PLANT NEMATOLOGY, EDUCATION AND TRAINING IN CHINA. **Liao[1], J. and H. Li[2].** [1]Laboratory of Plant Nematology/Guangdong Province Key Laboratory of Microbial Signals and Disease Control, South China Agricultural University, Guangzhou 510642, People's Republic of China; [2]Department of Plant Pathology, Nanjing Agricultural University, Nanjing 210095, People's Republic of China.

Due to the great losses caused by some parasitic nematodes on many crops in China, more and more researchers are involved in this area. Presently, there are about two hundred researchers located in different provinces in China. They focus on nematodes of agricultural importance, especially on species identification, basic biology, molecular aspects and disease management. In recent years, the Chinese government funded research on root-knot nematode, cyst nematode and pine wood nematode because of their serious damages on crops and forest. The interaction between nematodes and host plants and novel management techniques will be the ''hot'' research topics which attract Chinese nematologists. A good system for Nematology education and training has been developed through the efforts of Chinese nematologists. These include Bachelor, Master and PhD degree programmes. Incorporation of Nematology curriculums from USA and Europa at local universities is also a possibility.

THE GENOME SEQUENCE AND LIFE-STAGE SPECIFIC TRANSCRIPTOMES OF POTATO CYST NEMATODE. **Lilley[1], C.J., J.A. Cotton[2], V. Blok[3], S. Eves-van den Akker[1,3], L.M. Jones[1], A.J. Reid[2], P. Thorpe[1,3], M. Berriman[2], J.T. Jones[3] and P.E. Urwin[1].** [1]Centre for Plant Sciences, University of Leeds, Leeds LS2 9JT, UK; [2]Wellcome Trust Sanger Institute, Hinxton, Cambridge CB10 1SA, UK; [3]James Hutton Institute, Invergowrie, Dundee DD2 5DA, UK.

Potato cyst nematodes are major pathogens of potato crops in temperate regions, making them some of the most economically important plant parasitic nematodes. Research to develop novel approaches for control of these and other cyst nematodes will be significantly enhanced by a greater understanding of the molecular basis of the parasitic interaction and the key nematode genes required for this. A complete draft genome sequence of the white potato cyst nematode *Globodera pallida* has been assembled, together with transcriptomic data from most of the nematode life cycle, particularly focusing on the life cycle stages involved in root invasion and establishment of the biotrophic feeding site. Despite the relatively close phylogenetic relationship with root-knot nematodes, there is a very different gene family content between the two groups and in particular extensive differences in the repertoire of effectors, including an enormous expansion of the SPRY domain protein family in *G. pallida*, which includes the SPRYSEC family of effectors. This highlights the distinct biology of cyst nematodes compared to the root-knot nematodes that were, until now, the only sedentary plant parasitic nematodes for which genome information was available. The repertoires of genes likely to be important in understanding the unique biology of cyst nematodes and those that represent potential chemical targets and other targets for control have been analysed. A recently assembled draft genome for the closely related species *Globodera rostochiensis* will allow valuable comparative studies.

MOLECULAR CHARACTERIZATION OF RESISTANCE RESPONSES OF *COFFEA CANEPHORA* 'CLONE 14' UPON INFECTION WITH *MELOIDOGYNE PARANAENSIS*. **Lima[1,2], E.A., F.A. Carneiro[2], T.S. Costa[2], E.C.S. Rêgo[2], A. Jorge Júnior[2], C. Furlanetto[1], P. Marraccini[2,3], R.M.D.G. Carneiro[2] and A.C. Andrade[2].** [1]Dep. Fitopatologia, Universidade de Brasília, 70910-900 Brasília, DF, Brazil; [2]Embrapa Recursos Genéticos e Biotecnologia, 70770-917 Brasília, DF, Brazil; [3]CIRAD UMR AGAP, 34398, Montpellier, France.

Coffee is one of the major commodities in the world and an important source of income for producing countries. However, biotic and abiotic stresses are great limiting factors to coffee yield. In Brazil, root-knot nematodes cause considerable yield reduction and the use of resistant plants is the most promising method to control *Meloidogyne* spp. The aim of this work was to characterize the molecular mechanism underlining the previously identified resistance to *M. paranaensis* in *C. canephora* 'Clone 14' by means of RNAseq experiments. Differential expression using RNA extracted from roots of plants from clones 14 and clone 22 of *C. canephora,* previously identified as resistant and susceptible to *M. paranaensis,* respectively, were grown in sand and inoculated. Root samples were collected at different time points post inoculation as well as roots from an uninfected plant. The RNA was treated with DNAse and subsequently, a portion of the sample was lyophilized for RNAseq experiments and another portion kept for validation by qPCR experiments. Results of the identified candidate genes with differential expression among resistant (Clone 14) and susceptible (Clone 22) genotypes will be presented and discussed.

AGGRESSIVENESS OF *MELOIDOGYNE JAVANICA* POPULATIONS ON COMMERCIAL POTATO CULTIVARS. **Lima-Medina[1], I., J.T. Schafer[2], C.B. Gomes[1], M. Vizzoto[1], A.C. Krolow[1], R.M.D.G. Carneiro[3] and V. Correa[3].** [1]Embrapa Clima Temperado, Cx Postal 403, Pelotas/RS, Brazil; [2]Graduated student in Plant Pathology, PPGFS/Universidade Federal de Pelotas, Campus Universitario s/n C. P. 354, Pelotas/RS, Brazil; [3]Embrapa Recursos Genéticos e Biotecnologia, C.P. 02372, 70849-979, Brasília DF, Brazil.

The genus *Meloidogyne* is widely found in the different potato production regions of Brazil. However *Meloidogyne javanica* is the most frequent species that causes damage in potato crop. In order to study the aggressiveness of *M. javanica*, four populations (P1, P3 and P4: Est J3; P2: Est J2a) from southern Brazil was evaluated in two commercial potato cultivars (BRS Clara and Agata) in greenhouse conditions. Individual plants of the two cultivars, kept in pots with sterilized soil, were

inoculated with 5,000 eggs and second stage juveniles of *M. javanica* using six replicates. Fifty-five days after inoculation, each plant was evaluated for number of galls/root, galls number/1.76 cm^2/tuber, nematode reproduction factor (RF). Subsequently, the sensorial quality and the respective total phenolic compound levels in the tubers were also determined. P2 and P4 were the most aggressive *M. javanica* populations exhibiting the higher values of all studied nematode variables interfering in the expression of symptoms on both potatoes cultivars. Additionally, all the populations affected the flavour of cooked potatoes in both of the tested cultivars and higher levels of phenolic compounds were observed in potatoes infected with *M. javanica* P2 population.

REACTION OF POTATO CULTIVARS TO *MELOIDOGYNE HAPLA* AND *M. MOROCCIENSIS*. **Lima-Medina[1], I., J.T. Schafer[2] and C.B. Gomes[1].** [1]Embrapa Clima Temperado, Cx Postal 403, Pelotas/RS, Brazil; [2]PPGFS/Universidade Federal de Pelotas, Campus Universitário s/n C. P. 354, Pelotas/RS, Brazil.

In Brazil, different species of root-knot nematodes, affect potatoes. However, there are few studies of genetic resistance to *Meloidogyn*e species. The objective of this study was to evaluate the reaction of nine commercial potato cultivars to *Meloidogyne hapla* and *Meloidogyne morocciensis* in greenhouse conditions. Potato plants kept in pots with sterilized soil were inoculated with 5,000 eggs and second stage juveniles of *M. hapla* or *M. morocciensis*/plant using six replicates/genotype. 'Santa Cruz' tomato plants received the same inoculum level and were used as control. Fifty-five days after inoculation, each plant was evaluated for the number of galls, eggs and juveniles./root system. Subsequently, the reproduction factors (RF) of the two *Meloidogyne* species were determined in the different genotypes. Among the tested cultivars, BRS Ana, Asterix, BRSIPR Bel, Cota, Cristina, BRS Clara, Catucha, and Eliza were susceptible to both *Meloidogyne* species. Besides being susceptible to *M. morocciensis*, 'Agata' was also moderately susceptible to *M. hapla*.

FREE LIVING NEMATODES AS INDICATORS OF THE BIOLOGICAL STATUS OF AUSTRALIAN CEREAL SOILS. **Linsell[1], K., A. Stirling[2], D. Hartley[3], Herdina[1], A Cheshire[4], J. Nobbs[1], A. McKay[1], G. Stirling[2] and K. Ophel Keller[1].** [1]South Australian Research & Development Institute (SARDI), GPO Box 397, Adelaide, 5001, South Australia, Australia; [2]Biological Crop Protection Pty. Ltd., 3601 Moggill Road, Moggill, 4070, Queensland, Australia; [3]CSIRO Ecosystems Science, GPO Box 1700, Canberra, 2601, ACT, Australia; [4]Science to Manage Uncertainty, 24 Winding Way, Belair, South Australia, 5052, Australia.

The impact of management practices on the biological status of cereal-growing soils was investigated across a range of Australian soil types and climates through nematode community analysis, across multiple years. A multivariate statistical analysis approach identified the two key drivers influencing changes within free-living nematode communities to be soil type which is linked to regional rainfalls, particularly 1-3 months prior to crop sowing and the application of certain nutrients, particularly N, P, S and Cu. Significant shifts in nematode population structures were also characterised by tillage regimes when analysed by soil type. Stubble management and prior plantings did not influence community changes except where canola and legumes were included in the cereal rotations. A Bray–Curtis measure of similarity characterised the contribution of each species/genera driving the changes between each management/environmental treatment and seventeen free-living species were identified as good indicators. Since manual nematode community analysis is laborious and requires specialised taxonomic skills, molecular technologies were developed to allow routine indicator identification and quantification in soil, which can be delivered as part of diagnostic service for soil-borne pathogens. Nine DNA tests were developed incorporating eleven of the free-living nematode indicators and are predicted to detect more than 80% of the species present in Australian cereal cropped soils. There was a very strong correlation between free-living nematode community structures obtained from the manual count and DNA tests. Therefore, we concluded that DNA tests are a sensitive, quick and robust tool for assessing free-living nematode communities, and provide a useful indication of a soil's biological status.

DAMAGE FUNCTIONS OF *MELOIDOGYNE JAVANICA* ON ZUCCHINI SQUASH AND RELATIVE LEAF CHLOROPHYLL CONTENT. **López-Gómez[1], M., F.J. Sorribas[2], M. Talavera[3] and S. Verdejo-Lucas[1,4].** [1]IRTA. Crta de Cabirls Km 2. 08348 Cabrils, Barcelona, Spain; [2]Universitat Politècnica de Catalunya. 08860 Castelldefels, Barcelona, Spain; [3]IFAPA. Camino de Purchil s/n. Granada. Spain; [4]IFAPA. Camino de San Nicolás, 1. 04745 La Mojonera, Almería. Spain.

Yield losses in cucurbits have been reported in many horticultural regions. Zucchini-squash is an important crop in southern Spain accounting for one third of the production in the country. For sustainable management of root-knot nematodes in susceptible crops, it is essential to develop accurate information on population densities that cause yield losses and quantify them into plant damage functions. This study was conducted to determine maximum multiplication rate and equilibrium density of *Meloidogyne javanica* on zucchini squash cv Amalthee in response to increasing initial population densities and to develop damage function models. Seedlings were inoculated with 0, 0.5, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, and 1024 eggs of *Meloidogyne* per cm^3 of soil in repeated experiments in a greenhouse. The maximum multiplication rate was 511, and the equilibrium density 8135 eggs + J2 cm^{-3} soil. The relationship between Pi and relative plant top dry weight fitted the Seinhorst damage function model (R^2=0.53; P=0.0002). Values for minimum relative yield, tolerance limit, and constant z