untreated control consisting of tap water. Separate follow-up trials with each of the three test products included a range of dosage rates (400, 800, 1600, 3200 and 6400ppm) and the same intervals mentioned for the 500-ppm trial. All four trials consisted of randomised complete block designs with four replicates for each treatment. For the 500-ppm trial, the untreated control treatment resulted in 92% to 97% of J2's being motile at all of the respective time intervals. Data for J2's suspended in the three commercial standards, salicylic acid and the three test products, however, varied substantially in term of their motility for the duration of the trial. For the three dosage-response trials, significantly higher numbers of J2, compared to the untreated control, were immotile for Test Product 1 from the 800-ppm dosage rate from 48 hours onwards. Although the same effect was evident for Test Products 2 and 3, the majority of J2's was again motile after 72 and 96 hours. Salicylic acid was the only product with a 100% mortality rate for J2's, for both the 500ppm as well as the dosage-response trials, when stained with Tripan Blue after 96 hours. The effect of all treatments included in this study on the ultrastructure of J2's is currently being conducted by means of electronmicroscopy.

DNA BARCODE-BASED TOOL FOR THE MONITORING OF NEMATODE ASSEMBLAGES. **Vervoort[1], Mariëtte T.W., P.J.W. Mooijman[1], H.H.B. van Megen[1], S.J.J. van den Elsen[1], K.D. Rybarczyk[1], J.A. Vonk[2], C. Mulder[2], P.C. De Ruiter[3], J. Bakker[1] and J. Helder[1].** [1]Laboratory of Nematology, Wageningen University, Droevendaalsesteeg 1, 6708 PB, Wageningen, The Netherlands. [2]Laboratory for Ecological Risk Assessment, National Institute for Public Health and Environment (RIVM), A. van Leeuwenhoeklaan 9, P.O. Box 1, 3720 BA Bilthoven, The Netherlands.[3]Centrum Bodem, Wageningen University, Droevendaalsesteeg 4, 6708 PB, Wageningen, The Netherlands.

Within the vast complexity of the soil food web, nematodes are an informative group due to their representation at three different trophic levels. Environmental stress is not only reflected if it affects nematodes directly, but also if it results in major changes in (for instance) bacterial or fungal communities. Although nematodes possess several additional assets preferred for a bio-indicator (*e.g.* easy extractability, differential sensitivities to disturbances, ecological interpretability), the microscopic identification of so-called mass-slides demands skills, lots of time and endurance. For this reason, we have developed a database of currently ≈ 2,300 full-length small subunit ribosomal DNA sequences (appr. 1,700 bp each) from representatives of most major terrestrial and freshwater taxa (*e.g.* Van Megen *et al.* 2009). ARB (Linux-based freeware developed within the microbiology community) was used to design family and genus-specific PCR primers (all with an annealing temperature of 63°C). Currently, about 40 quantitative PCR assays are available for the analysis of nematode communities at family, genus or species level. Results will be presented of a field experiment in which 16 nematode families and genera were sampled every other week during a full season (period of 10 months). The results demonstrate that important ecological information is lost if nematodes are lumped into feeding groups. Substantial seasonal differences were

observed in presence and densities of individual families and genera belonging to the same trophic group.

Van Megen H, Van den Elsen S, Holterman M, Karssen G, Mooyman P, et al. (2009) A phylogenetic tree of nematodes based on about 1200 full-length small subunit ribosomal DNA sequences. Nematology 11: 927-950.

CELL CYCLE MANOEUVRING: A STRATEGY TAKEN BY PLANT PARASITIC NEMATODES TO INDUCE SPECIALIZED FEEDING SITES IN PLANT ROOTS.

Vieira, Paulo[1,2,3,4], G. Engler[1,2,3], M. Mota[4], P. Abad[1,2,3], L. Veylder[5], and J. Almeida-Engler[1,2,3]. 1INRA, UMR, 1301, 400 route des Chappes, F-06903 Sophia Antipolis, France, 2CNRS, UMR 6243, 400 route des Chappes, F-06903 Sophia Antipolis, France, 3Université de Nice Sophia Antipolis, UMR 1301, 400 route des Chappes, F-06903 Sophia Antipolis, France, 4Lab. Nematologia/ICAM, Dept. Biologia, Universidade de Évora, 7002-554 Évora, Portugal, 5Department of Plant Systems Biology, VIB, Ghent, Belgium.

Plant-parasitic nematodes of the genera *Meloidogyne* are capable to induce giant cells that undergo repeated mitosis without cytokinesis possibly alternated with endoreduplication cycles. Promoter activity and mRNA localization of key cell cycle genes like *CDKA;1*, *CDKB1;1*, *CYCB1;1*, and *CYCA2;1* showed early induction of these genes in both nematode feeding site (NFS). In addition, disturbance in NFS development and nematode maturation were observed during treatment of infected roots with cell cycle inhibitors. DNA synthesis experiments demonstrated that both feeding sites undergo extra endocycles possibly justifying the large nuclei present in NFC. How precisely nematodes manipulate the cell cycle in their favor remains to be understood. A systematic comparison of the temporal and spatial expression pattern of different classes of core cell cycle genes between uninfected roots and nematode infected *Arabidopsis thaliana* plants resulted in the identification of a collection of genes possibly implicated in NFC development. Among them, one member of the so-called interactors of cyclin-dependent kinase/Kip-related proteins (ICK/KRP), negative regulators of the cell cycle, showed to be upregulated during NFS development. Recent work has shown that KRP2 might regulate mitosis-to-endocycle transition during Arabidopsis leaf development and is highly expressed in endoreduplicating cells as potentially occurring in nematode feeding cells KRPs. To address the direct relevance of these cell cycle inhibitors genes for NFS ontogeny, mutant lines over- expressing and knocking-down are being used to determine how NFS development is affected, and which family members are potential involved in the NFS formation. Furthermore, *in vivo* subcellular localization of these cell cycle proteins in NFS has been followed to understand the dynamics of these proteins during giant cell development. Based on our preliminary results, some of these cell cycles inhibitors genes are promising candidates involved in NFS development.