

Epicoccum nigrum was the most dominant species in this ecosystem. Species richness was lower in the upland ecosystem, where *Fusarium oxysporum* isolates were extremely abundant. Nematodes were found only in the upland ecosystem, and were identified as *Pratylenchus zae* and *Pratylenchus goodeyi*. Previous records showed *P. zae* to be a rice pathogen, but *P. goodeyi* is described here for the first time in rice, a remarkable observation especially in coastal low altitude areas characterised by high temperatures. Preliminary results from greenhouse experiments indicate that *P. goodeyi* can indeed infect and multiply in rice. Based on available information from other crops studied, *Epicoccum nigrum* and *Talaromyces flavus* were selected and are currently tested for their biological activities against these lesion-nematodes.

DIVERSITY OF ENTOMOPHILIC NEMATODES AND THE THREAT OF CRYPTOGENIC INVASIVE SPECIES. Giblin-Davis¹, R.M., N. Kanzaki^{1, 2} and K.A. Davies³. ¹Fort Lauderdale Research and Education Center, University of Florida-IFAS, 3205 College Ave., Davie, Florida 33314, USA; ²Forestry and Forest Products Research Institute, 1 Matsunosato, Tsukuba, Ibaraki 305-8687 Japan; ³Australian Centre for Evolutionary Biology and Biodiversity, School of Agriculture, Food and Wine, University of Adelaide, Waite Campus, PMB 1, Glen Osmond, South Australia 5064, Australia.

Nematode fauna are often highly specialized for microniche utilization, *i.e.*, many nematode species are highly habitat specific. For example, a transect survey of soil, litter, epiphyte and insect-associated nematode fauna in the same site yields different nematode community strata, and the communities do not necessarily overlap each other. Thus, the “insect-associated nematode community” can potentially be considered as a specific “habitat” of specialized and divergent entomophilic nematodes. Based on entomophilic nematode surveys conducted by the authors, correlation between the nematode assemblage pattern (*e.g.*, feeding habitat groups) and the life history of their host/carrier insect (*e.g.*, feeding resource, habitat preference and life cycle) was expected, and the number of entomophilic nematode species was estimated at somewhere between 40,000 and 500,000 species. Considering that the number of currently described species for the entire phylum is about 27,000, most of the entomophilic nematodes are hypothesized to be undescribed species. Biodiversity can be affected by many different kinds of environmental alternations. Here, we focused on the potential for cryptogenic invasive species being introduced by international trade as a threat to the diversity of entomophilic nematodes by introducing several contemporary examples.

GENETIC IMPROVEMENT AND BREEDING OF EPN: THE RACE FOR THE “SUPER NEMATODE”. Glazer, I. Department of Nematology, Agricultural Research Organization, the Volcani Center, Bet Dagan 50250, Israel.

Entomopathogenic nematodes (EPN) which are used as commercial biocontrol agents were targeted for genetic improvement in recent years. Most studies were aimed at improvement of traits which were believed to contribute to the efficacy of these organisms under field condition. That included, enhancement of heat and desiccation tolerance, host finding and resistance to nematicides. In these studies substantial enhancement of the selected trait was demonstrated. The contribution of these traits to nematode efficacy under field condition was not yet demonstrated. In many cases the enhanced trait was not stable and rapid degradation was observed following relaxation of the selection pressure. Furthermore, reduction of fitness can occur during multiple reproduction cycles in large scale liquid culture of the nematodes. Modern genetic and molecular tools such as RNA-seq, transcriptomics can be utilised to follow and understand the molecular basis of a beneficial trait. Molecular markers and QTL can also help to develop new strategies for genetic improvement of EPNs. New techniques for genome editing (TALENs and CRISPR-Cas9) may be able to modify important traits. In the presentation, approaches to address the challenges concerning development of the “super nematode” will be discussed.

CHARACTERIZATION OF MELOIDOGYNE SPECIES FROM IRRIGATED RICE IN SOUTHERN BRAZIL. Gomes¹, C.B., R.R.D. Negretti², V.S. Mattos³, L. Somavilla², R. Manica-Berto², D. Agostinetto² and R.M.D.G. Carneiro³. ¹Embrapa Clima Temperado, C.P. 403, 96001-970 Pelotas RS, Brazil; ²PPGFS/Fac. Agronomia, Universidade Federal de Pelotas, C.P. 354, Pelotas RS, Brazil; ³Embrapa Recursos Genéticos e Biotecnologia, C.P. 02372, 70849-979, Brasília DF, Brazil.

Southern Brazil has the largest cultivated area of irrigated rice in the country. Nonetheless, rice production may be limited by several plant pathogens, including root-knot nematodes (*Meloidogyne* spp.). Considering the importance of root-knot nematodes in Brazil, a survey was carried out in irrigated rice fields in Rio Grande do Sul (RS) and Santa Catarina (SC) states. *Meloidogyne* populations were characterized biochemically by esterase (Est) and malate dehydrogenase (Mdh) phenotypes and morphologically by the female perineal patterns. Fifty five *Meloidogyne* spp. populations were detected in 48% of rice samples, and a total of five esterase phenotypes were identified. In Rio Grande do Sul state *Meloidogyne graminicola* (Est VS1, Rm: 0.70), *Meloidogyne* sp.2 (Est R2, Rm: 0.81, 0.91) and *Meloidogyne* sp.3 (Est VS1-2, Rm: 0.61, 0.70) were identified, which corresponded to 80, 40 and 10% of samples, respectively. In Santa Catarina state *M. graminicola*, *Meloidogyne javanica* (Est J3, Rm: 1.00, 1.20 and 1.35), *Meloidogyne* sp.1 (Est R1, Rm: 1.02), *Meloidogyne* sp.2 and *Meloidogyne* sp.3, accounted for 93.7, 12.5, 62.5, 12.5 and 6.2% of samples, respectively. *Meloidogyne javanica* showed a N1 Mdh phenotype (Rm: 1.0), while other populations exhibited a N1a (Rm: 1.4) phenotype. Morphology of female perineal patterns allowed identification only for *M. javanica* and *M. graminicola*. To further characterize these tree atypical

populations, sequencing and phylogenetic analyses of internal transcribed spacer-rRNA (ITS) and D2-D3 segment of 28S rRNA have been done. Future phylogenetic studies involving these atypical isolates will be performed.

USE OF NUTRITIONAL SUPPLEMENTS FOR THE MANAGEMENT OF ROOT-KNOT NEMATODE (*MELOIDOGYNE INCOGNITA*) INFECTING POTATO. **Gondal¹, A.S., N. Javed¹, S.A. Khan¹ and M. Shahid².** ¹Department of Plant Pathology, University of Agriculture Faisalabad, Pakistan; ²Plant Pathology Research Institute, Faisalabad, Pakistan.

A wide range of synthetic chemicals has been discriminately used as the major control measure against plant pathogens. Environmental pollution, degradation, insecticide resistance development and other agronomic concerns have prompted scientists to seek alternative disease management strategies. Present in-vitro studies were conducted to evaluate the efficacy of nutritional supplements including micro-power, humic acid and plant protectors containing benzoic acid against root-knot nematode (*Meloidogyne incognita*) infection on susceptible potato cultivar. Each treatment applied as single or in combined form significantly reduced the number of galls and egg masses and promoted overall plant growth as compared to un-amended control. Application of aqueous solution of 4% plant protector + 4% micro-power + 2% humic acid enhanced the number of leaves, root and shoot development and tuber weight and decreased the root weight, with the minimum number of females, root galls and egg masses recorded. Nematodes fecundity was observed to be the highest for the control treatment resulting in poor plant growth and development of higher number of galls and egg masses. The significantly lower number of galls and egg masses and enhanced plant growth observed with the combined application of plant protector 4%, micro power 4% and humic acid 2% indicated this treatment to be superior.

EFFECTS OF LONG-TERM CORN-SOYBEAN CROP SEQUENCES ON THE NEMATODE COMMUNITY. **Grabau, Z.J. and S.Y. Chen.** University of Minnesota Department of Plant Pathology, Southern Research and Outreach Center, 35838 120th Street, Waseca, Minnesota 56093, USA.

The effects of long-term corn-soybean crop sequences on the nematode community were studied at a field site that was established in 1982 in Minnesota, USA. The crop sequences were: (i) five-year rotation between crops such that both crops are in years 1, 2, 3, 4, and 5 of monoculture every year; (ii) annual rotation with both crops planted each year; (iii) continuous monoculture of each crop; (iv) annual rotation between two cultivars, but crop monoculture of each crop. Since 1995, sequence IV was single-cultivar monoculture of each crop. Since 2010, soybean susceptible to soybean cyst nematode (*Heterodera glycines*) and *Bt* corn were used for crop sequences i, ii, and iii while monoculture of a *H. glycines*-resistant soybean cultivar or a non-*Bt* corn cultivar was used for sequence iv. Beginning in 2010, half of each plot was treated with granular nematicide. In 2013, the nematode community in each plot was assessed at planting, midseason, and harvest. Nematicide was effective against plant-parasitic nematodes, but also reduced fungivore population and shifted the nematode community to a lower ecological succession. Crop sequences strongly affected plant-parasitic nematodes, but also affected fungivores, bacterivores, nematode community diversity, maturity, and enrichment. Differences in the nematode community were most dramatic when comparing crops rather than length of monoculture within a crop. After dramatic change in the initial years of growing a crop, changes in the nematode community continued incrementally as years in monoculture increased. This study shows the agronomic and ecological impact of crop rotation.

DIRECT AND INDIRECT CONSEQUENCES OF *GLOBODERA PALLIDA* SELECTION BY RESISTANT POTATO GENOTYPES. **Grenier, E., S. Fournet, M.C. Kerlan, D. Eoche-Bosy and J. Montarry.** INRA, UMR IGEPP, Domaine de la Motte au Vicomte, BP35327, 35653 Le Rheu, France.

In this study, we have first explored the variability of resistance durability in different potato genotypes harboring the same resistance QTL but differing by their genetic background. The indirect consequences of the resistance adaptation in terms of local (*i.e.* genotype-specific) adaptation and cross-virulence were then also investigated. Following the virulence of the potato cyst nematode *Globodera pallida* in a long-term experimental evolution protocol, our results showed that nematode populations were able to adapt to the resistance of four potato genotypes carrying the QTL *GpaV* from *Solanum vernei*, and that the plant genetic background has an impact upon the durability of resistance. The pattern of local adaptation observed here revealed a trade-off between the adaptation to a resistant potato genotype and the adaptation to another resistant genotype differing in its genetic background. In terms of cross-virulence between potato genotypes derived from different resistance sources (*Solanum sparsipilum* and *Solanum spegazzinii*), we showed that the adaptation to resistance QTL *GpaV_{vrn}* does not necessarily allow the adaptation to collinear *GpaV* loci. The results presented here will be useful for identifying durable strategies for resistance deployment. The virulent populations obtained from these experimental evolutions are actually used in order to identify, through a genome-scan approach, the genomic regions involved in that resistance breakdown.

DEVELOPMENTS IN THE IMPLEMENTATION OF ENTOMOPATHOGENIC NEMATODES IN INTEGRATED PEST MANAGEMENT SYSTEMS IN NORTH AMERICA. **Grewal, P.S.** Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN 37996, USA.

Entomopathogenic nematodes (EPNs) have emerged as excellent alternatives to chemical pesticides. They have been evaluated against nearly 200 insect pest species almost all of which can be controlled under field conditions. Broad host range