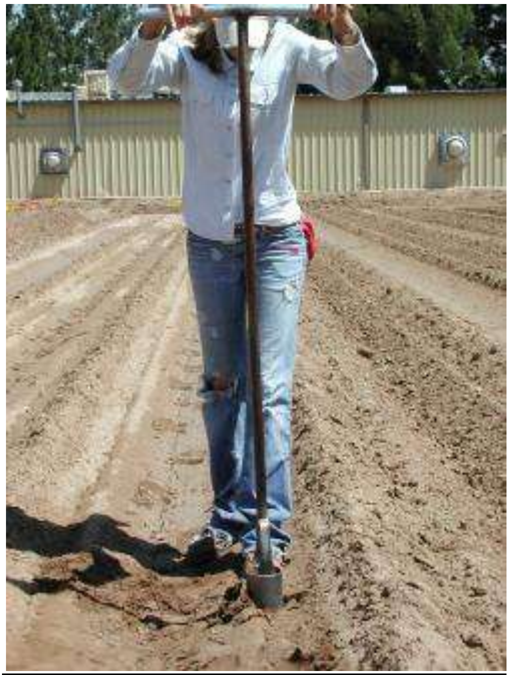
Some of the Research Conducted by the Nematology Lab:

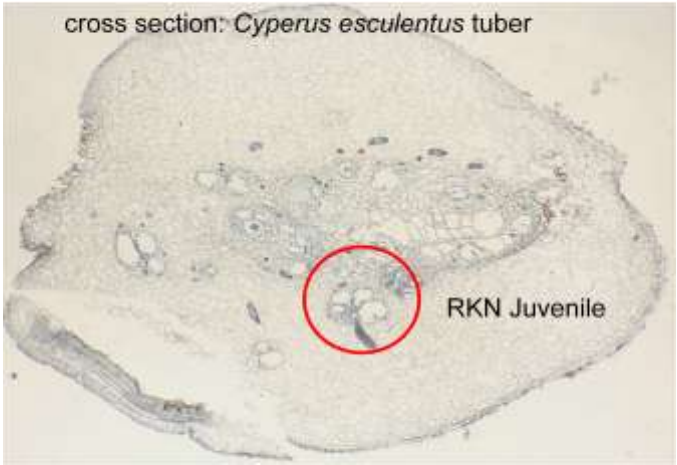
Our program focuses on plant-parasitic nematodes, which are persistent and often serious pathogens of many New Mexico crops. The most economically-damaging nematode in the state is the southern root-knot nematode, *Meloidogyne incognita*. It is widely distributed and, without proper management, can result in yield losses in most annual crops, exceeding 40% yield decline in chile and 25% in cotton. Other root-knot nematodes, including *M. chitwoodi* and *M. partityla* are less widely distributed but serious pests of potato and pecan, respectively. The northern root-knot nematode, *M. hapla*, can damage peanut, chile, and bean crops in eastern NM. In addition to crop damage, the presence of some of these nematodes results in regulatory restrictions on the shipment of NM produce. Historically, nematodes have been managed with pesticides but the availability of such materials to producers in NM and elsewhere have dwindled by 80% in recent years due to environmental concerns. As the expense of pesticide-based management has increased and use has tapered off, so has the level of nematode damage to many crops. Our program addresses a broad range of topics and strives to: determine how plant-parasitic nematodes interact with other pests and pathogens such as annual and perennial weeds and *Verticillium dahliae*; help develop sustainable management alternatives for pest complexes; enhance the efficacy of existing management options; determine relationships among various nematode trophic groups as they relate to plant and soil ecosystem health; evaluate the host status of important Southwestern ornamental plants; educate the agricultural community and homeowners regarding ways to manage existing nematode pathogens and avoid introducing new ones. Most of our research is interdisciplinary and collaborative.

Fabian Garcia

Pecan root-knot nematode:

A unique species of root-knot nematode, *Meloidogyne partityla*, which appears to only affect plants in the walnut family (pecan, walnut, and hickory), was discovered in 1996 from five pecan orchards around Texas. Shortly thereafter, we identified this nematode from mature trees in a diseased pecan orchard in New Mexico. Due to the difficulty in positively differentiating this root-knot species from other root-knot nematodes, we adapted an existing mt-DNA procedure for this purpose. Since then, we have confirmed the presence of M. partityla infested orchards in Arizona, Oklahoma, Georgia, Florida and additional locations in Texas. We have also monitored the seasonal population dynamics of this nematode on pecan for several years, and in so doing established the periods of peak nematode reproduction. There are no pesticide alternatives for management of *M. partityla* in pecan. Our goals with this project are to: examine the susceptibility of pecan and other perennial crops to *M. partityla* and other root-knot nematodes found in the state; determine the extent of pecan root-knot nematode infestation throughout NM orchards; assist in the curtailment of further dissemination of the pest; determine the potential for reducing pest severity through modification of cultural management practices. Collaborators: Mr. Brad Lewis, Entomologist and Dr. Richard Heerema, Pecan Specialist.





Leyendecker

Nematode/weed/crop interactions

A long standing collaborative effort has been working to understand the relationship between yellow and purple nutsedge (two perennial sedges that are among the world's worst weeds) and root-knot nematodes. We work with Drs. Jill Schroeder (EPPWS), Leigh Murray (Experimental Statistics, Kansas State University), and other scientists to understand the biological interactions between these two pest groups and to develop sustainable management strategies for fields infested with this pest complex. The research is unique and has determined that, unlike the crop plant, the weeds are either unaffected or grow better in the presence of the nematode and the nematode is protected within the tuber from nematicide applications and otherwise detrimental overwintering conditions. We have found that using alfalfa as a rotational crop with chile pepper may reduce populations of both pest groups enough to grow one season of chile without pesticide inputs. However, additional work is being conducted to further understand the biological interactions among these pests and to develop additional rotations to provide economically and environmentally sustainable options for fields infested with this pest complex.

During a three year rotation with an RKN-resistant alfalfa crop, it was determined, by monitoring the locations of nutsedge and RKN pest population suppression and resurgence of each, that the density of nutsedge in a field could be used as a predictor of RKN juveniles in the soil. Considering this association, there is no previous data from this environment characterizing the soil nematode community as influenced by crop sequence. The progression of the soil nematode community structure was and continues to be assessed in alfalfa and subsequent, conventionally tilled annual crops under flood irrigation practices in the semi-arid southwest.

Interactions among *Meloidogyne incognita*, annual weeds, and *Verticillium dahlia*: Implications for enhancement of pathogen and weed populations in chile pepper production.

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 and 2009 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. 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 was repeated in summer 2009 to confirm these findings. These 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.

Molecular identification and characterization of soil-inhabiting nematodes:

Numerous nematodes can only be morphologically identified by structures in adult specimens and such identification can often require an experienced nematologist. This can be very time consuming and still does not address the problem with identification of juveniles or the many species without official taxonomic designations. We and other universities are working to develop a simple, molecular system that will identify nematode diversity and abundance within a soil sample.

By generating sequence from single nematodes and comparing it to all previously sequenced nematodes that are available online, it is possible to identify all samples down to the genus level and many to species. In essence, the series of nucleotides specific to each nematode becomes an species identification barcode. Currently we utilize standard Polymerase Chain Reaction (PCR) with universal 18S ribosomal DNA primers. The successful PCR samples are then cleaned and sequenced. Sequences are trimmed and aligned using Geneious. Sequence generated from unknown nematodes is then aligned to a database of previously sequenced nematodes from around the world available on Genbank. A phylogenetic tree is then constructed to visualize the closest matches for the unknown samples. Even as hopeful as we are we need to consider that nematode description via genetic information is still a blossoming field. There are still many nematode species out there that will be discovered in years, months, or even days to come. Future reassessment and reworking of primers is necessary as new species are sequenced and published.