

## ABSTRACTS

### ABSTRACTS FROM 2009 SON/SES MEETING

TRAIN-THE-TRAINER WORKSHOPS AS A PLATFORM FOR EXTENDING NEMATOLOGICAL OUTREACH IN THE NORTHEAST REGION OF THE U.S. **Abawi<sup>1</sup>, George S., B. K. Gugino<sup>2</sup>, J. A. LaMondia<sup>3</sup>, and D. A. Neher<sup>4</sup>.**

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A full-day, hands-on workshop was developed to educate and train participants on nematode biology and ecology, diagnosis of symptoms, sampling, on-farm visual assessment using soil bioassays for *Meloidogyne hapla* and *Pratylenchus penetrans* and management of plant-parasitic nematodes on vegetables, small fruit and ornamentals. With financial support from the NE-SARE Professional Development program, from 2007 to spring 2009, a total of nine workshops have been held in New York, Connecticut, Vermont, Rhode Island, New Jersey and Maine. The participants were comprised of county extension educators, crop consultants, university personnel, federal and state government employees and interested growers. The workshops were advertised and promoted in state and regional newsletters, email list-serves, grower meetings, web-postings and through direct communication with project leaders, county extension educators and previous workshop participants. Participants received a binder containing hardcopy resources as well as a CD-Rom containing workshop Power-Point presentations, fact sheets and bioassay protocols. In addition, soil sampling and bioassay kits for root-knot and lesion nematodes were also provided. The goal of these workshops is to facilitate the dissemination of knowledge on the diagnosis, assessment and management of plant-parasitic nematodes to enable growers to manage nematode problems on an as needed basis with the ultimate goal of encouraging growers to design a whole-farm nematode management plan (whole-farm nematode management IPM program). Specific examples of workshop activities and feedback from participants will be shared during the workshop session. A follow-up survey will be distributed to all participants in the upcoming year to assess how the skills and knowledge acquired during the workshop were incorporated into their various and/or communications with growers or if the participant was a grower what impact has it had on their production practices and pest management decisions.

CHANGES IN PROTEIN CONTENT AND ENZYMATIC ACTIVITY OF TOMATO PLANTS IN RESPONSE TO NEMATODE INFECTION. **Abd-Elgawad<sup>1</sup>, Mahfouz M. M., Sanaa S. A. Kabeil<sup>2</sup> and A. E. Abd El-Wahab<sup>3</sup>.** <sup>1</sup>Plant Pathology Department, National Research Centre, Dokki 12622, Giza, Egypt, <sup>2</sup>Mubarak City for Scientific Research and Technology, Borg-Elarab, Alexandria, <sup>3</sup>Department of Agricultural Zoology and Nematology, Faculty of Agriculture, Al-Azhar University, Cairo, Egypt Corresponding author E-mail: sanaa5769@yahoo.com

The tomato cultivars, Super Marmand and GS-12 were susceptible to the root-knot nematode *Meloidogyne incognita* while the cultivar Castle Rock was moderately resistant as demonstrated by the common root gall index, nematode-reproduction factor and plant growth parameters. Protein content as well as endo- and exo-glucanase activities in leaf extracts of these cultivars were estimated one week after *M. incognita* inoculation and/or addition of garlic extract (600 g ground garlic cloves/ l water) as biocontrol agent. Also, catalase,  $\beta$ -1,3-glucanase and peroxidase activities in plant roots differed among these treatments, two weeks after nematode inoculation. The effects of such treatments on the tested protein and enzymes were presented and discussed.

TROPHIC PHYLOGEOGRAPHY: A RESEARCH PROGRAM FOR IDENTIFYING DRIVERS OF SOIL FOOD WEB COMPOSITION AND CONCERTED PATTERNS OF CHANGE OVER TIME AND SPACE. **Adams<sup>1</sup>, Byron J., and D. H. Wall<sup>2</sup>.** <sup>1</sup>Department of Biology and Evolutionary Ecology Laboratories, Brigham Young University, Provo, UT 84602-5253, USA. <sup>2</sup>Department of Biology and Natural Resource Ecology Laboratory, Colorado State University, Fort Collins, CO 80523, USA.

A pressing issue facing ecosystem ecologists today is the ability to predict how biodiversity will respond to global changes (land use, climate change). Additionally, little is known of the roles biotic and abiotic factors play in ecosystem assembly over space and time. We suggest that understanding how biodiversity responded to change in the past offers a logical framework for examining the range of potential changes that can be expected to occur in the future. Research programs in historical ecology, evolutionary biology, and molecular systematics have developed analytical tools that can inform the universe of possible future evolutionary responses. We propose a novel method for investigating soil food webs and distribution ecology that treats the players in soil food webs as co-evolving entities in time and space, with additional consideration for geophysical constraints. We suggest that our approach can reveal patterns of soil community assembly over time and space, and serve as a framework to test hypotheses of biotic and geophysical drivers of trophic relationships.

**CORRELATIONS BETWEEN ABOVE-GROUND AND BELOW-GROUND DIVERSITY RESPONSE TO MANAGEMENT.** **Adl, Sina, A. Mills, A. Maharning, M. Murray, and J. Murphy.** Department of Biology, Dalhousie University, Halifax, NS, B3H 4J1 Canada.

We conducted a five year study of pasture management, including experimental plots and commercial pastures. The experimental plots consisted of four management intensity treatments replicated four times. These ranged from intensive management, to extensive and stock-piling. The commercial pastures represented a 50 year chronosequence of sustainable management. Soil chemical & physical parameters were correlated with above-ground and below-ground diversity. Details of pasture species response over time to treatment were correlated with bacteria functional diversity, fungal biomass, and the diversity of amoebae, nematodes, micro-arthropods, spiders and beetles. Nematode maturity index was estimated. The multivariate statistical analysis included, RDA, CCA, path analysis, structural equation modeling (with confirmatory factor analysis), and modeling of the whole food web with "Foodweb-kb". We summarize the main conclusions, including a shift to fungi-fungivory over a decades under sustainable management.

**TURNOVER OF BACTERIA BIOMASS IN SOILS BY PROTISTS.** **Adl, Sina.** Department of Biology, Dalhousie University, Halifax, NS Canada.

Most species of soil protists are bacterivores, with fewer species contributing to cytotoxicity, fungivory or invertebrate predation. With pseudopodia and filopodia cells explore and feed in crevices inaccessible to the cell itself. With 106 to 108 cells.g<sup>-1</sup> active in most soils the grazing impact on the bacteria biomass is not negligible. The main competing grazers are bacterivorous nematodes. I present data on the magnitude and rate of field abundance changes over days. Both excystment and reproduction contribute to population explosions. In a detailed laboratory study we established the functional response of an omnivorous ciliate on various prey at different temperatures. There was optimal foraging behaviour with adjustments in size and a hierarchy of preferred prey. Stable and radioactive isotopes were used to assay the amount of bacteria grazing by protists, and the consumers on protists. A <sup>14</sup>C labeling study showed protists to be ingested by bacterivorous nematodes. From a multi-year field study of above-ground and below-ground diversity, we included the protist biomass into soil food web models to visualize the relative distribution of biomass in the system. From these data we attempt to calculate bacteria biomass turnover and impact of protists on soil nutrient flux. The map of grazing by categories of protists shows some functional differentiation. In a laboratory study, we established mobility to be about 1 cm.day<sup>-1</sup> or less through the pore network. However, a field study showed that protists could not establish in disturbed soil, even after several months. The recovery of diversity is slow and requires several years, and this is consistent with our field chronosequence studies. Recovery of the habitat and ped structure seems to be a limiting factor. This has consequences on soil remediation and rate of recovery, and the interpretation of short agricultural studies.

**WORKSHOP: INTEGRATING SOIL OBSERVING AND SENSOR NETWORKS IN SOIL ECOLOGICAL STUDIES.** **Allen, Michael F., N. Hasselquist, M. Taggart, K. Kitajima R. Vargas, and E. Mayzlish-Gati.** Center for Conservation Biology, University of California, Riverside, CA 92521.

We are developing networks of soil sensors that can be coupled with high-resolution automated minirhizotron (AMR) units to track dynamics of soil organisms and processes. These networks are comprised largely of off-the-shelf components, which can be configured and spatially arranged to best address questions of interest. Included are sensors for CO<sub>2</sub>, temperature, soil moisture, soil water potential, nitrate, and ammonium. In addition, at each location, we have atmospheric sensors for PAR, air temperature, precipitation, and relative humidity. We also utilize sapflow, tower flux estimates, and leaf phenology imagery describing plant activity. From the data output, we can model in situ respiration (CO<sub>2</sub> production) and soil CO<sub>2</sub> flux (soil respiration) using diffusion models modified for soil conditions. We have embedded conventional minirhizotron tubes at all locations for root and rhizomorphs observations. We have designed and are testing an automated minirhizotron built around a USB-port microscope for observing individual hyphal dynamics. By coupling camera, plant, and soil flux activity, we can begin to relate both timing and lags regulating integrated activities of soil organisms and plants. Finally we add direct soil extractions coupled with buried slides extracted and sequenced to characterize the fungal taxa present. The sensors and camera systems are web-based, so we will link into the James Mount San Jacinto NRS to observe streaming datasets and images. We will describe some of the benefits of these integrated systems as well as discuss issues problematic and in need of additional research. Our goal is to provide an overview of the potential for use of this approach, identify potential problems that can be further addressed, and begin to develop a network of soil ecologists interested in collaborations.

**ECOSYSTEM SERVICES PROVIDED BY TURFGRASS AND LANDSCAPE PLANTINGS.** **Amador, Jose A.** Laboratory of Soil Ecology and Microbiology, 024 Coastal Institute, Univ. of Rhode Island, Kingston, RI 02881.

Landscape plantings can provide important – and often ignored – ecosystem services, playing a role in the regulation of carbon, nutrient and hydrologic cycles in urban and suburban ecosystems. We present data from three studies that evaluated different aspects of the ecosystem services provided by landscape plantings, including turf. In the first study, comparisons

among an established turf plot, a wooded area, and a corn field indicated that turf had values that were intermediate between the wooded area and the corn field for soil bulk density, infiltration rate and soil organic matter content. No differences among land uses were observed for soil C and microbial biomass C. By contrast, the CO<sub>2</sub> flux for the turf plot was similar to the wooded area, and higher than that for the corn field. In the second study, the effects of turf death on nitrate leaching under established turf were examined. Nitrate levels were higher in pore water below the root zone following turf death, a difference that persisted for a year. Carbon mineralization and microbial biomass C were not different between soils from healthy and killed plots. The mass of NO<sub>3</sub> leached from killed plots was three times that from healthy plots. In the third study, NO<sub>3</sub> levels in pore water below the root zone were compared in areas with turf, areas with seven different types of ornamental landscape plantings, and a wooded area. Pore water NO<sub>3</sub> concentrations below the root zone were highest under ground covers, unplanted-mulched areas, turf, deciduous trees, and evergreen trees, with no differences among these vegetation types. Lower values of NO<sub>3</sub> were observed under woodlands, annual and perennial flowers, and evergreen and deciduous shrubs. Mass losses of NO<sub>3</sub> due to leaching were lowest for the woodlands and highest under ground covers. Together, these studies suggest that landscape plantings can carry out some of the same ecosystem services provided by vegetation in unaltered landscapes, although their magnitude may differ. Furthermore, the type of planting is an important factor in determining whether positive or negative effects on ecosystem services are observed, particularly with respect to NO<sub>3</sub> leaching.

**BIOLOGICAL CONTROL OF THE ROOT-KNOT NEMATODE *MELOIDOGYNE INCOGNITA* BY ALGINATE PELLETS OF *PAECILOMYCES LILACINUS* AND *POCHONIA CHLAMYDOSPORIA*. Aminuzzaman, F., W.J. Duan, H.Y. Xie, and X.Z. Liu.** Key Laboratory of Systematic Mycology and Lichenology, Institute of Microbiology, Chinese Academy of Sciences, No.3, 1st Beichen West Road, Chaoyang District, Beijing 100101, China.

Two hundred and thirty five isolates of fungi associated with naturally infected eggs and females of root-knot nematodes, *Meloidogyne* spp., were isolated and screened by the tissue culture plate method. Twenty-seven isolates, including 4 *Paecilomyces lilacinus*, 10 *Pochonia chlamydosporia*, 11 *Fusarium* spp. and 2 *Acremonium* spp., with high levels of egg parasitism, egg hatch inhibition and juvenile mortality were obtained. The alginate pellet formulations containing *P. lilacinus* and *P. chlamydosporia* separately were developed and evaluated against the root-knot nematode *Meloidogyne incognita* on tomato under greenhouse conditions. In pot experiment, dried pellets of both fungi were applied at ratio of 0.2%, 0.4%, 0.8% and 1.6% (w/w, pellets/soil). The highest root galling reduction by *P. lilacinus* was 50%, while the highest nematode population decrease by *P. chlamydosporia* was 91% both at the application rate of 1.6%. In the greenhouse plot experiment, the control effectiveness of alginate pellet formulation of *P. lilacinus*, the fumigant nematicide (Dazomet) and the non-fumigant nematicide fosthiazate alone or the combinations of the fungus with either chemical nematicide was evaluated. A significant reduction in root galling index was obtained with all the treatments compared with the control. The root galling index was reduced up to 60, 46 and 21% by *P. lilacinus* pellets, 80, 69 and 86% by Dazomet + *P. lilacinus* and 70, 69% and 71 by fosthiazate + *P. lilacinus* 43, 96 and 157 days after of tomato transplantation, respectively. The control efficacy of root-knot nematode was higher by fungal pellets combined with nematicides than nematicides along, suggested that the combined application of the fungal agents with fumigant or fosthiazate could be one of useful strategy for root-knot nematode control.

**THE EFFECTS OF PLANT COMMUNITY COMPOSITION AND RICHNESS ON METHANE PRODUCTION AND IRON REDUCTION IN EXPERIMENTAL MESOCOSMS. Andrews, Sarah<sup>1</sup>, R. Schultz<sup>2</sup>, S.D. Frey<sup>1</sup>, and V. Bouchard<sup>2</sup>.** <sup>1</sup>The University of New Hampshire, Dept. of Natural Resources and the Environment, Durham, NH, 03824, <sup>2</sup>The Ohio State University, School of Environment and Natural Resources, Columbus, OH, 43210.

We conducted a controlled outdoor mesocosm experiment over two growing seasons to assess the effects of plant community composition and functional group richness on wetland function, with a focus on methane cycling dynamics. The mesocosms are located at the Waterman Agricultural and Natural Resources Laboratory on the main campus of The Ohio State University. Four emergent macrophyte functional groups (facultative annuals, obligate annuals, reeds, and tussocks) were chosen to represent a range of plants known to associate closely in natural wetlands and were defined based on physiological, morphological, and life history traits. The functional groups were arranged in a completely random full-factorial design, for a total of 16 treatments including a no-plant control (n=5). Plantings occurred in spring 2007 and again in spring 2008, and soil samples were collected in June and August 2007 and June, August, and November 2008. Three to five 2 cm diameter cores (0-10 cm) were collected randomly from each mesocosm and bulked for analysis. Soils were shipped to The University of New Hampshire, where sub-samples were analyzed for soil moisture, organic matter, pH, and inorganic N content. To determine methane production and iron reduction potentials soils were mixed with deionized water or substrate (200 mM acetate or formate), or deionized water plus an H<sub>2</sub>-CO<sub>2</sub> gas mix (20% H<sub>2</sub>, 5% CO<sub>2</sub>). A second set of water-only slurries was analyzed immediately for initial reduced iron content using the Ferrozine reagent. Vials were incubated anaerobically and headspace samples were taken four times over an 11 day period and analyzed for CO<sub>2</sub> and CH<sub>4</sub> content. Post-incubation a sub-sample from each slurry was analyzed for final reduced iron content. Both methane production and iron reduction potentials were enhanced in the presence of either formate or the H<sub>2</sub>-CO<sub>2</sub> gas mix compared to acetate or water.

Initial results suggest that neither methane production nor iron reduction potentials were significantly related to plant community composition, though there may be a relationship with functional group richness.

**LINKING ABOVE AND BELOWGROUND RESPONSES TO GLOBAL CHANGE AT COMMUNITY AND ECOSYSTEM SCALES.** Antoninka, Anita<sup>1</sup>, J. Wolf<sup>1,2</sup>, M. Bowker<sup>1</sup>, A.T. Classen<sup>1,3</sup>, and N.C. Johnson<sup>1</sup>. <sup>1</sup>Biological Sciences, Northern Arizona University, Flagstaff, AZ, 86011-5694, <sup>2</sup>Department of Mycology and Microbiology Laboratory, United States Department of Agriculture, Beltsville, MD, 20705, <sup>3</sup>Environmental Sciences Division, Oak Ridge Laboratories, Oak Ridge, TN 37831-6422. Department of Ecology and Evolutionary Biology, 569 Dabney Hall, University of Tennessee, Knoxville, Tennessee 37996.

Cryptic belowground organisms are difficult to observe and their responses to global changes are not well understood. Nevertheless, there is reason to believe that interactions among above- and belowground communities may mediate ecosystem responses to global change. We used grassland mesocosms to manipulate the abundance of one important group of soil organisms, arbuscular mycorrhizal (AM) fungi, and to study community and ecosystem responses to CO<sub>2</sub> and N enrichment. Responses of plants, AM fungi, phospholipid fatty acids (PLFA) and community-level physiological profiles (CLPP) were measured after two growing seasons. Ecosystem responses were examined by measuring net primary production (NPP), evapotranspiration, total soil organic matter (SOM), and extractable mineral N. Structural equation modeling was used to examine the causal relationships among treatments and response variables. We found that while CO<sub>2</sub> and N tended to directly impact ecosystem functions (evapotranspiration and NPP, respectively), AM fungi indirectly impacted ecosystem functions by influencing the community composition of plants and other root fungi, soil fungi and soil bacteria. We found that the mycotrophic status of the dominant plant species in the mesocosms determined whether the presence of AM fungi increased or decreased NPP. Mycotrophic grasses dominated the mesocosm communities during the first growing season, and the mycorrhizal treatments had the highest NPP. In contrast, non-mycotrophic forbs were dominant during the second growing season and the mycorrhizal treatments had the lowest NPP. The composition of the plant community strongly influenced soil N; and the community composition of soil organisms strongly influenced SOM accumulation in the mesocosms. These results show how linkages between above- and belowground communities can determine ecosystem responses to global change.

**PREDATOR NEMATODES DECLINE WITH LONG-TERM CO<sub>2</sub> ENRICHMENT.** Antoninka,<sup>1</sup> Anita, P. Reich<sup>2</sup>, N.C. Johnson<sup>1</sup>. <sup>1</sup>Biological Sciences, Northern Arizona University, Flagstaff, AZ, 86011-5694, <sup>2</sup>Dept. of Forest Resources, University of Minnesota, St. Paul, MN 55108-6112.

Changing resource availability either above- or belowground can alter the structure and function of soil food webs. Understanding how soil food webs respond to long-term carbon dioxide (CO<sub>2</sub>) and nitrogen (N) enrichment either directly, or indirectly through plant community change, is important for predicting ecosystem responses to these global change factors. Nematode communities can be an excellent indicator of soil food web responses to resource enrichment because community members feed across many trophic levels. We studied responses of nematode feeding guilds to CO<sub>2</sub> and N enrichment in a Free Air CO<sub>2</sub> Enrichment (FACE) experiment at Cedar Creek Ecosystem Science Reserve, MN, USA. Nematode communities were assessed from field samples collected after nine years of treatment with all factorial combinations of ambient and elevated CO<sub>2</sub> (360 or 560 ppm) and ambient or elevated N (0 or 4 g N m<sup>-2</sup>). The overall community structure and abundance of nematodes was not affected by CO<sub>2</sub> or N enrichment. Likewise, no changes were found in the abundance of bacterial feeders, fungal feeders, plant feeders or omnivores. However, there were 50% fewer predators in the elevated CO<sub>2</sub> treatment (p<0.0001). This unexpected result may indicate that either the abundance or quality of preferred prey is impacted by CO<sub>2</sub> enrichment. Vector analysis revealed that the non-metric multidimensional scaling (NMS) axis most strongly related to predator abundance (r=0.45) was aligned with the abundance of arbuscular mycorrhizal fungal (AMF) hyphae (r=0.34), as well as the amount of organic matter (r=-0.21) and N (r=0.21) in the soil. Vectors corresponding to other NMS axes revealed that the nematode trophic community structure was also affected by AMF spore abundance (r=0.27), as well as organic matter (r=-0.24) and soil texture (r=-0.29). Changes in these factors under elevated CO<sub>2</sub> could alter the feeding patterns of nematodes in lower trophic levels and the abundance of particular species within a trophic level, resulting in a non-additive effect on predator abundance. A causal model relating measured biotic and abiotic variables to predatory nematode abundance will be presented. These results demonstrate that CO<sub>2</sub> enrichment can generate indirect effects which influence the structure of soil food webs such that the abundance of predatory nematodes is reduced. Future studies should examine how this change in trophic structure may impact the stability and functioning of soil food webs and consequently ecosystem function.

**HOST SUITABILITY OF SIXTEEN VEGETABLE CROP GENOTYPES FOR *MELOIDOGYNE INCOGNITA*.** Anwar, S. A.<sup>1</sup>, M. V. McKenry<sup>2</sup>, and A. U. Lughari<sup>1</sup>. <sup>1</sup>Department of Plant Pathology, University of Agriculture, Faisalabad, Pakistan; <sup>2</sup>Department of Nematology, University of California, Riverside, CA. 92521 USA.

*Meloidogyne incognita* is a major pest of vegetable crops in Pakistan and has been reported to parasitize most members of the plant kingdom. The purpose of this study was to increase our understanding of host suitability among various vegetable genotypes common to Pakistan. Sixteen crop genotypes of interest came from eight plant families including Apiaceae: carrot

(*Daucus carota*) and coriander (*Coriandrum sativum*); Asteraceae: lettuce (*Lactuca sativa*); Brassicaceae: cauliflower (*Brassica oleracea*) and radish (*Raphanus sativus*); Cruciferae: cabbage (*Brassica oleracea*) and mustard (*Sinapis alba*), Cucurbitaceae: bitter melon (*Momordica charantia*), Cucumber (*Cucumis sativus*), pumpkin (*Cucurbita argyrosperma*), sponge gourd (*Luffa cylindrica*) and watermelon (*Citrullus lanatus*); Fabaceae: pea (*Pisum sativum*); Malvaceae: okra (*Abelmoschus esculentus*); and Solanaceae: chilies (*Capsicum annuum*) and eggplant (*Solanum melongena*) were tested as hosts for *M. incognita* in a greenhouse. Tomato (*Lycopersicon esculentum* cv. Money Maker) was included as a susceptible check for comparison. Five seeds of each genotype were planted in 15-cm-diameter clay pots filled with sandy soil. One plant of each genotype was eventually selected for each pot. Each pot was inoculated with 5000 eggs and second-stage juveniles. There were ten replications for each genotype and pots were arranged in completely randomized design on a greenhouse bench maintained at  $28 \pm 4$  °C. Host suitability was assessed 60 days after inoculation. Soil and root nematode populations were determined to assess the rate of reproduction [ $Pf = \text{final population} / Pi = \text{initial population}$ ]. Roots were evaluated for root galling and egg mass production on 0-5 scale. The roots of all the genotypes produced galls of variable numbers and sizes in response to nematode infection. The gall and egg mass indices and rate of reproduction were also variable among the genotypes. Most resistant to *M. incognita* were mustard, radish, and cauliflower ( $< 3$  J2/ g root with gall (GI) and egg mass (MI) indices =1). The most susceptible genotypes were bitter melon, carrot, cucumber, eggplant, lettuce, okra, pea, pumpkin, sponge gourd and watermelon (20 to 350 J2/ g root with GI = 5, and MI = 4). Meanwhile, three plant species including cauliflower, chilies, and coriander provided an intermediate host response. Some plant genotypes appeared to be hypersensitive as they exhibited root galling but suppressed nematode reproduction. These included cabbage, radish, pumpkin, and sponge gourd.

EVALUATION OF *COFFEA ARABICA* L. ACCESSIONS FROM ETHIOPIA FOR RESISTANCE TO THE KONA COFFEE ROOT-KNOT NEMATODE, *MELOIDOGYNE KONAENSIS*. Aoki<sup>1</sup>, Sayaka, C. Nagai<sup>2</sup>, and B. Sipes<sup>1</sup>. <sup>1</sup>Dpt. of Plant and Environmental Protection Science, University of Hawaii at Manoa, 190 Maile Way, Honolulu, HI 96822, <sup>2</sup>Hawaii Agriculture Research Center, 99-193 Aiea Heights Drive, Suite 300, Aiea, HI 96701-3911.

The Kona Coffee root-knot nematode (*Meloidogyne konaensis*) infects coffee grown in the Kona district of Hawaii and reduces yield significantly. *Coffea liberica* var. dewevrei, Fukunaga is used as a root stock in Hawaii to control nematode. However, identifying new sources of resistance is necessary because of the possibility of nematode virulence against the resistance found in Fukunaga. Semi-wild Ethiopian *C. arabica* accessions were evaluated to obtain resistance to *M. konaensis*. Ten genotypes of Ethiopian accessions imported from CATIE, Costa Rica were compared to the well characterized *C. arabica* cv. Yellow Catuai and *C. arabica* cv. Typica (susceptible to *M. konaensis*). *M. konaensis* eggs were inoculated onto eleven seedlings of each genotype and three seedlings of each genotype received water only. The seedlings were maintained in the greenhouse for 8 months. *M. konaensis* eggs and J2 were collected from the roots by blending in NaOCl. The number of nematodes in Ethiopian accessions was significantly lower than in the susceptible controls. Nematodes found in Ethiopian accessions were 10 to 15 fold less than in the controls. Ethiopian accessions ET11C, ET15, ET17, ET25, ET28, ET 52, ET 57, ET 25-B and ET 32B showed Rf values  $< 1$ . These nine Ethiopian accessions can be used as root stock or cultivar, or as a source of resistance for future breeding.

THERE IS LITTLE VARIATION IN LIGNOCELLULOSIC FUNGAL COMMUNITY STRUCTURE ON DECOMPOSING WOOD OF TWO SPECIES *LIQUIDAMBAR STYRACIFLUA* AND *PINUS TAEDA* ACROSS 3 SITES IN OAK RIDGE, TN. Austin, Emily E. Knoxville, Tennessee.

The structure of lignocellulosic fungal communities differs between *L. styraciflua* and *P. taeda* wood in the Southeast; this has previously been demonstrated through fruiting body samples. Here I ask the questions: 1) Do fungal communities differ in *L. styraciflua* and *P. taeda* trees when measured with molecular techniques such as cloning libraries? And 2) Does the decomposition potential of lignocellulosic fungal communities vary in wood species or site? This study is a pilot for my PhD dissertation project that will focus on wood decomposition, lignocellulosic activity and microbial communities in decomposing wood in their response to environmental changes. We extracted DNA from *L. styraciflua* and *P. taeda* stands in adjacent young stands as well as separate stands a few miles away. Eight samples were included, two of each species from each site. Partial cloning libraries were performed on 16s rRNA gene, Large Sub-Unit (LSU) and genes coding for laccase and cellobiohydrolase. While we have observed variation in the fungal community structure, it is not clearly partitioned by site or species. My next project in this area will focus on variation of wood decomposition rates, lignocellulosic activity and microbial communities in decomposing wood of varying decay stage.

SOIL MICROBIAL COMMUNITY RECOVERY IN TWO GRASSLAND RESTORATION CHRONOSEQUENCES ON CONTRASTING SOILS. Bach, Elizabeth M.<sup>1</sup>, C.K. Meyer<sup>2</sup>, S.G. Baer<sup>1</sup>, and J. Six<sup>3</sup>. <sup>1</sup>Dept. of Plant Biology and Center for Ecology, Southern Illinois University Carbondale, Carbondale, IL 62901, <sup>2</sup>Dept. of Biology & Environmental Science, Simpson College, 701 N. C Street, Indianola, IA 50125, <sup>3</sup>Dept. of Plant Science, University of California, Davis, CA 95616.

Tallgrass prairies have some of the deepest and most fertile topsoils on earth. Widespread conversion of these grasslands to agriculture has decreased soil C storage by exacerbating erosion and disrupting aggregates that protect C from

decomposition, coupled with lower plant C inputs. Thus, a primary goal of some grassland restorations is to improve soil quality. Conversion of cultivated systems to perennial grasslands often increases soil C, microbial biomass, and soil aggregate size and stability. However, a few studies have documented changes in soil microbial community structure after restoration. We examined changes in soil microbial Phospholipid Fatty Acid (PLFA) profiles in two 0-19 year chronosequences of restored grasslands in Nebraska on different soil textures and compared them with native prairie. Soil was collected from the 0-10 cm soil depth at each site in May of 2007 or 2008. Different recovery trajectories for the two soil types were evident. The silty clay loam chronosequence exhibited linear increases in total PLFA biomass ( $P=0.005$ ,  $r^2=0.29$ ), fungi ( $P<0.0001$ ,  $r^2=0.65$ ), fungal:bacterial ratio ( $P<0.0001$ ,  $r^2=0.67$ ), Gram (+) bacteria ( $P=0.018$ ,  $r^2=0.22$ ), Gram (-) bacteria ( $P=0.046$ ,  $r^2=0.16$ ), and actinomycetes ( $P=0.016$ ,  $r^2=0.23$ ). Increases in number (richness) of PLFAs and mycorrhizal fungi PLFA were best described by power curves ( $P<0.0001$ ,  $r^2=0.25$  and  $r^2=0.75$ , respectively). Microbial stress indicators of saturated:unsaturated PLFA ratio and iso:anteiso PLFA ratio decreased with time since restoration ( $P<0.0001$ ,  $r^2=0.50$  and  $r^2=0.31$ , respectively). Restorations on loamy sand soils, on the other hand, showed no discernable recovery pattern, but restored sites as a whole had significantly less total PLFA biomass ( $P=0.0002$ ) and fewer numbers of PLFAs ( $P=0.0008$ ) than the native prairie sites. Non-metric multidimensional scaling (NMDS) analysis of the two sites show distinct PLFA profiles in each soil type (Stress=0.06). Thus, soil texture affects soil microbial community structure and microbial community recovery from disturbance, which has implications for accrual and protection of C during grassland restoration.

**TRANSCRIPTIONAL AND BIOLOGICAL DIFFERENCES IN TWO CLOSELY-RELATED STRAINS TTO1 AND GPS11 OF *HETERORHABDITIS BACTERIOPHORA*. Bai, Xiaodong, R. An, U. Uslu, and P.S. Grewal.** Department of Entomology, The Ohio State University - OARDC, Wooster, Ohio, USA.

*Heterorhabditis* and *Steinernema* with their respective symbiotic bacteria *Photorhabdus* and *Xenorhabdus* are important biological control agents of insect pests. We compared two strains, TTO1 and GPS11 of *H. bacteriophora*, for differences in insect pathogenicity, tolerance to heat and desiccation stress, gene expression profiles, and bacterial symbionts. We used the sequences of the ITS (internal transcribed sequence) region to establish the phylogenetic relationship between these two strains. The phylogenetic tree built with a maximum parsimony algorithm showed that TTO1 and GPS11 strains were more closely related to each other than to other *H. bacteriophora* strains. However, these two strains were drastically different in several important traits. First, they are associated with different species of *Photorhabdus* bacteria. TTO1 strain harbors *P. luminescens* while GPS11 strain harbors *P. temperata*. Second, the TTO1 and GPS11 nematode-bacterium complexes were different in pathogenicity to four white grub species (*Coleoptera: Scarabaeidae*): Japanese beetle *Popillia japonica*, Northern masked chafer *Cyclocephala borealis*, European chafer *Rhizotrogus majalis*, and Oriental beetle *Anomala orientalis*, but their associated bacteria were not. Third, these two strains differed in their tolerance to heat and desiccation stress, with TTO1 being more desiccation and heat tolerant than GPS11 strain. Finally, these strains were different in the gene expression profiles revealed by Illumina digital gene expression (DGE) tag profiling. The evidence presented here suggests that the relationships between *Heterorhabditis* and *Photorhabdus* species are not species-specific. *H. bacteriophora* TTO1 genome is sequenced and the annotation is underway. This research also demonstrates that GPS11 strain is an excellent target for complete genome sequencing in order to elucidate the genetic mechanisms underlying the different biological traits between these closely related strains.

**LATERAL DISPERSAL OF THE ENTOMOPATHOGENIC NEMATODE *HETERORHABDITIS BACTERIOPHORA* FROM INFECTED HOST CADAVERS IN SOIL. Bal, Harit K., Robin R. A. J. Taylor, and Parwinder S. Grewal.** Dept. of Entomology, OARDC, The Ohio State University, Wooster, OH 44691.

Although entomopathogenic nematodes are widely used as biological control agents for various economically important soil inhabiting insect pests, their population and spatial ecology has not been thoroughly investigated. Dispersal ability of entomopathogenic nematodes in soil is one of the key factors which play a role in their effectiveness as biocontrol agents. Three consecutive laboratory experiments were conducted to evaluate the lateral dispersal of *Heterorhabditis bacteriophora* GPS11 strain from infected host cadavers in 5 cm deep autoclaved soil with 24% moisture content placed in wooden trays at room temperature (21°C). Each of the three experiments had different sized trays: 22.86 cm x 22.86 cm, 61 cm x 61 cm and 122 cm x 122 cm for experiments 1, 2 and 3, respectively. A single 10-day old cadaver of final instar *Galleria mellonella* infected with 420 infective juveniles of *H. bacteriophora* was placed in the center of each tray. Soil core samples (2 cm in diameter and 5 cm deep) were collected in plastic cups at intervals from 6 to 240 hours and at distances from 7 to 61 cm from the cadaver. These distances were marked in different directions from the center, each corresponding to a time interval at which soil samples were collected. One uninfected *G. mellonella* larva was placed in each cup with the soil sample and examined for nematode infection three days later. Movement of at least one nematode from the cadaver to the site of the soil sample was inferred from death of the bait. Nematode infection in *G. mellonella* was determined by red coloration and leathery texture of the larva. All pans were covered with black plastic sheets throughout the experiment to minimize loss of moisture from the soil. Each experiment was replicated five times and all three experiments were repeated. The data collected

comprised the proportion of dead *G. mellonella* baits at all 96 combinations of distance and time computed from 10 replicates (5x2 repetitions). A two-dimensional modified Fick diffusion model was fit to the spatio-temporal data by least squares method and descriptive statistics were calculated. The average movement of infective juveniles in soil was 6 cm/day. The number of infective juveniles moving a given distance declined with increasing distance from the cadaver with 40% traveling >15 cm and 2.5% traveling >60 cm in up to 240 hours. This study has shown that the potential for movement of *H. bacteriophora* in soil in the absence of any source of attraction in the form of bait or carbon dioxide is much greater than had been previously thought. The ability of nematodes to disperse over this scale, particularly in its natural habitat, that is, soil is an important factor in their success as biocontrol agents.

#### MICROBIAL BIOMASS AND RESPIRATION RESPONSES TO NITROGEN FERTILIZATION IN A POLAR DESERT.

**Ball, Becky A.<sup>1</sup> and R. A. Virginia<sup>1</sup>.** <sup>1</sup>Environmental Studies Program, Dartmouth College, Hanover, NH.

How microbial communities respond to nitrogen (N) deposition will influence global carbon (C) and nutrient cycles. While it is assumed that release from N limitation increases the growth and abundance of organisms, there is evidence that N enrichment can negatively influence microbial communities. Several possible pathways have been suggested by which N enrichment may influence microbial growth and activity (both positively and negatively), including alterations to soil properties such as pH, cation concentrations, and carbon quality or availability. The simple (low biomass and biodiversity) soil communities of the McMurdo Dry Valleys of Antarctica may allow these potential pathways to be more easily examined independently from one another. We hypothesized that N enrichment would influence microbial biomass and respiration in dry valley soils, where any negative influences would be due to influences over soil ion content, while any positive influences would be due to release from the pressure of resource limitation. In a laboratory microcosm incubation, three increasing levels of N (0.2, 1, and 2 g N m<sup>-2</sup> as NH<sub>4</sub>NO<sub>3</sub>) were applied to soils, and microbial biomass and respiration were measured at regular intervals over the course of 4.5 months. Soil microbial C and N were measured, and C mineralization was calculated from periodic determinations of headspace CO<sub>2</sub> concentrations. Soil characteristics, including soil pH, conductivity, cation content, chlorophyll *a*, and organic carbon content were measured. To determine the soil carbon pool being utilized by the soil community,  $\delta^{13}\text{C}$  was measured on headspace CO<sub>2</sub> by mass spectroscopy. Soils from two sites in Taylor Valley (long-term field fertilization application) that differed in native soil N content were used to examine how preexisting soil N influences relationships between N fertilization and microbial biomass and respiration. Preliminary results show that N fertilization did not significantly influence C mineralization or  $\delta^{13}\text{C}_{\text{CO}_2}$  through time within a site, suggesting that microbial communities do not follow the classic response to N addition (i.e. increased or decreased C mineralization in response to N addition). There was a significant effect of N treatment on soil pH and conductivity, though the response did not appear to be directly related to the level of N fertilization and did not influence soil respiration. The lack of effect of N fertilization on microbial biomass and respiration could be due to N saturation occurring at very low levels given the low microbial biomass in these systems or limitation by some other nutrient that is out of stoichiometric balance. Despite a lack of response in C cycling from the added N, we observed a significant influence on some soil properties associated with proposed pathways by which N enrichment may influence microbial communities, suggesting that microbial communities may respond in time. For all properties measured, there were differences in how soils from the two different sites responded over time (significant time\*basin interaction), suggesting that future N enrichment responses may differ between the two sites.

#### EFFECT OF BIOCIDES AND SOIL DISTURBANCE ON NEMATODE COMMUNITY AND EXTRACELLULAR ENZYME ACTIVITY IN SOYBEAN CYST NEMATODE SUPPRESSIVE SOIL. **Bao<sup>1</sup>, Yong, D.A. Neher<sup>1</sup>, and S. Chen<sup>2</sup>.**

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Soybean cyst nematode (SCN), *Heterodera glycines*, is a major yield-limiting pathogen of soybean. Biological control, through soil suppression, to SCN becomes increasingly desirable with the environmental concerns raised by chemical nematicides and emergence of virulent populations following the use of resistant cultivars. A greenhouse experiment was performed to determine the effects of biocides and soil disturbance on nematode community and extracellular enzyme activities produced by soil microbes in the SCN-suppressive soil collected in 2008. Two treatment types were combined in a complete factorial design and replicated four times. A cultivation-like disturbance was created by passing soil through a 5-mm-aperture sieve and compared to a non-sieve (no disturbance) treatment. Effect of microbial community composition was manipulated by applying Captan (fungicide), Streptomycin (bactericide), a combination of Captan and Streptomycin, or no biocide. Three SCN-susceptible soybean plants were grown in each 10-cm-diameter pot. Soil samples were taken at 35 days after planting (DAP) and 70 DAP. Nematodes were extracted from 100 grams of soils by wet tray sieving, preserved, identified to genus, and enumerated. The activities of selected hydrolytic extracellular enzymes were detected: L-serine aminopeptidase (Serine) indicating serine protease, L-proline aminopeptidase (Proline) and L-phenylalanine aminopeptidase (Pheny) indicating collagenase, and  $\beta$ -1,4-N-acetylglucosaminidase (NAG), phenol oxidase (PO) and peroxidase (Pero) indicating chitinase. One gram of homogenized samples was incubated with fluorogenically-labelled substrates in a microplate format with appropriate controls. After the specific incubation times, fluorescence was measured

using a microplate fluorometer. Total nematode population increased by 106%, and SCN J2 population increased by 133% from 35 to 70 DAP (assuming one life cycle for SCN). Total nematode abundance was significantly greater in disturbed than undisturbed soil ( $p=0.0058$ ). All biocides treatments had significant stimulatory effect on SCN J2 abundance in the descending order of Captan&Streptomycin, Captan, and Streptomycin. Additionally, the most abundant SCN J2 population was found in disturbed soils treated with Captan&Streptomycin, suggesting that both fungal and bacterial antagonists may play important roles in SCN suppression. Values of Shannon Diversity Index ( $p=0.0019$ ) and Richness Index ( $p=0.0528$ ) were substantially smaller, while Simpson Dominance Index ( $p=0.0029$ ) declined in soils with disturbance than when left undisturbed at 35 DAP. The application of Streptomycin reduced the Maturity Index ( $p=0.0557$ ) at 70 DAP, while the other community indices did not differ significantly between the biocide treatments. Both soil disturbance and biocides did not affect all detected hydrolytic extracellular enzymes significantly. However, there was a trend for biocide treatments to decrease PO in the descending order of Captan&Streptomycin, Captan, and Streptomycin, indicating that biological suppression of SCN may be related to production of chitinase by fungal and bacterial agents in the suppressive soil.

**SURVEY OF LESION AND NORTHERN ROOT KNOT NEMATODES ASSOCIATED WITH VEGETABLES IN VERMONT. Bao, Yong and D. A. Neher.** Dept. of Plant and Soil Science, University of Vermont, 105 Carrigan Drive, Burlington, VT 05405.

A survey was conducted in Vermont to determine the frequency, abundance and distribution of nematodes associated with mixed vegetable production in 2008. Sixty-six soil samples were collected from tomato, green bean and lettuce fields on 36 vegetable farms across Vermont at the beginning and end of the growing season. In total, 175 hectares were sampled, which represents about 15% of the vegetable production area in Vermont. Each sample was collected as a composite of 20 cores (20 cm deep, 2 cm diameter) along a 100 m transect with a random starting point, sampling within 10 cm of the plant stem. The farmer managing each field provided data including cropping history, pest management, and crop rotation. Soil nematodes were extracted by wet tray sieving, preserved, identified to genus, and enumerated. Additionally, bioassays with indicator plants of soybean and lettuce were conducted in a greenhouse to visually assess the infestation level of northern root lesion (*Pratylenchus* spp.) and northern root knot (*Meloidogyne hapla*) nematodes in soil samples respectively. The survey revealed the presence of 20 families and 39 genera of nematodes in Vermont vegetable fields. Seven genera of plant-parasitic nematodes were identified: *Pratylenchus*, *Meloidogyne*, *Paratylenchus*, *Circonemoides*, *Heterodera*, *Helicotylechus* and *Hoplolaimus*. Among them, *Pratylenchus* was encountered most frequently, with detection being 97% of the fields sampled. *Meloidogyne* was only observed with low abundance in several particular fields in Vermont vegetable production area. Furthermore, *Pratylenchus* occurred at population levels above the economic threshold in 47% of the infested fields in the early season and increased to 70% in late fall. Out of thirteen surveyed counties in Vermont, populations of *Pratylenchus* exceeded the economic threshold in four counties in early season and then expanded to six counties in late season. The results of soil bioassay with soybean plants suggested that the number of lesions caused by lesion nematode on primary roots was correlated to soil infestation levels of *Pratylenchus*, although there was considerable variability. All cover crops commonly practiced in vegetable fields reduced *Pratylenchus* abundance, except vetch. And we found the significant ( $p=0.0072$ ) lower abundance of *Pratylenchus* covered by clover over winter. The application of animal manure also decreased *Pratylenchus* abundance, but not significantly. This survey indicated that *Pratylenchus* is the major economically important plant-parasitic nematode and is widespread in the vegetable production regions of Vermont.

**SPATIAL VARIATION IN SOIL BIOTA AND ORGANIC MATTER IN THE MCMURDO DRY VALLEYS, ANTARCTICA. Barrett<sup>1</sup>, J.E., D.W. Hopkins<sup>2</sup>, I. Hogg<sup>3</sup>, and S.C. Cary<sup>3</sup>.** <sup>1</sup>Dept. of Biological Sciences, Virginia Tech, Blacksburg, VA USA, <sup>2</sup>School of Biological and Environmental Sciences, University of Stirling, Stirling, Scotland, <sup>3</sup>Dept. of Biological Sciences, the University of Waikato, Hamilton, NZ.

The Antarctic Dry Valleys are among the most extreme soil environments on earth. In 1903 R.F. Scott described an apparent lack of life in the dry valleys, yet recent evidence reveals microbial diversity comparable to hot deserts. While Scott's impression has persisted into modern times, an emerging view of the dry valleys suggests a greater potential for biological influence over ecosystem functioning than previously recognized. We present data collected in 2008/2009 by the NZ-IPY Terrestrial Antarctic Biological Survey. The goal of this project is to elucidate the factors controlling assembly of soil communities from their most simple manifestation as strictly prokaryotic assemblages to the richest and most productive ecosystems consisting of linked microbial-metazoan trophic groups. Since availability of organic matter is hypothesized to be a major limitation to the assembly of active, multi-trophic communities, understanding the spatial variation in source pools of organic matter is essential to the broader goals of elucidating dry valley biocomplexity. Stable isotopic composition suggests that multiple pools of organic matter contribute to soil carbon and nitrogen in these environments, including cyanobacterial mats and moss associated with adjacent aquatic environments, and lichens and lithic communities in the dry mineral soils. Previous demonstrations of correlation between density and composition of these cryptogam communities with

below-ground microbial and metazoan assemblages suggest that soil diversity may be broadly predictable by the distribution of organic matter content and composition. The relative importance of these sources to regional stocks of carbon and food webs will be discussed.

**ASSESSING THE POTENTIAL DRUGABILITY OF Hp-FAR-1, FROM A FAR PROTEIN FAMILY SPECIFIC TO THE PHYLUM NEMATODA.** Bath<sup>1</sup>, Jennifer L., J.J. Drees<sup>1</sup>, E. Maetzold<sup>1</sup>, M.D. Scheidt<sup>1</sup>, M.E. Knox<sup>1</sup>, D. Ram<sup>1</sup>, P. Eneh<sup>1</sup>, and C.J. Clark<sup>1</sup>. Department of Biology, Concordia College Global Vaccine Institute (CCGVI), Moorhead, MN 56562, USA.

The parasitic nematode *Heligmosomoides polygyrus* is a laboratory mouse model frequently used to study the cellular mechanisms of chronic helminth infections. It has long been acknowledged that parasite-induced immunomodulation by the nematode *H. polygyrus* exists, yet the identification and detection of specific immunomodulatory molecules has been slow. Our lab has identified and isolated a novel protein, Hp-FAR-1, a major secreted antigen from *H. polygyrus*. To date, over a dozen FAR proteins have been discovered from a variety of nematodes, all of which, with the exception of *C. elegans*, are parasitic. The high homology of the FAR proteins across species suggests that the proteins themselves may be imperative for parasite survival and/or infection. The objective of this study is to assess the potential drugability of the Hp-FAR-1 protein utilizing bioinformatic, molecular and immunological data. We have found that Hp-FAR-1 itself is secreted by the parasite during the fourth larval stage of infection, at a time when the parasite is embedded in the muscularis externa of the host and therefore, it is reasonable to predict that the protein itself may play a direct role in immunomodulation of host immune mediators. We began this study with the extraction of cDNA encoding Hp-FAR-1 and production of the corresponding recombinant protein. Binding analyses performed on the recombinant protein demonstrate that the recombinant Hp-FAR-1 is indeed a functional fatty acid and retinol binding protein. Bioinformatic studies predict a leader sequence directing the protein to cellular secretory compartments. To confirm this datum, excretion of the protein from the host has been confirmed by western blot analysis, and confirms that Hp-FAR-1 itself, as an excretory protein, is thereby accessible outside of the host for targeting purposes. Similar to other known nematode FAR proteins, secondary structure analysis of Hp-FAR-1 predicts a predominantly alpha-helical conformation with no evidence of  $\beta$  extended structure. This structure is ideal for targeting Hp-FAR-1, as the alpha helical structure of the protein provides a unique target unlike any family of retinol binding proteins found in organisms outside the phylum Nematoda. RT-PCR using hp-FAR-1 specific primers indicates transcription of hp-FAR-1 throughout the lifecycle of the parasite (from the infective third stage larva through to the adult stage), increasing the probability that targeting Hp-FAR-1 for drug or vaccine use would work effectively early on during infection, as well as in later stages of disease. To support the data that Hp-FAR-1 is present throughout the lifecycle, we are able to detect antibodies specific for the recombinant Hp-FAR-1 in mice injected with E/S products from the fourth larval stage and the adult stage of the parasite. Taken together this data presents reasonable evidence that FAR proteins, prevalent throughout the phylum Nematoda, warrant further investigation as both a drug and an immunological target for helminth infections.

**NEMATOTOLOGY OUTREACH IN CALIFORNIA.** Becker, J. Ole, and J.A. Smith Becker. Department of Nematology, University of California, Riverside, CA 92521.

California's \$24 billion agricultural crop industry is by far the largest among the 50 US States. It is also the most diverse with hundreds of commodities, including dozens of crops that are produced exclusively in the state. California produces more than 50% of US grown fruits, nuts and vegetables on less than 4% of the country's farmland. Approximately 60% of California's 76,000 farms are less than 50 acres in size. Non-realized crop production value in California due to the activity of plant parasitic nematodes is conservatively estimated to exceed \$1.5 billion annually. Increasing regulatory restrictions on the use of soil fumigants and non-fumigant nematicides requires renewed focus on alternative nematode management strategies. The large number of specialty crops that are almost all host to various plant parasitic nematodes is a challenge for both research and outreach. As a center for international trade and tourism, California faces a high risk of potential introductions of several economically important invasive nematode species. Language and cultural obstacles with primarily first-generation immigrants from South America, Central America and Asia add further complexity to Cooperative Extension activities. The University of California's Agricultural and Natural Resources outreach model has relied successfully for many decades on an information flow from the University of California Agricultural Experiment Station and Cooperative Extension faculty to UC advisors located in almost every California county. State and Federal agencies as well as collaborators at other academic institutions or in industry have added further support to this continuum. However, with increasing focus of UC Nematology Departments on basic research and non-plant parasitic nematodes, the generation of grower-usable crop and nematode management information today relies almost exclusively on Cooperative Extension faculty research. Compounding the problem is the decline in federal and state funding over the past decade and university administrative decisions that have eliminated essential CE advisor positions in the counties and campus-based technical staff positions. The consequences will become more apparent with time when the lack of appropriately trained plant nematologists will pose significant challenges to mission-oriented nematology research and extension.

GREEN MANURE AND BIOFUMIGATION FOR ROOT LESION NEMATODE AND VERTICILLIUM WILT MANAGEMENT IN STRAWBERRY PRODUCTION. **Bélair<sup>1</sup>, Guy, and J. Coulombe<sup>2</sup>.** <sup>1</sup>Horticulture R&D Centre, Agriculture & Agri-Food Canada, St-Jean-sur-Richelieu, Québec, Canada, J3B3E6, <sup>2</sup>1551 Chemin Royal, St-Laurent, Île d'Orléans, Québec, Canada G0A3Z0.

From 2004 and 2006, a field experiment was conducted to assess the efficacy of 2-year crop rotation and biofumigation on verticillium wilt damage *Verticillium dahliae* and root lesion nematode density *Pratylenchus penetrans* in strawberry in Quebec, Canada. Crops tested as rotation were: canola followed white mustard (biofumigation), corn, forage pearl millet cv. CFPM 101, forage pearl millet cv. Tifleaf, and oats as the standard control. For the biofumigation treatment, canola was ploughed under at late bloom (end of July) followed by white mustard which was ploughed under at full bloom (October). Nematode population densities were significantly lower after biofumigation and both pearl millet than after corn and oats. In 2006, both pearl millet and biofumigation significantly reduced by an average of 21% incidence of verticillium wilt and allowed a 54% average increase in the development of strawberry plants cv. Jewel. In 2006 and 2007, two field trials were set out to investigate the potential of improving the efficacy of biofumigation by the incorporation of poultry manure (15 t/ha) at canola-crop ploughing time with and without the addition of a plastic mulch. In 2006, no significant improvement of biofumigation was observed by the addition of poultry manure and soil tarped with a transparent plastic much for 18 days. In 2007, the plastic mulch significantly improved the efficacy of biofumigation with a 95% reduction in the number of *P. penetrans* densities when compared canola biofumigation with poultry manure but no plastic mulch.

THE DISTRIBUTION OF SOIL INSECTS OVER DIFFERENT SPATIAL SCALES IN GRASSLAND. **Benefer, Carly, R. Blackshaw, M. Knight, and J. Ellis.** University of Plymouth, School of Biological Sciences, Portland Square, Drake Circus, Plymouth, PL4 8AA.

In the UK there are a number of insect taxa whose larvae are associated with grassland, including wireworms (*Agriotes spp.*), leatherjackets (*Tipula spp.*), bibionids (*Bibionidae*) and sciarid fly larvae (*Sciaridae*). Most research on these groups has arisen from their functional roles as pests in agricultural systems and as such each has been considered separately. Consequently there are no studies that consider the possible interactions between these different taxa. Here we present data on the occurrence of these pest groups. Insect larvae were recovered from soil cores using dry heat extraction (Blasdale 1974). Bibionid larvae were identified from morphological characteristics and *Agriotes spp.* using a T-RFLP genotyping method (Ellis et al. 2009). Leatherjackets were assumed to be *Tipula paludosa*, as no adults of other species were found at the sites. Sciarids were not identified to species. Samples were taken from 25 sites over six fields on a farm in south Devon, UK. At each site 96 5cm diameter soil cores were collected from points at the intersections of concentric circles (5, 10, 20 and 40m diameter) and regularly spaced (15°) radii. The distributions of the taxa were compared at three spatial scales: within soil cores, within study sites and within fields. Results are presented and the ecological and pest management implications discussed.

INSECTICIDE EFFECTS ON EARTHWORMS: LABORATORY AND FIELD STUDIES. **Benslim<sup>1</sup>, Hicham, J.K. Whalen<sup>1</sup>, and A. Vanasse<sup>2</sup>.** <sup>1</sup>Dept. of Natural Resource Sciences, McGill University, Ste-Anne-de-Bellevue, QC, Canada H9X 3V9, <sup>2</sup>Dept. of Botany, Laval University, Quebec, QC, Canada G1K 7P4.

Soybean aphid (*Aphis glycines*), an insect native of Asia, was accidentally introduced to North America in the late 1990s and first reported in Quebec, Canada in 2002. Outbreaks of this pest have led to severe yield losses in recent years. Many producers are now considering insecticidal sprays to protect their soybean crop. Among the products under consideration to control soybean aphid are dimethoate and lambda-cyhalothrin. The objective of this study was to determine if these insecticides affect earthworms, a non-target organism present in soybean fields. Standard laboratory test methods were used to determine lethal and sub-lethal effects on the earthworm *Eisenia fetida*. Earthworm populations in soybean fields on two farms were monitored during two field seasons. Ecotoxicology testing revealed an LC50 of 348 mg kg<sup>-1</sup> soil for dimethoate, but mortality of *E. fetida* exposed to lambda-cyhalothrin was negligible over the range tested (up to 1000 times greater than field exposure rates). Sublethal effects related to reproduction (cocoon production and hatchlings) were observed for both dimethoate and lambda-cyhalothrin. The concentrations of insecticide that would have no observable effect on earthworms were 25 mg dimethoate kg<sup>-1</sup> and 2.5 mg lambda-cyhalothrin kg<sup>-1</sup>. These values exceed the insecticide application rates recommended for control of soybean aphid. The earthworm populations at the two farms were distinct, with earthworms from various ecological groups (epigeic, endogeic and anecic) represented. Based on the sexually mature species present, Farm A had an earthworm population dominated by *Aporrectodea turgida* (64%) with important numbers of *Lumbricus terrestris* (22%) and *Allolobophora chlorotica* (12%). Earthworms on Farm B belonged to *A. turgida* (53%), *A. chlorotica* (21%) and *Eiseniella tetraedra* (26%). Assessment occurred twice during the season, shortly after insecticide application to the soybean crop. There was no difference in earthworm numbers and biomass in insecticide-treated plots and the untreated control. These results indicate that earthworm populations in the field were not affected by dimethoate and lambda-cyhalothrin applications, which confirms the results from laboratory ecotoxicology testing. We conclude that the standard laboratory test method is sufficiently robust that it can be used to predict insecticide effects on earthworm populations under field conditions.

HOST-PARASITE RELATIONSHIP OF *MELOIDOGYNE INCOGNITA* AND EPAZOTE. **Bernard, Ernest C., and P.J. Long.** Entomology and Plant Pathology, The University of Tennessee, 2431 Joe Johnson Drive, 205 Plant Sciences, Knoxville, TN 37996-4560.

Epazote (*Amaranthaceae: Dysphania ambrosioides*) a plant native to Mexico, is an increasingly popular herb used in cooking, especially bean dishes. Galls on epazote produced by *Meloidogyne incognita* were sectioned and stained for histological examination. Typically, giant cells were weakly developed and partially surrounded by isolated vascular elements or clusters of blind vessels without direction and unconnected to the main vascular system. In most galls, short vascular cells were oriented perpendicularly to typical xylem; these cells frequently abutted giant cells. Misaligned vascular cells probably are induced by the nematode shortly after infection, as the cells appear to have mature walls. This apparent resistance reaction in epazote likely reduces the flow of photosynthate to giant cells, with a consequent retardation of nematode growth and reproduction.

EVOLUTION OF PARASITIC ABILITY IN A PLANT-PARASITIC NEMATODE: HORIZONTAL GENE FLOW, GENE DIVERSIFICATION AND CONVERGENT EVOLUTION. **Bird<sup>1,2</sup>, David McK., C.H. Opperman<sup>1</sup>, E.S. Scholl<sup>1</sup>, J. Cromer<sup>1</sup>, P. DiGennaro<sup>1</sup>, M. Goshe<sup>3</sup>, and D. Nielsen<sup>1,2</sup>.** <sup>1</sup>Center for the Biology of Nematode Parasitism, <sup>2</sup>Bioinformatics Research Center, <sup>3</sup>Department of Structural Biology, NC State University, Raleigh NC, 27695.

Plant-parasitic nematodes are a major limit to global food, fiber and bio-energy production. To help catalog the biochemical basis for parasitism, we recently completed the 54 Mbp genome sequence of the diploid root-knot nematode *Meloidogyne hapla*. This genome encodes significantly fewer genes than does that of the free-living nematode *C. elegans* (most notably through a reduction of odorant receptors and other gene families), yet has acquired numerous genes suspected to be involved in adaptations to parasitism by horizontal gene transfer from other kingdoms. Genes thus acquired have undergone expansions and diversification in the *M. hapla* genome. A second class of candidate *M. hapla* genes encoding plant-like functions appears to have arisen via convergent evolution (molecular mimicry), and we have begun to use LC/MSE to confirm these candidates. In parallel, we have constructed a 90,000-element microarray spanning the entire set of known exons from our computationally predicted *M. hapla* proteome (HapPep3) and have used this array to interrogate the *M. hapla* transcriptome.

INFLUENCE OF PRECIPITATION ON POPULATIONS OF *HETERODERA GLYCINES* IN THE PRESENCE AND ABSENCE OF RESISTANT CULTIVARS. **Bird<sup>1</sup>, George W., L. Schumacher<sup>1</sup>, J. Davenport<sup>1</sup>, and T. Kendle<sup>2</sup>.** <sup>1</sup>Dept. of Entomology 243 Natural Science, Michigan State University, East Lansing, MI 48824, <sup>2</sup>Edwardsburg, MI 49112.

Soybean cyst nematode (*Heterodera glycines*, SCN) resistant variety trials have been conducted at the Tom Kendle Farm in Cass County, Michigan since 1999. Four fields, each approximately 25 acres, were used for the research. Each field was in a two-year rotation with wheat and used once every four years for the research. In addition to soybean yields and final SCN population densities, within-growing season precipitation data were recorded. The objective of this research is to describe the impact of precipitation on soybean yields and SCN population development in the presence and absence of SCN-resistant soybean cultivars. A mean of 22 resistant cultivars were evaluated every year. The data presented, however, are for the five highest-yielding resistant cultivars and the susceptible control cultivar. In the 10-year period between 1999 and 2008, there were four years with less than 40.6-cm and six years with greater than 50.8-cm of precipitation. For this analysis, the soybean yield data and final SCN population densities were grouped by these precipitation regimes. As expected, soybean yields were low in the dry years. Mean yield associated with the susceptible cultivar was 13.2-bu/acre, while the yield associated with the resistant cultivars was 23.6-bu/acre. For the years with greater than 50.8-cm of precipitation, the susceptible control yielded 22-bu/acre; whereas, the resistant cultivars yielded 38.7-bu/acre. In the dry years, the final SCN egg and second-stage juvenile population density associated with the susceptible cultivar was 50,784 per 100-cm<sup>3</sup> soil, while there were 4,310 per 100-cm<sup>3</sup> soil for the resistant cultivars. In the years with more than 50.8-cm of precipitation, there were only 21,785 and 2,442 SCN eggs and second-stage juveniles per 100-cm<sup>3</sup> of soil for the susceptible and resistant cultivars, respectively. There appeared to be a relationship between the number of times (1 to 5) a field was planted to a resistant variety and the final SCN population density. At-harvest population densities increased through the fourth time each field was planted to a resistant variety. This relationship will be evaluated further during the final two years of the experiment in 2009 and 2010. These results indicate that within-growing season precipitation had a major impact on both soybean yield and at-harvest population densities of SCN. At this commercial farm-research location in Cass County, MI, the highest at-harvest population densities of SCN were always associated with the years having within-growing season precipitation of less than 40.6-cm; whereas, the highest soybean yields were associated with years with greater than 50.8-cm of rainfall.

INTRA-GENERATIONAL MORTALITY OF LEATHERJACKETS (*TIPULA PALUDOSA*). **Blackshaw, Rod P.** Terrestrial Ecology Research Group, University of Plymouth, Drake Circus, Plymouth PL4 8AA, UK. E-mail: rblackshaw@plymouth.ac.uk

The larvae of *Tipula paludosa* (leatherjackets) are soil dwelling pests of grassland, cereals and some field vegetables. They are known to be susceptible to a range of pathogens and parasites, and are predated on by insects, birds and mammals. Some natural enemies have been associated with population collapse but there is no evidence of a sustained influence on population dynamics.

Their population dynamics from year to year have been the subject of several studies and there is strong evidence for density-dependent, inter-generational feedback that acts to regulate populations. However, within generation dynamics have received much less attention. In this paper I present data to show that intra-generational larval mortality is mainly associated with the final instar. Soil samples were collected monthly from four grass fields over five years (October to September) and leatherjackets extracted from them. Individuals were measured and allocated to an instar. These data were then analysed for sources of variability and used to estimate population changes over a single generation. There was no significant difference in measured parameters between fields or years, though there was between the monthly samples and the week/year interrelationship. October samples showed much greater sampling error than those collected in later months. Most mortality occurred from the onset of the fourth instar; the rate of decline from April to September was linear. Potential reasons for this result will be discussed.

**PREDICTING THE SIZE OF LEATHERJACKET (*TIPULA PALUDOSA* MEIG.) POPULATIONS IN GRASSLAND. Blackshaw, Rod P.** Terrestrial Ecology Research Group, University of Plymouth, Drake Circus, Plymouth PL4 8AA, UK. E-mail: rblackshaw@plymouth.ac.uk

The larvae of the crane fly *Tipula paludosa* ('leatherjackets') originate from temperate maritime regions of Europe but have now colonised areas of North America. They are pernicious pests of grassland causing steady yield losses and occasional sward destruction, but can be devastating to crops that follow grass in the rotation. They are easily controlled with insecticides in conventional agriculture, and these are generally applied in the spring when damage is seen. In organic agriculture control is much more challenging. Biocides (entomopathogenic nematodes and *Bacillus thuringiensis*) are more expensive and efficacy declines as the leatherjackets grow. Studies have shown that the optimal time for application of biocides is in early October at a time when direct sampling of first instar larvae to establish infestation levels is difficult. *Tipula paludosa* is univoltine and the adult period relatively short in comparison to the overall life-cycle. Females are gravid at emergence and poor fliers, and are thought not to disperse far before oviposition. It is also probable that there is density-dependent feedback between generations. This suggests that it may be possible to develop a monitoring system to predict leatherjacket population size so that rational decisions can be made about the application of biocides in October. This paper reports an investigation into the use of water traps to catch adults as predictors of subsequent larval populations. It is concluded that female trap counts will be a better predictor than male or total crane fly counts. It is also noted that there appears to be a spatial dimension to correlations suggesting that predictions may be specific to the immediate vicinity of the traps.

**THE STRUCTURE OF BELOWGROUND NEMATODE COMMUNITIES UNDER *PANICUM VIRGATUM* (SWITCHGRASS) IS IMPACTED BY ABOVEGROUND PLANT DIVERSITY. Bliss, TJ, C. E. Brassil, and T. O. Powers** University of Nebraska-Lincoln.

Previous research has shown that changes in above-ground diversity can drastically alter the diversity of below-ground communities. Less is known about the reciprocity of this relationship, however it is likely that changes in belowground diversity can have serious consequences for aboveground communities. This interaction is particularly important when combined with the process of agricultural domestication. Because most plant domestication occurred hundreds to thousands of years ago, little is known about the early effects of the plant domestication process on belowground communities. However, the domestication of Switchgrass (*Panicum virgatum*) in North America began less than 100 years ago, and provides an excellent opportunity to investigate these changes. Focusing on belowground nematode communities, we asked: How has the recent domestication of Switchgrass affected the community structure of soil nematodes? To answer this question, we analyzed soil nematode communities under Switchgrass in natural prairie systems and in domesticated Switchgrass monocultures. Knowing how the structure of soil nematode communities is affected by Switchgrass domestication may help us better understand the mechanisms by which high numbers of a few herbivorous species of nematodes are achieved, dramatically decreasing plant production in almost every domesticated crop plant on earth. Seven remnant prairies and 8 field monocultures of Switchgrass were identified and sampled in Eastern Nebraska. In a comparison of a pair of sites, one in a well-preserved remnant prairie and the other in a 20-year-old monoculture of Switchgrass, morphology-based taxonomic analysis of a subsample of the nematode communities shows that nematode genus diversity is higher in the prairie site with high plant richness than in the monoculture site. In the prairie site, a Switchgrass stand having an estimated area of 6.75 m<sup>2</sup>, 9 plant species including Switchgrass were present. Among the 161 randomly selected nematodes from a soil sample in this site, 29 genera were identified. In the monoculture site of equal area, 1 plant species was present. Among the 158 randomly selected nematodes from this site, 17 genera were identified. A dramatic increase in the abundance of a particular herbivorous nematode genus, *Basiria*, was also noted in the field site. These initial results indicate significant structural changes in the nematode community under a domesticated Switchgrass monoculture, highlighted by an increase in abundance of herbivorous nematodes. More rigorous investigations into the mechanisms that cause this change in nematode community structure are needed.

**CROSSING BOUNDARIES OF SPACE, CLIMATE, AND PHILOSOPHY: RESTORATION AND MANAGEMENT OF FIRE-PRONE FORESTS. Boerner<sup>1</sup>, Ralph, S. Hart<sup>2</sup>, K. Outcalt<sup>3</sup>, C. Skinner<sup>4</sup>, S. Stephens<sup>5</sup>, T. Waldrop<sup>6</sup>, D. Yaussy<sup>7</sup> and A. Youngblood<sup>8</sup>.** (Note: Authors presented in alphabetical order). <sup>1</sup>Department of Evolution, Ecology and Organismal

Biology, Ohio State University Columbus, OH 43210 USA. <sup>2</sup>School of Natural Sciences and the Sierra Nevada Research Institute, University of California - Merced, Merced, CA 95344 USA. <sup>3</sup>Southern Research Station, U.S. Forest Service, Athens, GA 30602 USA. <sup>4</sup>Pacific Southwest Research Station, U.S. Forest Service, Redding, CA 96002 USA. <sup>5</sup>Department of Environmental Science, Policy, and Management, University of California - Berkeley, Berkeley, CA 94720 USA. <sup>6</sup>Southern Research Station, U.S. Forest Service, Clemson, SC 29634 USA. <sup>7</sup>Northern Research Station, U.S. Forest Service, Delaware, OH 43015 USA. <sup>8</sup>Pacific Northwest Research Station, U.S. Forest Service, La Grande, OR 97850 USA.

The Fire and Fire Surrogate (FFS) network project is a continental-scale study of fire-prone forest ecosystems ranging from eastern Washington to central Florida. The overall objective was to test alternative management/restoration strategies using an experimental design, a decadal time frame, and a suite of study sites that would permit broad extrapolation of results across sites and in relation to changes in climate within individual regions. In this presentation we first describe the degree to which the manipulative treatments of the FFS study (prescribed fire, mechanical thinning of the canopy and/or understory, fire + mechanical treatment) achieved the *a priori* management and restoration goals from five different perspectives (wildfire hazard reduction, ecological restoration, biodiversity conservation, carbon sequestration, and sustainable forestry), then sharpen the analysis by focusing on how professionals from these five perspectives would alter their judgment (or not) by increasing their reliance on soil ecological parameters. We will conclude by discussing those factors that led to an increasing appreciation for and reliance upon soil ecological parameters over the course of this decade-long project.

**EXPLORING MECHANISMS THAT MAY EXPLAIN THE RESPONSE OF SOIL RESPIRATION TO LONG-TERM WARMING. Bradford, Mark A.** School of Forestry and Environmental Studies, Yale University, New Haven, CT 06511, USA.

The respiration of soil microbes releases dioxide from soils to the atmosphere. In the short-term, rates of soil respiration are strongly dependent on temperature. In the long-term the response of soil respiration to temperature is uncertain. Despite this uncertainty a sustained, positive response of soil respiration to temperature is included in all 11 coupled carbon-cycle climate models. These models are used by the Intergovernmental Panel on Climate Change (IPCC) to project climate. The positive feedback between climate warming and soil respiration, inherent within these models, is not observed in field experiments. Instead, experimental warming results in a short-lived stimulation of soil respiration. The explanations proposed for this ephemeral response include the depletion of labile soil carbon pools and thermal adaptation of soil respiration. Theoretical models attribute the response of soil respiration to sustained warming to the first mechanism (the 'substrate depletion' hypothesis). If empirically-validated this would suggest that positive feedbacks between the atmosphere and biosphere modelled by the IPCC arise through a reasonable assumption. If the 'thermal adaptation' hypothesis is supported, an outcome expected based on fundamental, evolutionary trade-offs between enzyme structure and function, the IPCC assumptions would seem unreasonable. I first test the 'substrate depletion' and 'thermal adaptation' hypotheses through investigation of soil carbon pool and microbial responses to experimental warming in replicated plots of the Harvard Forest Long-Term Warming Experiment. I present data that is consistent with both of these mechanistic hypotheses (i.e. smaller labile carbon pools and mass-specific respiration rates). These responses were consistently observed across the growing season. However, similar reductions in microbial biomass, which were also consistently observed, are not explicitly predicted by the substrate depletion or thermal adaptation hypotheses. This suggests that additional or alternate mechanistic hypotheses are required to explain soil respiration responses to prolonged warming. I present the results of two laboratory studies designed to tease out these additional mechanisms and show that substrate depletion and reductions in mass specific respiration rates are observed both in response to warmer environments and altered carbon substrate supply. The results indicate that our current understanding of soil organic carbon and microbial dynamics are not sufficient to explain combined microbial and process responses to long-term soil warming. I outline future areas for studies to focus on to develop the necessary understanding for more reliable climate prediction in the context of feedbacks between soil respiration rates and atmospheric carbon dioxide concentrations.

**IMPACTS OF LONG-TERM ORGANIC MATTER MANIPULATIONS ON NITROGEN CYCLING IN AN OLD GROWTH FOREST. Brewer<sup>1</sup>, Elizabeth A. and D.D. Myrold<sup>1</sup>.** <sup>1</sup>Department of Crop and Soil Science, 3017 ALS, Oregon State University, Corvallis, OR 97331.

The Detritus Inputs and Removal Treatments (DIRT) were established in the summer 1997 to examine the effects of long-term organic matter manipulations on SOM chemistry and nutrient cycling. After ten years of treatments, <sup>15</sup>N isotope dilution methods were used to estimate gross N mineralization and nitrification rates across six treatments that controlled the quality and rate of SOM inputs (control, double wood, double litter, no roots, no litter and no inputs). It was hypothesized that these changes in SOM will have altered the pace and dynamics of microbial nitrogen turnover. Respiration measurements taken throughout the incubation, showed lower rates from organic matter exclusion plots relative to the control, double litter and wood treatments. Compared to the control (1.4 mg N-NH<sub>4</sub><sup>+</sup> kg<sup>-1</sup> soil day<sup>-1</sup>), production and consumption of NH<sub>4</sub><sup>+</sup> decreased in the double wood treatment. Rates of NH<sub>4</sub><sup>+</sup> production and consumption did not significantly differ among any other

treatments. Gross nitrification rates were less than gross N mineralization and with the exception of double wood, rates did not significantly differ from zero. The higher rates of  $\text{NH}_4^+$  consumption compared to  $\text{NO}_3^-$  production suggests that  $\text{NH}_4^+$  consumption primarily occurred via immobilization. Microbial assimilation was further supported by an increase in  $^{15}\text{N}$  remaining in post extraction soils throughout the incubation time course. Although N mineralization rates did not significantly differ ( $p < 0.05$ ) from control, the overall trend of a decrease in N mineralization and respiration in the organic matter exclusions plots suggests that these plots may be becoming C limited. High rates of immobilization and low rates of nitrification in all treatments suggests that even after 10 years of altering SOM inputs, the microbial communities are also N limited.

**SOIL NEMATODE COMMUNITY RESPONSE TO LONG-TERM CROP ROTATION, ORGANIC MANAGEMENT AND PRAIRIE RESTORATION IN THE RED RIVER VALLEY OF CENTRAL NORTH AMERICA. Briar, Shabeg<sup>1</sup>, M. Tenuta<sup>1</sup>, C. Barker<sup>2</sup>, and M. Entz<sup>3</sup>.** <sup>1</sup>Department of Soil Science, <sup>2</sup>Formerly Department of Soil Science, <sup>3</sup>Department of Plant Science; University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2.

The response of soil nematode communities to crop rotation, organic management and tall-grass prairie restoration was assessed four times (June 2003, July and August 2004, and July 2005) at the Glenlea Long-term Crop Rotation and Management Study. The study treatments were initiated in 1993 at the site located just south of Winnipeg, Manitoba, in the Red River Valley. The soil is clay and seasonally saturated with moisture. Three four-year rotations (Wheat-Pea-Wheat-Flax, Wheat-Green manure -Wheat-Flax, and Wheat-Alfalfa-Alfalfa-Flax) under Conventional or Organic management and a restored tall-grass native Prairie treatment were analyzed for their nematode communities. No consistent difference was observed between Organic and Conventional systems for the abundance of nematode trophic groups including bacterial-, fungal- and plant-feeders over the sample occasions ( $P > 0.05$ ). High c-p (colonizer-persister  $\geq 3$ ) value carnivore, omnivore and fungal-feeders were marginally favored by Organic than Conventional management. Soil food web characteristics based upon nematode faunal analysis estimates of structure (SI) and enrichment (EI) indices revealed it to be of slightly higher-trophic structure for Organic (SI 35-74 and EI 41-72) than Conventional (SI 25-71 and EI 44-73) management while decomposition channels were dominantly bacterial for both. Rotation including a green manure favored bacterial-feeders dominated by c-p 1 and 2 nematodes compared to the two other rotations. The Prairie had higher abundance of c-p 3, 4 and 5 omnivore and carnivore but lower levels of bacterial-feeding nematodes than the Organic and Conventional management systems. The soil food web of the Prairie was highly structured but low to moderately enriched based on nematode faunal analysis with SI ranging from 84-97 and EI from 23-65. Higher abundance of bacterial-feeders in the rotation including green manure suggested accelerated nutrient and energy trophic interactions for this soil food web. The soil food web of the Prairie demonstrated the ability of high c-p, k-strategist nematodes, to establish upon restoration of native grasses, and cessation of tillage and use of agro-chemicals despite the soil being clay and seasonally saturated with moisture.

**FIRST REPORT OF *M. PARTITYLA* INFECTING LAUREL OAK (*QUERCUS LAURIFOLIA*). Brito<sup>1</sup>, Janete A., J. D. Stanley<sup>1</sup>, R. N. Inserra<sup>1</sup>, M. Hao<sup>1</sup>, and D. W. Dickson<sup>2</sup>.** <sup>1</sup>Division of Plant Industry, Gainesville, FL 32614; <sup>2</sup>Department of Entomology and Nematology, University of Florida, Gainesville, FL 32611.

Laurel oak (*Quercus laurifolia*) trees are deciduous plants native to the Atlantic and Gulf Coastal Plains including southeastern Virginia, southern Florida and southeastern Texas. The largest number of laurel oak trees occurs in north Florida and southern Georgia. This species of oak, characterized by narrow leaves and production of large number of acorns grows rapidly. In April 2007, laurel oak plants were found infected with root-knot nematodes in a home garden, Alachua County, Florida. Infected roots were severely galled and partially rotted. Distinct round galls were observed on secondary and tertiary roots with egg masses protruding from the root surface. Species identification was performed using morphology of male stylet, selected characters of the second-stage juveniles, perineal patterns and isozyme phenotypes (esterase and malate dehydrogenase). Isozymes patterns were resolved from young egg-laying females via polyacrylamide gel electrophoresis in a BioRad Mini Protean III system. Morphology of perineal patterns of females as well as body, stylet and tail length of J2 and males matched those of the original description of *Meloidogyne partityla*. Stylet morphology of males fit that of the species description and showed a blunt tip, a notable thickened basal portion of the shaft and each knob incised by a deep median longitudinal groove. The isozyme phenotypes (Esterase = Mp3; malate dehydrogenase = N1a) were consistent with those previously reported for *M. partityla*. To our knowledge, this is the first report of *M. partityla* occurring on *Q. laurifolia*. Also this is the first report of a plant host for this root-knot nematode species outside of the family Juglandaceae. Studies are in progress to determine the ability of the oak population of this nematode to infect and reproduce on other species of oaks as well as pecan.

**NEMATODE COMMUNITY ANALYSIS AS A POTENTIAL TOOL FOR DETECTING THE IMPACTS OF ORCHARD FLOOR MANAGEMENT. Brutcher, Lisa J.<sup>1</sup>, J. Moore-Kucera<sup>1</sup>, N.M. Wade<sup>2</sup>, R.E. Ingham<sup>2</sup>, and A.N. Azarenko<sup>1</sup>.** <sup>1</sup>Dept. of Horticulture, 4015 ALS Bld., Oregon State University, Corvallis, OR 97331, <sup>2</sup>Dept. of Botany and Plant Pathology, 20282 Corley Hall, Oregon State University, Corvallis, OR 97331.

Orchard floor management (OFM) impacts nutrient fluxes among soil faunal populations, soil microorganisms and the tree. Soil nematodes, which span multiple trophic levels, have been shown to reflect nutrient dynamics and functional

diversity in soils. This study examined the sensitivity of soil nematode community structure to different OFM strategies in Oregon sweet cherry production. The effects of two OFM strategy treatments applied to the tree row [high organic matter mulch (OrAM) vs. no added organic matter (NoAm)], and an alleyway sod treatment on nematode community structure were examined for two years during establishment of two organic sweet cherry research orchards and at one mature commercial orchard. Treerow treatments at the research orchards produced unique nematode communities distinguished by non-metric multidimensional scaling and perMANOVA techniques. Utilizing these same techniques, nematode communities under alleyway treatments were distinguishable from both tree row treatments for all three sites. Total nematode density and herbivorous nematode density correlated strongly with the ordination axes at all three sites. Density of bacterivores (at two of the sites) and the percentage of bacterivores (at the third site) also exhibited a strong correlation. The other trophic groups also correlated with the axes but were less consistent across sites. The percentage of omnivores correlated with the ordination axes for the commercial site, density of fungivores correlated at one research orchard, and density of predators, predators+omnivores and fungivores correlated with the axes from the other research orchard. In addition, potentially mineralizable N also correlated strongly with the ordination axes at two of the sites. An analysis of soil nematode communities may be a useful tool in evaluating the impacts of OFM strategies on the orchard soil ecosystem.

**ECOSYSTEM SERVICES IN URBAN SOILS: WHAT DO THEY DO AND WHAT DO WE WANT THEM TO DO?**  
**Byrne<sup>1</sup>, Loren B.** <sup>1</sup>Department of Biology, Marine Biology and Environmental Science, Roger Williams University, Bristol, RI 02809 USA.

Urbanized ecosystems continue to increase worldwide. During urbanization, humans dramatically modify land cover to meet their needs for diverse land uses. Subsequent landscape management maintains desired land cover patterns and dictates many characteristics of urbanized environments. Although soils are impacted by these processes, urban soils remain understudied. Nonetheless, information about their ecological characteristics is urgently needed to provide insights about the ecosystem services they do or do not provide and, in turn, guide their management for increased urban environmental quality and human well-being. To these ends, recent urban soil ecology studies have established foundational information. However, they have also begun to expose important challenges for continued progress toward understanding the many dimensions of urban soils including their associated ecosystem services. Two questions framing this area of study are: What do urban soils do and what do we want them to do? The objective of this presentation is not to answer these questions directly; instead, it is to facilitate their discussion through description of key challenges to answering them and development of conceptual frameworks that might facilitate overcoming those challenges. One of the main challenges for understanding urban soil ecology across scales is the high levels of land cover heterogeneity that characterize urbanized landscapes. Habitat structure provides a useful concept for approaching this challenge because it focuses attention on differences in abiotic and biotic physical conditions and inputs among land covers that are expected to drive small-scale soil ecology patterns. Comparative research among urban land covers that differ in habitat structure characteristics is needed to help provide insights into what urban soils do. In addition, the concept of habitat structure facilitates overcoming the challenge of integrating sociocultural variables into the study of urban soil ecology because management of aboveground habitat structure is a primary goal for many landscape management practices. Another challenge for examining the ecosystem services of urban soils is the diverse management and land use priorities that urban residents have for urbanized landscapes. This issue is effectively explored with a framework centered on individually managed landscape parcels. Within a parcel, priorities for specific ecosystem services can be elucidated to guide analysis and interpretation of relationships among management inputs, soil variables and ecosystem services. Straightforward analyses may prove difficult, however. Although soils collectively provide many ecosystem services, they may not provide all of them at the same time at desired levels under a given land cover or management regime. For soil ecologists, this translates into a challenge for investigating many ecological variables and services simultaneously so that insights can be generated into how management inputs may lead to trade-offs among ecosystem services. In the future, demand is likely to increase for information about how urban soils can be managed to enhance their ecosystem services. Hopefully, this presentation and subsequent analyses will help enable soil ecologists to more productively engage in discussions about what urban soils do and what we should want them to do to increase the well-being of urban human societies.

**INVASIVE EARTHWORM RESPONSES TO EXPERIMENTAL REMOVAL OF THE INVASIVE SHRUB *LIGUSTRUM SINENSE* (CHINESE PRIVET) IN RIPARIAN FORESTS OF THE SOUTHERN PIEDMONT.** **Callahan, Jr.<sup>1</sup>, Mac A., G.A. Langhenry<sup>1</sup>, J.L. Hanula<sup>2</sup>, and S. Horn<sup>2</sup>** <sup>1</sup>USDA Forest Service, Southern Research Station, Center for Forest Disturbance Science, Athens, GA, 30602, <sup>2</sup>USDA Forest Service, Southern Research Station, RWU-4552 – Insects, Diseases, and Invasive Plants, Athens, GA 30602.

The spread of Chinese privet (*Ligustrum sinense*, hereafter 'privet') in riparian forests of the southeastern United States has been ongoing since the introduction of the plant as an ornamental shrub in the mid-1800s. This invasion has deleterious effects on the midstory and understory plant communities and has been demonstrated to dramatically decrease plant community diversity when privet becomes dense. Recent work in other shrub invasion systems, in the Great Lakes states of the US, has

demonstrated that there is a putative synergistic relationship between invasive shrubs and non-native, invasive earthworms. We took advantage of an ongoing privet removal project in the Oconee river basin of east-central Georgia to address hypotheses about whether similar synergies were operating between privet and non-native earthworms. The larger project was aimed at evaluating responses of plant and arthropod communities to different privet removal treatments, and as part of this effort, ground dwelling invertebrates were sampled by pitfall traps. Frequent occurrences of earthworms as by-catch in these pitfalls (sometimes in large quantities) prompted a specific evaluation of earthworm community responses to the privet removal treatments. Two different privet removal techniques were employed on plots that were 1.5-2 ha in size. These treatments consisted of 1) chainsaw felling of all privet stems, with all slash reduced to 1 m height or less (Chainsaw), or 2) mechanical mastication by a tractor-mounted gyrotrac® apparatus (Mulch), resulting in a layer of privet mulch approximately 25-35 cm in depth across the entire treatment area. Both removal treatments were followed by herbicide application to residual privet stumps. Additional sampling was conducted on plots that had not been invaded by privet representing the desired condition (no-privet controls), and plots that were invaded by privet but did not receive any removal treatments (treatment controls). Preliminary results from the earthworm collections suggest that organic matter additions associated with wholesale removal of privet are highly favorable to European earthworm species. The earthworm fauna in these plots was dominated by *Lumbricus rubellus*, and this species was most abundant in the “mulch” treatment. Interestingly, *L. rubellus* was least abundant in the no-privet controls, (relative to all other plots), indicating that the plant may facilitate the establishment of the earthworm. Other European and Asian earthworms were also collected, but patterns of distribution were less clear-cut for these species. Native earthworm species were extremely rare, and only one genus, *Bimastos*, was well represented in our samples. *Bimastos* was most likely to be collected in the no-privet controls, but was also represented in the “mulched” plots, indicating that this group may recover quickly in response to privet removal treatments.

**ESTIMATING NUMBERS OF ENTOMOPATHOGENIC NEMATODES IN CITRUS ORCHARD SOIL SAMPLES USING REAL TIME QPCR. Campos-Herrera<sup>1</sup>, Raquel, E.G. Johnson<sup>1</sup>, F. E. El-Borai<sup>1,2</sup>, J.H. Graham<sup>1</sup>, and L.W. Duncan<sup>1</sup>.** <sup>1</sup>Citrus Research and Education Center, University of Florida, Lake Alfred FL 33850. <sup>2</sup>Plant Protection Dept. Faculty of Agriculture, Zagazig University, Egypt.

Entomopathogenic nematodes (EPN) from *Heterorhabditidae* and *Steinernematidae* inhabit most soils. These nematodes have potential for use as biological control agents and represent a promising non-chemical alternative for management of insect pests in a number of crops worldwide. Although commercial strains are available, native EPN populations occur in most soils at levels that sometimes regulate insect pests. The biotic and abiotic factors that affect their natural spatial patterns and their efficacy against target pests are largely unknown. A better understanding of the complex interactions between EPN, edaphic factors and food webs could provide new opportunities to more effectively employ EPN's for pest management. Traditional methods using insect baits are adequate for detecting EPN in soil, but current methods to assess population density are laborious. Consequently, we intend to employ quantitative real-time PCR (qPCR) to improve our ability to detect and quantify EPN in soil. Species-specific primers and TaqMan® probes were designed from the ITS rDNA regions of *Steinernema diaprepesi*, *S. riobrave*, *Heterorhabditis indica* and *H. zealandica*, all commonly encountered in Florida citrus orchards. Several populations of putative, undescribed species in the *S. glaseri*-group were also revealed during the design of primers. Species-specificity of the primers/probes were tested using several populations of each of these and other EPN species. Standard curves for each species were established using pure cultures reared in *Galleria mellonella*. Magnesium sulphate density gradient purification caused little additional loss of nematodes previously extracted from soil by sucrose centrifugation, but reduced interference with the PCR reaction by inhibitors in soil. Specificity and efficacy of qPCR to estimate numbers of EPN in nematode communities extracted from soil was confirmed by comparison with direct counts of nematodes in samples. We anticipate that use of this methodology will increase the capacity to quantify EPN in surveys and experiments by approximately an order of magnitude compared to traditional methods.

**FROM THE GROUND UP: CONSERVING SOILS AND ECOSYSTEM SERVICES IN URBAN WOODLAND PARKS. Carreiro, Margaret and E. Levine,** Department of Biology, University of Louisville, Louisville, KY 40292.

Urban woodland parks provide supporting and regulating ecosystem services, including primary production, biodiversity maintenance, air and water quality improvement, and heat island and flood reduction. But the ecosystem services most needed and readily appreciated by the public are cultural. These woodlands are iconic and well-loved places, since they provide city dwellers daily access to “wild” nature, and quiet places for passive recreation, spiritual rejuvenation and informal social interactions. However, the quality of these benefits is predicated on the continued regeneration of woody vegetation, which in turn depends on the condition of the woodland's soils. Urban park managers face many challenges involving soil conservation and regeneration of native plants, especially trees. These include poorly sited paved areas, rogue trail development and invasive plants. All of these soil impacts are even more difficult to remediate on wooded hill slopes, where leaf litter retention is low and soil loss can be considerable. The wooded slopes in 160 ha Cherokee Park, Louisville, Kentucky has had a history of natural disturbance, human usage and invasive shrub colonization that have left a legacy of compacted and eroding soils with low herbaceous cover and leaf litter protection. Leaf litter protects soils from erosion year-round, but especially in summer when

rainstorms are intense and ground-level plant cover is virtually non-existent ( $1.1 \pm 3.0\%$ ). On wooded slopes varying from  $11^\circ$  to  $22^\circ$  in this park, 52% to 100% of the soil surface was bare in summer. Summer leaf litter mass ranged from 0 to 44 g ODM/m<sup>2</sup>, offering little protection from sheet erosion and overland flow originating from rogue trails. Twenty plots have been established throughout the Park to determine the extent to which the invasive shrub, Amur honeysuckle, may be responsible for the low rate of plant regeneration and litter cover. Honeysuckle stem density in these plots ranged from 47 to 270 stems/100 m<sup>2</sup>. Since this study entails removal of honeysuckle in half the plots, the effect of shrub removal on downslope litter and soil movement was a concern. Therefore, soil erosion and leaf litter export is being quantified in control and removal plots using a silt fence capture method. After one month's rainfall in July-August of 5.8 cm (maximum intensity 3.4 cm/hr for 10 minutes), a 100% bare soil plot lost the equivalent of 0.51 metric tons ODM soil /ha. Since soil replacement from upslope is limited by paved areas and lawns, continued losses at these rates greatly compromises the sustainability of woodlands on hill slopes in this park and of the ecosystem services they provide. In subsequent years different methods for soil and leaf litter stabilization and tree seedling establishment will be evaluated. Stabilizing and improving the porosity of soils in this woodland is critical, if soils and vegetation are to withstand the more variable precipitation and higher drought risk predicted in this region from climate change.

**INTERACTIONS BETWEEN THE LEGACIES OF PLANT LITTER INPUTS ON SOIL CHEMISTRY AND SOIL COMMUNITIES AFFECT LITTER AND SOIL ORGANIC MATTER DYNAMICS.** Carrillo, Yolima<sup>1</sup>; B.A. Ball<sup>2</sup>; M. Strickland<sup>1</sup>, M.A. Bradford<sup>3</sup>. <sup>1</sup>Odum School of Ecology, University of Georgia, Athens, GA 30602, USA. <sup>2</sup>Dartmouth College, Environmental Studies Program, 6182 Steele Hall, Hanover, NH 03755, USA. <sup>3</sup>School of Forestry and Environmental Studies, Yale University, New Haven CT 06511, USA.

As spatial and temporal scales decrease decomposition in terrestrial ecosystems is largely dependent on the quality of resources and the decomposer community. The outcomes of interactions between these factors are for the most part not well understood. One way in which these two factors may interact to affect processes is through their legacy effects on contemporary processes. For example, the chemical and biotic environment in soil can be impacted by the history of plant litter inputs with potential effects on function. We tested whether legacy effects of plant litter inputs and soil community structure affected contemporary litter and soil organic matter (SOM) mineralization dynamics and, if so, whether or not these different mechanisms interacted to determine function. We established a microcosm experiment where the soil chemistry and community were manipulated by exposing them to two plant litters of contrasting chemical composition for 18 months. We characterized the soil chemical and biotic environment and monitored the initial stages of nitrogen (N) and carbon (C) mineralization of freshly-amended litters or resident SOM. The importance of the soil community legacy effects on contemporary decomposition processes was assessed by simplifying the soil community through freezing. We found that net N mineralization or immobilization was determined by strong interactive effects between litter pretreatment and the structure of the soil community. Interactions were dependent on whether the microcosms received fresh litter, the incubation period, and the species of fresh litter that was amended, suggesting that differences in mineralization manifested through both chemical and biotic legacies. In contrast to N dynamics, C mineralization of fresh litters was only influenced by litter pretreatment, suggesting that these legacy effects manifested mostly through changes to the soil chemical environment. Carbon mineralization of the SOM was only influenced by the community pretreatment, suggesting that these legacy effects manifested through changes to the soil decomposer community. We conclude that the manner in which legacy effects manifest will likely differ for C and N processes, and for litter and SOM decay. Our results highlight that some of the control exerted by decomposer communities might arise through legacy effects of litter inputs, and that the effects of the chemical composition of contemporary litters will likely depend on legacy effects on soil chemistry and biota. Our results suggest that knowledge of land use cover and management history may help explain variation in decomposition processes across a landscape.

**CULTURE AND MORPHOLOGY OF A NEW PARASITORHABDITIS (*RHABDITIDA*) FROM *DENDROCTONUS FRONTALIS* DEMONSTRATED WITH ALTERNATIVE METHODS FOR LOW TEMPERATURE-SEM.** Carta<sup>1</sup>, L.K., G. Bauchan<sup>2</sup>, C.-Y. Hsu<sup>3</sup> and C. Yuceer<sup>3</sup>. <sup>1</sup>USDA-ARS, Nematology Laboratory, Beltsville, MD 20705, <sup>2</sup>USDA-ARS, Electron and Confocal Microscopy Unit, Beltsville, MD 20705, <sup>3</sup>Mississippi State University, Forestry Department, Mississippi State, MS 39762.

*Parasitorhabditis* is a genus that currently includes 44 species of nematodes. A new species with males and females was discovered from the southern pine beetle *Dendroctonus frontalis* and its galleries in loblolly pine *Pinus taeda* from Mississippi. The new species (isolate LKC43) female has a cupola-shaped tail with a small, curved spike, and the male possesses a 2+(3+2)+3 ray pattern on the tail fan with rays 3 and 9 opening dorsally. LKC43 has some similarities to *Parasitorhabditis ateri* originally isolated from the black pine bark beetle *Hylastes ater* in Germany, and *P. malii* from the larger shot-hole borer *Scolytus mali* within the country of Georgia. It was initially grown on Luria Broth (LB) agar with its own microbial contaminants that included a bacterium, yeast and fungus. The nematode could also grow and reproduce on 2% water agar after chunks of LB agar with nematodes and microbial contaminants were transferred. When transferred to *E. coli* on NGM agar plates commonly used to raise other *Rhabditida*, the nematodes rapidly disintegrated and generally perished within days. Differential interference contrast and low-temperature SEM images are provided for the body, head, and tails of cultured

specimens. In order to optimize the likelihood that nematodes would turn their heads upward before flash-freezing, specimens were mounted in water on leaves with a variety of elevated structures.

**STUDIES ON BIOCONTROL OF *ROTYLENCHULUS RENIFORMIS* ON COTTON CROPS.** Castillo<sup>1</sup>, Juan D., K.S. Lawrence<sup>1</sup>, G. Morgan-Jones<sup>1</sup>, and E.S. van Santen<sup>2</sup>. <sup>1</sup>Department of Entomology and Plant Pathology, Auburn University, Auburn, AL 36849 and <sup>2</sup>Department of Agronomy and Soils, Auburn University, Auburn, AL 36849.

The objective of this work was to isolate, identify, and evaluate the biological control potential of naturally occurring fungal pathogens associated with *Rotylenchulus reniformis*. Soil samples were collected in cotton fields naturally infested with *R. reniformis* and from nematode stock pots grown in the greenhouse. Nematode samples were observed under the stereoscope and vermiforms colonized with mycelia and discolored eggs were collected. The percentage of parasitism of the reniform nematodes collected were Limestone county 3%, Henry 23%, Baldwin 5%, Escambia 0% and our greenhouse was 21%. These nematodes were cultured on 1.5% water agar, incubated at 27°C and fungal growth was transferred to Potato Dextrose Agar (PDASA) plus streptomycin sulfate to establish pure cultures. Identification of the nematophagous fungi was based on the morphological characters, and the ITS regions and 5.8S rDNA amplified by PCR using the primers ITS1 and ITS4. A total of 16 fungi were identified from *R. reniformis* with four of the fungal isolates previously reported as nematophagous to other nematodes species. The fungi include isolates of *Arthrobotrys dactyloides*, *Dactylaria brochopaga*, *Paecilomyces lilacinus*, and *Fusarium oxysporum*. Blasting the PCR product on GeneBank the *A. dactyloides* isolates were 99% similar to *Arthrobotrys anchonia* and 97% to *Drechslerella dactyloides*. The three isolates of *A. dactyloides* group together on the phylogenetic tree (Neighbor-joining, MEGA 4.1). In vitro pathogenicity tests for *Arthrobotrys dactyloides* and *Dactylaria brochopaga* revealed conidia germination after 14 hours and ring formation began after 16 hours. Ring formation was complete by 36 and 42 hours. Nematodes are observed near the ring structures after 60 hours and by 72 hours the nematodes were trapped. The pathogenicity of these fungi was further tested in the greenhouse in a with two soil types (autoclaved, and natural) and three fungal carriers (wheat, oat, and corn meal). In autoclaved soil, *A. dactyloides*, *D. brochopaga*, and *P. lilacinus* reduced ( $P < 0.05$ ) the number of vermiform *R. reniformis* nematodes in soil. *Paecilomyces lilacinus* and *F. oxysporum* reduced ( $P < 0.05$ ) the number of juveniles and eggs in the roots. In natural soil, *A. dactyloides* and *F. oxysporum* reduced *R. reniformis* numbers in soil, but the fungal isolates did not reduce *R. reniformis* numbers of eggs in roots. The fungal isolates exhibited no phytotoxicity and did not reduce plant shoot or root mass or reduce plant height. Interestingly, oat when used as a fungal carrier, plants root mass was increased. All six fungal strains of *A. dactyloides*, *D. brochopaga*, *P. lilacinus*, and *F. oxysporum* reduced *R. reniformis* numbers in autoclaved soil. The reduction in numbers of nematodes was consistently observed in autoclaved soil.

**SOIL CARBON STORAGE ACROSS A GRADIENT OF LAND USE IN MOUNTAIN ECOSYSTEMS.** Chapman<sup>1</sup>, Samantha K., R. Shaw<sup>1</sup>, and J.A. Langley<sup>1,2</sup>. <sup>1</sup>Department of Biology, Villanova University, Villanova, PA, <sup>2</sup>Smithsonian Environmental Research Center, Edgewater, MD 21037.

Soil carbon storage often depends on land-use history. We investigated the carbon storage potential of forests, pastures and Christmas tree farms (*Abies fraseri*) in the Southern Appalachian mountains in order to investigate land management impacts on soil carbon storage. We partitioned soil carbon into fractions delineated by stability, an important determinant of long-term sequestration potential. We measured NDVI and soil microclimate in tree farms, pastures and forests in order to assess plant and microclimatic variation across sites that might contribute to soil carbon differences. In order to assess land management impacts through time, we quantified soil carbon stocks in tree farms across a chronosequence of cultivation duration. By referencing soil carbon stocks in tree farms to those in adjacent pastures and native forests, we accounted for variability in other soil-forming factors. Labile soil carbon respiration rates were significantly higher in pastures and forests than in tree farms. Recalcitrant soil carbon pools were significantly greater in the forests than in the pastures and tree farms, which had similar amounts of recalcitrant soil carbon. Because of an oversupply of Christmas trees, some tree farms have been abandoned. These farms serve as an indicator of changing land use. We saw a 150% increase in labile soil carbon respiration on these farms as compared to active tree farms. Our findings can help inform land management decisions and soil carbon sequestration strategies. Further, ongoing investigations will allow us to determine if agro-ecosystems can concurrently provide an economically viable crop and the salient ecosystem service of carbon storage.

**SCREENING OF MICRO-ORGANISMS ISOLATED FROM THE NORTHEAST OF CHINA FOR TOXICITY TO NEMATODES.** Chen, Lijie, G.D. Zhang, B. Liu, J.S. Chen, J.R. Li, Y.Y. Wang, Y.X. Duan\*. College of Plant Protection, Shenyang Agricultural University, Shenyang, P.R.China, 110161. 1st Shenyang, SYAU 110161. Correspondence: duanyx6407@163.com

Thousands of fungal, actinomycete and bacterial isolates from the northeast of China were screened for toxicity to nematodes from 2006 to 2008. A significant number of the isolates were toxic to *Meloidogyne incognita*, *Heterodera glycines*, *Aphenlenchoides besseyi* and *Caenorhabditis sp.* in vitro. Greater than 70% corrected mortality rate of target nematodes was observed in 20 of 203 isolates of wild basidiomycete macro-fungi collected in Liaoning province. Basidiomycete isolate F149 induced a corrected mortality rate of 97.74% for *M. incognita*, F128 induced 96.55% mortality of *H. glycines*, F139 induced 90.40% mortality of *Caenorhabditis sp.*, and F130 induced 97.92% mortality of *A. besseyi*,

respectively, after 48h exposure. Twenty of 154 isolates of *Beauveria* from soil and insects were toxic to *H. glycines*, and nine of those isolates were toxic to other nematode species tested. Thirty of 400 isolates of actinomycetes from soil dilution samples could suppress *H. glycines*, and among them, there were 5 isolates that could strongly inhibit the activity of second juveniles (J2) and egg hatch of *H. glycines* (SCN). Actinomycete isolate C253 induced a 95% corrected mortality rate of SCN J2 after 24h exposure and was also toxic to the other nematode species tested except for weak activity against *Caenorhabditis* sp. Seven of 401 isolates of endophytic bacteria from soybean root tissue could inhibit egg hatch of SCN beyond 50%, however, endophytic bacteria generally had weaker toxicity to nematodes than other microorganisms. We also obtained several *Bacillus* isolates with toxicity to *H. glycines*. A number of micro-organisms with potential control activity against phytoparasitic nematodes were identified in this study.

**THE INVASIVE EARTHWORM *PONTOSCOLEX CORETHRURUS* INCREASES CO<sub>2</sub> EFFLUX AND NITROGEN MINERALIZATION IN THREE TYPES OF FOREST SOILS. Chen, Ting-Wen<sup>1</sup>, C.-P. Wang<sup>2</sup>, and P.-C.L. Hou<sup>1</sup>.**

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Effects of the invasive earthworm, *Pontoscolex corethrurus*, on ecosystem functions are controversial. We used a microcosm study to examine growth of *P. corethrurus* and its effects on soil CO<sub>2</sub> efflux and C, N mineralization in three types of forest soils from Taiwan (FS, high organic matter, clay-loam; NJS, low organic matter, clay-loam; TCG, low organic matter, sand). At the end of the experiment (101 days), the earthworms grew in body weight in all three soils and reproduced in FS and TCG soils, with the largest increases in FS soil. The earthworms also increased CO<sub>2</sub> production significantly in all three soils. In FS soil, the degree of CO<sub>2</sub> increase was depending on incubation time and the cumulative CO<sub>2</sub> production was highest among the three soils. No significant difference in CO<sub>2</sub> increase was found in the other two soils. *P. corethrurus* did not change microbial biomass-C in the three soils but decreased significantly microbial biomass-N in TCG soil at the end of experiment, suggesting the microbial community might have shifted from bacteria-domination toward fungi-domination. *P. corethrurus* did not change K<sub>2</sub>SO<sub>4</sub>-extractable organic carbon significantly, but increased K<sub>2</sub>SO<sub>4</sub>-extractable total nitrogen in the three soils. They increased ammonium in the two clay-loam soils and nitrate in the sandy soil, and also raised organic nitrogen in the low organic, clay-loam soil. The results suggest that, with high growth and reproduction rates, *P. corethrurus* per se might have a considerable contribution to CO<sub>2</sub> efflux and might change the activities of microbial community. The net effects of *P. corethrurus* and microbe interaction are increases in CO<sub>2</sub> efflux and nitrogen mineralization regardless of the soil types. Thus, the consequences of *P. corethrurus* invasion should not be overlooked.

**VERTICAL DISTRIBUTION OF SOIL FREE-LIVING NEMATODE COMMUNITY INHABITANTS IN A PLAYA AREA OF THE NORTHWESTERN NEGEV DESERT, ISRAEL. Cheng, Hu<sup>1,2</sup>, S. Pen-Mouratov<sup>1</sup>, and Y Steinberger<sup>1</sup>.**

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Inter-sand-dune desert sites are known to be one of the most prominent locations for generating playa surfaces characterized by compact floors, salt pavements, carbonate surfaces, and a high percentage (50% or more) of clay. Such physical and chemical soil properties have a strong influence on the vertical flow water by playing a crucial function in soil biotic community composition, density, and diversity. The aim of this research was to determine the vertical distribution of a soil nematode community in a playa area in the Nizzana inter-sand dune area in the northwestern Negev Desert, Israel. Soil samples from depths of 0-10, 10-20, 20-30, 30-40, and 40-50 cm were collected in a playa area while a sandy inter-dune area acted as control in dry and wet seasons. Soil moisture, organic matter, and electrical conductivity were determined in each sample, and nematode community composition and diversity were evaluated. The results showed that soil moisture, organic matter, and electrical conductivity were significantly influenced by sampling location. The total number of nematodes in the playa area ranged from 1 to 15 individuals per 100 g dry soils, while in the control sampling area, the number ranged from 66 to 508 individuals per 100 g dry soils, i.e., significant ( $p < 0.05$ ) differences between the sampling sites were found. This significant difference in nematode number lead to differentiation in the bacterivores, fungivores, and omnivores-predators between treatments, depths, and seasons ( $P < 0.05$ ). The plant-parasite trophic group was found to show a significant difference ( $P < 0.05$ ) only between the treatments and depths. Moreover, the total number of nematodes, bacterivores, fungivores, plant parasites, and omnivores-predators were significantly ( $p < 0.05$ ) greater in the control area than in the playa area in the dry and humid seasons. Soil free-living nematodes were found to mainly inhabit the upper soil layers (0-20 cm). Thirteen genera were found in the playa soil samples, with the Acroboloides being the dominant genus, in comparison to the control samples, in which fifty-five genera were found, with the genus Acrobeles being the dominant one. Nematode ecological indices such as Wasilewska index (WI), fungivore/bacterivore ratio (F/B), trophic diversity (T), genus dominance, Shannon Index (H'), maturity index (MI), plant parasite index (PPI), modified maturity index (MMI), evenness, species richness (SR), enrichment index (EI), basal index (BI), structure index (SI), and nematode channel ratio (NCR) significantly differentiated between treatments, other than PPI, which was found to be significantly affected by vertical sampling. The

results obtained from this study revealed that soil free-living nematode density, trophic group composition, and ecological indices are valuable tools for elucidating harsh soil habitats.

**HOW DO TALL FESCUE LAWNS ESTABLISHED ON COMMON URBAN SOIL MATRICES INFLUENCE THE NEMATODE FOOD WEB AND NUTRIENT POOLS? Cheng, Zhiqiang and P. S. Grewal.** Urban Landscape Ecology Program and Department of Entomology, The Ohio State University, 1680 Madison Ave., Wooster, OH 44691.

Human activity in urban areas often disturbs the soil profile, but little is known of its effects on subsequent soil food web dynamics and biogeochemical cycling. We assessed dynamics of the soil nematode food web and nutrient pools in tall fescue lawns created on either disturbed topsoil or subsoil for over two years. Overall, numbers of all nematodes and nematode genera remained higher in topsoil than subsoil plots even after two years. The nematode food web enrichment index was lower in subsoil plots compared with topsoil plots but steadily increased overtime. The nematode food web structure remained low in subsoil plots for one year and then increased rapidly to a level even higher than that in topsoil plots. The food web structure in topsoil declined in the first year and then increased over time. This temporal faunal profile analysis indicated that within two years, the soil food web condition became highly enriched but moderately structured, which is typical of what is found in turfgrass lawns, suggesting a strong bottom-up control. Soil macronutrients Ca, P, K, and soil organic matter remained higher in topsoil than subsoil even after two years. During the first two months after seeding, topsoil plots had lower turfgrass cover than subsoil plots, but had higher weed cover. After one year, turfgrass quality (greenness) was higher in topsoil than subsoil plots, and this pattern remained even after two years. We conclude that anthropogenic activities, resulting in the loss of topsoil, can have a profound effect on the soil nutrient pools and soil food web, which may severely affect soil's capacity to support optimal nutrient cycling, plant growth, and other essential functions.

**EFFECTS OF LANDSLIDE DISTURBANCE ON GROUND LITTER ORIBATID MITE COMMUNITIES IN A TROPICAL MONSOON FOREST IN TAIWAN. Chien, Hao-Chiang<sup>1</sup>, P.C.L. Hou<sup>1</sup>, and N. Kanaeko<sup>2</sup>.** <sup>1</sup>Department of Life Sciences, National Cheng Kung University, Tainan, Taiwan 70101, <sup>2</sup>Soil Ecology Research Groups, Graduate School of Environment and Information Sciences, Yokohama National University, Yokohama 240-8501, Japan.

Oribatid mites are often the most diverse group among litter arthropods. Their low mobility and low fecundity indicate that they may be sensitive to disturbances and are ideal for detecting environmental changes. In this study, effects of landslide disturbance on density and composition of the oribatid mites were investigated in a tropical monsoon forest in Taiwan. Oribatid mites collected bimonthly from litter layers of the control and the landslide forests were analyzed. A total of 87 morphospecies of oribatid mites across 49 families were identified from the litter samples. Mean density of oribatid mites was 1766.8 individuals/m<sup>2</sup> and did not differ significantly between the control and landslide forests. However, composition of the oribatid mites varied significantly between the two forests and time within each site. Juveniles of *Trhypochthoniidae* sp. 1 were more abundant in the landslide forests than the control forests. These results suggest that landslide disturbance does not change oribatid density but alter its composition in litter layer and appears to support the hypothesis that parthenogenetic oribatid mites are more abundant in the disturbed area than in the undisturbed area.

**THE EFFECT OF EARLY SOYBEAN CYST NEMATODE INFECTION ON SOYBEAN GROWTH AND PHYSIOLOGY. Cirrinicione, Peter, P. M. Tefft, and C. J. Springer.** Dept. of Biology, Saint Joseph's University, Philadelphia, PA 19131.

*Heterodera glycines*, the Soybean Cyst Nematode (SCN), a common pest of the important crop species, Glycine max (soybean) that causes an annual loss of 1.5 billion dollars in the United States. The Soybean Cyst Nematode is an obligate endoparasite that once inside the root of a soybean plant converts the phloem tissue into giant cells that form a nutrient sink. This provides nutrients and carbon to SCN that are normally supplied to the plant. Heavy infection causes economic loss due to decreased plant vigor and seed production. Despite this large economic cost, little is known about the specific changes in the physiology and morphology of soybeans as a result of infection with SCN. The current experiment examined the physiological and morphological changes in soybean plants infected with varying concentrations of SCN inoculum. Plants were inoculated with three concentrations of SCN eggs, as well as a non-inoculated group that served as the control. The number of larvae found inside the plant roots significantly increased with increasing SCN inoculum concentrations, with nearly a 16 fold increase between the number of worms found in plants inoculated with the highest doses of SCN eggs and those inoculated with the lowest dose of SCN. This large difference in SCN infection yielded a negative correlation between the physiological performance of the plants and the concentrations of the SCN inoculums. The plants exhibited a significant 33% decrease in stem mass between control plants and those inoculated with the highest dose of SCN eggs. Leaf mass also displayed a significant decrease with infection. For example, leaf mass decreased 85% between non-inoculated plants and those inoculated at the highest dose of SCN eggs. Coupled with this decrease in leaf mass was a decrease in total leaf area, whereby plants grown at the highest SCN dose exhibited a 59% decrease in leaf area when compared to control plants. Interestingly, steady-state net photosynthesis and total chlorophyll concentrations of the soybeans were not significantly different among the treatments. This finding suggests that the observed decrease in plant growth was primarily due to a decrease in leaf area among the inoculated plants. These findings

are contrary to the general conclusion that the observed decreases in soybean growth are primarily driven by a loss of chlorophyll concentrations in the leaves (chlorosis). The rate of leaf area production is likely far more limiting to plant growth and rigor early in the infection process as exemplified in this experiment.

**ECOSYSTEM PRODUCTIVITY AND SOIL FOOD WEB STRUCTURE – PAIRED FOREST AND GRASSLAND TRANSECTS ACROSS OREGON.** Colby<sup>1</sup>, Samantha E., and A.R. Moldenke<sup>1</sup>. <sup>1</sup>Dept. of Botany and Plant Pathology, 2064 Cordley Hall, Oregon State University, Corvallis, OR 97331. (samantha.colby@gmail.com, moldenka@science.oregonstate.edu)

The vast majority of organisms contributing to the biodiversity on Earth live in the soil; to what degree are this diversity and the ecosystem functions they perform regulated by climate and plant productivity? This study seeks to determine the relationship between climate/Net Primary Productivity (NPP) and soil food web structure. Seven research sites, each consisting of a conifer forest paired with a native grassland, are located along east-west transects in Oregon; these transects encompass climates producing the greatest productivity (maritime rain forest) and nearly the lowest productivity (sagebrush steppe) that occurs on the continent. Oregon climate is characterized by wet winters and dry summers, with snow-covered winters at the high elevations. Overall, the 14 experimental sites share the same basic flora and fauna, facilitating determination of the effect of productivity independent of the component species. Samples will be taken at each site once per season. Microbial abundance and biomass will be determined by direct counts. Nematode abundance, arthropod abundance, and species richness will also be determined by direct counts, and in addition will be expressed as biomass. The forested sites are characterized primarily by a fungally-based food web and soils with a deep humus layer. The paired grassland sites support a primarily bacterially-based food web with minimal organic soil layers. Because these energy pathways are so fundamentally different, we expect to see the greatest differences in food web structure between forest and grassland sites. Furthermore, at all of the sites we expect that the bacterially-driven components (rhabditid nematodes, flagellate protozoa, zerconid mites, etc.) will dominate during periods of maximum soil moisture, while the fungally-driven components (springtails, oribatids, gamasid mites, micryphantid spiders, etc.) will progressively dominate as the soil dries seasonally. Though annual fall litterfall (true of conifers too) adds labile nutrients, much of the actual food web is controlled by the rate and periodicity of litter-shredding by millipedes and isopods, and this activity takes place at different seasons along the transects. Thus energy and nutrients are made available at different times of year in the different systems. By monitoring the seasonal changes in food web structure along this gradient, we can capture a more complete picture of the dynamics of each system. The ultimate goal of this research is to produce a quantitative model relating climatic parameters (degree-days, precipitation), measures of nutrient input (NPP, litterfall), and food web structure (bacterial-based, fungal-based, relative emphasis on standing crop biomass of web components) with decomposition rate. We are especially interested in changes in species richness/diversity of each component of the food web as NPP increases.

**MOLECULAR FINGERPRINTING TO MONITOR NEMATODE POPULATIONS IN AGRONOMIC SOILS.** Conner, Kassie N. and R.N. Huettel. Dept. of Entomology and Plant Pathology 209 Life Sciences Bldg., Auburn University, AL 36849.

The nematode community within agronomic soils includes both plant-parasitic and free-living nematodes. These nematodes have direct and indirect affects on soil nutrition, other soil organisms and plant disease. Understanding the total nematode community includes identifying individual populations and determining interactions between them; however, identification based on morphology is time-consuming and requires extensive training. Alternative molecular approaches can generate population specific fingerprints by displaying ribosomal polymorphisms naturally present in microbial communities. Molecular fingerprinting methods, such as DGGE (denaturing gradient gel electrophoresis), are currently used to monitor bacterial and fungal populations in agronomic soils by separating fragments of DNA based on their unique sequence. In this study a DGGE protocol was set up to generate genetic profiles of nematode communities from peanut soils. Application of this method in agronomic soils under differing crop rotations can reveal differences in nematode composition. Understanding the entire nematode community within agronomic soils may provide management schemes to change soil microbial profiles and ultimately increase plant health.

**SEASONAL VARIATION IN MICROBIAL AND BIOGEOCHEMICAL PROCESSES IN CHRONICALLY WARMED AND FERTILIZED SOILS.** Contosta, Alexandra, S.D. Frey, and M.A. Knorr. Department of Natural Resources, Nesmith Hall, 131 Main Street, University of New Hampshire, Durham, NH 03824.

The objective of this work was to compare estimates of microbial and biogeochemical processes obtained from year round versus field season only data. We also aimed to capture the response of soils to simultaneous warming and nitrogen fertilization in both winter and summer months. Our research took place at the chronic Soil Warming and Nitrogen Fertilization experiment at the Harvard Forest Long Term Ecological Research site. The experiment includes four treatments in a completely randomized design: control, +heat, +N, and +heat +N. Heated plots are warmed to 5°C above ambient using buried heating cables, and N fertilization consists of monthly additions of NH<sub>4</sub>NO<sub>3</sub> in doses equivalent to a rate of 5 g N m<sup>-2</sup>

$\text{y}^{-1}$ . To date, year-round measurements of C and N fluxes and the soil microbial community show that soils were active during the winter months, and that our experimental manipulations impacted soils outside of the growing season. Across all treatments,  $\text{CO}_2$  flux underneath snowpack in January 2008 was approximately 10% of  $\text{CO}_2$  flux in July of 2007. Annual flux estimates corroborated this finding, and indicated that winter respiration contributed between 17-18% of the total annual flux. In addition,  $\text{CO}_2$  respiration in +heat and +heat +N plots was significantly higher than the control treatment both in winter and in summer months. Like  $\text{CO}_2$  respiration, N mineralization occurred during the colder months of 2007, though rates in November and December were about 5% of those during the summer maximum in June. Total annual net N mineralization was significantly higher in the +heat and +heat +N plots, though most of the difference in N turnover among treatments appeared to occur during the summer months. Like the C and N fluxes, microbial community function, as quantified by extracellular enzyme activity, also showed a seasonal pattern. Phenol peroxidase activity was highest in winter for all experimental manipulations, with the highest rates occurring when assays are incubated at  $0^\circ\text{C}$  as compared to  $25^\circ\text{C}$ . In contrast,  $\beta$ -glucosidase activity peaked in July and October, and showed higher rates of activity at  $25^\circ\text{C}$  than at  $0^\circ\text{C}$ . Measurements of microbial community composition as PLFA also showed seasonal differences. To date, PLFA estimates of fungal and bacterial biomass showed significantly higher F:B ratios in January as compared to April and July. Together, the  $\text{CO}_2$  respiration, N mineralization, and microbial community data suggest that soils are active in winter, and that microbial community composition and function differ between winter and the growing season. In addition, soil warming can accelerate  $\text{CO}_2$  flux outside of the typical field season. Failure to measure these processes after the field season ends could result in incorrect estimates of annual  $\text{CO}_2$  flux, and could also underestimate the impact of exogenous disturbances on ecosystem function.

**TAXONOMIC IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF NEMATODES IN THE SUBORDER CRICONEMATINA. Cordero, M.,<sup>1</sup> R. T. Robbins,<sup>1</sup> and A. L. Szalanski.<sup>2</sup>** 2009. <sup>1</sup>Department of Plant Pathology, 2601 N. Young Ave. Cralley - Warren Research Lab. University of Arkansas, Fayetteville, AR. 72704. <sup>2</sup>Department of Entomology, AGRI 330B, University of Arkansas, Fayetteville, AR. 72701. mcordero@uark.edu; rrobbin@uark.edu; aszalan@uark.edu

According to Siddiqi, nematodes in the suborder Criconematina belong to one of three Superfamilies: Criconematoidea, Hemicyclophoroidea, or Tylenchuloidea. The suborder has been studied since the 1880's and contains several important plant parasitic nematode species. Unfortunately, the taxonomy of many species is confusing, especially for members of the genera *Criconema*, *Mesocriconema*, and *Criconemoides*. The objective of this study is to clarify taxonomic relationships of the suborder Criconematina. Methodologies to be used will include: 1) morphological taxonomic identification of genera and species belonging to suborder Criconematina, and 2) molecular characterization of ITS1 and 18S rDNA sequences of all available genera and species of the suborder. Samples collected from Arkansas will be processed by standard extraction methods. For genera and species from superfamilies not found in Arkansas, specimens will be solicited in 1 M NaCl from researchers across the United States and worldwide. For each sample, at least 25 specimens will be mounted on glass microscope slides for identification and to serve as vouchers. Standard morphological data for each genus will be used, and new species will be described when warranted. For molecular characterization, ITS1 and 18S sequences will be amplified. Phylogenetic trees of ITS1 and 18S sequences will be constructed and compared with existing trees of D2-D3 regions of 28S-rDNA sequences. By providing complementary morphological and molecular identification of a wide range of genera and species of Criconematina, this study will help to resolve confusion surrounding the taxonomy of the suborder.

**INVESTIGATING SOIL FOOD WEBS – TRACKING THE TRANSLOCATION OF  $^{13}\text{C}$  AND  $^{15}\text{N}$  THROUGH MICROBIAL INTERACTIONS WITHIN THE SOIL. Crotty<sup>1,2</sup>, Felicity V., S.M. Adl<sup>3</sup>, C.D. Clegg<sup>1</sup>, R.P. Blackshaw<sup>2</sup>, and P.J. Murray<sup>1</sup>.** <sup>1</sup>North Wyke Research, North Wyke, Okehampton, Devon, EX20 2SB, UK, <sup>2</sup>School of Biological Sciences, University of Plymouth, Plymouth, Devon, PL4 8AA, UK, <sup>3</sup>Faculty of Science, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4R2.

Belowground processes are an essential part of the carbon and nitrogen cycles, litter decomposition and energy flow. There is evidence that the soil fauna has significant effects on these cycles but the interactions occurring or the connectedness between trophic levels is not clear. Within all soil food webs there are thought to be two distinct energy channels – bacterial and fungal, which form the basis of the food web pathway. There are very few studies which have observed soil food webs directly under field conditions; although many have inferred invertebrate food web position from laboratory or mesocosm studies, without fully distinguishing between the bacterial and fungal feeding channels. Stable isotopes can be used in situ to track feeding preferences of soil invertebrates without artificially manipulating the interactions that are occurring. Using a fluorescent pseudomonad cultured in  $^{13}\text{C}/^{15}\text{N}$ -labelled media, the bacterial feeding pathway was investigated. Bacteria (cultured to 99.9 atom%  $^{13}\text{C}/^{15}\text{N}$ -enrichment) were injected into intact soil cores, and mesofauna was subsequently extracted, identified and separated before analysis by mass-spectrometry. Results showed that some invertebrates were highly labelled indicating consumption of the added bacteria and provided an insight into the movement of C and N through the bacterial energy channel of the soil food web. Protozoa are mainly bacterial feeders and as an assessment of the next trophic level

within the soil, protozoa were cultured with  $^{13}\text{C}$ -sodium acetate. This was a preliminary experiment to determine whether protozoa could be effectively labelled with stable isotopes and introduced into soil mesocosms using the same introduction and extraction method as for the bacteria. Results from this experiment have shown that protozoa can be labelled with  $^{13}\text{C}$  and traced within higher invertebrates indicating their consumption. Further work is currently being developed to label fungi with stable isotopes to track this part of the soil food web in situ. Due to the nature of fungal growth introduction to the soil cannot be performed using a soil injector via a fluid medium, therefore development of a method to introduce the fungi back into the soil naturally – by growing back into the soil matrix has been performed. The ability for the hyphae to translocate high enrichment of  $^{13}\text{C}$  and  $^{15}\text{N}$  at varying distances within the soil matrix has been assessed. Potentially this method combined with the bacterial injection could be used to measure the contribution of these feeding channels to the soil food web and the feeding interactions occurring within the different trophic levels.

**NEMATICIDE POTENTIAL OF METHIONINE ON TURFGRASSES.** Crow,<sup>1</sup> William T., J. P. Cuda<sup>1</sup>, and B. R. Stevens<sup>2</sup>. <sup>1</sup>Entomology and Nematology Dept., PO Box 110620, University of Florida, Gainesville, FL 32611, <sup>2</sup>Dept. of Physiology and Functional Genomics, PO Box 100274, University of Florida, Gainesville, FL 32610.

Methionine is an essential amino acid that is commercially used primarily as an organic animal feed supplement. Certain amino acids and chemical analogues of methionine have been shown to affect several genera of plant-parasitic nematodes, but were deemed inappropriate, ineffective, and/or uneconomical as agricultural nematicides. However, the recent loss of fenamiphos has resulted in increased need for safe yet effective nematicides for use on turfgrasses. This, combined with changes in economics, has generated new interest in the development of methionine based nematicides for use on certain high-value commodities including sports turf. Two turfgrass field trials evaluated the effects of DL-methionine on *Belonolaimus longicaudatus* and *Mesocriconema ornata* on bermudagrass and zoysiagrass. Rates of 1120 kg/ha in a single application, and 224 kg/ha applied in two applications of 112 kg/ha each, were compared with untreated controls and fenamiphos. The effectiveness of the treatments was based on nematode population densities, and turf health. In these trials DL-methionine was equal to or better than fenamiphos in reducing nematode populations and promoting turf health. These trials indicate that DL-methionine may afford effective and economical nematode management on certain high value crops such as sports turf.

**ARBUSCULAR MYCORRHIZAL FUNGI DIVERSITY IN NATIVE TALLGRASS PRAIRIE AND AGRICULTURAL CROPLAND.** Damm, Mary C., K.M. Lankford, and J.D. Bever. Department of Biology, Indiana University, 1001 E. Third St., Bloomington, IN 47405.

In Kansas, the majority of agricultural land is planted to winter wheat, which receives approximately 70 kg nitrogen (N) fertilizer/ha/yr. A small percentage of land remains in native tallgrass prairie, with some harvested annually for hay. Wheat harvest and prairie hay mowing occur in July. In 2004, harvest data from the Kansas Census of Agriculture indicated no difference in amount of biomass per ha removed as wheat vs. prairie hay in 5 north-central Kansas counties. Total soil N; however, did differ, with N in tallgrass prairie significantly higher than in wheat fields. How does the tallgrass prairie maintain annual removal of aboveground biomass and high levels of soil fertility? Tallgrass prairie soils hold large reservoirs of organic matter and nutrients. Soil biota play a role in nutrient storage and dynamics and in the growth of tallgrass prairie plants. Arbuscular mycorrhizal (AM) fungi are common in the tallgrass prairie and are an important link between soil nutrients and plants' access to nutrients. AM fungi form a symbiotic relationship with plants generally providing benefits (increased uptake of nutrients and water) to plant hosts in exchange for plant carbon. Certain AM fungal species provide greater growth benefits to certain plant hosts. Heavy inputs of chemical fertilizers have reduced reliance of modern crops on natural symbiotic relationships with soil biota for nutritional needs. Many modern cultivars of winter wheat are non-symbiotic with mycorrhizal fungi or have reduced growth rates if colonized; whereas, older varieties benefited from mycorrhizal colonization. Future agricultural systems may need to rely again on soil sources for nutrients. Growth of perennial polyculture crops may depend on a diverse AM fungal community. To determine the role of AM fungal diversity in prairie and cropland soil fertility, we characterized the AM fungal community in 5 north-central Kansas tallgrass prairie and adjacent agricultural fields. At each site, 5 soil samples were taken using a 1-meter hydraulic soil corer. Each sample was separated into 6-depth intervals – 0-10, 10-20, 20-40, 40-60, 60-80, and 80-100 cm – and the samples per depth were pooled. In the lab, AM fungal spores were extracted from 100 cc of soil by wet sieving with sodium hexametaphosphate followed by sucrose centrifugation. AM fungi were identified by spore morphology using species descriptions from the International Culture Collection of VA Mycorrhizal Fungi (INVAM). Live spores were identified and counted using a stereomicroscope. Preliminary data indicate a 50% difference in AM fungal species composition between the tallgrass prairie and agricultural land. These results suggest that the unique species of AM fungi in the tallgrass prairie could play a role in the prairie's soil fertility.

**TRANSCRIPTIONAL PROFILING OF ROOT-KNOT NEMATODE INDUCED FEEDING SITES IN COWPEA (VIGNA UNGUICULATA L. WALP) USING A SOYBEAN GENOME ARRAY.** Das, Sayan<sup>1,2</sup>, J.D. Ehlers<sup>2</sup>, T.J. Close<sup>2</sup>, and P.A. Roberts<sup>1</sup>. <sup>1</sup>Department of Nematology, University of California, Riverside, CA 92521; <sup>2</sup>Department of Botany and Plant Sciences, University of California, Riverside, CA 92521.

Root-knot nematode (*Meloidogyne incognita*, RKN) causes damage to cowpea (*Vigna unguiculata*) directly and in interactions with Fusarium wilt (*Fusarium oxysporum* f. sp. *tracheiphilum*) as a disease complex. Host plant resistance is a primary means of managing RKN in cowpea production systems. The locus Rk confers resistance to several species of RKN in cowpea. Histological and reactive oxygen species (ROS) profiles of infected roots revealed that Rk confers a delayed resistance response without hypersensitive reaction-mediated cell death, in which juveniles develop but reproduction is blocked. We studied responses to *M. incognita* infection in roots of resistant CB46 and a susceptible near-isogenic line using the heterologous soybean Affymetrix GeneChip array at 3 and 9 days post inoculation (dpi). At 3 dpi, 746 and 623 genes were differentially expressed in incompatible (infected resistant tissue compared with non-infected resistant tissue) and compatible (infected susceptible tissue compared with non-infected susceptible tissue) interactions, respectively. At 9 dpi, 552 and 1,060 genes were differentially expressed in incompatible and compatible interactions, respectively. Comparison between inoculated resistant and susceptible genotypes revealed 638 and 197 genes differentially expressed at 9 and 3 dpi, respectively. More genes were suppressed than induced by infection of resistant compared to susceptible roots. Functional categorization by gene ontology indicated partial suppression of the typical defense response in resistant roots at both time-points. Variations of ROS concentrations, induction of toxins and other defense related genes were indicated to play a role in this unique resistance response, pointing to areas warranting further study by functional analysis.

EFFECT OF SIMULTANEOUS DROUGHT STRESS AND ROOT-KNOT NEMATODE INFECTION ON COTTON YIELD AND FIBER QUALITY. **Davis, R. F.<sup>1</sup>, H. J. Earl<sup>2</sup>, and P. Timper<sup>1</sup>.** <sup>1</sup>USDA-ARS, P.O. Box 748, Tifton, GA 31793, USA, <sup>2</sup>Dept. of Plant Agriculture, Univ. of Guelph, Guelph, Ontario, N1G 2W1, Canada.

Both drought stress and root-knot nematode (*Meloidogyne incognita*) infection can reduce cotton yield, and drought can affect fiber quality, but it not known what effect the nematodes have on fiber quality. To determine whether nematode parasitism affects fiber quality and whether the combined effects of nematode and drought stress on yield are additive (independent effects) or synergistic, we conducted a study in a field infested with *M. incognita*. A split-plot design was used in which the main plot factor was one of three irrigation treatments (drought, moderate water stress, and water-replete) and the sub-plot factor was one of two nematicide levels (1,3-dichloropropene at 0 or 56 l/ha). Surface drip tape irrigation was used for the three irrigation treatments. We prevented water stress in main plots designated as water-replete by irrigating twice weekly or as required. Drought plots received no irrigation, and the middle water stress treatment received half the water applied to the water-replete treatment. The severity of root galling was greater in non-fumigated plots and the severity increased as the level of water stress increased, but the degree of water stress did not influence the effect of fumigation. Cotton fiber length, weight of seed, and weight of lint produced were reduced in non-fumigated plots and decreased as the level of drought stress increased, but the degree of water stress did not influence the effect of fumigation. Fiber length and micronaire are two principal measures of fiber quality. Micronaire is a complex index that is affected by fiber wall thickness, and significant price reductions are applied to cotton with micronaire outside of specified ranges. Micronaire was increased by moderate to severe drought stress, but micronaire was not affected by fumigation. Therefore, we conclude that parasitism of cotton by *M. incognita* can affect fiber quality by reducing fiber length, and the detrimental effects of nematode parasitism and drought stress are additive rather than synergistic.

THE RELATIVE CONTRIBUTIONS OF SOIL BACTERIA AND FUNGI TO INORGANIC NITROGEN CYCLING IN SAGEBRUSH AND CHEATGRASS RHIZOSPHERE SOILS. **DeCrappeo<sup>1,2</sup>, Nicole M., P.J. Bottomley<sup>2</sup>, D.D. Myrold<sup>2</sup>, E.A. Brewer<sup>2</sup>, E.J. DeLorenze<sup>1</sup>, and D.A. Pyke<sup>1</sup>.** <sup>1</sup>Forest and Rangeland Ecosystem Science Center, U.S. Geological Survey, Corvallis, OR 97331, <sup>2</sup>Department of Crop and Soil Science, Oregon State University, Corvallis, OR 97331.

Exotic plant species can become ecosystem engineers in their new habitats and dramatically alter above- and belowground properties and processes. Cheatgrass (*Bromus tectorum*) is one such exotic annual grass that can potentially convert diverse, nitrogen (N)-limited sagebrush steppe ecosystems to homogenous, N-mineralizing environments. While many studies have characterized the pools and fluxes of inorganic N species (i.e., ammonium and nitrate) in sagebrush and cheatgrass rhizosphere soils, little research has focused on the relative contributions of specific microbial groups to N cycling in these soils. Soils collected from cheatgrass-invaded and uninvaded sagebrush/perennial bunchgrass plots from three sites each in eastern Oregon and southwestern Idaho were first subjected to soil community analyses. Phospholipid fatty acid (PLFA) data showed that fungal:bacterial ratios were not significantly different between sagebrush and cheatgrass rhizospheres ( $t = 0.01$ ,  $p = 0.38$ ), but analysis of the soil fungal communities using terminal restriction fragment length polymorphism (T-RFLP) showed striking differences in community structure and composition. In order to examine the effects of these different communities on N-cycling, we conducted an isotopic pool dilution experiment using <sup>15</sup>N tracers paired with bacterial and fungal antibiotics (bronopol and cycloheximide, respectively) that blocked protein synthesis in the target microorganisms. Forty-eight hour laboratory incubations were carried out to assess the partitioning of N to microbial biomass and inorganic N pools. Preliminary results showed that net N mineralization was higher in cheatgrass soils ( $t = 2.63$ ,  $p = 0.03$ ), while gross rates of ammonification were higher in sagebrush soils. The effects of the antibiotics treatments are currently being assessed to determine whether fungi or bacteria are primarily responsible for N turnover in these soils. Our preliminary analyses suggest

that fungi may play a more important role than bacteria in N cycling in sagebrush rhizosphere soils. As the sagebrush steppe becomes increasingly dominated by cheatgrass, the structure and composition of soil communities may shift to take advantage of short-term increases in N.

EFFECTS OF EXOTIC EARTHWORMS ON SOIL MICROBIAL COMMUNITY COMPOSITION IN A NORTHERN HARDWOOD FOREST. **Dempsey, Mark A.<sup>1</sup>, M. C. Fisk<sup>1</sup>, J. B. Yavitt<sup>2</sup>, T. J. Fahey<sup>2</sup>, P. M. Goffman<sup>3</sup>, and J. C. Maerz<sup>4</sup>.** <sup>1</sup>Zoology Department, Miami University of Ohio, 212 Pearson Hall, Oxford, OH 45056. <sup>2</sup>Department of Natural Resources, Cornell University, Ithaca, NY 14851. <sup>3</sup>Cary Institute of Ecosystem Studies, Box AB, 2801 Sharon Turnpike, Millbrook, NY 12545. <sup>4</sup>Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA 30602.

Exotic earthworms, introduced by agricultural trade, are invading forests in the northern United States. Exotic earthworms alter physical, chemical and biological soil properties, and one notable effect of earthworms is the elimination of organic horizons, which are incorporated into underlying mineral soils, altering the environment in which decomposer microorganisms exist. We hypothesized that such changes may increase the abundance of bacteria and decrease the abundance of fungi, as bacteria may take better advantage of structurally modified carbon (C) substrates than fungi, and as fungi may better tolerate the variable moisture conditions of organic horizons than bacteria. To test the effect of earthworms on soil microbial community composition we quantified bacterial and fungal biomass using direct counts in paired earthworm-invaded (earthworm) and earthworm-free (reference) plots in forests in central New York state three times (early-, mid-, and late-season) over the course of one season. <sup>13</sup>C-enriched leaf litter was applied in a subset of sites, and microbial <sup>13</sup>C was quantified by phospholipid fatty acid (PLFA) analysis to trace the flow of C from leaf litter into the microbial food web. Earthworms substantially increased the ratio of bacteria:fungi in surface mineral soils by the late-season ( $p = 0.01$ ). These results indicate an increase in the abundance of bacteria vs. fungi, and suggest that the effect of earthworms may be related to time since leaf senescence, becoming greater as the previous year's leaf litter is incorporated into mineral soils. Sites with applied <sup>13</sup>C-enriched leaf litter will test more directly the effect of organic matter incorporation on the proportion of microbial C that is leaf litter-derived in earthworm vs. reference plots, and may confirm the importance of shifting C processing pathways within the microbial food web. By indicating a significant shift in soil microbial community composition this study sets the stage for future research into potential links between changes in the soil microbial community and soil nutrient dynamics, and other ecosystem-level processes.

NEMATODE CONTROL WITH OXAMYL FOLIAR SPRAYS: EFFECT OF SPRAY CONCENTRATION, VOLUME AND SOIL AND PLANT COVER. **Desaeger, Johan and M. Rivera.** DuPont Crop Protection, Newark, DE, 19711.

Oxamyl (Vydate®) is an oxime carbamate used to control nematodes and insects, with excellent systemic activity. Oxamyl is the only nematicide that is effective by foliar application as it moves from the leaves through the phloem into the roots. Oxamyl foliar sprays are commonly used in the southeastern US to control plant-parasitic nematodes on cotton. Many growers use an early-season foliar Vydate® spray. The efficacy of oxamyl foliar applications was evaluated using a 7-nozzle boom sprayer at the Stine-Haskell laboratory, Newark, DE. Foliar applications of oxamyl were effective and reduced root-knot nematode infection on cotton (*Meloidogyne incognita*). Nematode control was partially due to downward movement of oxamyl from foliage to roots. In addition, a significant proportion of nematode control was accounted for by direct contact between oxamyl and soil (spray ending up on soil + run-off from foliage onto soil). Higher spray concentration, and to a smaller extent spray volume, also improved nematode control. Plant stage (4-leaf vs 6-leaf) did not significantly affect nematode control. These data support the current oxamyl (Vydate® CLV) label recommendations for nematode management in cotton with foliar applications beginning at the 2<sup>nd</sup>-5<sup>th</sup> true leaf stage.

SOIL RESPONSES FOLLOWING EXOTIC PLANT INVASION AND RESTORATION OF COASTAL SAGE SCRUB OF SOUTHERN CALIFORNIA. **Dickens, Sara Jo M., E. B. Allen and L. S. Santiago,** University of California Riverside, Riverside CA 92521.

The invasion of exotic plants into coastal sage scrub (CSS) has caused large scale habitat conversion associated with increased displacement of rare and endangered species, fire, and alteration of ecosystem function. Few studies have looked at restoration of invaded soil. Therefore, the level of alterations caused by the non-native plants is little known, or the extent or rate of recovery of soil processes from exotic plant invasions once invaders have been removed and native plants restored. Our hypotheses are: (1) Presence of exotic plant species changes the characteristics of the soils beneath them by altering soil inputs via litter and root exudates. (2) If exotics are controlled and natives restored, soil characteristics will return to pre-invaded conditions because the soil inputs of the native plants will be restored. Soil nitrogen, carbon and phosphorus to 10cm depth, plant species richness, and percent cover were recorded three times during the growing season from two coastal sage scrub locations. Nitrogen mineralization rates were determined in lab incubations and plant litter decomposition rates determined using litter bags located in both restored and invaded areas. Contrary to our predictions, plants invading CSS did not alter the total carbon and nitrogen pools or nitrogen mineralization rates to a significant level. However, invaded soils

appear to experience greater NO<sub>3</sub> drawdown earlier in the season than do soils of native and restored areas. By summer, differences in extractable N decreased in invaded soils, whereas NO<sub>3</sub> decreased in restored plots. Because total N and N-mineralization rates were not significantly different, changes in NO<sub>3</sub>-N during the growing season may be controlled more by uptake than by supply. Implications of varying plant litter decomposition rates among species and in response to reciprocal transplants will be discussed.

EFFECTS OF LEAF LITTERS ON THE ECTOMYCORRHIZAL FUNGAL COMMUNITY AND SOIL FAUNA IN PITCH PINE MESOCOSMS. **Dighton, John<sup>1</sup>, L. Jonsson<sup>1</sup>, and J. Lussenhop<sup>2</sup>**. <sup>1</sup>Rutgers University Pinelands Field Station, PO Box 206, 501 Four Mile Road, New Lisbon, NJ 08064. <sup>2</sup>University of Illinois at Chicago.

Pitch pine, oak, huckleberry, a mixture of all three litters or no leaf litter were placed over horizontal mini-rhizotron tubes in mesocosms. The mesocosms contained intact organic horizon of NJ pine barrens soils placed over three 2m long mini-rhizotron tubes placed horizontally in 2 x 1 m mesocosms. The original litter layer of soil was replaced by patches of leaf litter of either separate or mixed litter types and sown with gnotobiotically grown pitch pine seedlings. Litter was kept in place using 2.5 cm mesh, such that successive year's litter could be separated by a coarse mesh. After three years, the mycorrhizal community of the pine seedlings, the leaf litter chemistry and the soil fauna under each leaf litter type was evaluated. Leaf litters of all types significantly reduced pitch pine growth as seen by the presence of litter polyphenols by Jonsson et al. (2005) and Garnett et al. (2004). In particular, abundance of ectomycorrhizal fungal type HS was significantly suppressed in the presence of any leaf litter type and may be influenced by litter chemistry in the same way as pine seedlings. The abundance of oribatid mites, collembolan and total fungivorous microarthropods was significantly and negatively correlated to plant growth. Relative abundance of soil faunal groups was related to leaf litter type. Oribatid mites, collembolan and total fungivorous arthropods were significantly more abundant under pine litter than huckleberry litter and this higher than other litters. In contrast, mesostigmatid mite abundance was highest under huckleberry litter, though not statistically significant. These results reinforce our findings that heterogeneity of leaf litter accumulation in the New Jersey pine barrens and its composition has a significant effect on the ectomycorrhizal and soil faunal community (Conn & Dighton, 2000).

COMMERCIAL INTRODUCTION OF BIONEMATOCIDES BASED ON *PAECILOMYCES LILACINUS*. **Dimock, Michael B.**, Certis USA, 9145 Guilford Road, Columbia, MD 21046.

The nematophagous fungus *Paecilomyces lilacinus* strain 251 recently has been introduced as an agricultural bionematicide in the USA after several years of commercial use in southern Europe. Produced and registered by ProPhyta GmbH of Germany, it is currently marketed by Intrachem Bio Italia under the tradename "BioAct" and by Certis USA as "MeloCon." The principal economic targets have been root knot nematodes (*Meloidogyne* spp.) in vegetable crops, but research and practical experience has shown that *P. lilacinus* can be used effectively against a wide range of plant parasitic nematodes in annual and perennial cropping systems. Field trials have also shown that well-timed applications of *P. lilacinus* are at least as effective as currently available post-planting chemical nematicides. As with other microbial biopesticides, development of efficient manufacturing and delivery systems has been a key requirement in bringing *P. lilacinus* to market. This presentation will discuss these practical aspects as related to biological characteristics of *P. lilacinus* and its performance in the field.

*PASTEURIA NISHIZAWAE* STUDIES IN TENNESSEE. **Donald, Patricia A<sup>1</sup>, and T. E. Hewlett<sup>2</sup>**. <sup>1</sup>Crop Genetics and Production Unit, ARS, 605 Airways Blvd, Jackson, TN 38301, <sup>2</sup>Pasteuria Biosciences, 12085 Research Drive, Alachua, FL. 32615.

Spores of *Pasteuria nishizawae* were first recovered in Tennessee in 2008 attached to soybean cyst nematode juveniles, *Heterodera glycines*, and inside cysts extracted from soil collected at Ames Plantation, Grand Junction, TN. The field had a 15% increase from 1997 through 2004 in number of samples where soybean cyst nematode was not detected, even in the presence of favorable conditions and susceptible cultivars. There was a 16% decrease in soybean cyst nematode population density in greenhouse bioassays of collected soil samples from 2001 through 2004. Fifty percent of the original samples examined contained parasitized juveniles or cysts. Preliminary studies of levels of infestation in Tennessee soybean production fields indicated 78% of the soil samples with greater than 5 cysts per 100 cm<sup>3</sup> of soil were infested with *P. nishizawae*. Cyst and juvenile infestation levels within the samples were highly variable. Studies were initiated to increase the spore level of *P. nishizawae* in greenhouse cultures containing soybean cysts. Cysts free of eggs, as well as abnormally developed eggs within cysts, were present after 35 days. Seven populations of soybean cyst nematode corresponding to HG Types 1.2.3.4.5.6.7 (2 populations), 5.7 (2 populations), 2.5.7, 1.2.5.7, 1.3.5.7 (races 1, 2, 3, 5, 14, and 2 populations which reproduce on all indicator lines) were exposed to 100,000 spores of *P. nishizawae*. Average spore incidence ranged from 0.8 to 4.5 spores per juvenile. Frequency of attachment ranged from 50 to 100%. No differences in spore attachment were found between the various HG Types. Spores were detected on males; however, no spore attachment was observed on dead juveniles. Calibration curves were developed from 1 x 10<sup>4</sup> to 1 x 10<sup>6</sup> spores per mL to determine the level of spore addition needed for consistent detection of *P. nishizawae*.

**RISING ATMOSPHERIC CO<sub>2</sub>, CLIMATE CHANGE AND CARBON BALANCE IN TERRESTRIAL ECOSYSTEMS. Drake, Bert G**, Smithsonian Environmental Research Center, Edgewater, Maryland USA.

Photosynthesis and growth of plants is stimulated by rising atmospheric CO<sub>2</sub> and temperature. But climate change also increases drought and fire in arid lands, insect invasion in northern forests, warming in the Arctic, and expansion of subtropics. These effects may severely reduce the capacity of terrestrial ecosystems to store carbon and increase the urgency to control rising atmospheric CO<sub>2</sub>. In the end, the availability of water may determine whether land ecosystems continue to account for nearly a third of anthropogenic emissions of CO<sub>2</sub>. This talk will review experimental evidence in the context of the expected impacts of climate change on carbon and water cycling.

**BACTERIAL AND FUNGAL CONTRIBUTIONS TO NITROUS OXIDE PRODUCTION AS INFLUENCED BY THE EARTHWORM *LUMBRICUS TERRESTRIS*. Durocher<sup>1</sup>, Simon, and J.K. Whalen<sup>1</sup>**. <sup>1</sup>Dept. of Natural Resource Sciences, McGill University, Ste-Anne-de-Bellevue, QC, Canada H9X 3V9.

Soil emissions contribute significantly to the atmospheric levels of nitrous oxide (N<sub>2</sub>O), a potent greenhouse gas. Earthworms fragment and mix organic residues with soils, accelerating decomposition and nitrogen cycling processes, which leads to an increase in carbon dioxide (CO<sub>2</sub>) and N<sub>2</sub>O production in earthworm-worked soils. The objective of this study was to determine the relative contribution of bacterial and fungal populations to N<sub>2</sub>O production using inhibitors, and to confirm the pathway leading to N<sub>2</sub>O production with the acetylene block method. Microcosms (30-cm long x 10-cm wide polyvinyl chloride pipes with a sealed bottom) were filled with soil moistened to about 40% water-filled pore space and two juveniles of *L. terrestris* were added. Microcosms were incubated at 15°C for two weeks in the dark to allow the earthworms to modify the soil environment. Then, the microcosms were capped and gas samples were taken to assess CO<sub>2</sub> and N<sub>2</sub>O emissions. Next, a soil core was taken from the geometric center of each microcosm using a stainless steel T-sampler and a minimally disturbed sample (10-cm long x 2-cm dia.) was gently transferred to a polycarbonate plastic tube. Control tubes with the original field-moist soil, not incubated or in contact with earthworms, were also prepared. The plastic tube was capped at both ends with air-tight rubber septa. Tubes were then treated with antibiotics (streptomycin to inhibit bacterial communities, cycloheximide to inhibit soil fungi, or deionized water) and soil was moistened to 84% water-filled pore space. Tubes were flushed with argon gas and then treated with 0 Pa, 10 Pa or 10 kPa of acetylene. Each factorial treatment (antibiotics, acetylene) was replicated four times. All of the earthworms survived and maintained their weight whilst in the microcosms. The CO<sub>2</sub> and N<sub>2</sub>O emissions tended to be greater in microcosms with earthworms than without earthworms. Although N<sub>2</sub>O production can occur via nitrification and denitrification pathways, this study demonstrated that *L. terrestris* stimulated N<sub>2</sub>O production via denitrification only. Most of the denitrification in earthworm-worked soil apparently came from soil bacterial activity, with a smaller contribution attributed to fungal denitrifiers. However, we cannot rule out the possibility that the archaea were also involved in denitrification, as the antibiotics used would not have inhibited this group. We conclude that soil mixing and reorganization by *L. terrestris* favors the activity of denitrifying microorganisms, thus contributing to soil N<sub>2</sub>O emissions.

**HEAT TOLERANCE OF ANHYDROBIOTIC SEED GALL NEMATODES, *ANGUINA AGROSTIS*. Eisenback, J. D.<sup>1</sup>, C. W. Roane<sup>1</sup>, J. R. Way<sup>1</sup>, and Neil Selz<sup>1</sup>**. <sup>1</sup>Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg, VA 24060.

*Anguina agrostis*, a seed gall nematode found parasitizing redtop creeping bentgrass (*Agrostis stolonifera*), overwinters in a dehydrated state of suspended animation (anhydrobiosis). Specimens were collected on August 24, 2003 from a naturally infested site near the fire watchtower on Butt Mountain Lookout, between Pembroke and Ripplemead, Virginia. They were stored in an open plastic bag in a laboratory cabinet for more than 5 years. Recovery of living nematodes was evaluated from infested seeds by soaking seed galls in spring water for 24 hr. Additional seed galls were exposed to high temperatures in a glass test tube immersed in hot water for 30 min. at 80, 90, and 100°C each. After the gall cooled, it was placed in water for 24 hr. and the nematodes were freed from the gall with sharply pointed forceps. Nematodes in each gall were counted as living if they were moving, or as dead if they were not. Likewise, galls, collected on Aug. 9, 1990 in St. Louis County, Minnesota and stored in a paper envelope in a drawer, were immersed into water for 24 hr. and evaluated for the presence of living nematodes. All treatments were replicated 7 times. Five-year-old galls contained an average of 694 nematodes, of which 70% were alive. The survival of nematodes in galls that were heat-treated at 80°C for 30 min. was reduced to 66% with an average of 785 nematodes per gall. Galls exposed to 90°C for 30 min. contained an average of 990 specimens and survival was reduced to 9%. All of the individuals were killed in galls that were treated at 100°C for 30 min. In the galls that were more than 18 years old, the survival was 40% with an average of 463 nematodes in each gall.

**GROWTH OF CITRUS SEEDLINGS IN 3 SOILS WITH COMBINATIONS OF WEEVIL HERBIVORES AND ENDEMIC SPECIES OF ENTOMOPATHOGENIC NEMATODES. El-Borai<sup>1,2</sup>, Fahiem E., R. J. Stuart<sup>1</sup> and L. W. Duncan<sup>1</sup>**. <sup>1</sup>University of Florida, IFAS, Citrus Research and Education Center, 700 Experiment Station Road, Lake Alfred, FL 33850. <sup>2</sup>Plant Protection Dept. Faculty of Agriculture, Zagazig University, Egypt.

Entomopathogenic nematodes (EPN) are used for augmentation biological control of the root weevil, *Diaprepes abbreviatus*, in Florida citrus groves. Field surveys suggest that soil texture might influence *D. abbreviatus* populations

indirectly by affecting EPN species diversity and abundance. At various sites, the percentage of caged weevil larvae infected by EPN is directly related to the percentage of coarse sand. More EPN species are generally detected in orchards on the central ridge (coarse sand) than in the flatwoods regions (sandy loam), where a single species, *Heterorhabditis indica*, predominates. The prevalence of *D. abbreviatus* is inversely related to both EPN prevalence and percentage of coarse sand in soils. To test the hypothesis that patterns of *D. abbreviatus* prevalence are regulated indirectly by soil properties that influence their natural enemies, a greenhouse experiment was conducted to measure the persistence, efficacy, and plant protection ability of three EPN species (*Steinernema diaprepesi*, *S. riobrave*, and *H. indica*) in pasteurized sandy soils of three different textures. One hundred citrus seedlings were grown individually in pots containing each of three soil types: coarse sand (97% sand with >60% >0.25 mm); fine sand (94% sand with <20% >0.25 mm); and sandy loam (58% sand with <10% >0.25 mm). One month after planting, 3 *D. abbreviatus* larvae were added to each of 80 pots of each soil type. Twenty-four h later, IJs of each EPN species (50 IJ cm<sup>-3</sup> soil surface) were added to 20 pots of each soil that received weevil larvae. Twenty pots of each soil served as negative controls (no larvae and no EPN), and 20 as positive controls (larvae, but no EPN). Subsequently, weevil larvae were added to the pots monthly and the experiment continued for 9 months. ANOVA of plant root and top weights showed highly significant main effects of soil and nematode species ( $P \leq 0.0001$ ), and a highly significant interaction between soil type and nematode species ( $P \leq 0.0001$ ). *S. riobrave* afforded protection to citrus plants in all 3 soils and the plants often had significantly higher root and top weights than positive controls and other EPN treatments. Top and root weights were greater than positive controls in pots treated with *S. diaprepesi* in coarse and fine sand but not in sandy loam; and *H. indica* protected plants significantly only in coarse and very fine sand. Based on root weight, both *S. riobrave* and *S. diaprepesi* protected plants better in coarse sand than fine sand; and better in fine sand than in sandy loam. Mortality of caged sentinel weevil larvae in all soils at the end of the experiment was highest in pots treated with *S. diaprepesi*, and *S. diaprepesi* was the only EPN species recovered by baiting soil with *Galleria mellonella*. These results are consistent with field observations of EPN and weevil distributions across soil types in Florida citrus groves.

**A COMPARISON OF PLANT ROOT EXTRACELLULAR ENZYME ACTIVITIES BETWEEN NATIVE AND EXOTIC PLANTS. Elk<sup>1</sup>, Michael, R. and M.N. Weintraub<sup>1</sup>.** <sup>1</sup>Dept. of Environmental Sciences 2801 West Bancroft Street Mail Stop 604, The University of Toledo, Toledo, OH 43606.

Invasive exotic species are widely recognized as a major threat to biodiversity. An aspect of invasive plant species that has not been well studied is enzymes secreted from roots. Extra-cellular enzymes are produced by both microbes and plants and directly mediate organic matter breakdown. These enzymes can be present on root surfaces or secreted by roots into the rhizosphere and are used to exploit pools of organic nutrients in the soil. It is hypothesized that extracellular enzymes of invasive plants might have a greater capacity to acquire nutrients than native plants. Testing this hypothesis might shed some light on the success of these invasive plants. To accomplish this goal, the objectives of this project include: 1) measuring plant root enzyme activity of both native and invasive plant species in the Oak Openings region of NW Ohio and 2) comparing enzyme activities between invasive and native plants to determine if differences in root enzymes might play a role in the success of invasive plants. To accomplish these objectives, roots from invasive species, *Lonicera maackii* (Bush Honeysuckle), *Rhamnus frangula* (Glossy Buckthorn), *Rosa multiflora* (Multiflora Rose), *Saponaria officinalis* (Bouncing Bet or Soapwort), *Centaurea maculosa* (Spotted Knapweed), and *Vicia villosa* (Hairy Vetch), and surrounding native plants will be screened for three types of enzymes: chitinase, phosphatase, and peptidase. These enzymes provide access to organic nitrogen and phosphorous, principal limiting nutrients to plant growth so that differences may affect competitive outcomes for limiting nutrients.

**GEOGRAPHIC DIFFERENCES IN FIELD POPULATIONS OF SOYBEAN CYST NEMATODE (SCN). Faghihi, Jamal<sup>1</sup>, P. Donald<sup>2</sup>, T. Welacky<sup>3</sup>, G. Noel<sup>4</sup>, and V. Ferris<sup>1</sup>.** <sup>1</sup>Department of Entomology, Purdue University, West Lafayette, IN 47907; <sup>2</sup>USDA ARS, Jackson, TN 38301; <sup>3</sup>Agriculture and Agri-Food Canada, Harrow, ON N0R 1G0, Canada; <sup>4</sup>Dept of Crop Science University of Illinois, USDA ARS, Urbana, IL 61801.

As a follow-up to a recent study of soybean cyst nematode funded by NCSRP to evaluate current soybean resistance potential of PI88788 in the North central region of the U.S., we have been determining HG types for many field populations in three broad geographic areas. We found some indication that field populations in these discrete geographic areas may share inherent differences in virulence characteristics. We speculated that although field populations may change in virulence after repeated exposure to resistance genes (e.g. PI88788), the inherent virulence characteristics of SCN also differ among widespread different geographic areas. Such information is important for breeders as they develop new varieties that employ a variety of resistance genes. Our data showed that although soybeans are grown in all three climatological areas of TN, most soybeans are produced in west TN (where varieties with PI88788 have been grown for more than 30 years). In west and middle TN all field populations tested but one were able to reproduce on PI88788. In historical west TN (three counties near the Mississippi river), field populations were able to reproduce on PI548402 (Peking). Populations bordering western Kentucky were also able to reproduce on PI90763. Of the 261 IN SCN populations that were HG typed, most of the PI 88788

resistance-breaking populations were concentrated in the west to the mid-north part of Indiana. Cultivars with PI 88788 resistance have been grown extensively in these areas for the past 25 years, but for many years we have considered these SCN populations to be more “aggressive” compared with the rest of the Indiana field populations. A total of 26 Illinois populations were collected from 11 counties in east central IL. Of these, nine were capable of reproduction on PI88788. A larger than expected number of populations in Ontario, Canada, were able to develop on PI548402 and on PI209332, although soybeans with these resistance genes are not generally grown in Ontario. In Ontario, reproduction on PI88788 was evenly spread throughout the area with the longest history of soybean production. Reproduction on PI548402 was also found in this area but more centralized in a north-south oval pattern. The proximity of Ontario to soybean fields of northern U.S. raises questions about the virulence characteristics of those U.S. populations that might be of interest to soybean breeders.

**SOIL EXTRACELLULAR ENZYME ACTIVITIES AS INDICES OF MICROBIAL NUTRIENT LIMITATION AND SOIL CNP DYNAMICS. Fatemi<sup>1</sup>, Farrah R., I.J. Fernandez<sup>1</sup>, K.S. Simon<sup>1</sup>, and D.B. Dail<sup>1</sup>.** <sup>1</sup>School of Ecology and Environmental Science, University of Maine, 5722 Deering Hall, Orono, ME 04469-5722.

The activity of extracellular enzymes produced by soil microbes can be used as indices of organic matter decomposition, rates of nutrient cycling and microbial response to environmental change. Recent research suggests that some soil extracellular enzyme activities are inhibited by elevated N deposition, particularly ligninases such as phenol oxidase and peroxidase. The activity of phosphatases, on the other hand, should be increased by N supply because these enzymes are rich in N, but some studies suggest that phosphatase activity is non-responsive to elevated N deposition. We examined the response of extracellular enzyme activity to enhanced N and/or P supply in O horizon and mineral soils at the Bear Brook Watershed in Maine (BBWM). In this long-term paired-watershed experiment, the West Bear (WB) watershed has received bimonthly additions of  $(\text{NH}_4)_2\text{SO}_4$  since 1989 while the East Bear (EB) watershed serves as a reference. Forest composition at the BBWM is characterized by two distinct forest types with different litter qualities: northern hardwoods at lower elevation and red spruce at higher elevation. Phosphorus dynamics are different in the treated and reference watersheds; soil solution ortho-P concentrations are 1.5 times higher in WB softwoods compared to EB softwoods. We measured the activities of seven extracellular enzymes involved in microbial acquisition of C, N and P ( $\alpha$ -glucosidase,  $\beta$ -glucosidase, xylosidase, phenol oxidase, peroxidase, N-acetylglucosaminidase, and acid phosphatase). We also experimentally manipulated soil N and P concentrations to explore extracellular enzyme response to these changes in nutrient supply. Our initial findings suggest that there are differences in extant enzyme activity by treatment, forest type and soil horizon. For example, average phenol oxidase activity in O horizon soil in softwoods is 3 times higher in the reference watershed compared to the N-enriched watershed. Suppressed ligninase activity in N-enriched soils is consistent with results from previous research in other ecosystems. Contrary to expectations, extant phosphatase activity in both O and B horizon soils was lower in the treated watershed compared to the reference watershed. Results from nutrient supply experiments will help to define microbial mechanisms controlling soil CNP dynamics at the BBWM.

**CONTRIBUTION OF NEMATODES TO THE STRUCTURE AND FUNCTION OF THE SOIL FOOD WEB. Ferris<sup>1</sup>, Howard.** <sup>1</sup>Department of Nematology, University of California, Davis, CA 95616.

Carbon and energy flow through, and reticulate in, the soil food web, driving the metabolic processes of successive consumers. However, they are depleted rapidly by the metabolic and production functions of organisms. A “long” food web, with a large biomass at higher trophic levels, must receive a high rate of rhizodeposition or detrital subsidy, or be top-populated by organisms of slow growth and long life cycle, or both. Disturbed soil food webs tend to be bottom heavy and recalcitrant to restoration due to the slow growth of upper predator populations, physical and chemical constraints of the soil matrix, biological imbalances, and the relatively low mobility and invasion potential of soil organisms. Nematodes affect food web structure and function by: 1) channeling resources derived through herbivory; 2) predation on other organisms; 3) serving as prey for higher level predators; 4) redistributing organisms in the soil matrix; 5) sequestering minerals, C and energy; 6) mineralizing organic molecules to mineral forms available for uptake by plants and microbes; and 7) regulating opportunistic species. Subjectively, metabolic and behavioral functions of organisms in the soil food web may be categorized as ecosystem services, disservices or effect-neutral. Clearly, some of the functions through which nematodes affect food web structure are services; others are disservices. Among the disservices attributable to nematodes are overgrazing, which diminishes services of prey organisms, and plant-damaging herbivory, which reduces carbon fixation and availability for all organisms in the food web. However, not all plant-feeding is a disservice. Nematodes of the family Tylenchidae may be abundant around roots without causing measurable plant damage; their apparently non-damaging herbivory may be considered a service in providing resources for other functions of the food web. Opportunities for managing the service roles of nematodes in soil food webs include enhancement of mineralization by edaphic and environmental alteration, prolonging service effects through space and time by enhancing biodiversity and, consequently, functional complementarity and functional continuity. Further, managed increase of non-damaging prey of top predators provides an opportunity for enhancing predators in common of target prey species. In many instances, management to ameliorate potential disservices results in unintended but long-lasting diminution of services.

COMPARING THE CONTINENTAL-SCALE STRUCTURE OF SOIL ARCHAEAL, BACTERIAL, AND FUNGAL COMMUNITIES. **Fierer<sup>1</sup>, Noah.** <sup>1</sup>Dept. of Ecology and Evolutionary Biology and Cooperative Institute for Research in Environmental Sciences, University of Colorado, Boulder, CO 80309-0216.

The biogeographical patterns exhibited by plants and animals have been studied for centuries. As a result, the diversity and distribution of these 'macrobial' taxa across larger spatial scales are reasonably well understood. In contrast, we know very little about the biogeographical patterns exhibited by the microorganisms living in soil, arguably one of the most diverse habitats on Earth. Here we compare the continental-scale patterns exhibited by archaea, fungi, and bacteria, the three dominant groups of soil microorganisms. Not surprisingly, the factors correlated with microbial abundances in soil are distinct from those factors correlated with changes in diversity and community composition. Total microbial biomass across biomes is well-correlated with soil organic carbon (SOC) concentration ( $r^2 = 0.91$ ), but SOC concentrations do not predict the composition of bacterial, fungal, or archaeal communities. Fungal:bacterial ratios are correlated with soil C:N ratios ( $r^2=0.65$ ), but archaeal:bacterial ratios are very difficult to predict as they are not correlated with any commonly-measured soil or site parameters. Soil pH is a good predictor of bacterial community diversity and composition, but soil fungal diversity and composition are most strongly correlated with estimates of soil nutrient availability. Soil archaeal community structure is less predictable at this scale of inquiry; a number of factors (including pH and soil nutrient concentrations) appear to be correlated with archaeal community composition and diversity, but these individual correlates are weak, suggesting that archaea are very diverse with respect to their functional capabilities and environmental tolerances. Together these results suggest that the structure of soil bacterial and fungal communities is surprisingly predictable across biomes but key gaps remain in our understanding of the natural history of soil archaea.

MELOIDOGYNE PHYLOGENY: A SUPERTREE APPROACH. **Finlinson, Camille E., Peat, S. M. and B. J. Adams.** Evolutionary Ecology Laboratories, Dept. of Biology, Brigham Young University, Provo, UT 84602.

In order to better understand the evolution of pathogenesis and develop more effective control strategies, a clearer image of how the many species of Meloidogyne are related is needed. While many phylogenies of the genus have been created in the past, a single phylogenetic analysis that combines all of the previous datasets (total evidence approach) is not feasible because not all taxa are common to all of the datasets. Alternatively, supertree construction algorithms can search the topologies of trees produced by non-overlapping datasets to produce an optimal solution. We mined genetic databases and generated phylogenetic trees, maximizing the number of genetic lineages, and constructed gene trees using standard approaches (bayesian, likelihood and parsimony). We identified significant discrepancies in rates of morphological and molecular divergence. The topologies of the resulting analyses were used to construct supertrees using 'matrix representation of parsimony' and 'most similar supertree' approaches. Overall, most of the gene tree topologies are remarkably similar, with the exception of the mitochondrial and nuclear datasets. Our supertree analysis reveals that the nodes involving putatively hybridogenic lineages involve species (*sensu lato*) that do not have unique evolutionary origins or fates, and thus should not be expected to exhibit resolved, congruent, gene genealogies. Our analysis provides the most comprehensive framework to date for generating and testing hypotheses of Meloidogyne evolution.

THE COMPOSITION AND FUNCTIONS OF BIOLOGICAL SOIL CRUSTS IN THE NORTHEASTERN U.S. **Finn, E.S. and Thiet, R.K.** Department of Environmental Studies, Antioch University New England, 40 Avon Street, Keene, NH 03431.

Biological soil crusts (BSCs) consist of green algae, cyanobacteria, bryophytes, and lichens that colonize the top 5 mm of soils. Generally found in arid and semi-arid biomes around the world, they influence soil moisture, reduce soil erosion, and contribute substantial carbon and nitrogen to soils in nutrient-limited ecosystems. The vast majority of ecological research about BSCs has been conducted in deserts, particularly in the American west, Australia, and Israel. However, biological soil crusts are quite widespread in patchily-distributed ecosystems in temperate climates such as the eastern U.S., where they appear to comprise a very early stage of vegetation re-establishment following disturbance and soil erosion. Only a few studies have documented the composition and function of BSCs in temperate ecosystems. In this study, we evaluated the composition and functions of well-developed green algal, cyanobacterial, bryophytic, and lichen crusts that colonize extensive soil surfaces in the unique pine barrens of Concord, NH, and Wells, ME, and in beachgrass-heath habitat at Parker River National Wildlife Refuge, Plum Island, MA. We simulated rainfall on crusted and uncrusted soil cores in a 12-week laboratory experiment and quantified the effect of BSCs at all three sites on water and nutrient (N) infiltration to soil below crusts. At each study site, we collected 10 uncrusted and 10 crusted soil cores (9 cm h x 5 cm d); the cores were transported to a greenhouse and suspended over jars to collect rainfall that infiltrated through the cores during rainfall simulations. Inorganic nitrogen ( $\text{NH}_4^+$  and  $\text{NO}_3^-$ ) in each infiltration sample was analyzed using standard colorimetric methods and the effects of BSCs on total soil C content were evaluated using standard LOI procedures. Species composition of BSCs was determined by visual identification using microscopes and taxonomic keys. Analyses are currently in progress, and results will be presented in this poster. This study will provide insight for managers and ecologists about the species composition and ecological functions of biological soil crusts in inland and coastal temperate biomes, and will contribute valuable new information to our understanding of biological soil crusts in plant, soil, and ecosystem ecology.

EARTHWORMS AND LITTER INPUTS DRIVE SOIL ORGANIC MATTER STABILIZATION, NUTRIENT DYNAMICS, AND PLANT NUTRIENT UPTAKE IN THE QUESUNGUAL AGROFORESTRY SYSTEM OF WESTERN HONDURAS. **Fonte<sup>1</sup>, Steven J. and J. Six<sup>1</sup>**. <sup>1</sup>Dept. of Plant Sciences, University of California, Davis, CA 95616.

The development of sustainable agricultural systems ultimately depends upon improved management of non-crop species to enhance overall agroecosystem functioning and the provision of ecosystem services. To address this need, our research examines the role of earthworms and residue management on aggregate-associated soil organic matter (SOM) stabilization, nutrient dynamics and maize growth in the Quesungual agroforestry system of western Honduras. Field mesocosms were established with two earthworm treatments (worms excluded, -W, vs. 8 *Pontoscolex corethrurus* individuals per mesocosm, +W) and four litter quality treatments (low quality *Zea mays*, LQ; high quality *Diphyssa robinoides*, HQ; mixture of low and high quality litter, MQ; and a control with no organic residues applied, C). Mesocosms included a single maize plant and additions of <sup>15</sup>N labeled inorganic N. At maize harvest, the mesocosms were destructively sampled for analysis of soil and plant material. Surface soils (0-15 cm) were dried and wet-sieved to determine the distribution of C, N and <sup>15</sup>N among different aggregate size classes. Bulk soils were also analyzed for available (Olsen P and Bray P) and total P, as well as potentially mineralizable N. Maize plants were divided into grain, roots and non-grain aboveground components and analyzed for total P, N and <sup>15</sup>N. In general, earthworms yielded greater influence on soil properties and nutrient dynamics than residue treatments. Earthworms increased the mean weight diameter by 10% ( $P = 0.024$ ) through an increase in large macroaggregates ( $P = 0.031$ ), leading to a 15% increase in C and N stored within large macroaggregates ( $P < 0.05$ ). Increased C storage in microaggregates within large macroaggregates ( $P = 0.033$ ) suggests increased stabilization of SOM in the presence of earthworms. However, this benefit of earthworms only occurred in the presence of residues and not in the control. Earthworms also decreased available P ( $P < 0.001$ ) and total soil P ( $P = 0.024$ ), indicating that earthworms may facilitate the loss of labile P from this system. Although earthworms had no effect on plant biomass or yield, they did appear to alter N and P content in the grains and non-grain components. Residue quality yielded greater effects on plant growth with the LQ treatment exhibiting the highest total plant biomass, but there was no effect on grain yield. Earthworms decreased the recovery of fertilizer derived N in the soil ( $P < 0.006$ ), but increased <sup>15</sup>N uptake by maize plants by 7% ( $P = 0.018$ ). Our results indicate that the management of earthworm populations and litter inputs can have important implications for SOM dynamics, nutrient cycling, and plant growth within agroforestry systems.

EFFICACY OF NEMATOCIDAL SEED TREATMENTS FOR CONTROL OF SOYBEAN CYST NEMATODE. **Frye, Jeffrey W.** Dept. of Plant Pathology, 2510 Gardner Hall, Raleigh, NC 27695-7616.

Among the most damaging pathogen to soybean (*Glycine max*) is the soybean cyst nematode (SCN) *Heterodera glycines*. Annual losses caused by this pathogen have been reported to exceed 5 million metric tons. Management programs that involve rotation with non-host crops and (or) resistant cultivars have been used with some success. While there are nematostatic chemicals available they are generally not recommended in soybean production due to cost, environmental and potential health hazards. Seed treatments are becoming more popular because of the reduced hazards associated with handling, environmental effects and ease of implementation. Abamectin has been used in other cropping systems with some success for management of plant-parasitic nematodes (PPN). The efficacy of both abamectin treated seed and a imidicloprid+thiodicarb treated seed at both high and low rates were evaluated in microplots and the greenhouse. In this time-course study we stained PPN's in planta and found that second stage juvenile (J2) infections/plant were highest at 70.7, 39.3, and 116.7 for the high rate of the abamectin seed treatment at 8, 14, and 21 days after planting (DAP) respectively, however, the only significant difference among other treatments was seen at 14 DAP. Similar results were found in the greenhouse with 20.1 J2's/plant on the abamectin treatment at 5 DAP and 9.5 and 1 J2/plant for the imidicloprid+thiodicarb treatment and untreated control respectively. We hypothesize that ineffectiveness of these seed treatments may be attributed to the nature of the SCN and are influenced by soil physical and chemical properties, as well as environmental factors.

GENES ASSOCIATED WITH DESSICATION TOLERANCE IN THE FOLIAR NEMATODE *APHELENCHOIDES FRAGARIAE*. **Fu, Zhen<sup>1</sup> and P. Agudelo<sup>1</sup>**. <sup>1</sup>Dept. of Entomology, Soils, and Plant Sciences. 114 Long Hall, Clemson University, Clemson, SC 29634.

Dessication tolerance is an important survival adaptation for foliar nematode *Aphelenchoides fragariae*, but little is known about the genes involved in anhydrobiosis of this species. In contrast, much has been documented on the participation of specific genes in the anhydrobiotic stages of the free-living nematode *Aphelenchus avenae*. A comparative study on the induction of genes associated with dehydration in these two species was conducted. Both nematode species were exposed to dehydration, cold, and osmotic stress treatments (90% relative humidity, 4°C, and 500mM sucrose solution, respectively, for 24 hours). Survival after stress treatments was compared to untreated nematodes, and assessed by observation of motility after 24 h recovery in tap water at 25°C. The foliar nematode showed higher survival (89.42%, 94.22%, and 94.47% after desiccation, cold, and osmotic stress, respectively) than *Aphelenchus avenae* (82.21%, 92.10%, and 92.54%, respectively). During dessication, *A. fragariae* formed compact yellow clusters on the filter paper that were not observed with *A. avenae*. After treatments, RNAs were isolated, and an SL1-based mRNA differential display technique was used to clone genes that were upregulated by dehydration. The expression of genes *Aav-lea-1*, *Aav-ahn-1*, and *Aav-glx-1* was confirmed by Northern blotting.

PLANT AND SOIL MICROBIAL COMMUNITY STRUCTURE ASSOCIATED WITH NATIVE AND EXOTIC ANNUAL BROME DOMINATED RANGELAND IN WYOMING. **Gasch Salava, Caley<sup>1</sup>, S. Enloe<sup>2</sup>, P. Stahl<sup>1</sup>.** <sup>1</sup>Department of Renewable Resources, University of Wyoming, Laramie, WY, <sup>2</sup>Department of Agronomy and Soils, Auburn University, Auburn, AL.

We conducted a study to quantify aboveground vegetation, ground surface characteristics, soil carbon, nitrogen, and phosphorus, and soil microbial abundance of Wyoming rangeland either (1) extensively invaded by *Bromus tectorum* and *Bromus japonicus*; or (2) dominated by native species. Sampling sites were located in semi arid north central Wyoming and have a history of wildfire and livestock use. Nine plots, each with four sampling subplots, were established in both native sagebrush steppe and rangeland dominated by exotic annual bromes since a wildfire in 1996. Subplots were quantified for vegetation functional group cover, and surface soils (0-5 cm) were analyzed for soil organic carbon, nitrogen, and phosphate, and soil microbial community structure determined by phospholipid fatty acid analysis. Subplots with greater than 20% exotic annual brome cover had significantly less cover of all native vegetation functional groups (including cool season perennial grasses, perennial shrubs, perennial forbs, and warm season perennial grasses), resulting in lower functional group richness and evenness than native plots. Cover of bare ground and biotic crusts was also reduced in invaded subplots. Invaded soils also had 85-92% lower abundance of all major soil microbial groups, including arbuscular mycorrhizal fungi, and a lower bacterial:fungal ratio (native = 0.93; invaded = 0.64). Lower abundance of arbuscular mycorrhizal fungi spore propagules was not observed in invaded soils, suggesting that fungal symbionts, and perhaps other microbial groups, are present in dormant form in invaded soils. Native and invaded soils both had low levels of nitrogen, phosphorus, and carbon; however, invaded soils had higher levels of total nitrogen and available phosphorus and a lower C:N ratio (native = 20.23; invaded = 12.11) than the native soils. This data suggests that rangeland dominated by exotic annual bromes is structurally and functionally different than the native sagebrush steppe community.

ANALYSIS OF TWO TRANSCRIPTION FACTORS THAT ARE UPREGULATED IN EARLY NEMATODE FEEDING SITES. **Gheysen, Godelieve and W. Grunewald.** Department of Molecular Biotechnology, Faculty of Bioscience Engineering, Ghent University, B-9000 Gent, Belgium.

During the interaction between sedentary plant-parasitic nematodes and their host, complex morphological and physiological changes occur in the infected plant tissue, finally resulting in the establishment of a nematode feeding site. This cellular transformation is the result of altered plant gene expression most likely induced by proteins injected in the plant cell by the nematode. Here, we report on the identification of a WRKY transcription factor expressed during nematode infection. Using both promoter-reporter gene fusions and in situ reverse transcription-polymerase chain reaction, we could show that AtWRKY23 is expressed during the early stages of feeding site establishment. Knocking down the expression of WRKY23 resulted in lower infection of the cyst nematode *Heterodera schachtii*. WRKY23 is an auxin-inducible gene and in uninfected plants WRKY23 acts downstream of the Aux/IAA protein SLR/IAA14. Although auxin is known to be involved in feeding site formation, our results suggest that, during early stages, auxin-independent signals might be at play to activate the initial expression of WRKY23. We have also identified a transcription factor from the JAZ/TIFY family that is upregulated very early after nematode infection in syncytia induced by cyst nematodes and in giant cells induced by rootknot nematodes. In addition, the gene is also rapidly upregulated by several plant hormones.

NEMATODE ASSOCIATIONS WITH WILD BEES FROM GLOBAL DIVERSITY SURVEYS. **Giblin-Davis<sup>1</sup>, Robin M., N. Kanzaki<sup>1,2</sup>, C. Hazir<sup>3</sup>, S. Hazir<sup>3</sup>, W. Wcislo<sup>4</sup>, W. Ye<sup>1,5,6</sup>, and W. K. Thomas<sup>6</sup>.** <sup>1</sup>University of Florida-IFAS, Fort Lauderdale, FL 33314, USA, <sup>2</sup>Forestry and Forest Product Research Institute, Tsukuba, Japan, <sup>3</sup>Adnan Menderes University, 09100, Aydin, Turkey, <sup>4</sup>Smithsonian Tropical Research Institute, Balboa, Panama, <sup>5</sup>North Carolina Department of Agriculture & Consumer Services, Raleigh, NC 27607, USA, <sup>6</sup>University of New Hampshire, Durham, NH, 03824, USA.

Adults of the wood nesting bees *Megalopta genalis* and/or *M. ecuadoria* were surveyed from Barro Colorado Island, (BCI), Panama and La Selva, Costa Rica for associated nematodes. Nematodes were recovered as dauer juveniles from the Dufour's gland of female and aedeagus of male bees and cultured as RGD 96 (*ex M. genalis*, BCI), RGD 807 (*ex M. genalis*, La Selva) and RGD 900 (*ex M. ecuadoria*, BCI). All three populations were identified as a single new species of "*Aduncospiculum*". Sequences from the three geographical/host isolates were not significantly different for near full length (1,666 bps) SSU, ca 600 bps of D2/D3 LSU; and 658 bps of a fragment of mitochondrial cytochrome oxidase I (mtCOI). Molecular, biological and morphological comparisons support the resurrection of the diplogastrid genus *Aduncospiculum*, which is a putative sister of *Acrostichus*. The new species of *Aduncospiculum ex Megalopta* was closest to *Aduncospiculum halicti* from *Halictus ligatus* and A. sp. from *Augochlora pura* from North America. *Aduncospiculum* is distinguished from *Acrostichus* by morphology and the autapomorphy of synchronized phoretic associations with halictid bees in North and Central America. In Turkey, a total of 9,456 wild bees were surveyed for the presence of nematodes and 173 female and 22 male bees were positive for an overall association level of 2.1%. *Halictus resurgens* was the most widely encountered bee to be associated with nematodes (52%). In 3.9% of all Halictidae (173/4417), mostly dauer nematodes were observed in the

Dufour's gland, poison sac, oviducts, and abdominal cavity of dissected females and from the aedeagus of male bees. Only abdominal glands of 0.6% (21/3279) of females from the Andrenidae were observed with dauers. Nematodes were isolated from the genital capsule of one male Melittidae. Sequence analysis using D2/D3 LSU and mtCOI allowed for putative identification of nematode isolates. There were two or three species of *Bursaphelenchus* (*B. anatolius*, *B. debrae*, and potentially one or more cryptic species closest in morphology to *B. anatolius*) isolated from six different halictid species (*Halictus* and *Lasioglossum*). There were four species of diplogastrids recovered from the abdominal glands of andrenids; a new species of *Koerneria* from *Andrena limata* and a separate sister clade to *Mononchoides* composed of three other possible species from four *Andrena* species. An additional unknown species in the order Tylenchida (nr Allantonematinae) was recovered from three species of *Lasioglossum*. Three mermithid juveniles were recovered from two *Andrena* and one *Halictus* species. The nematode associations for most nematode isolates of bees of the families Halictidae and Andrenidae were phoretic, whereas the tylenchid and mermithids were parasites.

**INTRON GAIN AND LOSS IN CAENORHABDITIS.** Giese, Gabrielle E.<sup>1</sup>, M. Srivatsavai<sup>2</sup>, Z. Hadadian<sup>3</sup>, P.J. Hatcher<sup>2</sup>, R.D. Bergeron<sup>2</sup>, W.K. Thomas<sup>4</sup>, and J.J. Collins<sup>1</sup>. <sup>1</sup>Dept. of Molecular, Cellular and Biomedical Science, Rudman Hall, University of New Hampshire, Durham, NH 03820. <sup>2</sup>Dept. of Computer Science, Kingsbury Hall, University of New Hampshire, Durham, NH 03820, <sup>3</sup>Dept. of Plant Biology, Rudman Hall, University of New Hampshire, Durham, NH 03820, <sup>4</sup>Dept. of Molecular, Cellular and Biomedical Science, Gregg Hall, University of New Hampshire, Durham, NH 03820.

With the rapid progress of sequencing technology we are now able to compare the genomes of multiple, closely related species of *Caenorhabditis*. This gives us the ability to use comparative genomics to address biological questions that require a much finer timescale of analysis. We are using it to investigate the dynamic nature of introns in eukaryotic genes. Studies to date on the question of intron gain and loss have been limited by comparisons of fewer and/or more distantly related genomes. We are using a data set of 6,546 orthologs identified in four species of *Caenorhabditis*: *C. elegans*, *C. briggsae*, *C. remanei*, *C. brenneri*. The ortholog list was assembled by reciprocal best blast. Alignment of the ortholog set and analysis using PHYLIP will identify intron loss and gain events. We are particularly interested in testing the hypothesis that recent intron gains are caused by transposable element insertion.

**EFFECTIVENESS OF SOIL SOLARIZATION ON MANAGEMENT OF *PHYTOPHTHORA RUBI* AND *PRATYLENCHUS PENETRANS* IN NORTHWESTERN WASHINGTON.** Gigot, Jessica.<sup>1</sup>, I. Zasada<sup>2</sup> and T. Walters<sup>1</sup>. <sup>1</sup>Washington State University-NWREC 16650 State Route 536, Mount Vernon, WA 98273 and <sup>2</sup>USDA-ARS Horticultural Crops Research Unit, 3420 NW Orchard Avenue, Corvallis, OR 97330.

Soil solarization is an important component of soil borne disease management systems in many regions. Over 90% of the nation's processed raspberries are grown in Washington State. Currently, broadcast pre-plant fumigation is used to manage soil borne pathogens; a practice that is expensive and chemically intensive. Solarization (SOL) and a combination of SOL plus drip-line fumigation (Inline™ Telone:chloropicrin 61:33, 400 L/HA) were investigated as alternatives for control of *Phytophthora rubi* (Pr) and *Pratylenchus penetrans* (Pp) in northwestern WA. Field plots were established at Washington State University-Northwestern Washington Research and Extension Center in Mount Vernon, WA in June 2007. Plots (3 x 30 m) were set up as a randomized complete block with five replications. Nylon mesh bags of Pr inoculum were placed at 15, 30 and 45-cm depths and harvested in March 2008. Pathogen survival in these bags was assessed in a greenhouse bioassay with tissue culture-propagated raspberry plants. Soil samples for nematode population density assessment were collected after SOL and fumigation in Oct 2007. Raspberry roots samples were collected in November 2008 for Pp quantification. At 15, 30 and 45-cm, SOL plots accumulated 358, 38 and 0 hrs of heat units above 29 °C, respectively. There was no significant affect of SOL on the proportion of diseased roots as compared to the untreated control (UTC) or SOL-Inline treatments. The average root rot rating at all three depths for SOL (6.6) was significantly ( $P < 0.05$ ) higher than the UTC (5.7) and similar to SOL-Inline (6.3). Root and shoot dry weights were not different between treatments. The Pp population density per g soil was significantly ( $P < 0.05$ ) lower in SOL-Inline (8) compared to SOL (82.8) or the UTC (142.2). *Pratylenchus penetrans* per gram of fresh root was significantly lower in SOL (14.5) and SOL-Inline (1.7) compared to the UTC (62). Combining SOL with additional soil management techniques, such as drip-line fumigation, may increase the effectiveness of this technology. Further work is underway to explore the use of organic amendments with SOL for increased control of Pr and Pp in raspberry systems.

**PARTITIONING OF HABITABLE PORE SPACE IN EARTHWORM BURROWS.** Gorres, Josef H.<sup>1</sup> and Jose A. Amador<sup>2</sup>, <sup>1</sup>Plant and Soil Science, University of Vermont, jgorres@uvm.edu, <sup>2</sup>Natural Resources Science, University of Rhode Island, jamador@uri.edu

The effect of earthworms on physical nematode habitat structure was investigated for aggregates approximate 1 cm<sup>3</sup> in size. The aggregates were obtained from soil columns (sandy loam) that were incubated with earthworms (*Lumbricus terrestris*). One set of aggregates was taken from burrow soil (Drilosphere, 'D') and another from locations 2 cm from the burrow (Bulk, 'B').

Samples were taken three, five and sixteen weeks after the beginning of the incubation. Pore volumes and pore sizes were measured in triplicate with Mercury Intrusion Porosimetry (MIP). This method is ideally suited to establish pore size structure in the context of habitat, because it measures the stepwise intrusion of mercury from the outside of the aggregate into ever smaller pores. The progress of mercury into the aggregate interior thus resembles potential paths of a nematode into accessible habitable pore spaces residing in an aggregate. Mercury volumes intruding into pores with neck sizes smaller than nematodes body diameters indicate void space inaccessible to nematodes. This method more closely describes the potentially accessible pore space in aggregates than the measurement of a soil water retention curve. However, the method is costly and measures only small samples. In this study, pore space was classified as nematode habitat when the void spaces were greater than 10  $\mu\text{m}$ , based on prior image analysis results of nematode diameters. Additional classification was into micro (<5  $\mu\text{m}$ ), mesopores type 1 (5 – 25  $\mu\text{m}$ ), mesopores type II (25– 60  $\mu\text{m}$ ) and macropores (> 60  $\mu\text{m}$ ). Total specific pore volume,  $V_s$ , varied between 0.13 and 0.18 mL/g and increased from 3 to 16 weeks in both burrow and bulk soil. Differences between  $V_s$  of D and B samples were not significant on any sampling date. However, some differences were significant for particular pore size fractions. The macropore volume was significantly greater in D than B, after 3 ( $P < 0.022$ ), but not after 5 weeks ( $p < 0.10$ ) and less in D than B after 16 weeks ( $P < 0.035$ ). There was no significant difference for mesopores type 1. After 3 weeks, the specific pore volume of mesopores type 2 was less for D after 3 weeks ( $p < 0.004$ ) and greater for D than B after 16 weeks ( $p < 0.03$ ). There was no significant difference in this pore size range after 5 weeks, although the specific pore volume was less in D than B. The specific pore volume of micropores was not significantly different on any sampling date. When examining the specific pore volume >10  $\mu\text{m}$ , i.e. nematode habitat, specific pore volume was greater after 3 and 5 weeks, but only significantly so after 3 weeks ( $p < 0.05$ ). Nematode habitat was identical after 16 weeks. These data agree with the ephemeral effect that earthworms observed in mesocosm experiments for C and N mineralization and nematode abundance reported elsewhere. The pattern of drilosphere total specific pore volume found for the sandy soil used in this study differs from another study on a silt loam in which drilosphere soil was less porous.

**NITROGEN FERTILIZER EFFECTS ON SOIL COMMUNITIES AND DECOMPOSITION DYNAMICS IN AGRICULTURAL SYSTEMS. Grandy<sup>1</sup>, A. Stuart, K. Wickings<sup>1</sup>, and N Fierer<sup>2</sup>.** <sup>1</sup>Department of Crop and Soil Sciences, Michigan State University, East Lansing, MI 48823, <sup>2</sup>Cooperative Institute for Research in the Environmental Sciences and Department of Ecology and Evolutionary Biology, University of Colorado at Boulder, Boulder, CO 80309, USA.

Many ecosystems, including grassland, forest, alpine, and desert, have shown responses to N enrichment. These responses vary considerably but include changes in soil respiration rates, enzyme activities, and microbial community structure. Surprisingly, little work has examined the effects of N enrichment on soil communities and processes in agricultural systems despite the high rates of N applied in most crop production systems. We investigated litter decomposition rates and their relationship to soil communities in replicated corn-soybean-wheat rotations receiving three levels of N (0, 134, and 291 kg/ha). We found that N fertilizer resulted in modest and temporally variable increases in the activity of four C and N cycle enzymes and modest changes in microbial community structure. We also found that N fertilizer increased mesofaunal abundance by >30% in September but not at other times of the year. There were no differences in the decomposition rates of either corn or wheat. We are in the process of determining whether litter chemistry or soil respiration rates were altered by N fertilization. Our results, although still rolling in, suggest that N fertilization in agricultural systems can alter soil communities. However, we see little evidence that these changes, at least in the short-term, modify litter decomposition rates or soil C dynamics. We interpret our results in the context of current theories, mostly developed in other kinds of ecosystems, regarding N saturation and ecosystem function.

**MIXED DISTURBANCE EFFECT ON SOIL NUTRIENTS AND PLANT SPECIES COMPOSITION. Gray, Dennis M. and J. Dighton.** Rutgers Pinelands Field Station, PO Box 206, 501 Four Mile Road, New Lisbon, NJ 08064.

The upland forest shrub layer of the New Jersey Pinelands is dominated by ericaceous species. Interspersed throughout the region graminoid species dominated patches are found where disturbance was severe or frequent. Ericaceous shrubs maintain dominance by space and nutrient preemption. Where graminoid species dominate they prevent ericaceous species recruitment and vegetative ingrowth by producing a large root mass extending into the soil. We believe ericaceous and graminoid assemblages constitute alternative stable state communities. Each attains dominance due to differing disturbance tolerances. Ericaceous shrubs tolerate moderately frequent and severe disturbance; whereas graminoid plants are tolerant of substantially more frequent and severe disturbance events. In a field study using mixed species plots dominated by *Gaylussacia baccata* and *Vaccinium palida* with a minor *Carex pensylvanica* component we are attempting to shift herb layer species dominance by employing frequent disturbance at increasing levels of severity. Our overarching hypothesis is that a controlled disturbance regime will result in replacement of an ericaceous plant assemblage by a graminoid community which will positively influence soil nutrient dynamics, and improve soil quality as measured by nitrogen and phosphorus availability and increased microbial biomass. The disturbance regime includes annual winter prescribed fire, spading of the soil surface to 20 cm and a fire plus spading treatment. Treatments were applied to three replicate circular 7.1 m<sup>2</sup> plots in March 2007 and 2008. *G. baccata* and *V. palida* stems and *C. pensylvanica* ramets were counted in August 2006, 2007 and 2008. Periodically 20 cm soil cores were obtained and analyzed for microbial biomass nitrogen (MBN), KCl extractable NO<sub>3</sub> and NH<sub>4</sub> and Bray

extractable  $\text{PO}_4$ . After two years of treatment results indicate a nonsignificant trend toward greater ramet production following repeated soil disturbance. Both ericaceous species reacted positively to all disturbance regimes following the first disturbance event but declined following the second annual disturbance. MBN increased in all disturbance regimes three days after treatment and nitrate increased in the soil disruption treatments. After two months MBN and nitrate levels did not vary significantly from the unmanipulated controls; however extractable ammonium increased significantly in the soil disruption treatments. At the end of two growing seasons following consecutive disturbance treatments the soil disruption treatments had significantly greater MBN levels than the control and fire treated plots. At no time did the treatment extractable phosphorus concentrations vary significantly from that of the control. The results indicate a high frequency soil disturbance regime results in ericaceous plant species elimination and a significantly greater soil microbial biomass component. However *C. pensylvanica* coverage has not expanded, and despite the reduction in plant biomass there is little difference in nutrient availability in treated plots. It appears that the nutrient base of this system is tied up in biomass and that nutrients released by a disturbance must be taken up quickly or lost.

**CARBON SEQUESTRATION, NUTRIENT POOLS, AND SOIL FOOD WEBS IN URBAN SOILS. Grewal<sup>1</sup>, Parwinder.** <sup>1</sup>Department of Entomology, Ohio State University, Wooster, Ohio 44691.

Urban soils tend to be highly disturbed due to the impact of anthropogenic activities. We have initiated studies on the impact of human activities on nutrient cycling, carbon sequestration and soil food web dynamics in urban soils. We find huge spatial variation in carbon pools, organic matter, pH, and nutrient pools, nematode community indices, and diversity and abundance of nitrogen fixing bacteria in urban areas. In manipulative experiments we have assessed temporal dynamics of the soil nematode food web and nutrient pools in tall fescue lawns initiated on either topsoil or exposed subsoil, with or without compost amendment (Cheng et al., 2009). We found that nematode abundance, genus diversity, food web enrichment, and structure indices were lower in subsoil compared with topsoil plots. Compost amendment increased nematode food web enrichment index but had no effect on structure index. Temporal faunal profile analysis indicated that the soil food webs converged in all treatments overtime resulting in a pattern typical for turfgrass lawns. Soil macronutrients Ca, P, K, total N, total C, microbial biomass, and soil organic matter contents were higher in topsoil than subsoil, and were increased by compost amendment in both substrates. After one year, turfgrass quality (greenness) was higher in topsoil than subsoil plots, in plots with compost amendment than those without. The implications for these findings for sustainable vegetation management will be discussed.

**MICROBIAL FUNCTIONAL DIVERSITY PROFILES IN RESPONSE TO SIMULATED NITROGEN DEPOSITION AND VARIABLE PRECIPITATION IN THE CHIHUAHUAN DESERT, BIG BEND NATIONAL PARK, TX. Grizzle, Heath W., N. Van Gestel, T. Robertson, D. Tissue, and J. C. Zak.** Department of Biological Sciences, Texas Tech University, Lubbock, TX.

The amount of anthropogenic nitrogen (N) deposition in arid ecosystems is relatively low when compared to mesic systems. Because arid ecosystems are characterized by low precipitation and high potential evapotranspiration rates (PET) in addition to nutrient limitations, anthropogenic N deposition will likely have major effects on community structure and function of soil microorganisms differing from effects found in mesic systems. Determining the impacts of N deposition in arid systems is critical as they cover more than 40% of the global land surface, contain a large portion of agricultural lands and are inhabited by more than 1 billion humans. This study evaluated how a simulated increase in annual N deposition (2 and 4 times background of 3.9 kg/ha) and variable precipitation affected soil microbial functional diversity (FD) in a mid-elevation Sotol grassland and high-elevation Oak-Pine forest in the Chihuahuan Desert in Big Bend National Park, TX. Monthly precipitation was measured and microbial functional diversity parameters were evaluated at both sites from August 2003 to August 2006. Differences in bacterial and fungal FD on carbon (C) substrates and fungal FD on nitrogen (N) substrates were estimated via substrate utilization profiles from Biolog microtiter plates. Bacterial FD was not impacted by either N treatments or precipitation in either site. In the Oak-Pine forest site, Fungal FD on C substrates was increased by low level N treatments but activity was depressed back to control values with the high level N treatment. Fungal FD on N substrates was not affected by N deposition in the Oak-Pine forest site. Variable precipitation and N deposition had a synergistic effect on microbial functional diversity in the mid-elevation grassland site. The high level N treatments differed significantly from controls when coupled with high seasonal precipitation. This difference was due primarily to increases in fungal FD on N substrates. During periods of average rainfall microbial function did not differ between treatments. The lack of bacterial response to additional nitrogen input suggests that bacterial functional diversity is limited by soil moisture rather than by N. The overall impact of N deposition on fungal FD in the Oak-Pine forest site is likely due to the higher precipitation and the more diverse litter makeup of the site when compared to the grasslands. This response suggests a shift to a fungal rather than a bacterial dominated system with increased nitrogen deposition. Microbial dependence on precipitation in arid systems is illustrated by the lack response to N additions with low precipitation amounts in the grasslands system. With continuing increases in global N deposition the results of this study suggest a potential for major changes in microbial function as precipitation patterns are altered with climate change.

EFFICACY OF DMDS AND *BACILLUS FIRMUS* COMPARED TO OTHER COMMONLY USED NEMATOCIDES FOR CONTROL OF *MELOIDOGYNE CHITWOODI* IN POTATO. **Hafez, S.L., and P. Sundararaj.** University of Idaho, Parma Research and Extension Center, 29603 U of I Ln, Parma, Idaho 83660, USA.

Two field experiments were conducted at the University of Idaho, Parma Research and Extension Center, Parma, Idaho to study the efficacy of DMDS and Chancellor compared to Telone II or Temik15G for control of *Meloidogyne chitwoodi* in potato. The first experiment was laid out in a randomized complete block design with ten treatments each and five replications in a sandy loam field. Telone II was applied broadcast by ripper to a depth of 16-18". Different rates (200, 300 or 400lb/A) of DMDS were applied by ripper shank. Immediately after application, all the water sealed area was surface irrigated with half an inch of water. Potato cv. Sheppody seed pieces were planted in rows three ft apart. Second experiment was conducted under field conditions to evaluate the efficacy of a biopesticide active ingredient, *Bacillus firmus*, at different rates and combinations as an alternative to soil fumigation. The experimental design was a completely randomized blocks with seven treatments and five replications. Different rates of biopesticide were incorporated in the soil and chemigated after planting at the respective rates. Vydate was applied six times at two week intervals. Five months after planting, the tubers were harvested, graded and evaluated for nematode infection. Nematode population was significantly reduced in treated plots with an increase in clean and total yield compared to control plots. Nematode infected tubers as well as percent of nematode infection were also significantly reduced by the treatments compared to control plots. Percent of tubers with nematode infection in DMDS treated plots ranged from 0.2 to 25.6. Data from the second experiment indicated that percent of tubers with nematode infection in treated plots ranged from 31.5 to 97.8. Lowest level of nematode infection was recorded in the plots treated with Temik + Vydate treatment followed by the highest rates of *Bacillus firmus* treatments.

EVALUATION OF GREEN MANURE CROPS FOR BIOFUMIGATION POTENTIAL TO CONTROL *M.CHITWOODI* UNDER GREEN HOUSE CONDITIONS. **Hafez, S.L., P. Sundararaj and R. Porteneir.** University of Idaho, Parma Research and Extension Center, 29603 U of I Ln, Parma, Idaho 83660, USA.

Three green house experiments were conducted to demonstrate the effects of oil radish and mustard varieties on *Meloidogyne chitwoodi*. These experiments were laid out in a completely randomized block design with five, six and eleven varieties with six replications for the first, second and third experiment, respectively. Seeds of green manure varieties were planted in 1500 cc pots filled with sterile soil mixture and individually inoculated with 5000 J2 of *M.chitwoodi* and harvested eight weeks after planting. Data from the first experiment indicated that the lowest level of nematode population per g dry root was observed in Defender (149) followed by Colonel (926). Data from the second experiment indicated that among all varieties lowest nematode multiplication in the soil and root was with oil radish variety Bracco (814 and 149). In third experiment, among eleven green manure varieties tested, the maximum reduction of *M.chitwoodi* was in the oil radish variety Defender (95.9%).

EVALUATION OF TRAP CROPS FOR *HETERODERA SCHACHTII* MANAGEMENT IN SUGAR BEET PRODUCTION. **Hafez, S.L. and P. Sundararaj.** University of Idaho, Parma Research and Extension Center, 29603 U of I Ln, Parma, Idaho 83660, USA.

Green house and field experiments were conducted to study the effects of oil radish (Colonel and Ramses) and mustard (Saloon) varieties on *Heterodera schachtii*. In green house, all three varieties were planted in individual pots (500 cc) filled with soil infested with sugar beet cyst nematode (14 eggs and larvae/cc soil) in a completely randomized block design with five replications each. Eight weeks after planting, the crop was harvested and data on eggs and larval population in soil along with viable cysts were recorded. Data indicated that there was a significant difference in the cyst, eggs and larval population among the varieties tested. Among all varieties, lowest level of cyst, eggs and larvae were observed with Colonel followed by Ramses. For the field study, three varieties were planted in the fall 2006 in a field that was naturally and heavily infested with SBCN. They were mechanically chopped three months after planting and roots and shoots were incorporated into the soil by double-disking. Sugar beet was planted over all treatments in spring, 2007 following incorporation of the green manure trap crops. At maturity, sugar beet was harvested, yield data and sugar percent were recorded. Data indicated that there was a significant increase of beet yield in trap crop planted plots compared to the fallow. The maximum yield increase was in the Colonel planted plots followed by Ramses and Saloon. There was no significant difference in sugar percent of beet due to the planting of trap crops.

SEED TREATMENT – AN EFFICIENT STRATEGY FOR *HETERODERA SCHACHTII* MANAGEMENT IN SUGAR BEET. **Hafez, S.L., and P. Sundararaj.** University of Idaho, Parma Research and Extension Center, 29603 U of I Ln, Parma, Idaho 83660, USA.

Two field experiments were conducted at the University of Idaho, Parma Research and Extension Center, Parma, Idaho to evaluate the efficacy of Temik 15G along with Admire Pro and Poncho Beta seed treatments on the sugar beet cyst

nematode management in sugar beet. First and second experiments were laid out in a randomized complete block design with ten and twelve treatments each with five replications. Temik was applied at planting to individual plots (6 rows x 50 ft) and sugar beet seeds were planted in rows 22 inches apart. Vydate was applied at planting and two more foliar applications were made at 14 day intervals and Temik was side dressed eight weeks after planting to respective plots. Admire was applied at planting, by using the CO<sub>2</sub> powered plot sprayer, with spray nozzles mounted behind planting shoe in front of packing wheel, two inch band over each row. Plant protection, weeding and other standard cultural practices were followed. Plant vigor was recorded in the scale of 1-5. Five months after planting beets were harvested from 20 ft of the middle two rows of each plot, weighed and yield data recorded. In the first experiment, application of Temik at planting plus the seed treatment significantly increased the beet yield compared to the untreated control. Percent yield increase (25.9%) was also greatest in that treatment. The highest plant vigor was observed in the plots treated with Temik plus the seed treatment. The combination of seed treatment and Temik performed better than other treatments in terms of beet yield and plant vigor. Maximum reduction of nematode population and yield increase were in the plots of seed treated with Poncho Beta plus Temik, followed by the treatment Poncho Beta plus EXP3. In the second experiment, application of Temik at planting and side dressing (20lb/A + 13lb/A) or single application of Temik along with seed treatment (Poncho Beta Fs 453, 68 G A/Unit + Exp3 90 G A/Unit) significantly increased the beet yield compared to the untreated control. The highest plant vigor and percent yield increase (58.7 and 49.1) was also maximum in the same treatments. In general, split application Temik alone or single application of Temik along with seed treatment performed better than other treatments in terms of beet yield.

ON THE DESCRIPTION OF TWO NEW SPECIES OF *PAURODONTELLA* (NEMATODA: PAURODONTINAE) WITH A KEY AND DIAGNOSTIC COMPENDIUM TO THE SPECIES OF THE GENUS. **Handoo<sup>1</sup>, Zafar A., I.E. Yawar<sup>2</sup>, N. Kazi<sup>2</sup>, and S. Fayyaz<sup>2</sup>.** <sup>1</sup>Nematology Laboratory, USDA, ARS, Beltsville, MD 20705, USA, <sup>2</sup>National Nematological Research Centre, University of Karachi, Karachi 75270, Pakistan.

Two new species of *Paurodontella* collected around the roots of wheat (*Triticum aestivum*) are described and illustrated. One new species is characterized by having a short, cylindrical, robust body markedly tapering at both ends, an anteriorly located vulva, short post-uterine sac, lateral field with four incisures, excretory pore at the base of esophagus, fusiform median bulb and straight pointed tail with a long, thorn-like, mucronate terminus. The other new species has a longer and very slender body with posterior vulva, lateral field with four incisures, and short, conoid, mucronate tail. An identification key to 10 valid species of *Paurodontella* is given. A compendium of the most important diagnostic characters with illustrations of each species is included as a practical alternative and supplement to the key. The diagnosis of *Paurodontella* is emended and a list of all worldwide valid species of the genus is given. Additional information regarding distribution of the two new species and their importance is needed.

INVASIVE PLANT SPECIES AS AGENTS OF BELOWGROUND CHANGE. **Hawkes, Christine V.<sup>1</sup>, N.T. Hausmann<sup>2</sup>, and S.N. Kivlin<sup>3</sup>.** <sup>1</sup>Section of Integrative Biology, University of Texas at Austin, Austin, TX 78712, <sup>2</sup>Land, Air, and Water Resources, University of California-Davis, Davis, CA, <sup>3</sup>Department of Ecology and Evolutionary Biology, University of California-Irvine, Irvine, CA 92697.

Exotic plants can maintain different root fungal communities compared to native plant species and, in some cases, the presence of exotic plants can alter fungal communities in neighboring native plant roots. Understanding these interactions will elucidate top-down drivers of plants on fungi, as well as how fungi may contribute to invasion success. In a series of field and greenhouse studies we asked how the impacts of exotic plants on local neighborhood characteristics, including composition and diversity, affected root fungal communities. Specifically, we examined (1) the effects of neighbor identity by growing a native perennial with each of three annuals (one native, two exotic), (2) the influence of plant priority by establishing plants first or with a three-week delay, and (3) the relative importance of neighborhood diversity vs. host origin by growing five natives and five exotics separately and in mixtures at three levels of richness. These experiments collectively allow us to consider the host specificity of root fungi on native plants and the factors associated with the arrival of exotic plants that may alter these associations. We found that neighborhood characteristics can matter as much as host identity in determining root fungal communities. In manipulating pair-wise neighborhood composition, host specificity was neighbor-specific with exotic neighbors that either had no effect or a controlling effect on and native neighbors that had a synergistic effect on root fungi. These patterns could be partly predicted from the strength of aboveground interactions between neighbors, suggesting a hierarchy of plant influence belowground. In examining priority effects, plants that arrived first were strong determinants of root fungal community composition regardless of origin. Priority likely allows plants to act as a host-specific filter through development of a standing fungal network prior to the establishment of other plants. These effects may be particularly important in communities where the phenology of exotics is different from natives. In the context of neighborhood diversity, native and exotic plants had very different impacts on root fungi. Exotic plant communities were associated with similar fungal communities at all levels of diversity, suggesting that exotics have a narrow pathway of influence. However, that impact was changed by exotic plant interactions with local native hosts and native host diversity. It is possible that more

diverse native plant communities may be able to moderate the impacts of invaders more successfully than less diverse communities. In all experiments, fungal taxa in exotic roots had some overlap with those in native roots. Taken together, the observed effects of host and neighbor origin, priority, and diversity define several potential pathways of influence for exotic plants on root fungal communities that are likely to be relevant to invasion success and ecosystem function.

**MUSTARD BIOFUMIGATION DISRUPTS BIOLOGICAL CONTROL BY *STEINERNEMA* SPP. NEMATODES IN THE SOIL.** Henderson, Donna R.<sup>4</sup>, E. Riga<sup>1,2</sup>, R.A. Ramirez<sup>3</sup>, J. Wilson<sup>1,2</sup>, and W.E. Snyder<sup>3</sup>. <sup>1</sup>Irrigated Agriculture Research and Extension Center, Washington State University, Prosser, WA 99350, USA. <sup>2</sup>Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA. <sup>3</sup>Department of Entomology, Washington State University, Pullman WA 99164, USA. <sup>4</sup>University of California Cooperative Extension, Imperial County.

Mustard green manures or seed meal high in glucosinolates, which produce a natural biofumigant upon incorporation into the soil, form an alternative to synthetic fumigants. However, the non-target impacts of these biofumigants in the field are unclear. We examined the effectiveness of soil incorporation of *Brassica carinata* seed meal both in controlling the plant-parasitic Columbia root-knot nematode (*Meloidogyne chitwoodi*), and on the biological control exerted by the entomopathogenic nematodes *Steinernema feltiae* and *S. riobrave* on root-knot nematodes and the Colorado potato beetle (*Leptinotarsa decemlineata*). Singly, both the seed meal and *Steinernema* spp. reduced root-knot nematode damage to potato tubers and increased marketable tuber yields. However, there was a negative interaction between the two bioagents such that their combination did not further improve suppression of plant-parasitic nematodes. Thus, mustard seed meal applications harmful to the target root-knot nematode also disrupted the ability of *Steinernema* spp. to act as biocontrol agents. Further, we observed modest disruption of the biological control of potato beetles following biofumigation, and the potato beetles were less likely to lay eggs on potato plants grown in mustard-amended soil, suggesting a counteracting benefit of mustard application. Multiple, complementary controls must be integrated to replace the very effective pest suppression typical of synthetic soil fumigants. Our study suggests significant interference between biofumigation and biocontrol agents in the soil, presenting challenges in combining these two environmentally friendly approaches to managing plant-parasitic nematodes and other pests.

**IMPROVING COTTON MANAGEMENT SYSTEMS IN RENIFORM NEMATODE FIELDS USING HERBICIDES TO PROMOTE WEED CONTROL AND REDUCE COTTON RE-GROWTH.** Herring<sup>1</sup>, Dustin M., K. S. Lawrence<sup>1</sup>, S. R. Moore<sup>1</sup>, and C. H. Burmester<sup>2</sup>. <sup>1</sup>Department of Entomology and Plant Pathology, Auburn University, Auburn, Alabama 36849 and <sup>2</sup>Agronomy and Soils Department, Auburn University, Auburn, Alabama 36849.

The reniform nematode (*Rotylenchulus reniformis*) has emerged as the most economically damaging pest to cotton in the southeastern United States. Eliminating late season generations by killing the cotton re-growth and decreasing fall weeds could be an effective management tool to reduce nematode populations for the subsequent season. Tests were conducted in the greenhouse and in four field trials in to evaluate the effect of herbicides on weed densities, re-growth of harvested cotton, and *R. reniformis* nematode populations. Treatments were: 1) 2, 4-D Amine 1.8 L/ha, 2) 2, 4-D Amine 2.4 L/ha, 3) Dicamba 1.8 L/ha, 4) Dicamba 2.4 L/ha, and 5) untreated control arranged in a RCBD with 4 to 6 replications. In the greenhouse, *R. reniformis* was increased on cotton for 120 days and the herbicide treatments were applied. Plant height and weight, and nematode populations were determined at application and 60 days later. In the field, herbicides were applied immediately after harvest and at 30 day intervals samples were taken and weed densities rated. In the greenhouse, the herbicide treatments killed the cotton plants and reduced ( $P < 0.05$ ) root and stem dry weights as compared to the untreated control. All *R. reniformis* life stages present in the soil were reduced an average of 61% in the herbicide treatments ( $P < 0.05$ ) compared to the control. Eggs extracted from the cotton root systems were 69% lower ( $P < 0.05$ ) in the herbicide treatments. Field trials indicated a trend for *R. reniformis* populations to decline in the herbicide treatments over the winter season in December, February, and March. Significant nematode reductions were observed 5 months after herbicide application in April. At cotton planting; the *R. reniformis* populations were 51% lower in the 2, 4 D and Dicamba treatments as compared to the control. Cotton yield in the 2, 4 D at 1.8 L/ha and both Dicamba treatments over all locations averaged a 59.5 kg/ha increase as compared to the control; however, the yield boost was not significant ( $P < 0.10$ ). The combined average data from all tests showed an increase in net profit for both rates of 2,4D. The increase in net profit was \$9.20 and \$37.88, respectively for the 1.8 L/ha and 2.4 L/ha rates as compared to the control. Dicamba at the 1.8 L/ha rate resulted in a \$1.13 net profit while the 2.4 L/ha rate lost \$1.35 compared to the control. An economic analysis indicated that all 2, 4 D treatments had a positive net return above the direct cost of the herbicides on the *R. reniformis* infested cotton farm.

**EFFECTS OF SOIL TYPE, IRRIGATION AND *ROTYLENCHULUS RENIFORMIS* ON COTTON YIELD.** Herring, Stephanie L., and S. R. Koenning, Dept. of Plant Pathology Campus Box 7616, North Carolina State University, Raleigh, NC 27695-7616.

The effects of soil type, irrigation, and population density of *Rotylenchulus reniformis* on cotton were evaluated in a microplot experiment in 2008. Six soil types, Fuquay sand (91% sand, 6% silt, 3% clay, 0.6% organic matter), Norfolk sandy

loam (84% sand, 12% silt, 4% clay, 1.4% organic matter), Portsmouth loamy sand (72% sand, 18% silt, 10% clay, 3.8% organic matter), Muck (58% sand, 33% silt, 9% clay, >30% organic matter), Ceil sandy loam (53% sand, 18% silt, 29% clay, 2.2% organic matter), and Ceil sandy clay (48% sand, 13% silt, 39% clay, 0.9% organic matter), were arranged in randomized complete blocks with four replications. Final population (Pf) densities of *R. reniformis* were greatest in Portsmouth loamy sand. However, irrigated crops planted in this soil and in a high organic matter content, Muck soil, had the greatest cotton total lint yields in spite of high *R. reniformis* populations. The addition of irrigation was significant in these and most of the other soil types. An exception was in the Fuquay sand and Ceil sandy clay where irrigation did not result in a total yield increase. Irrigation effects on cotton earliness was measured by conducting four separate manual harvests of the crop and showed irrigation dependence for most soil types. The initial population (Pi) of *R. reniformis* and its significance on cotton yield varied by soil type. For example, in the Fuquay sand, Ceil sandy clay and Norfolk sandy loam Pi was found to be a significant factor on total yield. The effect of mid-season population (Pm) on yield also varied by soil type and was shown to be important in the Fuquay sand. Transformation of the data showed other significant relationships between Pi or Pm and total yield among the other soil types. An interaction effect of soil type and irrigation was found to act on Pi and Pm values; however, only soil type had an effect on the Pf values.

**EXOTIC PLANT *ALLIARIA PETIOLATA* ASSOCIATED WITH CHANGES IN SOIL RESOURCE AVAILABILITY AND SOIL BIOTA ABUNDANCE AND FUNCTION.** Herrmann, Dustin L, S. J. Morris, K. D. McConaughay, S. Tun, J. McClain, and D. S. O'Keefe, Bradley University, Department of Biology, 1501 W. Bradley Ave., Peoria, IL 61625.

The importance of belowground processes in exotic plant invasions is becoming widely recognized. The direction and magnitude of exotic plant-mediated effects on soil resources in infested native communities has been species-specific and context dependent. More detailed properties and mechanisms of invasion may lead to new generalizations of species effects, particularly the role of positive feedbacks to maintain and facilitate species establishment. *Alliaria petiolata* (garlic mustard), an exotic biennial herb in North American forests, has great potential to affect resource availability of infested soils. To broadly examine the effects of garlic mustard on soil biota and ecosystem processes, we sampled soil from infested and non-infested sites at a pine plantation on sandy soils in central Illinois. Some sites within the plantation were mixed with the dinitrogen-fixing tree *Robinia pseudoacacia* (black locust) which increased garlic mustard density and soil fertility. Plots were studied in pine stands and mixed pine/black locust stands so that soil chemistry and biology could be examined with and without garlic mustard and with and without black locust. Stands with black locust but without garlic mustard presence could not be located for study. Results indicate that soils with garlic mustard infestations exhibit higher rates of soil respiration, lower fungal:bacterial ratios, greater bacterial numbers, higher rates of N mineralization and nitrification, and lower C:N ratios. Catabolic response profiles, a measure of functional diversity of soil microbiota, indicate a shift in substrate use accompanying garlic mustard presence. As black locust is also present on this site it is likely that garlic mustard is either attracted to soils with high nitrogen and bacterial components or that garlic mustard alters soil chemical and microbiological parameters. Current studies on pine only sites are following the changes to soil conditions of non-invaded soils as garlic mustard is experimentally introduced. This relatively simple, but natural model system is providing some clear signals for understanding invasion ecology. Invasion by garlic mustard should be explored under the following hypothesis. Its competitive superiority over many native species is a result of interference mechanisms that have little cost or are beneficial to reproduction. Its establishment of dense stands is maintained through priority effects, whereas superior resource exploiters are excluded from the increased nutrient availability associated with garlic mustard infestation. The cycle is primarily driven by changes to soil chemistry and biology and may have considerable effects on ecosystem function.

**IDENTIFICATION OF *PASTEURIA* SPP. THAT PARASITIZE *ROTYLENCHULUS RENIFORMIS*.** Hewlett<sup>1</sup>, Thomas E., S.R. Stetina<sup>2</sup>, L.M. Schmidt<sup>1</sup>, J.P. Waters<sup>1</sup>, L.J. Simmons<sup>3</sup> and J.R. Rich<sup>4</sup>. <sup>1</sup>Pasteuria Bioscience, 12085 Research Dr., Alachua, FL 32615. <sup>2</sup>USDA ARS, P.O. Box 345, Stoneville, MS 38776. <sup>3</sup>209 Life Sciences Building, Plant Pathology Nematology, Auburn, AL 36849. <sup>4</sup>University of Florida, 155 Research Dr., Quincy, FL 32351.

Reniform nematodes (*Rotylenchulus reniformis*) collected from cotton research plots in Quincy, Florida, a commercial field in Huxford, Alabama, and from multiple west central Mississippi cotton farms were observed to have Pasteuria-like spores attached to their cuticles. Reniform nematodes with spores attached from the Huxford, Alabama sample were surface sterilized, ruptured and cells were propagated in-vitro by Pasteuria Bioscience, INC. Endospores produced from this culture were attached to uninfected reniform nematodes and incubated in sterilized soil at 29.5 C. Spore-filled reniform nematodes were recovered from the soil after 10 days. Genomic DNA extracts were prepared from spores recovered from the infected cadavers. PCR using degenerate primers provided partial coding sequences for spoIIAB, atpA, atpF, and 16s rDNA, having significant homology to *Pasteuria* spp., thus establishing the first reported infection and in-vitro propagation of *Pasteuria* spp. for the reniform nematode.

STRATEGIES FOR USING PASTEURIA TO CONTROL PLANT PARASITIC NEMATODES. **Hewlett<sup>1</sup>, Thomas E., J.P. Waters<sup>1</sup> and L.J. Simmons<sup>2</sup>.** <sup>1</sup>Pasteuria Bioscience, 12085 research Dr., Alachua, FL 32615. <sup>2</sup>Auburn University, 209 Life Sciences Building, Auburn, AL 36849.

Control of nematode populations using predominately *Pasteuria penetrans* have been demonstrated in laboratory and small plot trials. In the past, large scale efficacy tests were not practical or possible to conduct as mass production technology of the bacterium (specifically the endospores) did not exist. Recently, Pasteuria Bioscience, Inc. developed a mass production method and is presently testing efficacy of several *Pasteuria* species for plant parasitic nematode control. Comparison of efficacy trials using *P. usgae* to control sting (on turf) and efficacy trials using reniform nematode specific *Pasteuria* spp. (for agronomic crops), it is evident that different treatment strategies must be utilized to optimize plant parasitic nematode control. These strategies must address a number of variables such as: regional locations, soil types, endospore percolation rates, agricultural production systems, application techniques, number of applications and timing of applications.

INTERRELATIONSHIPS BETWEEN *HETERODERA SCHACHTII* AND *RHIZOCTONIA SOLANI* ON SUGAR-BEET: DISEASE DISCRIMINATION BY HYPERSPECTRAL DATA ANALYSIS. **Hillnhütter, Christian, R.A. Sikora and E.-C. Oerke.** Institute for Crop Science and Resource Conservation (INRES) – Phytomedicine: Phytopathology and Nematology in Soil-Ecosystems, Rheinische Friedrich-Wilhelms-Universität Bonn, Nussallee 9, 53115 Bonn, Germany.

*Heterodera schachtii* and *Rhizoctonia solani* are major factors limiting economic sugar-beet production in Europe and elsewhere. Nematicides are not registered for use against *H. schachtii* and control relies on the effective use of resistant mustard and oil-seed radish varieties and recently developed resistant sugar-beet. However, losses are increasing due to changes in crop rotation that prevents use of the green manure crops. Observations in the field have also shown significant increases in *R. solani* crown rot where the pathogen is found simultaneously with *H. schachtii*. Fungicides for direct application and seed treatment against the disease in later stages are not registered. For the control of *R. solani*, tolerant varieties are used. The increasing importance of energy crops like *Zea mays* and *Brassica napus* in sugar-beet crop rotations further promotes crop loss, because corn is a host for *R. solani* anastomosis group (AG) 2-2 IIIB and oil-seed rape for the beet cyst nematode, respectively. Therefore, precise diagnostics for the early detection and discrimination of the two diseases are required for the spatio-temporal distribution; hyperspectral data acquisition seems to be a promising tool for finding the pathogens in the field. Characteristically, damage due to both soil-borne pathogens appears in clusters. In addition, *R. solani* and *H. schachtii* may occur either alone or simultaneously on one plant making detection and optimum treatment of one or both difficult. High capacity sensors in combination with geo-referencing systems could be used to detect and evaluate the occurrence and the development of single or complex diseases as well as the distribution of the individual pathogens in the field. Optical methods such as hyperspectral imaging and non-imaging sensors have been proved to be useful tools to detect changes in plant vitality due to soil-borne diseases. In greenhouse experiments, sugar-beet varieties differing in the level of resistance to *R. solani* or *H. schachtii* were inoculated at different growth stages with *R. solani* and *H. schachtii* alone or concomitantly. Plants with “split tap-roots” were prepared to distinguish between direct or indirect interactions. To determine variation in symptoms by the pathogens a hyperspectral sensor was used to record the spectral reflectance of leaves at different times after infection. Hyperspectral vegetation indices were calculated to determine vitality changes and disease intensity of the plants. The results demonstrated significant interactions between *H. schachtii* and *R. solani* AG 2-2 IIIB. Leaf yellowing and wilting occurred faster when both organisms were present. Attempts were made to discriminate between the occurrence of each disease alone or in combination by hyperspectral data acquisition. Various vegetation indices generated additional information concerning the disease complex.

LINKING ECTOMYCORRHIZAL SPECIES COMPOSITION TO BELOWGROUND FUNCTION AND EXPLORATION TYPES. **Hobbie, Erik A.** Complex Systems Research Center, Morse Hall, University of New Hampshire, Durham, New Hampshire, USA.

Mycologists have devoted considerable effort to mapping species composition of ectomycorrhizal communities using newly available genetic techniques but how this newly discovered diversity relates to function has been understudied. The functional attribute of how ectomycorrhizal fungi explore the soil (termed exploration type) is probably conserved within taxa and may provide a useful framework by which to relate diversity to functionality. Analyses of carbon and nitrogen isotopic ratios in ectomycorrhizal sporocarps are proving to be a useful integrator of functional information about the role of different taxa in carbon and nitrogen cycling, the extent of hyphal development, and where in the soil profile specific taxa operate. Low levels of nutrient availability should favor exploration types evolved for transport of patchily distributed resources through hydrophobic rhizomorphs, such as long-distance (e.g., *Leccinum*), medium-distance mat (e.g., *Hydnellum*), and medium-distance fringe (e.g., *Cortinarius*) exploration types. These types in general require higher hyphal biomass. In contrast, exploration types with hydrophilic mycorrhizae, such as medium-distance smooth (e.g., *Amanita*), short-distance (e.g., *Inocybe*), and contact (e.g., *Hygrophorus*) exploration types should rely on labile, mobile forms of

nitrogen and generally have poor enzymatic capabilities to access other nitrogen forms. Here, isotopic patterns and compositional data for ectomycorrhizal fungi were compared from a worldwide database. Ecosystems with low nitrogen availability supported a higher proportion of high biomass exploration types than ecosystems with high nitrogen availability. Nitrogen isotope patterns corresponded to exploration type, with long-distance and medium-distance fringe higher in  $^{15}\text{N}$  than short-distance, medium-distance smooth, and contact exploration types, presumably because of the sequestration of large amounts of  $^{15}\text{N}$ -depleted chitin in the mycelia of high biomass exploration types. Within taxa of similar biomass demand, differences in  $^{15}\text{N}$  content of sporocarps appeared to correspond with where hyphae were found in the soil profile. Combining the exploration type concept with nitrogen isotope measurements on sporocarps appears to provide useful information on nitrogen dynamics, carbon demand, and soil exploration patterns for ectomycorrhizal fungi, and will therefore help to evaluate the importance of ectomycorrhizal fungi for ecosystem processes.

**VARIATION PRESENT IN THE COI GENE OF MELOIDOGYNE AND ITS POTENTIAL FOR MOLECULAR IDENTIFICATION. Holterman<sup>1</sup>, Martijn H.M., M. Oggenfuss<sup>1</sup>, S. Kiewnick<sup>1</sup>, and J.E. Frey<sup>1</sup>.** <sup>1</sup>Forschungsanstalt Agroscope Wädenswil, Schloss, 8820 Wädenswil, Switzerland.

Root-knot nematodes (*Meloidogyne spp.*) are important plant pathogens worldwide and cause an estimated 5% of total crop losses world-wide. Morphological identification is difficult and requires expert-knowledge. Therefore molecular methods are especially important for routine diagnostics of this genus. Most available molecular data are from the ribosomal DNA repeat. The advantage of ribosomal DNA is that it is abundant and contains both very conserved and very variable regions. However, not all copies of the rDNA repeats in a genome are necessarily identical, especially in the non-coding regions, which can make their use for diagnostics problematic. Therefore it is useful to have a second region for molecular diagnostics. The cytochrome oxidase subunit I (COI) gene is the standard molecular barcoding gene in many organisms and could provide a good alternative. Furthermore, being a mitochondrial gene it is totally independent of the ribosomal DNA. To establish the suitability of the COI gene for molecular diagnostics of *Meloidogyne*, most (~80%) of the COI gene of eleven *Meloidogyne* species was sequenced and the variation within and between species and populations was assessed. It could be demonstrated that sufficient variation is present in the COI gene to distinguish between different *Meloidogyne* species (except tropical *Meloidogyne spp.*), with species displaying ~2-50 species-specific single nucleotide polymorphisms (SNP's). Furthermore, variation within species appears to be very limited (0-2 SNP's). This shows the potential of the COI gene for routine molecular diagnostics of *Meloidogyne*. To further demonstrate the genes suitability, a high resolution melting curve analysis (HRMC) assay is being developed using the COI data.

**INFLUENCE OF LEAF SPECIES AND BELOW CANOPY WINDS ON LITTER INVERTEBRATES AND LITTER DECOMPOSITION RATES IN A TROPICAL MONSOON FOREST IN TAIWAN. Hou, Ping-Chun L.<sup>1</sup>, T.-Y. Chen<sup>1</sup>, and K.-C. Lin<sup>2</sup>.** <sup>1</sup>Department of Life Sciences, National Cheng Kung University, Tainan, Taiwan 701, <sup>2</sup>Taiwan Forestry Research Institute, Taipei, Taiwan 100.

Litter decomposition is an important ecological process in forest ecosystem and is influenced by factors such as climate, substrate quality, and soil fauna. In this study, we set up wind-shield and control plots in a tropical lowland monsoon forest in southern Taiwan to investigate invertebrate communities and rates of litter decomposition in 6 leaf species with different nitrogen contents (1.33-2.78%). Total numbers of invertebrates extracted from the litterbags peaked at the end of the third month and were positively correlated with nitrogen contents of the leaf species ( $r = 0.875$ ,  $P = 0.022$ ). However, total numbers of invertebrates were not affected by wind shield. Composition of the invertebrate community was affected by time, wind shield, and leaf species. The mean annual decomposition rates ranged from 1.66 in *Illicium arborescens* to 4.07 in *Diospyros morrisiana* and were not related to either nitrogen contents of the leaf species or total number of invertebrates. The decomposition rates were not significantly influenced by wind shield. The lack of differences between wind-shield and control treatments indicate below canopy winds in the forest are less important than litter species to litter decomposition.

**CONTROL OF MELOIDOGYNE CHITWOODI IN POTATO WITH REDUCED RATES OF 1,3-DICHLOROPROPENE, SUDANGRASS AND OXAMYL. Ingham, Russell E.<sup>1</sup>, N.L. David<sup>2</sup>, and N.M. Wade<sup>1</sup>.** <sup>1</sup>Dept. of Botany and Plant Pathology, 2082 Cordley Hall, Oregon State University, Corvallis, OR 97331. <sup>2</sup>Dept. of Plant Sciences, 474G Lotsgard Hall, North Dakota State University, Fargo, ND 58105.

Fumigation with 1,3-dichloropropene (1,3-D) to control Columbia root-knot nematode (*Meloidogyne chitwoodi*, CRKN) damage to potato is a common practice in the long, warm growing season of the Columbia Basin but rates of 140 l/ha (with metam sodium) to 187 l/ha are required. However, the high altitude growing region of the San Luis Valley (SLV) of Colorado has a short, cool growing season which supports less nematode reproduction than in the Columbia Basin. Yields are also lower and growers have less revenue to invest in fumigation which can cost as much as \$650/ha. This study examined whether lower rates could be effective in this environment. 1,3-D was applied at 0, 112, 140 and 187 l/ha in fall of 2004 in a randomized block design with five replications. Prefumigation densities of CRKN across the site averaged 500/250 g soil.

Potato was grown in 2005 and 2007. A green manure crop of sudangrass cv Sordan 79 was grown in 2006. All rates of 1,3-D reduced population densities of CRKN to very low levels for three years after application and controlled the expression of tuber symptoms due to CRKN infection to 0 in 2005 and trace amounts in 2007. Since a low amount of infection is permitted in domestic markets, tuber quality in all 1,3-D treatments would be considered acceptable in both years. However, no CRKN infection is permitted in tubers for seed or export markets. After warm storage of tubers to encourage CRKN and symptom development, small (4% or less) amounts of infection were discovered at all rates in 2005 and large amounts (20%) in 2007. This indicated that some tubers that did not express symptoms at harvest were infected with CRKN that had not yet developed. Therefore, these tubers should not be marketed as seed or exported. Another set of fumigated plots were treated in 2007 with six in-season applications of oxamyl at 1.1 kg/ha delivered through center pivot irrigation. Tuber infection at harvest averaged less than 2% and did not increase after warm storage. In a second field treated with the three rates of 1,3-D that had prefumigation densities of CRKN as high as 2,090/250 g soil, all examined tubers from harvest and stored samples were free of CRKN for all rates of 1,3-D. These results suggest that reduced rates of 1,3-D in the SLV would provide acceptable control of CRKN in tubers for domestic markets and that one application may provide control for two potato crops which would improve profitability. Sudangrass suppressed population densities of CRKN substantially and may have contributed to the extended excellent performance of 1,3-D in the second potato crop. If a good host crop for CRKN, such as wheat, had been grown in 2006, it is uncertain if 1,3-D would have continued to protect the second crop of potato. However, even the highest rate of 1,3-D did not eliminate all tuber infection, so fields with high population levels of CRKN should not be used to produce potatoes intended for seed or export.

APPLICATION OF ENTOMOPATHOGENIC NEMATODES CAN INDUCE COMPONENTS OF SYSTEMIC RESISTANCE IN PLANTS. **Jagdale<sup>1\*</sup>, Ganpati B., S. Kamoun<sup>2\*\*</sup> and P. S. Grewal<sup>1</sup>.** <sup>1\*</sup>Present address: Extension Nematology Lab, Department of Plant Pathology, University of Georgia 2350 College Station Road, Athens, GA, 30602, USA, <sup>2\*\*</sup>Present address: The Sainsbury Laboratory, Colney Lane, Norwich NR4 7UH, United Kingdom and Departments of Entomology<sup>1</sup> and Plant Pathology<sup>2</sup>, Ohio State University, OARDC, Wooster, OH USA 44691.

Antagonism between entomopathogenic nematodes (EPNs) and plant-parasitic nematodes (PPNs) has been documented over the past two decades but its mechanism and ecological significance remain elusive. We investigated the effects of *Steinernema carpocapsae* and its symbiotic bacterium, *Xenorhabdus nematophila* applied to the potting medium on *pyrogallol peroxidase* (P-peroxidase), *guaiacol peroxidase* (G-peroxidase) and catalase activities in *Hosta* sp and *Arabidopsis thaliana* leaves as components of induced systemic resistance. We found that P-peroxidase activity was significantly higher in the leaves from *Hosta* plants treated with *S. carpocapsae* infective juveniles (IJs) and *S. carpocapsae* infected insect cadavers than in the leaves from the control plants 2 weeks after treatment. The G-peroxidase activity was significantly higher in *S. carpocapsae* infected cadaver and *X. nematophila* treatments 10 and 15 days after treatment (DAT) and in *S. carpocapsae* IJs treatment 5 and 15 DAT. The catalase activity in *Hosta* leaves was significantly higher in *S. carpocapsae* infected cadaver and *X. nematophilus* treatments compared with the control 5 and 15 DAT and in *S. carpocapsae* IJs treatment 5 and 10 DAT. Further, the catalase activity in *A. thaliana* leaves was significantly higher in *S. carpocapsae* IJs treatment than in the control 7 DAT. We also determined the effects of *S. carpocapsae* infected cadavers and *S. carpocapsae* IJs on PR1-gene expression in transgenic *A. thaliana* leaves through GUS ( $\beta$ -glucuronidase) activity assay and found that the PR1-gene was expressed in leaves from all treatments except the control. Thus, we conclude that the EPNs and their symbiotic bacteria can induce systemic resistance in plants which may explain the elusive antagonistic effect of EPNs on PPNs.

THE EFFECTS OF *STEINERNEMA CARPOCAPSAE* DENSITY AND SOIL MOISTURE ON MORTALITY OF THE LARGER BLACK FLOUR BEETLE, *CYNAEUS ANGUSTUS*. **James<sup>1</sup>, Jacob, C. Nansen<sup>2</sup>, P. Porter<sup>3</sup>, and T. A. Wheeler<sup>2</sup>.** <sup>1</sup>Dept. of Plant and Soil Science, Texas Tech University, Lubbock, TX 79404, <sup>2</sup>Texas Agrilife Research, Lubbock, TX 79403, <sup>3</sup>Texas Agrilife Extension Service, Lubbock, TX 79403.

Texas produces 30 to 50% of the U.S. cotton, and large amounts of gin trash (plant debris including cotton burs) are produced as part of the ginning process and deposited in piles sometimes near urban communities. The larger black flour beetle thrives in cotton gin piles and has become a severe nuisance when emerging from these gin trash piles, because it may then invade homes, schools, businesses, etc. There has been no success in controlling this pest with chemical strategies, and no insecticides are registered for use in gin trash piles. The larger black flour beetle larvae prefer drier soil, and adults move away from the high moisture areas in gin piles toward drier areas, particularly at the soil/gin pile interface. Based on laboratory experiments, we have demonstrated that *Steinernema carpocapsae* can kill the larger black flour beetle and the effect of soil moisture, insect density, and nematode density were assessed. Soil was placed in petri dishes after being adjusted to 0, 7, or 14% moisture. Larger black flour beetles were added to the test dish at a density of 1 or 5 per dish and either in larval or adult stages. The second-stage (J2) juveniles of *S. carpocapsae* were added to the soil at a density of 0, 250, or 1000/dish. With both 1 and 5 insect larvae/dish, soil with 7 and 14% moisture had higher levels of insect mortality than soil with 0% moisture, and 1000 J2 killed more insect larvae than did 250 J2/dish. With 1 adult insect/dish, 1000 J2 killed approximately 80% of the insects at all moisture levels. However, 250 J2 killed more adult insects as soil moisture increased

(ranging from 15 to 58% mortality). When five adult insects were placed in each dish, then an interaction occurred between J2 density and soil moisture that resulted in the best insect mortality with the combination of 1000 J2 and 0 or 14% moisture, or 250 J2 and 7% moisture. Based on these petri dish studies a series of additional tests will be conducted in Mason jars with four different soil moisture contents, untreated or inoculated with *S. carpocapsae*, and gin trash will be added to all jars to simulate the environment in the interface between gin trash piles and soil surface. The population dynamics of larger black flour beetles will be followed over time. Utilizing *S. carpocapsae* as a biocontrol agent of larger black flour beetles in gin trash piles does not appear to be limited by soil moisture.

**AVICTA® BRAND NEMATICIDE FOR EARLY SEASON NEMATODE MANAGEMENT IN UNITED STATES CROPPING SYSTEMS. Jones, Kurt, D. Long, K. Shetty, C. Watrin, L. Xing, and B. Ulmer.** Syngenta Crop Protection, Greensboro, NC.

Awareness of plant parasitic nematodes and their impact on field crops is increasing in many crops and cropping systems. In 2007, a survey of parasitic nematodes of corn was conducted across the Midwest. Each county with at least 3000 acres of corn was sampled at three random locations for corn parasitic nematodes. The survey results demonstrate the potential for significant damage from various genera of nematodes across the corn belt. Abamectin is being developed as a seed treatment for nematode management in several cropping systems. Research studies with Avicta® brand nematicide, active ingredient abamectin, as a seed treatment demonstrate broad spectrum nematocidal activity. Field trials with Avicta® brand nematicide applied as Avicta Complete Cotton® and Avicta Complete Corn® have improved yields in both crops. Results from both greenhouse and field trials have demonstrated the positive effects of abamectin seed treatment on improving root health and increasing yields of both cotton and corn. In 2008, a set of 35 large-block side-by-side on-farm trials were conducted in Iowa, Indiana, Illinois, Kansas, Nebraska and South Dakota. The yield advantage of the Avicta Complete Corn® averaged 8.7 bushels per acre above Cruiser Extreme® 250. Avicta Complete Corn has also shown similar effectiveness in Southern corn fields. A 15-trial summary from Arkansas, Alabama, Georgia, Louisiana, Mississippi, North Carolina, South Carolina and Texas, demonstrated a 5.3 percent yield increase in fields treated with Avicta Complete Corn versus Cruiser Extreme 250.

**IS BIODIVERSITY REALLY A BARRIER TO ECOSYSTEM INVASION?: AN ANALYSIS OF THE MECHANISMS OF PLANT INVASION. Jones, Rachel O. and S. K. Chapman.** Dept. of Biology, Villanova University, Villanova, PA 19085.

Understanding the mechanisms driving biotic invasions is of great importance to contemporary ecology, especially considering the environmental and economic impacts of losses in native biodiversity. The prevailing theory for a time was that native diversity would protect against non-native invasions (theory of biotic resistance); however, it has been shown that in some instances more diverse areas are actually more susceptible to non-natives (theory of biotic acceptance). Recently, it has been suggested that non-native plant invasions may be the result of anthropogenic disturbances such as nitrogen deposition. Previous studies have suggested that non-native plants often take up larger proportions of soil nitrogen which, coupled with increases in soil nitrogen from deposition, could serve to reduce native species richness and diversity in favor of non-native plants. During the summer of 2008, we collected diversity, richness and productivity data for native and non-native plants within 25 randomly selected sites throughout Ridley Creek State Park, Pennsylvania. Soil cores were also taken from each site and extracted in order to measure available soil nitrogen. Native diversity was found to be significantly negatively correlated with non-native diversity ( $p=0.067$ ) and richness ( $p=0.0372$ ), lending support to the theory of biotic resistance. Native richness was also negatively correlated with increases in nitrates ( $\text{NO}_3$ ), ammonium ( $\text{NH}_4$ ), and total nitrogen. In addition, there was a positive relationship between non-native richness and the percent cover of a native nitrogen fixer, *Trifolium* sp. ( $p=0.0282$ ) which suggests that increased available soil nitrogen benefited non-native plants at the expense of natives. As a continuation of this study, during the 2009 field season I conducted fertilizer manipulations within 8 sites at Ridley Creek State Park as well as within a controlled greenhouse setting to investigate the form of nitrogen (organic or inorganic) driving these effects. This study will advance our knowledge of how nitrogen can impact plant invasion, a critical factor to understand for mitigating invasions.

**MORPHOLOGY AND MOLECULAR PHYLOGENY OF TWO PANAMANIAN FIGWASP NEMATODES, *PARASITODIPLOGASTER CITRINEMA* AND *P. POPENEMA*. Kanzaki<sup>1,2</sup>, Natsumi, R.M. Giblin-Davis<sup>1</sup>, E.A. Herre<sup>3</sup>, and B.J. Center<sup>1</sup>.** <sup>1</sup>Fort Lauderdale Research and Education Center, University of Florida-IFAS, 3205 College Avenue, Fort Lauderdale, FL 33314-7719, USA, <sup>2</sup>Forest Pathology Laboratory, Forestry and Forest Product Research Institute, 1 Matsunosato, Tsukuba, Ibaraki, 305-8687, Japan, <sup>3</sup>Smithsonian Tropical Research Institute, Box 0843-03092, Balboa, Ancon, Republic of Panama.

Currently, the genus *Parasitodiplogaster* contains 13 valid species from figwasps and figs from Africa, North America, Australia and the Neotropics. However, because most of these species were described based upon ethanol-fixed materials, many important morphological characters were missing from the original descriptions. We observed newly-collected living

and formalin-fixed materials to confirm detailed morphological traits of Panamanian species. The survey was conducted at Barro Colorado Island Research Station, Smithsonian Tropical Research Institute in Panama in May of 2008 with NSF support. The nematodes were handpicked alive from dissected syconia into distilled water, and some of them were stored in modified Worm Lysis Buffer for DNA extraction, amplification, and sequencing attempts of near full length SSU, D2/D3 LSU and mtCOI, or collected, heat-killed, and placed into 5% formalin for measurements by light microscopy and then processed into permanent mounts. Six species of *Parasitodiplogaster* were collected in total from six species of *Ficus*. In the morphological observations, *P. citrinema* and *P. popenema* were similar to each other, but were distinguished from the other species examined. These two species have relatively wide and short stomas with large claw-like stegostomatal teeth that extend through the gymnostom. These two species are distinguished from each other by lip morphology, *i.e.*, *P. citrinema* has three small bristle-like setae on the outer surface of each sector, and arrangement of male caudal papillae, *i.e.*, the fifth pair is located ventro-laterally in *P. citrinema* and dorso-laterally in *P. popenema*. Based upon the figures in the original descriptions, these two species are hypothesized to be closest to *P. sycophilon*, but the type or voucher material of *P. sycophilon* was not available for this study for comparisons. Based upon the molecular phylogenetic analysis, the genus *Parasitodiplogaster* is tentatively separated into four clades, *i.e.*, *P. laevigata* group (*P. laevigata*, *Parasitodiplogaster* sp. RGD579 and *P. trigonema*: each possessing a shallow stoma with large claw-like teeth), *P. citrinema*/*P. popenema* group (a wide and cylindrical stoma with large teeth), *P. maxinema* (a narrow stoma, described as “longer than wide”) and *P. australis* (shallow stoma with large claw-like teeth with squared tips). Until recently, the stoma of *Parasitodiplogaster* species was considered to be a simple tube or cylinder. However, recent descriptions of newly discovered species of *Parasitodiplogaster* and our re-examination of live nominal species suggest that the stomatal morphology of *Parasitodiplogaster* is complicated and may be as or more diverse than other diplogastrid genera. More sampling, molecular phylogenetic analyses and ecological (life cycle) studies will be necessary to understand the adaptive radiation and morphological evolution of this interesting genus.

**TERMITE-ASSOCIATED NEMATODES IN KENTING NATIONAL PARK, TAIWAN. Kanzaki<sup>1</sup>, Natsumi, H.-F. Li<sup>2</sup>, Y.-C. Lan<sup>3</sup>, H. Kosaka<sup>4</sup>, and R.M. Giblin-Davis<sup>2</sup>.** <sup>1</sup>Forestry Microbiology Dept., Forestry and Forest Product Research Institute (FFPRI), 1 Matsunosato, Tsukuba, Ibaraki, 305-8687, Japan, <sup>2</sup>Fort Lauderdale Research and Education Center, University of Florida-IFAS, 3205 College Avenue, Fort Lauderdale, FL 33314-7719, USA, <sup>3</sup>Leader Univ., Taiwan, and <sup>4</sup>FFPRI, Hokkaido, Japan.

Termite-associated nematodes were surveyed in Kenting National Park, Taiwan. Eight species (41 colonies) of termites were collected and examined for nematode associates. Twenty workers were randomly chosen from each colony and squashed onto a 2.0% water agar plate to establish cultures of associated nematodes. The culture plates were kept at room temperature and examined daily for one month. Nematodes from successful cultures were isolated and used to establish isofemale lines. The successfully cultured nematodes were observed with a light microscope for identification and sequenced for molecular typing. Based upon fragments of SSU (ca. 600 bps.) and D2/D3 LSU (ca. 600-730 bps.), seven MOTUs (*Poikilolaimus floridensis*, an un-described *Poikilolaimus* species, and five *Halicephalobus* species) were identified from five species of termites, *Odontotermes formosanus*, *Coptotermes formosanus*, (Rhinotermitidae), *Nasutitermes takasagoensis* (Termitidae), *Neotermes koshunensis* and *Cryptotermes domesticus* (Kalotermitidae). *Poikilolaimus floridensis* is considered to have wide distribution, because there were only minor differences in D2/D3 LSU between Taiwanese and South Florida populations. *Poikilolaimus* sp. is close to *P. floridensis* based upon inferences from molecular sequence data and typological morphological similarities, *i.e.*, possessing regular thin cuticle and triangular flap at the stomatal opening and lack of stegostomatal teeth, however it is distinguished from *P. floridensis* by molecular sequence data and cheilostomatal morphology, spicule morphology, male caudal papillae arrangement and female tail morphology. More research is necessary to elucidate the biology and systematics of this Taiwanese *Poikilolaimus* sp. *Poikilolaimus floridensis* and *Poikilolaimus* sp. have been isolated only from Kalotermitidae termites, *i.e.*, *Neotermes*, *Cryptotermes* and *Incisitermes*, suggestive of association by descent or a co-evolutionary radiation with drywood termites. Contrastingly, *Halicephalobus* species are difficult to distinguish from each other using general morphology because of parthenogenetic reproduction and the lack of males, although they were distinguishable with molecular sequence data from the chosen loci. More morphological and biological studies are necessary. Interestingly, the genera *Poikilolaimus* and *Halicephalobus* have been isolated from termites in South Florida and Central America (Panama and Costa Rica). The association ratios in South Taiwan appeared similar to those in the American Neotropics.

**PLANT COMPOSITIONAL SHIFTS MODERATE CLIMATE CHANGE EFFECTS ON SOIL ENZYME ACTIVITIES AND SOIL NEMATODES. Kardol<sup>1,2</sup>, Paul, M.A. Cregger<sup>2</sup>, C.E. Campamy<sup>1,2</sup>, and A.T. Classen<sup>2</sup>.** <sup>1</sup>Oak Ridge National Laboratory, Environmental Sciences Division, Oak Ridge, TN 37831, <sup>2</sup>Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37919.

Feedbacks of terrestrial ecosystems to climate change depend on soil ecosystem dynamics. Soil ecosystems can directly and indirectly respond to climate change. For example, warming directly alters microbial communities by increasing their

activity. Climate change may also alter plant community composition, thus indirectly altering the microbial communities that feed on their inputs. To better understand how climate change may directly and indirectly alter soil ecosystem functioning, we investigated old-field plant community and soil ecosystem responses to single and combined effects of elevated [CO<sub>2</sub>], warming, and water availability. Specifically, we collected soils at the plot level (plant community soils), and beneath dominant plant species (plant-specific soils). We used microbial enzyme activities and soil nematodes as indicators for soil ecosystem functioning. Our study resulted in two main findings: 1) Overall, while there were some interactions, water, relative to increases in [CO<sub>2</sub>] and warming, had the largest impact on plant community composition, soil enzyme activities, and soil nematodes. Multiple climate change factors can interact to shape ecosystems, but in this case, those interactions were largely driven by changes in water availability. 2) Indirect effects of climate change, via changes in plant communities, had a significant impact on soil ecosystem functioning and this impact was not obvious when looking at plant community soils. Climate change effects on enzyme activities and soil nematode abundance and community structure strongly differed between plant community soils and plant-specific soils, but also within plant-specific soils. In sum, these results indicate that accurate assessments of climate change impacts on soil ecosystem functioning require incorporating the concurrent changes in plant function and plant community composition. Climate change-induced shifts in plant community composition will likely modify or counteract the direct impact of climate change on soil ecosystem functioning, and hence, these indirect effects should be taken into account when predicting how climate change will alter ecosystem functioning.

THE ROLE OF POPULATION SOURCE AND GRASS DOMINANCE ON RECOVERY OF ECOSYSTEM STRUCTURE AND FUNCTION IN TALLGRASS PRAIRIE RESTORATIONS. **Klopf, Ryan P. and S.G. Baer.** Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901.

Two important filters in community re-assembly through ecological restoration include population source selection and seed mix composition, but their consequence for belowground recovery and functioning is largely unexplored. Our objectives were to evaluate whether two soil properties that are sensitive to changes in management, i.e., soil microbial biomass C (MBC) and inorganic N availability, respond differently to dominant species population seed source and seeded grass:forb ratio across a precipitation gradient. We established two split plot experimental restorations at the Konza Prairie LTER (KNZ), and the Belleville Research Station in southern Illinois. These field sites were located at similar latitude, but across a 500 km longitudinal precipitation gradient within the historic range of tallgrass prairie. The whole plot treatment was dominant C<sub>4</sub> grass seed source (i.e., cultivar or non-cultivar). The subplot treatment was the ratio of C<sub>4</sub> grasses to forbs. After three years of restoration, plant cover of ruderal species was greater in non-cultivar than cultivar plots at KNZ (P=0.003). Growing season inorganic N availability, as measured in-situ on ion exchange resin bags, was lower in these non-cultivar plots (P=0.096), likely due to the lower nutrient use efficiencies of weedy species. Recovery of MBC was similar in cultivar and non-cultivar plots at KNZ. In the wetter climate of Illinois, cover was dominated by planted species in all plots. Soil inorganic N was lower and MBC was greater than at KNZ. Within Illinois, inorganic N availability was low in both cultivar and non-cultivar sources, while MBC was greater in cultivar plots than non-cultivar plots (P=0.051). In response to the dominance treatment, C<sub>4</sub> grass cover was similar across subplots at KNZ, but forb cover was greatest in the subplot with the lowest grass dominance. MBC was higher in the low grass dominance subplot relative to the high dominance subplot (P=0.078). In Illinois, planted grasses and forbs established according to the percent grass dominance treatments, but there was no difference in MBC between composition treatments. Our results suggest source and dominance of the C<sub>4</sub> grasses differentially influence belowground recovery across a precipitation gradient due to both direct and indirect mechanisms. The effect of source may be direct (i.e., greater recovery of MBC in Illinois plots restored with cultivars), where greater productivity of the C<sub>4</sub> grass cultivars may have stimulated the microbial community. The influence of source may be indirect (i.e., lower N availability in non-cultivar plots at KNZ) due to greater cover of weeds in non-cultivar plots. Higher MBC in the plots with a lower seeded grass:forb ratio suggests the presence of both functional groups may facilitate soil restoration to a greater extent than higher grass dominance. In general, greater ecosystem recovery in Illinois emphasizes the importance of climate in modulating the influence of population source and functional group dominance on the recovery of ecosystem function during tallgrass prairie restoration.

EVALUATION OF SPK, A NOVEL COMBINATION OF ORGANIC COMPOUNDS FOR ROOT-KNOT NEMATODE CONTROL IN TOMATO. **Kokalis-Burelle<sup>1</sup>, Nancy, E.N. Rosskopf<sup>1</sup>, and F. Iriarte<sup>2</sup>,** <sup>1</sup>USDA, ARS, U.S. Horticultural Research Lab, 2001 S. Rock Rd., Ft. Pierce, FL, 34945, <sup>2</sup>Iowa State University, Plant and Insect Diagnostic Clinic, 327 Bessey Hall, Ames, IA, 50011.

Laboratory, greenhouse, and field microplot trials were conducted to evaluate the efficacy of a novel combination of organic compounds, referred to as SPK, for control of root-knot nematode (*Meloidogyne incognita*) on tomato. SPK has zero ozone depletion potential, has a short half-life in soil (3-7 days), has low mammalian toxicity, is composed of widely available material, and is economically feasible for field-scale application. In laboratory studies complete control of nematode egg hatch was achieved at 0.4% SPK (v:v) and above. SPK at 0.2% resulted in a decrease in egg viability compared to the control. In greenhouse experiments, application rates of 6% SPK to soil controlled *M. incognita* J2 in both

soil and tomato roots, and improved root condition ratings, while 9% SPK reduced root galling. In field microplot studies using tomatoes, SPK reduced the number of J2 in roots and soil at 5% and above, and reduced galling at 10% and higher. In addition to controlling nematodes, SPK is a broad-spectrum fungicide, and controls a variety of weed species including yellow and purple nutsedges (*Cyperus esculentus* and *C. rotundus*), goosegrass (*Eleusine indica*), crabgrass (*Digitaria ciliaris*), and pigweed (*Amaranthus hybridus*). A patent is currently pending on SPK in cooperation with researchers from the University of Florida.

**SOIL MICROBIAL COMMUNITY ALTERATIONS WITH DISTURBANCE IN SHORTGRASS STEPPE AND NORTHERN MIXED-GRASS PRAIRIE RANGELANDS. LaFantasie, Jordana<sup>1</sup>, C.C. Gasch Salava<sup>2</sup>, and S.F. Enloe<sup>3</sup>.**

<sup>1</sup>Department of Biological Sciences, 600 Park St., Fort Hays State University, Hays, KS 67601, <sup>2</sup>Department of Renewable Resources, 1000 E. University Ave., University of Wyoming, Laramie, WY 82071, <sup>3</sup>Department of Agronomy and Soils, 119 Extension Hall, Auburn University, Auburn, AL 36849.

Soil microbiota are critical components of ecosystem function; mediating essential soil chemical transformations, and interacting with plant communities. Anthropogenic disturbance in rangelands is increasing due to exurban and energy development. An understanding of how microbial communities respond to disturbance is essential for the remediation of microbial community structure and therefore plant community structure. The objective of this study was to quantify differences in microbial community structure following soil and plant community disturbances (soil disturbance, vegetation clipping, vegetation removal via non-selective herbicide and undisturbed control) in two rangeland ecosystems (shortgrass steppe and northern mixed grass prairie). Both of our field locations were on USDA Agricultural Research Service research stations, with the shortgrass steppe site on the Central Plains Experimental Range in NE Colorado and the Northern Mixed Grass Prairie on the High Plains Experimental Grasslands Research Station in SE Wyoming. We hypothesized that microbial abundance would be highest in the undisturbed control and lowest with soil disturbance. Disturbances were initiated in early spring 2005 and maintained through soil collection in spring 2006. Phospholipid fatty acids were extracted from total soil using a modified Bligh-Dyer methodology and analyzed with an Agilent 6890N gas chromatograph and Sherlock software. In addition, we monitored changes in aboveground plant communities by disturbance and rangeland ecosystem. Results for both shortgrass steppe and northern mixed grass rangelands indicate significant differences in total abundance between treatments. In the northern mixed grass prairie we found differences between all soil microbial functional groups between treatments, with lower bacterial:fungal ratios being associated with a stronger representation by perennial grasses. Differences in soil microbiotic functional group diversity were also evident, with higher amounts of diversity associated with established perennial plant species, regardless of whether they were defoliated under the clipping treatment. Soil disturbance in northern mixed grass prairie and shortgrass steppe rangelands appears to have the most impact on soil microbial community structure and, likely, soil and ecosystem function. These results suggest that establishment of plant communities similar to native communities are the first step in reestablishing soil ecological function.

**LEAF LITTER CHEMISTRY CHANGES DUE TO BURNING. Lammers Kristin<sup>1</sup>, J. Dighton<sup>2</sup>, and G. Arbuckle-Keil<sup>3</sup>.**

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Low intensity control burns are a standard fuel reduction management tool used in the New Jersey pine barrens ecosystem. Periodic disturbances through fire can be an important influence on the cycling of nutrients within the ecosystem and is important for sustained forest growth. The control burns release mineral nutrients, but the changes in the organic composition of leaf litter due to burning have not been documented. Our study compared chemical changes in white oak (*Quercus alba*), pitch pine (*Pinus rigida*) and black huckleberry (*Gaylussacia baccata*), characteristic of the New Jersey pine barrens, during thermal decomposition (100, 200, 300, 400 and 550°C) using FT-IR spectroscopy. Principal component analysis (PCA) of the presence/absence of vibrational modes in IR spectra revealed changes in the carbohydrate chemistry of the leaf litter at each temperature. In general, it appears that there is clear separation of leaf litter species chemistry at low temperatures. At 300°C the chemistries of all species become similar, but then separate again at higher combustion temperatures. Infrared spectroscopy illustrated that all three species shared wavenumbers characteristic of the primary components of leaves such as cellulose, lignin and hemicellulose, but that ratios of these constituents varied during heating. Evolved gas analysis (EGA) was applied to each litter species using Thermal Gravimetric Analysis (TGA-IR) to further characterize the changes induced by heating. EGA indicated that a major weight loss including CO, CO<sub>2</sub>, H<sub>2</sub>O, aliphatic compounds (CH) and a combination of hydrocarbons were indicative of the degradation process while heating from ~225°C to ~600°C. Time series ANOVA verified different weight loss steps in the IR gaseous regions with respect to temperature. The repeated measures ANOVA was also performed on frequently measured wavenumbers in the three litter species. Generally, in all wavenumbers analyzed, there was no difference overall between species, despite species variation at the main weight loss event. The precise identification of the functional groups and compounds is difficult; complex mixtures such as leaf material are composed of various polymers with various degradation processes.

**BRASSICA GLUCOSINOLATE PROFILES ASSOCIATED WITH BIOFUMIGANT ACTIVITY AGAINST *MELOIDOGYNE HAPLA*.** LaMondia, James A.<sup>1</sup> and N. A. McHale<sup>2</sup>. The Connecticut Agricultural Experiment Station, <sup>1</sup>Valley Laboratory, 153 Cook Hill Rd. Windsor CT 06095 and <sup>2</sup>Department of Biochemistry and Genetics, 123 Huntington St. New Haven CT 06504.

*Brassica* spp. produce a broad range of glucosinolates (GSLs) that break down to toxic metabolites that can be utilized in biofumigation for nematode management. Seeds of these species make a number of minor GSLs, but typically produce one predominant type. Using reverse phase HPLC, we characterized species by predominant GSL type, and conducted bioassays to determine which GSLs are most toxic to Northern root knot nematodes (*Meloidogyne hapla*). The predominant GSLs tested from plant seed sources were as follows: progoitrin (*Brassica napus* 'Dwarf Essex', 'Sterling'), sinigrin (*B. juncea* 'Pacific Gold' and *Brassica nigra*), 4-methylsulfinylbutyl (*B. oleracea* 'Calabrese'), not identified (*Camelina sativa*), epiprogoitrin (*Crambe abyssinica* 'Meyer'), 4-methylthiobutyl (*Eruca sativa*), and sinalbin (*Sinapis alba* 'Ida Gold'). Bioassays were performed using ground seeds of the above plants plus lettuce *Lactuca sativa* 'Simpson Elite' as a no GSL control. A 250 µl suspension of 140 to 200 J2 of *M. hapla* in water was placed in small vials. Seeds of test plants were frozen, ground in a mortar and pestle, and mixed with air-dried pasteurized Windsor loamy sand (pH 6.2) at rates of 20, 15, 10, 5; 2.5, 1.3, 0.6, or 0 g seed per L soil. One g of amended soil was added to the nematode suspension in vials. Vials were capped and incubated at 21 °C. After 48 hr, vial contents were washed into pie pans with 250 ml of additional water for nematode recovery and J2 were collected after 72 hrs, scored as viable or non-viable, and counted. There were 3 replicates of each treatment. Data were normalized for the soil alone treatment recovery, and the LD50 was determined. The lowest lethality scores were observed in *S. alba* and *E. sativa* treatments. LD50 values were greater than 1.3 g seed per L soil, similar to the *L. sativa* control, suggesting relatively low toxicity for sinalbin and 4-methylthiobutyl GSL. Higher toxicity was observed in the *Crambe* treatments (60% mortality at 1.3 g/L soil), where epiprogoitrin predominates. The highest toxicity levels (LD50 less than 1.3 g per L soil) were observed with *B. nigra*, and *B. juncea* Pacific Gold (70 and 100% mortality at the 1.3 g seed per L soil rate, respectively), both of which have sinigrin as the predominant GSL. Sinigrin levels were 3 fold higher in seeds of Pacific Gold vs. *B. nigra*, which correlated with substantially higher mortality scores. The results point to sinigrin as the glucosinolate with the most activity and Pacific Gold as the most promising crop for management of *M. hapla* by biofumigation.

**TEMPORAL DYNAMICS OF THE MICROBIAL RESPONSE TO A TWO-YEAR RAIN EXCLUSION.** Landesman, William J.<sup>1,2</sup> and J. Dighton<sup>2</sup>. <sup>1</sup>Graduate Program in Ecology & Evolution and Rutgers Pinelands Field Station, Rutgers University, New Brunswick, NJ 08901, <sup>2</sup>Rutgers Pinelands Field Station, Rutgers University, New Lisbon, NJ 08064.

The effect of altered precipitation amount on soil microbial community structure was evaluated in an Oak-Pine stand of the New Jersey pinelands. Treatments included drought (no rainfall), normal (100%), high (200%) and ambient rainfall. Samples were removed from the surface soils, predominantly organic matter with small quantities of sand, and analyzed using the phospholipid fatty acid analysis. We hypothesized that the bacterial:fungal and gram+:gram- ratios would be highest in the drought plots and lowest in the high rainfall plots. Microbial biomass was not statistically different between treatment levels on any sampling date (repeated measures ANOVA,  $p = .49$ ). The manipulations had no effect on community composition, as measured by the bacteria:fungi ( $p = .84$ ) and gram+:gram- ( $p = .34$ ) bacteria ratio. In order to measure the short-term temporal response of microbial communities to rainfall, the equivalent of two inches of rain was applied to the drought and ambient plots at the conclusion of the two-year experiment. The response of microbial communities was measured three hours, eight hours, one day, two days, one week and three weeks following the rain application. The water application resulted in a highly significant treatment effect ( $p < .005$ ). After only three hours, microbial biomass was significantly higher in the ambient plots. After 8 hours, biomass in the ambient plots was more than double the microbial biomass in the drought plots. There was no difference between microbial biomass at any other sampling time, with the exception of the 1 week sampling event. The bacteria:fungi biomass ratio was significantly higher in the drought plots after three and eight hours but was not statistically different at any other sampling time. This research demonstrates that soil microbes can rapidly increase their biomass in response to rainfall. Sampling in the long-term experiment were never removed less than 48 hours following the most recent rain event. This, combined with the fact that most of the treatment effects in the short-term temporal experiment were found within 1 day of watering suggests that microbes rapidly enter dormant states when water is not available. Although microbes can rapidly return to an active state after a two-year drought, there is evidence that drought stress limits their growth rate, at least in the short term (days to weeks). Our research highlights the need for greater temporal resolution when sampling the response of microbial communities to precipitation manipulations.

**USING PYROSEQUENCING TO COMPARE THE PHYLOGENETIC AND FUNCTIONAL ATTRIBUTES OF SOIL BACTERIAL COMMUNITIES.** Lauber<sup>1</sup>, C.L., and N. Fierer<sup>1,2</sup>. <sup>1</sup>Cooperative Institute for Research in Environmental Sciences, University of Colorado, UCB 216, Boulder, CO 80309. <sup>2</sup>Department of Ecology and Evolutionary Biology, University of Colorado, UCB 334, Boulder, CO 80309.

Soils harbor enormous amounts of bacterial diversity and soil bacterial communities can vary greatly in composition across space. However, our understanding of the specific changes in soil bacterial community structure that occur across larger

spatial scales is limited because most previous work has either focused on surveying a relatively small number of soils in detail or analyzing a larger number of soils with techniques that provide little detail about the phylogenetic structure of the bacterial communities. Here we used a barcoded pyrosequencing technique to characterize bacterial communities in 88 soils from across North and South America, obtaining an average of 1501 sequences per soil. We find that overall bacterial community composition, as measured by the pairwise UniFrac distances, and phylogenetic diversity were significantly correlated with differences in soil pH ( $r=0.79$  and  $0.50$ , respectively), and largely due to changes in the relative abundances of Acidobacteria, Actinobacteria and Bacteroidetes across the range of soil pHs. In addition we surveyed the functional metagenomes of three distinct soils (desert, temperate hardwood forest and grassland) using a similar barcoded pyrosequencing method. We find each soil contains a unique set of functional genes which can readily differentiate soil communities in each of these distinct ecosystems. Together these results suggest that the structure of soil bacterial communities is, to some degree, predictable across larger spatial scales, and the effect of soil pH on bacterial community composition is evident at even relatively coarse levels of taxonomic resolution.

**BIOCONTROL EFFICACY OF THE ENDOPHYTIC *FUSARIUM MONILIFORME* ISOLATE Fe<sub>14</sub> TOWARDS THE RICE ROOT-KNOT NEMATODE *MELOIDOGYNE GRAMINICOLA* UNDER OXIC AND ANOXIC SOIL ENVIRONMENTS.** **Le, Huong T.T.,<sup>1</sup> J.L. Padgham<sup>2</sup> and R. A. Sikora<sup>3</sup>.** <sup>1, 3</sup>Institute of Crop Science and Resource Conservation (INRES) - Phytomedicine, Phytopathology and Nematology in Soil-ecosystems, University of Bonn, Nussallee 9, Bonn 53115, Germany, <sup>2</sup>Environmental Risk, Vulnerability and Adaptation Program International START Secretariat, 2000 Florida Av. NW, Washington, DC 20009, USA.

*Meloidogyne graminicola* is one of the most damaging nematodes in rice, causing yield losses of 20 up to 50 % in upland, lowland, and deepwater rice ecosystems in Asia. While this nematode cannot penetrate roots in flooded soils, it can survive long periods in anoxic soil environments and rapidly reinvade roots whenever soils are drained. Anoxic conditions do not inhibit the development of *M. graminicola* already in the root at the onset of soil flooding. Therefore, there is a need to devise control strategies that not only impact the oxic host penetration phases, but that also target subsequent nematode developmental stages in the root, which generally occur under anoxic soil conditions. The endophytic *Fusarium moniliforme* isolate Fe<sub>14</sub>, which was isolated from a rice growing region of Vietnam, was shown to have biocontrol activity toward *M. graminicola* by reducing gall formation and juvenile penetration by up to 50 %. The colonization of this endophytic fungus and its ability to control the rice root-knot nematode under oxic and anoxic soil environments was investigated under glasshouse conditions. Fungal spores were inoculated twice to the rice seedlings at sowing and three weeks later. One week after the second fungal inoculation the rice plants were subjected to either oxic or anoxic soil water environments. To create anoxic condition, half the number of experimental pots were slowly submerged under water from the bottom to top for 3 days. The experiment was terminated 4 weeks after flooding the soil. Colonization rate was evaluated by calculating percentage of root pieces showing Fe<sub>14</sub> growth. To test the biocontrol activity, the same methods were applied except that one week after the second fungal inoculation, *M. graminicola* J2 were inoculated to rice plants at a density of 4 J2 / g soil. The development of the nematode was synchronized by washing all of the experimental pots 3 days after nematode inoculation and replanting rice seedlings in new pots which were under both soil water conditions. Experiment was harvested 8 weeks after nematode inoculation. The total number of nematodes in control and treated plants in both soil water conditions was recorded. The results showed that colonization of Fe<sub>14</sub> was very high regardless of soil water conditions and was up to 89 %. Inoculation of Fe<sub>14</sub> significantly reduced the number of nematode inside the rice plant by 60 % in oxic soil and by 45 % under anoxic soil. These results suggest that the mutualistic fungus *Fusarium moniliforme* Fe<sub>14</sub> is an effective biocontrol agent under anoxic soil environment.

**EFFECT OF CROP ROTATION ON *ROTYLENCHULUS RENIFORMIS* POPULATION STRUCTURE.** **Leach<sup>1</sup>, Megan M., P. Agudelo<sup>1</sup>, and A. Lawton-Rauh<sup>2</sup>.** <sup>1</sup>Dept. of Entomology, Soils, and Plant Sciences 114 Long Hall, Clemson University, Clemson, SC 29634, <sup>2</sup>Dept. of Genetics and Biochemistry 100 Jordan Hall, Clemson University, Clemson, SC 29634.

*Rotylenchulus reniformis* is a highly variable species and an economically important pest in many cotton fields across the southeast. Rotation to resistant or nonhost crops has the potential to contribute to management of reniform nematode. A number of rotation studies have documented the suppression of reniform nematode in cotton fields, but the effect of these rotations on the genotype of reniform nematode populations has not been studied. In order to study this effect, an initial population of *R. reniformis* was obtained from an infested field in Calhoun County, SC. The field population was subjected to six planting schemes covering four planting cycles in a greenhouse. The cropping cycles were: 1) cotton, corn, cotton, corn; 2) susceptible soybean, corn, susceptible soybean, corn; 3) resistant soybean, cotton, resistant soybean, cotton; 4) corn, cotton, corn, cotton; 5) continuous susceptible soybean; 6) continuous cotton. Cotton cultivar Deltapine 50, corn hybrid Funk's Waxy, and soybean varieties Braxton and Forrest were used for the described rotations. Each cycle allowed for reproduction over a 120 day period. After 120 days, nematodes were extracted, counted, and combined into 1,000 reniform nematode aliquots. DNA was extracted and digested using *EcoR* I and *Mse* I. Amplified fragment length polymorphisms

(AFLPs) were used to determine the effect of crop rotation on the genotype of reniform nematode populations after each cropping cycle. Selective amplification was conducted using primer pairs consisting of three selective nucleotides. Each AFLP genotype produced was compared to the initial field population following rotation cycles with the purpose of identifying DNA markers associated with the reniform nematode's ability to parasitize particular hosts. The characterization of field population variability of reniform nematode and of population responses to host plants used in rotations will help extend the durability of resistant varieties and will help growers choose effective rotation schemes.

**A COMMUNITY-LEVEL PHYSIOLOGICAL PROFILING APPROACH TO EVALUATING IN SITU SOIL CARBON SUBSTRATE UTILIZATION AND ITS INTERACTION WITH BIOAVAILABLE NITROGEN. Lehman, R. Michael, J. L. Garland, M. C. Zabaloy, C. L. Mackowiak, and S. D. Frey** USDA-ARS, Bookings, South Dakota.

We used microtiter plates loaded with an oxygen-sensitive fluorophore to assay respiration of endogenous carbon and added organic substrates by soil microbial communities. The respiration of soil slurries was measured at low substrate concentrations (0.5 mg substrate per g soil) with and without added inorganic nitrogen over a short (< 7 h) incubation period in the lab. Soil samples collected from field plots that were manipulated to receive amendments of organic substrates and/or nitrogen were examined with the method. We found that the measured community respiratory response to added nitrogen in the microplate assay was significantly correlated with the analytical determinations of inorganic nitrogen in the field plots. Soils from field plots amended with non-nitrogen-containing substrates (i.e., glucose) exhibited increased respiration in the assay to nitrogen-containing substrates (i.e., amino acids). In contrast, soils from field plots amended with amino acids exhibited increased respiration of both sugars and amino acids. When no nitrogen is added during the laboratory assay, little growth occurs within the microplate wells during the incubation period based on quantitative PCR of bacterial and fungal ribosomal genes. When nitrogen is added, moderate growth (e.g., doubling) may be observed. Previous work has shown minimal effect of soil disruption during the performance of this assay and inclusion of fungal activities in the measured responses. This assay significantly advances the ability to examine in situ relations between carbon and nitrogen utilization in soils and generate ecologically-relevant community-level physiological profiles.

**EFFECT OF LONG-TERM FERTILIZATION ON SOIL NEMATODE COMMUNITIES UNDER GREENHOUSE CONDITION. Li, Q., W.J. Liang, Y.L. Lou, and J.N. Zhang.** Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang, 110016, China.

Vegetable production in greenhouses is characterized by intensive use of fertilizers and management, and relatively higher temperature and moisture content compared with the open-air systems. There is a paucity of studies that focus on the impact of fertilization on soil nematode communities under greenhouse conditions. Nematodes were identified and enumerated by trophic groups and functional guilds (bacterivores, fungivores, plant-parasites and omnivore-predators combination with their cp-scaling) in a long-term fertilization (10-year) vegetable greenhouse experiment in Northeast China. Treatments included inorganic nitrogen fertilizer or manure (M). Controls received no fertility amendments. Inorganic nitrogen was applied in either low (N1, 69 kg N ha<sup>-1</sup> per year), or high (N2, 138 kg N ha<sup>-1</sup> per year). Effects of inorganic and organic fertilizers were also tested in combination with potassium and phosphorus (N1PK, MN1, MN2, and MN1PK). Soil samples were collected in a tomato field at 0-10 and 10-20 cm depths in January (winter) and July (summer) of 2008. The most abundant trophic groups were bacterivores and fungivores followed by plant-parasites and omnivore-predators with progressively fewer nematodes. The effects of high doses of inorganic fertilizer were greatest in January ( $P < 0.05$ ), decreasing the numbers of total nematodes and different trophic groups. Bacterivores were least abundant with low levels of inorganic fertilizer with (January) or without (July) phosphorus and potassium. No omnivore-predators were observed when high doses of inorganic fertilizer were applied, regardless of season. Community indices were affected differently by applications of inorganic or organic fertilizer. For example, MI values were less with manure than control plots. Channel index values were greater in control and low doses of inorganic fertilizer than any dose of organic fertilizer. Based on the community index values, we conclude that soil environment in the M, MN1, MN2 and MN1PK treatments were subject to high degree of disturbance due to the manure fertilization. And the food web in the N1 and N2 treatments were degraded due to the stressed soil condition by the extremely low or high level of inorganic nitrogen fertilization. Canonical correspondence analysis (CCA) based on the absolute abundance of nematode functional guilds and environmental variables suggested that soil pH and electric conductivity were most relevant in explaining the patterns of nematode distribution. The first axis defined by soil pH explained 41.3% of the species-environment relationships. Soil nematode community analysis may provide a useful tool to assess the impact of soil environmental change on soil processes in vegetable production under greenhouse conditions.

**IMPACTS OF THE INVASIVE EUROPEAN FIRE ANT (*MYRMICA RUBRA*) ON COASTAL NEW ENGLAND SOILS. Lin, Mao T.<sup>1</sup>, R.K. Thiet<sup>1</sup>, and K.R. Cangialosi<sup>2</sup>.** <sup>1</sup>Dept. of Environmental Studies, Antioch New England Graduate School, 40 Avon Street, Keene, NH 03431, <sup>2</sup>Dept. of Biology, Keene State College, Keene, NH 03435.

The complex ecological impacts of fire ant invasions are still poorly understood. The European fire ant (*Myrmica rubra*) is an exotic species documented in several counties along the coast of Maine and other coastal New England states. Since its first

reported sighting in the United States in 1906, *M. rubra* has slowly expanded its range over the last century, with a sudden increase in population in the 1990s. Extensive literature suggests that ants can physically and chemically alter soils within and beyond the vicinity of their nests. They directly impact soils through bioturbation and by excreting wastes, transporting food (nutrients) into their nests, and concentrating into trash piles organic matter that is unusable to the colony. Ants may indirectly impact soils by influencing populations of other important soil organisms via habitat modification or predator/prey interactions. For example, *M. rubra* invasions can cause a displacement and restructuring of native ant communities and an increase in plant-parasitic insects. However, most field studies have been unable to establish a causal relationship between ants and altered soil properties because they cannot prove that ants do not simply choose particular soil types and soil properties in which to establish their nests. To establish a causal relationship between invasive ants and altered soil properties, we quantified the effects of *M. rubra* on coastal Maine soils, and compared their effects to those of native ants (*Formica* sp.), in a controlled laboratory experiment. Each of thirty cylindrical tubes (32 cm x 5.1 cm) were filled with 20 cm (~450 g) of sieved sandy loam from Bar Harbor, ME; 10 tubes contained *M. rubra*, 10 contained *Formica* sp., and 10 served as controls. Tubes were maintained at field moisture capacity, a vial of sugar water was added to each tube to provide food, and 1 g of shredded organic matter was added to each tube to replicate field conditions. Each week for six weeks, a 1 g soil sample was taken from each tube at 0-12 cm and >12 cm to test for total C and N. At the end of six weeks, each experimental tube was destructively sampled and soil bulk density, aggregation, and texture were evaluated at 0-5 cm, 5-12 cm, and >12 cm. Analyses are currently in progress, and results will be presented in this talk. This study will provide valuable new insight for managers and ecologists into the effects of the invasive European fire ant on coastal New England soils, and will add important information to our understanding of belowground invasion ecology.

**ECOSYSTEM CONSEQUENCES OF TOP-DOWN EXTINCTION IN A DETRITAL MICROECOSYSTEM. Lindo,<sup>1</sup> Zoë, A. Gonzalez<sup>1</sup>, P. Staddon<sup>2</sup>, F. Gilbert<sup>2</sup> and P. Crittenden<sup>2</sup>.** <sup>1</sup>Dept. of Biology, McGill University, Montreal, Canada QC H3A 1B1; <sup>2</sup>School of Biology, Nottingham University, NG7 2RD, United Kingdom.

Non-random extinction and cascading changes in community composition following habitat alteration (loss and fragmentation) are expected to impact ecosystem processes, yet few experiments have clearly demonstrated ecosystem impacts of altered habitat connectivity in naturally complex communities. We examined how extinction, driven by habitat loss, affected ecosystem functioning in a moss microcosm, consisting of a species rich decomposer food web spanning multiple trophic levels. We show that non-random extinction caused by habitat fragmentation, and subsequent community compensation, markedly affected carbon and nitrogen dynamics. Community-level changes were associated with top-down biodiversity loss via the extinction of large-bodied top predators and compensatory increases in lower trophic levels (prey). These changes in the food web caused a trophic cascade that affected the ecosystem-level processes of cumulative N and C dynamics. The functional effects of the trophic cascade are likely driven by grazing-stimulated fungal growth and fungal-driven decomposition, and immobilization of nutrients within prey biomass. The presence of corridors ameliorated the effects of fragmentation and habitat loss on both biodiversity loss and ecosystem dynamics. Our results reveal that knowledge of spatial processes will be essential for a full understanding of the link between biodiversity and ecosystem functioning in human transformed landscapes.

**BIOLOGICAL AND GENETIC CHARACTERISATION OF RESISTANCE TO ROOT LESION NEMATODE *PRATYLENCHUS* SPP. IN WHEAT. Linsell<sup>1,2,3</sup>, Katherine J., K. Davies<sup>2</sup>, I. Riley<sup>1,2</sup>, H. Wallwork<sup>1,3</sup>, and K. Oldach<sup>1,2,3</sup>.** <sup>1</sup>South Australian Research and Development Institute, <sup>2</sup>University of Adelaide, <sup>3</sup>Molecular Plant Breeding CRC, Waite Campus, Glen Osmond, SA 5064, Australia.

The root lesion nematodes (RLN) of the genus *Pratylenchus* feed and reproduce in the root cortex of many plants, including wheat. Migration through root tissue causes extensive root damage, thus in turn severe reductions in growth and yield. The majority of studies analysing biological resistance mechanisms have focussed on the sedentary endoparasitic nematodes such as Cereal Cyst Nematodes but very little is known about RLN resistance. This study has investigated a wheat population, which has shown very strong resistance to *Pratylenchus thornei*, made by a bi-parental cross between the synthetic-wheat derived line Sokoll and the Australian wheat cultivar Krichauff. Each stage of the nematode life cycle has been analysed to identify at which point(s) biological resistance is manifested. Soil and agar analyses have confirmed that there is no difference in penetration between resistant and susceptible lines. Attraction assays have shown that RLN are equally attracted to both resistant and susceptible lines in the soil. Thus, the resistance mechanism is expressed after RLN root entry. Several symptoms indicate reduced nematode reproduction in the resistant genotype. Juvenile development, as shown by timecourse soil analysis, is suppressed at early developmental stages (moulting from juvenile stage 2 to 3). In addition, suppression of egg development/hatching, decreased nematode mobility and migration has also been observed in the presence of resistant root exudates and soluble root compounds. Previous genetic studies have identified nine regions in the wheat genome containing RLN resistance loci (QTL). However, closely linked molecular markers to these QTL are required to implement RLN resistance in breeding programs. Here, two QTL associated with *P. thornei* resistance have been identified in the Sokoll/ Krichauff doubled haploid population. Using a variety of mapping techniques, markers closely linked to the QTL have been detected. Combining the information of the biological resistance mechanisms and the genetic information will allow the correlation of a biological role for each QTL.

**DISTRIBUTION AND DENSITIES OF PLANT-PARASITIC NEMATODES ON *ZEА MAYS* IN NORTHERN ILLINOIS.** Lopez-Nicora, H., J. Morrison, D. Feltes, and T. L Niblack. Department of Crop Sciences, University of Illinois, Urbana, IL.

The recent labeling and marketing of products intended for nematode management in corn (*Zea mays*) in Illinois prompted interest among extension educators in the occurrence, distribution, and population densities of putative corn-pathogenic nematodes. A pilot study was conducted during 2008 in 19 northern Illinois counties in order to test protocols that will be used in a future study to include 80 additional counties, excluding those which are predominantly urban. For the 2008 study, eight cooperators were each assigned randomly-generated GPS coordinates along a pre-determined route in two to four counties per cooperator. A total of 76 soil samples were collected from corn fields at or near the assigned coordinates from corn plants at the V3 to V6 growth stage. Samples comprised 10 to 20 soil cores (2.5-cm-diam) taken to a depth of 25 to 30 cm within the rows. A 100 cm<sup>3</sup> soil subsample was washed through a series of sieves including 20-, 60-, and 400-mesh (850, 250, and 38- $\mu$ m-apertures, respectively). Material collected on the 20 and 60 mesh sieves was placed on Baermann funnels for 48 hrs. Material collected on the 400-mesh sieve was processed by centrifugal flotation for extraction of vermiform nematodes. Data collected from each sample included numbers of nematodes in each of five trophic groups: microbivores, fungivores, plant parasites, omnivores, and predators. Plant parasites were identified to morphological group or to genus, and individuals were collected, fixed, and mounted to facilitate species identification. Overall, the nematode communities were composed of about 50% microbivores and 50% plant parasites; very few fungivores, omnivores, or predators were observed. The most frequently (97%) occurring group of nematodes was the "tylenchid," with delicate stylets, nonoverlapping glands, and acutely pointed tails. Genera and species of animals in this group were not determined, but they were counted as plant parasites rather than fungivores. The second most frequent (94%) group was the spiral nematode complex, consisting mostly of *Helicotylenchus* species. The most frequent (92%) genus of possibly corn-pathogenic nematodes was *Pratylenchus*, including at least four species. Other genera of potential corn pathogens observed were *Hoplolaimus* (36%), *Xiphinema* (18%), and *Paratylenchus* (11%). The stunt nematode group was found in 24% of the samples, and comprises at least three species in two genera. Juveniles of *Heterodera* were observed in 57% of the samples. Species identification will provide additional insight into the potential for any or all of these groups or genera to reduce corn growth or yield.

**EFFECTS OF IRRIGATION, THATCH, AND A WETTING AGENT ON 'CANDIDATUS PASTEURIA USGAE' ENDOSPORE PLACEMENT IN TURF.** Luc<sup>1</sup>, John E., W.T. Crow<sup>1</sup>, R. McSorley<sup>1</sup>, J.B. Sartain<sup>1</sup>, and R.M. Giblin-Davis<sup>3</sup>. <sup>1</sup>Entomology and Nematology Department, University of Florida, Gainesville, FL, 32611, <sup>2</sup>Soil and Water Science Department, University of Florida, Gainesville, FL, 32611, <sup>3</sup>Fort Lauderdale Research and Education Center, University of Florida, 3205 College Ave., Davie, FL 33314.

In the past, endospores of *Pasteuria spp.* have been incorporated into the soil profile using various sources of inoculum laden with endospores. However, these methods required disturbance of the soil profile. Unlike seasonal crops which are cultivated regularly allowing for introduction of endospores throughout the soil profile, turfgrass is a perennial crop which is relatively undisturbed. Application of endospores into the turfgrass soil profile could be hindered by dense turf growth, thatch, and black layers. However, once in the mineral soil, increased percolation and irrigation following treatment may cause endospores to move below the rootzone, reducing effectiveness. Greenhouse experiments were conducted to evaluate ten treatments including five watering levels: 0.6cm of water with a wetting agent (Lesco Wet) at 2.54 ml/m<sup>2</sup>, 0.6cm of water without a wetting agent, 2.5cm, 7.6 cm, 15.2 cm of water, and two thatch levels: with thatch (2.5-cm depth) or without thatch. Fifty lysimeters were used to simulate a soil profile typical of a golf course putting green. 'Tifdwarf' bermudagrass (*Cynodon dactylon* x *C. transvaalensis*) grown from aerial sprigs or plugs taken from a putting green were harvested and planted to simulate turf with no thatch or heavy thatch layer, respectively. Turf was allowed to establish a root system for 7 months. *Pasteuria usgae* endospores were applied as a drench at 200,000 endospores/cm<sup>3</sup> of soil to treat the top 10cm of the soil profile (202 cm<sup>3</sup>). Endospores remained undisturbed for 2 days, and then water treatments were applied once. One week after water treatments were applied the soil profiles were cut into sections to determine relative endospore density at four soil depths (0 to 2.5, 2.5 to 10, 10 to 20, and 20 to 30 cm) providing four samples per soil profile. Each sample was placed in a paper bag and allowed to air dry for 4 months. A bioassay was conducted to determine endospore attachment for each treatment at the respective soil depths. Application of 15.2 cm of irrigation reduced percent endospore attachment by as much as 32% and 40% at soil depths 0 to 2.5 and 2.5 to 10.2 cm respectively, and increased percent endospore attachment by as much as 71% and 819% at soil depths 10 to 20 and 20 to 30 cm, respectively compared to 0.6 cm of irrigation. Thatch and wetting agent treatments showed no effect on placement of endospores into the soil profile.

**SOIL NEMATODE COMMUNITIES AS INDICATORS OF THE INTER-DEPENDENCY OF ABOVEGROUND AND BELOWGROUND BIOTA IN SUB-ARCTIC TERRESTRIAL SYSTEMS: PRELIMINARY RESULTS.** Lumactud, Rhea and M. Tenuta. Department of Soil Science, University of Manitoba, Winnipeg, MB R3T 2N2.

The ubiquity of nematodes, their importance in soil nutrient recycling, and that they occupy most trophic levels in the soil food web, makes them useful indicators of soil ecological processes and an important determinant of food web function. To know whether plant communities have relationships with belowground biota, nematode communities were assessed from

different plant-habitat types in the subarctic coastal environments at Churchill, Manitoba, Canada. Five sites were chosen from the coast of Hudson Bay to inland locations; Coastal Sand Dunes with mats of *Elymus arenarius* and *Honckenya peploides*, Tundra Heath, Polygonized-peat Plateau, Hummocky-Eutrophic Fen and Spruce-lichen Forest. A total of 38 genera covering 27 families were observed. Multivariate analysis revealed four distinct groupings of the nematode communities: (1) Coastal Sand Dune- *E. arenarius*; (2) Coastal Sand Dune- *H. peploides*; (3) Tundra Heath, Polygonized-peat Plateau and Hummocky-eutrophic Fen; (4) Spruce-lichen Forest. We found distinct differences in taxa and trophic structure between the contiguous mats of *E. arenarius* and *H. peploides* at the Coastal Sand Dune site. *E. arenarius* showed dominance of plant-feeders (65%), whereas, *H. peploides* exhibited dominance of bacterial-feeders (80%) and its plant-feeder composition was only 5%. Communities of *E. arenarius* were dominated by the migratory plant-feeding nematode, *Pratylenchus*, while *H. peploides* by the bacterial-feeding nematode, *Panagrolaimus*. The diversity of plant species reflected belowground diversity as sites with diverse plant communities- Tundra Heath, Polygonized-peat Plateau, Hummocky-eutrophic Fen and Spruce-lichen Forest had higher functional diversity of nematode communities. More specifically, predators were absent in both Coastal Sand Dune mats dominated by *E. arenarius* and *H. peploides*. The Spruce-lichen Forest site had significantly higher omnivores ( $p < 0.05$ ) indicating a more ecologically complex and stable ecosystem. Our results provide evidence that plant communities influence nematode communities, which consequently mirror changes in the soil food web structure, thus showing great inter-dependency between aboveground and belowground biota.

**SPATIAL VARIATION OF NEMATODE COMMUNITIES IN A RELATIVELY HOMOGENEOUSLY FIELD AT THE SUB-ARCTIC COASTAL ENVIRONMENT AT CHURCHILL, MANITOBA, CANADA: A PRELIMINARY ANALYSIS.** Lumactud, Rhea and M. Tenuta. Department of Soil Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2.

A heathland plant community of site that was level and uniform in plant species composition was chosen to investigate the spatial distribution of nematode communities in the sub-arctic coastal environment at Churchill, Manitoba. Nematodes are not only the most abundant soil microfauna but they also have a key role in soil food web and nutrient recycling among other important attributes, as such, knowledge of their spatial pattern will give us more understanding on the functioning of soil biota in soil ecosystem processes. Soil samples were taken using a 10-cm diameter core to a 15 cm depth from three, 300-m parallel transects, for a total of 93 geospatially controlled sampling points. Soil samples were partitioned for nematode and soil physical-chemical analyses. Nematode samples were identified to genus level. Preliminary results showed a total of 38 genera from 24 families dominated by *Filenchus*, *Tylencholaimus*, *Prodesmodora* and *Rhabdolaimus* taxa. Variability in abundance of each taxon was of normal distribution with coefficient of variations ranging from 25-80%. Correlation between some taxa was observed. *Filenchus* was negatively associated with bacterial/unicellular-feeding nematodes *Prodesmodora*, *Prismatolaimus* and *Rhabdolaimus*. *Malenchus* coexisted with *Teratocephalus*, while it was negatively associated with *Tylencholaimus*. *Plectus* was negatively associated with *Acrobeles* and *Prodesmodora* though positively with *Eumonhystra*. Possible reasons of negative and positive associations between taxa may be specialized niche selection, competition, specific plant species' effects through differences in litter quality and influence of soil environmental characteristics. Further analyses may clarify relationships of these taxa. Data analysis is ongoing with spatial dependency and autocorrelation of nematode taxa using geostatistical techniques being pursued.

**DEAD ROOTS ARE A HABITAT OF *PRATYLENCHUS PENETRANS*.** MacGuidwin, A. E. Dept. of Plant Pathology, University of Wisconsin-Madison, Madison, WI 53706.

*Pratylenchus penetrans* is a versatile root parasite that moves in and out of roots at all points in its life cycle. We studied the role of dead roots in sheltering nematodes after plant senescence and during the winter months in agricultural fields in Wisconsin. For all studies, nematodes were recovered from 100 cm<sup>3</sup> soil using a modified sugar flotation-centrifugation technique. Roots retained on a 0.25-mm sieve during the soil assay were incubated on Baermann funnels for nematodes. For field studies, census data were collected from soil sampled at five locations within fields at the time potatoes were planted. There were no significant differences among 22 fields for the percentage of the nematodes recovered from the root fragments using the criteria of soil fumigation (+/-) or short (< 6 days) versus long-season (> 100 days) crop, with an overall mean of 43% of nematodes recovered from the root portion of the samples. For eight different fields sampled using the same methods in a different year, the fraction of the population recovered from roots was 69%. Samples collected from a wide range of studies confirmed the importance assaying dead root fragments to estimate population densities of *P. penetrans*. Observations from the field led us to test the hypothesis that plant residues influenced the location of nematodes between soil and root habitats. Corn roots recovered from the field in October were placed in mesh bags and embedded in microcosms filled with 100 cm<sup>3</sup> pasteurized soil with or without fragments of dried sorghum leaves (0.5 gm). The microcosms were held at room temperature in the dark and destructively sampled for three weeks. The experiment was repeated three times. Nematodes recovered from soil were considered to have egressed from roots in the mesh bags since no nematodes were recovered from soil-only microcosms. Nematodes remaining in the roots were recovered by incubating the mesh bags in Baermann Funnels for 5 days, and then crushing roots to release any nematodes remaining. All data were expressed as percentages to account for

variation in the number of nematodes per root. Egress was significantly greater from the roots buried in soil with plant residues, with the rate of egress influenced by experiment and time. In both field and laboratory studies, nematodes egressed from dead roots were mobile and active, indicating that the shelter provided by this habitat is important for the persistence of *P. penetrans*.

**SOIL ORGANIC MATTER RESPONSES TO CHRONIC NITROGEN ADDITIONS IN A TEMPERATE FOREST.** **Maclean<sup>1</sup>, Rich, S.D. Frey<sup>1</sup>, S. Ollinger<sup>2</sup>, K. Nadelhoffer<sup>3</sup>, M. Day<sup>2</sup>, and J. LeMoine<sup>3</sup>,** <sup>1</sup>Dept. of Natural Resources & the Environment, University of New Hampshire, <sup>2</sup>Complex Systems Research Center, University of New Hampshire, <sup>3</sup>Dept. of Ecology and Evolutionary Behavior, University of Michigan.

This past year marked the 20th anniversary of the Chronic Nitrogen Addition Experiment at Harvard Forest. Started in 1988, the Chronic N experiment is an investigation into the effects of increasing anthropogenic atmospheric N deposition on forests in the eastern United States. Located in an old red pine plantation and a mixed hardwood forest the treated plots have received 50 and 150 kg N·ha<sup>-1</sup>·yr<sup>-1</sup>, as NH<sub>4</sub>NO<sub>3</sub>, in six equal monthly applications during the growing season each year since the start of the experiment. Additionally, the control and low N treatments were given a single pulse label of <sup>15</sup>NO<sub>3</sub> and <sup>15</sup>NH<sub>4</sub> in 1991 and 1992. Regular measurements have been made over the past 20 years to assess woody biomass production and mortality, foliar chemistry, litter fall, and soil N dynamics. Less frequent measurements of soil C pools, soil respiration, fine root dynamics, and microbial biomass and community structure have been made. For the 20th anniversary an intensive sampling campaign was carried out in fall 2008 with a focus on evaluating how the long-term N additions have impacted ecosystem C storage and N dynamics. The primary objective of our 2008 sampling effort was to assess the amount of C and N stored in wood, foliage, litter, roots, and soil (to a depth of ~50 cm). We also wanted to examine the fate of N by comparing patterns of <sup>15</sup>N recovery to those observed previously. An additional objective was to further examine how chronic N additions impact microbial biomass, activity and community structure. Results to date indicate that chronic N additions over the past 20 years have increased forest floor mass and soil organic matter across the soil profile; decreased microbial biomass, especially the fungal component; and altered microbial community composition (i.e., significantly lower fungal:bacterial biomass ratios in the N amended plots).

**VARIATION IN EARTHWORM DENSITY ACROSS URBANIZED LAND COVERS AND EFFECTS ON SOIL CHEMISTRY.** **Mancarella<sup>1,2</sup>, Taryn, L. Byrne<sup>1</sup>, and S. O'Shea<sup>2</sup>.** <sup>1</sup>Department of Biology and <sup>2</sup>Department of Chemistry, Roger Williams University, One Old Ferry Road, Bristol, RI 02809.

The presence of earthworms in terrestrial ecosystems affects soil physicochemical characteristics and rates of biogeochemical cycles, specifically those of carbon and nitrogen. The spatial patterns of earthworm abundance are expected to therefore relate to spatial patterns of ecosystem structure and function. In addition, human activities such as urban landscape management may strongly affect earthworm distributions and spatial soil patterns and their relationships. Greater understanding of relationships among urban land cover management, earthworm populations and soil properties is needed to understand ecological functions and services in urbanized ecosystems. In this study, we examined the distribution of earthworms and patterns of soil variables across an urbanized landscape, specifically the campus of Roger Williams University in Bristol, RI. In the summer of 2008, earthworms were sampled from four land cover types (lawns, wood mulched areas, forest remnants, low-maintenance fields) by hand-sorting from 25x25x25 cm soil samples. Earthworm densities were highly variable within and among the land cover types (range in mean density of 0-45 earthworms 625cm<sup>-3</sup>) suggesting that local (and perhaps historical) environmental factors may affect earthworm abundances more than land cover per se. In several locations, very high earthworm densities resulted in ~5cm deep accumulation of cast material ("hotspots"). These locations were used as natural experiments to examine the effects of earthworm casting on soil properties as compared to those of surrounding bulk soil without earthworms. The average carbon-to-nitrogen ratio of casts was 13.33 as compared to 12.93 for that of the bulk soil. The bulk soil was more acidic (pH of 4.83) than cast samples (5.86). Colorimetric analyses indicate that nitrate (cast: 33.42 ppm, bulk soil: 15.25 ppm) and nitrite (cast: 18.67 ppm, bulk soil: 15.42 ppm) were higher in cast than bulk soil. These differences between cast and bulk soil indicate that earthworm activity and density influence spatial patterns of biogeochemical cycling and soil properties. The differences in earthworm density across diverse urban land cover types may have implications for the levels of ecosystem services and disservices created at different locations. Future studies on our University's campus will be conducted to provide further insight into the causes and consequences of highly variable earthworm distributions and densities within urbanized landscapes. In particular, examining the set of factors that may lead to localized "hotspots" of earthworm populations may provide valuable insights into how urban land cover can be managed to favorably affect earthworms and associated ecosystem services.

**EFFECTS OF A STRIP-TILL COVER CROPPING SYSTEM ON NEMATODE COMMUNITIES.** **Marahatta, Sharadchandra P., K.-H. Wang, and B.S. Sipes.** Department of Plant and Environmental Protection Sciences, University of Hawaii, 3050 Maile Way, Honolulu, HI 96822.

Strip-till cover cropping is a combination of conventional cover cropping and conservation tillage. Cash crops are grown in tilled cover crop strips, and non-tilled cover crop strips serve as 'living mulch'. Conventional cover cropping allows cover

crops with allelopathic compounds against plant-parasitic nematodes to be incorporated into soil so as to suppress nematode pests while enhancing beneficial nematodes involved in nutrient cycling due to the organic input into the soil. Conservation tillage practices reduce soil erosion and nutrient leaching while increasing soil moisture and improving soil structure. Two field trials were conducted between 2007 and 2009 in a commercial farm at Kunia, Oahu, Hawaii to examine the effect of strip-till cover cropping on nematode communities. *Crotalaria juncia* (SH), and *Tagetes patula* (MG), were grown, for 3 months and alternate rows of cover crops were strip-tilled. Seedlings of bitter melon, *Momordica charantia*, were transplanted into the tilled strips. A bare ground (BG) treatment was included as the control. Nematode faunal analysis that included enrichment index (EI), structure index (SI), channel index (CI), and basal index (BI) was performed on soil food web conditions. At termination of cover crops in both trials, strip-tilling of SH resulted in greater ( $P < 0.05$ ) population densities of bacterivorous and fungivorous nematodes. MG enhanced ( $P < 0.05$ ) bacterivorous and fungivorous nematode population densities at termination of cover crop only in Trial I. Population densities of omnivorous and predatory nematodes were close to undetectable and were not affected by cover cropping. The most prominent plant-parasitic nematode in this site was *Meloidogyne incognita*. SH and MG suppressed ( $P < 0.05$ ) *M. incognita* at bitter melon harvest in Trial I and at termination of cover crops in Trial II. At bitter melon harvest of both trials, effects of strip-tilling of cover crops did not affect abundance of all nematode trophic groups. On the other hand, nematode community indices were more sensitive in detecting changes in soil food web conditions. Higher EI in SH as compared to BG ( $P < 0.05$ ) at termination of cover crop and at crop harvest in both trials indicated that SH consistently enriched soil nutrients even after one cash crop cycle. Lower CI in SH as compared to BG at bitter melon harvest in Trial II indicated a domination of bacterial decomposition. Cover cropping did not affect ( $P > 0.05$ ) nematode community structure as indicated by SI. No difference in BI among treatments throughout both trials except for higher BI in MG plots at cover crop termination in Trial I indicated a uniform resource stress conditions of the field site. Strip-till of SH was able to increase EI up to cash crop harvest. Longer term strip-till cover cropping might be needed to improve SI in both SH and MG plots.

**DISCOVERY AND DEVELOPMENT OF MICROBIAL AND PLANT NATURAL PRODUCTS FOR CONTROL OF PLANT PARASITIC NEMATODES. Marrone, P.G. and M.E. Koivunen.** Marrone Organic Innovations, Inc. 2121 Second Street, B-107, Davis, CA 95618.

Natural product compounds in plant extracts have known activities against plant pathogens, insects, weeds and nematodes. In addition, microbes and microbial metabolites have been successfully used for natural product pesticides. There are fewer nematicidal compounds discovered than insecticidal, herbicidal and fungicidal compounds and a review of known compounds will be presented. Marrone Organic Innovations (MOI) is currently developing biopesticides from both plant and microbial sources. On the microbial side, MOI screens for active compounds produced by bacteria, actinomycetes and fungi in vivo against plant parasitic nematodes. An overview of the process for discovery, development and commercialization of a bionematicide will be discussed.

**USING NMR TO UNDERSTAND THE ECOLOGICAL ROLES OF CHARCOAL. Masiello<sup>1</sup>, Caroline A. and W. C. Hockaday<sup>1</sup>.** <sup>1</sup>Department of Earth Science, Rice University, 6100 Main St, MS 126, Houston, TX 77005.

Nuclear magnetic resonance (NMR) has been used for the past 25 years to understand the basics of soil organic chemistry, and a recent methods intercomparison study has made it clear that NMR is one of the best tools available to quantify the amount of charcoal in soils. But NMR can do more than simply quantitatively determine the amount of charcoal in a soil: it can also be used to understand the chemical structure of charcoal. Charcoal chemistry exerts a fundamental control on its environmental behavior: charcoals with high degrees of oxidation act as nutrient sponges, while charcoals with less oxidation do not interact with nutrients, at least initially. In this talk I will discuss the use of NMR to understand the roles of charcoal in the environment. I will also describe the natural variation in charcoal chemistry observed in a 2009 fire in New Jersey.

**RESIDUAL EFFECTS OF BENZYL ISOTHIOCYANATE ON HATCHING IN THE ROOT-KNOT NEMATODE, MELOIDOGYNE INCOGNITA. Masler<sup>1</sup>, Edward P., I. A. Zasada<sup>2</sup>, S. Sardanelli<sup>3</sup>, S. T. Rogers<sup>1</sup>, and J. M. Halbrendt<sup>4</sup>.** <sup>1</sup>USDA-ARS Nematology Laboratory, Beltsville MD 20705, <sup>2</sup>USDA-ARS Horticultural Crops Research Laboratory, Corvallis OR 97330, <sup>3</sup>Plant Nematology Laboratory, University of Maryland, College Park MD 20742, <sup>4</sup>Pennsylvania State University, Biglerville PA 17307.

Brassicaceous plants, when used as materials for amending soil to control plant-parasitic nematodes, release nematotoxic isothiocyanates (ITCs) upon tissue breakdown. While numerous studies have addressed the levels of ITCs, and consequent effects upon nematode survival, in soil environments, our research addressed precisely what specific nematode responses are affected by ITCs and what minimum ITC levels are required to produce these effects. We exposed *Meloidogyne incognita* infective juveniles (J2) to various doses of benzyl isothiocyanate (BITC) *in vitro* and observed both J2 behavior and subsequent infectivity on host plants (soybean, *Glycine max*; pepper, *Capsicum annuum*). Behavior was affected qualitatively with disruption of the typical J2 sinusoidal movement, and the frequency of overall movement was reduced significantly ( $P < 0.05$ ),

with as little as 1 hr exposure to 0.01mM BITC. Effects of BITC on *M. incognita* infectivity (95-98% reduction) and subsequent egg production (75-98% reduction) were also significant ( $P < 0.05$ ). Hatching from eggs produced on either soybean or pepper by *M. incognita* that had been exposed to BITC as J2 was also suppressed (75% reduction,  $P < 0.05$ ). This was unexpected, since neither the developing juveniles nor the eggs had ever been directly exposed to BITC. Possible explanations include the potential for carryover of trace levels of BITC from treated juveniles to eggs, or the possibility that the selective effect of BITC treatment exposed a sub-population of *M. incognita* relatively resistant to BITC but with a developmental rate lower than the overall population. These and other possibilities will be discussed.

**INTERACTION OF BRASSICACEOUS SEED MEAL AND ROOTSTOCK ON RECOVERY OF *PRATYLENCHUS PENETRANS* FROM ROOTS OF APPLE GROWN IN REPLANT ORCHARD SOILS. Mazzola, Mark<sup>1</sup>, Brown, J.<sup>2</sup> and Fazio, G.<sup>3</sup>** <sup>1</sup>USDA-ARS, Wenatchee, WA; <sup>2</sup>University of Idaho, Moscow, ID; <sup>3</sup>USDA-ARS, Geneva, NY.

Lesion nematode is a significant component of the biological complex that incites replant disease of apple in Washington state. This program has sought to develop non-fumigant methods for control of the nematode and fungal components of the parasite/pathogen consortium that incites replant disease, and has included the evaluation of brassicaceous seed meal amendments in concert with rootstock tolerance. In initial field trials, *Brassica napus* seed meal (SM) provided suppression of *Pratylenchus penetrans* populations recovered from Gala/M26 apple, and suppression was equivalent to that attained with Telone-C17 pre-plant soil fumigation. However, suppression of *P. penetrans* in response to *B. napus* SM was transient and nematode numbers recovered by the end of the second growing season. In controlled environment trials *Brassica juncea* SM was superior to *B. napus* SM or *Sinapis alba* SM in suppressing lesion nematode populations. Apple rootstocks from the Geneva series consistently supported lower populations of *P. penetrans* than did Malling or Malling-Merton rootstocks. Significant rootstock  $\times$  seed meal interaction was detected. When utilized with rootstocks such as G11 or G30, which inherently supported lower lesion nematode numbers, all seed meals significantly suppressed *P. penetrans* root populations. In contrast, although *B. juncea* SM provided effective nematode suppression irrespective of rootstock, in general, *B. napus* and *S. alba* seed meals were less effective or ineffective in suppressing *P. penetrans* root populations when used in concert with a highly susceptible rootstock such as M26 or MM111. This response is likely a function of multiple factors including seed meal mode of action in nematode suppression and fecundity of *P. penetrans* on the individual rootstocks. *B. juncea* SM induced nematode suppression functions in part through the nematicidal activity of allyl isothiocyanate, which is generated in response to hydrolysis of 2-propenylglucosinolate. In contrast, ITCs produced by soil incorporation of *B. napus* SM and *S. alba* SM have lower or lack nematicidal activity, and nematode suppression realized in response to these and other high N containing seed meals, such as soybean meal, likely functions predominantly through the liberation of ammonia. Similarly, significant rootstock effects were observed in the capacity of these seed meals to suppress root infection by and additional component of the pathogen complex inciting replant disease, the oomycete *Pythium* spp. resident to orchard soils. These findings demonstrate that utilization of brassicaceous seed meal amendments for replant disease suppression must employ an appropriate rootstock in order to achieve optimal disease control.

**MOLECULAR DIALOGUES AND DEFENSE MECHANISMS IN BACTERIA-PROTOZOA INTERACTIONS. Mazzola, Mark<sup>1</sup>, I. de Bruijn<sup>2</sup> and J. M. Raaijmakers<sup>2</sup>.** <sup>1</sup>USDA-ARS, Washington State University, Wenatchee, WA 98801, USA; <sup>2</sup>Laboratory of Phytopathology, Wageningen University, Wageningen, The Netherlands.

The composition and activity of soil microbiota is influenced by a myriad of biotic and abiotic factors resident to the ecosystem of interest. The grazing activity of bacterivores is an instrumental process contributing to the cycling of nitrogen in soil systems, but also has a significant impact in shaping bacterial community structure. Preferential feeding by protozoan predators significantly impacts the dynamics, diversification and evolution of bacterial communities. To evade protozoan predation, bacteria employ various defense mechanisms including pre-ingestional strategies such as altered morphology and post-digestional strategies such as the release of bioactive metabolites. Soil-dwelling *Pseudomonas fluorescens* strains SS101 and SBW25 produce the cyclic lipopeptide surfactants (CLPs) massetolide and viscosin, respectively. The antibiotic activity of CLPs is largely attributed to the disruptive effects on cell membranes, leading to lysis of various microbial life stages including zoospores of oomycete plant pathogens and trypomastigotes of the human protozoan pathogen *Trypanosoma cruzi*. Here we explored the function of CLPs as a highly effective defense mechanism of soil-dwelling *Pseudomonas fluorescens* against predation by the amoeba *Naegleria americana* and determined whether bacterial perception of predation regulates the expression of CLP biosynthesis genes. CLP production was shown to protect these bacteria from predation as, relative to the corresponding CLP-deficient mutants, strains SS101 and SBW25 exhibited resistance to grazing by the protozoa *N. americana* in vitro and superior persistence in soil in the presence of this bacterial predator. CLP-producing strains had a direct deleterious impact on survival of *N. americana* in the rhizosphere, however, protozoan sensitivity differed in a CLP-specific manner. Exposure of SS101 or SBW25 to *N. americana* in vitro resulted in the up-regulation of CLP biosynthesis genes in both strains. Enhanced gene expression did not require physical contact between these two organisms and functions through a pathway that operates in a quorum-sensing independent manner. These findings highlight the functional versatility

of these natural microbial detergents and document the existence of a previously unknown sensing-signaling mechanism in the interactions between soil bacteria and protozoan predators.

DEVELOPING GREEN TECHNOLOGY FOR NEMATODE CONTROL. **McCarter, James P.** Divergence, Inc. 893 North Warson Road, St. Louis MO 63141.

Improved nematode control is a key part of a movement toward environmentally sustainable agriculture. Global trends will double demand for crops by 2050. Meeting this demand without further conversion of natural ecosystems to agriculture will require yield improvements far outstripping historical trends. Climate change is expected to alter the geographical distribution of plant diseases and have an additional negative impact on crop yields. Nematode control has been an underappreciated opportunity for yield gains in many crops. Nematicides such as organophosphates (OPs) and carbamates are non-specific neurotoxins with poor environmental and worker-safety profiles and many have been restricted in use or withdrawn. The fumigant methyl bromide has been largely phased out because of its role in ozone depletion. Nematicides with favorable efficacy, cost, and a greatly improved toxicology profile could replace neurotoxic molecules and further expand nematicide usage into markets where current nematicides are unregistered, restricted, or where unfavorable toxicology makes their use impractical. Divergence Inc. ([www.divergence.com](http://www.divergence.com)) is a biotechnology company developing both crops with nematode resistance and a safe and effective nematicide with a novel mode-of-action. Divergence is currently conducting field trials with its lead nematocidal chemistry and has demonstrated significant nematode control and yield gains at rates comparable to OPs. While providing broad-spectrum nematode control, Divergence's chemistry differs greatly from OPs in toxicology profile with a safety improvement of several orders of magnitude for acute mammalian exposure. This presentation will review the Company's progress in characterizing this chemistry. By contributing to improved yields of both temperate and tropical crops, new green technology for control of plant parasitic nematodes has a major role to play worldwide for both food security and environmental protection in the coming decades.

EVALUATION OF MOVENTO™ (SPIROTETRAMAT) FOR EFFICACY AGAINST NEMATODES INFESTING PERENNIAL CROPS. **McKenry, Michael, S. Kaku and T. Buzo.** Nematology Department, UC Riverside, Riverside, CA 92521.

MOVENTO™ (spirotetramat) is a novel active ingredient from the new chemical class of tetramic acids. When applied to foliage, this highly systemic insecticide is converted into an enol form and translocated in an acropetal and basipetal manner within the plant, resulting in effective pest control on roots and shoots. Three years of field evaluations have shown up to a 70% reduction in population levels of *Xiphinema americanum* collected from *Vitis spp* using sieve/mist extraction procedures 18 days after treatment. Soil extractions of *Xiphinema* index involved a sieve/cheesecloth procedure with impact detectable at 18 days but population declines undetectable until 36 days after treatment. Soil extractions for *Criconeoides xenoplax* involved sieve/centrifugation methodology, a procedure that provided no indication of reduced population levels until 54 days after treatment. It is apparent that nematode extraction procedures that necessitate nematode motility are the quickest to show nematicidal impact associated with spirotetramat. Work conducted to date has shown varying degrees of impact with spirotetramat against all plant parasitic nematode species associated with roots of *Citrus spp.*, *Vitis spp.* and *Juglans spp.* and to a lesser extent, saprophytic nematodes. Population reductions of all plant parasitic nematode species have been reduced by 50% for up to three months, provided that irrigation was delayed for two weeks following treatment. Late fall treatments to *Juglans spp.* reduced population levels of *Pratylenchus vulnus* by 45% for 4 months, whereas populations of *Tylenchulus semipenetrans* infecting *Vitis spp* were reduced for only 6 weeks. Spring treatments involving *Meloidogyne spp.*, as well as those listed above, have provided 50% population reductions for 3 months. Infection percentages of *T. semipenetrans* by an un-described *Pasteuria* species were not impacted after three years of spirotetramat applications. First-year yield improvements of 10% from treated vines were common but seldom significant. One data set involving a 2-year test provided significantly improved yield as a result of treatment. Phloem transport of molecules having relatively subtle effects on nematodes will require a greater understanding of application timing relative to nematode development, as well as environmental and prevailing field conditions. Currently, spring/fall treatment timings are associated with avoidance of post-treatment irrigations rather than toward date of root flush. This strategy will change depending on the crop and method of irrigation. Two well-timed treatments per year provide a starting point toward better understanding of the pest management complexities when multiple target pests are involved.

PLANT-PARASITIC NEMATODES ASSOCIATED WITH ASSOCIATED WITH PLANTS (*MISCANTHUS SPP.* AND *PANICUM VIRGATUM*) USED FOR BIOFUELS. **Mekete, Tesfamariam<sup>1</sup> and Terry Niblack<sup>2</sup>.** <sup>1</sup>Energy Bioscience institute, University of Illinois, 1206 W Gregory Dr, 61801, Urbana, USA, <sup>2</sup>Department of Crop Sciences, University of Illinois, 1102 S Goodwin Ave, Urbana, IL 61801.

The distribution, frequency, and population levels of plant-parasitic nematodes were surveyed from 14 different Miscanthus and switchgrass field sites throughout Illinois, Iowa, and South Dakota. Nematodes were extracted and identified based on morphology and molecular methods. The predominant genera of plant-parasitic nematodes recovered were *Pratylenchus*,

*Xiphinema*, *Helicotylenchus*, *Longidorus*, *Heterodera*, *Hoplolaimus*, *Tylenchorynchus*, *Criconemella*, *Hemicriconemoides* and *Pratylenchus*. All of these genera contain one or more species of plant pathogenic nematodes capable of causing significant biomass reductions on monocotyledonous hosts. Four species of *Pratylenchus* (*P. penetrans*, *P. hexincisus*, *P. scribneri*, *P. brachyurus*), two of *Xiphinema* (*X. rivesi* and *X. americanum sensu stricto*), one of *Longidorus* (*L. breviannulatus*), one of *Hoplolaimus* (*H. galeatus*), *Heterodera glycines* and two unidentified populations of *Heterodera* were found. This survey indicates that *Pratylenchus*, *Xiphinema*, *Helicotylenchus*, and *Hoplolaimus* are wide-spread and have a high Prominence value. Concomitant infestations of *Pratylenchus*, *Xiphinema*, and *Hoplolaimus* were observed in multiple sampling sites. Population levels were also recorded above the established economic thresholds for corn in most of the concomitantly infested fields.

**CROSS-DISCIPLINARY EFFICIENCY ASSESSMENT OF SOIL AMENDMENTS. Melakeberhan, Haddish**, Agricultural Nematology Laboratory, College of Agriculture and Natural Resources, Michigan State University, East Lansing, MI 48824 USA.

Maintaining soil's biological, physiochemical, nutritional, and structural health is necessary to formulate the foundation for food security and global ecosystem sustainability. However, soil degradations in natural, managed, and disturbed ecosystems present mitigation and/or adaptation challenges and will require integrated approaches to solve. Nematodes, the most abundant metazoan, can be guiding indicators for identifying soil biological conditions and nutrient cycling processes in rehabilitating soil degradations and maintaining healthy ecosystems. While there is a substantial body of interdisciplinary science on understanding function and structure of soil ecosystems, key gaps must be bridged to exploit the best traits of nematodes to monitor management of natural, managed and disturbed ecosystems. These include assessing integrated agrobiological, ecological, economical, and environmental efficiency of soil manipulation practices in time and space across ecosystems. Against this background and focusing on nematode community structure's (NCS) bioindicator and nutrient cycling traits, this presentation discusses the application of a fertilizer use efficiency (FUE) model for assessing agronomic, economic, ecological, environmental, and nematode (pest) management efficiency of soil amendments (organic or synthetic). Defined as increase in host productivity and/or decrease in plant-parasitic nematode population density in response to a given fertilizer treatment, the FUE model separates nutrient deficiency and toxicity from nematode parasitism as well as suitability of treatments designed to achieve desired biological and physio-chemical soil health conditions. By recognizing variable responses, the FUE model allows the user to make an efficiency analysis necessary for integrated management decisions such as identifying and monitoring changes in soil conditions through integrated analysis of NCS, soil parameters (eg. pH, nutrients, %OM), and plant response to treatments. Thus, the FUE model creates the proof-of-concepts needed to bridge disciplinary and cross-disciplinary gaps, which, in turn, will lead to developing integrated soil biological adjustment markers.

**PATHOGENICITY OF MELOIDOGYNE JAVANICA RACE 3 TO PEANUT AND SOME OTHER CROPS COMPARED TO M. ARENARIA RACE 1 AND M. JAVANICA RACE 1. Mendes, Maria de Lourdes, J. I. Orajay, and D. W. Dickson.** Entomology and Nematology Department, University of Florida, Gainesville, FL 32611.

*Meloidogyne javanica* race 3 is a newly discovered root-knot nematode pathogen of peanut in Florida. Our objective was to compare its pathogenicity with that of *Meloidogyne arenaria* race 1 and *M. javanica* race 1. Each nematode was tested on six peanut cultivars and eight other horticultural and agronomic crops. Each host was replicated six times, and inoculated with 10,000 second-stage juveniles and eggs of each root-knot nematode. The test plants were maintained in the greenhouse for 82 days, after which nematode galling and reproduction were assessed along with host growth parameters, namely plant heights, fresh and dry shoot weights, and fresh root weights. Root-knot nematode susceptible peanut cvs. Florunner, Georgia Green, and C99R were hosts for both *M. arenaria* race 1 and *M. javanica* race 3, but not for *M. javanica* race 1. Both *M. arenaria* race 1 and *M. javanica* race 3 produced numerous galls and egg masses on all three susceptible peanut cultivars. Only *M. javanica* race 3 produced a large number of galls and egg masses on the root-knot nematode resistant cv. Coan. There was no galling observed on the root-knot nematode resistant cvs. Nema Tam or Tiftguard. However, *M. arenaria* race 1 and *M. javanica* race 3 produced an average of 15.6 and 1.7 egg masses on Nema Tam, and 8.7 and 9.0 respectively on Tiftguard. The reproductive factor on the three resistant peanut cultivars was low (< 1.00), both for *M. arenaria* and *M. javanica* race 3. Pepper and cotton were nonhosts for all three nematodes, whereas tobacco, watermelon, eggplant, and tomato were good hosts. Both field corn (cv. Yellow Dent) and sweet corn (cv. Silver Queen) were moderately good hosts for all three nematodes. There were few differences among plant growth parameters measured for the three nematode species and the crop hosts tested.

**DIACETYLPHELOROGLUCINOL (DAPG); IS IT ACTIVE AGAINST NEMATODES? Meyer, Susan L.F.<sup>1</sup>, J.M. Halbrendt<sup>2</sup>, L.K. Carta<sup>1</sup>, A.M. Skantar<sup>1</sup>, T. Liu<sup>3</sup>, H.M.E. Abdelnabby<sup>4</sup>, and B.T. Vinyard<sup>5</sup>.** <sup>1</sup>USDA ARS Nematology Laboratory, Henry A. Wallace Beltsville Agricultural Research Center (BARC)-West, Beltsville, MD 20705, USA, <sup>2</sup>Pennsylvania State University Fruit Research and Extension Center, Biglerville 17307, USA, <sup>3</sup>Institute of Plant and Environmental Protection, Beijing Academy of Agricultural and Forestry Science, Beijing, 100097, China, <sup>4</sup>Department of

Plant Protection, Faculty of Agriculture, Benha University, Qaliubia, Egypt, <sup>5</sup>USDA ARS Biometrical Consulting Service, BARC-West, Beltsville, MD 20705, USA.

The antibiotic compound diacetylphloroglucinol (DAPG) is produced by various isolates of the beneficial bacterium *Pseudomonas fluorescens*. DAPG can be toxic to plants, bacteria, fungi and viruses, and DAPG production has been associated with activity against some plant pathogens. This study was undertaken to investigate toxicity of DAPG to certain soil-dwelling nematodes. The study included the following free-living and plant-parasitic nematodes: *Caenorhabditis elegans*, *Heterodera glycines*, *Meloidogyne incognita*, *Pratylenchus scribneri*, *Pristionchus pacificus*, *Rhabditis rainai* and *Xiphinema americanum*. Eggs, juveniles and/or adults of these nematodes were exposed to synthetic DAPG: DAPG concentrations ranged from 1 µg/ml to 75 or 100 µg/ml. Percentages of egg hatch and of mobile vermiform stages were recorded. Egg hatch of *M. incognita* was inhibited by DAPG; mobility of second-stage juveniles was not affected. Conversely, egg hatch of *C. elegans* was stimulated by DAPG, at least during early hours of exposure. However, as with *M. incognita*, juvenile (J1) mobility was not altered, nor was mobility of adults. DAPG was toxic to adults of *X. americanum*. The other four nematode species did not respond to DAPG (based on the measured parameters). The data indicate that DAPG production by soil-dwelling bacteria would not directly result in suppression of population numbers of every plant-pathogenic or bacterial-feeding nematode species. Augmentation of DAPG-producing *P. fluorescens* populations for biological control of nematodes should be targeted to pathogenic nematode species that have been shown to be sensitive to the compound, or used for indirect effects, such as induced systemic resistance.

LONG-TERM EFFECTS OF ELEVATED CO<sub>2</sub> AND O<sub>3</sub> ON EXTRAMATRICAL MYCORRHIZAL HYPHAL BIOMASS PRODUCTION AND STANDING CROP IN QUAKING ASPEN. **Miller, R. Michael**. Biosciences Division, Bldg 203, Argonne National Laboratory, Argonne, IL 60439.

We have been evaluating for the last seven years the interactive effects of eCO<sub>2</sub> and eO<sub>3</sub> on the sequential growth and allocation of both ectomycorrhizal fungi (ECM) and arbuscular mycorrhizal fungi (AMF) associated with quaking aspen (*Populus tremuloides*) at the Aspen FACE site. We have used several different approaches to quantifying treatment effects on the mycorrhizal fungal network, especially how host responses influence root associated colonization and extramatrical hyphal (EMH) production and symbiotic benefit. We are able to determine net EMH production directly by using hyphal in-growth bags. EMH are isolated from the bags by elutriation followed by measuring C and N content, and isotopic <sup>13</sup>C and the <sup>15</sup>N on the recovered hyphae. The proportion of hyphae consisting of AMF from ECM fungi is determined using marker phospholipid 16:1w5c and 18:2w6. By using allometric models for tree growth we determine incremental C gain for trees associated with bag placement. Foliar N content of these trees is also determined. Host C flux to mycorrhizal fungi is calculated from the in-growth bag hyphal mass. We find the average C demand of the fungus for new growth corrected for metabolic efficiency to be around 15.6 g C m<sup>-2</sup> y<sup>-1</sup> for the ambient treatment. When fungal C demand for the treatments are expressed as a response ratio [(treatment – ambient)/ambient] we find a 15% increase with eCO<sub>2</sub> and a 53% reduction with eO<sub>3</sub> fumigation. The combined eCO<sub>2</sub> + eO<sub>3</sub> treatment demonstrated a 16% reduction in C transfer to the fungus from the host. Preliminary measures indicate that correcting for winter mortality of hyphae will likely account for a 30% increase in host C flux to mycorrhizal fungi. EMH standing crop was determined by using marker phospholipids along with loss on incubation. Total EMH standing crop for the ambient treatment for year eight years after stand establishment was found to be around 103 g C m<sup>-2</sup>, with a 30% increase found with eCO<sub>2</sub> and a 17% reduction with eO<sub>3</sub> fumigation. The standing crop of EMH in the eCO<sub>2</sub> + eO<sub>3</sub> treatment demonstrated a 24% increase above ambient. When EMH standing crop is expressed as a ratio of ECM/AMF biomass we find that eCO<sub>2</sub> fumigation favors ECM fungi whereas eO<sub>3</sub> favors AMF. It appears that with eO<sub>3</sub> fumigation we find a decrease in ECM biomass suggesting competitive release of AMF. These observed fumigation treatment influences on the amount and kinds of EMH biomass produced have implications for future forest trajectories.

CALCIUM INFLUENCES MICROBIAL C AND N MINERALIZATION IN NORTHERN HARDWOOD FOREST SOILS: A FIELD AND LABORATORY STUDY. **Minick<sup>1</sup>, Kevan J., M.C. Fisk<sup>1</sup>, and P.M. Groffman<sup>2</sup>**. <sup>1</sup>Dept. of Zoology, Miami University, 212 Pearson Hall, Oxford, OH 45056, <sup>2</sup>Cary Institute of Ecosystem Studies, Box AB 2801 Sharon Turnpike, Millbrook, NY 12545.

Long-term base cation depletion from soils appears to be detrimental to the health and productivity of hardwood forests in the northeastern U.S. Understanding and predicting forest responses to acidic deposition and changes in soil chemistry would benefit from better knowledge of limitations to soil microorganisms, given their critical role mediating the supply of essential nutrients to plants. In a recent study at the Hubbard Brook Experimental Forest (HBEF), NH, soil microbial activity was not stimulated by calcium (Ca) additions to the base-poor forest ecosystem, despite an increase in forest floor pH of approximately 1 unit. We examined this result further by testing the hypothesis that Ca reduces the availability of labile carbon (C) to microorganisms. We conducted a plot-scale field experiment in which we added two levels of Ca (850 kg Ca/ha and 4250 kg Ca/ha) as the mineral wollastonite (CaSiO<sub>3</sub>), to four blocks of 2 x 2 m plots. Wollastonite addition rate at the lower level was intended to restore soil base status to pre-acid deposition levels. Two years after the Ca additions, we incubated soils in the

laboratory to test treatment effects on C mineralization and net nitrogen (N) transformations. Mineralization of soil organic C (SOC) was reduced by the high level of Ca addition to field plots. To distinguish between mineralization of SOC and more recent C inputs, we added  $^{13}\text{C}$ -labeled ground leaf litter to laboratory incubations. Mineralization of this added C substrate was not sensitive to plot-level Ca addition. However, Ca added directly to laboratory incubations (as  $\text{CaCl}_2$ ) reduced C mineralization in the presence and absence of labeled leaf litter. Preliminary  $^{13}\text{C}$  data suggest that added Ca suppressed the mineralization of SOC as well as that of leaf litter. Net N transformations followed the same trends as C mineralization, except that there was virtually no nitrification in incubations amended with Ca in the laboratory. Our results suggest that base status of these soils influences mineralization of soil organic matter, but they do not clearly support our hypothesis that Ca binds with labile pools of C. Understanding the mechanisms by which Ca influences nutrient recycling will require further work distinguishing which organic C pools are most sensitive to interacting with soil Ca.

**HOW GENERAL IS THE CURRENT PN CONTROLS ON  $\text{CO}_2$  FLUX PARADIGM? Mitchell<sup>1</sup> Robert. J., B. Mortazavi<sup>2</sup>, and J. O'Brien<sup>3</sup>.** <sup>1</sup>Joseph Jones Ecological Research Center, Route 2, Box 2324, Newton GA 39870; <sup>2</sup>University of Alabama, Dauphin Island Sea Lab, 101 Bienville Blvd, Dauphin Island, AL 36528; <sup>3</sup>USDA Forest Service Southern Research Station, Athens, Georgia 30602 USA.

A variety of methods including girdling experiments and stable and radioisotope labeling approaches have provided evidence for a tight coupling between current photosynthate and soil  $\text{CO}_2$  flux. The implications from these investigations are that a greater emphasis should be placed on the role of the autotrophic community as a controlling factor on soil  $\text{CO}_2$  flux. If the results from these investigations are generalized then how patterns and regulation of below ground C dynamics and the means by which ecosystem controls are studied and modeled will have to be reconsidered. While evidence for a coupling between current photosynthate and soil carbon dynamics has been conspicuous, data that may challenge the relationship has not been as thoroughly examined or clearly presented. Results from foliar scorching treatments in longleaf pine (*Pinus palustris*) ecosystem that removed 95% of the foliage demonstrate that (i) mycorrhizal fungi production was not significantly reduced as a result of scorching, (ii) root mortality was not significantly affected because of disturbance of the carbon source, and (iii) total root non-structural carbohydrates were not significantly reduced after scorching. These results together combined with findings from other systems suggest that in some systems soil  $\text{CO}_2$  fluxes are less sensitive to variations in current photosynthate and stored C is used to buffer against variations in environmental variables. We propose that natural history response to disturbance and recovery from disturbance may explain the observed patterns and discrepancies in the coupling between above and belowground carbon dynamics.

**POSITIVE AND NEGATIVE FEEDBACKS AFFECT ON COMMUNITY STRUCTURE: A THEORETICAL APPROACH. Molofsky<sup>1</sup>, Jane.** <sup>1</sup>Department of Plant Biology, University of Vermont, Burlington, Vermont 05405.

Plant-soil feedbacks are known to be important drivers of plant community composition and ecosystem function. Simple theoretical models of feedbacks can provide a way to understand how differences in the direction (whether positive or negative), magnitude and scale of feedback can influence both the introduction of a new species into a community and the coexistence patterns found within communities. Here we show using a simplified theoretical framework that the interplay of positive and negative feedbacks that each species experiences in the community can influence both coexistence and invasive success. We develop criteria to predict when the introduction of a new species into a community results in extirpation, naturalization or complete takeover of the existing community. Our results suggest that complex interactions taking into account both the nature and scale of the feedback relationships can greatly alter the conclusions about the importance of feedbacks. Thus, we suggest that experimental approaches that specifically examine the nature and spatial scale of the feedback interaction be considered in both field and greenhouse experimental studies on feedbacks in plant communities.

**APPARENT COMPLEXITY AND THE STABILITY OF REAL AND MODEL ECOSYSTEMS. Moore<sup>1</sup>, John C.** <sup>1</sup>Natural Resource Ecology Laboratory, Ft. Collins, CO 80525.

Most representations of food webs (connectedness structure) are aggregates of multiple sub-webs that occur over space and time. In soils the sub-webs arise from different types of resources (roots, detritus, algae, pollen, etc.), the distribution of water, spatial heterogeneity and arrangements of organic matter and aggregates within soils, season, plant phenology, and the life histories of species. The food web diagrams and model, and the measures of complexity, energy flux, and stability that are derived from them do not capture this. Instead, we tend to think of food webs as possessing a single connectedness structure with energy flux and interaction strength represented by average values that were functions of the population densities of species and their physiological and life history attributes. An implicit assumption of the models is that for the system to persist the population densities of all species must be greater than zero, else species go locally extinct, and that the species that were present are all active. In soils, species go from active to inactive states depending on conditions, resulting in the soil food web being characterized by pulse dynamics - periods of intense biological activity punctuated by periods of lesser activity.

Systems that possess these pulse dynamics are often hierarchically organized with interacting subunits of species whose activities are constrained by a single factor (e.g., water availability) or multiple factors (e.g., water, temperature, and nutrients). When conditions are optimal, all the interactions within the connectedness structure are in place and the food web is fully operational. In this case, the rules governing food web dynamics and stability are in play. When conditions are less than optimal, a subset of the interactions within the web fails to fully materialize. The rules are still operating but only on the subset that is active. The implications to the scenario presented above with regards to nutrient dynamics and dynamic stability will be discussed. The implications of this to the theme of this symposium, “The two faces of soil community ecology – interactions within and among trophic groups” are as follows. First, the study of a single species or trophic group usually includes some influence by other resources or trophic groups that it interacts with, resembling the sub-webs. Second, food webs at a given spatial scale and within a given timeframe are not as complex as their diagrams represent, often collapsing to the sub-webs. So when contrasting the ecology of a single trophic level or species to whole systems, the differences in many cases may not be that great as one might think.

**ROTYLENCHULUS RENIFORMIS** DISPERSAL PATTERNS UPON INTRODUCTION INTO A COTTON FIELD. **Moore<sup>1</sup>, Scott R., K. S. Lawrence<sup>1</sup>, F. J. Arriaga<sup>2</sup>, E. van Santen<sup>3</sup>, and C. H. Burmester<sup>3</sup>.** <sup>1</sup>Dept. of Entomology & Plant Pathology, Auburn University, Auburn, AL 36849, <sup>2</sup>USDA-ARS, Auburn, AL 36849, and <sup>3</sup>Dept. of Agronomy and Soils Auburn University, Auburn, AL 36849.

The reniform nematode, *Rotylenchulus reniformis*, has rapidly spread across cotton fields in Alabama since it was identified in the 1980's. This study was conducted to observe the vertical, horizontal, and temporal spread and the subsequent population development of *Rotylenchulus reniformis* upon introduction in a cotton field under irrigated and non-irrigated conditions. Vermiform life stages of *R. reniformis* were applied in an in furrow spray into the top 3 cm of selected rows at planting. Horizontal movement and population density increase was determined monthly through the season. Vertical movement was determined at planting and harvest. In the first year, vertical movement of the *R. reniformis* males, juvenile stages and vermiform females were observed to the maximum sampling depth of 91cm in both the irrigated and non-irrigated tests. Horizontal movement of *R. reniformis* vermiform life stages did not differ between tests, as both were observed an average of 75cm (< 1 row) from the inoculated row. Movement of *R. reniformis* males was affected by irrigation, with males in the irrigated test being observed to have moved an average of 150cm (between 1 and 2 rows) from the inoculated row at 60 and 90 days after planting (DAP) then reducing to 100cm (< 1 row) at 120 DAP. Males in the non-irrigated test had moved 25cm (< half a row) from the inoculated row at 60 DAP, increasing to an average of 125cm (> 1 row) at 90 DAP and finally reducing to an average of 75cm (< 1 row) at 120 DAP. In 2008, both males and vermiform life stages were observed at planting to a depth of 75cm in the irrigated test and to the maximum sampling depth of 91cm in the non-irrigated test. At harvest, both males and vermiform life stages were found to the depth of 91cm in both the irrigated and non-irrigated tests. Populations were observed only in the originally inoculated rows at planting in 2008, however at 30 DAP both males and vermiform life stages were observed at the maximum sampling distance of 200cm (> 2 rows) from the originally inoculated row and remained throughout the season. *Rotylenchulus reniformis* population levels through the soil profile at harvest were the highest in the top 30cm in both the irrigated and non-irrigated tests. Horizontal population development was highest in the originally inoculated rows and declined with increasing distance from the inoculated row. At 120 DAP, *R. reniformis* populations peaked in the inoculated rows at 6,000/150cm<sup>3</sup> of soil in the irrigated test and 3,000/150cm<sup>3</sup> of soil in the non-irrigated test. The results of this trial illustrate how quickly *R. reniformis* populations can spread and reach economic threshold levels upon introduction into a cotton field.

**MICROBIAL BIOMASS DYNAMICS ASSOCIATED WITH LITTER MASS DYNAMICS AND CHEMISTRY.** **Moorhead<sup>1</sup>, Daryl, J. Herman<sup>1,2</sup> and E. Hammer<sup>1</sup>.** <sup>1</sup>Department of Environmental Sciences, University of Toledo, Toledo, OH 43617. <sup>2</sup>Present address: Coastal Carolina Community College, Jacksonville, NC 28546.

We reviewed published reports of microbial biomass associated with decaying plant litter in both terrestrial and aquatic systems to evaluate relationships between microbial:litter mass (B:C) and litter quality. Sixty-seven papers from the past 30 years provided 1016 observations. Results of analyses showed that microbial biomass averaged 2.53% of total system organic matter (microorganisms + litter), but was more than twice as large in aquatic (3.43%, N=632) as terrestrial (1.05%, N=384) studies. A Mann-Whitney U test confirmed that B:C values were significantly different between habitats. Partial Mantel analyses performed separately by habitat found significant relationships between B:C values and incubation period, litter mass loss and changing litter chemistry (lignin index) in aquatic studies, and time and initial nitrogen concentration in terrestrial studies. Analyses of only the most detailed studies with >5 observations per experiment found that both slopes and strengths of B:C relationships varied over time and with litter type: relationships became increasingly non-linear with progressive decay and also varied with initial lignin content of litter. Unfortunately, too few studies to date have included sufficiently detailed, simultaneous observations of microbial biomass, litter mass and litter chemistry to unequivocally define consistent controls.

**SUSCEPTIBILITY OF THE ADULT JAPANESE BEETLE TO ENTOMOPATHOGENIC NEMATODES.** **Morris, Elizabeth Erin<sup>1</sup> and P. S. Grewal<sup>1</sup>.** <sup>1</sup>Department of Entomology 222 Thorne Hall, OARDC/Ohio State University, Wooster, OH 44691.

We evaluated the susceptibility of the adult Japanese beetle to 20 strains of *Steinernema* and *Heterorhabditis*. All strains infected the beetle and caused 55% to 95% mortality. The most pathogenic strains were: *Steinernema* sp. R54 (90% mortality, LT50 = 4.06 d, LT90 = 7.51 d), *Steinernema* sp. R45 (83% mortality, LT50 = 4.29 d, LT90 = 8.40 d), *Steinernema* sp. FC48 (79% mortality, LT50 = 4.41 d, LT90 = 8.80 d), *H. zealandica* D61 (98% mortality, LT50 = 3.82 d, LT90 = 11.06 d), *H. bacteriophora* D60 (94% mortality, LT50 = 4.54 d, LT90 = 12.35 d), *H. bacteriophora* D2 (90% mortality, LT50 = 6.25 d, LT90 = 13.01 d), *H. bacteriophora* R96 (90% mortality, LT50 = 5.93 d, LT90 = 12.68 d), and *H. bacteriophora* GPS11 (79% mortality, LT50 = 5.36 d, LT90 = 9.03 d). The ability of four nematode strains to infect and reproduce in the beetle was examined to assess the potential of infected beetles to disseminate nematodes upon their death. All strains infected and killed beetles, but only *Steinernema* strains reproduced in the cadavers. We conclude that while *Heterorhabditis* and *Steinernema* strains can be effective against the adult Japanese beetle, only *Steinernema* strains may reproduce and be disseminated by infected adults.

**EVALUATING PUTATIVE ORTHOLOGS FOR PHYLOGENOMIC ANALYSIS ACROSS THE PHYLUM NEMATODA.** **Morris<sup>1</sup>, Krystalynne, T. Fogal<sup>2</sup>, P.J. Hatcher<sup>2</sup>, R.D. Bergeron<sup>2</sup>, P. Datla<sup>2</sup>, W.K. Thomas<sup>1</sup>.** <sup>1</sup>Hubbard Center for Genome Studies, University of New Hampshire, 35 Colovos Road, Durham, NH 03824, <sup>2</sup>Department of Computer Science, University of New Hampshire, 33 Academic Way, Durham, NH 03824.

Phylogenomic approaches aim to use the entire complement of orthologous genes to infer the evolutionary history of species. Here we have identified hundreds of putative orthologs among five nematode taxa with complete genome sequences from species that span the diversity of the phylum. Two different methods, reciprocal best BLAST (RBB) and per cent maximal bit score threshold, were used to predict orthologs. For each putative ortholog from each method, we found the tree that had the best support using both parsimony and maximum likelihood methods, on both the nucleotide and amino acid data partitions. For these five taxa, there are fifteen possible trees. We tested the support of each putative ortholog for each of the fifteen possible trees. Among all data partitions and inference methods, the same tree was favored by the greatest number of genes. No single ortholog gave significant support for the consensus tree or any other tree. In addition, large numbers of genes (62 %) support one of the other fourteen trees. These data support a single consensus tree but also demonstrate that a large number of genes are necessary to ensure correct support of a consensus tree.

**CONTROLS ON SOIL CARBON SEQUESTRATION.** **Morris<sup>1</sup>, Sherri J., E.A. Brewer<sup>2</sup>, and E.A. Paul<sup>3</sup>.** <sup>1</sup>Bradley University, Biology Department, 1501 W. Bradley Avenue, Peoria IL 61625. <sup>2</sup>Department of Crop and Soil Science, 3017 Agricultural and Life Science Building, Oregon State University, Corvallis, OR 97331. <sup>3</sup>Natural Resource Ecology Laboratory, Colorado State University, Fort Collins, CO 80523.

Soil carbon sequestration is the result of the interactions of soil chemical and biological factors. Decomposition results from biotic processing of organic matter as it enters soil pools. Controls on decomposition include substrate (root and litter) quantity and quality, physical environment and microbial community. Studies that examine controls on soil carbon sequestration seek to understand the role of these, as they alter the rate at which materials enter and leave soil organic carbon (SOC) pools. These controls also determine the quantity and quality of C retained in SOC pools vs the amount lost as CO<sub>2</sub> to the atmosphere and speed with which that C is lost. Management can alter the biotic and abiotic characteristics of sites in ways that alter C storage. Understanding the consequences of management on SOC pools can aid in our understanding of the controls on C sequestration. Our studies have focused on a range of managed afforested sites. While most of our study sites are on former agricultural lands, some are on former sand prairies. Overall, our results have suggested that interactions of soil type, plant and environment impact potential soil C sequestration. For example, we have found C retention in sandy soils vs. litter pools above-ground is determined by the vegetation established. We have also identified a possible link between calcium and C retention in afforested prairie and agricultural sites that appears dependent upon the tree species planted. Of recent concern is C retention in managed forests, which leads to the question could be calcium used as an amendment such as in agriculture to increase SOC. To evaluate calcium additions as a management tool, we established plots in C poor pine forest sites in Michigan and Illinois. Rather than add a stable, mined form of calcium to soils we added CaCl<sub>2</sub> alone and in concert with N and with incorporation of litter pools. Our results suggested increases in total and resistant C pool sizes with addition of CaCl<sub>2</sub> and litter incorporation, but without changes to the mean residence times of SOC. Data from field respiration measurements supported our laboratory data showing decreased respiration from CaCl<sub>2</sub> amended plots suggesting sequestration; however, additional measurements on these sites are necessary to assess long-term effects of amendments on soil C stabilization. These results suggest that soil carbon sequestration is currently being managed intentionally or unintentionally through the choices made at time of planting. Careful manipulation of the controls on carbon sequestration within managed sites could increase SOC so as to provide gains in terrestrial C storage, more important however, would be the improvements to soil fertility and site productivity that are associated with soils with large SOC pools.

**HISTOLOGICAL CHANGES INDUCED BY *BURSAPHELENCHUS XYLOPHILUS* IN SEEDLING TISSUES OF *PINUS PINASTER*.** Mota, Luísa<sup>1</sup>, P. Barbosa<sup>2</sup>, M. Mota<sup>2</sup>, and L. Ascensão<sup>1</sup>. <sup>1</sup>Universidade de Lisboa, Faculdade de Ciências de Lisboa, DBV, IBB, Centro de Biotecnologia Vegetal, C2, Campo Grande, 1749-016 Lisboa, Portugal, NemaLab-ICAM, Departamento de Biologia, Universidade de Évora, 7002 – 554 Évora, Portugal. [mmota@uevora.pt](mailto:mmota@uevora.pt)

Pine wilt disease, caused by *Bursaphelenchus xylophilus*, the pine wood nematode (PWN), inflicts significant damage on the coniferous forests of Portugal. First detected in Europe in 1999, on *Pinus pinaster* growing on the Setúbal Peninsula of Portugal, it has spread dramatically throughout the country where it has become a serious threat to Portuguese pine forests. Despite considerable research on this disease, a detailed mechanism of PWN invasion has not yet been described. To understand the host reaction during the course of disease development, knowledge of the anatomy of the host tree is essential. In this communication, structural changes in stems of two-year old *P. pinaster* seedlings infected with PWN were studied. Seedlings were inoculated by placing a 1mL water suspension containing 1,000 nematodes (mixed stages) on debarked apical shoots. Water without nematodes was used for controls. Samples harvested at three, five and seven weeks were fixed with buffered glutaraldehyde and prepared, following standard methods, for SEM and embedding in Leica Historesin®. Sections of embedded tissue for general histology were cut 3µm thick and stained with Toluidine O and Safranin. Because it is difficult to distinguish nematodes from pine tissues with these stains, we also experimented successfully with other stains, such as PAS/Comassie Blue and Ponceau/Azur II. In *P. pinaster* stem, as in other pine species, vertical resin ducts occur both in the cortex and xylem, where horizontal resin ducts are also present. In the control trees, resin ducts were surrounded by a layer of cytoplasm-rich epithelial cells, which are primary sites for biosynthesis of the resin's terpenoid compounds. The initial symptom of disease, began about four weeks after inoculation. Symptom development varied among specimens. At the "early stage" of infection, when no external symptoms were visible, PWN was observed within the lumen of cortical resin ducts. Compared to controls, more tanniniferous idioblasts and a certain degree of degradation in the parenchyma cell walls also were observed. Severe tissue degradation occurred during the "advanced stage" of infection, when external symptoms were plainly visible. Cortical parenchyma cells were degraded or even collapsed as were cambial cells and epithelial cells of the vertical and horizontal resin ducts. Cavities with irregular boundaries developed from degraded resin ducts and surrounding parenchyma cells and PWN were present in the xylem vertical and horizontal ducts where the number of PWNs per duct had increased. As the disease progressed, the cambial zone degraded and the cavities expanded and fused. Seven weeks after inoculation, the number of nematodes increased dramatically and all pine tissues were severely damaged.

**PINE WILT DISEASE IN PORTUGAL: RECENT PROGRESS AND NEW APPROACHES TO THE UNDERSTANDING AND CONTROL OF THE PINWOOD NEMATODE AND ITS INSECT VECTOR.** Mota<sup>1</sup>, M., S. Oliveira<sup>2</sup>, C. Vicente<sup>2</sup> and P. Vieira<sup>1</sup>. <sup>1</sup>NemaLab-ICAM, <sup>2</sup>Soil Microbiology Lab-ICAM, Departamento de Biologia, Universidade de Évora, 7002-554 Évora, Portugal.

Pine wilt disease (PWD) is one of the most serious threats to forest ecosystems worldwide, and in some countries, such as Japan and Korea, it has become the number one problem of certain pine species. The pinewood nematode, *Bursaphelenchus xylophilus*, was detected for the first time in the EU (in Portugal) 10 years ago, in declining maritime pines (*Pinus pinaster*), in a small area, 30km SE of Lisbon. Despite efforts developed by the national forestry and quarantine authorities to control the nematode and its insect vector (*Monochamus galloprovincialis*) the nematode spread rapidly, in less than 10 years, to new forest areas in the center of the country, more than 200 km from the original detection site. In 2008, the nematode was reported to be present in Spain, from a site close to the Portuguese border. Control strategies have been based on capturing the vector by using chemical traps, cutting down more than 500,000 symptomatic trees, heat-treatment of lumber that is to be used in industry, and the monitoring of main roads and ports through which lumber and wood products are transported. These efforts have obviously not been successful in containing the nematode which now threatens to spread to the rest of Europe. Also, a significant body of scientific knowledge has been generated that includes nematode and insect bioecology, aspects of the nematodes' pathogenicity, use of molecular biology in diagnostics and detection, etc. A brief overview of the progress in these areas will be presented. In 2009, a major national program was initiated to research new ways of controlling PWD.. It includes five main lines of research, namely (1) detection and molecular biology studies of the nematode, (2) direct control of the nematode (chemical and biological), (3) associated bacteria putatively involved in the disease, (4) control of the insect vector, and (5) plant biotechnological approaches to breeding and resistance. The University of Évora is directly involved in lines 1 and 3, and an overview of the ongoing research in these areas will be presented.

**QTL MAPPING OF ROOT-KNOT NEMATODE RESISTANCE IN COWPEA (*VIGNA UNGUICULATA*) USING EST-DERIVED SNP MARKERS.** Muchero<sup>1</sup>, Wellington<sup>1</sup>, W.C. Matthews<sup>1</sup>, N.N. Diop<sup>2</sup>, P.R. Bhat<sup>2</sup>, S. Wanamaker<sup>2</sup>, J.D. Ehlers<sup>2</sup>, T.J. Close<sup>2</sup>, and P.A. Roberts<sup>1</sup>. <sup>1</sup>Department of Nematology, University of California, Riverside, CA 92521; <sup>2</sup>Department of Botany and Plant Sciences, University of California, Riverside, CA 92521.

Root-knot nematodes (*Meloidogyne incognita*, *M. javanica*, RKN) are highly damaging to cowpea (*Vigna unguiculata*) directly and in interactions with Fusarium wilt (*Fusarium oxysporum* f. sp. *tracheiphilum*) as a disease complex. Breeding

cultivars with resistance to RKN is an effective management strategy for cowpea production systems. The locus *Rk* confers resistance to several species of RKN in cowpea. We developed EST-derived SNP markers from 17 cDNA libraries and used the markers to construct genetic maps for six RIL populations (288 to 436 markers per population) and a consensus genetic map from these RILs (928 markers) using an Illumina 1536-SNP GoldenGate genotyping assay. Three RIL populations segregated for RKN resistance, and they were phenotyped for resistance to *M. incognita* and *M. javanica* in replicated screenings in infested field plots and growth-pouch inoculation tests in controlled environment chambers. QTL mapping for resistance was performed using the Kruskal-Wallis and Multiple-QTL model mapping (MQM) packages of MapQTL 4.0 software. The *Rk* locus and other resistance loci were mapped to 6 of the 11 cowpea linkage groups. Nine QTL were identified in the three populations each explained from 8.7 to 83.1% of the variation for resistance phenotype. These data and genomic resources will be valuable for marker-assisted breeding for RKN resistance, functional analysis of RKN resistance candidate genes, and positional cloning of these resistance genes.

**ARBUSCULAR MYCORRHIZAL FUNGI PRE-INOCULANT IDENTITY DETERMINES COMMUNITY COMPOSITION IN ROOTS. Mummey<sup>1</sup>, Daniel L. and M. C. Rillig<sup>2</sup>.** <sup>1</sup>Division of Biological Sciences, University of Montana, Missoula, MT, USA, <sup>2</sup>Freie Universität Berlin, Institut f. Biologie, Berlin, Germany.

Arbuscular mycorrhizal fungi (AMF) are obligate biotrophs that form symbiotic associations with the majority of terrestrial plant species. Due to their salient roles in plant nutrient acquisition, there is considerable interest in using AMF as “bio-fertilizers”. Indeed, pre-inoculation of seedlings with commercial, typically non-indigenous, AMF species has become common practice in the horticultural and land reclamation industries. Although frequently viewed as ecologically friendly or benign, very little information is available regarding how non-indigenous AMF inoculants influence indigenous AMF communities [1]. In this study we specifically examine how AMF pre-inoculation influences the structure of AMF communities that subsequently assemble within roots of seedlings after planting in field soil. We exposed seedlings to five different AMF treatments (preinoculation with **Glomus A**, **Glomus B**, one of two *Gigaspora sp.*, or no AMF) for 30 days prior to planting in a whole-soil, mixed AMF community inoculum. After a growth period of 75 additional days, the plants were harvested and aboveground biomass and foliar nutrient concentrations determined. AMF community composition was analyzed in roots collected away from the initial inoculum sites using an approach combining LSU rDNA sequencing and T-RFLP analysis. Our results indicate that the AMF communities that assembled within roots were strongly influenced by the identity of the AMF species to which seedlings were initially exposed. Pre-inoculation with *Glomus A* or *Glomus B* representatives greatly decreased the richness of other AMF ribotypes subsequently colonizing roots. In contrast, pre-inoculation with either *Gigaspora* species didn’t significantly influence overall AMF ribotype richness. Our results also indicate that, concurrent with changes in AMF communities, changes in AMF community functionality, as indicated by differences in plant aboveground biomass and foliar P content, also occurred. Our results indicating the potential for exclusion of indigenous AMF species may have important implications regarding the introduction of non-indigenous AMF and serves to highlight the importance of considering life-history differences when designing AMF inoculants.

**SPATIAL ANALYSIS OF MICROBIAL COMMUNITY COMPOSITION IN A CONIFEROUS FOREST AND ADJACENT CLEARCUT SITES: EVIDENCE FOR DISPARATE ENVIRONMENTAL CONTROLS. Mummey, Daniel L. and P. W. Ramsey.** Division of Biological Sciences, University of Montana, Missoula, MT, USA.

Ecosystems show characteristic variability in biotic and abiotic components on a range of spatial and temporal scales and there is increasing recognition that ecosystem disturbance can result in the disruption of these relationships. Since differences in spatial characteristics are indicative of disparate controls on populations and processes, spatial analyses can be useful for evaluating the effects of ecosystem disturbance and to direct reclamation strategies aimed at reintroducing natural variation patterns. The aim of this study was to compare spatial variation in soil physical, chemical and biotic properties in adjacent areas of a coniferous forest ecosystem subject to different management. We collected soil samples from 140 locations on 4.57 X 36.57 M rectangular grid bisecting virgin forest and clearcut areas. We documented plant locations in relation to each sample and examined each soil sample for aggregate stability, SOM content, chemical properties and fungal hyphae, both AMF and non-AMF. Microbial communities were assayed using PLFA analysis. In addition spatial analyses involving variography, we examined PLFA data using canonical variance partitioning with principal coordinates of neighbor matrixes (PCNM) spatial models as environmental or co-variables in RDA or db-RDA analyses. Our results indicate that soil aggregate stability decreased significantly following timber harvest. Fungi, Gram-negative bacteria and total microbial biomass were found to be significantly greater in samples collected from the forest area. Total bacteria and Gram-positive bacteria were significantly greater in samples from the clearcut. Variography indicated that the spatial range at which autocorrelation between samples was evident was greater in samples from the clearcut area for bacteria, Gram-negative bacteria and Gram-positive bacteria, actinobacteria and microbial biomass, and greater in the forest area for fungi. The high nugget variance of many of our variogram models suggested substantial spatial variance at distances less than were sampled (<0.9 m). Variance decomposition using PCNM spatial variables indicated that soil aggregate stability predicted more of the variation in most PLFA biomarkers than other environmental variables, followed by non-AMF hyphae and vegetation characteristics. Separate analyses of forest and clearcut areas indicated differences in the environmental factors that predicted

significant variation in microbial communities, with pH being more important to the forest and SOM to the clearcut. Taken as a whole, our results indicate clear shift to bacterial dominance after timber harvest and highlight differences between environmental factors driving soil microbial community composition in forest and clearcut systems.

**IMPACTS OF TALLGRASS PRAIRIE RESTORATION ON PLANT COMMUNITIES, SOIL BACTERIAL COMMUNITIES AND ECOSYSTEM FUNCTIONING. Murphy<sup>1</sup>, Cheryl A. and B. L. Foster<sup>1</sup>.** <sup>1</sup>Dept. of Ecology and Evolutionary Biology, University of Kansas, 2045 Haworth Hall, 1200 Sunnyside Ave., Lawrence, KS 66045.

Restoring vegetation and ecosystem function in degraded systems are often goals for land managers. However, restoration typically focuses on plant community establishment. Little is known about the impacts of plant restoration upon soil bacterial communities (SBC) even though they mediate up to 90% of soil processes and are predicted to have enormous diversity. Furthermore, research suggests that the composition and diversity of plant communities could influence SBC structure and diversity. Yet, the links between plant diversity, soil biodiversity and soil functioning are poorly understood. Our goal was to utilize an on-going tallgrass prairie restoration experiment and prairie remnant to investigate the impacts of restoring native prairie plant communities upon SBC. We had three objectives: 1) compare SBC structure and diversity from soils under control and restored plant communities; 2) explore if SBC under restored plant communities are similar to those in a native prairie remnant; and 3) determine if SBC could aid in explaining observed patterns in ecosystem processes. The experiment was initiated in 1999 (University of Kansas Field Station and Ecological Reserves (Lawrence, Kansas)) to explore the effects of restoring native plant species diversity on ecosystem processes. Forty blocks were scattered throughout a 20-ha old-field dominated by introduced cool-season perennial grasses. In each block, four 1m<sup>2</sup> plots contained one of four randomly assigned treatments: control, disturbance; restored (24 native prairie species seeded); and restored plus disturbance. By 2004, restored plots had greatest plant diversity and productivity, thereby establishing distinct plant communities compared to control plots. In June 2005, using 18 of the 40 blocks, we collected soils from control and restored plots for SBC analyses. Additional variables measured from the experiment included available soil N, soil microbial biomass, plant diversity and above- and belowground biomass. Soil samples and plant diversity data were also collected from 18 randomly selected locations throughout a native tallgrass prairie remnant located 200m-500m from the experiment. Soil bacterial community analyses from bulk soils were conducted using Terminal-Restriction Fragment Length Polymorphism (T-RFLP), a reproducible method having sufficient resolution to detect differences in SBC structure. This technique entails extracting SB DNA, amplifying the 16S rDNA region and cutting DNA into different sized fragments via restriction enzymes. These fragments are then sequenced to generate SBC profiles. Preliminary analyses indicate that soils from control plots tend to have lower SB diversity than both the restored and remnant prairie plots, consistent with differences in plant diversity among plots. Further, multivariate analyses suggest that variation in SBC could be partially influenced by topography. Soil bacterial diversity was positively correlated with soil microbial biomass, but negatively correlated with root biomass. These results suggest that plant communities could be shaping soil bacterial communities. However, several other factors, both biotic and abiotic, appear

**ARE LONG-TERM CHANGES IN SOIL ORGANIC MATTER REFLECTED IN THE SOIL COMMUNITIES? Murray<sup>1</sup>, Phillip J., P.R. Hirsch<sup>2</sup>, L.M. Gilliam<sup>2</sup>, S.P. Sohi<sup>2</sup>, J.K. Williams<sup>1</sup>, I.M. Clark<sup>2</sup>, and P.C. Brookes<sup>2</sup>.** <sup>1</sup>North Wyke Research, North Wyke, Okehampton, Devon, EX20 2SB, UK, <sup>2</sup>Rothamsted Research, Harpenden, Hertfordshire, AL5 2JQ

The 'Highfield experiment' is based on an existing study where there are plots of grass, arable and bare-fallow that have been in continuous management for over 50 years. Consequently, differences in the soil organic matter content and soil structure have built up over time.

In initial studies we found that soil microbial biomass carbon, phospholipid fatty acids (PLFAs), soil-extracted DNA, mesofauna (mite and collembolan) communities and heterotrophic bacteria followed the trend, fallow<arable<pasture. However, the relative abundance of PLFAs differed in the three soils and the Shannon diversity index (H') in the bare-fallow soil was significantly lower than that of the pasture. The patterns of Biolog<sup>TM</sup> substrate utilisation by heterotrophic soil bacteria varied between the three soils but H' was not significantly different. When we compared 16S rRNA genes extracted from soil, the pattern of bands representing different bacteria phyla differed in the three treatments, with more being visible in the bare-fallow and fewest in the arable soil. This order was reflected in H' from the three soils and in the number of phyla. The active bacterial population revealed from 16S rRNA extracted from soil appeared to be most diverse in the pasture and least diverse in the arable soil. Despite dramatic difference in soil microbial abundance and community composition, there is no reduction in phylum "richness" when soil is deprived of plant inputs. There is also no evidence of loss of metabolic activity in the three soil types. This implies that, in the bare-fallow soil, either small contributions from minor weed growth between tilling operations is sufficient to sustain part of the original community, or that a large and diverse subset of the soil bacteria thrives on residual carbon substrate inhabiting increasingly distinct and discrete physical locations. These results raise the question of what will happen if the bare-fallow soil is planted and how will the soil communities react. The first phase of the experiment is now underway with areas of the bare-fallow planted to either grass or arable; areas of the grass

plots being made fallow or planted with arable; areas of the arable plots being made fallow or planted with grass. The changes in the biology, chemistry and physics of the experiment will be followed over the next few years.

**PROPOSAL FOR A STANDARD GREENHOUSE METHOD OF ASSESSING SOYBEAN CYST NEMATODE RESISTANCE IN SOYBEAN: SCE08 (STANDARDIZED CYST EVALUATION 2008).** Niblack, T. L.<sup>1</sup>, G. L. Tylka<sup>2</sup>, P. Arelli<sup>3</sup>, J. Bond<sup>4</sup>, B. Diers<sup>1</sup>, P. Donald<sup>3</sup>, J. Faghihi<sup>5</sup>, V. R. Ferris<sup>5</sup>, K. Gallo<sup>6</sup>, R. D. Heinz<sup>7</sup>, H. Lopez-Nicora<sup>1</sup>, R. Von Qualen<sup>8</sup>, T. Welacky<sup>9</sup>, and J. Wilcox<sup>7</sup>. <sup>1</sup>University of Illinois, Urbana, IL; <sup>2</sup>Iowa State University, Ames, IA; <sup>3</sup>United States Department of Agriculture – Agricultural Research Service, Jackson, TN; <sup>4</sup>Southern Illinois University, Carbondale, IL; <sup>5</sup>Purdue University, West Lafayette, IN; <sup>6</sup>Syngenta Seeds, Inc.; <sup>7</sup>University of Missouri, Columbia, MO; <sup>8</sup>Agricultural Consulting and Testing Services, Inc., Carroll, IA; <sup>9</sup>Agriculture Canada, Ontario, CA.

The soybean cyst nematode (SCN) remains the most economically important pathogen of soybean in North America. Despite this, according to surveys conducted in Illinois and reports from nematologists, most farmers do not sample for SCN and believe that the use of SCN-resistant varieties is sufficient to avoid yield losses due to the nematode. This creates problems for sustainable high-yield soybean production either continuously or in rotation because SCN populations vary widely in population densities (numbers) and virulence (ability to reproduce on resistant cultivars), both of which characteristics influence soybean yield; in addition, the word “resistant” on the seed label does not necessarily mean that the cultivar is actually resistant in the traditional meaning of the word (i.e., a Female Index [FI] less than 10, where the FI is calculated as the number of females produced on a soybean cultivar, divided by the number produced on a standard susceptible, expressed as a percentage). Although there are loosely agreed-upon methods for determining the level of SCN resistance of a soybean line during cultivar development, there are currently no widely accepted standards for verifying and labeling a soybean cultivar “SCN resistant.” Several studies have shown that many cultivars marketed as SCN-resistant actually have little or no effective resistance. During the 4th National Soybean Cyst Nematode Conference held in Tampa, FL, in March 2008, approximately 80 members of the assembly discussed and agreed upon a set of standards originally offered by members of a workshop on SCN resistance held in March 2007 in Champaign, IL, for assessing SCN resistance in released cultivars. These standards, which include the use of specific protocols and the host reaction scale proposed by Schmitt & Shannon (Crop Science 32:275-277), will allow direct comparisons of cultivars carrying SCN resistance genes. Adoption of the standards by soybean seed companies will be strictly voluntary, allowing the seed to be labeled as “according to SCE08 standard protocol.” Such labeling will permit soybean farmers to compare soybean cultivars directly and make better-informed cultivar choices.

**THE DIVERSITY OF TARDIGRADES AND THEIR ROLE IN THE SOIL FOOD WEBS IN THE MCMURCO DRY VALLEYS, ANTARCTICA.** Nielsen, Uffe N.<sup>1</sup>, D. H. Wall<sup>1</sup>, and B. J. Adams<sup>2</sup>. <sup>1</sup>NREL and Department of Biology, Colorado State University, Fort Collins, Colorado <sup>2</sup>Department of Biology, and Evolutionary Ecology Laboratories, Brigham Young University, Provo, Utah.

The McMurdo Dry Valleys, Antarctica, represents one of the most inhospitable environments on earth. Yet, the landscape offers microhabitats that support distinct soil food webs. In dry areas the soil food web is dominated by the nematode *Scottinema lindsayae*, whereas the wet areas support more complex food webs dominated by the nematode genus *Plectus* and with high abundances of tardigrades. Before the latest Antarctic field season (i.e. the Austral summer 2008-09) only 4 species of tardigrades had been recorded, but a more systematic approach to this group during the latest field season showed a greater diversity of tardigrades within the Dry Valleys than expected. The presence of two previously unrecorded species has been confirmed, one of which belongs to a genus not previously recorded in the Dry Valleys. Whether the specimens of *Milnesium* sp. represent a new species is currently being scrutinized using images taken with a scanning electron microscope, high resolution microscopy and DNA. The discovery of several individuals at multiple locations across the Dry Valleys representing the genus *Milnesium* is of particular interest. None of the tardigrade species recorded from the Dry Valleys to date are considered predatory, but some members of the genus *Milnesium* are known predators. Observations of live specimens indicated that the Dry Valley *Milnesium* specimens are also predatory. Previously, the soil food webs in the Dry Valleys were considered not to support ‘top-predators’. Hence, the find of the predatory *Milnesium* sp. suggests greater biotic interaction within the soil food webs than expected.

**SEPARATE AND CONCOMITANT EFFECTS OF MELOIDOGYNE PARTITYLA AND MESOCRICONEMA XENOPLAX ON PECAN.** Nyczepir, A.P. and B.W. Wood. USDA-ARS, SE Fruit & Tree Nut Research Laboratory, 21 Dunbar Road, Byron, GA 31008.

Mouse-ear (ME) of pecan is a nutrient disorder that has increasingly manifested itself in recent years as an orchard “replant” disorder in the southeastern United States. Mouse-ear has been found to be caused by a nickel (Ni) deficiency, with timely foliar application of Ni correcting this disorder. In many of the affected ME orchards sampled in Georgia,

*Mesocriconema xenoplax* occurs in the same soil as *Meloidogyne partityla*. The interactive effects of *M. partityla* and *M. xenoplax* on nematode reproduction as well as growth of 'Desirable' pecan were studied in field microplots. *Meloidogyne partityla* suppressed reproduction of *M. xenoplax*, whereas the presence of *M. xenoplax* did not affect the populations of *M. partityla* second-stage juveniles in soil. Trunk diameter was reduced in the presence of *M. partityla* alone or in combination with *M. xenoplax* as compared with the uninoculated control trees 32 months following inoculation. The interaction between the two nematodes was significant for dry root weight 37 months after inoculation. Although the combined nematode treatment (*M. partityla* + *M. xenoplax*) caused a greater reduction in root growth than *M. xenoplax* alone, it was not less than *M. partityla* alone. Mouse-ear symptom severity in pecan leaves was increased in the presence of *M. partityla* compared with *M. xenoplax* and the uninoculated control. *Meloidogyne partityla* is an economically important pest to the pecan industry in the southeastern United States; however, the economic impact of *M. partityla* on orchard longevity, yield, and nut quality remains unknown.

**DOES MYCORRHIZAL INOCULUM INCREASE FUNGAL COLONIZATION OF HYBRID WILLOW ROOTS (*SALIX VIMINALIS*)?** Ohsowski<sup>1</sup>, Brian M., A. Straathof<sup>2</sup>, R. Schierholt<sup>1</sup>, J.N. Klironomos<sup>1</sup>, K.E. Dunfield<sup>2</sup>, C. Wagner-Riddle<sup>2</sup>, M.M. Hart<sup>1</sup>. <sup>1</sup>Department of Integrative Biology, University of Guelph, Guelph, ON, N1G 2W1, Canada, <sup>2</sup>Department of Land Resource Science, University of Guelph, Guelph, ON, N1G 2W1, Canada.

Hybrid willows are increasingly important for land reclamation due to their erosion control attributes and high rates of nutrient / contaminant uptake. In addition to land reclamation, willows can be periodically coppiced for use in plant-derived biofuel production. Since *Salix sp.* are known to form symbiotic relationships with arbuscular mycorrhizal (AM) and ectomycorrhizal (EM) fungi, soils supplemented with mycorrhizal inoculum may benefit overall willow primary production. However, the fate of inoculum in the field is not known. Mycorrhizal inoculation may result in root colonization, failure to establish, or uncontrollable spread. Currently, there is little data documenting the outcome of mycorrhizal inoculum in the field. A further consequence of inoculum addition may include a shift in microbial community structure within hybrid willow root tissues and the associated rhizosphere. This greenhouse study examined the root colonization ability of two fungal inocula: *Glomus intraradices* (AM) and *Hebeloma cylindrosporum* (EM) grown with the hybrid willow clone, *Salix viminalis*. Attempting to mimic *in situ* conditions, two replicates of each unsterilized field soil texture (clay, loam, or sand) were collected from unique sites in Southern Ontario. Soils were subsequently amended with one of four inocula treatments (AM, EM, AM + EM, none). After four months of greenhouse growth, freshly collected roots were processed, freeze-dried, and DNA extracted. Fungal primers specific to each isolate were designed to determine inocula presence within DNA root tissue extracts. To quantify the extent of mycorrhizal colonization in root tissue and soils, we used a quantitative PCR assay. Changes to the background microbial community were investigated with Terminal Restriction Fragment Length Polymorphism (T-RFLP). Results of this investigation will indicate both the utility of adding mycorrhizal inoculum in the field and consequences for resident soil microbes.

**DETECTING MICROBIAL NUCLEIC ACIDS WITHIN NEMATODE BODIES: A PHOTO ESSAY.** O'Leary<sup>1</sup>, Cecilia A., A.M. Treonis<sup>1</sup>, C. Marks<sup>1</sup>, and I.A. Zasada<sup>2</sup>. <sup>1</sup>Dept. of Biology 28 Westhampton Way, University of Richmond, Richmond, VA 23173, <sup>2</sup>USDA-ARS Horticultural Crops Research Laboratory, 3420 NW Orchard Ave., Corvallis, OR 97330.

We developed a taxa-specific, fluorescence *in situ* hybridization (FISH) technique to localize microbial nucleic acids within nematode bodies. This technique involves hybridization of a nucleic acid probe to target microbial sequences. Hybridization is detected microscopically, as the probes have fluorescent labels attached to them. Here, we present an overview of this molecular microscopy technique and a photo essay portraying several applications. Using bacteria-specific rRNA FISH probes, this method has been used to successfully localize the passage of microbial food sources through the esophageal region of *Caenorhabditis elegans*. The same technique was applied to bacterial-feeding nematodes (Cephalobidae spp.) isolated from soils from the Mojave Desert. We were also able to detect the presence of archaeal rRNA within these nematodes, using archaea-specific FISH probes. To our knowledge, this is the first time that consumption of archaea by nematodes has been documented. We have also been able to visualize intestinal symbionts using this technique. Phylogenetic staining is a promising tool for the study of nematode food sources and symbionts.

**PLANT NEMATODE GENOMICS: LOOKING BACK AND MOVING FORWARD.** Opperman, Charles H.<sup>1</sup>, D.McK. Bird<sup>1</sup>, E.S. Scholl<sup>1</sup>, and M. Burke<sup>2</sup>. <sup>1</sup>Center for the Biology of Nematode Parasitism, NC State University, Raleigh, NC 27695, <sup>2</sup>David H. Murdoch Research Institute, Kannapolis, NC 28081.

Just over a decade ago, the first genome sequence of a multicellular animal was reported in the journal Science. Because the animal was a nematode, this milestone had tremendous impact on the Nematology/Parasitology scientific community. The free-living nematode, *Caenorhabditis elegans* possesses a 100 Mb genome with slightly more than 20,000 genes, and has proved to be a robust biological model for many systems, including humans. Indeed, the sequencing consortium

assembled for the *C. elegans* genome was largely responsible for the public effort to sequence the human genome. Since the release of the *C. elegans* genome, there has been a growing effort to complete genome sequences from both plant and animal parasitic nematodes, and as premissed in 1998, *C. elegans* has proved to be an important tool to guide parasite biologists in the post-genomic era. We have developed a large EST database that has set the stage for numerous genome projects. In the past few years, genome sequences have been reported from *Meloidogyne hapla*, *M. incognita*, *Brugia malayi*, *Pristionchus pacificus*, and *Trichinella spiralis*. There are ongoing projects on numerous other species, including *Heterodera glycines*, *Globodera pallida*, *Heterorhabditis bacteriophora*, *Haemonchus contortus*, *Onchocerca volvulus*, *Strongyloides ratti*, and *Nippostrongylus brasiliensis*. Others species are planned for the future. Individually, these sequences are a digital record of an organism, but collectively they represent a hugely significant resource to study the evolution of parasitism. As a comprehensive comparative genomics study we are developing these resources, which will be made available to the scientific community via our Gbrowse site at [www.pngg.org](http://www.pngg.org).

**POST-FUMIGATION POPULATION DYNAMICS OF *MELOIDOGYNE ARENARIA* AND *PASTEURIA PENETRANS* IN A PEANUT FIELD. Orjay, Joey I.<sup>1</sup>, G. K. Kariuki<sup>2</sup>, M. L. Mendes<sup>1</sup>, W. T. Crow<sup>1</sup>, and D. W. Dickson<sup>1</sup>.** <sup>1</sup>Entomology and Nematology Department, University of Florida, Gainesville, FL 32611; <sup>2</sup>Kenyan Agricultural Research Institute, Nairobi, Kenya.

*Meloidogyne arenaria* race 1 is the most prevalent and damaging nematode pathogen of peanut in the southeast United States and many other countries. *Pasteuria penetrans* is a highly suppressive bacterial parasite of root-knot nematodes that occurs naturally in many peanut fields in Florida. Our objective was to monitor the population densities of both *M. arenaria* and *P. penetrans* over a 5-year period following their introduction in a peanut field site in 2003. Both *M. arenaria* and *P. penetrans* were maintained on a peanut-vetch cropping system. The fumigants 1,3-D and chloropicrin were applied in 2004 and 2005 and nonfumigated plots served as the control. The experiment was arranged in a randomized complete block design with four blocks consisting of three plots per each of the three treatments. Beginning in 2004, root-knot nematode and endospore densities were estimated from soil samples taken at the end of each crop season and continued through 2008. Throughout the study, the population densities of *M. arenaria* and *P. penetrans* in the nonfumigated plots fluctuated slightly within a low density range. Fumigation by 1,3-D suppressed the nematode and bacterial population densities, whereas chloropicrin suppressed the bacterial population densities only during the years when they were applied. When treatments stopped, a population density resurgence of root-knot nematode was immediately observed in all fumigated plots. The mean densities at harvest in 2006 were 526 and 365 J2/100 cm<sup>3</sup> of soil, for plots previously fumigated with 1,3-D and chloropicrin, respectively. These levels were higher ( $P \leq 0.05$ ) than in nonfumigated plots which had 92 J2/100 cm<sup>3</sup> soil. *Pasteuria* densities increased rapidly in the previously fumigated plots in a host density-dependent manner with time delay. This swift build-up of the parasite caused suppression of the nematode to levels that were barely detectable in some replicate plots. The Lotka-Volterra simulation model indicated stability of both the nematode and parasite populations in the nonfumigated plots but predicted nematode extinction in plots whose dynamics were disturbed by the fumigants. The fumigant-induced nematode and *Pasteuria* population resurgence that led to eventual suppression of the former followed the ecological concept of “paradox of enrichment”. This approach may be used as a paradigm in managing soil suppressiveness toward *M. arenaria*.

**CLIMATE PATTERNS DETERMINE SOIL ORGANIC MATTER DYNAMICS AND ASSOCIATED FUNGAL CARBON RESPIRATION. Oren, Adi and Y. Steinberger.** The Mina and Everard Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan 52900, Israel.

We explored mechanisms by which climatic factors direct soil organic matter dynamics and resultant carbon and nitrogen availabilities, and by which these, in turn, shape soil fungal communities with regard to biomass and carbon-substrate-respiration activities. A unique platform was selected to that aim, along a large-scale climatic slope in Israel, shifting from a humid-Mediterranean climate type in the north to the Negev Desert in the south, thus forming an exceptionally steep climatic gradient (from 780 to only 90 mm mean annual rainfall) over a drastically-condensed geographical area. The impact of environmental conditions was evaluated on two different scales: 1. Geographic; and 2. Temporal - conferred by the seasonal dynamics at the Mediterranean region. We faced up the challenge of distinguishing seasonal from spatial climatic effects by a separate analysis of data at each location (perceiving the difference among seasons) as well as at each individual season (portraying the geographic variation). When both scales of examination were mutually found to exert an independent control on a considered parameter, their relative power was assessed. A modified MicroResp<sup>TM</sup> procedure was used which was fit to test fungal competence for utilization of complex, low-solubility substrates, reflective of the bulk input of organic substances in soils. Subsequently, sole-carbon-source utilization profiles were constructed, which were analyzed against potential abiotic soil determinants. Clear distinctions could be made along the geographic axis of the gradient in soil abiotic parameters, with mean soil moisture, total organic carbon, dissolved organic carbon, and total soluble nitrogen levels all being statistically different from site to site, and gradually descending from the humid toward the arid location. All of these abiotic parameters were positively correlated with each other along the geographic axis, however, on the seasonal scale, only soil moisture and total soluble nitrogen were positively correlated in every location. Variable mechanisms were proposed to be involved in the

control over soil organic matter dynamics under the various climate types comprising the Mediterranean region, depending on patterns of rainfall, primary production, and soil texture. Fungal-community CO<sub>2</sub> evolution data demonstrated considerable correspondence to abiotic attributes, similarly descending with enhanced aridity level. Fungal basal respiration, as well as all substrate-induced respiration rates, was found to positively correlate with total, as well as dissolved organic carbon, over the spatial axis. The seasonal element of the climatic framework formulated was less decisive than geography in determining soil organic carbon – fungal carbon respiration relationships. In sharp contrast to all tested abiotic, as well as biotic parameters, the metabolic quotient ( $q\text{CO}_2$ ) was found to increase with climate aridity level, along both the spatial and temporal axes of the gradient. This was probably the result of increased fungal energy demand and decreased carbon-use efficiency with intensifying dryness and heat stress levels.

**BERMUDAGRASS (*CYNODON SPP.*) AND SEASHORE PASPALUM (*PASPALUM VAGINATUM*) RESPONSES TO STING NEMATODES (*BELONOLAIMUS LONGICAUDATUS*). Pang<sup>1</sup>, Wenjing, W. T. Crow<sup>1</sup>, and K. E. Kenworthy<sup>2</sup>.**

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Bermudagrass (*Cynodon spp.*) and seashore paspalum (*Paspalum vaginatum*) are commonly grown warm-season turfgrasses in Florida. Sting nematode (*Belonolaimus longicaudatus*) is considered the most serious nematode pest of these grasses in Florida. Utilization of resistant or tolerant cultivars is the most efficient and least costly practice for nematode management on turf, but information about the responses of most cultivars to *B. longicaudatus* is not available. The objective of this study is to evaluate newer cultivars for their resistance and tolerance to sting nematode. In two trials, eight bermudagrass and three seashore paspalum cultivars were evaluated for their responses to *B. longicaudatus* in a greenhouse in 2008. The experimental design was randomized complete block with six replications. Grasses were grown in 1500 cm<sup>3</sup> sand-filled clay plots and then inoculated with 0 or 200 *B. longicaudatus* per pot. The experiment was harvested 90 days after inoculation with nematodes. Cultivar tolerance was determined by the percent reduction in root length of inoculated grass compared with the uninoculated control. Resistance was determined by the nematode reproductive factors at harvest. The same turfgrass cultivars, with the addition of ‘Tifway 419’ bermudagrass, were evaluated for *B. longicaudatus* responses in the field beginning in 2008. In the greenhouse *B. longicaudatus* caused significant reductions in the root length of several cultivars of both grasses. The population of *B. longicaudatus* was doubled on ‘Champion’ while populations decreased on ‘Tifspport’ and ‘Celebration’ bermudagrass. Final population of *B. longicaudatus* was the highest on ‘Sea Dwarf’ among the seashore paspalum cultivars. The field study showed that populations of *B. longicaudatus* increased to the highest on ‘Mini Verdi’ and ‘Floradwarf’ and did not increase on ‘Tifspport’ bermudagrass. Results on seashore paspalum were not consistent between greenhouse and field trials. Both greenhouse and field studies showed that final populations of *B. longicaudatus* were higher on bermudagrass cultivars used on putting greens than those used on fairways. These studies will be continued and expanded in 2009. Data from these studies will help turfgrass managers select cultivars with fewer sting nematode problems in the future. Resistant cultivars can be planted to reduce soil nematode population; while tolerant cultivars can be used when the grass growth is the main concern.

**DO SOIL NEMATODE COMMUNITY REFLECT ALTERED URBAN SOIL CHEMICAL PROPERTIES? Park<sup>1,2</sup>, Sun-Jeong, Z. Cheng<sup>2</sup>, H. Yang<sup>1,2,3</sup>, E. E. Morris<sup>2</sup>, M. Sutherland<sup>2</sup>, B. B. McSpadden Gardener<sup>1,4</sup>, and P. S. Grewal<sup>1,2</sup>.**

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Urban development causes substantial disturbance to the soil ecosystem. Removal of topsoil, compaction, and addition of transported materials modify physical, chemical and biological conditions of the soil. This initial disturbance, coupled with subsequent anthropogenic inputs including fertilizers, pesticides, atmospheric deposits, urban contaminants, extreme heat, and foot traffic, have the potential to produce unique soil communities in urban ecosystems. The main objective of the study was to determine whether differences in soil chemical properties can be detected in soil nematode community assemblages along temporal and spatial gradients related to urban development. Urban boundaries from 1920’s (old), 1960’s (middle) and 2000’s (new) were identified for three cities in northeast Ohio; Massillon, Wooster and Canton. Soil samples were collected from two road-side and two interior lawns in one public school site within each urban age ring. Soil texture and basic chemical properties including pH, available P, exchangeable K, Ca, and Mg, cation exchange capacity, nitrate, total carbon, and nitrogen, and soil organic matter were measured. Nematodes were extracted, counted, identified to genus-level and assigned to a functional guild. Along the temporal gradient of urban development, total carbon, total nitrogen and organic matter were significantly lower in the soils of newly developed areas of Massillon and Wooster ( $P < 0.01$  for each). And, the abundance and genus-level richness of nematodes were also lower in new sites as compared to old sites in Massillon and Wooster ( $P < 0.10$ ). However, none of the community indices were able to detect such an urban age gradient. On the more local spatial gradient, road-side soils had significantly higher soil carbon and nitrogen than interior sites, particularly in old and middle-aged sites in all three cities ( $P < 0.05$  for each). However, there were no significant differences in nematode

abundance, genus-level richness and community indices with respect to distance from the road. In conclusion, initial urban development and subsequent human activities in urban areas can have profound influence on key soil chemical properties. Such changes in urban soil were reflected in abundance and genus-level richness of nematodes, but not in community indices.

**INCORPORATING SPATIAL DISTRIBUTION INTO THE NEMATODE FUNCTIONAL GUILD CONCEPT. Park<sup>1,2</sup>, Sun-Jeong, R. A. J. Taylor<sup>2</sup>, and P. S. Grewal<sup>1,2</sup>.** <sup>1</sup>Environmental Science Graduate Program, Urban Landscape Ecology Program, <sup>2</sup>Department of Entomology, The Ohio State University-OARDC, Wooster, OH 44691.

Functional guilds defined by nematode feeding types (bacteria-feeding, fungal-feeding, omnivore, predatory and plant-feeding) are further refined by colonizer-persister class (i.e. r- and K-strategists) which reflects life-history strategy. We compared spatial organization of nematode genera belonging to the same functional guild or colonizer-persister class to determine intraguild spatial distribution behavior. A total of 360 soil samples from turfgrass lawns were collected from three locations in each of the three Ohio cities, Wooster, Massillon and Canton, in July and October, 2007. The index of aggregation, 'b' of Taylor's power law, was used to compare the spatial distribution of 21 nematode genera, six different functional guilds, five colonizer-persister classes and total nematodes. The index of aggregation for the total nematodes was 2.0, which is the value of 'b' averaged over all the examined vertebrate and invertebrate taxa. The individual genera, the functional guilds and colonizer-persister classes had indices of aggregation that differed from 2.0. Functional guild as a group had higher 'b' value than individual genera, suggesting higher degree of aggregation at functional guild level. We found that 'b' value and colonizer-persister class is related. Low cp-scale nematodes have higher 'b' value. We conclude that the examination of spatial organization of nematodes may lead to further improvements in the practical value of nematodes as soil bioindicators.

**PHYLOGENETIC SIGNAL IN FUNCTIONAL DIVERSITY AND COMMUNITY ASSEMBLY OF ARBUSCULAR MYCORRHIZAL FUNGI. Parrent<sup>1</sup>, Jeri L., Maherali<sup>1</sup>, H., Powell<sup>2</sup>, J., Klironomos<sup>1</sup>, J. N.** <sup>1</sup>Dept. of Integrative Biology - University of Guelph - Guelph, Ontario, Canada- N1G 2W1. <sup>2</sup>Freie Universität Berlin, Institut für Biologie - Ökologie der Pflanzen, Altensteinstraße 6, 14195 Berlin, Germany.

In contrast to many other guilds of plant symbiotic fungi, arbuscular mycorrhizal fungi (AMF) are a relatively low diversity, monophyletic and ancient lineage. Consistent with many other fungal communities, our understanding is limited with regard to the factors that govern AMF community assembly and the functional consequences of AMF community composition for their plant hosts. Previous studies have shown that AMF taxa vary in a number of traits relevant to their performance as plant partners, such as plant colonization intensity, soil hyphal biomass, and pathogen protection. Here we combine data from field and greenhouse studies with a phylogenetic approach to examining AMF communities to ask: (1) Are functional traits of AMF taxa phylogenetically conserved; (2) what is the spatial organization of phylogenetic community structure; and (3) what are the consequences of phylogenetic diversity in AMF community assemblages for plant productivity? Reconstructing functional trait evolution across the AMF phylogeny we find evidence for conservation of a number of traits, and this pattern is largely driven by the partitioning of trait variance between the two orders within this phylum. Our studies also show that AMF communities are phylogenetically overdispersed at spatial scales ranging from 4-576 m<sup>2</sup>, and that plant productivity increases as phylogenetic diversity is increased within constructed AMF community assemblages. These results suggest that phylogenetic structure may be an honest signal for functional diversity within AMF communities, and that phylogenetic overdispersion of AMF communities may represent functional complementarity of AMF community members, which can have a positive, synergistic effect on their plant associates.

**GRANITE ROCK OUTCROPS: AN EXTREME ENVIRONMENT FOR SOIL NEMATODES? Parsons, Charles H.H., E. Austin, K. Semmens, and A.M. Treonis.** Dept. of Biology, 28 Westhampton Way, University of Richmond, VA 23173.

We studied soil nematode communities from the surface of granite flatrock outcrops in the eastern Piedmont region of the United States. The thin soils that develop here host unique plant communities and experience high light intensity and extreme fluctuations in temperature and moisture. We collected soils from outcrop microsites in Virginia (VA) and North Carolina (NC) in various stages of succession (Mature, Minimal, and Primitive) and compared soil properties and nematode communities to those of adjacent forest soils. Nematodes were prevalent in outcrop soils, with densities comparable to forest soils ( $P > 0.05$ ). Nematode communities in Mature and Minimal soils had lower species richness than forest soils ( $P < 0.05$ ), and contained more bacterial-feeders and fewer fungal-feeders ( $P < 0.05$ ). Primitive soils contained either no nematodes (NC) or only a single species (*Mesodorylaimus* sp., VA). Nematode communities were similar between Mature and Minimal soils, according to trophic group representation, MI, PPI, EI, SI, and CI ( $P > 0.05$ ). Forest soils had a higher PPI value ( $P < 0.05$ ), but otherwise communities were similar to outcrop soils ( $P > 0.05$ ). Outcrop nematode communities failed to group together in a Bray-Curtis cluster analysis, indicating higher variability in community structure than the Forest soils, which did cluster together. A high proportion of the nematodes were extracted from outcrop soils in coiled form (33-89%), indicating that they used anhydrobiosis to persist in this unique environment.

MINERAL NUTRIENT DYNAMICS OF TREMBLING ASPEN AND PAPER BIRCH UNDER ELEVATED CO<sub>2</sub> AND O<sub>3</sub>. **Parsons<sup>1</sup>, William F.J., J. G. Bockheim<sup>2</sup> and R. L. Lindroth<sup>3</sup>**. <sup>1</sup>Department of Biology, University of Sherbrooke, Sherbrooke, QC, Canada J1K 2R1; <sup>2</sup>Department of Soil Science, University of Wisconsin, Madison, WI 53706 USA; <sup>3</sup>Department of Entomology, University of Wisconsin, Madison, WI 53706 USA.

Ongoing changes in atmospheric composition are likely to affect how forest ecosystems will cycle mineral nutrient elements in the future, especially through trace gas-mediated shifts in litter chemistry. We evaluated the independent and interactive effects of elevated CO<sub>2</sub> (560 µl l<sup>-1</sup>) and O<sub>3</sub> (55 nl l<sup>-1</sup>) on the decomposition of the early successional species trembling aspen (*Populus tremuloides* Michx.) and paper birch (*Betula papyrifera* Marsh.) at the Aspen FACE facility in northern Wisconsin, USA. Dynamics of macro- (N, P, K, Ca, Mg, S) and micro- (B, Zn, Mn, Cu, Fe) nutrients were followed in aspen and birch leaves that had been grown, senesced, and decayed in the field for 23 mo under ambient CO<sub>2</sub>+O<sub>3</sub>, elevated CO<sub>2</sub>, elevated O<sub>3</sub>, or elevated CO<sub>2</sub>+O<sub>3</sub> treatments, i.e., when litter was placed back into its native plot. After 693 days, overall mineral nutrient release rates did not differ greatly among the four treatments, consistent with previous studies on the site. Temporal variation in their respective concentrations, however, did differ and reflected CO<sub>2</sub>- and O<sub>3</sub>-mediated shifts in secondary metabolite levels, as determined from partial least-squares and procrustes analysis.

DEVELOPING REAL TIME qPCR ASSAY TO MEASURE THE PREDATION RATE OF ENDEMIC NEMATOPHAGOUS FUNGI ON ENTOMOPATHOGENIC NEMATODES. **Pathak<sup>1</sup>, Ekta, R. Campos-Herrera<sup>1</sup>, E.G. Johnson<sup>1</sup>, F. E. El-Borai<sup>1,2</sup>, J.H. Graham<sup>1</sup>, and L.W. Duncan<sup>1</sup>**. <sup>1</sup>Citrus Research and Education Center, University of Florida, Lake Alfred FL 33850. <sup>2</sup>Plant Protection Dept. Faculty of Agriculture, Zagazig University, Egypt.

Nematophagous fungi (NF) are a diverse group of organisms that either prey upon or parasitize nematodes, and might be among the primary antagonists that regulate the effectiveness of entomopathogenic nematodes (EPN) as biological control agents of insects in soils worldwide. Thus, knowledge of the interactions between NF and EPNs could be crucial for understanding the conditions under which EPNs can act as effective biological control agents. Most of the predacious NF species exist along a continuum from mainly saprophytic to mainly predatory and, consequently, their predation rates are often unrelated to their abundance. Moreover, many methods of studying NF predation and parasitism rates from field samples involve the observation of NF on agar and might give results that are completely unrelated to NF activity and abundance in soil. Therefore, we are developing a quantitative real-time PCR (qPCR) assay using Taqman® probes to accurately assess the relative predation and parasitism rates on EPN by individual endemic species of NF in Florida citrus orchards. The bioassay involves the inoculation of EPNs in undisturbed soil, incubation, recovery of the EPNs from the soil, DNA extraction from the EPNs, and qPCR to quantify the associated NF. For this purpose, species-specific primers and probes were designed from the ITS region of rDNA for the most common trapping fungi in Florida citrus orchards: *Arthrobotrys oligospora*, *A. dactyloides*, *A. musiformis* and *Monacrosporium geophyropagum*. Similarly, we are designing primers for the endemic endoparasitic fungi *Catenaria spp.* and *Myzocyttium spp.*. Specificity of the primers was determined by conventional PCR using pure cultures of different fungi. Each primer set selectively detected its target organism and no cross reaction occurred with other NF. A separate experiment using conventional PCR was conducted to test the detection of fungal DNA from EPNs incubated with fungi in raw soil vs. clean soil. Each pair of these species-specific primers successfully detected each species of fungus from DNA extracted from nematodes recovered from soil inoculated with *Arthrobotrys oligospora*, *A. dactyloides*, *A. musiformis* and *Monacrosporium geophyropagum*. The bioassay is currently being evaluated using qPCR in situ, and these results will be presented.

URBAN GREENSCAPE, SOILS, AND ECOSYSTEM FUNCTIONING IN A SEMI-ARID URBAN ECOSYSTEM. **Pavao-Zuckerman<sup>1</sup>, Mitchell A.** <sup>1</sup>Biosphere 2, University of Arizona, Tucson, AZ 85721.

As rates of urbanization continue to rise and a greater proportion of the population lives in urban and suburban areas, the provision of ecological services and functions become increasingly important to sustain human and environmental health in urban ecosystems. Soils play a primary role in the healthy functioning of ecosystems that provide supporting, provisioning, regulating, preserving, and cultural ecosystem services, yet developing our understanding of how urban soils function to provide these services within an ecological context is just getting underway. Soils in urban ecosystems are highly heterogeneous, and are affected by both direct and indirect influences and local modifications which alter their functioning relative to non-urbanized local soils. Here I discuss the ecosystem functioning of patches of the urban landscape in and around Tucson, AZ, that have been transformed with the purpose of providing various ecosystem services to local residents and the greater urban ecosystem, such as rain gardens. This study compares soil properties, microbial function, and ecosystem functions among different patches of the Tucson urban ecosystem to determine how urbanization alters soils in semi-arid environments, and to determine if green urban modifications in desert cities can improve soils and ecosystem services. Soils in rain gardens have higher organic matter contents than native soils, and correspondingly, greater microbial function, higher abundance, and community complexity in these green modifications. These preliminary data indicate that soil quality is improved in arid system rain gardens. Such urban modifications both improve soils and reconnect ecohydrologic flows in

Tucson neighborhoods, suggesting that the provision of ecosystem services in cities can be assisted with small scale modifications.

**SPATIAL AND TEMPORAL DYNAMICS OF SOIL FREE-LIVING NEMATODE COMMUNITIES IN THE NIZZANA SAND DUNE ECOSYSTEM, NORTH-WESTERN NEGEV, ISRAEL. Pen-Mouratov<sup>1</sup>, Stanislav, C. Hu<sup>1,2</sup>, E. Hindin<sup>1</sup>, Y. Steinberger<sup>1</sup>.** <sup>1</sup>The Mina & Everard Goodman Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan 52900, Israel, <sup>2</sup>Institute of Plant Protection and Soil Science, Hubei Academy of Agricultural Sciences, Wuhan 430064, P. R. China.

In order to determine slope orientation impact on a soil free-living nematode community, its spatial and temporal dynamics and composition were studied at the xeric southern and the mesic northern facing sand dune slopes. Soil moisture, organic matter, and nematode population size and composition were determined monthly in samples collected from 0-10 and 10-20 cm layers, at the top and middle of two sand dune slopes. A significant ( $p < 0.05$ ) effect of sampling location on organic matter, total number of free-living nematodes, and trophic diversity was found, whereas soil moisture indicated only seasonal dependence. Moreover, soil moisture was found to be one of the most important abiotic variables that determined the total number of free-living nematodes, fungi-feeding and omnivore-predator trophic groups. Trophic diversity indices (TD) (which define trophic community composition), modified maturity index ( $\Sigma$ MI) (which reflects the degree of disturbance of the soil ecosystem and the monitoring of soil conditions), and basal index (BI) (which is used as a guide of a food web diminished by stress or marked by limited nutrient resources), indicated significant differences between both opposite slopes and between sampling locations on the same slope. However, trophic diversity (TD) and nutrient resource availability (BI) were higher at the southern slope, while the  $\Sigma$ MI indicated more unfavorable ecological conditions at the southern top and the northern middle plots. The results obtained in our current study elucidate the effect of slope orientation on soil free-living nematode communities in a sand dune ecosystem.

**THE EFFECT OF GARLIC MUSTARD (*ALLIARIA PETIOLATA*) DENSITY ON SOIL ENZYME ACTIVITY IN NORTHWEST OHIO. Pisarczyk, Elizabeth W., E.L. Hammer, M.N. Weintraub, and D.L. Moorhead.** Dept. of Environmental Sciences, The University of Toledo, 2801 W. Bancroft St., Toledo, OH 43606.

Garlic mustard (*Alliaria petiolata*) is a biennial herb, native to Eurasia that may have been imported to North America in the 1800's and since has invaded most of the Eastern and Midwestern United States. It possesses allelopathic compounds in its leaf litter and root exudates that decrease the presence of arbuscular mycorrhizal fungi, suppressing the germination of several hardwood tree species and other mycorrhizal species. Suppression of mycorrhizae suggests possible effects of garlic mustard on other soil microorganisms, and preliminary studies show impacts on bacterial community diversity and extracellular enzyme activity. We examined the effect of garlic mustard densities on soil enzyme activity in three forested plots in NW Ohio. Garlic mustard density gradients were identified at each site, and each gradient was divided into areas of high, medium and low density. A manipulative weeding experiment was also performed on other plots of high-density garlic mustard: plots were divided in half and one side was weeded whereas the other half remained a control. Monthly soil samples from both experiments were analyzed for enzyme activity, nutrient availability and microbial carbon and nitrogen content. Stepwise regressions produced few models that included garlic mustard density as a predictor of any single enzyme activity. A multi-variate analysis of variance (MANOVA) suggested that there were significant differences in enzyme activity with density for one site, however similar results were not observed in the manipulative weeding experiment. The MANOVA for the split-plot weeding experiment revealed several significant differences in enzyme activity, however the majority of these differences were only observed once during the course of the study. These results suggest that garlic mustard density does not have a consistent effect on microbial enzyme activity over time and between study sites.

**REPRODUCTION OF THREE MELOIDOGYNE SPECIES ON CRUCIFEROUS BIOFUMIGANT CROPS. Ploeg, A.** Department of Nematology, University of California Riverside, Riverside, CA92521, USA.

Biofumigation has been successfully employed as a strategy to manage soil borne diseases and weeds. Many cover crop cultivars used for biofumigation are hosts for root-knot nematode species, potentially resulting in a nematode build-up during the cover crop cultivation. To optimize the use of this strategy for root-knot nematode management, we have evaluated the host status of a range of cruciferous cover crop cultivars for three Meloidogyne species, in order to identify poor – or non-host varieties. Pots with different cruciferous crops were inoculated with *M. incognita*, *M. javanica*, or *M. hapla*. Eight weeks later, plants were harvested, and root galling severity, and nematode population levels in the pots were determined. The host status of the different cultivars was generally similar for *M. incognita* and *M. javanica*, with *Raphanus sativus* cultivars being poor hosts, and *Brassica juncea* being good hosts. Differences in host status for *M. hapla* were less pronounced, and did not reflect the results obtained with the other two Meloidogyne species. Results indicate that only few varieties can be used to avoid risk of nematode build-up of three common and agriculturally important Meloidogyne species. Field and microplot trials on *M. incognita* or *M. javanica* infested soil, confirmed the pot-test results, as moderate or good host cover crop varieties resulted in increased damage in following susceptible crops.

**EFFICACY OF BIO-FUMIGATION AND SOIL SOLARIZATION FOR THE MANAGMENT OF DAGGER NEMATODES IN FRUITS.** Pokharel<sup>1</sup>, Ramesh R., H. J. Larsen<sup>1</sup>, and S. Palanisamy<sup>2</sup>, <sup>1</sup>Western Colorado Research Center, Colorado State University, Grand Junction Colorado 81503. <sup>2</sup>Southwest Idaho R & E Center, Idaho State Universities, Parma, ID.

Dagger nematode (*Xiphinema spp.*) is an important problem for western Colorado fruit industries; it transmits plant virus and reduces productivity of trees. Surveys were carried out from 2006 to 2008 in western Colorado fruit orchards to assess distribution, frequencies and densities of dagger nematode in stone and pome fruit orchard soils. The nematode was widely distributed, had higher frequencies in most of the orchards surveyed, and had densities that varied with location, crop, soil and variety in western Colorado. Increased incidence and severity of cherry rasp leaf virus, vectored by the dagger nematode, have been observed in western Colorado cherry orchards. The virus also causes flat apple disease and peach is a symptomless host. Efficacy of bio-fumigation to control dagger nematode populations was evaluated in a naturally infested peach orchard soil using mustard (*Brassica juncea*) as green manure. The mustard crop was grown to maturity and the above ground portion either removed or incorporated into the soil with the roots. Dagger nematode populations were assessed before planting mustard and 2 months after mustard harvest. Dagger nematode populations were drastically reduced (almost 90%) by incorporating the whole mustard as compared to simply growing and harvesting mustard at maturity without incorporation. Soil solarization, was done using different colored and layers of plastic in a peach orchard soil naturally infested with dagger nematodes. Dagger nematode populations were reduced by more than 80% by soil solarization from June 18 to August 1 in western Colorado. Reduction in dagger nematode populations varied with different colors of plastic mulch. Further studies are underway on ways to enhance soil solarization via different layers of plastic and different soil amendments including mustard greens and meal cakes, manures and their combinations

**LINKING OPERATIONAL CLUSTERED TAXONOMICAL UNITS TO NEMATODE SPECIES IN PARALLEL-TAGGED ULTRASEQUENCING.** Porazinska<sup>1</sup>, Dorota L., R.M. Giblin-Davis<sup>1</sup>, T.O. Powers<sup>2</sup>, W. Sung<sup>3</sup>, and W.K. Thomas<sup>3</sup>. <sup>1</sup>Dept. of Entomology and Nematology, IFAS 3025 College Ave, University of Florida, Fort Lauderdale, FL 33314, <sup>2</sup>Department of Plant Pathology, 406 Plant Sciences Hall, University of Nebraska, Lincoln, NE 68583, <sup>3</sup>Hubbard Center for Genome Studies, 35 Colovos Rd., University of New Hampshire, Durham, NH 03824.

Parallel-tagged ultrasequencing (PUS) provides fast access to large amounts of microbiotic diversity data from environmental samples, but without proper bioinformatics infrastructure, the analysis of the sequence data becomes a major obstacle. We used PUS sequences from SSU and LSU rDNA diagnostic regions generated from control samples (artificially assembled nematode communities with known identities and quantities) to assess a relationship between nematode species and operational clustered taxonomical units (OCTUs) formed in a newly developed OCTUPUS pipeline. OCTUs formed at 95% similarity level underestimated number of species by ~25%, and OCTUs formed at 99% recovered almost all species. Although the total number of OCTUs increased from an average (across the two diagnostic loci) of 35 at 94% to 673 at 99%, a predictable pattern of the distribution of OCTUs around each species allowed an assignment of clusters of OCTUs to specific species by using a suite of parameters (e.g. OCTU length, bitscore, % similarity to database) at emerged cut-off levels. We examined the approach using environmental samples from a transect from a tropical rainforest in Costa Rica that had been previously characterized using standard (single nematodes) PCR amplification and sequencing methods. Just as in control samples, the number of OCTU-species estimated using 95% within OCTU similarity was lower by ~28% than when using OCTUs formed at 99% similarity. In addition, the patterns of species abundance were remarkably similar to those achieved by standard PCR methods. For instance, nematode richness within litter and understory habitats was approximately two times higher than within the soil environment. The total number of species predicted by rarefaction curves were also similar. We propose that our approach might provide a useful operation for approximating nematode species diversity from PUS reads clustered into OCTUs in the OCTUPUS pipeline.

**A DNA-BASED SYSTEM FOR DEFINING SPECIES BOUNDARIES IN MICROBIAL COMMUNITIES.** Powell<sup>1</sup>, Jeff R., M.T. Monaghan<sup>2</sup>, M. Öpik<sup>3</sup>, and M.C. Rillig<sup>1</sup>. <sup>1</sup>Institut für Biologie, Freie Universität Berlin, Altensteinstr. 6, 14195 Berlin, Germany, <sup>2</sup>Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), 12587 Berlin, Germany, <sup>3</sup>Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, 40 Lai St., 51005 Tartu, Estonia.

Microbiologists are constrained by the sheer diversity of organisms present within most environmental samples, the vast majority of which are unculturable. A common approach to dealing with this problem is to rely almost entirely on DNA sequence data to estimate microbial diversity and detect shifts in community structure. However, we currently lack the ability to quantify the taxonomic richness within the environment aside from arbitrarily-defined limits in sequence similarity. New quantitative approaches using likelihood-based methods that integrate phylogenetic and coalescent models seek to objectively define species boundaries in DNA surveys. The generalized mixed Yule-coalescent (GMYC) model distinguishes population-level processes within lineages from processes associated with speciation and extinction, thus identifying a distinct point where extant lineages became independent. Here, we tested the GMYC model on a functionally-important

group of soil microorganisms, the arbuscular mycorrhizal (AM) fungi. DNA was extracted from plant roots obtained from several boreal forest, dry meadow, and border sites across Estonia and the AM fungal 18S region was amplified, cloned, and sequenced. Most sequences were associated with the *Glomeraceae*, and further analyses focused on this family. A single-threshold GMYC model provided a significantly better fit to the data than a null model of uniform coalescent branching across the entire tree, suggesting that the technique could capture the transition point. A multiple-threshold GMYC model, allowing the transition point to vary among lineages, did not significantly improve the fit to the data. The model identified 26 distinct species clusters and three singleton sequences apparently representing the only observations of these clades. This objective approach to defining species limits, based on criteria of phylogenetics and coalescence rather than sequence similarity, will enhance our ability to estimate and compare microbial diversity in natural, managed, and impacted systems and could facilitate attempts to understand the structure and assembly of microbial communities.

**THE INFLUENCE OF PLANT GENOTYPE AND ENVIRONMENT ON NITROGEN CYCLING IN A MODEL POPULUS SYSTEM. Pregitzer, Clara.** Knoxville, Tennessee.

Abiotic and biotic variation has been shown to be important in regulating nutrient cycling and belowground communities in natural systems. Yet only recently has intraspecific variation been considered significant to these processes, and almost no studies have looked at these interactions across multiple environments. Using *Populus* as a model system in a common garden approach we hypothesized that: Genetic, environment and genetic by environment (G X E) interactions will affect plant-microbe-soil linkages. We used three different common gardens separated by elevation (low, mid and high elevation sites) in northern Utah, and five common *Populus* genotypes to measure the genotype and environmental effects on microbial pools of nitrogen as well as rates of nitrogen availability. We measured annual rates of net nitrogen mineralization/nitrification from genotypes across 3 environments that differ in soil moisture, soil/air temperature, precipitation, and soil pH. Preliminary results (from one season) show environmental variation is significant ( $p < 0.001$ ) in influencing nutrient cycling under these trees yet genotype has no significant influence on nitrogen availability. Overall, the greatest amount of nitrogen nitrified (N mg/kg) occurred at the low elevation site and the greatest amount of nitrogen mineralized (N mg/kg) occurred at the high elevation site suggesting N is more limited in the high elevation sites. Soil pH varied significantly by garden ( $p < 0.001$ ), not by genotype, but there was a significant G X E ( $p < 0.0259$ ) effect suggesting variation in the plant influence on soil pH across environments. Overall this study will allow for a better understanding of the role of both environment and genetic variation on above- and belowground species interactions and the consequences of these interactions on ecosystem processes.

**SOIL TOXICITY TESTS FOR ASSESSING CANADIAN BOREAL FOREST SOILS USING ECOLOGICALLY-RELEVANT PLANT AND SOIL INVERTEBRATE SPECIES. Princz<sup>1</sup>, Juliska I., M. Moody<sup>2</sup>, L. Van der Vliet<sup>1</sup> and R. Scroggins<sup>1</sup>.** <sup>1</sup>Environment Canada, Biological Methods Section, 335 River Rd., Ottawa, ON Canada K1A 0H3, <sup>2</sup>Saskatchewan Research Council, 1125-15 Innovation Blvd., Saskatoon, SK Canada S7N 2X8.

Environment Canada and the Saskatchewan Research Council are developing new toxicity tests for assessing contaminants present in soils found across the Canadian boreal forests. Two unique aspects were included within the scope of this method development: (i) the assessment of two different soil testing systems, both meant to mimic the boreal forest environment; and (ii) the use of ecologically-relevant test species. The soil test system options included the collection of individual soil horizons present within the forested regions and re-layering the horizons within the test vessels, and collection of intact soil cores. Most test species were collected directly from the field for the establishment of cultures. Established test populations were used to derive baseline reproduction values in uncontaminated soils for each species. The control data generated to date has contributed to the establishment of test performance criteria for boreal forest soils. The sensitivity of these new species (e.g., six plants: *Populus tremuloides*, *Pinus banksiana*, *Calamagrostis canadensis*, *Picea mariana*, *Picea glauca* and *Solidago canadensis*; three invertebrates: *Folsomia nivalis*, *Dendrodrilus rubidus*, and *Oppia nitens*) to contaminated forest soils was assessed through comparison to results from testing using standard agronomic soil species (e.g., *Trifolium pratense*, *Elymus laneolatus*, *Eisenia andrei*, *Folsomia candida*). The results from these studies will be presented and discussed. The development of these methods will improve the ability for industry to perform site-specific ecological risk assessments and assess remediation programs for the maintenance of soil ecological function within the forest ecosystems.

**NEMATODE COMMUNITY STRUCTURE OF SOIL FROM ALTERNATIVE MANAGEMENT AND NATURAL ECOSYSTEMS. Quintanilla, Marisol<sup>1\*</sup>, and G. Bird<sup>2</sup>.** <sup>1</sup>Northern Marianas College Cooperative Research and Extension Service, P.O. Box 501250, Saipan, MP 96950, <sup>2</sup>Department of Entomology, Nematology Program, Michigan State University, E. Lansing MI, 48824.

Nematode community structure (biological diversity, maturity and stability) was determined for soil from a pristine deciduous forest, two old-field successions (early and mid-succession) and three agricultural ecosystems (conventional, no-till, and bio-based) at the Michigan State University Long-Term Ecological Research (LTER) site at the Kellogg Biological

Station (KBS) in Hickory Corners, MI. Each ecosystem is replicated six times and three sampling dates were included. The early succession replicates were burned during the spring of each of the past five years. Fifteen ecological indicators were evaluated. These included absolute population density, total number of taxa, Shannon-Weiner Diversity, Simpson Dominance, Simpson 1-D, Simpson 1/D, Shannon's Equitability, Nematode Channel Ratio, Nematode Maturity Index (MI), Enrichment, and Structural Indices plus a multivariate canonical correspondence bi-plot analysis. Nematode community structure assessment indicated that the forest and old field successions were the most biologically diverse, mature and stable ecosystems. These nematode communities were different from those associated with the agriculture soils. The conventional and no-till systems had the lowest biodiversity, maturity and evenness. Ecosystem specific taxa were observed. Soil moisture apparently played a significant role in relation to detectable taxa. Nematode community structure differences among the ecosystems were most clear when the soil was dry. It appeared that increases in soil moisture potential made resources more available and opportunistic nematodes (r-strategist, or lower c-p values) more abundant. In a separate trial with compost, water was shown an ecosystem pulsing agent. In addition, the deciduous forests and mid old field succession had higher soil organic matter, lower pH, and lower bulk density than soil from the agricultural ecosystems and the early old field succession. The water stability of soil aggregates from the deciduous forest was greater than that of agricultural ecosystems when analyzed with both traditional and acoustical technologies. The nematodes recovered from this KBS/LTER nematode community structure research were photographed and are posted at [www.nemasoil.com](http://www.nemasoil.com).

THREE-DIMENSIONAL RECONSTRUCTION OF THE ANTERIOR, NON-AMPHID SENSORY ANATOMY IN *APHLENCHUS AVENAE* (TYLENCHOMORPHA) WITH PHYLOGENETIC COMPARISON TO RHABDITIDA OUT-GROUPS. **Ragsdale, Erik J.<sup>1</sup>, P. Ngo<sup>1</sup>, J. Crum<sup>2</sup>, M. H. Ellisman<sup>2</sup>, and J. G. Baldwin<sup>1</sup>.** <sup>1</sup>Department of Nematology, University of California, Riverside, CA 92521, <sup>2</sup>National Center for Microscopy and Imaging Research, University of California, San Diego, La Jolla, CA 92063.

The anterior sensory anatomy (not including amphids) of the nematode *Aphelenchus avenae* (Tylenchomorpha) has been three-dimensionally reconstructed from serial, transmission electron microscopy thin sections. Models, showing detailed morphology and spatial relationships of cuticular sensilla and internal sensory receptors, are the first computerized reconstruction of sensory structures of a Tylenchomorpha nematode. Results are analyzed with respect to similarly detailed reconstructions of Rhabditida outgroup nematodes, *Acrobeles complexus* (Cephalobomorpha) and *Caenorhabditis elegans* (Rhabditomorpha). In a comparison of three model taxa, several features have been putatively identified as synapomorphic between *A. avenae* and *A. complexus*, constituting the first strong morphological evidence for a clade including Tylenchomorpha and Cephalobomorpha and exclusive of Rhabditomorpha. Similarities between *A. avenae* and *A. complexus* include: the presence of a second, internal outer labial dendrite (OL1); a second cephalic dendrite in the female (CEP2/CEM); an accessory process loop of inner labial dendrite 1; terminus morphology and epidermal associations of internal sensory receptors BAG and URX; the presence of a lateral pair/syncytium of epithelial cells, "HypD," associated with all outer labial, cephalic, and amphid sheath cells. Unique to *A. avenae* is a pair of peripheral, lateral neurons of unknown homology but with axial positions and intercellular relationships nearly identical to, and thus possibly homologous with, the "posterior branches" of URX in *A. complexus*. Knowledge of homologies and connectivity of anterior sensory structures provides a basis for expansion of the experimental behavioral model of *C. elegans* to the economically important, largely plant parasitic Tylenchomorpha.

A PROPOSED APPROACH FOR THE ASSESSMENT OF SOIL CONTAMINANTS ON INDIGENOUS BOREAL FOREST SOIL MICROORGANISMS. **Rahn<sup>1,2</sup>, Jessica H., L.A. Beaudette<sup>1,2</sup>, J.T. Trevors<sup>2</sup>, H. Lee<sup>2</sup>, R. Theal<sup>1</sup>, P. Gillespie<sup>1</sup>, and R. Scroggins<sup>1</sup>.** <sup>1</sup>Environment Canada, Biological Methods Section, 335 River Rd. Ottawa, ON K1A 0H3, <sup>2</sup>Dept. of Environmental Biology, University of Guelph, Guelph, ON N1G 2W1.

The health of soil microbes and terrestrial ecosystems are clearly linked. Soil microorganisms play a significant role in nutrient cycling and organic matter decomposition. Tens of thousands of sites across Canada contain contaminated soils, so it is imperative that methods be developed to assess the toxic effects of soil contaminants on indigenous soil microbial communities. The development of these methods directly supports Canadian provincial and federal regulatory efforts to deal with contaminated land issues. Endemic soil microbial communities vary from site to site; therefore a set of tests with different assessment endpoints is needed. The proposed group of tests will assess microbial activity and biomass, as well as diversity and community structure. The measurement of soil microbial activity will be pursued using bait lamina, substrate induced respiration (SIR), microbial soil respiration, nitrification, and organic matter decomposition methods. The fumigation/extraction (FE) method will be used to evaluate soil microbial biomass. Soil microbial diversity and community structure will be examined using denaturing gradient gel electrophoresis (DGGE), community level physiological profiling (CLPP), and enzyme assays.

Preliminary results with the bait lamina, CLPP, and DGGE tests indicate that microbial communities differ between reference and contaminated soils. In a study using a lab-based bait lamina test to compare metal-contaminated and reference soils, a higher feeding activity was observed in the reference soil in comparison to the contaminated soil. DGGE results with salt-brine contaminated soils indicated a greater number of microbial species in the contaminated soil than in the reference

soils. It was also observed that the dominant microbial species differed between the two soil types. In contrast, DGGE results with a petroleum-hydrocarbon contaminated soil indicated a greater number of microbial species in the contaminated soils. While the communities in each soil types differed, similar DNA bands were observed, indicating similar species composition. CLPP analysis indicated a greater activity diversity in the reference soil compared to metal-contaminated soils. Much lower diversity of microbial activity was observed in the salt-brine contaminated soil than its two respective reference soils. When comparing soil horizons, the A horizon of a petroleum-contaminated soil exhibited similar activity than a comparable reference soil when analyzed by CLPP. In contrast, the more organic reference soil showed higher activity than its respective petroleum-contaminated soil. Method development is still underway for SIR, microbial respiration, nitrification, and organic matter decomposition tests as well as various enzyme assays. Once all tests have been applied in the laboratory, they will be evaluated using weighted criteria to determine which tests should be pursued for further validation and possible standardization. Additionally, the results of the final microbial tests will be directly compared to test results from Environment Canada single-species soil toxicity tests (earthworm, plant, and collembolan).

**SOIL MICROBIAL COMMUNITIES AND SOIL CHEMICAL CONDITIONS IN A RECENTLY RESTORED SALT MARSH. Rajaniemi, Tara K. and J. Breton.** Biology Department, University of Massachusetts Dartmouth, 285 Old Westport Road, North Dartmouth, MA 02474.

A salt marsh restoration was completed in Fall 2007 at the Atlas Tack Superfund Site in Fairhaven, MA. Contaminated sediments were excavated and filled with soil from an inland site. Restored portions of the marsh with new soils occur side-by-side with undisturbed marsh against which the recovery of restored portions can be judged. Here, we present data comparing soil chemical characteristics and microbial communities in restored and undisturbed marsh. In July and October 2008, soil cores were collected from 24 plots, with 19 plots in new, restored soils and 9 in intact marsh soils (4 at the edge of the restored area near intact marsh, 5 in an undisturbed section of the marsh). Soil pH, organic matter, total C and N, and  $\text{NO}_3^-$  and  $\text{NH}_4^+$  were measured in each core. DNA was extracted from soil at depths of 3cm and 20cm and the soil microbial community characterized by ARISA. Restored soils had lower pH, organic matter, total C and N, and plant-available N. Soil microbial communities differed between restored and undisturbed soils, but it remains unclear which environmental factors drive microbial community composition. Plots near the edge of the restored area did not differ from those in the remainder of the restored area. These data provide a baseline for monitoring the recovery of structure and function in the restored soils.

**SOIL MICROBES AND PLANT INVASIONS—HOW SOIL-BORNE PATHOGENS REGULATE PLANT POPULATIONS AND AFFECT PLANT INVASIONS. Reinhart, Kurt O.<sup>1</sup>** <sup>1</sup>USDA-Agricultural Research Service, Fort Keogh Livestock & Range Research Laboratory, Miles City, Montana.

Exotic plant invaders are a major global threat to biodiversity and ecosystem function. Here I present multiple lines of evidence suggesting that soil microbial communities affect the population growth rates of *Prunus serotina* in its native range and affect its invasiveness abroad. Research often reveals complex regulatory effects of oomycetes (specifically *Pythium* spp.) on *P. serotina* populations in its native range. *Prunus serotina* appears highly susceptible to some *Pythium* spp. even when they are at relatively low densities. Although research indicates oomycetes (and often more specifically *Pythium*) negatively affect *P. serotina* throughout its native range, results exhibit a high degree spatial complexity. For example in its native range, field and laboratory experiments reveal that pathogenic effects and *Pythium* densities vary among sites, among individual *P. serotina* trees, and with distance from *P. serotina* trees. At a biogeographical scale, plant-soil biota interactions appear more negative in the native than the non-native ranges, and biogeographical comparisons of the virulence of *Pythium* associating with *P. serotina* in its native vs. non-native ranges reveal that the *Pythium* species in its native range are considerably more virulent than those in its non-native range. A phylogenetic comparison of *Pythium* isolates associating with *P. serotina* revealed taxonomic shifts with virulent taxa associating with *P. serotina* in its native but not its non-native ranges. In total, these various lines of evidence support the idea that oomycetes, specifically *Pythium* species, are an important biological factor regulating the density of numerous populations of *P. serotina* in its native range but not in its invasive range. This biogeographical variation in regulation by *Pythium* pathogens is likely an important factor affecting its invasive success abroad. I also highlight the general challenges scientists face when determining whether soil microbes affect plant population growth rates and invasions and attempting to uncover the taxa driving these effects.

**SOIL BIOTA INTERACTIONS AND SOIL AGGREGATION. Rillig<sup>1</sup>, Matthias C., and D.L. Mummey<sup>2</sup>.** <sup>1</sup>Freie Universität Berlin, Institut für Biologie, 14195 Berlin, Germany. <sup>2</sup>Division of Biological Sciences, The University of Montana, Missoula, MT 59812, USA.

Soil aggregation is a fundamentally important ecosystem process mediated by a complex and diverse community of biota through a range of different mechanisms, active at different scales. Given a set of abiotic conditions (e.g., texture, climate), organisms play a central role in soil aggregation and are in turn influenced by soil structure in important but generally

non-quantified ways. Nevertheless, soil aggregation is often studied in agroecosystems and from the perspective of management practices (like organic matter additions, tillage, etc.). An organism-centered approach is generally not as common. Next to roots, arbuscular mycorrhizal fungi (AMF) are probably among the most important soil biota groups that influence soil aggregation, often displaying strong correlations with aspects of soil structure. Evidence is mounting to suggest that AMF species identity and diversity of the assemblage matter; but soil aggregation is definitely an underrepresented function in AMF research (compared to plant nutrition and pathogen protection). Still fewer studies have endeavored to test the importance of trophic (microarthropods, earthworms) or other interactions (e.g. associated bacteria) with AMF on soil structure. We summarize the work done and point to the importance of studying interactions involving multiple organism groups, as well as patterns within an assemblage.

**THE RELATIONSHIP BETWEEN ENZYME ACTIVITY AND MICROBIAL BIOMASS DURING LITTER DECOMPOSITION. Rinkes<sup>1</sup>, Zachary L. and M. N. Weintraub<sup>1</sup>.** <sup>1</sup>Department of Environmental Sciences, Mail Stop #604, University of Toledo, Toledo, Ohio 43606.

Soils are an important reservoir for carbon (C) in the global C cycle, because they can accumulate significant quantities of organic matter. As soil organic matter accumulates, it is decomposed by a succession of microorganisms, which have the ability to produce extracellular enzymes that can break down even the toughest plant litter constituents. Decomposition serves as a key control on carbon sequestration, yet the relationship between enzyme activity and microbial biomass dynamics that determine the amount of carbon sequestered are unclear. Research has shown that disturbances, such as elevated levels of carbon dioxide and increasing amounts of atmospheric nitrogen deposition, alter microbial activity during decomposition. This change in the level of activity may modify the amount of carbon stored in soils and influence soil nutrient availability, which is a key regulator of plant community composition. We examined this relationship between enzyme activity and microbial growth during litter decomposition in a high resolution lab incubation experiment. Our specific hypothesis was that the ratio of enzyme activity to microbial growth during decomposition will be strongly affected by nutrient availability and energy tradeoffs, with this relationship serving as a key regulator of soil carbon storage. A lab incubation experiment was set up using ½ pint Mason jars containing soil adjusted to 40% water-holding capacity mixed with finely ground *A. saccharum* litter. Litter was ground to increase surface area, which maximized accessibility to soil microbes. Jars were incubated at 20°C and replicates were destructively harvested over a three-month period. Replicates were analyzed for microbial biomass, microbial enzymes that drive carbon, nitrogen and phosphorus cycling, rate of carbon mineralization, bacteria to fungal biomass ratios, and soil nitrogen and phosphorus availability. Further exploration of the mechanisms that drive litter decomposition will give insight into how global climate change may impact soil carbon storage and nutrient cycling.

**INFLUENCE OF POPULATION DENSITIES OF *DACTYLELLA OVIPARASITICA* AND *HETERODERA SCHACHTII* ON SUGARBEET CYST NEMATODE POPULATION SUPPRESSION. Rocha, Fernando S.<sup>1</sup>, J. Smith Becker<sup>1</sup>, S. Benecke<sup>2</sup>, D.R. Jeske<sup>2</sup>, J. Borneman<sup>3</sup>, and J.O. Becker<sup>1</sup>.** Departments of <sup>1</sup>Nematology, <sup>2</sup>Statistics, <sup>3</sup>Plant Pathology and Microbiology, University of California, Riverside, CA 92521.

*Dactylella oviparasitica* is the primary causal agent of beet cyst nematode-suppressiveness located in field 9E at the University of California Riverside Campus Agricultural Operations. The fungus is an effective parasite of the *Heterodera schachtii* female, its eggs, and late juvenile stages that are exposed to the rhizosphere. In this project the relationship between fungal and nematode population densities was evaluated. Pots with methyl iodide-fumigated 9E soil were infested with *D. oviparasitica* inoculum obtained from potato dextrose cultures. The lowest density of the fungus was  $2 \times 10^1$  cfu/cm<sup>3</sup> soil with a 10-fold increase for each of the next three treatments. The pots were seeded with Swiss chard (*Beta vulgaris*) and incubated in a greenhouse at  $25 \pm 2^\circ\text{C}$  and ambient light. Four weeks later, the pots were infested with freshly hatched *H. schachtii* at 25, 50, 100 or 200 second-stage juveniles (J2) per 100 cm<sup>3</sup> soil. This resulted in 16 treatments with all possible combinations of fungal and nematode infestation levels. The trial design was a randomized complete block with 5 replications. After 9 weeks, the number of cysts, eggs, J2, fungal egg parasitism and plant weights were assessed. In treatments without *D. oviparasitica*, all final nematode population densities were positively correlated to the initial nematode infestation levels while the opposite was found with plant weights. There was a significant negative correlation between the fungal infestation level and the final nematode egg and J2 population density. Likewise, the percentage of egg parasitism by *D. oviparasitica* increased with increasing fungal inoculum.

**RENIFORM NEMATODE (*ROTYLENCHULUS RENIFORMIS*) RESISTANCE LOCUS FROM *GOSSYPIUM ARIDUM* IDENTIFIED AND INTROGRESSED INTO UPLAND COTTON (*G. HIRSUTUM*). Romano<sup>1</sup>, Gabriela B., E.J. Sacks<sup>1</sup>, S.R. Stetina<sup>1</sup>, A.F. Robinson<sup>2</sup>, D.D. Fang<sup>1</sup>, O.A. Gutierrez<sup>3</sup>, and J.A. Scheffler<sup>1</sup>.** <sup>1</sup>USDA-ARS CGPRU, P.O. Box 345, Stoneville, MS 38776, <sup>2</sup>USDA-ARS CPRU (retired), 2765 F&B Rd., College Station, TX 77845, <sup>3</sup>Dept. Plant and Soil Science, Mississippi State University, P. O. Box 5367, Mississippi State, MS 39762.

SSR markers associated with reniform nematode (*Rotylenchulus reniformis*) resistance were identified and mapped using progeny from a cross between a tri-species hybrid [*Gossypium arboreum* × (*G. 371* - *G. hirsutum* × *G. aridum* -)] and *G.*

*hirsutum* MD51ne. The 50 most resistant and 26 most susceptible progeny were genotyped with 104 markers. Of these, 25 markers were associated with a resistance locus. Two markers, BNL 3279\_132 and BNL 2662\_090, were mapped within 1 cM of the locus. Results indicate that the resistance is simply inherited, possibly controlled by a single dominant gene. Because the SSR fragments associated with resistance were found in *G. aridum* and the progenitor G 371 (*G. hirsutum* × *G. aridum*), *G. aridum* is the likely source of this resistance. The availability of this source of resistance in a *G. hirsutum* background, along with related molecular markers, should facilitate development of cotton cultivars with a high level of resistance to reniform nematode.

SOIL PROPERTIES, UNDERSTORY VEGETATION AND MICROBIAL COMMUNITY STRUCTURE AND STABILITY IN PURE AND MIXED-WOOD STANDS OF TREMBLING ASPEN AND JACK PINE FROM SOUTHERN BOREAL FOREST IN NORTHWESTERN QUEBEC. **Royer-Tardif, Samuel and R. L. Bradley.** Écologie des sols, Département de biologie, Université de Sherbrooke, Sherbrooke, Québec, J1K 2R1.

While mixed-wood stand management is experiencing increased interest from foresters, little is known about the consequences of tree mixtures on soil environments. Here we report on a study where we explored soil chemistry, understory vegetation and microbial community structure and stability in mixed-wood stands of jack pine and trembling aspen on two different geological parent materials. Basing on assumptions that plant diversity increases microbial beta-diversity and that this diversity is likely to increase microbial stability, we hypothesized that microbial stability in the presence of disturbance and stress would be greater in mixed-wood stands than in corresponding pure stands. Microbial stability was measured as microbial biomass resistance and resilience to a dry-wet disturbance and as tolerance to incremental additions of copper and HCl. Soil properties, understory vegetation and microbial structure and functional diversity were also measured to provide insights into the factors regulating microbial biomass stability. According to our results, mixed-wood stands possess a unique combination of soil, vegetation and microbial properties in comparison to single-species stands. We also find greater microbial resistance to dry-wet cycles in mixed-wood stands, probably a result of their greater microbial beta-diversity. Microbial communities in aspen-jack pine mixtures were also the more tolerant to stresses on both parent materials in comparison to single-species stands. Although stand composition did not affect significantly microbial resilience to dry-wet disturbance, we show that nutrient availability, driven by parent material identity, can be a strong factor regulating microbial resilience.

MOLECULAR MECHANISM OF SYMBIOSIS BETWEEN ENTOMOPATHOGENIC NEMATODES AND BACTERIA. **Ruisheng, An and P.S. Grewal.** Department of Entomology, The Ohio State University, Wooster, OH 4469, USA.

Association between bacteria *Photorhabdus* or *Xenorhabdus* and their nematode hosts represents an emerging model of animal-microbe symbioses. Here, we investigated transcriptomes of *Photorhabdus temperata* and *Xenorhabdus koppenhoeferi* during interaction with the infective juvenile (IJ) of nematode *Heterorhabditis bacteriophora* and *Steinernema scarabaei*, respectively. By using the cDNA selection method of selective capture of transcribed sequences and enrichment for the isolation of differentially expressed transcripts, a total of 50 and 29 transcripts were identified to be induced in *P. temperata* and *X. koppenhoeferi*, while 58 and 53 were repressed in the respective bacteria. Annotation of these transcripts suggests the development of biofilm only in *P. temperata* but not in *X. koppenhoeferi* and the limited cell motility and cell growth in both bacteria while in association with IJs. Differential expression of genes related to H<sup>+</sup> regulation indicates that both bacteria share cellular acidification process to maintain survival in their nematode hosts. Regulation of genes related to metabolism implies the utilization of TCA and pentose phosphate pathways in *X. koppenhoeferi* and *P. temperata*, respectively. To further obtain clues concerning importance of identified genes in bacteria-nematode association, we performed mutation studies on five genes identified in *P. temperata*. Compared to the wild type, bacterial mutant of gene *dnaK*, *metL*, or *tktA* supported nematode growth better, but mutant of *ileS* or *purL* was defective and all mutants exhibited lower level in the yield of and colonization of IJs, suggesting that these genes are required for bacterial retention in the IJs. In conclusion, in vivo gene expression of *P. temperata* and *X. koppenhoeferi* depicted molecular features which enable the bacteria to maintain the symbiotic life in their nematode hosts.

HEAT AND DESICCATION TOLERANCE OF LINES OF ENTOMOPATHOGENIC NEMATODES. **Ruiz-Vega, Jaime, and F. Ruiz-Carballo.** Mexico.

Entomopathogenic nematodes possess many attributes as ideal biological control agents; however, temperature extremes and low moisture levels (Aw) may restrict their use. The objectives of our study were to generate lines with tolerance to heat and desiccation in three entomopathogenic nematode species (*Steinernema glaseri*, *Steinernema riobrave* and *Heterorhabditis bacteriophora*). The nematode species were produced separately in *Galleria mellonella* larvae in the laboratory, harvested and stored at 8° C. One week after harvest, the nematodes were exposed to different temperature regimes and water stress. Treatments that selected for heat tolerance were applied to nematodes for six generations at temperatures of 25°, 30° and 35° C for 48 h; for selection for resistance to desiccation, the nematodes were exposed to Aw values of 0.86, 0.90 and 0.97 for 48 h. As the Aw decreased, the survival of all nematode species decreased, but after generation F3, *S. glaseri* was the most tolerant to desiccation, followed by *S. riobrave*. After generation F3, all nematode species increased their tolerance to

high temperatures, especially *Steinernema glaseri* and *H. bacteriophora*, which in generation F6 reached 80 and 70% survivorship at 35° C, respectively. The evaluation of the desiccation tolerance of the lines, which first was done on *Phyllophaga vetula* larvae showed that *H. bacteriophora* and *S. riobrave* were the most tolerant to low Aw's, whereas *S. glaseri* and *S. riobrave* were most tolerant to high temperatures. The generated lines were also evaluated against wild *G. mellonella* larvae; the results indicated that *S. glaseri* and *S. riobrave* were outstanding in their ability to infect and kill them at high temperature (35° C), while *H. bacteriophora* and *S. riobrave* showed good efficacy at low moisture levels. Taking into account their ability to kill both *P. vetula* and *G. mellonella* larvae, *S. glaseri* was the most effective at high temperatures, while *H. bacteriophora* had a better capacity of control at lower Aw's.

POPULATION-LEVEL GENETIC DIFFERENTIATION IN POPULUS AND EUCALYPTUS IMPACT SOIL NUTRIENT AVAILABILITY. **Schweitzer, Jennifer A.<sup>1</sup> J.K. Bailey<sup>1</sup>, R. Barbour<sup>2</sup>, J.A. O'Reilly-Wapstra<sup>2</sup>, T.G. Whitham<sup>3</sup> and B. M. Potts<sup>2</sup>.** <sup>1</sup>Dept. of Ecology & Evolutionary Biology, University of Tennessee, Knoxville TN 37996, <sup>2</sup>Dept. of Plant Sciences, University of Tasmania, Hobart TAS 4001, <sup>3</sup>Dept. of Biological Sciences, Northern Arizona University, Flagstaff AZ 86011.

Recent data demonstrating the importance of intra-specific variation to soil microbial communities and ecosystem processes highlights the importance of genetic variation to ecological and possibly evolutionary interactions between species. A next step in exploring the evolutionary consequences of genetic variation to soil processes is to examine the role of population-level genetic differentiation and local adaptation on nutrient processes. Using population level variation within *Populus* spp. and *Eucalyptus* spp. that have been planted in longterm common gardens in northern Utah, USA and northern Tasmania, Australia, respectively, we examined the hypothesis that genetic differentiation between plant populations of the same species will influence nutrient availability in soils beneath those trees. We found that, in both species, variation in soil total nitrogen (ammonium and nitrate) varied by plant population. Variation in plant productivity and secondary chemistry between populations are the putative mechanisms for these patterns, suggesting tight linkages between above- and below-ground processes. Across both species, our results indicate that evolution in plants leads to change in soil nutrient availability which has important applied and theoretical implications.

FATTY ACID FINGERPRINTS USED FOR THE IDENTIFICATION OF PLANT-PARASITIC NEMATODES. **Sekora, Nicholas S.<sup>1</sup>, K. S. Lawrence<sup>1</sup>, E. van Santen<sup>2</sup>, P. Agudelo<sup>3</sup>, and J. A. McInroy<sup>1</sup>.** <sup>1</sup>Dept. Entomology and Plant Pathology, Auburn University, Auburn, AL 36849, <sup>2</sup>Dept. Agronomy and Soils, Auburn, AL 36849-5412, <sup>3</sup>Dept. Entomology, Soils, and Plant Sciences, Clemson, SC 29634-0315.

For several years, chromatographic analysis of fatty acid methyl esters (FAME) has been used to identify bacteria more quickly than traditional methods. The objective of this study was to determine the applicability of FAME analysis for the identification of plant-parasitic nematodes for use in diagnostic laboratories. *Meloidogyne incognita*, *Rotylenchulus reniformis*, and *Heterodera glycines* were statistically distinct ( $P < 0.0001$ ) and could be identified in samples containing at least 100 total individuals for *M. incognita* and *R. reniformis* and 5 cysts for *H. glycines*. Two fatty acids (16:1  $\omega$ 5c and 18:1  $\omega$ 5c) indicate the presence of *R. reniformis* when comparing samples containing 100 or greater individuals of either *R. reniformis* or *M. incognita*. Significant variation ( $P < 0.0001$ ) in the fatty acid profiles of *M. incognita* and *R. reniformis* was observed when either species was increased on tomato, cotton, or soybean plants, but variations of the FAME profile for each nematode allowed for identification of each species regardless of host. Mixed-species samples of *M. incognita* and *R. reniformis* could be differentiated ( $P < 0.0075$ ) from one another and single-species samples of each species in 100% of comparisons when samples contained 5000 total individuals and in 95% of comparisons when samples contained 500 total individuals. In samples containing 500 total individuals, it was not possible to differentiate between a (50:50) ratio of *M. incognita* and *R. reniformis* or a sample with a (25:75) ratio of *M. incognita* and *R. reniformis*. However, all other comparisons, including these two ratios separately, were identifiable. Three *Meloidogyne* species (*M. arenaria*, *M. hapla*, and *M. javanica*) and three *M. incognita* races (races 1, 2, and 3) all produced distinct ( $P < 0.0001$ ) fatty acid profiles and could be identified with 85.6% overall accuracy to the race level. Soil containing *R. reniformis* produced a fatty acid profile significantly different ( $P < 0.0001$ ) from soil without *R. reniformis* and contained higher percentages of fatty acids found in nematodes. Certain fatty acids found in *R. reniformis* were found in higher quantities in soil infested with the nematode and may indicate its presence. The compiled library identified nematode samples with 90.4% total accuracy. Genus level identification was accurate at 100% for the samples studied and species level identification was 94.4% accurate. FAME analysis appears to be a promising alternative for identification of plant-parasitic nematodes.

ARBUSCULAR MYCORRHIZAL FUNGI FROM DIFFERENT SUCCESSIONAL STAGES DO NOT CHANGE PLANT PERFORMANCE. **Sikes, Benjamin A., J.N. Klironomos.** Dept. of Integrative Biology, University of Guelph, Guelph, Ontario, Canada.

Plant communities are generally thought to become increasingly more mycorrhizal dependent during succession, attributed to a reduction in available nutrients over time. It is unclear, however, if the composition or functioning of mycorrhizal

communities changes over time to account for this shift in dependency. We conducted a greenhouse experiment to test whether arbuscular mycorrhizal (AM) fungi from different stages of a well-defined sand dune chronosequence (Early dunes- 10-35ybp, Mid-dunes- 235-295ybp, Late dunes-450-745ybp) caused differential growth in plants from these different stages. We used eight plant species that were most abundant across the succession at different stages: Early- *Ammophila breviligulata*, *Artemisia campestris*, *Calamovilfa longifolia*; Mid- *Schizachyrium scoparium*, *Pinus strobus*; Late- *Acer rubrum*, *Deschampsia flexuosa*, *Pinus resinosa*. Plants were grown for four months in  $\chi$ -irradiated field soil mixed from all source dunes and re-inoculated with one of the following: sterile water, common microbial wash (<30 $\mu$ m), wash + Early (E), Mid (M), or Late (L) AM fungal inoculum, or a combined (EML) inoculum. All AM fungal inoculum was isolated by sucrose gradient centrifugation. Leaf number, average leaf length, diameter and chlorophyll concentration were estimated biweekly and at harvest, root and shoot biomass were measured. Across the different plant species, we found no differences in plant biomass ( $p>0.5$ ) or root:shoot ratios ( $p>0.5$ ) at the end of the experiment, based on the origin of the mycorrhizal inoculum. Furthermore, plants inoculated with AM fungi showed no significant differences from plants inoculated with a common microbial wash alone or completely un-inoculated plants. Analyses of time-series data will be presented. While preliminary, these data suggest that the soil microbial factors, including AM fungi from different successional stages, may have little effect on plant growth within this chronosequence.

**OCCURRENCE OF PLANT-PARASITIC NEMATODES ON GOLF COURSES IN ONTARIO AND QUÉBEC. Simard, Louis<sup>1</sup>, G. Bélair<sup>1</sup>, and J. Dionne<sup>2</sup>.** <sup>1</sup>Horticulture Research and Development Centre, Agriculture and Agri-Food Canada, St-Jean-sur-Richelieu, Québec, Canada J3N 1V3, <sup>2</sup>Royal Canadian Golf Association, Oakville, Ontario, Canada L6M 4X7.

In Canada, plant-parasitic nematodes (PPNs) are important pests of several annual and perennial plants such as carrot, potato, red clover, spring wheat and tomato, whereas PPNs are not currently recognized as a major turfgrass problem. During the last decade, golf course superintendents have been observing on a more regular basis various turfgrass damages not related to a disease and an insect problem. Thus, an extensive survey on thirty-eight golf courses located in the provinces of Ontario and Québec was conducted for PPNs on greens, fairways, and roughs in 2002 and 2003. Soil samples were taken and PPN numbers were estimated by processing two sub-samples of 50 g by the Baermann pan method. Sixteen, 15 and 12 genera of PPNs were found on golf greens, fairways and roughs, respectively. *Pratylenchus* was the most frequent genus recovered on greens and fairways, whereas *Tylenchus* was the most common on roughs. Among the genus *Pratylenchus*, *P. crenatus* was frequent and widespread, whereas *P. penetrans* and *P. thornei* were uncommon. PPN densities obtained were occasionally above the known damage thresholds but no visual symptoms were observed during this study. However, in 2005, an unidentified disease on an annual bluegrass green was recorded on a golf course in the Montréal area (Québec). Irregular yellowish/chlorotic patches were monitored on the collar of one green and a lower turfgrass density in the diseased areas was noticed. When roots were examined under a dissecting microscope, galling was found. Upon dissection of washed galls, root-knot nematode egg masses and mature females inside the roots were observed. Morphological identification of mature females and juveniles were performed and confirmed to be *Meloidogyne naasi*. This is the first report of the occurrence of *M. naasi* in Canada where it is causing noticeable damage to turfgrass in Québec. In 2006, irregular yellowish/chlorotic and dead turfgrass patches were again observed on several sand-based creeping bentgrass greens on a golf course in Bromont (Québec). Numerous nematode extractions were performed using soil from damaged but also healthy areas. Identification was determined by morphological examination of a small number of adult female nematodes ( $n=7$ ) and confirmed to be *Longidorus breviannulatus*. This is the first report of the occurrence and turfgrass damage caused by *L. breviannulatus* in Québec. In 2008, turfgrass damage with an important decline of the turfgrass root system was observed on few creeping bentgrass greens on a golf course in Ste-Julie (Québec). High populations of PPNs were recovered from soil samples using the pan method. Preliminary identification indicated that turfgrass damage is associated to the presence of an unknown species of *Meloidogyne* sp.

**RELATIONSHIPS BETWEEN INVERTEBRATE HABITAT PREFERENCE, STREAM FLOW AND DIEL TEMPERATURE FLUCTUATION IN AN ANTARCTIC MELTWATER STREAM. Simmons, B.L.<sup>1</sup>, B.J. Adams<sup>2</sup>, D.M. McKnight<sup>3</sup> and D.H. Wall<sup>1,4</sup>.** <sup>1</sup>Natural Resource Ecology Laboratory, Colorado State University, Fort Collins, CO 80523, <sup>2</sup>Department of Microbiology and Molecular Biology, Brigham Young University, Provo, UT 84602, <sup>3</sup>Institute of Arctic and Alpine Research, University of Colorado, Boulder, CO 80309, <sup>4</sup>Department of Biology, Colorado State University, Fort Collins, CO 80523.

The glacier-fed ephemeral streams that flow into Lake Fryxell (Taylor Valley, Antarctica) exhibit strong, predictable diel temperature patterns, peaking at similar times regardless of stream orientation or length. Stream temperatures can reach maximums of 10°C above air temperatures, and are controlled by solar radiation, not stream flow, which peaks separately. We hypothesized that invertebrates move between aboveground (cyanobacterial mats) and belowground (sediment) habitats in response to physical perturbation, such as changes in water temperature or stream flow. Cyanobacterial mats and the aquatic sediments directly beneath were sampled at five sites along Von Guerard Stream. Samples were taken from two locations (where mats are constantly or only intermittently submerged by stream flow) at each site every 4 hr for 24 hr ( $N = 140$ ). With the exception of the nematode *Eudorylaimus* sp., all other invertebrate groups were significantly more abundant in cyanobacterial

mats compared to aquatic sediments directly beneath ( $P < 0.01$ ), regardless of sample location. This supports previous work indicating that *Plectus* spp are well-suited to exploiting patchy resources in aquatic and semi-aquatic areas, and that rotifers and tardigrades prefer vegetative habitats over aquatic sediments when available. *Eudorylaimus* sp. is suspected to prefer moist but not saturated environments, and is typically more abundant in moist sediments in wetted zones compared to cyanobacterial mats. Abundances of *Eudorylaimus* sp. were generally higher in aquatic sediments compared to cyanobacterial mats, and in areas where mats were only submerged during periods of high flow, but these variables did not significantly affect their distribution ( $P = 0.15$  and  $P = 0.13$ , respectively). Preliminary analysis across time provides evidence for movement of *Eudorylaimus* sp. between above- and belowground habitats regardless of sample location ( $P = 0.04$ ). Abundances of *Eudorylaimus* sp. in the cyanobacterial mats peaked twice over the course of the experiment, and were inversely related to smaller peaks in abundances in associated sediments. It is unclear at this time whether these peaks are related to changes in stream temperature or flow, but further analysis will allow for testing of correlations between densities of *Eudorylaimus* sp. and stream dynamics. No other invertebrate groups appeared to be affected by sampling time, and abundances remained steady throughout the course of the experiment. The results of this and other recent work on invertebrate community dynamics across aquatic-terrestrial interfaces in the McMurdo Dry Valleys highlight the need for more information on the relationship between invertebrates, the major transformers of nutrients in this system, and stream variables such as percent vegetative cover, cyanobacterial species composition, dimensions of the wetted zone, or nutrient flow. Linking stream dynamics and function with invertebrate biology would allow for better prediction of total ecosystem response to global changes.

**RESPONSE OF CARICA PAPAYA TO MELOIDOGYNE JAVANICA IN THE GREENHOUSE. Sipes, Brent<sup>1</sup>, M. Berry<sup>1</sup>, R. Manshardt<sup>2</sup>, and S. Ferreira<sup>1</sup>.** <sup>1</sup>Department of Plant and Environmental Protection Sciences, and <sup>2</sup>Department of Tropical Plant and Soil Sciences, University of Hawaii, 3190 Maile Way, Honolulu, HI 96822.

Papaya (*Carica papaya* L.) trees infected with root-knot nematodes (*Meloidogyne javanica*) can be stunted, have lower yields, and increased sensitivity to stresses. We conducted two separate greenhouse experiments to quantify root-knot nematode susceptibility of different cultivars and breeding lines of papaya and to quantify damage to a standard commercial cultivar. In the first experiment, papaya cultivars Kapoho, Maradol, Saipan, Sunrise and Vietnam, and breeding lines UH Poamoho, Richter 181.OM20-1, Richter 192.OM3-1, and Richter 192.OM3-2 were inoculated with 5,000 root-knot nematode eggs. Each genotype was replicated 8 times. Four months later, a nematode reproductive factor (Rf) was determined for each genotype. All the papayas supported nematode reproduction. Saipan supported the least nematode reproduction (Rf = 0.6) among the papaya tested. Vietnam, UH Poamoho, Kapoho, and Richter 192.OM3-1 supported moderate nematode reproduction with Rfs between 1.5 to 1.9. Richter 192.OM3-2 and Maradol were more susceptible with Rfs of 3.5 and 3.7 respectively. Richter 181.OM20-1 and Sunrise had the greatest Rfs (8.9 and 14.0 respectively). In the second experiment, 2-month-old Sunrise papaya seedlings were inoculated with 0, 500, 1000, 5000, 10,000 or 50,000 eggs with each treatment being replicated 8 times. Three months later, plant growth and nematode numbers were measured. Root and shoot weight decreased with increasing nematode Pi, such that plant dry weight = 23g - 0.00015(Pi). Papaya genotypes differ in their response to *M. javanica*. The Hawaiian papaya cultivars are among the more susceptible genotypes to *M. javanica*. Damage caused by *M. javanica* is not especially on Sunrise papaya however.

**MOLECULAR AND MORPHOLOGICAL DESCRIPTION OF MELOIDOGYNE ARENARIA FROM TRAVELER'S TREE (RAVENALA MADAGASCARIENSIS). Skantar, Andrea M.,<sup>1</sup> L.K. Carta,<sup>1</sup> and Z.A. Handoo<sup>1</sup>.** <sup>1</sup>Nematology Laboratory, USDA, ARS, Henry A. Wallace Beltsville Agricultural Research Center, Bldg. 011A, Room 165B, Beltsville, MD 20705-2350.

An unusual variant of *Meloidogyne arenaria* was discovered on roots of a traveler's tree (*Ravenala madagascariensis*) intended for display at a public arboretum in Pennsylvania. The population aroused curiosity by the lack of visible galling on the roots of the infected plant. Morphometrics of the population fit within the ranges reported for *M. arenaria*, with a mosaic of features in common with either *M. platani* or other tropical *Meloidogyne* spp. Molecular characterization included analysis of four loci. The mitochondrial sequence, extending from cytochrome oxidase II (*COII*) to the 16S (*IRNA*) gene, was nearly identical to another *M. arenaria* population and closely related to sequences from *M. morocciensis* and *M. thailandica*. The 28S D2-D3 expansion segment was most similar to those from *M. arenaria*, *M. incognita* and *M. paranaensis*, and the IGS-2 was most related to those from *M. thailandica*, *M. arenaria* and *M. incognita*. Analysis of partial Hsp90 genomic sequences revealed the greatest similarity to *M. arenaria*, *M. thailandica* and an Hsp90 haplotype from *M. floridensis*, and a composite sequence comprised of EST from *M. arenaria*. While highly unusual in some aspects, there were no molecular or morphological features that clearly set this population apart as a new species; taken together, the data points to its identification as *M. arenaria*.

**ESTIMATION OF CARBON POOLS BASED ON RESPIRATION FROM AGGREGATE SIZE FRACTIONS. Smith, Jeffrey L.** USDA-ARS, Department of Crops and Soil Sciences, Washington State University, Pullman, Washington, 99164.

Microbial transformation and turnover of soil organic matter (SOM) can influence the magnitude of soil C storage. These microbially-mediated reactions, among soil organisms, enzymes and SOM, fractionate organic material into various reactive

C pools. These C pools have traditionally been designated as labile, slowly decomposable, and resistant with respect to their persistence in soil. In many studies the fractionation into C pools is calculated from respiration data obtained from soil incubation experiments. However, these calculations may be dependent upon the pretreatment of the soil, specifically sieving to a particular aggregate size fraction. We fractionated four different soils into aggregate size classes and incubated them for 128 days using the CO<sub>2</sub> respired to calculate C pool sizes and kinetic parameters. In addition we determined the non-hydrolyzable total C and N for each fraction. The less than 1 mm and 1-2 mm aggregate fractions showed similar C pool sizes and C dynamics except for the high organic matter forest soil. The highest rates of C mineralization occurred in the 2-4 mm size fraction. The calculated kinetic parameters varied with aggregate size fractions and predicted different C mineralization potentials. Except for the sandy loblolly pine soil non-hydrolyzable C was similar within fractions of each soil. In general in each soil the non-hydrolyzable C was a consistent fraction of the total C of each aggregate size. Thus overall the pretreatment of the soil may influence the calculation of C pools and kinetic parameters when using the long-term incubation method for determining these parameters.

**BIOLOGICAL NEMATODE CONTROL IN CHANGING CLIMATES. Smith, Kelly S., and T.E. Hewlett.** Pasteuria Bioscience, Inc. 12085 Research Dr., Suite 185, Alachua, FL 32615.

Nematodes are currently estimated to be a \$1 billion problem in global agriculture, and the largest unmet need in pest control. Fumigants and other traditional pesticides are increasingly unavailable to growers due to safety and environmental hazards, cost, and a growing demand for alternative pest control strategies. Climate change is likely to exacerbate the problem of nematode control as with many other pests. Changing temperatures may be correlated with shifts in population dynamics, including changes in the geographic ranges of known nematode pests. The host ranges of these nematodes may also shift as they move into new areas. Biological control is well-suited to managing these pest problems, as it can be rapidly adapted to changing nematode populations and host preferences without creating additional unintended effects on crop safety or the environment. In contrast, approaches using genetic modification of crop plants take years or decades to become marketable, and require much more extensive safety and environmental testing before they can be fully deployed. Biological control also avoids the often negative public perception of GMO food plants and thus can also be more rapidly marketed and sold. Therefore biological control methods for nematodes will be of increasing importance in the growers' arsenal of pest control products in changing climatic conditions.

**INCREASED SOIL MOISTURE AVAILABILITY RESULTING FROM SUBSURFACE ICE MELT HAS AN IMPACT ON NEMATODE ABUNDANCES AND COMMUNITY STRUCTURE IN A POLAR DESERT ECOSYSTEM. Smith, Tracy E.<sup>1</sup>, D.H. Wall<sup>1</sup>, I.D. Hogg<sup>2</sup>, and B.J. Adams<sup>3</sup>.** <sup>1</sup>Department of Biology, Colorado State University, 200 W Lake St, Fort Collins, CO 80523-1878. <sup>2</sup>Department of Biology, Natural Resource Ecology Laboratory, and School of Global Environmental Sustainability, Colorado State University, 200 W Lake St, Fort Collins, CO 80523-1499, <sup>3</sup>Centre for Biodiversity and Ecology Research, Department of Biological Sciences, University of Waikato, Private Bag 3105, Hamilton, New Zealand. 685 WIDB, Brigham Young University, Provo, UT 84602.

Polar desert ecosystems are experiencing decadal events of high temperatures, which can result in increased soil moisture from glacier and permafrost melt. The McMurdo Dry Valleys of Antarctica are an ice-free polar desert ecosystem characterized by limitations of water and carbon. Nematodes, the dominant faunal species in the system, are highly adapted to this extreme environment. The microbial-feeding *Scottinema lindsayae* is an endemic nematode that is the most widely-distributed species across the Dry Valleys, and is known to occur in soils of low moisture and high salinities. In the region's moist soils, on the other hand, the other two inhabiting genera *Plectus* (also a microbial-feeder) and *Eudorylaimus* (an algal feeder) tend to be more abundant. During the austral summer 2008-09, occurrences of subsurface ice melt resulted from warming events in the Dry Valleys. We examined soils at two locations in Taylor Valley, to test the hypothesis that increases in soil moisture alter nematode life demographics, community structure, and depth distribution. We compared sites that had no seepage (dry soils) with those having visible seepage, and dug soil pits to the surface of the ice-cemented permafrost. We sampled the soils in 10 cm depth increments from surface soil through the active layer to and including the depth of permafrost surface, to investigate whether additional water (seepage) increases moisture throughout the soil profile and alters the depth distribution, abundance and species composition of nematodes. This experiment included three replicates of each treatment (seep versus dry soils) per site, across two watersheds in the dry valleys. We found varying effects between the two locations. One of the locations had much higher soil moisture contents in both the seep and dry sites compared to their replications at the other location. In this instance the seep significantly accounted for the variation in nematode abundances between sites ( $p < .01$ ), with the seep soils nearly devoid of individuals. This suggests that increased temperature affecting permafrost melt and subsequently soil moisture may have a major impact on nematode abundances and distribution, and the level of impact may be controlled by soil moisture prior to increased seep. Community composition did not differ between dry and wet soils, although based on a recent study it is possible that there will be a one-year lag time before shifts are apparent. Our study has implications for how organisms in terrestrial polar desert ecosystems might be affected by changes in climate, as the region is expected to experience both periodic short-term warming events as well as future increased warming trends over a much longer timescale. An understanding of how the biota in these systems may be impacted by such changes will in turn contribute to the understanding of consequent changes in the ecosystem's functioning.

FORMS AND FUNCTIONS OF MESO AND MICRO-NICHE CAPACITIES WITHIN SOIL AGGREGATES. **Smucker, Alvin, E.J. Park, W. Wang, W.J. Sul and M. Rivers.** Michigan State University, Gyeonggi Research Institute and Univ. of Chicago.

Aggregate black boxes include soil clay-water-ion-organic matter contents combined with natural dry/wet cycling alters intra-aggregate pore continuity, connectivity, dead-end storage volumes, and tortuosity. Surface aggregates in the 0-5 cm depths of most soils experience from 34 to 57 DW cycles with delta water content exceeding 10%. Both the rates of drying or wetting, (intensity) and the contrasting delta values of soil water contents (severity) alter the transport of water, C and N through micro and mesofaunal habitats at the both the micro and mesoscales. These changes alter gaseous compositions, C and N storage capacities and microbial communities among different regions within soil aggregates. Recent advances in X-ray microtomography enable the examination of intact pore networks within soil aggregates at resolutions as small as 4 microns. Geostatistical and multifractal methods provide concise characteristics of pore spatial distributions within the aggregates and are useful for comparing these alterations among soils. In collaboration with the Advanced Photon Source at the ANL, we compared similar air-dried aggregates from the same soil type which were subjected to multiple wetting and drying (WD) cycles. X-ray microtomography is a great tool that offers quantitative descriptions which can be used to summarize and compare intra-aggregate structures and internal organizations among different soil types, agricultural practices and land uses. Aggregates with WD pretreatments developed greater spatial correlation ranges that parallel with increased  $^{13}\text{C}$  sorption away from respiring microorganisms. T-RFLP electropherograms of PCR-amplified 16S rDNA microbial nucleotides demonstrated significant shifts in the abundance of unique microbial ribotypes within exterior and interior regions of macroaggregates subjected to 0 and 5 D/W cycles. Modifications of intra-aggregate pores to reduce aerobic and anaerobic greenhouse gases will be described in greater detail. Past research indicates that microbial activities within the soil aggregate matrix are spatially heterogeneous due to complex pore geometries within aggregates. Geostatistical and multifractal methods provide concise characteristics of pore spatial distributions within the aggregates and are useful for comparing these alterations among soils. Illumination of the "blackbox" interiors of soil aggregates by synchrotron microtomographic 2D and 3D imaging and improved image analyses, provide a physical form of the biophysical and biogeochemical functions controlling flow rates of soil solutions through intra-aggregate pore geometries. This presentation includes a discussion of natural and anthropogenic alterations of solution flow, carbon sequestration, and respiration of soil aggregates containing biological, chemical and physical gradients.

EFFECTS OF HURRICANE DISTURBANCE ON SOILS IN A CHANGING WORLD. **Stanturf<sup>1</sup>, John A., S. L. Goodrick<sup>1</sup>, M. A. Callahan<sup>1</sup>, Jr. and J. J. O'Brien<sup>1</sup>.** <sup>1</sup>Center for Forest Disturbance Science, Southern Research Station, U.S. Forest Service, Athens, GA 30602 USA.

From a soil-centric view, hurricanes are just another disturbance of varying recurrence with both direct and indirect effects, which depend on disturbance intensity, distance from the coast, and vulnerability of the vegetative cover. Near the coast, storm surge and overwash of salt water affect soils in ways that other wind-related disturbances do not. Changes in inundation regimes of coastal rivers are generally short-term and cause anaerobiosis, but longer-term effects arise from changes in coastal morphology. In general, however, the greatest (and most studied) hurricane effect on soils is through damage to the vegetative cover. A severe hurricane will extensively influence the composition, structure and subsequent development of vegetation. Stripped leaves, broken branches, and broken or tipped stems are a pulse of carbon and other nutrients to the soil surface, and dislocated or severed root systems are similarly available for decomposition. Loss of vegetative cover, especially in coastal forests, affects soil microclimate through greater insolation and heating. An immediate impact of hurricanes is a massive conversion of living forest biomass to dead fuel, an increase in fuel bed depth, and a decrease in dead fuel moisture that can increase the risk of severe wildfires that remove organic layers and heat mineral soil. Thus, hurricane damage to vegetation can affect soils by altering pools of carbon and some other nutrients and generally by accelerating decomposition, altering nutrient cycling, and elevating respiration. Global change potentially will impact soils in hurricane-impact zones in various and complex ways. Climate change in terms of altered maximum and minimum temperatures and precipitation and their distribution (seasonality) as well as increased frequency and severity of extreme events (particularly hurricanes, drought, and lightning) and sea-level rise will alter composition and structure of vegetative communities. Demographic changes and human responses to climate change effects on coastal areas will constrain management of wildland areas, especially in managing hazardous fuels and increasing the potential for human-caused ignition of wildfires. Change in vegetation over large areas feeds back to the climate system, leading to a cascade of further change and impact on soils.

INHERITANCE OF RESISTANCE TO *MELOIDOGYNE INCOGNITA* IN PRIMITIVE COTTON ACCESSIONS. **Starr, J. L.<sup>1</sup>, R. L. Nichols<sup>2</sup>, E. Moresco<sup>1</sup>, and C. W. Smith<sup>3</sup>.** <sup>1</sup>Dept Plant Pathology and Microbiology, Texas A&M University, College Station, TX 77843; <sup>2</sup>Cotton Incorporated, Cary, NC 27513; <sup>3</sup>Dept Soil & Crop Sci., Texas A&M University, College Station, TX 77843.

Most of the resistance in upland cotton (*Gossypium hirsutum*) to the root-knot nematode *Meloidogyne incognita* used in research and breeding programs has been derived from the accessions Cleve-wilt-6 (CW) and Wild Mexico Jack Jones

(WMJJ). There are conflicting reports on the genetic basis for resistance to root knot in CW and no data are available on WMJJ. There are numerous other cotton accessions reported to express resistance to *M. incognita*, including the accessions TX-1174, TX-1440, TX-2076, TX-2079, and TX-2107; however no data on inheritance are available for these lines. A half-diallel cross experiment that included all of these genotypes plus the susceptible cotton DP-90 was established. The parents, F1, and F2 generations were screened in greenhouse tests for ability to support reproduction of *M. incognita*, measured as eggs per g roots, to estimate allelic relationships and inheritance of resistance of each resistant genotype. In these tests, F1 progeny from crosses of CW or WMJJ with DP-90 were susceptible, supporting similar numbers of eggs per g root as the susceptible DP-90, indicating that the resistance in these two accessions was inherited as a recessive trait. The segregation of resistant phenotypes in the F2 generation further suggested that resistance of CW and WMJJ was conditioned by multiple genes and that at least some of the resistance genes differed between the two genotypes. Resistance in each of the TX accessions appeared to be inherited as a dominant trait, as all F1 individuals in crosses with DP-90 were resistant, supporting relatively low levels of reproduction. Resistance in TX accessions appears to be conditioned by a single major gene, which may be allelic in some of these accessions. Collectively, these data suggest that there are multiple unique genes for resistance to *M. incognita* in the *G. hirsutum* germplasm collection and that resistance gene(s) in the TX accessions are different from those present in CW and WMJJ. Therefore, the number of resistance genes presently being used in cotton breeding programs can be expanded beyond its current narrow base.

THE INTERACTION OF *VICIA FABA* BEANS WITH DIFFERENT POPULATIONS OF *DITYLENCHUS DIPSACI*. **Stawniak, Natalia**. National Institute of Agricultural Botany, Huntingdon Road, Cambridge, CB3 0LE, natalia.stawniak@niab.com.

Stem nematode *Ditylenchus dipsaci* (Kühn) causes deterioration of bean seeds, yield loss, and persistent soil contamination in the UK. In the past, the oat-onion race was reported to be at higher levels than the giant race. However, recent analyses using restriction fragment length polymorphism (RFLP) of very heavy infected seed lots showed that 92% of lots were contaminated by the giant race. This race identification was used to develop a resistance screening programme and host range study. Cultivars grown in the UK showed a significant variation in susceptibility to the giant race. Damage caused by *D. dipsaci* was marked by a severe brown lesion and swelling on the stem. Line 29H, reported as resistant in several locations, was confirmed as resistant with UK giant race populations under glasshouse conditions. However, more severe symptoms were observed after inoculation of this line with the oat-onion race. Resistant cultivars should help to decrease soil and seed infestation. Host-range experiments confirmed the higher susceptibility of field beans to the giant race than to oat-onion race. Lupin, sugar beet and pea were all sensitive to the oat-onion race but not to the giant race. The results indicate the importance of effective field bean cultivar resistance evaluation to different *D. dipsaci* populations and the significance of specific crop rotations.

INDIRECT EVIDENCE FOR REDUCED ENZYME TURNOVER UNDER EXPERIMENTAL DROUGHT AT THE BOSTON AREA CLIMATE EXPERIMENT. **Steinweg, J. Megan**<sup>1,2</sup> and **M.D. Wallenstein**<sup>1,2</sup>, <sup>1</sup>Natural Resource Ecology Laboratory, Campus Delivery 1499, Colorado State University Fort Collins, CO 80523-1499, <sup>2</sup>Graduate Degree Program in Ecology, 206 Natural Resources, Colorado State University Fort Collins, CO 80523.

Currently there is little consensus on how soil organic matter (SOM) decomposition will respond to climate change over the long-term. Moisture and temperature are key drivers of SOM decomposition rates, however it is not clear how changes in these drivers will affect the degradation of different soil compounds over the long-term with new climate regimes. Soil enzyme activity is a relevant metric of soil community function because it is related to decomposition of specific substrates in soil. Enzymes are released in response to nutrients an organism needs as well as what is available in the soil matrix. Enzyme activity is measured as potential activity, and it is an indicator of the enzyme pool size. We collected soils from the Boston Area Climate Experiment (BACE), an old field site located in Waltham, MA. There are three precipitation treatments (ambient, plus 50% precipitation, and minus 50% precipitation) and four temperature treatments (ambient, +200 W m<sup>-2</sup>, +600 W m<sup>-2</sup>, and +1000 W m<sup>-2</sup>) arranged in a full-factorial design with three replicates. Precipitation treatments began in June 2007, and warming started in July 2008. Soils were collected in June 2008, August 2008 and January 2009, sieved and stored at -80°C until enzyme analysis. Enzyme assays for  $\beta$ -glucosidase, cellobiohydrolase, xylosidase, N-acetyl glucosamidase, and leucine amino peptidase were performed at 15, 25 and 35°C using fluorescent substrates. These enzymes are involved in the cycling of carbon, nitrogen, and phosphorus in the soil. There was no effect of warming on enzyme activity, however the drought treatment decreased microbial biomass but significantly ( $p < 0.05$ ) increased activity of several enzymes in both August 2008 and January 2009 compared to control plots. An increase in activity under drought could be due either to increased enzyme production or decreased turnover rates. Under drought, the diffusion of enzymes, substrates and products is constrained and microorganisms may have increased enzyme production to compensate for lower diffusion rates. However, microbial biomass was lower in August under drought potentially ruling out increased enzyme production as a likely hypothesis. Alternatively, increased enzyme activity in January may be due to decreased enzyme turnover in the colder months. The temperature sensitivity of enzyme activity was higher in the reduced precipitation treatment in January 2009. The increased temperature sensitivity could be explained by increased

production of enzymes in late summer and a decrease in turnover during the winter, since enzymes produced during the summer may have higher temperature sensitivities. These results indicate that precipitation reduction due to climate change may lead to increases in enzyme activity and soil organic matter decomposition.

**OCTUPUS: A PACKAGE FOR DEFINING “OPERATIONAL CLUSTERED TAXONOMIC UNITS FROM PARALLEL-TAGGED ULTRA-SEQUENCING”.** Sung<sup>1</sup>, Way, D. Porazinska<sup>2</sup>, S. Creer<sup>3</sup> R.M. Giblin-Davis<sup>2</sup>, and W.K. Thomas<sup>1</sup>. <sup>1</sup>Hubbard Center for Genome Studies, University of New Hampshire, Durham, NH 03824, <sup>2</sup>Fort Lauderdale Research and Education Center, University of Florida, IFAS, 3205 College Avenue, Fort Lauderdale, FL 33314, USA, <sup>3</sup>School of Biological Sciences, University of Wales, Bangor, Gwynedd LL57 2UW, UK.

The ability to catalog multiple samples using parallel-tagged ultra-sequencing in conjunction with low cost sequencing technology has revolutionized the use of metagenetics in the study of biodiversity. The massive amount of data generated from high throughput sequencing has led to a need for an efficient pipeline for the organization and definition of metagenetic diversity. Here we introduce OCTUPUS, a program designed for the definition of Operational Clustered Taxonomic Units from data generated through Parallel-tagged Ultra-Sequencing. OCTUPUS works in tandem with a number of well-refined bioinformatic tools in order to generate a list of operational clustered taxonomic units (OCTUs). During processing, OCTUPUS uses a novel method of sequence clustering and pairwise comparisons which are uninfluenced by sequence entry order, generating a list of OCTUs that represent dominant species found in the sample. Not only can these OCTUs be compared against available databases, they can also be directly compared against OCTUs generated using the same methodology from other sources. OCTUPUS is optimized for speed and does not require a computing cluster. OCTUPUS has been benchmarked on two separate environmental samples, each using different tagged diagnostic ribosomal DNA sequences and approximately 300,000 meiofaunal sequences.

**THE EFFECTS OF HABITAT TYPE IN STRUCTURING ASSEMBLAGES OF ORIBATID MITES.** Sylvain<sup>1</sup>, Zachary A. and C.M. Buddle<sup>2</sup>. <sup>1</sup>Dept. of Biology, Colorado State University, 200 W. Lake St., Fort Collins, CO 80523-1878, <sup>2</sup>Dept. of Natural Resource Sciences, McGill University, Macdonald Campus, 21,111 Lakeshore Road, Ste.-Anne-de-Bellevue, QC, Canada H9X3V9.

As landscapes shift through climate or land-use change, aboveground plant communities may also shift altering local dynamics in the soil/litter system. This could result in loss of biodiversity from the soil system, which may result in changes to ecosystem functioning, such as a reduction of ecosystem services. Oribatid mites (Order Acari suborder Oribatid) represent a hyperdiverse taxon and are ubiquitous within soil and litter, where they feed on a range of substrates from bacterial mats and fungal hyphae to coarse organic matter such as leaf litter, thus they are important in decomposition dynamics within forest systems. The effects of finer-scale factors such as soil type, humidity and pore-space size on oribatid assemblages have been investigated in detail, however, we know little of the effects of large scale factors such as forest stand type on the biodiversity and assemblage composition of oribatids or how large scale factors may be altered with climate. To address this we examined oribatid mite assemblages found under forest stands dominated by American beech (*Fagus grandifolia*), sugar maple (*Acer saccharum*), and stands of mixed deciduous and conifer plantations at the Morgan Arboretum of McGill University, Quebec, Canada. Four replicated sites were established within each of four forest stand types, and from these sites 1 L of densely packed litter was collected on each of three sampling dates: July and September 2005 and June 2006. Oribatids were extracted at 32°C for 5 days using modified Tullgren funnels and identified to species. A total of 6920 individuals within 51 species was collected. The most abundant species collected was *Anachipteria magnilamellata* and comprised 11.4% of all individuals sampled; of the ten most abundant species collected most were found more often in conifer plantations than any other stand type. Results of ANOVA testing showed that all four forest stand types supported significantly differing abundances, while beech stands and conifer plantations supported more species rich assemblages than did sugar maple or mixed deciduous stands. The resulting 3-dimensional NMS ordination revealed that conifer plantations and beech stands supported assemblages differing significantly from all other stand types, while maple and mixed deciduous stands featured assemblages of similar composition. These results show that landscape-scale factors such as forest stand type cannot be ignored when investigating determinants of oribatid mite diversity. We suggest that these effects may be due to litter characteristics determined by above-ground plant diversity, which may influence the heterogeneity of the litter habitat by dictating litter fragment size and nutrient composition. Additionally, these results suggest that global changes acting regionally across landscape-scale may influence belowground assemblages, even at the scale of soil organisms.

**URBAN SOIL FAUNA AND ECOSYSTEM SERVICES: EXAMPLES FROM THE BALTIMORE ECOSYSTEM STUDY.** Szlavecz<sup>1</sup>, Katalin, R.V. Pouyat<sup>2</sup>, W. Carroll<sup>3</sup>, S. M. Lev<sup>3</sup>, P.M. Groffman<sup>4</sup>, R. Casey<sup>4</sup> and E. R. Landa<sup>5</sup>, <sup>1</sup>Dept. of Earth and Planetary Sciences, Johns Hopkins University, <sup>2</sup>USDA Forest Service, <sup>3</sup>Urban Environmental Biogeochemistry Laboratory, Towson University, Towson, MD, <sup>4</sup>Institute of Ecosystem Studies, Millbrook NY, <sup>5</sup>U.S. Geological Survey, Water Resources Division-National Research Program, Reston, VA.

Even though soils in urban and urbanizing landscapes are predominately altered by human activity, they provide many of the same ecosystem services as unaltered soils. As such, soils can function in urban landscapes by reducing the bioavailability of pollutants, storing carbon and mineral nutrients, serving as habitat for soil fauna, and moderating the hydrologic cycle through absorption, storage, and supply of water. While soil abiotic factors determine the occurrence and abundance of soil biota, organisms are active participants in soil biogeochemical cycles and thus the ecosystem services mentioned above. Urban soil fauna and the urban soil food web is altered due to 1/ local extinction of native species 2/high percentage of non-native species, and 3/highly modified base of the decomposer food web. In this talk I will provide three examples on urban soil fauna and ecosystem services from Baltimore, MD: 1/ Effects of earthworms on the fate of roadway derived dust. We carried out mesocosm experiments using conditions observed in bioretention cells receiving direct storm water input. Earthworms influenced the roadway contaminant distribution and increased the trace metal (Zn) availability 2/ Earthworm species effects on nitrogen cycling. We compared three large earthworm species (*Eiseniodes loennbergi*, native; *Lumbricus terrestris*, European; *Amyntas hilgendorfi*, Asian) in their effect on N-mineralization and nitrification rates. While all three species increased the rates significantly, the Asian species had the largest effect both in natural and in commercially bought soils. 3/ The effect of forest fragmentation on carrion beetle (Silphidae) communities. This study showed that the likelihood of carrion burial was decreasing with declining species diversity. Some ecosystem services provided by soil biota is inversely related to the level of land management. The altered decomposer food web in urban environment provides opportunities to test general hypotheses on the relationship between biodiversity and ecosystem function.

**ROLLING CIRCLE MITOCHONDRIAL DNA AMPLIFICATION UNMASKS NEW MERMITHID PARASITISM OF COMMON TERRESTRIAL ISOPODS. Tang, S.,<sup>1</sup> G. O. Poinar, Jr.,<sup>3</sup> G. Wang,<sup>2</sup> E. G. Platzer,<sup>2</sup> and B. C. Hyman.<sup>1,2</sup>**

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Previous studies have shown that the mermithid nematode *Thaumamermis cosgrovei*, parasitizing local populations of the common terrestrial isopod *Armadillidium vulgare* (Latr.), carried numerous mitochondrial DNA (mtDNA) haplotypes. Recent surveys for additional haplotypes using rolling circle mtDNA amplification revealed the presence an unusual RFLP variant within a mermithid whose macroscopic appearance was strikingly similar to that of *T. cosgrovei*. Exposure of this nematode to distilled water resulted in spontaneous body fragmentation, whereas *T. cosgrovei* remained intact under identical hypotonic conditions. Guided by a morphology-based phylogeny that divides the nematode family Mermithidae into seven subfamilies (Gafurov, 1997), a Maximum Likelihood molecular phylogenetic analysis employing mitochondrial COI and nuclear 18S and 28S rDNA nucleotide sequences consistently yielded a single tree after a series of full heuristic searches. The subfamily Agamermethinae was resolved as monophyletic, and within this clade the tested nematode was a sister taxon to *Agamermis*. Morphological characters from juvenile and adults also support a tentative assignment as *Agamermis* (Cobb, Steiner and Christie, 1923). The complete nucleotide sequence of the *Agamermis* sp. mitochondrial genome has been determined; unlike the hypervariable *T. cosgrovei* mitochondrial genome, only a single *Agamermis* sp. haplotype is found. We infer an ancient, large duplication encompassing the mitochondrial genes for NADH dehydrogenase subunits 3, 4 and 6, (ND3, ND4, ND6) and the small mitochondrial rRNA (*rrnS*), followed by random loss of duplicate gene copies. These observations provide the first report of any mermithid parasite found in the common pillbug *A. vulgare* beyond that of *T. cosgrovei*.

**THE EFFECTS OF CALCIUM AND NITROGEN AMENDMENTS ON SOIL ORGANIC MATTER DYNAMICS IN PINE FORESTS STANDS AT SAND RIDGE STATE FOREST. Taura<sup>1</sup>, Joseph, J.A. Koch<sup>1</sup>, E.A. Paul<sup>2</sup>, K.D. McConaughay<sup>1</sup>, and S.J. Morris<sup>1</sup>.**

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Concern over the increase in atmospheric CO<sub>2</sub> content has created interest in the mechanisms that increase and stabilize organic matter in soils. The present study examined the impacts of calcium and nitrogen on soil organic matter (SOM) in nutrient poor pine soils. There is evidence that Ca additions reduce decomposition rates and increase soil organic matter retention in slightly acidic sandy soils. The impacts of N additions on soil organic matter retention are divided. Some studies have found that increased N results in increased C turnover and some studies have found SOM stabilization. Calcium and N are relatively inexpensive and easily applied to soils. There are many management practices, mostly in agriculture, that use these additions to sustain soil fertility or plant productivity. Increases in SOM resulting from additions of calcium and N to non-agricultural soils, such as forest plantations, would have potential to increase C sequestration on the terrestrial surface in degraded systems. Our study focused on low nutrient pine plantation stands in the Sand Ridge State Forest in central Illinois. Pine plantations were established at this site on native sand prairie in 1950's. Soil organic matter in these stands is generally low. Amendments consisting of CaCl<sub>2</sub> and NH<sub>4</sub>NO<sub>3</sub> were made in the summer of 2007. Amendments were made separately and together on the surface of the soil and incorporated into the soil to a depth of 20 cm. For the former treatment litter was removed and replaced before amendment. For the latter treatment litter was incorporated into soils with the amendment to roughly mimic tillage. There were four blocks in two pine stands – two per stand - with eight plots per block (one plot = one

treatment). Carbon mineralization incubations were initiated in the laboratory to examine the initial effects of each of these treatments. There were significant differences detected in the amount of C released from soils even 500 days after treatment. Calcium alone and with N had low rates of C evolution. Calcium and Ca/N added with pine litter had higher C release than control but less than when litter was added without amendment or with N alone. Results suggest that Ca additions in forest soils decrease C loss through mineralization. Whether this results in long term stabilization of SOM without affecting plant nutrient availability remains to be seen. Forest plots will be evaluated for the next several years to determine the extent to which these trends continue and the impacts on above and belowground communities.

**NEMATODE EXTENSION ACTIVITIES IN PRAIRIE CANADA: TO BOLDLY GO WHERE NONEONE HAS GONE BEFORE. Tenuta, Mario.** Department of Soil Science, University of Manitoba, Winnipeg, MB R3T 2N2.

Awareness of nematode pests of crops is greatly lacking in the prairie provinces of Canada, Manitoba, Saskatchewan and Alberta. Nematode pests are thought to be not of concern in these provinces. This is because of a belief that winter conditions are too cold for survival of nematodes and that there has been an absence of nematologists working in these provinces. In my short time working in Prairie Canada, I have found growers and industry very interested in learning about various aspects regarding nematodes. The major questions include, do they survive the cold winters, how to interpret nematode pest soil analyses, can the potato cyst nematodes become established, and are all nematodes detrimental to crops? Through combination of presentations at grower annual meetings, experimental station field days, provincial extension field days, provincial extension annual disease and pest conferences, and in advising provincial and national commodity groups on nematode issues, the Soil Ecology Laboratory has worked to provide some answers to growers and industry. Unlike other regions where a considerable history of extension activities and awareness of nematode issues exist, in Prairie Canada, all extension activities start with describing what nematodes are and dispelling that cold winters will protect crops from all nematode pests. Among the various approaches used by the Laboratory, probably none is more effective than showing growers live nematodes or movies. The impact to growers of being able to visualize plant-parasitic nematodes and as-well, beneficial nematodes, is the simplest and most effective means of generating interest and starting on the road to understanding nematodes in cropping systems of Prairie Canada.

**UTILITY OF GRAFTING FOR MANAGING SOUTHERN ROOT-KNOT NEMATODE, *MELOIDOGYNE INCOGNITA*, IN WATERMELON. Thies<sup>1</sup>, Judy A., J. J. Ariss<sup>1</sup>, R. L. Hassell<sup>2</sup>, and S. Olson<sup>3</sup>.** <sup>1</sup>U.S. Vegetable Laboratory, USDA, ARS, 2700 Savannah Highway, Charleston, SC 29414; <sup>2</sup>Coastal Research and Education Center, Clemson University, 2700 Savannah Highway, Charleston, SC 29414; <sup>3</sup>University of Florida, North Florida Research & Education Center, 155 Research Road, Quincy, FL 32351.

Four bottlegourd (*Lagenaria siceraria*) cultivars, one squash (*Cucurbita moschata* x *C. maxima*) hybrid, four wild watermelon (*Citrullus lanatus* var. *citroides*) germplasm lines, and one commercial wild watermelon (*C. lanatus* var. *citroides*) cultivar were evaluated as rootstocks for cultivated watermelon (*C. lanatus* var. *lanatus*) in a field infested with the southern root-knot nematode (*Meloidogyne incognita*) in Charleston, SC in 2007 and 2008. Commercial watermelon 'Fiesta' (diploid seeded) and 'Tri-X 313' (triploid seedless) scions were grafted onto the rootstocks in 2007 and 2008, respectively. In 2007, the plants with rootstocks of the wild watermelon germplasm lines and the commercial wild watermelon had significantly less ( $P < 0.05$ ) root galling than non-grafted 'Fiesta' watermelon, and plants with the squash hybrid and bottleneck gourd rootstocks. In 2008, plants with rootstocks of three wild watermelon germplasm lines had significantly less ( $P < 0.05$ ) root galling than non-grafted 'Tri-X 313' watermelon, and plants with the squash hybrid and bottleneck gourd rootstocks. Root galling of the squash hybrid and bottleneck gourd rootstocks was severe (80 to 96%) in both years. Root galling was moderately severe for non-grafted 'Fiesta' (40%) and non-grafted 'Tri-X 313' watermelon (56%). Root galling for the wild watermelon germplasm lines ranged from 11 to 34% and 32 to 42% in 2007 and 2008, respectively. Root galling of the commercial wild watermelon rootstock was 24% and 39% in 2007 and 2008, respectively. Wild watermelon germplasm lines derived from *C. lanatus* var. *citroides* may be useful as resistant rootstocks for managing root-knot nematodes in watermelon.

**THE EARTH BENEATH OUR FEET: SOIL ECOLOGY GRADUATE STUDENTS TACKLE THE MYSTERY SOIL LAB. Thiet, R.K., B.M. Dempsey, N. Gertz-Young, L. Schottenfeld, J. Skinner, V. Snowdon, and M.F. Vinson.** Environmental Studies Department, Antioch University New England, Keene, NH.

Despite increasing emphasis on student-centered and experiential learning at the college level, many ecology classroom laboratory exercises still do not provide students with the autonomy to generate their own questions and experiments. Further, stand-alone laboratory exercises often illustrate ecological concepts out of context or abstracted from the landscape in which students live. Developing and implementing meaningful ecology laboratory exercises is particularly challenging in soil ecology courses, where learning requires leaps of imagination, since most soil organisms and their interactions are difficult to observe. In this Master's level Soil Ecology course laboratory exercise at Antioch University New England, a graduate school in Keene, NH, environmental studies students were presented with a Mystery Soil sample to explore and interpret over the

course of four weeks. Their charge was to use any tools at their disposal to characterize the soil thoroughly and deduce the specific geomorphic setting and plant community under which the soil was collected within a 40-mile radius of the university. To start, each of four small student groups was given a different Mystery Soil and told only which southern NH county the soil was collected from. Students were allowed four full weeks to develop questions and test their soils in whatever way they chose, both inside and outside of class. Student groups chose to characterize soil texture, aggregation, bulk density, moisture, color, total C, microbial activity, and microarthropod community composition. Using conceptual content from other classroom lessons about relationships among soil physical, chemical, and biological properties and aboveground-below-ground feedbacks, student groups hypothesized the landscape geomorphic history and plant community origin of their soil. At the end of the four-week laboratory exercise, student groups presented their results to the class using visual displays that included samples of their Mystery Soil; they were not permitted to use electronic presentations. Students were highly successful at pinpointing the landscape context and plant communities under which their soil was collected, and one group was able to use the NRCS County Soil Survey to locate the precise landscape location where their Mystery Soil was collected. This long-term soil ecology laboratory exercise had the following positive learning outcomes: the exercise (1) gave students autonomy to generate their own questions and methods for testing their questions about a unique soil; (2) allowed students to explore a soil in the context of complementary, conceptual course content; (3) challenged students to make connections among various soil properties and landscape geomorphic history, plant community composition and land management, resulting in a broader, more thorough view of soil processes on the New England landscape and; (4) helped students develop hypothesis-generation and field and laboratory skills for a longer-term, independent soil ecology research project assignment in the course.

INTERACTIONS AMONG *MELOIDOGYNE INCOGNITA*, ANNUAL WEEDS, AND *VERTICILLIUM DAHLIAE*: IMPLICATIONS FOR ENHANCEMENT OF PATHOGEN AND WEED POPULATIONS IN CHILE PEPPER PRODUCTION. **Thomas<sup>1</sup>, Stephen. H., J. M. Trojan<sup>1</sup>, J. Schroeder<sup>1</sup>, C. Fiore<sup>1</sup>, S. Sanogo<sup>1</sup>, L. Leiss<sup>1</sup>, and L. W. Murray<sup>2</sup>.** <sup>1</sup>Dept. of Entomology, Plant Pathology and Weed Science, New Mexico State University, Las Cruces, NM 88003 and <sup>2</sup>Dept. of Statistics, Kansas State University, Manhattan, KS 66505.

A late-season survey of chile pepper (*Capsicum annuum*) in Luna County, NM in 2007 revealed the presence of southern root-knot nematode (*Meloidogyne incognita*) and a high incidence of certain annual weeds in fields containing chile plants that expressed severe wilt symptoms due to infection by *Verticillium dahliae*. The predominant weeds included spurred anoda (*Anoda cristata*, =SA), Wright's groundcherry (*Physalis wrightii*, =WG) and tall morningglory (*Ipomoea purpurea*, =TM), none of which expressed the wilt symptoms prevalent in the crop, despite being suitable hosts for *V. dahliae*. All three weeds are also hosts for *M. incognita*, with symptoms of infection being evident on roots of TM and chile in some of the affected fields. The limited expression of visible symptoms of infection by *M. incognita* and *V. dahliae* among weeds in these infested fields led us to hypothesize that weeds may serve as refugia that maintain or enhance populations of pathogens that can in turn injure chile. A greenhouse experiment was conducted in summer 2008 to determine the effects of *M. incognita* and *V. dahliae*, alone and in combination, on growth of SA, WG, TM, and chile compared to non-inoculated control plants. *Meloidogyne incognita* reproduction, incidence of *V. dahliae* infection ascertained through stem and root culturing, and plant shoot and root growth proportional to non-inoculated controls were measured six weeks post-inoculation. Preliminary results from 2008 showed shoot and root biomass of chile were not affected by *M. incognita* alone, but were reduced 26% and 63% respectively by *V. dahliae* and the two pathogens combined. Nematode reproduction was largely unaffected when chile was co-infected with *V. dahliae*, despite the reduction in root biomass. *Meloidogyne incognita* reproduction was similar among chile, TM and WG, ranging from 309,000 to 399,000 eggs per plant. Spurred anoda was a poorer host for *M. incognita*, yielding approximately one third the eggs observed on other species. Nematode reproduction was slightly greater in all three weed species when plants were co-infected with *V. dahliae*. Unlike the results observed in chile, weed root and shoot biomass were not reduced by *V. dahliae* infection or co-infection by both pathogens. Tall morningglory shoot and root biomass increased substantially when infected by *V. dahliae*. The study is being repeated in summer 2009 to confirm these findings. These preliminary results suggest that all three weeds will support either pathogen, or both together, without pathogenic effects, and that TM and WG support *M. incognita* reproduction at levels similar to those found in highly-susceptible chile plants. Failure to effectively manage the weeds examined in this study may enhance weed and pathogen populations to the detriment of future chile crops.

IDENTIFICATION AND MAPPING OF GENETIC TRAITS INVOLVED IN PLANT PARASITISM IN *MELOIDOGYNE HAPLA*. **Thomas, Varghese P. and Valerie M. Williamson.** Department of Nematology, University of California-Davis.

*Meloidogyne hapla* (northern root-knot nematode) is an important pest of tomato, potato, carrot, alfalfa and other crops in temperate climates. A better understanding of the genes involved in the complex interactions between nematodes and their hosts is needed to develop novel control strategies. The genome sequence has been obtained and a genetic map constructed for *M. hapla*, providing powerful resources to transform the way we study nematode parasitism and host plant-parasite interactions. The main objective of this work is to characterize the inheritance of the genetic factors involved in nematode

parasitism. We have sequenced 80 AFLP markers and used these sequences to align the genetic map with the assembly sequence of *M. hapla* strain VW9. These markers include co-dominant and dominant AFLP markers and were picked to cover all the 15 linkage groups (LGs) in the genetic map. Using BLAST N, we identified the physical contigs that contained the AFLP DNA marker sequences. All the AFLP sequences had good matches in the genome assembly, validating both the *M. hapla* physical assembly and the genetic markers. In this study, we are focusing on the interaction between *M. hapla* and *Solanum bulbocastanum*, a wild diploid species of potato. To identify genetic loci contributing to the variation in parasitism observed between parental strains, we applied quantitative trait loci (QTL) mapping to an inbred population of F2 progeny. We discovered that the variation in nematode reproduction (egg-masses/plant) and percentage root-galling on *Solanum bulbocastanum* are inherited as complex traits resulting from the combined effects of multiple genetic loci. QTL analysis (using QTL Cartographer V2.5) has identified several loci with major contribution to nematode reproduction level on linkage groups (LG's) in the genetic map. Differences in root-galling on *S. bulbocastanum* also segregated in the F2 population and showed significant association with two loci on different chromosomes. High-through put SNP genotyping of the inbred F2 population is in progress to increase the resolution of available *M. hapla* genetic map. This will identify markers closer to the genetic loci responsible for the identified nematode parasitism traits.

PHYLOGENOMIC ANALYSES IN THE AGE OF NEXT-GEN SEQUENCING: THE SCOURGE OF GENE DUPLICATION AND THE USE OF TRANSCRIPTOME DATASETS. **Thomas<sup>1</sup>, W. Kelley, K. Morris<sup>1</sup>, and P.J. Hatcher<sup>2</sup>.**

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Comparative genomics aims to incorporate a rich knowledge of patterns of gene family expansion, gene loss, as well as changes in the rates and patterns of evolution across the genome that accompany adaptive evolution. Dramatic improvements in DNA sequencing have facilitated the ability to collect genome-wide datasets for ever-expanding numbers of species. These new data extend our knowledge of gene content well beyond traditional model systems or a few taxa of agro-economic or biomedical importance. These new opportunities to create gene catalogs for large numbers of species with distinct and diverse ecological roles, expand our potential to correlate genes and biological function advancing our understanding of the genetic basis for diverse biological processes. Critical to inferring the potential functions for genes is an effective understanding of gene family relationships (orthology and paralogy) and the phylogenetic framework for the species involved. Extension of functional annotation across species assumes orthology. So called next-generation sequencing brings both the ability to sequence whole genomes as well as large-scale transcriptome datasets. To support large scale comparative genomics analysis, we have developed methods for genome-wide gene family analysis. We have applied these approaches to several whole genome datasets for nematodes across multiple levels of diversity from within the *Caenorhabditis* to phylum-wide analysis. In addition, we test the utility of large-scale transcriptome analysis using a deep-coverage dataset for *Romanomermis*.

SOIL MOISTURE DISTURBANCE INFLUENCES MICROBIAL COMMUNITY FUNCTION AND STRUCTURE WITH IMPACTS ON SOIL CARBON AND NITROGEN DYNAMICS. **Tiemann, L. K.<sup>1</sup> and S. A. Billings<sup>1</sup>.** Department of Ecology and Evolutionary Biology, Kansas Biological Survey, University of Kansas, 2101 Constant Ave., Lawrence, KS 66047.

In this study, we assess soil microbial community function and the degree of coupling between ecosystem process rates and microbial community structure after disturbance. Soil moisture variability can be a major source of disturbance causing ecosystem scale alterations in C and N cycling processes because it is a critical determinant of microbial growth, activity, and community structure. We explored these issues in grasslands of the Great Plains, where large fluctuations in soil moisture are common and microbial activities are likely limited by organic C and N substrates only when soil moisture is limiting. We collected soils from four sites in Kansas along a precipitation gradient ranging from 485 to 960 mm y<sup>-1</sup>. We manipulated the frequency and size of water additions and dry down periods in these soils by applying the same amount of water, but in three different, 2-week long wetting-drying cycles, in laboratory incubations lasting a total of 58 days. In soils undergoing a long interval (LI) treatment, with all water added at the beginning of each 2-week cycle, soils from all four sites mineralized 1.4 - 2.0 times more carbon, and exhibited greater C acquisition enzyme activity than soils undergoing a short interval (SI) treatment that consisted of 4 wetting events spread evenly over the two-week cycle. All soils, regardless of moisture treatment, experienced general declines in microbial biomass C and increases in inorganic N throughout the incubation. Soils from all sites experiencing the SI treatment had greater inorganic N than LI soils, and greater denitrification potential in soils from the more mesic sites. To assess coupling between community structure and function after disturbance, we used qPCR to measure the abundance of functional genes in these soils at the end of the incubation. We quantified functional genes associated with denitrification, including *nirK*, *norB* and *nosZ*, because of the anaerobic nature of this process and the strong link between moisture availability and anaerobic conditions. We observed greater numbers of functional gene copies in soils from the more mesic sites compared to soils from the most xeric site, consistent with the observed differences in denitrification

potential across the precipitation gradient. We also found a significant relationship between *nosZ* gene copies and denitrification potential in the LI soils across all sites. The positive relationship in LI and lack of relationship in SI soils between N transformation rates and the abundance of an associated functional gene suggests that altering precipitation regimes in this region may result in variation in the degree of coupling between soil microbial gene expression and biogeochemical functions. This information is particularly important in light of predicted alterations in precipitation patterns with global climate change and will help us to understand how C and N dynamics will change as our climate changes.

**RESPONSE OF A NEMATODE COMMUNITY TO TILLAGE AND NEMATICIDE APPLICATION IN COTTON. Timper, Patricia<sup>1</sup>, R.F. Davis<sup>1</sup>, and G. B. Jagdale<sup>2</sup>.** <sup>1</sup>USDA ARS, P.O. Box 748, Tifton, GA 31793, <sup>2</sup>Plant Pathology Dept., University of Georgia, Athens, GA 30602.

We hypothesized that tillage and nematicide use would reduce the relative abundance of predatory and omnivorous nematodes, which in turn would result in greater survival and reproductive potential of plant-parasitic nematodes later in the season. To test this two-part hypothesis, we conducted a split-plot experiment in a cotton field where half the main plots had been in conservation tillage (strip tillage) for 4 years and the other half in conventional tillage (subsoiled and bedded). The subplots received either the fumigant nematicide 1,3-dichloropropene (Telone) or no nematicide. The field site was naturally infested with the southern root-knot nematode, *Meloidogyne incognita*. To determine the nematode community structure, soil samples were collected pre-tillage and fumigation, post-plant, and midseason. We also assayed the survival and population increase of plant-parasitic nematodes in soil collected from different treatments. We found that the numbers of predatory and omnivorous nematodes were unaffected by tillage, but were lower in the Telone than the control plots in the post-plant and midseason samples. Predators were also reduced in the pre-fumigation samples from Telone plots, suggesting a residual effect from fumigation the previous spring. The Structure Index (SI), a measure of the relative abundance of omnivorous and predatory nematodes in the community, was lower in Telone compared to control plots in the post-plant and midseason samples. In the pre-fumigation samples, the SI was only reduced in the conventional tillage plots (tillage x nematicide interaction). In the first bioassay, survival of *M. incognita* juveniles was generally greater in soil from the control compared to Telone plots; however, this result was confounded by a larger population of resident juveniles in the control plots. Reniform nematode will be used as an assay nematode to avoid this problem in the future. In the second bioassay, population increase of *M. arenaria* on peanut was similar in soil from Telone and control plots, and was less in conventional tillage than in strip tillage. In summary, conventional tillage had only a small impact on the relative abundance of predators and omnivores; whereas, Telone application had a large and lasting impact on both the absolute and relative abundance of these two trophic groups. Nevertheless, we were unable to demonstrate that the reduction in predators and omnivores following Telone application resulted in greater survival or reproductive potential of plant-parasitic nematodes.

**ISOLATION AND CULTURE OF THE ANTARCTIC NEMATODE, PLECTUS MURRAYI UNDER LABORATORY CONDITIONS. Tomasel, Cecilia M. de<sup>1</sup>, G. Li<sup>1</sup>, B. J. Adams<sup>2</sup>, B. Adhikari<sup>2</sup> and D. H. Wall<sup>1</sup>.** <sup>1</sup>Department of Biology and Natural Resource Ecology Laboratory, Colorado State University Fort Collins CO 80523- 1499 <sup>2</sup>Department of Biology and Evolutionary Ecology Laboratories, Brigham Young University Provo, UT-84602.

The McMurdo Dry Valleys of Antarctica are considered one of the most extreme desert ecosystems on Earth, and in the ice-free areas, nematodes constitute the top of the soil food webs and play an important role in nutrient cycling and belowground carbon cycling. The endemic bacteria-feeding nematode *Plectus murrayi* is one of only four species found in this region, capable of surviving multiple stresses including extreme cold temperatures, desiccated soils, and frozen, dark winters. Generally this nematode species has a habitat of relatively high organic carbon, low soil salinity and moist habitats. To date there have been no systematic studies of this species' life cycle under laboratory conditions. Previous attempts to culture *P. murrayi* on bacteria in Bold Modified Basal Freshwater Nutrient Media without sand in our laboratory were unsuccessful. In this paper we describe a technique developed to produce cultures of *P. murrayi* in the laboratory. The technique includes the use of a culture medium that combines Bold's Modified Basal Freshwater Nutrient Media (BMBFN) and Standard Ottawa sand (granular silicon dioxide) in the Petri plates. To make the media 20 ml/L of BMBFN solution was added to deionized water and the pH of the solution was adjusted to 6.6 using NaOH or HCl. Fifteen grams of Bacto-agar were added to this solution, heated, and autoclaved for 15 min at 121°C. After cooling, the center of each plate was sprinkled with 0.2 g of previously autoclaved Ottawa sand spread evenly over each plate. Nematodes and associated bacteria were first isolated and inoculated onto the original plates from a water-soil slurry from Antarctica and incubated at 15°C, a temperature within the range of Antarctic austral summer soil temperatures. Cultures were established by serially moving small pieces of media with *P. murrayi* onto fresh plates every 3-5 days until the cultures contained only microbes and this single species of nematode. Every three weeks, when the populations covered 40 % of the plate they were transferred to new plates by chunking and moving a quarter of the media-sand segment to a new media plate. The new Petri plates were sealed with ParafilmTM, placed in plastic bags, and incubated at 26°C for a week. Each bag of plates was turned over to place the dishes face down, and incubated at 15°C for three weeks until they were transferred to new plates. As observed in field samples, only females were found in the laboratory cultures, but eggs were also noted. Other bacteria (*E. coli* OP50) were also tried as a

food source after sterilizing nematodes, and *E. coli* OP50 seemed to be preferred. The combination of BMBFN + Ottawa sand and alternating temperatures seems to be suitable for culturing *P. murrayi* and its associated food source.

**MODELING URBAN SOIL CARBON STORAGE AND SEQUESTRATION POTENTIAL USING CENTURY, A PLANT-SOIL ECOSYSTEM MODEL. Trammell<sup>1</sup>, Tara L.E., R.V. Pouyat<sup>2</sup>, M.M. Carreiro<sup>1</sup>, and I.D. Yesilonis<sup>2</sup>.**

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Soil carbon dynamics in urban landscapes are understudied and current soil carbon field studies may provide insight to the possible response of soils in urban environments. However, predicting the soil carbon dynamics under continued human impact will provide important knowledge as to the potential for highly altered soils to sequester and store carbon (C). The CENTURY model is a mechanistic model simulating plant-soil ecosystem interactions. One advantage of modeling urban soil carbon using CENTURY includes its ability to simulate responses to different management manipulations. Urban landscapes are highly heterogeneous land mosaics with varying degrees of management, and we can expect that soil carbon will vary tremendously across patch types. Urban residential lawns represent an aerially extensive urban patch type that is highly influenced by human activities, such as water and nutrient subsidies, mowing, and tree pruning. Model calibration for urban lawns may be useful for future model applications in other urban patches. CENTURY simulations were conducted for the Baltimore Ecosystem Study (BES) using soil data collected throughout the metropolitan area in residential patches. Initial CENTURY model runs showed that parameters controlling soil carbon stabilization in urban soil formation (e.g., year residence built) are not the factors that typically control soil formation in natural areas (e.g., soil texture). Correlation between observed and CENTURY-simulated soil organic carbon was poor ( $y = -0.03x + 5053$ ;  $r^2 = 0.027$ ), and variation observed in residential soil carbon was much greater than simulated by CENTURY (range = 10.8 vs. 1.0 kg m<sup>-2</sup>; respectively). CENTURY model runs were then conducted to represent individual lawn management regimes typically observed in urban residences. Individual lawn manipulations consisted of various levels of fertilizer application, tree pruning, and erosion during development. Including variation in individual management greatly improved the correlation between observed soil carbon and simulated soil organic carbon ( $y = 0.87x + 819$ ;  $r^2 = 0.881$ ). Data from the Urban Forestry Effects model, which estimates aboveground carbon storage and sequestration was also available for these BES residential sites. Thus, comparisons were made between UFORE and CENTURY model output for aboveground C storage and sequestration. Individual management manipulations for the residential lawns improved the correlation between UFORE and CENTURY output (C storage  $r^2 = 0.003$  vs.  $r^2 = 0.665$ , C sequestration  $r^2 = 0.010$  vs.  $r^2 = 0.224$ ); however, improvement is still needed for aboveground carbon CENTURY estimates. Results from these initial CENTURY model runs identified the need to obtain information of existing individual lawn management to improve predictions of C storage and sequestration potential in urban residential soils. CENTURY model runs will be further explored for other urban landscape patch types. Modeling current and future urban soil carbon storage and sequestration potential is important for understanding the future carbon offset potential of urban areas.

**SOIL BIOTA IN A CHANGING ENVIRONMENT: MICRO- AND MESOFAUNAL RESPONSES TO ELEVATED ATMOSPHERIC CO<sub>2</sub>. Treonis<sup>1</sup>, Amy M. and J. F. Lussenhop<sup>2</sup>.** <sup>1</sup>Dept. of Biology, University of Richmond, Richmond, VA 23173, <sup>2</sup>Dept. of Biological Sciences, University of Illinois, Chicago, IL 60607.

Understanding the impact of rising levels of atmospheric carbon dioxide on terrestrial ecosystems has been a fertile area of research for decades. Numerous studies have investigated the responses of soil bacteria, fungi, protozoa, nematodes, and microarthropods. The elevated CO<sub>2</sub> paradigm is a unique opportunity to empirically assess the impact of increased resource availability on the soil food web (i.e., bottom-up effects). Here, we review foundational studies of soil food webs under elevated CO<sub>2</sub>, including the results of our analyses of rhizosphere micro- and mesofauna. During the summer of 1992, we grew hybrid *Populus* saplings under ambient and elevated atmospheric CO<sub>2</sub> using a Free-Air CO<sub>2</sub> Enrichment (FACE) system at the University of Michigan Biological Station. Measured variables included microbial biomass, protozoan density, arbuscular mycorrhizal colonization of roots, hyphal length, and microarthropod density (as observed through minirhizotron tubes). Protozoan density, fungal variables, and microarthropod density all increased in the rhizosphere of elevated CO<sub>2</sub> plants. During the summer of 1994, we grew *Brassica nigra* under elevated and ambient CO<sub>2</sub> and measured bacterial and protozoan density. Bacterial and protozoan densities were not different between CO<sub>2</sub> treatments. Protozoan communities were altered under elevated CO<sub>2</sub>, however, with increased density of flagellates and decreased density of amoebae. Overall, these results, and the results of subsequent studies, suggest that soil food webs are sensitive to the changes in plant-based resource availability that accompany growth under elevated atmospheric CO<sub>2</sub>. Soil biota assimilate and transform carbon, nitrogen, and other soil nutrients. The response of these organisms is a critical aspect of the sustainability of soils as a natural resource in a changing global environment.

**EFFECTIVENESS OF GREEN TREE RETENTION AND TREE REGROWTH IN MAINTAINING THE DIVERSITY OF ECTOMYCORRHIZAL FUNGI IN HARVESTED AREAS OF COASTAL FOREST IN BRITISH COLUMBIA. Trofymow, J.A. and Outerbridge, R.A.** Canadian Forest Service, 506 Burnside Rd. W., Victoria, BC. V8Z1M5.

*Ectomycorrhizae* fungi (EM) play an important role in nutrient cycling and tree protection from drought and disease. Douglas-fir (*Pseudotsuga menziesii*), for example, a dominant tree species in coastal British Columbia (BC) is known to form such symbioses with nearly 2000 different fungi. Variable retention (VR) is a new forest practice that is replacing clearcutting in coastal BC. Previously we found clear evidence of edge effects, observing significantly lower abundance and diversity of EM fungi with increased distance from the retained forest patches. In this study, we extend our research to survey different EM fungal species, along transects from retained portions of mature forest into adjacent replanted forests of increasing ages (5, 27, 57 yrs), in order to assess their recolonization rate. We also examined how different levels of individual green tree retention affect recolonization, by studying a VR experimental site containing 4 treatments: uncut, 0% (clearcut), 5%, 10%, and 30% green tree retention. We hypothesized that edge effects would decline as the replanted forest grows and that EM diversity and abundance will increase with the increased number of retained live trees in harvested areas. In the VR experiment the steepness of the edge effect curve for EM richness declined with increasing retention, however the steepness of the curve for % EM colonization was not as well related to retention level though this depended upon the suite of EM species examined and if preexisting microsite differences were accounted for. Edge effects on % colonization and richness did decline with age of regrowth and were not significantly different in the 57 year stand, though some differences in community structure did occur. Implications of finding for forestry and maintenance of EM diversity will be discussed.

SOIL NEMATODE COMMUNITY STRUCTURE IN AN ALFALFA, CHILE AND COTTON CROP SEQUENCE. **Trojan<sup>1</sup>, Jacqueline M., S.H. Thomas<sup>1</sup>, J. Schroeder<sup>1</sup>, L.W. Murray<sup>2</sup>, and N. Schmidt<sup>3</sup>.** <sup>1</sup>Dept. of Entomology, Plant Pathology and Weed Science, New Mexico State University, Las Cruces, NM 88003, <sup>2</sup>Dept. of Statistics, Kansas State University, Manhattan, KS 66505, <sup>3</sup>Dept. of Economics and International Business, New Mexico State University, Las Cruces, NM 88003.

Previous research on the management of the nutsedge (*Cyperus spp.*) and the southern root-knot nematode (*Meloidogyne incognita*) pest complex in irrigated systems in New Mexico has found that an extended rotation with a resistant alfalfa crop can suppress the resurgence of both pests. A crop sequence study was conducted to assess the influence of a shortened two year rotation with a *M. incognita*-resistant, nondormant alfalfa (*Medicago sativa* cultivar 'Mecca II') for suppression of the nematode/weed pest complex and its affect on pest resurgence in two subsequent annual crops. In addition, soil nematode community structure was compared in the alfalfa and the subsequent, conventionally tilled annual crops, chile pepper (*Capsicum annum*, 'NM 6-4') in year 3 and cotton (*Gossypium hirsutum*) in year 4. Replicated, composite soil samples were taken in May (n=20), July (n=27) and September (n=31) of each cropping year. Soil nematodes were processed by elutriation/sucrose centrifugation and categorized according to trophic level. Plant parasitic nematodes were identified to genus and grouped according to feeding behavior (sedentary or migratory endoparasite and ectoparasite). Community dynamics were assessed according to differences ( $\alpha = 0.10$ ) in ratios among trophic groups and among plant-parasitic nematode feeding behaviors which were analyzed by sampling date across years. The trophic ratios analyzed were: FB (fungivores/[fungivores + bacteriovores]); BH (bacteriovores/[bacteriovores + all plant parasites]); and HT (all plant parasites/total nematode population). The plant parasite feeding behavior ratios were: SM (sedentary endoparasites/[sedentary +migratory endoparasites]); SE (sedentary endoparasites/[sedentary endoparasites +all ectoparasites]); and ME (migratory endoparasites/[migratory endoparasites +all ectoparasites]). Significant changes in trophic ratios were observed among end of season ratios (September). Two years of alfalfa decreased the FB ratio due to increased bacteriovore populations. As the crop sequence progressed, the BH ratio decreased and the HT ratio increased each year as total herbivore populations increased. Feeding behavior of the predominant herbivore population was influenced by crop type. Considering end of season nematode populations, two years of alfalfa decreased the SM ratio as populations of the sedentary endoparasite *M. incognita* decreased, while populations of migratory endoparasitic *Pratylenchus spp.* increased. During the subsequent two years of annual crops, *M. incognita* numbers increased significantly from 5 J2 per 100 cc soil at the end of the alfalfa rotation to 286 J2 at the end of the second annual crop. End of season ectoparasitic nematode populations showed the greatest annual fluctuation among crops. Greater presence of yellow nutsedge (*Cyperus esculentus*) was correlated with a greater overall abundance of herbivores and a greater abundance of sedentary endoparasites within the herbivore community.

ENTOMOPATHOGENIC NEMATODES FROM CONTINENTAL PORTUGAL. **Valadas<sup>1</sup>, Vera\*, P. Vieira<sup>1</sup>, S. Oliveira<sup>2</sup>, and M. Mota<sup>1</sup>.** <sup>1</sup>NemaLab-ICAM, <sup>2</sup> Lab. Microbiologia do Solo-ICAM, Departamento de Biologia, Universidade de Évora, 7002-554 Évora, Portugal.

Entomopathogenic nematodes (EPN) of the families Steinernematidae and Heterorhabditidae are parasites of insects, and can be found under diverse ecological conditions, including cultivated fields, grasslands, deserts, forests and oceanic beaches. The need to find new alternatives that may reduce the use of harmful insecticides has promoted the exploitation of these nematodes as biological agents. Until recently, the only region in Portugal where EPN have been studied is in the Azores archipelago. However, in continental Portugal there have been no known reports of EPN. In 2006, a national survey was initiated in order to study the distribution of EPN in all the territory, especially in areas that are considered suitable habitats

(e.g. sandy soils, dunes, natural forests, cultivated fields, grasslands) in order to understand the diversity of these nematodes. During a random survey in Alentejo, southern Tejo valley and Algarve regions, soil samples from different habitats were collected and assayed for the presence of EPN. To confirm the identification of the nematodes harvested by the baiting method, from *G. mellonella* cadavers, a molecular characterization of its ITS region was conducted. The DNA base sequences obtained for the Portuguese isolates were compared with other sequences deposited in the GenBank database and two species of entomopathogenic nematodes were identified. Isolates of *Steinernema feltiae* (accession numbers EF595633 (isolate I1), EF595634 (isolate I8), EF595635 (isolate H9) showed that they are almost identical (2-6 nucleotide substitutions) to, and share a high degree of homology with a UK population (accession number AY230170). The three isolates display 100% similarity among each other (accession numbers EU435138 (isolate I3), EU435139 (isolate R7), EU435140 (isolate X7)). *Steinernema feltiae* and *Heterorhabditis bacteriophora* have a wide distribution in temperate regions, being the most common species of the genus found in Europe, as well as in many other parts in of the world.

**SOIL MICROBIAL COMMUNITY – PLANT COVER RELATIONSHIP IN A DESERT ECOSYSTEM. Vered, Saul-Tcherkas and Y. Steinberger** The Mina & Everard Goodman Faculty of Life Sciences, Bar-Ilan University, Ramat-Gan 52900, Israel.

The Negev Desert is characterized by spatial and temporal patterns of resource distribution, in which soil biota are considered to be among the most sensitive biological parameters. Soil water availability and organic matter are among the most important factors, acting as triggers that determine the length of activity and composition of the soil biota. In order to overcome this xeric environment, plant and soil biota have evolutionarily developed over time ecophysiological abilities in order to fulfill their biological role and function. As plant ecophysiological adaptations consist of salt (*Reaumuria negevensis*) and chemical compound (*Artemisia sieberi*) excretion, generating “islands of salinity” or active germination inhibitors, the interplay with biotic components began to attract attention. In the present study, we report on the plant ecophysiological adaptation and microbial community interaction in relation to wet and dry seasonality, reflecting the mesic and xeric environments, respectively. Soil samples were collected monthly under the canopy of *A. sieberi*, *Noae mucronata*, and *R. negevensis*, from a depth of 0-10 cm. Samples collected from inter-shrub spaces acted as control. Soil microbial biomass and functional diversity were measured using the MicroResp™ method and the data obtained were compiled to represent dry and wet seasonality. A significant difference ( $p < 0.05$ ) was obtained between the two periods for most of the examined parameters. CO<sub>2</sub> evolution, microbial biomass, and H' values in soil samples collected beneath the canopies of *N. mucronata* and *R. negevensis* and from an open area were found to be higher during wet periods in comparison to the dry seasons, while no differences were found in soil samples collected beneath *A. sieberi*. In integrating all the data using RDA analysis, a similar trend was obtained, elucidating the importance of plant ecophysiological adaptation as well as the strong effect of the wet period, where both were expressed in soil moisture and the biotic variables measured, including microbial biomass, CO<sub>2</sub> evolution and microbial functional diversity index (H'). This study enabled us to make a relevant ecological interpretation, particularly in face of plant ecophysiological adaptations as governing below-canopy microbial community activity and functional diversity in desert xeric environments, without being able to dispatch this process from rainfall unpredictability in its broad sense.

**EARTH'S FRAGILE SYSTEMS: THE MACHAIR OF SCOTLAND – A CASE STUDY. Vink, Stefanie N.<sup>1,2</sup>, T. Daniell<sup>1</sup>, D. Robinson<sup>2</sup>, and R. Neilson<sup>1</sup>.** <sup>1</sup>SCRI, Dundee, DD2 5DA, Scotland, UK, <sup>2</sup>School of Biological Sciences, University of Aberdeen, Aberdeen, AB24 3FX, Scotland, UK.

Machair is one of the rarest coastal grassland habitats in Europe, found primarily in the north and west of Great Britain and Ireland. It is estimated that Machair is restricted to an area of approximately 25,000 ha world-wide, with 17,500 ha in Scotland, predominantly in the Western Isles archipelago. The Machair ecosystem is characterized by extensive, low-lying fertile plains on a bed of calcareous sand which have traditionally been subjected to low-input agriculture. Historically, land management is focused on family/community sustainability operating on small parcels of land leading to a rich mosaic of habitat diversity. Rotations are based around extensive grazing, fallow periods and cropping of typically potatoes, a mixture of small oats and rye and bere barley. In recent decades social demographics have altered substantially with population movement from the Scottish Islands to the mainland and the management of Machair has increasingly become a secondary profession or hobby. The concomitant effect is that the Machair ecosystem is now under threat due to changing management practices such as the use of artificial fertilizer instead of traditional composted seaweed and/or abandonment resulting in concerns regarding the maintenance of habitat diversity. In contrast to the numerous above-ground studies which have well characterized the diversity of vegetation and associated invertebrate assemblages, there is a paucity of below-ground studies on the Machair. This has resulted in a significant knowledge gap in an area key to the current and future functioning of the system. To assess the gross impacts of land management on below-ground components of the Machair, we temporally sampled 10 discrete geographic locations in the Uists and associated islands in spring, summer and autumn for one year. Thereafter, four key sites were identified and temporal sampling occurred as previously. Hypothesis-led microcosm experiments were also initiated to identify potential drivers of the below-ground Machair ecosystem. Using Terminal-Restriction Fragment Length Polymorphism (T-RFLP) we

have characterized the nematode, *arbuscular mycorrhizal*, bacterial and fungal assemblages under each of three studied land uses. Nematode analysis was performed at a functional level using both molecular and morphological methods, allowing us to make comment upon the impact of different land management practices on below-ground microbial assemblage structure and faunal functional diversity. We will postulate that, in addition to playing a key role in maintaining settlement of the Western Isles through tourism associated with high floristic and animal diversity, the Machair ecosystem has the potential as an excellent model system to study the impact(s) of agricultural intensification.

**CAN NEMATODE COMMUNITY INDICES ELUCIDATE PLANT HEALTH CONDITIONS? Wang<sup>1</sup>, Koon-Hui, R. McSorley<sup>2</sup>, and R. N. Gallaher<sup>3</sup>.** <sup>1</sup>Dept. Plant and Environmental Protection Sciences, University of Hawaii at Manoa, Honolulu, HI 96822; <sup>2</sup>Dept. Entomology and Nematology, <sup>3</sup>Dept. Agronomy, University of Florida, Gainesville, FL 32611.

Two field trials were conducted in Gainesville, FL to demonstrate if nematode community analysis could elucidate plant health conditions. Sunn hemp (SH), *Crotalaria juncea*, was planted as a summer cover crop prior to vegetable crops to generate a regime of soil organic inputs and levels of soil disturbance. Field plots were planted with sunn hemp or left fallow (F) with weeds. At the middle of the cover cropping season, sunn hemp was either clipped (C) or unclipped (UC). Prior to vegetable planting, sunn hemp plots were either tilled (T) or not-tilled (NT). The fallow treatment was followed by tilling (FT). Thus, five treatments were imposed: CT, UCT, FT, CNT, and UCNT. In the fall, lima bean (*Phaseolus lunatus*) and turnip (*Brassica rapa*) were planted in 2005 and 2006, respectively. Nematode communities were monitored at termination of the cover crop (Pi) and at cash crop harvest (Pf). Sunn hemp UC plots generally produced more biomass than the C plots. At cash crop harvest, UC plots had greater ( $P < 0.05$ ) abundance or percentages of fungivorous and predatory nematodes than C in both years. In 2006, clipping of sunn hemp enhanced soil nutrient enrichment more than UC as indicated by an increased ( $P < 0.05$ ) abundance of bacterivores and enrichment index (EI) and reduction ( $P < 0.05$ ) in maturity (MI) and channel indices (CI). However, tillage did not affect nematode communities in either year. Regardless of clipping or tillage, planting of sunn hemp increased fungivorous and omnivorous nematodes, but suppressed plant-parasitic nematodes and percentage of predatory nematodes as compared to FT ( $P < 0.05$ ) in 2005. In 2006, SH did not suppress plant-parasitic nematodes, but increased EI and suppressed structure index (SI) and CI at harvest. A series of regression analysis was performed between plant health parameters and nematode community indices at Pi and Pf. In 2005, lima bean yield did not regress linearly with any of the nematode community indices individually, lima bean yield regressed significantly with  $y = EI_i - CI_i + EI_f + SI_f - CI_f$  ( $R^2 = 0.2372$ ,  $P = 0.03$ ) where i and f indicated sampling at Pi and Pf, respectively. In the same year, nitrogen content (N) in lima bean leaves at harvest only was regressed with  $N = EI_i$  but not with any combination of indices. In 2006, turnip yield and N in turnip related individually with several indices. In addition, these two turnip plant health parameters were also regressed with  $y$  or  $N = EI_i - CI_i + EI_f + SI_f - CI_f$  ( $R^2 = 0.1912$ ,  $P = 0.02$  and  $R^2 = 0.1913$ ,  $P = 0.05$ , respectively). We concluded that plant health parameters were related to a combination of nematode community indices, specifically EI, CI and SI, measured before planting or at cash crop harvest. However, slight changes in this relationship occurred from trial to trial.

**BACTERIVORUS NEMATODE POPULATION DYNAMICS IN A PORE NETWORK MATRIX MODEL. Weicht<sup>1</sup>, T. R., J. Gorres<sup>1</sup>, D. L. Moohead<sup>2</sup> and D. A. Neher<sup>1</sup>.** <sup>1</sup> University of Vermont, Plant and Soil Science, <sup>2</sup> University of Toledo, Environmental Sciences.

Nematodes are active under dry soil conditions, when nominal water-filled pore sizes are calculated to be smaller than body diameters. This suggests that bulk soil water retention properties insufficiently describe the habitat of nematodes. Population dynamics models use correlations between soil water content and anhydrobiosis to capture the dynamics of field populations. However, these models do not account for spatial patterns and therefore, do not contribute to a spatial understanding of soil habitat. Understanding interactions between nematodes and their microbial prey within a soil water context may explain field observations that differ from expectations. For example, in dry soils greater microbial respiration was observed in the absence of net nitrogen mineralization. This may be explained by compensatory microbial growth stimulated by nematodes continue grazing in isolated water-filled voids. Autonomous agent models provide a framework for spatially explicit modeling. However, to implement this class of models, one has to consider models of soil pore and water release, individual-based growth and dispersal, and microbial growth and decomposition. In all aspects, both informational and computational constraints exist. Direct observations of pore space are limited by scale and variability in small soil volumes. We chose to parameterize a conditional probability model with empirical data from thin sections of intact soil cores. This technique failed to capture the large pore diameters observed in this soil. Consequently, the model had to be implemented at two levels of resolution, increasing computational time. Available data of modeled pore structure agrees with mercury intrusion porosimetry measurements. Modeling water release requires indentifying and sorting pore pathways with increasing displacement resistance. Identifying pathways through the network requires skeletonization by eroding pores to a single voxel (a 3D pixel) center line. This is proving to be computationally costly for sandy soil (mm diameter pores). Therefore, parallel computing solutions become necessary. To date, only small pore networks have been skeletonized. Our current code will be moved to the supercomputer at the Vermont Advanced Computer Center. Individual-based growth models differ from population growth models. Population dynamics models drive population growth with temperature and moisture. These models do not account for food resources.

However, an individual's development is governed by energy. In culture, first stage juvenile development is delayed until sufficient bacterial biomass exists. Further, spatially explicit models must account for directed dispersal, and studies are scarce. Microbivorous nematodes initially cull microbial stocks by feeding. In return, carbon and nutrients are supplied for compensatory growth through egestion, mineralization, molting and death. Feeding, assimilation, egestion and respiration rates are widely available in the literature. Least is known about molted cuticle: 1), most life history studies do not specifically account for stages; 2), the mass of cuticle lost is in question since cuticle may be lost in its entirety or only as the epicuticle.

**EFFECT OF RIPARIAN HEDGEROWS ON BENEFICIAL ORGANISMS AND ECONOMIC PESTS IN ONTARIO. Welacky, T.W., C. Fox, T. Anderson, D. Hunt, and R. Michelutti.** Agriculture & Agri-Food Canada, Research Centre, 2585 County Rd. 20, Harrow, Ontario, Canada, N0R 1G0.

The objective of the project was to investigate the influence of planted shelterbelts (mixed spruce and white cedar) and native hedgerows on the adjacent soybean crop for evaluation of the benefits or liabilities by providing refugia for pests and pathogens. The project was undertaken for 3 years on 3 paired field locations with planted or natural hedgerows. A field area of 100 meters X 100 meters directly adjacent to the hedgerow was monitored for differences in beneficial organisms and economic pests. Soybean cyst nematode (SCN) *Heterodera glycines* population differences over the growing season for the natural sites were significantly ( $p < 0.5$  level) different with distance from the hedgerows in 2004 and 2006 but not in 2005 and not at the planted sites during the 3 year study. Parasitic amoebae that attack fungi and nematodes were generally more common in the field than the hedgerow. The incidence and occurrence of fungi in each field differed. Per cent occurrence of *Fusarium spp.* tended to be greater at planted shelterbelt sites 2 out of 3 years, *F. oxysporum* was greater at planted shelterbelts throughout the study, *Trichoderma spp.* and Dpc/Ps tended to be higher in occurrence at the natural shelterbelts for 2 out of the 3 years. In 2006 average seed germination of harvested seed increased with distance from the hedgerow ( $r = 0.7904^{**}$ ). Seed pathogens decreased with distance from the hedgerow, *Alternaria spp.* ( $r = .07569^{**}$ ), *Diaporthe spp.* ( $r = -0.4441^{*}$ ) and *Phomopsis longicolla* ( $-0.9064^{**}$ ). These results suggest that the shelterbelt altered the microclimate to promote seed infection near the shelterbelt. In all 3 years, leaf litter and topsoil from the natural windbreaks contained significant numbers of over wintering bean leaf beetles but none were found in leaf litter samples from the planted windbreaks. Spring sampling of soybeans adjacent to the natural shelterbelt did not show higher numbers of beetles in the fields or more defoliation of the soybeans. There was no correlation between the number of soybean aphids and the type of shelterbelt or distance from the shelterbelt. In 2006 only, the average number of soybean aphids per plant correlated to increased distance from the windbreak. Bean leaf beetle counts in soybean fields adjacent to natural and planted windbreaks were slightly higher at 1 m (2006) and 5 m (2005) from the windbreak compared to 90 m from the windbreak for some sampling dates. There were no apparent differences between bean leaf beetle numbers in soybeans adjacent to natural or planted shelterbelts. Alfalfa mosaic virus, soybean dwarf virus, soybean mosaic virus, bean pod mottle virus, and tobacco ringspot virus were detected by ELISA on some weed species in the hedgerows.

**EXTENSION SUPPORT FOR GERMAN FARMERS: HOW DOES IT WORK? Westphal, Andreas.** Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Toppheideweg 88, D-48161 Münster, Germany.

Agricultural production depends on scientific information to improve economic sustainability of production and minimize impacts on the environment. In the densely populated Germany, public acceptance of agricultural production practices is crucial. Mainstream agriculture has an educational system that includes organic farming practices. The system is divided into three levels. Vocational training is certified as a trade job, and advanced schooling results in a vocational degree that prepares new educators for vocational trainees. A second tier is on the college level: degrees allow for trainee education and confer permission to enter the university. At the university level, students earn B.S., M.S., and Ph.D. degrees. These degrees prepare students for advisory or academic positions. The public, continued-education programs are not embedded within the university system. Instead, variety testing and management strategies are investigated at state offices that provide regional implementation of production methods. These offices carry the legal obligation of "official advisors." Federal and state research institutes support applied and fundamental aspects of field problems. In addition to advisory functions, these institutes carry regulatory responsibilities. This network of state government advisors exists alongside private consultants from chemical companies, cooperatives, or commodity groups. In summary, the offerings of public education are multifold in Germany, and the growers make their management decisions based on a variety of these sources.

**FEEDING BY THE ORIBATID MITE SCHELOBATES ALTERS MICROBIAL ACTIVITY AND CARBON CYCLING. Wickings<sup>1</sup>, Kyle G. and A. S. Grandy<sup>1</sup>.** <sup>1</sup>Department of Crop and Soil Sciences, 599 Plant and Soil Science Building, Michigan State University, East Lansing, MI 48824.

Oribatid mites are among the most diverse soil mesofauna, and they possess a variety of metabolic and morphological feeding adaptations. Unfortunately, our understanding of the mechanisms by which oribatids may influence decomposition dynamics is incomplete. A microcosm experiment was conducted in which corn and oak leaf litter were incubated in the presence and absence of actively feeding oribatid mites *Scheleobates sp.* Our objective was to quantify the effects of *Scheleobates sp.* on

microbial activity and carbon cycling within litter. Microbial activity was assessed by measuring C mineralization and microbial enzyme activity over a 3 month period. Respiration rates were measured using infrared gas analysis at three-day intervals and the activity of seven microbial extracellular enzymes was assessed weekly to bi-weekly using fluorometric and spectrophotometric techniques. Carbon dynamics were assessed by comparing the molecular chemical composition of the feces of *Scheloribates* sp. with that of the original litter using pyrolysis-gas chromatography/mass spectroscopy (py-GC/MS). Carbon mineralization rates increased slightly in the presence of an actively feeding mite population after 60 days of incubation. Similarly, the activity of many extracellular enzymes, including beta-glucosidase, chitinase, phenol oxidase and urease, was consistently higher in the presence of *Scheloribates* sp. than in their absence after 60 days. While the chemical composition of feces was similar to that of the original detritus, differences existed in the relative abundance of many compounds. This suggests that *Scheloribates* sp. may be feeding selectively on specific microbial and plant-based compounds within the detritus and that their ability to assimilate some compounds more efficiently than others results in the excretion of organic matter with a unique chemical structure. Our experiment demonstrates that *Scheloribates* sp. can influence carbon cycling indirectly by increasing the activity of microbial extracellular enzymes and directly by altering the molecular chemistry of decomposing organic matter through detritus feeding. Past work shows that many soil mesofauna can alter soil microbial and chemical processes. Given that soil mesofauna differ in food preference and digestive capabilities, we predict other taxa to vary considerably in their effects on these processes in litter. This prediction will serve as the basis for future work in our lab.

**MICROORGANISMS AND ECOSYSTEM DEVELOPMENT: DO SOIL MICROBIAL COMMUNITIES SHOW PATTERNS OF SUCCESSION? Williams<sup>1</sup>, Mark A., S. Tarlera<sup>2</sup>, K. Jangid<sup>3</sup>, and W.B. Whitman<sup>3</sup>.** <sup>1</sup>Mississippi State University, Department of Plant and Soil Sciences MS State, 39759, <sup>2</sup>Universidad de la Republica-Uruguay Catedra de Microbiología, Montevideo, Uruguay. <sup>3</sup>University of Georgia, Department of Microbiology, Athens, GA 30602.

Stemming from its ability to provide order and predictability in very complex ecosystems, succession has survived nearly a century as a paradigm in ecosystem ecology. Soils and their microorganisms have long been considered key to ecosystem function, but the changing composition of microbial communities have not been adequately studied in the context of ecosystem development. To gain a better understanding of how bacterial communities change during soil ecosystem development, we studied their composition and diversity in soils that developed over ~77,000 years of intermittent eolian deposition. 16S rRNA gene clone libraries were used to assess the diversity and composition of the communities. The bacterial community composition changed with soil age, and the overall diversity, richness and evenness of the communities increased as the soil habitat matured. Bray-Curtis ordination suggested an orderly pattern of change of the bacterial community associated with the depositional age of the soil. While the bacterial communities along the chronosequence were relatively rich, the plant diversity was low and changed in a pattern that appeared to be unrelated to changes in the bacterial communities. Microbial community change along the chronosequence, nevertheless, was reminiscent of successional processes often evoked to describe plant community change during the development of in terrestrial ecosystems.

**CONNECTING THE GENETIC AND PHYSICAL MAPS OF THE MODEL ROOT-KNOT NEMATODE *MELOIDOGYNE HAPLA* AND MAPPING A TRAIT FOR AGGREGATION. Williamson, Valerie M.<sup>1</sup>, J. Schaff<sup>2</sup>, S. Fudali<sup>1</sup>, V.P. Thomas<sup>1</sup>, and C. Wang<sup>1</sup>.** <sup>1</sup>Dept. of Nematology, University of California, Davis, CA 95616, <sup>2</sup>Genomic Sciences Lab, North Carolina State University, Raleigh, NC 27695.

The genome sequence of the northern root-knot nematode *Meloidogyne hapla* strain VW9 has been obtained and a genetic map produced, making it an excellent system for investigating traits important for parasitism. The genetic map was produced by analysis of DNA polymorphisms identified as AFLP markers in 183 F2 lines derived from parental strains VW8 and VW9. The F2 lines also differ in behavioral and pathogenicity traits. To identify additional DNA polymorphisms, we obtained 125 Mb of sequence from pooled F2 progeny using an FLX 454 sequencer. The sequence obtained comprised 503,980 reads of 250 bases average length. Over 99% of the reads mapped to the VW9 reference genome assembly. More than 57,000 polymorphisms were identified, approximately 21,000 of which were single nucleotide polymorphisms (SNPs). A subset of these SNPs was tested and confirmed to be segregating in our F2 lines by PCR and sequence analysis. A set of 96 SNP loci was selected based on multiple criteria including proximity to loci of interest (e.g., putative parasitism genes), distribution across linkage groups, and representation on un-mapped contigs. These SNP markers are being used to map new loci in the F2 population with the Illumina Golden Gate assay system. An exciting finding has been that the parental strains differ in whether they aggregate into tight balls in agar and pluronic gels. We hypothesize that the aggregation is part of a survival mechanism. The ability to aggregate or not segregates as a single locus in our F2 population and has been mapped to a linkage group. Fine mapping is in progress with the goal of localizing and identifying the responsible gene(s).

**FIRE AND FUNGI IN THE TALLGRASS PRAIRIE: RESULTS FROM LONG-TERM STUDIES AT KONZA PRAIRIE BIOLOGICAL STATION. Wilson<sup>1</sup>, Gail W. T.** <sup>1</sup>Department of Natural Resource Ecology and Management. Oklahoma State University, Stillwater, OK 74078.

Arbuscular mycorrhizal fungi are ubiquitous in terrestrial plant communities forming mutualistic symbiotic associations with roots of most plant species. Benefits to host plants include enhanced nutrient acquisition and growth, improved water relations, and reduced pathogenic infections. Our previous studies have shown that this symbiosis is a key factor in influencing the structure and function of North American grassland ecosystems. These associations strongly regulate plant growth, reproduction, competition, plant population and community dynamics, as well as play an important role in regulating plant responses to fire. North American grasslands have been maintained for the last 5000 years by frequent fires attributed historically to Native Americans. Although cool-season ( $C_3$ ) grasses, forbs, and warm-season ( $C_4$ ) grasses coexist in these grasslands, frequent fires increase the dominance of  $C_4$  grasses. The stimulation of mycorrhizal activity following burning might be one mechanism for increased productivity of the warm-season grasses. This hypothesis is supported in that warm-season grasses are obligately mycorrhizal. Further, burning stimulates both plant growth and mycorrhizal colonization. However, this stimulation of AM activity is temporary, with no differences observed later in the season. In tallgrass prairie grasslands, the absence of fire increases the density and size of *Juniperus virginiana* (eastern red cedar). Currently, reductions in fire frequency have resulted in encroachment of eastern red cedar into grasslands in the Central Great Plains at an unprecedented rapid rate affecting millions of hectare. Intra- and extra-radical AM fungal abundance is two to three times higher beneath eastern red cedar, as compared to adjacent warm-season grass dominated communities. Fire frequency and mycorrhizal symbiosis may strongly interact to influence vegetation patterns across grasslands of the Central Great Plains. Mycorrhizal symbiosis is a key biotic interaction important to the sustainability of the dominant warm-season grasses.

**BELOWGROUND MACROINVERTEBRATE RESPONSE TO GRASSLAND RESTORATION. Wodika, Ben R. and Sara Baer, Carbondale, Illinois.**

Over 99% of the tallgrass prairie in Illinois has been lost to cultivation, fire suppression, and urbanization, resulting in the decline of many consumer groups associated with this ecosystem. Grassland restoration is typically focused on planting historic vegetation, however less is known about changes in belowground invertebrates in response to aboveground community assembly. Our objectives were to: (1) characterize soil macroinvertebrate assemblages of restored prairies in northern Illinois, (2) quantify changes in abundance of soil macroinvertebrate groups across a restoration chronosequence, and (3) assess whether diversity of seeded plant species affects composition and abundance of soil macroinvertebrates. Soil monoliths were extracted from two agricultural fields, multiple high-diversity restored prairies ranging in age from 1-13 years since planting, three low diversity grasslands restored through the Conservation Reserve Program (CRP), and one prairie remnant. Ant (Formicidae) abundance increased with time since restoration ( $P=0.037$ ,  $r^2=0.31$ ), whereas total beetle (Coleoptera adult and larval) decreased with time since restoration ( $P=0.088$ ,  $r^2=0.22$ ). Total earthworm abundance showed no change with time since restoration. There were no differences in the abundance of macroinvertebrates between high and low diversity restorations. Beetle and earthworm abundances were similar to the remnant prairie. Average ant abundances in the oldest restorations were almost 60 times higher than the remnant. Thus, change in macroinvertebrate abundance during restoration varies among these coarse taxonomic groups. Understanding the recovery dynamics of these belowground consumer groups during restoration is needed to evaluate their role in restoration of ecosystem properties and processes during grassland redevelopment following long-term cultivation.

**DEVELOPMENT OF AFLP-DERIVED STRAIN-SPECIFIC DNA MARKERS AND PERSISTENCE ASSESSMENT OF 10 DOMESTIC SUBSTANCE LIST MICROORGANISMS IN SOIL MICROCOSMS. Xiang, Shu-Rong, M. Cook, S. Saucier, P. Gillespie, R. Socha, R. Scroggins, and L.A. Beaudette. Biological Methods Section, Science and Technology Branch, Environment Canada, 335 River Rd. Ottawa, ON, K1A 0H3.**

For the protection of human health and the environment, there is a requirement under the Canadian Environmental Protection Act (CEPA) to assess the risk of all microbial substances used in Canada after implementation of the New Substances Notification Regulations (NSNR) which came into effect in 1997. Substances with a microbial ingredient that were declared as being in Canadian commerce between 1984 and 1986 were put on a Domestic Substances List (DSL). Given that DSL substances were in commerce prior to the NSNR, industry was not obligated to provide fate or effects data. To fill this information gap, Environment Canada is generating data on the persistence of 10 high priority DSL microorganisms. Strain-specific DNA markers for each of the 10 DSL strains were developed by the amplified fragment length polymorphism (AFLP) technique, and the fate of introduced DSL strains in Alberta clay loam soil microcosms were assessed by real-time quantitative PCR (qPCR). The results indicated that all of the AFLP-derived DNA makers had high specificity at the strain level, and that detection of the target microorganisms were sensitive with a limitation of detection range between  $1.3 \times 10^2$  to  $3.25 \times 10^5$  CFU/g dry soil. qPCR data indicated that all of the introduced microbial strains showed a trend towards a declining persistence in soil and could be categorized into three pattern types. The first was long term persistence over the incubation period. For example, *Pseudomonas aeruginosa* 31480 and *Pseudomonas dinitrificant* 13867 remained at a high concentration,  $3.4 \times 10^5$  and  $1.4 \times 10^7$  CFU/g dry soil respectively for 180 days. In the second pattern, the inoculated strain dropped dramatically below the detection threshold after 10 to 21 days, while the third pattern resulted in a gradually decrease falling below detectable level

within the incubation period. These patterns indicate a selection effect related to ecological function of the introduced microbial strain in soil. In conclusions, the DSL stains can be quantitatively tracked in soil microcosms with high sensitivity and specificity at the strain level using qPCR. Results from this research together with toxicity and pathogenicity data will be used to assist Environment Canada regulators in preparing their risk assessment reports for the priority DSL strains.

**NEMATODE COMMUNITY ASSOCIATED WITH A NEW BI-PHASIC BIORETENTION RAIN GARDEN ECOSYSTEM. Yang, Hanbae<sup>1, 2, 3, 4</sup>, S-J. Park<sup>1, 2, 4</sup>, E. L. McCoy<sup>1, 2, 3</sup>, W. A. Dick<sup>1, 2, 3</sup>, and P. S. Grewal<sup>1, 2, 4</sup>.**

<sup>1</sup>Environmental Science Graduate Program, <sup>2</sup>Center for Urban Environment and Economic Development, <sup>3</sup>School of Environment and Natural Resources, and <sup>4</sup>Department of Entomology, 1680 Madison Ave., The Ohio State University-OARDC, Wooster, OH 44691.

Rain gardens are small, landscaped storm water bioretention areas that may reduce peak runoff flow and improve water quality in a natural and aesthetically pleasing manner. Rain gardens remove runoff pollutants by a combination of physicochemical and biological processes. However, there is little information on soil organisms involved in pollutant removal processes occurring in rain gardens. Using a novel bi-phasic (i.e., sequence of anaerobic to aerobic) concept for improving retention and removal of storm water runoff pollutants, three replicate field-scale bioretention rain gardens were constructed. A mixture of sand, topsoil, and compost (6:2:2, volume ratio) was used as a soil medium in the rain gardens and six native plant species selected for their habitat suitability were planted. Natural and simulated runoffs with spiked concentrations of runoff pollutants were introduced and monitored from April, 2008 to March, 2009. To monitor population dynamics of nematode species in the rain gardens, three composite soil cores (5 cm diameter and 15 cm depth) were collected from anaerobic and aerobic zones over a period of 1 year. Abundance of nematodes was very low in the initial soil medium (average 4 individuals/10 g of soil sample) and the population size did not increase even three months after the establishment of the rain gardens. There were slight differences in nematode abundances in the aerobic and anaerobic zones; the aerobic zone contained higher number of nematodes (8 individuals/10 g of soil) compared to the anaerobic zone (2 individuals/10 g of soil). Free-living nematodes *Acrobeloides*, *Panagrolaimus*, and *Rhabditis* and plant-parasitic nematodes *Pratylenchus* and *Tylenchus* were observed in the rain gardens. Nematode community succession following the introduction of runoff pollutants is currently being monitored and will be presented.

**LINKING THE ABOVEGROUND AND BELOWGROUND COMPONENTS OF COMMUNITIES: 17-YEAR PERIODICAL CICADAS AS RESOURCE PULSES IN NORTH AMERICAN FORESTS. Yang<sup>1</sup>, Louie H.** <sup>1</sup>Department of Entomology, University of California, Davis, California, 95616.

Increasingly, ecologists have begun to integrate the aboveground and belowground components of natural communities into a comprehensive view of terrestrial ecology. I present evidence that resource pulses of periodical cicadas (*Magicicada* spp.) contribute to substantial aboveground-belowground links at landscape and ecosystem scales. Using manipulated cicada densities in field experiments, I investigated the effects of cicada pulses on a belowground forest community including macroarthropods, soil microbes, soil nitrogen, an annual understory plant (the American bellflower, *Campanulastrum americanum*), and a large mammalian herbivore (the white-tailed deer, *Odocoileus virginianus*). These experiments demonstrated rapid changes in the macroarthropod community under experimental cicada litter supplementation. Bacterial biomass increased by 12% compared to controls during the first 28 days of this experiment, and fungal biomass increased by 28%. High natural densities of cicada litter increased mean nitrate levels more than 3-fold relative to controls, and mean ammonium levels increased more than 2-fold relative to controls. American bellflowers which received experimental cicada litter supplementation showed elevated foliage nitrogen content and 9% larger seeds, and also experienced higher rates of deer browsing herbivory. These results suggest that cicada litterfall during emergence years causes substantial pulsed enrichment of forest ecosystems and facilitates strong, if transient, links between aboveground and belowground ecosystem components. In order to identify general patterns among resource pulse events, the results of these field studies are compared with resource pulse-consumer interactions observed in other systems.

**SPERMATOGENESIS IN *PARACTINOLAIMUS MICRODENTATUS* (NEMATODA: DORYLAIMIDA: ACTINOLAIMIDAE). Yushin, Vladimir V. A.V.** Zhirmunsky Institute of Marine Biology of the Far Eastern Branch of the Russian Academy of Sciences, Vladivostok 690041, Russia.

The nematode spermatozoa represent an aberrant type of male gametes; they are characterized by the absence of an axoneme and acrosome. The basic type of nematode spermatozoon is an amoeboid bipolar cell with anterior pseudopod and posterior main cell body which includes condensed nucleus, mitochondria and so called 'membranous organelles' (MO), unique aberrant organelles characteristic of developing and mature sperm of many nematodes studied. The MO appear as a part of the complexes with paracrystalline fibrous bodies (FB) composed from densely packed parallel filaments. The complexes of FB and MO ('FB-MO complexes') during late stages of spermatogenesis dissociate into separate FB and MO. The nematode spermatozoa have been studied in a lot of nematode taxa including the order Dorylaimida. However, all information on the dorylamid spermatozoa

is based on the representatives of only one genes, *Xiphinema*, belonging to the family Longidoridae (*X. diversicaudatum*, *X. pinoides*, *X. theresiae*). The data obtained are unusual and somewhat controversial. It is interesting to widen our knowledge on the dorylaimid male gametes using a representative distant from the longidorids. The structure and development of spermatozoa from the male gonads of the freshwater dorylaimid *Paractinolaimus microdentatus* (Actinolaimidae) were studied using TEM technics. Each testis contains successive stages of sperm development: spermatocytes, spermatids and spermatozoa. The spermatocytes have irregular outlines and highly lobated nucleus each containing one spherical nucleolus. Late spermatocytes have voluminous cytoplasm with numerous clustered mitochondria and components of cell synthesis: ribosomes, cisternae of the RER, Golgi bodies. Unusual spindle-shaped complex of nucleus with mitochondria start to form in the spermatids and persists in the immature spermatozoa. The nucleus which consists of chromatin clumps embedded in electron-light matrix is surrounded by continuous monolayer of mitochondria. This complex is covered by dense filamentous layer isolating central part from the rest cytoplasm. The peripheral cytoplasm of the early spermatid contains the synthetic components which removed from the cell as the residual body of the late spermatid. The latter accumulates large amount of filamentous matter filling prominent pseudopod-like protrusions of the cell. The immature spermatozoa are elongated cells 8-10  $\mu\text{m}$  long 2-3  $\mu\text{m}$  wide. Each spermatozoon contains the central complex of nucleus with mitochondria which is surrounded by electron-light cytoplasm containing numerous dense bundles of filaments and microtubule-like fibres 16 nm in diameter. The spermatozoon surface bears numerous slender pseudopodia resulting in specific star-like images of spermatozoa on the thin sections through the testis. No inclusions resembling MO and FB of other nematode spermatozoa were observed in the male germ cells of *P. microdentatus*. This unusual situation were observed rarely in some representatives of such distant taxa as Mononchida, Chromadorida, Desmodorida and Rhabditida. The deviant pattern of the dorylaimid sperm and spermatogenesis is discussed in details using data on *Xiphinema* spp.

**PATHOGENICITY OF PLANT-PARASITIC NEMATODES ON BLUEBERRY. Zasada<sup>1</sup>, Inga A., J.N. Pinkerton<sup>1</sup>, and T.A. Forge<sup>2</sup>.** <sup>1</sup>USDA-ARS Horticultural Crops Research Laboratory, 3420 NW Orchard Ave., Corvallis, OR 97330, <sup>2</sup>Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, P.O. Box 1000-6947, Agassiz, BC V0M1A0.

Very little is known about the effects of plant-parasitic nematodes on commercial production of blueberries (*Vaccinium* spp.). We conducted field surveys in the Pacific Northwest and Canada, as well as controlled experiments in microplots and in the greenhouse, to discover what plant-parasitic nematode species are present in these production systems and to assess their pathogenicities. Field surveys revealed widespread distribution of *Paratrichodous renifer* in blueberry plantings in British Columbia and northern Washington. *Xiphinema americanum* was found in southern Washington and northern Oregon, and *Pratylenchus* spp. were distributed across all geographic regions examined, occurring in about 45-50% of sampled fields. Inoculation of Northern and Southern highbush and lowbush genotypes in field microplots and in pots in the greenhouse with *P. renifer*, *P. penetrans* and *X. americanum* revealed that blueberry genotypes vary in their susceptibilities to *P. renifer*, and that blueberry does not appear to be a host for *P. penetrans*.

**ESTIMATING VIRULENCE OF SOYBEAN CYST NEMATODE FIELD POPULATIONS IN RESPONSE TO USE OF RESISTANT CULTIVARS. Zheng, Jingwu<sup>1,2</sup>, and S.Y. Chen<sup>1</sup>.** <sup>1</sup> University of Minnesota, Southern Research and Outreach Center, 35838 120th Street, Waseca, MN 56093. <sup>2</sup>Current address: Institute of Biotechnology, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou 310029, P. R. China.

Use of resistant cultivars is the most common practice in managing the soybean cyst nematode, *Heterodera glycines*. Currently, most commercial *H. glycines*-resistant soybean cultivars were developed from a single source of resistance, Plant Introduction (PI) 88788. The effect of crop sequences including rotations of *H. glycines*-susceptible soybean 'Sturdy' with *H. glycines*-resistant soybean 'Freeborn' carrying resistance derived from PI 88788, soybean 'Pioneer 9234' carrying resistance derived from PI 548402 (Peking), and nonhost corn was studied at two field sites in southern Minnesota. Parasitic ability of *H. glycines* measured as a Female Index (FI) on PI 88788 and Freeborn increased with the number of years Freeborn was planted. After more than 5 years of Freeborn, either in monoculture or rotation with other soybean cultivars and corn, the *H. glycines* population changed from the original race 3 (HG Type 0 or 7) to race 1 (HG Type 2.7 or 2.5.7). After 10 years of Freeborn, the resistant cultivar was susceptible (FI > 60) to the changed nematode population. There was no selection pressure from the use of PI 88788-resistance on *H. glycines* populations towards adaptation on Peking. Planting 3 or fewer years of Pioneer 9234 had no noticeable effect on the virulence phenotype of the *H. glycines* population. This study suggests that more cultivars from resistance sources other than PI 88788 are urgently needed for effective management of the nematode in Minnesota and other regions.