to M. incognita infection at three time points (5dpi, 15 dpi, and 33 dpi). Our results indicate that unique sets of genes are expressed within each of these lines in response to M. incognita infection, and we have identified candidate genes that are differentially expressed in resistant and susceptible lines under infected conditions. These candidate genes require further investigation to determine if they could be useful targets for breeding M. incognita resistance into cultivated watermelon.

Relationships between nematode community and incidence of asparagus crown and root rot. Wang, K.-H., P. Waisen, R. Paudel, S. Budhathoki and J. Uyeda. University of Hawaii at Manoa, Honolulu, HI 96822.

Fusarium crown and root rot caused by F. oxysporum f. sp. asparagi (Foa) is a major disease of asparagus worldwide. The fungus survives in the soil indefinitely and can interact with root-knot nematodes (Meloidogyne spp.) to cause a replant problem. Managing soil health has been suggested to help asparagus tolerate the disease pressure. Two field trials were conducted in Wailua, HI to assess the effects of a series of soil biostimulants on disease incidence. Pratylenchus penetrans was collected at 2-month intervals and subjected to soil respiration test (Solvita Gel System, Solvita and Woodend Laboratory) and nematode community analysis. Root pieces of asparagus were plated on Komada medium to estimate the percentage of roots colonized by Foa. Disease incidence was rated in the field at each sampling date. Canonical Correspondence Analysis (first two axes explained 91% of the variations) for both trials revealed that disease incidence and Fusarium colonization on Komada medium were highly correlated,
but they were not related to abundance of root-knot nematodes in the soil. However, these parameters were related to nematode eggs and root-knot nematodes/g root of asparagus. In Trial I, Fusarium colonization on Komada and disease incidence were negatively related to Enrichment Index (EI) and Structure Index (SI), but positively related to Channel Index (CI) indicating soil treatments that increased nutrient enrichment and improved soil food web structure would lead to less disease incidence. In Trial II, disease incidence was negatively related to abundance of bacterivores and fungivores, EI but not to SI and CI. This study demonstrated that enhancement of soil health can reduce Fusarium crown and root rot disease on asparagus.

DEVELOPMENT OF AN INTEGRATED MANAGEMENT STRATEGY FOR THE INVASIVE GUAVA ROOT-KNOT NEMATODE (MELIODOGYNE ENTEROLOBII) IN LOUISIANA. Watson, Tristan1, and J. S. Rezende1. 1Department of Plant Pathology and Crop Physiology, LSU AgCenter, Baton Rouge, LA 70803.

Since 2018, the guava root-knot nematode (Meloidogyne enterolobii) has been detected entering Louisiana twice on contaminated sweetpotato planting material imported from North Carolina and twice on ornamental plants imported from Florida. Entry into the state on contaminated sweetpotato storage roots poses a serious threat to crop production in Louisiana, as many of the crops rotated with sweetpotato are highly susceptible to this nematode, including soybean and cotton. Our previous studies have suggested that corn and grain sorghum varieties are non-hosts to M. enterolobii and could be used as a component of an integrated management strategy for this pest should it establish in the future. The aim of this study was to preemptively develop an integrated management plan for M. enterolobii specifically tailored to production practices in Louisiana. Greenhouse, growth chamber, and in vitro lab studies were conducted in 2020 to evaluate the suitability of commercially available soybean varieties, winter cover crops, and non-fumigant nematicides for management of M. enterolobii. All nine soybean varieties evaluated were susceptible to M. enterolobii parasitism; however, variation in susceptibility among varieties suggests that some level of resistance to this nematode may exist in currently available germplasm. Of the eight winter cover crop species that were evaluated, only winter rye and winter wheat did not support M. enterolobii reproduction. In the in vitro nematicide exposure studies, both M. enterolobii and M. incognita showed similar sensitivity to oxamyl, flusulfone, fluopyram, and fluazaindolizine. Greenhouse nematicide efficacy trials on sweetpotato demonstrated similar efficacy toward M. enterolobii and M. incognita when the four different nematicides were applied at the label recommended rate; however, flusulfone and fluazaindolizine provided a greater reduction in root parasitism by both Meloidogyne species relative to that of oxamyl and fluopyram. Overall, our data suggest cover cropping with winter wheat or winter rye between cash crops alongside the use of non-fumigant nematicides during cash crop establishment shows potential to be a component of an integrated management strategy for M. enterolobii in Louisiana.

IMPLICATIONS OF THE RATE OF DECLINE OF SUGARBEET CYST NEMATODE IN CENTRAL CALIFORNIA UNDER NONHOST CROPS FOR GROWING SUGARBEETS AS BIOFUEL. Westerdahl, Becky1, E.P. Caswell-Chen1, and F.R. Kegel. 1University of California, Davis, CA 95616, 2University of California Cooperative Extension, Stockton, CA 95206.

Crop rotation has been a commercial practice for managing sugarbeet cyst nematode (Heterodera schachtii, SBCN) on sugarbeets since the 1950s. Research conducted in southern California established that SBCN populations decline at the rate of 40 to 80 percent per year, leading to estimates that 3 to 4 year rotations to nonhost crops would be sufficient to reduce SBCN densities to nondamaging levels. Following grower reports that much longer rotations were needed in northern California, trials were conducted to establish the rate of decline of SBCN in the San Joaquin Valley. Seven commercial fields with a history of SBCN infestation were sampled periodically for 6.5-years. In each field, 10 circular subplots located 30.5 meters apart (each with a 6 m radius) were established with reference to a permanent landmark. On each sampling date, 12 subsamples from each subplot were taken randomly from the top 0-30 cm of soil and composited into a single sample. Standard techniques were utilized to extract and count cysts and eggs from soil samples. Average yearly rates of population decline in the sampled fields ranged from 11.4 to 25.8 percent. This finding has implications for SBCN management in California sugarbeets grown for biofuel, as the lower decline rates indicate that nonhost rotations of longer duration than previously anticipated may be necessary.

EFFECTS OF SALTR’ SEED TREATMENT, ACTIVE INGREDIENT PYDIFLUMETOFOEN, ON EGGS AND JUVENILES OF THE SOYBEAN CYST NEMATODE. Wlezien, Elizabeth and G. L. Tylka. Department of Plant Pathology and Microbiology, Iowa State University, Ames, IA 50011.

It is important to understand how different stages of a nematode life cycle are affected by nematode-protectant seed treatments. Some have been shown to alter nematode hatching, movement, root penetration, and reproduction. Saltr’ seed treatment, active ingredient pydflumetofen, is marketed for control of soybean sudden death syndrome disease, caused by Fusarium virguliforme, and for management of soybean cyst nematode (SCN), Heterodera glycines. Laboratory experiments were conducted to study effects of Saltr’ seed treatment on hatching and chemotaxis of SCN. Seeds of three SCN-resistant soybean varieties (GH2981X, S24-K2, Jack) and the susceptible variety Williams 82 were treated with Saltr’ plus base fungicides (thiamethoxam, mefenoxam, fludioxonil, sedaxane), the base fungicides alone, or left untreated resulting in a 4 by 3 factorial treatment arrangement. Exudates from treated seeds and exudates from radicles grown from treated seeds were collected and used in hatching and chemotaxis assays. Also, leachates from soil planted with treated seeds were collected and used in experiments. To evaluate effects on hatching, SCN eggs were incubated in exudates or leachates at 25°C and hatched second-stage juveniles (J2s) were counted on days 3, 7, and 14. Unhatched eggs remaining on day 14 were counted, and percent hatching was calculated. There was no interaction of the main factors of seed treatment and variety and no significant main effect of seed treatment on hatching in exudates or leachates. However, there was a significant main effect of variety in seed hatch and exudates. Hatchling in seed exudates from the resistant variety Jack was significantly less than with the other three varieties and hatchling in leachates of the susceptible variety Williams 82 was greater than with the other three varieties. To study effects on movement of SCN J2s, the leachates and exudates described above were deposited into randomly selected reservoirs at the ends of lanes of microfluidic chemotaxis chips and deionized water was placed in the opposite reservoir of the same lanes. Newly hatched SCN J2s were placed in the center of
each lane, and the chips were incubated at 25°C for 24 hours then observed microscopically. The number of J2s that moved towards or away from the treatments during incubation period were counted. The SCN J2s were not attracted to or repelled by seed exudates or by leachates. However, exudates from radicles of the resistant varieties GH2981X and Jack grown from seeds treated with Saltro® plus the base fungicides significantly repelled J2s of SCN. In contrast, J2s were not attracted or repelled by exudates of radicles of the same two varieties grown from untreated seeds or seeds treated with just the base fungicides; the effect was associated only with Saltro®. Repelling J2s from radicles may be a mechanism of nematode protection provided by Saltro®, although one would expect the effect to be consistent among all soybean varieties.

GLOBAL COMPARATIVE GENOMICS OF RADOPHOLUS SIMILIS. Wram, Catherine1, C. Hesse2, P. Vieria3, S. Eves-van den Akker4, R. Myers5, D. Humphreys-Pereira6, D. Coyne7, P. DiGennaro8, H. Lopez-Nicora9, A. Cedeno10, O. Emmanuel11, K. Saikai12, L. Duncan13, O. Guzman14, O. Adewuyi15, J. Cobon16, B. Chinnasari17, R. Inserra1, and I. Zasada1. 1Oregon State University, Dept. of Botany and Plant Pathology, Corvallis, OR 97331, 2USDA-ARS HCRU, Corvallis, OR 97331, 3USDA-ARS Molecular Plant Pathology Laboratory, Beltsville, MD 20705, 4School of Plant and Environmental Sciences, Virginia Tech, Blacksburg, Virginia, 24061, 5Department of Plant Sciences, University of Cambridge, UK, 6Daniel K. Inouye U.S. Pacific Basin Agricultural Research Center, USDA ARS, Hilo, Hawaii, 96720, 7Laboratorio de Nematología, Centro de Investigación en Protección de Cultivos, Escuela de Agronomía, Universidad de Costa Rica. San José, Costa Rica, 2060, 8International Institute of Tropical Agriculture, PMB 5320, Oyo Road, Ibadan, Nigeria, 9Entomology and Nematology Department, University of Florida, Gainesville, FL 32611, 10Departamento de Producción Agrícola, Universidad San Carlos, Asuncion, Paraguay, 11Corteva Agriscience, Costa Rica, 12Nematology Research Unit, Department of Biology, Ghent University, K.L. Ledeganckstraat 35, 9000 Gent, Belgium, 13University of Florida, IFAS Citrus Research and Education Center, Lake Alfred, FL 33850, 14Laboratorio de Nematología, departamento de Producción Agropecuaria, Universidad de Caldas, Manizales, Colombia, 15Department of Agriculture and Fisheries, Queensland Government, Brisbane QLD 4001, Australia, 16Department of Plant Pathology, Kasetsart University, Bangkok, 10900 Thailand, 17Division of Plant Industry, Florida Department of Agriculture and Consumer Services, Gainesville, FL 32614.

Radopholus similis is a devastating pest to many economically important crops including banana and citrus. To better understand host preference, effector diversity, global relatedness, and associated endosymbiont and microbial communities of R. similis, 22 populations were received from five continents (Nigeria, Kenya, Uganda, Colombia, Costa Rica, Australia, Thailand, Malaysia, and the United States of America), which were genomically sequenced. Populations originated from a range of hosts, including banana, plantain, citrus, and ornamental plants. Meta-genomes were assembled for each population using metaSPAdes and the taxonomy of assembled contigs was identified using BlobTools. From meta-genome assemblies, bacterial endosymbionts were identified and further filtered using BlobTools to contain only nematode identifying contigs. BUSCO (Benchmarking Universal Single-Copy Orthologs) scores were calculated for each filtered assembly and QUAST was used to calculate assembly statistics. Assemblies ranged from 48-58% in BUSCO score completeness, genome size was on average ~50 Mb, CG content ranged from 47%-49%, and N50 scores comprised on average 15,737 contigs. Using quality filtered reads, >120,000 single nucleotide polymorphisms (SNPs) were identified across the different populations, using Freebayes, which were filtered using VCFtools. SNPs were identified after mapping to a previously published R. similis genome using BWA (NCBI Accession No. VAHH00000000). SNPs were then used to generate UPGMA phylogenomic trees using R packages “vcf”, “poppr” and “adegenet”. Phylogenomic trees revealed that populations generally fell into clades based on geographic location, irrespective of whether the populations contained the endosymbiont bacteria Wolbachia. Multi-genic mitochondrial trees were also generated using across all populations to confirm SNP results. Additionally, SNPs were also used to generate PCA plots to assess genomic similarities in populations based on geographic location, host, and effector content.

AN OMICS APPROACH TO ANSWERING APPLIED NEMATOLOGY QUESTIONS. Wram, Catherine1, C. Hesse2, and I. A. Zasada2.
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Understanding the complexities of how plant-parasitic nematodes interact with their host, the conditions that dictate host preferences, and the mechanisms behind chemical and biological controls can help guide their management. As sequencing technologies have become increasingly more accessible and economical, the use of genetic resources is now available to help address these research questions. Two case studies of the use of -omics sequencing to help address basic questions about plant-parasitic nematodes are presented here. In one study, the aim was to provide foundational knowledge of how novel the nematicides fluopyram, fluensulfone, and fluazaindolizine affect Meloidogyne incognita movement, reproduction, and transcription in comparison with the traditional nematicide oxamyl. To ask these questions, 24-hr dose-response curves were established for M. incognita second-stage juveniles (J2) exposed to the nematicides. Using RNAseq, transcriptional changes were examined in M. incognita J2 after a 24-hr exposure to the above nematicides. Although the most toxic nematicide fluopyram had limited impacts on expression of cellular detoxification or other stress-responses, expression in the citric acid cycle and oxidative phosphorylation pathways supported the mode-of-action, succinate dehydrogenase inhibitor. Fluensulfone and fluazaindolizine produced robust transcriptional responses with 1,208 and 2,611 differentially expressed genes, respectively. Expression data indicated two potential pathways of interest for modes-of-actions: β-fatty acid oxidation pathway and 2-Oxoglutarate dehydrogenase of the TCA cycle for fluensulfone and fluazaindolizine, respectively. Oxamyl negatively affected expression of cellular detoxification, but expression changes in acetylcholine neuron components also provided strong evidence to support its functionality as an acetylcholinesterase inhibitor. This study provided context for the physiological responses observed in M. incognita to nematicides. Radopholus similis was the focus of the second study. To better understand host preference, effector diversity, global relatedness, and associated microbial communities of R. similis, genomes were sequenced from 22 populations from five continents. Populations originated from a range of hosts, including banana, plantain, citrus, and ornamental plants. Single nucleotide polymorphisms (SNPs) were identified across the different populations in comparison to a previous published R. similis genome and used to generate phylogenomic trees. Phylogenomic trees revealed that populations generally fell into clades based on geographic location unless the population contained the endosymbiont bacteria Wolbachia. Multi-genic mitochondrial trees were also generated to confirm SNP results. SNPs were used to generate PCA plots to assess genomic
similarities in populations based on geographic location, host, and effector content. These results provide context for host preference, global movement of *R. similis*, and new genomic resources for the nematology community.

**PINEWOOD NEMATODE DIAGNOSTIC SERVICES IN NORTH CAROLINA DEPARTMENT OF AGRICULTURE & CONSUMER SERVICES.** Ye, Weimin. 1Nematode Assay Section, Agronomic Division, North Carolina Department of Agriculture & Consumer Services, Raleigh, NC 27607.  

*Bursaphelenchus xylophilus*, the pine wood nematode (PWN), is the causal agent for pine wilt disease. The nematode was first discovered in the timber of longleaf pine (*Pinus palustris*) in Louisiana, USA. PWN is native to North America where it causes relatively minor damage to native conifers but is labeled as an EPPO-A-2 pest and a quarantine nematode for many countries because of its potential for destruction of their native conifers. The Agronomic Division of the North Carolina Department of Agriculture & Consumer Services has a publicly-operated nematode assay lab providing nematode diagnostic services and control recommendations. In the past ten years, due to more strict regulations on PWN, many pine wood samples have been submitted to the lab. From fiscal year 2012 to 2021, 65,310 pine wood samples were analyzed and 6,753 reports were generated for USDA/APHIS/PPQ in connection with the issuance of phytosanitary certificates for export of pine wood logs. A large industrial funnel (30-cm diameter, 32-cm high, 6800-ml water capacity) and a movable rack (2.2-m x 1-m x 1.3-m H, 18 samples in total per rack) were designed and used to extract PWN. The required sample size is minimum 200 grams of wood-drilled shavings shipped overnight to the lab. Identification of PWN is accomplished by using traditional morphology, primarily by female tail shape and vulva flap and male spicule and bursa. The identification can also be confirmed by DNA sequencing and real-time-PCR if necessary to comply with the zero-tolerance export regulations. Overall, PWN prevalence in submitted samples has been 2.08%. These results indicate the low presence of PWN in exported pine wood logs and the importance of regulatory measures and laboratory testing.

**BACTERIALLY SECRETED DEFENSE PEPTIDE PEP1 STIMULATES ROOT-KNOT NEMATODE RESISTANCE.** Zhang, Lei1,2, K. Hamel1, and C. Gleason1. 1Washington State University, Dept of Plant Pathology, Pullman, WA 99164, USA, 2Current address: Purdue University, Dept. of Botany and Plant Pathology and Dept. of Entomology, West Lafayette, IN 47907.  

The root-knot nematode *Meloidogyne chitwoodi* is present in the Pacific Northwest region of the United States and is a major pest of potatoes within the region, infecting both potato roots and tubers. The tuber infections lead to blemishes on the skin that significantly affect the value of the potatoes. There are no commercially available potato cultivars that are resistant to root-knot nematodes. We investigated the use of the potato defense elicitor StPep1 as a new method for root knot nematode control. StPep1 is a plant peptide that is made and released by the plant when it is under attack or damaged. The neighboring plant cells can detect the released StPep1, and this results in plant cells that are primed for enhanced immune responses. We found that exogenous treatment of potato roots with synthetic StPep1 reduced root-knot nematode galling by ~50%. The StPep1 treatment triggered changes in gene expression in the plant roots and leaves resulting in increased nematode resistance. Next, we wanted to create an alternative method of elicitor delivery to potato roots. We transformed the bacteria *Bacillus subtilis* to produce and secrete StPep1. Pre-treating potatoes with *B. subtilis* that secretes StPep1 resulted in a significant decrease in root-knot nematode galling without triggering a negative impact on plant growth. In addition, the *B. subtilis* treatment lacking synthetic StPep1 had no effect on galling, showing that the bacteria used in the experiments did not have antagonistic activity towards nematodes. Furthermore, we replicated our findings in tomato to illustrate the adaptability of the system in other crop plants. Pretreatments with *B. subtilis* secreting the tomato specific Pep1 significantly reduced tomato galling. Overall, plant defense elicitors secreted by bacteria can provide enhanced immunity against root-knot nematodes.