

MONDAY 1 JUNE

Plenary session 1

Lamoraalzaal

Chair: Geert Smant

15:10- 15:40 hrs

Free-living nematodes in the deep sea: From fundamental ecological research to monitoring human impacts for environmental management and governance

Ellen Pape

Marine Biology research Group, Ghent University

The deep sea, defined as the ocean below 200 m water depth, represents the largest biome on Earth, yet remains one of the least explored. Within deep-sea sediments, meiofauna (>32 µm) become increasingly important with water depth and often constitute the dominant component of metazoan abundance and biomass in abyssal (> 3000 m) ecosystems. This size class is strongly dominated by nematodes, which occur in high densities, display remarkably high local diversity, and are thought to play key roles in benthic ecosystem functioning.

In this keynote, I will present selected results from deep-sea nematode research, with a focus on work conducted by our research group, covering biodiversity patterns, feeding ecology, functional traits, and links with ecosystem functioning across different deep-sea ecosystems.

The talk will then address the growing footprint of human activities in the deep sea. Although once considered remote and relatively undisturbed, deep-sea ecosystems are increasingly exposed to fisheries, hydrocarbon extraction, and potentially polymetallic nodule mining. Using deep-seabed mining as a framework, I will discuss how nematodes can serve as indicators of human impacts, highlight past and ongoing research on nodule-mining effects, and reflect on how meiofauna and nematodes are currently considered in environmental management and mining regulations.

16:25-17:00 hrs

How plant pathogens co-opt ancient antimicrobials for host manipulation

Bart Thomma

University of Cologne, Germany

Effector proteins are molecules secreted by pathogens to manipulate host biology and promote infection. Evolutionary histories of fungal effector proteins that mediate plant colonization remain poorly understood. While most characterized effectors are known for their roles in modulating plant immunity, recent evidence suggests that some also target host-associated microbiota.

We recently developed AMAPEC, a computational predictor for antimicrobial activity in effector candidates, and use it to uncover a large repertoire of antimicrobial effectors, including many that are highly conserved—pointing to ancient evolutionary origins. Notably, we find that several effectors previously characterized as plant immunomodulators also exhibit antimicrobial activity. This suggests that such proteins may have evolved from ancestral antimicrobials while retaining, at least in part, their original functions.

Collectively, our findings support a model in which microbial antagonism represents a fundamental and ancestral function of fungal effectors. We propose that fungi have repurposed ancient antimicrobial proteins to fulfill diverse roles during host–pathogen coevolution, including both microbiota manipulation and immune modulation.

TUESDAY 2 JUNE

Parallel Session 1

08:30 — 10:00 GMT+2

Lamoraalzaal

Parallel session 1: High resolution insights in nematode/plant interactions

Chair: Jose Lozano-Torres & Almudena Gómez Rojas

8:30-8:48 hrs Almudena Gomez Rojas

Galls and GCs ontogeny: Transcriptional changes within the meristem studied at single cell resolution during Root Knot nematode infection in Arabidopsis

Almudena Gomez Rojas^{□1}, Maite Saura SANCHEZ^{□2,3}, Patricia Abril Urias¹, Thomas Eekhout^{2,3}, Bert De Rybel^{*2,3}, Tina Kyndt^{*4}, Tom Beeckman^{*2,3}, Carolina Escobar^{*1}.

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Root-Knot nematodes (RKNs; *Meloidogyne* spp.), are one of the most important groups of sedentary endoparasites characterized by the formation of galls within the plant root. RKNs penetrate the plant through the elongation zone and migrate towards the meristem to access the vasculature where nematodes select between 5-8 cells to become giant cells (GCs). To unravel the cell-type specific transcriptional responses to nematode infection at very early infection stages, when GCs presumably begin to acquire their identity from precursor cells, we performed a single cell RNA sequencing (scRNAseq) at 36 hours post inoculation (dpi). Three independent replicates from mock and inoculated samples were processed obtaining 35594 and 14153 high quality cells with a median of 1970 and 2005 genes per cell respectively. An unsupervised clustering grouped cells into 28 major clusters, identifying a heterogeneous cell population of enriched cells responding to RKN infection that grouped together forming the “nematode cluster”. This “nematode cluster” include undifferentiated quiescent-like cells only present in the infected sample. These pluripotent cells have suffered massive reprogramming acquiring new cell identity. Additionally, we identified transcription factors differentially expressed in the specific quiescent stem-like

cells infected cell population during early stages of infection, some of them with main roles during RKN infection.

8:48-9:06 hrs Tina Kyndt

Unravelling nematode feeding site formation in plant roots using single cell RNA sequencing

Maite Saura-Sanchez^{1,2,3}, Almudena Gómez Rojas⁴, Melissa Deveux³, Carolina Escobar Lucas^{4,*}, Tom Beeckman^{1,2}, Bert De Rybel^{1,2} and Tina Kyndt³

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Plant-parasitic nematodes lead to large economic losses in agriculture worldwide. Root-knot nematodes (*Meloidogyne* spp.) induce the formation of root galls, containing feeding cells called giant cells (GCs). The GCs develop by a series of drastic cellular changes, induced by massive reprogramming of gene expression. The molecular mechanisms underlying the very early stages of this developmental reprogramming are still poorly understood.

A comparative single-cell RNAseq analyses of infected root samples of two plant species, *Arabidopsis thaliana* and *Oryza sativa*, revealed that the early nematode-responsive cells are highly similar between species, both at transcriptional and functional level. We identified novel conserved genes activated in nematode infected samples and validated their induction upon infection using transcriptional reporter lines and Fluorescence in situ hybridization. A cell-type-specific regulatory network analysis identified conserved transcription factors and their targets that are specifically induced or repressed upon infection. Finally, we selected conserved genes for functional genetic studies and confirmed their role as nematode susceptibility genes. This work provides an unprecedented resource that will help design biotechnological tools against nematode infection in crops.

9:06-9:24 hrs Rahul S. Lathe

Deciphering Feeding Cell Development in *Arabidopsis* and *Tomato* by Plant Parasitic Nematodes (PPNs): Spatial Transcriptomics and Single-Nucleus RNA Sequencing (snRNA-seq) Approaches

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Resistance conferred by dominant R-genes against plant-parasitic nematodes (PPNs) offers an environmentally sustainable solution. However, the emergence of resistance-breaking populations and elevated temperatures due to climate change compromise its long-term efficiency. To address this, our research identifies R-gene-independent resistance strategies by dissecting the molecular mechanisms underlying feeding cell development in root-knot and cyst nematodes.

Previously, we developed spatial transcriptomics using RNA-tomography to systematically map gene-expression dynamics at near-cellular resolution during feeding cell development in *Arabidopsis* (Pijnacker and Wang et al., 2026; <https://doi.org/10.1111/nph.70674>). Here, we complement this dataset with single-nucleus RNA sequencing (snRNA-seq). Promising candidates identified through these multi-omics approaches were spatially validated using high-throughput techniques, including single molecule FISH (smFISH) and hybridization chain reaction (HCR), and functionally characterized to determine their role in feeding-site ontogeny.

Furthermore, we present an update on the translation of RNA-tomography and snRNA-seq developed to Tomato. By comparing these transcriptional landscapes, we aim to elucidate the evolutionary pathways that lead to the complex giant cells and syncytia induced by root-knot and cyst nematodes, respectively. Ultimately, blocking key developmental transitions by targeted mutagenesis and gene silencing may reveal novel targets for breeding crops with durable and broad- spectrum nematode resistance.

9:24-9:42 hrs Yuhao Wang

Revealing spatiotemporal parasitism of *H. schachtii* by integrating spatial transcriptomics and single-cell RNA-seq data

Yuhao Wang¹, Anna Pijnacker¹, Jaap-Jan Willig^{1,2}, Mark G. Sterken¹, Steffen Werner³, Geert Smant¹, Rik Korswagen⁴, Jose Lozano Torres¹

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Plant-parasitic cyst nematodes threaten agricultural production worldwide. To cause infection, these nematodes depend on specialized feeding cells induced in host plants, yet our understanding of how feeding sites are initiated is limited. To better understand the molecular events of early cyst nematode infection, we generated high-resolution spatiotemporal transcriptomes of *Arabidopsis thaliana* roots infected by *Heterodera schachtii* at 1-, 2-, and 4-days post-inoculation using RNA tomography (Tomo-seq). Our spatial expression maps reveal a highly localized and dynamic host response at the infection sites. We identified specific gene clusters involved in nutrient transport, cell wall remodelling, and developmental processes that were rapidly induced at the nematode's head, preceding visible feeding cell formation. Importantly, by simultaneously mapping to *H. schachtii* transcriptome, we correlate the expression of key parasitic effectors with these localized host responses. Furthermore, by integrating our spatial data with single-cell RNA-seq, we reveal the targeted reactivation of key host developmental pathways that may contribute to the formation of feeding cells. Our work provides a powerful framework for studying plant-nematode interactions at cellular resolution and delivers a detailed molecular roadmap of the transcriptional events underlying feeding cell formation.

9:42-10:00 hrs Peter DiGennaro

Improved Approaches to Single-Cell Recovery and Sequencing of Plant-Parasitic Nematodes

Kwon, K.¹, Henthorn, C.², Wijaya, S.³, Richardson, C.³, Zamanian, M.², DiGennaro, P.¹

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Single-cell sequencing technologies are powerful tools to unravel basic biology of model organisms. Complex symbioses, like that of plant parasitic nematodes (PPN), necessitate single-cell resolution to unravel intricate interactions and characterize specific signaling events that dictate plant and animal development over time. One such interaction is the decision of some PPN to initiate development; second stage juveniles are often compared to free-living dauer stages. Here, we evaluated single-cell dissociation, fluorescence-activated cell sorting (FACS), and transcriptome sequencing methods in the root-knot nematode *Meloidogyne hapla* naive dauer larvae compared with those of *Caenorhabditis elegans*. Improved enzymatic digestion and mechanical disruption protocols followed by standard FACS gating strategies allowed for the comparison of viable singlet cells recovery from *M. hapla* and *C. elegans*. Normalization of cell recovery was based on the estimated total somatic cells per individual, reflecting the different innate biology of differences of parasite and free-living nematodes. Individual cells were sorted based on viability (Calcein-AM+ and DRAQ5+) and on RNA-richness (Cresyl Violet+). Improved methodologies for single-cell recovery allow for comparative transcriptional studies on the signals of *C. elegans* dauers

and their PPN counterparts, providing new insights into the transcriptional control at the cellular level of these nematodes.

Parallel session 2

08:30 — 10:00 hrs

Abdijzaal

Parallel session 2: Management - systems approach

Chair: Leendert Molendijk & Anne Sophie van Bruggen

8:30-8:48 hrs Deliang Peng

Occurrence and Integrated Management of Potato Cyst Nematode (*Globodera rostochiensis*) in China

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Golden cyst nematode (*Globodera rostochiensis* = *Globodera vulgaris*) is most important quarantine nematodes on potato. The *G. rostochiensis* was first found in Guizhou province in 2018, it has now distributed in seven counties of Yunnan and Guizhou in China. The sudden outbreak of the potato cyst nematode poses a serious threat to the safe production of potato seed bases. 200 potato cultivars and lines from the southwest mixed-cropping zone were tested resistance to *G. rostochiensis* even in greenhouse and infected filed. Two molecular markers 57R and TG689, linked to the H1 for resistance to *G. rostochiensis* Ro1 pathotype were used to identify those cultivars of the bioassay. Eight major potato cultivars including Huishu 15, Xuan 5, Xuan 6, Yun 505, Yun 304, Atlantic, Long 14, and Jizhangshu 12 are found highly resistant to *G. rostochiensis*. Those cultivars above were identified as harboring the H1 gene conferring resistance to the potato cyst nematode. Five Nematicides effects against the Potato Golden Nematode (*Globodera rostochiensis*) were evaluated in the Field in Zhaotong, Yunnan Province. Non-fumigant nematicides such as 1% abamectin granules, 41.7% fluopyram suspension, 40% Fluensulfone emulsion, 450g/L cyclobutirfluram suspension, 10% fosthiazate granules could effectively control potato cyst nematode. The fumigant nematicide, such as 98% dazomet microgranules could achieved over 99% efficacy against PCN. Rotation measures including marigold, Chinese medical plant,

broccoli, Chinese cabbage were tested. The Integrated Nematode Managements of potato cyst nematodes were developed. This work was supported by the grants from National Key R & D Program of China (2023YFD1400400)

8:48-9:06 hrs Alessandro Cabianca

A Comprehensive Study of *M. chitwoodi* and *M. fallax* in Switzerland: Characterization, Phylogenetic Analysis and Investigation of Resistant Plants

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Meloidogyne chitwoodi and *M. fallax* are root-knot nematodes adapted to temperate climates, with host ranges encompassing crops such as tomato and potato. These species have quarantine status in Europe, and their polyphagy makes them difficult to control.

In Switzerland, *M. chitwoodi* and *M. fallax* infested fields are left fallow, a practice which controls nematode populations but also decreases soil health. Cultivating non-host plants would be a better control technique, reducing nematode populations while improving soil health. Both species occur in Switzerland, and investigating genetic similarities between populations could clarify population movements and points of entry.

In this study, morphological and molecular characterization of Swiss *M. fallax* and *M. chitwoodi* populations was carried out. *M. chitwoodi* was identified as Race 1, pathotype Roza, using a differential host test and a race-specific PCR. A phylogenetic study was performed with barcodes commonly used in phylogenetic studies and diagnostic identification. Although high sequence conservation hindered the analysis, Swiss populations often grouped within the same cluster, suggesting a common point of origin. The host status of *M. chitwoodi* and *M. fallax* for several plants was tested over one and two generations, with promising results for *Tagetes* spp. and *Raphanus sativus*.

9:06-9:24 hrs Wim Wesemael

Survival of *Meloidogyne enterolobii* in soil under temperate conditions in the absence of host plants

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Meloidogyne enterolobii is a highly aggressive and invasive root-knot nematode listed as quarantine pest in the EU. Native to tropical and subtropical regions, this pest is now infiltrating temperate zones, aided by climate change and global trade. Knowledge on its ability to survive during intercrop periods and its possible adaptation to cooler climates is needed to anticipate introduction and further spread. Survival and infectivity of second-stage juveniles (J2) of *M. enterolobii* were assessed under outdoor conditions during three consecutive winter periods in Flanders, Belgium. Additionally, survival was also examined under controlled temperature regimes. In the outdoor experiments, infective J2 were still present in the soil after 28 weeks during autumn, winter and spring. The *in vitro* experiment showed highest survival at lower temperatures (5°C) during the initial 6 weeks. At later time points there was no difference in survival between low and higher temperatures. We can conclude that *M. enterolobii* is able to survive at low temperatures (<10°C) during several weeks and remain infective. These findings stress the need to prevent introduction of *M. enterolobii* into agricultural areas in temperate zones.

9:24-9:42 hrs Solveig Haukeland

Potato cyst nematode (*Globodera* spp.) invades Africa - distribution and dynamics in Eastern and Southern Africa.

Haukeland, S.^{1,2}, Murithi, H.³, Otieno, W.⁴, Sosa, O.⁴ Onkendi, E.⁵, Atieno, E.O.⁶, Kamau, J.⁷, Jones J.^{8,9} and Coyne, D.^{3,10}

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¹⁰Ghent University, Ghent, Belgium

The potato cyst nematode (PCN; *Globodera rostochiensis*) was reported for the first time in eastern Africa over 10 years ago in the highlands of Kenya. Since then, it has been reported in Rwanda (2019), Tanzania (2026) and Uganda (2020). In Kenya its distribution is well

documented and PCN is present in all major potato growing regions. Additionally, *G. pallida* was reported in 2018 in Kenya. The need to understand PCN dynamics and its distribution across the eastern and southern Africa region is urgent towards containing and managing the threat. In 2023 the Standards and Trade Development Facility of the World Trade Organization (STDF) approved a project (2023-2026) to strengthen capacity of phytosanitary services in their knowledge of PCN in 12 countries (Burundi, Ethiopia, Kenya, Lesotho, Malawi, Mozambique, Rwanda, South Sudan, Tanzania, Uganda, Zambia and Zimbabwe). Activities have been focused on capacity building (trainings) and creating awareness to reduce the impact of PCN and other emerging pests on potatoes across the region. The project aims to facilitate a regional and harmonized approach to addressing the risks from PCN and emerging potato pests in the 12 countries. Current findings from this highly collaborative project will be presented.

9:42-10:00 hrs Evelyn Van Heese

MAKANDRA: Together stronger! Government to Government project to strengthen Food security and Plant Health.

van Heese, E.Y.J.¹, Zebeda, S²., Mitrosentono, D.², Boschma³, S., Karssen¹, G. and van Bruggen A.S¹.

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The Makandra project is a collaborative initiative between the Netherlands and Suriname, aimed at improving food safety, animal health, and plant health in Suriname, both for the domestic market and export purposes. This project facilitated knowledge exchange between government institutions from both countries, with the NPPO of Suriname as the beneficiary and the NVWA playing a key role as partner. The project consisted of two main components: phytosanitary and veterinary.

In the phytosanitary domain, activities such as courses and study visits were organized to strengthen policy makers, inspectors and laboratory employees regarding their awareness, skills and knowledge. Knowledge transfer occurred through reciprocal visits of experts, with a focus on enhancing the capacity of Surinamese services to meet EU standards. This to support Suriname in exporting more easily within their region and to the EU.

A key aspect of the project was training Surinamese colleagues at the LVV laboratory in Paramaribo, where they were educated about plant diseases caused by bacteria, insects,

nematodes and fungi. Additionally, training covered performing phytosanitary inspections for import and export and developing risk management strategies.

The project contributed to strengthening the relationship between the Netherlands and Suriname, with both countries gaining valuable insights and knowledge.

Parallel session 3

08:30 — 10:00 GMT+2

Room 522

Parallel session 3: Plant resistance to nematodes (I)

Chair: James Price & Aska Goverse

8:30-8:48 hrs Rick Faesen

Screening for novel sources of resistance to virulent *Globodera rostochiensis* populations in wild potato genotypes.

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Potato cyst nematodes (PCN) are an economically destructive pest in both temperate and tropical regions where potatoes are grown and can reduce the potato yield. The reliance on a single major resistance gene has led to heavy selection pressure and breaking of the resistance. This challenge creates a need for new sources of resistance to be incorporated into commercial potato cultivars. Within the RostoResist project we aim to increase our arsenal with novel resistance genes against two of the most virulent *Globodera rostochiensis* populations (AmPOP43 and AmPOP44). To this end we have screened a panel of 300+ wild *Solanum* genotypes to determine their level of resistance, by inoculating *in vitro* grown potato explants. Moreover, we were able to closely follow the infection process under the microscope and monitor resistance mechanisms such as hypersensitive responses (HR) and concurrent effects on nematode development. At 60 days-post inoculation, the number of females and cysts were counted and compared to our susceptible control cv. Desiree. Several of the wild genotypes were found to be resistant with several different mechanisms of resistance. Promising genotypes were later validated in pots inoculated with PCN eggs. Details of the result and future prospects will be presented.

8:48-9:06 hrs Leidy Van Rijt

Breeding lines with novel resistance sources from wild *Solanum* species utilise a combination of resistance mechanisms against virulent *Globodera pallida* population 'Oberlangen'

Leidy van Rijt & Dr. Sebastian Kiewnick

Institute for Plant Protection in Field Crops and Grasslands, Julius Kühn-Institut, Messeweg 11-12, 38104 Braunschweig, Germany

Intensive use of limited sources of resistance caused an emergence of GpaV-virulent *Globodera pallida* populations in starch potato-growing regions in Germany and in the Netherlands. The project ASPARA is developing durable resistance with resistance sources from wild potato species. Because of the wide variety of species, a high diversity of (undiscovered) resistance mechanisms can be present in the breeding lines. Resistance mechanisms can affect hatching, attraction and penetration or syncytium formation of *G. pallida*. The latter limits nematode reproduction by masculinisation or disruption of female development.

To investigate the mechanisms underlying the novel sources of resistance, different resistant genotypes were investigated for their effects on the *G. pallida* populations “Oberlangen” (virulent) and Chavornay (a-virulent). Our results point to a combination of mechanisms, namely prevention of juvenile entry, masculinisation and potentially reduced egg production. Further hatching, attraction and penetration tests were conducted to identify the source of reduced juvenile entry. Next to that, to exclude the possible effect of nutrient-poor soil on reduced egg production, bioassays using a more nutrient-rich substrate are used.

These experiments highlight the variety of strategies in the plant’s defence against virulent *G. pallida* populations and the importance of utilising novel sources of resistance in potato breeding.

9:06-9:24 hrs Danny Coyne

Potato cyst nematode (*Globodera rostochiensis*) dynamics in repeat potato cropping systems in East Africa

Kisaakye, J.¹, Mwesigye, R.^{2,3}, Mbiyu, M.⁴, Nyongesa, M.⁴, Jones, J.⁵ and Coyne, D.^{1,3}

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Potato (*Solanum tuberosum*) is a key food crop globally. In East Africa, potato production is threatened by potato cyst nematodes (PCN; *Globodera rostochiensis*), regulated quarantine pests responsible for substantial yield losses. Continuous cultivation of PCN-susceptible cultivars, frequent use of farm-saved seed, and limited crop rotation have accelerated PCN population build-up in the region. PCN-resistant cultivars have recently been deployed as a sustainable management strategy. However, there is limited knowledge on how repeated

cultivation of resistant cultivars would influence PCN population dynamics under the sub-tropical conditions. Multi-season field trials are therefore being conducted in Kenya and Uganda to evaluate the effects of repeated cropping on PCN dynamics and potato yield. The trials include two recently introduced PCN-resistant cultivars (Malaika, Glen) plus an existing one (Markies) and one susceptible control (Shangi). Preliminary results following two consecutive seasons indicate that repeated cultivation of resistant cultivars a consistent decline in PCN cyst densities, reduced eggs per cyst, and lower egg viability, while maintaining satisfactory yields, particularly with Malaika and Glen. These findings highlight the significance of using PCN-resistant cultivars in suppressing nematode populations, sustaining potato productivity, and supporting phytosanitary compliance for regional and cross-border trade.

9:06-9:24 hrs Milad Rashidifard

Resistance of Soybean Cultivars to *Meloidogyne incognita*: Greenhouse Screening and Histopathological Evaluation

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Soybean is one of the most valuable grain crops in South Africa and is cultivated across all provinces of the country. However, its production is severely constrained by root-knot nematodes, which are the primary nematode problem in soybean cultivation. This study evaluated the host resistance of twenty-four soybean cultivars and seven genotypes against *Meloidogyne incognita* under greenhouse conditions. Resistance levels were primarily determined using the reproduction factor (Rf) value. To validate the results, selected cultivars were subjected to histopathological evaluations.

The results indicated that cultivar LS 5995 and genotype GCI 7 exhibited the highest level of resistance, whereas cultivars LS 6248 R and Dundee were highly susceptible.

Histopathological evaluations using light and transmission electron microscopy confirmed resistance in both GCI 7 and LS 5995. This resistance was attributed to the development of giant cells that differed markedly from those observed in susceptible cultivars. Both greenhouse screenings and histopathological evaluations confirmed the susceptibility of cultivar Egret, previously identified as resistant, to *M. incognita*. Overall, greenhouse screenings proved to be a reliable method for identifying resistance in local soybean cultivars. Furthermore, histopathological observations revealed resistance mechanisms at the cellular level, highlighting hypersensitivity as an additional defence mechanism.

Plenary session 2

10:30 — 12:30 GMT+2

Lamoraalzaal

Plenary session2

Chair: Hans Helder

10:30-11:00 hrs Peter Geldhof (INVITED SPEAKER)

Emerging Challenges in Managing Nematode Infections Across Human and Veterinary Health

Peter Geldhof

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Parasitic nematode infections continue to pose a major challenge to both human and animal health worldwide. Control of these infections still relies heavily on the use of anthelmintic drugs, but the long-term sustainability of this approach is increasingly under pressure. In veterinary medicine, decades of intensive and often frequent drug administration have led to widespread anthelmintic resistance in gastrointestinal nematodes of livestock, particularly in sheep and cattle. In addition, concerns are growing regarding the environmental impact of drug residues and the effects of parasite control practices on ecosystem biodiversity.

Although the situation in human health remains less critical, large-scale preventive chemotherapy programs targeting soil-transmitted helminths and other neglected tropical diseases continue to increase global drug pressure. Reports of reduced drug efficacy and genetic markers associated with resistance are emerging, highlighting the importance of proactive surveillance and sustainable control strategies before widespread clinical resistance develops. At the same time, climate change, changing farming systems, globalization and increased movement of humans and animals are influencing parasite epidemiology and transmission dynamics, creating new challenges for integrated parasite management across the human–animal interface. Despite these evolving threats, the development of novel anthelmintic compounds has remained limited, emphasizing the urgent need for alternative and complementary control approaches. This presentation will provide an overview of the current challenges in managing nematode infections across both veterinary and human health sectors, with particular emphasis on anthelmintic resistance, advances in diagnostics and surveillance, sustainable parasite control strategies, and recent progress in the search for novel therapeutics or vaccines and integrated management approaches.

11:00-11:20 hrs Lisa van Sluijs

A Model Phage Resource (CePhi) to Study Ecological, Molecular and Evolutionary Consequences of Nematode-Phage Hitchhiking on the Soil Microbiome

Annamaria Mattia, Amarenz Ringia, Stefan van de Ruitenbeek, Lisa van Sluijs

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Bacteriophages (phages) infect bacteria and hitchhike along with nematodes to travel through the hostile soil environment. By hitchhiking, phages overcome a diverse range of spatial and physical barriers, and as a result, nematode-phage interactions could shape microbial soil communities. Existence of a biological model system would facilitate studies investigating these interactions, but naturally cooccurring nematode-bacteria-phage trios are not available yet. Here, we create a phage resource, called CePhi, with naturally co-occurring nematode-bacteria-phages trios to study their ecological, molecular and evolutionary interactions. Therefore, we set out to identify phages associated with the model nematode *C. elegans* and its well-characterized bacterial microbiome. We enriched ephemeral substrates, on which we find *C. elegans*, for phages that infect members of the nematode's bacterial microbiome. Thereby, lytic phages were identified, propagated and characterized via genome sequencing. So far, using only a small set of ephemeral samples, our results show natural phages of *C. elegans* can readily be discovered. Next sampling season, we will use this method to expand the CePhi collection. The initial isolates are currently used in experiments determining molecular and evolutionary nematode-phage interactions. Together, these experiments give insight in how previously undiscovered interactions between nematodes and phages could determine the soil microbiome.

11:20-11:40 hrs John Jones

Managing *Globodera rostochiensis* in Kenya using genotypes that combine resistance with grower- and consumer-preferred traits under sub-tropical conditions

Coyne, D.^{1,2} Price, J.A.³, Haukeland, S.², Cortada, L.^{1,2} Orage, C.¹, Mwaura, O.^{1,2}, Kuhfuss, L.³ & Jones, J.T.^{3,4}

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The potato cyst nematode (PCN) *Globodera rostochiensis*, causes serious damage to potato production across East Africa. In Kenya, it is present in all major potato growing regions, often at exceptionally high densities. The most preferred cultivar, Shangi, which dominates the Kenya market is susceptible to PCN. It has very low dormancy, has high taste acceptability and cooks quickly. The sub-tropical conditions support multiple cropping cycles per year, facilitating high PCN densities. To manage PCN in Kenya, cultivars with H1 resistance have been introduced for evaluation. For successful adoption however, resistant

cultivars need to possess a suite of traits and characteristics favoured by growers as well as consumers. New potential cultivars were selected from advanced breeding lines based on their resemblance to cv. Shangi. Field tests demonstrated that the new lines performed well in the field, including under high levels of PCN. In consumer acceptability tests the lines were favoured compared to a PCN-resistant check cultivar, but also in relation to Shangi. Two new cultivars - Glen and Malaika have now been officially registered. Current work is focused on scaling up production of seed tubers and assessing suitability of the cultivars for growers in other countries.

11:40-11:50 hrs Short Break

11:50-12:10 hrs Pallavi Shakya

High-Resolution Genome Assembly and Linkage Mapping in *Meloidogyne hapla* Reveal Non-Canonical Telomere Repeats and Recombination Hotspots Associated with Effector Proteins

Pallavi Shakya¹, Muhammad I. Maulana^{2,3}, Etienne GJ Danchin⁴, M. Laurens Voogt², Stefan J.S. van de Ruitenbeek², Jacinta Gimeno¹, Adam P Taranto^{1,5}, Alison C. Blundell¹, Evelin Despot-Slade⁶, Nevenka Meštrović⁶, Ana Zotta Mota⁴, Dadong Dai⁷, Valerie M. Williamson¹, Mark G. Sterken^{2,*}, Shahid Siddique^{7*}

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Root-knot nematodes cause significant yield losses across diverse crops. *Meloidogyne hapla* is a valuable model for studying root-knot nematodes due to its small diploid genome and reproductive strategy that facilitates genetic analysis. We report the most contiguous genome assembly to date for any plant-parasitic nematode, built using PacBio HiFi, Oxford Nanopore, Illumina, and Hi-C sequencing. Genetic linkage analysis of F2 populations derived from crosses between *M. hapla* strains validated the assembly but revealed anomalies indicating chromosome structure differences between parental isolates such as fissions, fusions, and rearrangements. Strikingly, we identified sharply delimited zones with extraordinarily high recombination on most chromosomes. Several of these high recombination zones were significantly enriched for genes encoding secreted proteins that contribute to parasitism. These findings suggest that meiotic recombination facilitates effector diversification and offer insight into how these parasites diversify their effector repertoire to expand their extraordinary host range. We further report the discovery of a novel 16-nucleotide tandem repeat and lack of canonical telomere repeats at chromosome ends. The localization of this 16-nt repeat at chromosome ends highlights a potentially divergent mechanism of chromosome-end maintenance. Overall, our study integrates high-resolution structural genomics, genetic mapping, and functional inference to uncover links between genome architecture, recombination landscapes, and host–parasite interactions.

12:10-12:30 hrs Peter Marhavy

Sound as a hidden modality shaping plant–animal interactions

Zahid, N.,¹Anjam, S.¹, Hiltl, C.³, Rollo, M.⁴, Lin, J.^{1,2}, Chen, C.^{5,6}, Klaminder, J.⁴, Jensen F.C.², Grundler, F.³, Marhavý, P.¹.

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Plants generate sound that functions as an ecological signal for animal behaviour. Ultrasonic emissions from plant roots vasculature, produced by cavitation associated with xylem hydraulic conductivity, elicit robust and directional locomotory responses in nematodes. Behavioural responses are niche-dependent: the free-living *Caenorhabditis elegans* avoids ultrasound, whereas the plant parasite *Heterodera schachtii* is attracted and uses these cues for host invasion. Disruption of mechanosensitive ion channels abolishes these responses. Loss of the TRP-4 channel reduces ultrasonic sensitivity in *C. elegans*, while silencing of *mec-4* and *trp-4* in *H. schachtii* impairs host localization and root invasion. Together, these findings establish plant-derived sound as a functional sensory cue and reveal an acoustic axis of plant–parasite interactions.

Parallel Session 4

14:00 — 15:30 GMT+2

Lamoraalzaal

Parallel session 4: Adaptations, plasticity, and novel approaches

Chair: Clarissa Hiltl & Sophie Mantelin

14:00-14:18 hrs Sophie Mantelin

Host imprint in the root-knot nematode *Meloidogyne incognita*

Mantelin, S., Da-Rocha, M., Van-Ghelder, C., Julien-Portier, U., Lartigue, S., Pierre, O., and Favery, B.

INRAE-Université Côte d'Azur, Institut Sophia Agrobiotech, 400 Route des Chappes, 06903 Sophia- Antipolis, France

Soil-born, plant-pathogenic nematodes that infest plant roots cause severe damage to crops worldwide. *Meloidogyne incognita* is of particular concern due to its broad host range. However, the patterns of host compatibility are often discussed in relation to nematode populations that differ in their ability to efficiently infect different host plants. Using acclimatised nematode populations generated through experimental evolution of the *M. incognita* model on two distant hosts (tomato and fig tree), we observed that the rearing host plant has a significant impact on the nematode aggressiveness, affecting both infectivity and fecundity. Additionally, it modulates the chemotaxis behaviour of *M. incognita* towards root extracts. RNA-seq analysis of naïve pre-parasitic juveniles from these populations further revealed that host plants significantly influence the nematode transcriptional landscape. Notably, acclimatisation led to switches in the usage of homoeologous gene copies in the triploid hybrid *M. incognita*, which most likely correlates with an epigenetic imprint at the chromatin level. Overall, these results suggest that pathogen adaptation occurs to balance nematode reproduction rate with the sustainability of its food source.

14:18-14:36 hrs Olaf Kranse

Controlling the Clock: New Tools for Inducing and Studying Nematode Tanning

Kranse, O.P., Dang, L., Leproni, A., and Eves-van den Akker, S.

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Tanning of the cuticle coincides with the final life stage of female cyst nematodes. The tanned cuticle is thought to enable encysted eggs to remain viable within the soil for decades, creating a persistent inoculum. This long-term survival requires extended crop rotations and complicates eradication, leading to economic losses.

Our understanding of the triggers of tanning remain largely unknown, due in part to technical limitations of observing the phenomenon. We address this constraint using a custom-engineered test-bed that integrates specialised hardware and software for monitoring tanning *in planta*, as well as an optimised cyst-inducing protocol *ex planta*, for *Heterodera schachtii*. While the stochastic onset of tanning has historically limited research to static, binary assessments (tanned vs. untanned), this platform enables high-resolution, real-time observations, effectively unlocking the temporal dimension of this biology for study. Using this new approach we found that *in planta* tanning, progresses as a wave across the cuticle, which may indicate some form of self-amplifying reaction.

Taken together, these tools pave the way for developing a deeper understanding of this fundamental part of cyst nematode biology, perhaps enabling the exciting prospect of interventions which prevent tanning and thereby may reduce dormancy from decades to a single season.

14:36-14:54 hrs Jaap-Jan Willig

Interspecific adaptations in root system architecture define host tolerance of Arabidopsis to biotic stresses by root feeding nematodes

Willig, J.-J.^{1,2}, van Schaik, C.C.¹, Faesen, R.², Sterken, M.G.¹, Teklu, M.G.², Smant, G.¹

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Plants tolerate belowground biotic stress through developmental plasticity, yet how root system adaptations contribute to tolerance remains poorly understood, particularly when stresses differ in location, duration, and severity. Root-feeding nematodes provide a model, as migratory, vascular-feeding, and gall-inducing species impose different types of damage. We investigated how Arabidopsis responds to three nematode species with contrasting infection strategies: the root-lesion nematode *Pratylenchus penetrans*, the cyst nematode *Heterodera schachtii*, and the root-knot nematode *Meloidogyne incognita*. Using high-throughput phenotyping, we quantified canopy growth dynamics and root architecture upon increasing nematode densities. All species induced a shared temporal pattern in canopy growth, with early inhibition during migration, reduced growth during nematode establishment, and partial recovery at later stages. Despite this similarity aboveground, belowground responses were species specific. *Heterodera schachtii* reduced primary root growth but induced compensatory lateral root formation, maintaining total root length. *Pratylenchus penetrans* caused extensive cortical damage without inducing root system plasticity, leading to canopy collapse beyond a density threshold. In contrast, *M. incognita* strongly suppressed primary root growth but induced gall formation, which may preserve

vascular connectivity and confer a higher tolerance limit. These results show that plant tolerance to nematodes is stress-type specific and relies on distinct root developmental strategies.

14:54-15:12 hrs Megann Tran

Genome-Informed Approaches to Nematode Management in Walnuts Using Rootstocks and Cover Crops

Castro, B.¹, Dai, D.¹, Zhang, Y.¹, Latina, R.¹, Yang, X.¹, Tran, M.¹, Williamson, V. M.², Groen, S. C.³, Shamsullah, S.¹, Leslie, C. A.⁴, Siddique, S.¹.

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The root lesion nematode *Pratylenchus vulnus* is a migratory endoparasite that penetrates and feeds on walnut roots, leading to reduced vigor, lower yields, and decreased nut quality. While some commercially used walnut rootstocks show partial tolerance, effective resistance to *P. vulnus* is currently unavailable. Because walnuts are grafted crops, the use of rootstocks provides a unique opportunity to target belowground pest interactions while leaving the scion genotype and nut quality unchanged. This project aims to improve nematode management using biotechnological strategies in walnut root stocks and associated cover crops. We generated a high-quality genome of *P. vulnus* and identified key genes involved in parasitism and survival. These targets are being used to guide the development of genome-informed biotechnological approaches that disrupt nematode infection and survival. Current efforts focus on plant transformation and early-stage evaluation of these strategies in walnut and candidate trap or cover crops. Overall, this research provides new strategies for managing damaging belowground pests in orchard production systems through nematode-resistant rootstocks and complementary trap crop approaches.

15:12-15:30 hrs Clarissa Hiltl

Non-destructive siRNA-induced gene silencing in Arabidopsis via root tip delivery

Clarissa Hiltl¹, Vivien Lenz¹, Laura Oé¹, Jessica Dekinger¹, Anna Schubert¹, Florian M.W. Grundler¹

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The extensive insertion mutant collections available for *Arabidopsis thaliana* have greatly advanced our understanding of gene function; however, many essential genes remain poorly characterized. This limitation is particularly pronounced in long-term interactions with

sedentary endoparasitic nematodes, if loss-of-function mutants cause lethality or severe phenotypes that impede functional analysis during infection. As essential genes are increasingly recognized as host susceptibility factors exploited by plant-parasitic nematodes, alternative approaches to study their function are required. RNA interference (RNAi) enables targeted and reversible suppression of gene expression and thus provides a powerful strategy to investigate essential genes. RNAi is mediated by small interfering RNAs (siRNAs), which induce mRNA cleavage and degradation. Several transgenic and topical delivery methods exist, but most exogenous siRNA applications have focused on foliar delivery. Here, we established two root tip-based siRNA delivery methods that exploit the plant's natural uptake pathways to study essential genes during the interaction between *Arabidopsis* and *Heterodera schachtii*. Targeting vitamin B7 biosynthesis pathway as a proof of concept resulted in systemic gene silencing lasting up to 11 days post treatment and significantly reduced nematode pathogenicity, highlighting the importance of this essential nutrient during this biotrophic parasitism.

Parallel Session 5

14:00 — 15:30 GMT+2

Abdijzaal

Parallel session 5: Genomic perspective on genetic diversity

Chair: Eric Grenier & Yi-Chien Lee

14:00-14:18 hrs Yi-Chien Lee

Natural genetic variation related to host range in *Ditylenchus dipsaci*

Yi-Chien Lee¹, Dennie M. te Molder¹, Joost Riksen¹, Stefan J.S. van de Ruitenbeek¹, Jaap Bakker¹, Geert Smant¹, Mark G. Sterken¹

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The stem nematode *Ditylenchus dipsaci* is a plant-parasitic nematode with a remarkably broad host range. *D. dipsaci* is an obligate endoparasite of higher plants and is a cosmopolitan species mostly prevalent in temperate climates. Although over 500 plant species are described hosts, individual *D. dipsaci* isolates reportedly can only infect a subset of hosts; which led to the suggestion that there are many races within this species. For better understanding of this complex species, we genetically characterized over 50 population of *D. dipsaci*.

We characterized the genetic diversity in *D. dipsaci* based on three chromosome-scale genome assemblies. These were generated for isolates infecting sugar beet, garlic, and potato, using PacBio HiFi sequencing and Hi-C scaffolding. The assembled genome sizes range from 160 to 240 Mb and comprise 12 chromosomes, with BUSCO completeness of approximately 92%. Repetitive elements account for ~60% of each genome, and between ~14,000 and ~18,000 protein-coding genes were identified. Using these genomes, we characterized over 50 re-sequenced *D. dipsaci* isolates isolated from various host-plants, including bulbous flowers.

We found genetic variation related to host-range as well as geography. However, in general the populations seem to form a genetic continuum, rather than distinct sub-populations with a limited host-range.

14:18-14:36 hrs Rocio Silvestre Casas

Genetic diversity of *Globodera* spp. from South America

Silvestre, R.¹, Bhatta, B.¹, Zasada, I.², and Dandurand, L.M.¹

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²Oregon State University, Corvallis, Oregon, USA

The Andean region is the center of origin of potatoes, however the evolutionary pathway and global dissemination of potatoes' main pests, potato cyst nematodes (PCN; *Globodera pallida* and *Globodera rostochiensis*), remains complex. This research investigates the genetic diversity of *Globodera* spp. populations from South America compared to populations found worldwide. Using a combination of nuclear (ITS rDNA) and mitochondrial (*COX* and *Cytb*) genomic regions, we characterized diverse *Globodera* populations from South America. Phylogenetic analysis reveals significantly higher allelic diversity in native South American populations than in other regions. Our data aligns with the emerging hypothesis that PCN populations may have complex diversification and spread in multi directional dispersal pathways. While South America is the native source, the spread of PCN to countries such as the United States may have resulted from introductions via European populations rather than direct from the Andean region. To further understand these evolutionary patterns, high-resolution genomic datasets from Andean PCN populations will be compared with global populations. This study emphasizes the importance of the Andean gene pool in understanding the global biosecurity risks and potential adaptive traits of *Globodera* spp.

14:36-14:54 hrs Eric Grenier

A first insight into the importance in polyandry in *Globodera pallida* during its adaptation to masculinizing potato resistances

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Polyandry is known to occur in several plant parasitic cyst nematodes. For the potato cyst nematode *Globodera pallida*, polyandry has never been demonstrated and quantified. Since the potato resistance used to control this nematode acts by masculinizing populations, leading to an unequal sex ratio, and because polyandrous mating are more frequent in male-skewed populations, the level of polyandry can be expected to decrease during the nematode adaptation process to potato resistance. Aims of this study were thus to determine whether polyandry occurs in *G. pallida*, to estimate the number of fathers per cyst, and to explore the polyandry evolution during the adaptation process to the potato resistance. Using *G. pallida* lineages obtained from experimental evolution on susceptible and resistant potato cultivars, we explored and quantified the genetic evidences of multiple paternity within cysts by genotyping juveniles using microsatellite loci. Results showed that 100% of females were polyandrous, with an average of seven fathering males. At contrario to the our expectation, multiple mating appeared to remain stable during the adaptation process to a masculinizing resistance. The level of polyandry highlighted here would be an

important parameter to consider in demo-genetic models designed to compare control strategies of nematode populations.

14:54-15:12 hrs Vincent Hanlon

How plant-parasitic nematodes edit *HYP* genes in their somatic cells

Vincent Hanlon, Luisa Kalkert, Unnati Sonawala, Hans Helder, Sebastian Eves-Van Den Akker

Crop Science Centre, Department of Plant Sciences, University of Cambridge, UK

The *HYP* genes of plant-parasitic *Globodera* nematodes encode secreted effector proteins with staggering sequence diversity. Previous work on *HYP*s strongly suggests that this diversity is allelic and that it is produced by developmentally-programmed rearrangements: that is, the nematodes edit *HYP* genes in their somatic cells by shuffling a set of short DNA sequence motifs within a hypervariable domain. Although the germline diversity of *HYP* alleles is small, such editing is thought to create hundreds or thousands of distinct somatic alleles across a population. The genetic mechanism responsible for *HYP* editing is unknown. In this talk, we discuss a DNA repair hypothesis for the editing mechanism, and we present preliminary results from a test of the hypothesis in a heterologous yeast system. We also present new population-level deep sequencing data from inbred nematode lines and from mixed populations, with which we characterise the diversity and pattern of germline and somatic *HYP* alleles.

15:12-15:30 hrs María Córdoba Sánchez

Screening for resistance to *Meloidogyne hapla* in pea (*Pisum sativum*) germplasm collection

Córdoba-Sánchez, M.¹, Rubiales, D.¹, Pablo Castillo, P.¹ and Palomares-Rius, J.E.¹

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Pea (*Pisum sativum*) is a grain legume widely cultivated in temperate regions and is well known for its agricultural and environmental benefits. These include improving soil fertility through biological nitrogen fixation, biodiversity, and providing an important source of food and feed. However, pea crops are susceptible to several diseases, making integrated plant disease management strategies essential. Within this framework, genetic resistance represents an effective and environmentally sustainable control tool.

Among the pathogens affecting pea, plant-parasitic nematodes are of particular relevance, especially sedentary endoparasitic root-knot nematodes (*Meloidogyne* spp.), which can cause significant yield losses. The objective of this study is to identify sources of resistance to *Meloidogyne hapla* in pea.

A screening is being conducted on a genotyped pea collection comprising 320 accessions. Experiments are performed under controlled growth chamber conditions using a susceptible control cultivar (Messire). Each accession is inoculated with a constant number of *M. hapla* eggs. At 45 days post-inoculation, roots are harvested and assessed for the number of egg masses and total egg counts, and the nematode reproduction factor (Rf). These phenotypic data is used to identify single nucleotide polymorphisms (SNPs) associated with resistance through a genome- wide association study (GWAS).

Parallel session 6

14:00 — 15:30 GMT+2

Room 522

Parallel session 6: Taxonomy, species identification, and phylogenic analyses

Chair: Wim Bert

14:00-14:18 hrs Mariam El Khatib

Mitochondrial phylogeny and species identification in Root-Knot nematodes

Mariam El Khatib, Ana Paula Zotta-Mota, and Etienne Danchin

Institute Sophia Agrobiotech, 400 Rte des Chappes, 06903 Sophia Antipolis, France

Root-knot nematodes (*Meloidogyne* species) are among the most agriculturally damaging pests, causing billions of dollars in annual loss. Accurate species identification and delineation of evolutionary relationships is crucial to understanding transitions in their life history and their adaptation to a wide range of hosts, but also towards proposing improved control and species identification methods.

Most of the phylogenetic studies done on these species primarily used nuclear sequences to infer relationships. However, this approach has not been successful in deciphering phylogenetic relationships in Clade I of Root-Knot nematodes, which comprises the most destructive *Meloidogyne* species, including *Meloidogyne incognita*, *M. javanica*, *M. arenaria* and *M. enterolobii*. This is mainly due to the polyploid nature of their genomes, with the presence of multiple diverged nuclear sub-genomes and common hybrid ancestry.

Here, I present a reconstructed phylogeny using 12 mitochondrial protein-coding genes (PCGs) and two ribosomal RNAs (rRNAs) of 14 *Meloidogyne* species, covering 114 different populations. This approach successfully recapitulates the three previously described main *Meloidogyne* clades and distinguishes different species within these clades.

I also propose a pipeline for identification of *Meloidogyne* species from uncharacterized samples based on a ca. 5kb mitochondrial barcode region. After long-read sequencing of the corresponding PCR amplicons, phylogenetic placement on the reconstructed phylogenetic tree allows accurate species identification.

14:18-14:36 hrs André Bertran

Long-read mitochondrial DNA amplicon sequencing enables accurate tropical *Meloidogyne* spp. Recognition

Wilten, J.¹, Belousova, M.¹, Teklu, M. G.², Meressa, B.H.³, Kefelegn, H.^{4,5,9}, Couvreur, M.⁵ Bert, W.⁵, du Pré, R. ⁶, van Heese, E.Y.J.⁶, Susič, N.⁷, Gerič Stare, B.⁷ Wesemael, W.M.L.⁸ and Bertran, A. G. M.^{1,2}

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Due to climate change, it is expected that tropical root-knot nematodes (RKN, *Meloidogyne* spp.) will spread from the Mediterranean towards northern Europe posing increased and different risks to crops and cropping systems that have been optimized for resistance and management strategies to temperate RKN species. The correct identification of RKNs is therefore paramount in our surveillance and preparedness strategy. However, accurate identification of tropical RKN species is difficult due to their hybrid (allopolyploid) nature, showing the characteristics of multiple species. Species-specific mitochondrial DNA motifs were recently suggested as suitable for tropical RKN identification. Our research established a practical approach to tropical RKN identification based on qPCR screening (triage stage) using i) Clear Detections® Real-Time *Meloidogyne* spp. Diagnostic Kit followed by ii) long amplicon generation iii) Nanopore sequencing, and iv) phylogenetic analyses using a curated database of mtDNA obtained from pure cultures maintained by Wageningen Plant Research, NIVIP and KIS. Together, these steps enable accurate identification of tropical RKN including cases involving mixed infections. This methodology has recently been applied to determine the complete mtDNA genomes of several tropical RKN, including a new Ethiopian population of *Meloidogyne luci* and constitutes a deliverable of the NEM-EMERGE project.

14:36-14:54 hrs Yincai Ren

Nematode metagenomics enables accurate taxonomic profiling and abundance estimation

Yincai Ren, Zhiyin Liu, Fan Guo, Hongmei Li, Xue Qing

Metagenomics and metabarcoding has emerged as a powerful tool for resolving the diversity of bacteria but has not yet been widely applied to eukaryotes. Several bioinformatics tools developed for metagenomic profiling are primarily designed for prokaryotes, necessitating validation in eukaryotes. Consequently, current taxonomic profiling of microbial eukaryotes relies heavily on 18S rRNA-based metabarcoding. While abundance correction methods have been established for prokaryotes using metabarcoding or metagenomic annotation, equivalent methods for eukaryotes are limited. This study benchmarked three metagenomic classification pipelines—reads-based, 18S rRNA-based, and protein-based—against morphological and metabarcoding methods using two mock datasets (one mock community containing different phyla while the other corresponding to nematodes). Results indicate that 18S rRNA-based metagenomics outperforms other taxonomic profiling methods when targeting taxa at order level. Furthermore, community abundance estimation can be significantly improved using 18S rRNA gene copy number corrections, with sample-specific correction methods outperforming species-specific approaches in the nematode mock community. In addition, we demonstrated marine and soil communities can be distinguished by several marker genes like cellulase, pectate lyase and chorismate mutase, suggests protein composition is promising method to predict function of microbial community.

14:54-15:12 hrs Joseph Maosa

My journey through integrative nematode taxonomy

Joseph Maosa, Marjolein Couvreur and Wim Bert

Nematology Research Unit, Department of Biology, Ghent University, K.L. Ledeganckstraat 35, 9000 Ghent, Belgium.

Nematodes are among the most ubiquitous and diverse organisms on Earth, with millions of species estimated to exist, yet only a few thousand formally described. This large gap reflects substantial undocumented diversity, even among economically important PPNs. A key limitation in nematode taxonomy is reliance on traditional classifications based primarily on morphology, often without molecular support, leading to both under and overestimation of diversity due to subtle morphological differences and cryptic species. The absence of a universal DNA barcode further complicates species identification. Integrative taxonomy, which combines morphological and molecular evidence, has begun to address these limitations. In this study, we applied an integrative approach using sequences from multiple gene regions (18S, 28S, COI, & ITS), light and scanning electron microscopy, drawings, and several species delimitation methods to characterize various African plant-parasitic nematodes. This strategy enabled: resolution of cryptic species, distinguishing *Scutellonema brachyurus* and *S. afribrachyurus*; clarification of conflicting molecular signals through morphology, as in *Meloidogyne africana*; molecular characterization of morphologically

known but genetically unresolved taxa, such as *Trophotylenchulus obscurus*; and discovery of new species including *Pratylenchus mahindii* and *Paratylenchus cacao*. These results highlight that substantial nematode diversity remains undiscovered and that integrating morphological and molecular methods is essential for accurate taxonomy.

15:12-15:30 hrs Jianfeng Gu

Field applied quick PWN detection and screening methods, and *Bursaphelenchus* grouping
Jianfeng Gu

Ningbo Key Laboratory of Port Biological and Food Safety Testing (Technical Centre of Ningbo Customs/Ningbo Inspection and Quarantine Science Technology Academy), No. 8, Huikang Road, Ningbo 315100, Zhejiang, P. R. China

Three quick PWN (Pine wood nematode) detection methods, an enzyme-mediated duplex exponential amplification (EmDEA) method, together with a CPCR (convention PCR) and LAMP fluorescence detection method were developed for detecting PWN from extracted nematodes or pinewood sawdust. Above methods comprised freeze-dried enzyme pellets that can be stored at room temperature for one year, a dry block heater, and a portable fluorescence amplification instrument. The whole procedure was completed within 30 min (5 min for DNA extraction and 20 min for amplification). The detection limit was 10 copies/tube or 1/10000 of single PWN per reaction. Therefore, the EmDEA, CPCR or LAMP fluorescence detection methods have potential applications in PWN detection in the field, as well as quarantine inspection in international trade.

Moreover, a new revised grouping system for 157 *Bursaphelenchus* species (including subspecies) is suggested. The genus is divided into 10 groups with four incisures in the lateral field (*xylophilus*, *pterocarpi*, *okinawaensis*, *africanus*, *tokyoensis*, *fungivorus*, *posterovulvus*, *kevini*, *cocophilus*, and *sexdentati*), 3 groups with three incisures (*eggersi*, *hofmanni*, and *leoni*) and 3 groups with two incisures (*abietinus*, *hylobianum* and *sinensis*). This system exhibiting a high correlation with phylogenetic analysis based on rDNA partial sequences.

Parallel session 7

14:00 — 15:30 GMT+2

Room 532

Parallel session 7: NEM-EMERGE, PCN Action Scotland, PAPAS

Chair: Cynthia Gleason

14:00-14:18 hrs James Price

PCN Action Scotland

James A. Price¹ & PCN Action Scotland.

¹Cell & Molecular Sciences Department, The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, UK.

The UK is the 5th largest potato producer and exporter in Europe with an industry worth approximately £928 million at farmgate value and many billions in downstream industries. 77% of seed potatoes used in Great Britain originate from Scottish farms. However, this industry is under threat from potato cyst nematodes (PCN) which have been spreading across many UK potato growing areas. Legislation in Scotland prevents seed potatoes from being grown on land where PCN have been detected. However, it is expected that approximately 35% (59,000 ha) of all Scottish potato land remains infected with PCN.

Following a report in 2020, PCN Action Scotland was initiated under the management of Scotland's Plant Health Centre. This group, consisting of over 50 government, academic and industry partners, collaborated across 9 key work packages. In addition to core research, the group proposed new policy changes and created new tools to help growers with PCN management. The initial PCN Action Scotland project has now finished. This presentation will provide an overview of the project for the PAPAS, PCN Action Scotland and Nem-Emerge workshop, detailing how industry perception and responsiveness has changed in Scotland over the past 5 years and how our goals were achieved.

14:18-14:36 hrs Yuk Woon Cheung

Phased Potato Genome Assembly and Association Genetics Enable The Delineation of the H1 Resistance Locus Against Potato Cyst Nematodes

Yuk Woon Cheung^{1,2*}, Lynn H Brown^{1,2*}, Thomas M Adams¹, Brian Harrower¹, Amanpreet Kaur^{1,3}, Gaynor McKenzie¹, Jamie Orr¹, James Price¹, Vikrant Singh¹, Moray Smith², Micha Bayer¹, Ingo Hein^{1,2}

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Potato cyst nematodes (PCN) are among the most economically damaging parasitic nematodes of potato, threatening both yield and long-term land use. In Scotland, where legislation restricts seed potato production on infested land, the spread of PCN poses a major challenge for sustainable crop management. Durable host resistance, integrated with other pest management strategies, is therefore central to effective PCN control. This work contributes to those efforts through high-resolution genetic delineation of the H1 resistance locus, which confers resistance to *Globodera rostochiensis*.

Using haplotype-resolved genome assembly of a dihaploid potato plant, generated with Oxford Nanopore sequencing, we achieved a detailed structural characterisation of the H1 resistance gene cluster in potato. By integrating ONT sequencing, association genetics and resistance gene enrichment sequencing (RenSeq), we developed an ONT-AgRenSeq-d pipeline that enables precise mapping and validation of resistance loci. This approach supports the rapid identification of functional resistance gene variants and the development of locus-specific molecular markers.

These tools provide a practical foundation for resistance-informed breeding, enabling more reliable deployment of nematode-resistant cultivars as part of integrated PCN management. This work will be presented at the PAPAS, PCN Action Scotland and Nem-Emerge workshop, supporting coordinated strategies to manage parasitic nematodes in potato production systems.

14:36-14:54 hrs Inga Zasada

Systems approach to controlling nematodes in US potato production.

Dandurand, L.M.¹, Kuhl, J.¹, Gleason, C.², Watson, P.¹, DeJong, W.³, and Zasada, I.A.⁴

¹University of Idaho, Moscow, ID USA

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³Cornell University, Ithaca, NY, USA

⁴NemaSolutions LLC, Corvallis, OR USA

Productivity of the U.S. potato industry depends upon successfully implementing a systems approach to managing invasive nematode species such as potato cyst (PCN) or root knot nematodes (RKN). Highly susceptible varieties, lack of rapid diagnostics, unreliable thresholds, and limited selection of nematicides are constraints to effective control of plant-parasitic nematodes for the potato industry. Currently, nematode control largely relies on nematicides, yet many are being phased out or are no longer available. Although use of resistance is one of the most sustainable and effective measures for plant pest control, commercially acceptable potato varieties resistant to RKN and PCN do not exist in the U.S.,

and a systems approach is, as yet, undeveloped. Our goal is to provide information, tools, and best management practices for the decision-making process for nematode control. In the “PAPAS, PCN Action Scotland and Nem-Emerge workshop”, measures to improve diagnostic methods and decision support tools, efforts to develop potatoes resistant to the Columbia root knot nematode, *Meloidogyne chitwoodi*, pale cyst nematode, *Globodera pallida*, and to the golden nematode, *Globodera rostochiensis* pathotype Ro2, and continued development of novel nematicides from the trap crop *Solanum sisymbriifolium* will be discussed.

14:54-15:12 hrs Paige Hickman

Controlling *Globodera pallida* with trap crops and crop rotation

Hickman, P. and Dandurand, L. M.

University of Idaho, Dept. of Entomology, Plant Pathology, and Nematology, Moscow, ID, USA 83844

In Idaho, the potato cyst nematode, *Globodera pallida* is under quarantine and infested fields are fumigated to eradicate the nematode. Trap cropping and crop rotation are being investigated as ways control *G. pallida* in Idaho. Various cropping sequences using the trap crops *Solanum sisymbriifolium* (litchi tomato) or *Chenopodium quinoa* (quinoa), the resistant potato variety ‘Innovator’, or the nonhost, *Hordeum vulgare* (barley) have been investigated for their impact on *G. pallida*. Remaining encysted eggs of the initial *G. pallida* population and progeny cysts were assessed at the end of each season. *Solanum sisymbriifolium* reduced *G. pallida* by 80 to 100% when followed by susceptible potato. *Chenopodium quinoa* caused 35 to 45% reduction in *G. pallida* in rotation with potato. When the rotation included the resistant potato ‘Innovator’, *G. pallida* densities were reduced even further. The value of a highly resistant potato was illustrated in a 3-year rotation, where rotations including resistant potato reduced *G. pallida* 90 to 93% when compared to 3 years of barley. Our studies indicate that quinoa can be useful in reducing *G. pallida* populations in rotation, but the use of *S. sisymbriifolium* or a highly resistant potato in rotation are more effective in controlling *G. pallida*.

15:12-15:30 hrs Aska Goverse & Misghina Teklu

NEM-EMERGE: Managing potato cyst nematodes that have overcome current host plant resistances due to genetic selection

Goverse, A. & Helder, J. (coordinators)

Laboratory of Nematology, Wageningen University, Droevendaalsesteeg 1, 6708PB Wageningen, The Netherlands

Soil-borne plant-parasitic nematodes are a biosecurity risk for global food production with an estimated annual loss of €110 billion worldwide. Root-knot nematodes (RKN) and potato

cyst nematodes (PCN) rank 1 and 2 in the Top 10 of high-impact plant-parasitic nematodes. For decades, non-specific, environmentally harmful agrochemicals have been applied to manage PCN and RKN. The increasing awareness about their negative impact prompted the phasing out of most nematicides. Consequently, there is an urgent need for alternative, durable control strategies that enable adequate responses by stakeholders to prevent crop losses. Application of resistant varieties is an essential instrument to control PCN and RKN in a sustainable manner in crops like potato. However, recent reports document the emergence of nematode problems in potato across Europe and beyond due to genetic host selection by the application of a limited set of resistance genes over decades. By using a multi-actor and interdisciplinary approach the Horizon EUROPE project NEM-EMERGE aims to join efforts and provide a spectrum of sustainable, science-based solutions for both the conventional and organic farming sector based on the principles of IPM. In this workshop, the NEM-EMERGE project goals as well as R&I pathways to achieve this will be presented and discussed.

Misghina Teklu

Wild Potatoes as a Reservoir of Resistance to Virulent PCN

Jaap-Jan Willig^{1,2}, Rick Faesen¹, Jack Vossen³ & Misghina Goitom Teklu¹

¹Agrosystems Research, Wageningen University & Research, Wageningen 6708 PB, The Netherlands

²Laboratory of Nematology, Wageningen University & Research, Wageningen 6708 PB, The Netherlands

³Plant Breeding, Wageningen University and Research, Wageningen 6708 PB, The Netherlands

Potato cyst nematodes remain a major threat to potato production, particularly as emerging virulent populations overcome widely deployed resistance genes. To identify new sources of resistance, we screened a wild potato germplasm panel against two highly virulent *Globodera rostochiensis* populations, AmPOP43 and AmPOP44. Using an in vitro infection system, 364 wild *Solanum* accessions were screened and their relative susceptibility quantified based on the number of cysts. This revealed extensive quantitative variation in resistance, with several accessions showing strong resistance ($\leq 5\%$ relative susceptibility) and a larger group displaying intermediate resistance ($\leq 15\%$) to one or both nematode populations. Microscopic analysis during infection uncovered resistance mechanisms acting at different stages of the nematode life cycle, including reduced attraction, penetration, early immune responses, hypersensitive reactions during feeding site formation, and male-biased nematode development. To validate the relevance of the in vitro screening, selected accessions were tested in pot experiments. Resistance phenotypes and quantitative reductions in cyst formation were largely consistent between in vitro and in vivo conditions.

Together, these results demonstrate that large-scale in vitro screening reliably identifies resistance levels and mechanisms that translate to whole-plant conditions, highlighting wild potatoes as a valuable resource for PCN resistance breeding.

Workshop 1: Nematode-Microbiome Interactions

16:00 — 17:15 GMT+2

Lamoraalzaal

Workshop 1: Nematode-Microbiome Interactions

Chairs: Olivera Topalovic, Sigal Brown and Lisa van Sluijs

Presenters: Olivera Topalovic, Sigal Brown, Lisa van Sluijs, Chris Bell, Qing Xue, Sabine de Graauw and Samad Ashrafi

During this workshop we will dissect nematode–microbe interactions across scales, from early host recognition to community-level dynamics and disease suppression strategies. The workshop highlights how microbial communities influence nematode behavior and infection, supporting sustainable management, and concludes with an audience-steered panel discussion on challenges and future directions for the field.

Workshop 2: Nematode Genomics

16:00 — 17:15 GMT+2

Abdijzaal

Workshop 2: Towards highly contiguous and well-annotated plant parasitic nematode genomes

Chairs: Mark Sterken, Shahid Siddique, Etienne Danchin and Sebastian Eves-van den Akker

Presenters: Mark Sterken, Yi-Chien Lee, Marjam Saleh, Erik Andersen, Shahid Siddique, Etienne Danchin and Sebastian Eves-van den Akker

We aim to bring together groups with interests in genomics, in particular related to plant parasitic species. With the advent of HiC-aided scaffolding, highly contiguous genomes now become available for our species. There will be presentations and a discussion session for which attendees can share their interest and projects beforehand.

Workshop 3: NEM-EMERGE, PAPAS, PCN Scotland

16:00 — 17:15 GMT+2

Room 522

Organized and contributions by NEM-EMERGE, PAPAS, PCN Action Scotland partners and stakeholders (by invitation)

Workshop 4: Citizen science & outreach

16:00 — 17:15 GMT+2

Room 531

Workshop 4: The Hidden Majority: How Can We Make Nematology Accessible to the Public?

Chairs: Jose Lozano Torres and Solveig Haukeland

Presenters: Jose Lozano Torres, Solveig Haukeland and Joost Riksen

Help demystify the phylum Nematoda! We will demonstrate classic extraction methods alongside modern 3D-printed microscopes. In working groups, participants will tackle a community challenge: designing simplified frameworks, visual narratives, or educational toolkits that empower the public to generate large-scale distribution data and elevate global awareness of nematodes.

Poster session 1

17:15 — 18:15 GMT+2

Lounge 1

Poster session 1

Poster 1

Litylenchus crenatae, the beech leaf disease nematode: an emerging threat to European forests potentially exceeding the impact of pinewood nematode.

Viaene, N.^{1,2}, Ebrahimi, N.^{1,2}, Prior, T.³, and Orlando, V.³

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³Fera Science Ltd. York Biotech Campus, Sand Hutton, York, YO41 1LZ, UK

Litylenchus crenatae, the foliar nematode that causes beech leaf disease, is spreading through the USA and Canada. It was originally described in Japan as associated with native beech species. Unlike *Bursaphelenchus xylophilus*, the pinewood nematode, it does not rely on an insect vector but spreads through wind and rain, facilitated by massive population densities within beech foliage and buds. Entrance and spread of *B. xylophilus* is under control due to a rigorous surveillance program and mandatory wood treatment. Current EU and UK legislation prohibit import of *Fagus* plants for planting, although import of seeds and dwarfed trees (bonsai) is allowed with phytosanitary certificate. This measure should prevent entrance of the nematode into our regions, but thorough and accurate inspection is required during export and import surveillance. The nematode was added to the EPPO alert list in 2019 and a Diagnostic Standard of *L. crenatae* is in preparation. *Given the high environmental importance of beech forests and the commercial value as quality timber, L. crenatae could have significant impacts in Europe. It is therefore advisable for nematologists to raise awareness among relevant authorities to assess this nematode as a potential threat to forest ecosystems and evaluate the need for regulatory attention.*

Poster 2

Bacillus velezensis NTU-8 enhances resistance against *Meloidogyne enterolobii* in tomato by modulating hormone signaling and metabolic profiles

Sook-Kuan Lee^{1,2,#}, Yi-Ling Chiang^{1,#}, Jia-Heng Hung¹, Chih-Yu Lin³, Kung-Ta Lee⁴, Chiu-Ping Cheng^{1,5}, Pei-Chen Janet Chen⁶, Hieng-Ming Ting^{1,5,*}

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⁵ Department of Life Science, National Taiwan University, Taipei 10617, Taiwan

7 Department of Plant Pathology, National Chung Hsing University, Taichung 402202, Taiwan

Tomato (*Solanum lycopersicum*) yield and quality are severely compromised by root-knot nematodes like *Meloidogyne enterolobii*. This study investigates the biocontrol potential of *Bacillus velezensis* NTU-8, focusing on its ability to induce systemic resistance and promote plant growth. Experimental results demonstrate that NTU-8 pre-treatment significantly reduces root galling while simultaneously enhancing root development. To elucidate the underlying defense mechanisms, phytohormone levels and gene expressions were analyzed. The findings reveal a significant increase in salicylic acid (SA) content and the up-regulation of ethylene (ET) biosynthesis genes in NTU-8 treated plants 24 hours post-inoculation. Furthermore, LC-MS/MS metabolomic analysis indicates that NTU-8 triggers an upward trend in glycolysis-related metabolites and significantly elevates defense-associated compounds, including GABA, β -alanine, and glutamate. In conclusion, *B. velezensis* NTU-8 enhances tomato defense by regulating hormonal balance and reprogramming primary and secondary metabolic pathways. These results resolve the tripartite interactions between the host, beneficial bacteria, and pathogen, supporting NTU-8 as a sustainable and environmentally friendly strategy for nematode management.

Poster 3

Efficacy and long-term assessment of saturated steam heat treatment for the elimination of the pinewood nematode in conifer bark

Fonseca, L.^{1,2}, Nestler, H.³, Oliveira, R.⁴, Verdasca, J.⁵, Serra, C.⁶, Abrantes, I.¹

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⁶DGAV, Tapada da Ajuda, Edifício 1, 1349-017 Lisboa, Portugal

The Portuguese Standard “*NP 4515:2020+Emenda1:2023*, Softwood bark and wood chips — Phytosanitary heat treatment for the elimination of the pinewood nematode (*Bursaphelenchus xylophilus*) and other harmful organisms” establishes technical criteria for the thermal treatment of conifer bark to mitigate phytosanitary risks associated with harmful pests. Considering the possible presence of the pinewood nematode (PWN) in the conifer bark, it is mandatory to eliminate its presence in the final products. The standard responds to international trade regulations by providing a validated heat treatment methodology ensuring the effective eradication of PWN and its insect vector, *Monochamus galloprovincialis*. The treatment involves the application of saturated steam at temperatures ≥ 100 °C, with the material conveyed continuously through a thermally insulated chamber. Bark must reach a minimum temperature of 64 °C throughout their entire volume and mass for at least 30 consecutive minutes. This study presents a quantitative analysis of thermally treated bark samples collected over a ten-year period from three Portuguese industrial facilities, demonstrating the efficacy, consistency and long-term compliance of *NP 4515:2020+Emenda1:2023* under industrial conditions.

Poster 4

Soybean seed coating with *Hyalorbilia oviparasitica* suppressed *Heterodera glycines* population development in greenhouse trials

Smith Becker, J. and Becker, J.O.

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The ascomycete *Hyalorbilia oviparasitica* suppresses populations of several endoparasitic nematodes. Strain HslmV27, isolated from parasitized *H. schachtii* cysts in California and amended to soil infested with *H. glycines*, was highly effective in greenhouse trials. Here, we report that seed-coating soybeans with HslmV27 suppresses soybean cyst nematode populations. The fungal strain was cultured in reed sedge peat to a concentration of 4.1×10^5 CFU/g of moist peat. An emulsion of HslmV27 peat culture prepared in 10% Agrimer30™ was used to coat soybean seeds. Autoclaved peat cultures served as controls. Coated seeds were either planted immediately or dried overnight before planting. HslmV27 CFU/seed for coated seeds was 5.6×10^3 for seeds planted immediately and 2.5×10^3 for seeds dried overnight. Two weeks after planting into cones with 200 cm³ sterile sandy loam, each cone was infested with 1000 *H. glycines* eggs. After 1,260 DD, cysts and females were collected by flotation sieving and enumerated. Autoclaved peat treatments had no effect on nematode numbers, whereas seeds coated with live HslmV27 reduced cysts and females by approximately 50%.

Poster 5

Grape pomace biochar from consecutive harvests consistently suppresses root-knot nematodes *via* nematode- and plant-directed mechanisms

Martínez-Gómez, A^{1*†}, Díaz-Manzano, F.E^{1†}, Carrión, A.M¹, Domínguez-Figueroa, J¹, Martín-Trillo, M¹, Giné, A², Fullana, A.M², Expósito, A.², Gómez-Torres, O¹, Díaz, E³, Martínez-Sánchez, L³, Hamzaoui, M.A⁴, Santander, K⁵, Sorribas, F.J², Hernández, L.E⁴, Escobar, C^{1*}.

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† Both authors have contributed equally to this work

Phytoendoparasitic nematodes are a major constraint to crop productivity worldwide. Root-knot nematodes (RKNs; *Meloidogyne* spp.) infect plant roots and induce gall formation containing multinucleate feeding cells known as giant cells (GCs). The development of sustainable nematode control strategies is increasingly urgent, as most effective nematicides have been restricted due to environmental and health concerns. Here, we show that biochar produced from grape pomace derived from different harvests and pyrolyzed at 350 °C efficiently suppresses *Meloidogyne* spp. infection and reproduction in tomato plants after one nematode generation, with the suppressive effect persisting for two generations, regardless of grape variety composition. Despite minor compositional differences among grape pomaces, the resulting biochars exhibited stable physicochemical properties and consistently reduced nematode infection when applied at 0.75% (w/w), supporting their potential for standardization. The mode of action of biochar significantly impaired egg hatching and reduced second-stage juvenile (J2) mobility. Notably, biochar treatment primed tomato defense responses, as indicated by the induction of defense- and redox-related genes and enhanced reactive oxygen species (ROS) accumulation. This biochar-induced activation of plant immunity likely underlies the reduced RKN infection and reproductive performance. Overall, grape pomace-derived biochar represents a sustainable and reproducible strategy for RKN management.

Evidence of virulent and avirulent *Meloidogyne* spp. populations on *Mi*-resistant tomato in slovenia

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Root-knot nematodes (RKN; *Meloidogyne* spp.) are among the most damaging plant-parasitic nematodes, causing substantial yield losses worldwide. Although resistance genes from the *Mi* family are widely used in tomato, some RKN populations have evolved virulence, enabling reproduction on resistant hosts. We assessed the virulence of five Slovenian RKN populations in a greenhouse pot experiment. Tomato cv. Velasco F1 (*mi/mi*, susceptible hybrid) and cv. Rally F1 (*Mi/mi*, resistant hybrid) were inoculated with second-stage juveniles (J2) (10 replicates per population and cultivar) and grown at approximately 25 °C for six weeks. The galling index and egg production were evaluated and the reproduction index (RI) was calculated as the ratio of eggs on resistant versus susceptible plants. Four populations—*M. incognita* NE13-110, *M. arenaria* NE12-110, *M. luci* NE12-69, and *M. luci* Dornberk (the first three isolated from Vrtojbensko polje in 2024, the last isolated from Dornberk in 2003) were classified as avirulent. In contrast, *M. luci* SI-Šmartno/1, isolated from Šmartno pri Ljubljani in 2015, was virulent, showing similar reproduction on susceptible and resistant tomatoes. These results will serve as the basis for the design of molecular markers specific to virulent RKN isolates.

Poster 7

Novel hardware for *in planta* nematicide screening

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Plant-parasitic nematodes cause \$157 billion in annual agricultural losses, yet nematicide discovery is limited to screening against second-stage juveniles or the non-parasitic model *Caenorhabditis elegans*. This approach systematically excludes compounds that disrupt plant-parasite interactions occurring during later developmental stages. Here, we present a high-throughput imaging platform for phenotyping nematode infection throughout the complete lifecycle under media-limited conditions compatible with chemical library screening. We developed an affordable (£280) automated system by modifying an Ender 3 3D printer with Raspberry Pi-controlled camera components and open-source firmware. Key features include higher resolution imaging revealing fine morphological features such as individual eggs within gelatinous matrices, Z-stack imaging, and dyed media layers providing

separation of root and shoot compartments for improved segmentation. Integration with ARADEEPOPSIS extracted 78 shoot-level traits while custom machine-learning models achieved complete detection of mature female nematodes. We confirmed *Heterodera schachtii* infection and lifecycle progression under media-limited conditions. This system enables longitudinal screening of shoot health, root architecture, nematode population dynamics, and individual morphology—creating aggregate phenotypic fingerprints for mode-of-action clustering of nematicidal compounds. By extending chemical screens beyond second-stage juvenile-active compounds, this platform addresses a fundamental gap in nematicide discovery and could build the foundation for novel approaches targeting host-pathogen interactions at any lifecycle stage.

Poster 8

Study of a combination of agroecological levers to control root-knot nematodes in vegetable cropping systems

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The reduction in authorized nematicides and the emergence of virulent root-knot nematodes (RKN) highlight the need for alternative control strategies. We investigated the combination of three agroecological levers: genetic resistance (G), co-culture with *Tagetes erecta* (Te), and association with arbuscular mycorrhizal fungi (AMF), on tomato and sweet pepper grown in soils naturally infested with RKN. Crop development and yield, RKN population dynamics, and root infestation were monitored.

In sweet pepper, G alone strongly reduced root infestation and RKN populations (-90% RKN population), with even greater reductions when combined with Te and/or AMF. Te also had a suppressive effect on *Meloidogyne* populations in soil, which was doubled when combined with AMF. Moreover, G increased the abundance of non-phytopathogenic nematodes, indicators of soil health, and this effect was amplified when levers were combined.

In tomato, AMF failed to establish and Te was severely affected by pests. Nevertheless, the GxTe combination reduced root infestation and RKN populations in soil, while non-phytopathogenic nematodes were unaffected.

In both crops, resistant genotypes were infected by virulent RKN populations, confirming that G should not be used alone. Te and AMF show promising potential to strengthen and protect genetic resistance, although their implementation requires further optimizations.

Poster 9

EUPHRESCO V-PCN: Standardized testing of potato varieties to assess resistance affected by testing location and facilities?

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In the European Union, potato varieties must be tested for their resistance against the potato cyst nematodes *Globodera rostochiensis* and *G. pallida* following the directive EU2022/1192. The testing is performed utilising the standard reference populations such as *G. rostochiensis* Ecosse (Ro1) or *G. pallida* Chavornay (Pa3) and uses the nematode multiplication rate on a tested variety as evaluation criterium. This EUPHRESCO project addresses whether the reference populations in the EU still perform as needed, or show changes in their virulence over time, due extensive multiplication on a susceptible variety, such as Desiree. However, the geographic location and type of the testing facilities might also affect the outcome of the resistance tests. Due to the relocation of the testing facilities in Germany from Münster to Braunschweig (approx. 250km apart), the Pf/Pi-levels and resulting relative susceptibility values of reference varieties seemed affected. Furthermore, besides the fact that temperature and lighting regimes, as well the substrate were identical, the observed length of the diapause and the level of spontaneous hatching were different between testing locations. However, the overall results according to the international recognized standard scheme were not affected or altered the final resistance rating of a variety when tested at both locations.

Poster 10

Detection and distribution of root-knot nematodes in potato fields in England

Celestine Oduori^{1,2}, Aleeshaban Shinas², Katarzyna Dybal¹, Eleanor Jones², Simon Edwards¹, Thomas Prior², Matthew Back¹, Valeria Orlando².

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A survey was conducted across fifteen major potato-growing counties in England to detect and characterise root-knot nematode species associated with potato production. The study analysed 205 archived soil DNA extracts originally collected during a national survey of *Pratylenchus* spp. conducted in 2017 and 2019. Real-time PCR assays incorporating an internal amplification control were used to assess DNA integrity, of which 109 samples yielded amplifiable DNA. Species-specific assays targeted six economically important

Meloidogyne species, namely *Meloidogyne chitwoodi*, *M. fallax*, *M. hapla*, *M. incognita* type, *M. minor* and *M. naasi*.

Meloidogyne naasi was the dominant species, detected in 98.2% of all positive samples, while *M. minor*, *M. hapla*, and *M. fallax* were detected at low frequencies. *Meloidogyne chitwoodi* and *M. incognita* type were not detected. The presence of *M. fallax*, a regulated non quarantine pest in the United Kingdom, was confirmed at two sites. Spatial analysis indicated higher prevalence of *M. naasi* in Norfolk, Yorkshire, and Lincolnshire.

The predominance of *M. naasi*, a cereal-associated nematode, is likely linked to widespread cereal rotation practices. These findings provide baseline data on the distribution of *Meloidogyne* spp. in English potato fields. However, an updated national survey is required to ascertain the current phytosanitary risk.

Poster 11

Efficacy of control of high-levels of root-knot nematodes (*Meloidogyne* spp.) in soil and improvement of soil health using Crescent Sunn (*Crotalaria juncea*), *Sorghum sudanense* (Sudan Grass) and *Trichoderma harzianum*

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Root-knot nematodes are a major constraint in greenhouse cultivation. Nematicides and resistance genes remain the primary management tools; however, nematicides are increasingly restricted by regulatory frameworks, and resistance genes are limited by the risk of selecting for virulent nematode populations. In this context, the use of cover crops and biological control may offer complementary strategies for nematode suppression. Nevertheless, these approaches have been mainly evaluated predominantly under low to moderate *Meloidogyne* inoculum levels and typically using second-stage juveniles. This study assessed four treatments under high *Meloidogyne incognita* inoculum levels in large pots (17 L) with tomato grown under greenhouse conditions: a) untreated control; b) biocontrol agent addition (*Trichoderma harzianum*); c) use of cover crop Crescent Sunn (*Crotalaria juncea*); and d) use of cover crop Sudan grass (*Sorghum sudanense* cv. Belle). Crescent Sunn effectively suppressed *M. incognita* even at high inoculum levels (around 20 J2/cm³ of soil at the time of sowing the cover crop), whereas *T. harzianum* showed no detectable effect, and Sudan grass increased *M. incognita* populations. Both cover crops

enhanced mycorrhizal inoculum in the soil, with the strongest mycorrhizal association in tomato observed following Crescent Sunn. Additionally, cover crops also promoted higher abundances of beneficial soil nematode populations.

Poster 12

Solanum linnaeanum extracts for the management of *Meloidogyne chitwoodi*

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Root-knot nematodes are key factors in reducing crop quality and yield. This study explores the potential of aqueous extracts from *Solanum linnaeanum* roots to manage *Meloidogyne chitwoodi*. Roots of *S. linnaeanum* were macerated with liquid nitrogen into a powder. A decoction was prepared by treatment of the powder with distilled water (100 g/3 L) and boiling for 60 min with constant agitation. The extract was tested in a pot experiment against *M. chitwoodi* in field-like conditions. Four-weeks-old tomato plant pots were irrigated with 15 mL of extract and the control with 15 mL of distilled water on the day prior to inoculation. On the following day, they were inoculated with 1000 J2 (Pi) of *M. chitwoodi* and not irrigated. Then, plants were irrigated daily for 15 days with 15 mL of extract or distilled water (control). Each treatment consisted of five replicates. Sixty DAI the plants were uprooted and the root systems stained with phloxine B and galls and eggs masses counted. Eggs were extracted as described above and counted to determine the final population (Pf) and the Reproduction Factor (Pf/Pi). The results indicate the potential of *S. linnaeanum* roots as a natural alternative to commercial synthetic nematicides.

Poster 13

Molecular marker assisted selection for nematode resistance in *Raphanus sativus* plants

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Root-knot and cyst nematodes are considered the most devastating plant parasitic nematodes. Nematode infestations are often controlled using resistances in the host plant. However, nematode resistant cover crops can also contribute as a sustainable strategy to control plant-parasitic nematodes. *Raphanus sativus* (fodder radish) has strong resistances

against *Heterodera Schachtii*, *Meloidogyne chitwoodi*, and *M. hapla*. However, efficiently combining these resistances in one variety requires the development of molecular markers.

We develop molecular markers based on loci identified by bulk segregant analysis on pooled individuals with contrasting resistance phenotypes in segregating populations. By now, loci associated with resistance in three nematode species have been identified and markers are being developed.

Poster 14

Community dynamics of predatory and plant-parasitic nematodes in banana cultivars: implications for soil and microbial health in the tropics

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Banana is a staple and economically important crop for Guam and many Pacific Island countries and territories, yet its production is severely constrained by plant-parasitic nematodes (PPNs). These pests reduce yield, compromise plant health, and threaten long-term soil sustainability in tropical systems. This study examined nematode community dynamics in banana cultivars, focusing on interactions between predatory nematodes (*Mononchus* spp.) and PPNs, particularly *Meloidogyne* spp., and their implications for soil health. Soil and root samples from multiple banana cultivars were analyzed for nematode community structure and soil chemical properties. In addition, controlled pot experiments using tomato as a model host were conducted to evaluate predator–prey interactions over time. Across cultivars, no significant differences in PPN densities were observed, indicating uniform susceptibility. Three major PPN genera were identified: *Meloidogyne*, *Helicotylenchus*, and *Pratylenchus*, with *Meloidogyne* dominating root samples. In contrast, soil samples showed higher abundances of bacterivores and predatory nematodes, alongside elevated organic matter, carbon, and nitrogen levels. Pot experiments revealed increasing interaction strength between predatory and plant-parasitic nematodes over time, resulting in significant reductions in gall formation, egg-laying females, and juvenile populations. These findings highlight the potential of predatory nematodes as biological regulators of PPNs and support their integration into sustainable banana pest management strategies.

Poster 15

Breeding cereal crops for *Heterodera avenae* resistance

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Cereal cyst nematodes (CCN; *Heterodera* spp.) are plant-parasites that damage cereal crops by weakening root systems and reducing plant development. Persistent infestations cause major yield losses. Because CCN depend on hosts, populations decline when cereals are removed, making crop rotation with resistant cultivars and non-grass crops the most effective control strategy. Access to resistant varieties is therefore essential for limiting yield loss.

The CeNem project examines resistance and tolerance to *Heterodera avenae* in a three-year cereal field trial. Yield levels were recorded, and nematode population dynamics were monitored through frequent soil sampling. Yield responses were strongly influenced by overall nematode pressure.

Although cyst numbers declined substantially across the period, environmental variation made it difficult to associate population decline with varietal resistance. Barley demonstrated higher tolerance to *H. avenae* than oat and wheat. Pot experiments supported resistance classifications, and molecular markers reliably identified resistance under controlled conditions. Barley consistently showed strong tolerance, while oat and wheat were more sensitive, even resistant varieties were used.

Overall, annual variation had a dominant effect on both nematode populations and crop performance. Choice of resistant and tolerant crops and varieties must therefore be combined with robust agronomic management to remediate nematode infested fields.

Poster 16

Volatile-mediated nematicidal activity of *Bacillus subtilis* zwz-19 against the potato rot nematode *Ditylenchus destructor*

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Endophytic bacteria offer an eco-friendly strategy for controlling the potato rot nematode *Ditylenchus destructor*. Among eight screened strains, *Bacillus subtilis* ZWZ-19 exhibited strong contact and fumigant toxicity, causing up to 86.94% and 72.79% mortality, respectively. Pot and field trials confirmed its effective nematode suppression. GC–MS identified 18 volatile organic compounds (VOCs), among which hexamethylcyclotrisiloxane showed high nematicidal activity. Integrated transcriptomic and proteomic analyses revealed that VOC exposure disrupted detoxification pathways, energy metabolism, stress responses, and motility-related processes in *D. destructor*.

Poster 17

Integrating research and practice: Aa norwegian adaptation of the best4soil nematode management tool

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Crop rotation is a key measure for preventing and controlling plant-parasitic nematodes. Best4Soil is a digital decision-making tool designed to help farmers and advisors reduce the risk of nematode damage in agricultural production (<https://www.best4soil.eu/database>). The tool is part of a European collaboration funded by the EU's Horizon 2020 program. Best4Soil provides an overview of host status and expected damage of nematode–crop combinations, based on research and validated local experience. To make Best4Soil more accessible and relevant to Norwegian farming conditions and users, NIBIO has contributed by providing a translation of the nematode platform to Norwegian. Additionally, the database has been expanded with information from 30 years of research in Norway and local common knowledge. This includes new information especially relevant for nematodes in cereal production. The current Norwegian version, launched in late 2025, now includes seven extra plant-parasitic nematode species, nine major crops, and fact sheets that provide information on symptoms and management strategies.

Best4Soil strengthens knowledge-based advisory work and offers an accessible foundation for strategic decisions that help reduce yield loss and promote better soil health. This enables farmers to plan effective crop rotations tailored to current nematode challenges. The nematology community is invited to participate and add valuable information.

Poster 18

Decoding endoparasitic nematodes feeding-sites formation and their relation with auxins

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Plant-parasitic nematodes, including cysts (CNs) and root-knot nematodes (RKNs), cause serious agronomic losses worldwide through complex parasitism behavior. RKNs develop giant cells (GCs) contained in a pseudo-organ named gall, whilst CNs establish syncytia by selecting cambial or procambial cells. Although the ontogenesis of both structures differs markedly, their formation requires an auxin maximum. To clarify the molecular divergences between these feeding-sites, we investigated the auxin transduction pathways during CNs interaction through several genes that play key roles during gall and lateral root

development. The promoters *pGATA23* and several deletions of *pmiR390a* were active in both feeding-sites, whilst *AHP6* and/or putative up-stream regulators as *ARF5* were only active in galls. However, none of these genes seemed to display a crucial role during CNs establishment. Analysis of promoters active exclusively in galls (*AHP6*, *LBD16*) revealed the presence of only canonical AuxRe elements in their proximal promoter regions, whereas the analyzed promoters active in syncytia (*pmiR390a*, *pGATA23*), carry AuxRe elements overlapping core cis-elements recognized by other transcription factor families (i.e., bHLH, bZIP). Furthermore, *in silico* transcriptomic analysis showed a few common upregulated IAA responsive genes in both feeding-sites. These results suggest that complex and partially divergent auxin-driven regulatory pathways operate during both interactions.

Poster 19

Drought affects the molecular response of *Meloidogyne incognita* during tomato parasitism.

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To understand the effect of water stress during parasitism and the molecular responses of *Meloidogyne incognita*, we performed a comparative transcriptome study. The analyses were carried out at 7- and 14-days post inoculation (dpi) in parasitized tomato plants, exposed or not to a moderate drought. Gene ontology and KEGG-pathway-based analyses were applied to investigate *M. incognita* differentially expressed genes (DEGs) that were exclusive and common in the water stress treatments (RKN_WS), at 7 and 14 dpi. Common and upregulated DEGs included dynein, peptidases, metalloproteases, C2H2 (Zinc Finger Type 2C) zinc finger superfamily proteins, Cysteine-Rich Secretory Proteins (CRISP) family, and CCCH-type zinc finger proteins. Exclusive DEGs in RKN_WS at 7-dpi were integral membrane proteins, involved in crucial cellular processes, inositol phospholipid synthesis regulating cellular metabolism, membrane synthesis and trafficking, and energy homeostasis, indirectly influencing fat storage. Exclusive DEGs in RKN_WS at 14-dpi were related to nematode development and host metabolism manipulation, such as Glutathione-S-Transferase or Essential Lipid Oligosaccharide (ELO) protein family, involved in lipid synthesis, crucial for nematode survival within roots. These findings show a significant impact of water stress on *M. incognita* gene expression, providing valuable insights into the complex mechanisms elicited during tomato parasitism.

Poster 20

Functional analysis of the TRPV channel gene *osm-9* in host recognition of plant-parasitic nematodes

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Root-knot nematodes and cyst nematodes recognize host roots by responding to host-derived signals after hatching. While root-knot nematodes parasitize a wide range of plant species, cyst nematodes exhibit strict host specificity. To elucidate the molecular basis underlying differences in host range between these nematodes, we analyzed the function of the TRPV channel gene *osm-9*, previously reported as a host-recognition-related gene in root-knot nematodes, using RNA interference in *Meloidogyne incognita* (Mi) and *Heterodera glycines* (Hg).

Suppression of *osm-9* expression did not affect attraction toward host roots in Hg. In contrast, Mi showed a clear disruption of attraction to host roots following *osm-9* knockdown, demonstrating that the contribution of TRPV channels to host recognition differs between the two species. Furthermore, in Mi, *osm-9*-silenced juveniles exhibited a significant reduction in stylet protrusion frequency after serotonin treatment. Because stylet activity is essential for host invasion and the establishment of parasitism, these results indicate that TRPV channels in Mi play multifaceted roles not only in host attraction behavior but also in host–parasite interaction processes.

Poster 21

NILR1-mediated brassinosteroid-type signaling contributes to nematode resistance

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Plant-parasitic nematodes trigger rapid transcriptional reprogramming in host roots, yet how receptor-mediated perception is coupled to early regulatory outputs remains poorly understood. The leucine-rich repeat receptor-like kinase NEMATODE-INDUCED LRR-RLK 1 (NILR1) has been implicated in nematode resistance and immune signaling, suggesting a role as a primary immune transcriptional activator. However, its genome-wide transcriptional role during early root–nematode interactions has remained unresolved. Here, we define NILR1-dependent transcriptional responses during early *Heterodera schachtii* exposure in *Arabidopsis thaliana* using time-resolved RNA sequencing at 30 minutes and 3 hours post inoculation combined with genotype × treatment interaction analysis. Canonical PTI-associated genes were robustly induced in both wild-type and *nilr1* roots, demonstrating that NILR1 is dispensable for activation of classical PTI transcription at these early stages. Instead, NILR1 selectively biases infection-associated transcription toward growth-, hormone-, and cell wall-related programs. These responses converge on a focused brassinosteroid-responsive regulatory module enriched in elongating cortex cells and centered on the transcription factor GTL1, without widespread induction of canonical brassinosteroid marker genes. Together, our findings provide the first genome-wide, time-

resolved evidence that NILR1 selectively engages a conserved brassinosteroid-type signaling backbone during nematode perception, thereby contributing to effective resistance against parasitic nematodes.

Poster 22

From tropics to temperate: The journey of an adaptive and cold-resilient invader —
Meloidogyne enterolobii

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Meloidogyne enterolobii, an aggressive root-knot nematode (RKN), poses a major economic risk due to its ability to infect plants with resistance genes effective against other RKN species. With a host range exceeding 100 plant species and reports from at least 37 countries, it is regulated as a quarantine pest in many regions. Management remains challenging due to few resistant cultivars, limited nematicides, and insufficient knowledge of host preference and adaptability.

Considering the known adaptability of other RKN species, the adaptive potential of seven geographically distinct *M. enterolobii* populations on cotton and phacelia was investigated under greenhouse conditions. After one life cycle, populations were transferred to new plants for a second cycle, followed by multiplication on a susceptible tomato cultivar to assess fitness costs. All populations showed significantly increased reproduction in the second cycle, with population-specific variation and no loss of reproductive fitness.

Although native to tropical and subtropical regions, *M. enterolobii* has been detected in Europe threatening temperate crops. A semi-field study showed five of nine populations survived winter (1–17 °C) across soil depths (20 and 40cm) and tomato cultivars (MoneyMaker & Phantasia). These findings highlight its adaptability, cold tolerance, and supports development of sustainable preventive management strategies.

Poster 23

Host range and susceptibility of parsley and mint to *Meloidogyne* spp.

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Peppermint (*Mentha × piperita*) and parsley (*Petroselinum crispum*) are widely cultivated medicinal and aromatic plants valued for their essential oils and fresh leaves. Like many other crops, they are vulnerable to infections caused by plant-parasitic nematodes of the genus *Meloidogyne*. However, the host status of commonly cultivated varieties and the damage potential of *Meloidogyne* species occurring in temperate climates remain poorly understood for these crops. In the present study, we evaluated the impact of *Meloidogyne* species on peppermint and parsley under controlled greenhouse conditions. The results showed that the tested mint and parsley varieties are hosts for *Meloidogyne* species, although host status varied depending on both nematode species and plant variety. All studied varieties were susceptible to *M. hapla* but exhibited tolerance to infection, as no significant reduction in plant growth was observed. Nevertheless, at the highest nematode density, *M. hapla* significantly reduced essential oil content in peppermint, indicating that tolerance was limited to vegetative growth and did not extend to secondary metabolite production. Importantly, peppermint cultivar 'Multimentha' was identified as a non-host for *M. chitwoodi* and *M. fallax*, highlighting its potential role in crop rotation strategies aimed at managing these economically important root-knot nematodes. Overall, our findings contribute to a better understanding of host-nematode interactions in medicinal and aromatic plants and provide practical information for sustainable nematode management in herb production systems.

Poster 24

Characterizing natural tomato resistance to root-knot nematodes under heat stress

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California dominates U.S. processing tomato production, accounting for over 90% of national output and more than 25% of the global supply. This industry faces increasing pressure from root-knot nematodes (RKNs; *Meloidogyne* spp.), which cause an estimated \$88 million in annual yield losses. Management of RKNs relies heavily on the resistance gene *Mi-1*, which is present in most commercial cultivars. However, prolonged reliance on *Mi-1* has selected for resistance-breaking nematode populations, recently identified in 27 of 30 symptomatic fields surveyed in California. The durability of *Mi-1*-mediated resistance is further threatened by rising global temperatures, as resistance is compromised at soil temperatures above 28°C while nematode infectivity and reproduction increase.

Concurrently, increasingly restrictive regulations on fumigants and nematicides have reduced chemical control options, intensifying the need for durable, non-chemical management strategies. This project evaluates the effectiveness of the heat-tolerant resistance gene *Mi-9*, derived from wild tomato (*Solanum arcanum*), together with three additional candidate resistance genes, in conferring resistance to RKN populations across

temperature regimes. Resistance will be assessed using transgenic tomato lines in replicated greenhouse experiments and field microplot trials. Successful deployment of heat-tolerant resistance would provide a temperature-resilient approach to nematode management in California processing tomato production systems.

Poster 25

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Soybean cyst nematode is a major constraint on soybean production worldwide, and management remains difficult due to limited durability of resistance and concerns over chemical control. Host attraction and host-finding by the pre-infective juvenile stage represent critical early steps, yet the receptor mechanisms underlying cue detection remain poorly understood. We used transcriptomics and differential expression analysis under host-attraction–relevant conditions to identify candidate sensory receptors linked to host recognition. A prioritized receptor candidate was examined in a heterologous cell-based signaling assay and used as a molecular target for chemical screening. Screening of diverse libraries yielded compounds that modulate receptor-associated signaling in vitro. Ongoing work assesses whether these candidates perturb nematode orientation and attraction behaviors in controlled assays, with the longer-term objective of developing mechanism-based inhibitors that interfere with host recognition. Our approach connects gene discovery to ligand screening and provides a framework for receptor-guided, sustainable control strategies.

Poster 26

Potato metabolomics for the control of plant-parasitic nematode *Pratylenchus penetrans*

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Pratylenchus penetrans is one of the most damaging root-lesion nematode species, causing significant yield losses in agricultural production worldwide. In Portugal, *P. penetrans* is widely distributed in potato-growing regions and is frequently associated with reduced crop productivity. Control strategies remain limited due to the lack of resistant cultivars, highlighting the urgent need for alternative and sustainable management approaches. In this study, untargeted metabolomics was used to identify plant metabolites differentially produced in resistant-like (R) and susceptible (S) potato cultivars in response to *P. penetrans* infection. Three cultivars - Agria (S), Kennebec (S), and Laura (R) - were inoculated with mixed-stage nematodes and grown under controlled conditions. Root samples were collected 30 days after inoculation and subjected to metabolite extraction and analysis. A total of 375 metabolic features were annotated by UPLC-MS-QTOF, using spectral libraries, representing a wide range of chemical classes. Multivariate analyses revealed clear metabolic differentiation between infected and non-infected plants. The resistance-like cultivar Laura exhibited a distinct metabolic profile characterized by elevated levels of glycosylated flavonoids, diterpenes, and phenolic derivatives, suggesting a potential role for these compounds in nematode egression and reduced nematode development and highlighting promising targets for sustainable nematode management and potato improvement.

Poster 27

Effects of the Invasive Black Locust (*Robinia pseudoacacia* L.) on Soil Nematode Communities in Temperate Forests

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Invasive tree species are known to modify aboveground vegetation and soil properties; however, their influence on soil biota remains less well documented. This study examined the effects of the invasive *Robinia pseudoacacia* L. on soil nematode communities in temperate forests of Europe (southern Slovakia), using native pedunculate oak (*Quercus robur* L.) stands as a reference. A paired-site design was applied across nine localities to compare nematode abundance, richness, diversity, trophic and functional structure, ecological indices, and metabolic footprints. A total of 107 nematode genera were identified across all sites. Overall, no significant differences were found between black locust and oak forests in total nematode abundance, diversity, biomass, or most ecological indices, indicating similar soil food web structure and stability. Bacterivorous nematodes dominated in both forest types, followed by plant parasites, omnivores, fungivores, and predators. A significantly higher plant parasitic index was observed in black locust stands, driven by increased abundance of obligate plant-parasitic nematodes. These findings suggest that,

despite its invasive status, *R. pseudoacacia* does not cause major shifts in soil nematode community structure under the studied conditions.

Poster 28

Study of Ascension Island Nematode communities

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Ascension Island's unique environment offers an ideal setting for studying soil nematode communities and their responses to environmental change. This study establishes the first baseline of nematode diversity on Ascension and identifies key taxa that may serve as indicators of soil health and environmental disturbance. Soil samples were collected across multiple elevations and slope orientations. Diversity metrics, trophic groups, and ecological indices of isolated nematodes were calculated to assess distribution, community structure and soil condition. Statistical analyses evaluated how environmental gradients influenced nematode assemblages.

Nematodes on Ascension exhibited spatial variation. Species richness increased with elevation and highest richness recorded at 800m. Some rare, widespread, and potentially undescribed species, including genera *Trissonchulus*, *Belondira*, *Mylonchulus* were recorded, alongside important plant-parasites such as *Xiphinema* and *Meloidogyne*. The discovery of rare, biogeographically notable, and undescribed species emphasizes Ascension's unique belowground biodiversity. Nematode communities showed ecological differentiation, with higher elevations and northeast-facing slopes supporting richer, more mature, and functionally complex assemblages, while low-elevation sites harboured more simple and opportunistic communities shaped by environmental stress. Results highlight the sensitivity of belowground biodiversity to fine-scale environmental heterogeneity in structuring soil food webs and provide a foundation for future monitoring and development of nematode-based soil health indicators.

Poster 29

End of the beginning: the strange chromosome ends of root-knot nematodes

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Telomeres are nucleoprotein complexes that prevent chromosome fusion; and their ends from being recognized as double-strand DNA breaks. Their shortening following DNA replication as cell divide accompanies ageing. Canonical telomeres are composed of G-rich DNA repeats associated with a complex of proteins and RNA. Telomeres shortening is partially compensated by telomerase reverse transcriptase that multiply the DNA repeat using RNA template. This system is thought to be widely conserved across evolution, including in nematodes. The model nematode *C. elegans* has (TTAGGC)_n telomeric repeats multiplied by telomerase enzymes, and a whole set of characterized single-strand and double-strand telomeric DNA-binding proteins.

Long-read genome sequencing technologies have yielded chromosome scale genome assemblies for a variety of nematodes. This allowed exploring telomeric systems in the nematode tree of life. We found substantial variations in nematode telomeric systems. For instance, simple repeats and telomerase were missing in many animal and plant-parasitic nematodes. In the root-knot nematodes, we identified a diversity of complex repeats at chromosome ends. These repeats lack homology in the rest of species. Telomerase and orthologs of the *C. elegans* shelterin complex were missing, suggesting an alternative lengthening of telomeres. This discovery opens new perspectives, including possible control methods specifically targeting telomeres.

Poster 30

Cryptobiosis induces Fragmentation and Rearrangements in the Genomes of *Panagrolaimus* Nematodes

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Cryptobiosis is a state of absent metabolic activity in an organism and is rarely observed in animals. The most common types are anhydrobiosis (desiccation-tolerance) and cryobiosis (freezing-tolerance). Cryptobiotic nematodes survive harsh environments, like the Siberian permafrost or the hyper-arid Atacama Desert, yet the genomic basis and molecular mechanisms remain unclear. We studied the impacts of cryptobiosis on the genome structure of cryptobiotic and non-cryptobiotic representatives of the roundworm family

Panagrolaimidae. For this, we generated high quality assemblies, including phased genomes. Additionally, the survival rates of anhydrobiotic nematodes were assessed and a differential expression analysis was performed at multiple time points of the process.

On the genomic side, we found a potential fusion between chromosomes present in more basal Panagrolaimidae, forming a larger chromosome in a derived, freezing-tolerant branch of *Panagrolaimus*. *Panagrolaimus* genomes also show more fragmentation than those of closely related genera, as well as major rearrangements.

Physiologically, high survival rates were found to not be restricted to nematodes from dry environments, and an upregulation of genes possibly involved in drought-tolerance was observed. We conclude that cryptobiosis may be linked to genome fragmentation in *Panagrolaimus* nematodes and involves the upregulation of specific genes associated with tissue protection and DNA repair.

Poster 31

Measures to Reduce the Incidence of Oat Cyst Nematode in Organic Cereal Production-
investigation of biology and cultivar susceptibility

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Fields with damage from cereal cyst nematodes, especially oat cyst nematode (*Heterodera avenae*; HCN), are increasing in cereal cultivation. Farms with organic production are especially vulnerable since oats are frequently grown. The extent of the damage depends on the proportion of eggs that hatch and the timing of hatching. The biology of HCN regarding egg hatching under Swedish conditions is not fully understood. Recommended countermeasures include crop rotation with non-host crops, which is challenging since most cereals and grasses maintain the nematode population in the soil. Access to resistant cultivars of oats and barley has previously been effective, but today, the range is limited to two barley varieties and one oat variety. The project aims are to provide cereal growers and advisors with guidelines to reduce yield losses caused by HCN. The overarching goal is to increase knowledge about HCN biology and provide the agricultural sector with a rapid screening method for assessing the susceptibility of oat and spring wheat varieties. We will provide results on how HCN egg hatching is affected by temperature.

Poster 32

Understanding interactions between viruses and their plant-parasitic nematode hosts.

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Viruses naturally infecting plant-parasitic nematodes (PPNs) drive host biology, potentially altering nematode fitness, reproduction, and pathogenicity. Despite their ecological importance, the molecular mechanisms governing these interactions remain obscure. A previous small RNA analysis identified seven viral types—including Picorna-like and Bunya-like viruses—in *Globodera rostochiensis* and *Heterodera schachtii* populations. Leveraging insights from *C. elegans*, where viral infection triggers extensive gene regulation and RNA interference (RNAi)-mediated responses, we aim to characterize the biological and molecular basis of PPN-virus interactions. To this end, we will isolate previously detected viruses, specifically focusing on Picorna-like and Bunya-like viruses, and determine their transmission routes (vertical and/or horizontal). Then we will assess viral localization within nematode tissues using fluorescence-based approaches. Finally, we will use high-throughput sequencing to characterize virus-induced changes in host gene expression and RNAi pathways. This work will provide fundamental insights into nematode–virus biology and establish a conceptual framework for exploring their potential relevance in future applications.

Poster 33

Detection of tropical root-knot nematode *Meloidogyne luci* infecting tomato in a field in Slovenia

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Root-knot nematodes (RKN, *Meloidogyne* spp.) are obligate endoparasites causing significant yield losses in agricultural production systems worldwide. *Meloidogyne luci* is a tropical RKN species that requires relatively high temperatures for survival and reproduction in the field. To date, *M. luci* has been reported in Iran, Brazil, Chile, European Union countries (Slovenia, Italy, Greece and Portugal), Turkey, Guatemala, Serbia, Argentina, Bolivia, Ecuador and Ethiopia. *M. luci* was included in the European and Mediterranean Plant Protection Organization (EPPO) A2 Quarantine List of pests due to its economic significance. In Slovenia, *M. luci* had previously only been found in greenhouses. In 2024, *M. luci* was detected in 20% of the sampled tomato plants in a small field near Vrtojba village, mixed with *M. arenaria*. The species were identified using morphological, molecular and biochemical analyses. Present detection demonstrated that *M. luci* has spread in Slovenia not only in protected growing areas such as greenhouses, but also in fields. Climate change, higher soil temperatures and the polyphagous nature of *M. luci* can facilitate its future spread (greenhouses and fields), not only in Slovenia, but also in other regions with sub-Mediterranean and continental European climates.

Poster 34

Comparative Genomics of *Mi-1.2*-Virulent *Meloidogyne incognita* Isolates Selected on Resistant Pepper Using GBS

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Root-knot nematodes (*Meloidogyne* spp.) are one of the main pests of cultivated plants belonging to the Solanaceae family. Virulent root-knot nematodes are one of the most important factors limiting the use of resistant cultivars. To prevent the formation of virulent populations, it is important to use plants carrying genes that confer resistance to *Meloidogyne* in rotational manner. This study investigated the responses of *Me1* gene conferring resistance to root-knot nematodes in pepper to *Mi-1.2* naturally virulent *M. incognita* V6 isolate during the selection process. According to pathological data, the *Me1* gene was exceeded by the naturally virulent *M. incognita* isolate (V6) and it completed three selection process. In the molecular data, the changes in the genomes after the selection processes were investigated using the Genotyping by Sequencing (GBS) method using double digest Restriction-site Associated DNA (ddRAD) technology. For this process, DNA was isolated from the initial J2s of the isolates and from the J2s obtained at the end of the third selection of isolate. The libraries were prepared for next-generation sequencing (NGS). Libraries were sequenced on Illumina HiSeq SBS. As a result of GBS, total 6970 SNPs were identified and among them 3888 SNPs were determined as high-quality and reliable.

Poster 35

First report of *Globodera rostochiensis* and *Globodera pallida* in Swiss greenhouse tomato systems

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Potato cyst nematodes, *Globodera rostochiensis* and *Globodera pallida*, rank among the most economically important plant-parasitic nematodes and remain a threat to potato production. Their occurrence in open-fields is well documented, yet records from protected cultivation are rare. During routine survey, both PCN species were detected for the first time in Swiss greenhouses producing tomato, expanding the known epidemiological context of these quarantine pests.

Soil samples from greenhouses and plastic tunnels revealed *G. rostochiensis* in Valais and Aargau, and *G. pallida* in Valais. Species identity was confirmed using morphological and

molecular analyses. Koch's postulates demonstrated reproduction of both PCN species under greenhouse conditions and identified tomato as a potential bridge host.

Phylogenetic analyses suggested that two *G. rostochiensis* populations likely share a common origin or reflect secondary spread between sites, while a third appears to result from an independent introduction.

The presence of PCN in greenhouse raises significant biosecurity concerns. Protected cultivation systems may act as overlooked reservoirs, enabling population persistence, increasing the risk of transfer to open-field potato crops via contaminated soil, equipment, or planting material. These findings highlight the need for targeted monitoring, strict hygiene measures, and the inclusion of protected cultivation systems in PCN surveillance and management programmes.

Poster 36

Non-invasive detection of virulent *Globodera pallida* populations by hyperspectral imaging

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The potato cyst nematode, *Globodera pallida*, poses a significant threat to potato crops. Since effective chemical nematicides have been largely banned, alternative control methods are required. While crop rotation and biological controls have limitations, genetically resistant cultivars offer a promising alternative. However, intensive cultivation has facilitated the emergence of new virulent populations in Germany and the Netherlands. For early detection and management, we developed a method using hyperspectral sensor data, focusing on identifying latent infestations without visible symptoms. The system employs a hyperspectral camera (@SPECIM, Spectral Imaging LTD.) operating within 400–1000 nm. Under greenhouse conditions, susceptible and resistant potato cultivars were inoculated with three different virulent *G. pallida* populations. Hyperspectral images were produced at various time points, and nematode development was determined via destructive root sampling and staining. At the end of the experiments, reproduction rates (Pf/Pi) were assessed. The virulent *G. pallida* populations showed a relative susceptibility of 10%, 18%, and 23%, with Pf/Pi values of 1.7, 2.9, and 4.2 on the resistant variety, respectively. This virulence allowed the detection of differences in hyperspectral signatures between each population and the control at 42 days past inoculation.

Poster 37

Host status of common weeds to plant-parasitic nematodes

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Due to the expected decline in herbicide availability in agricultural practice weed control will become an increasingly greater challenge in the future. Despite the possibilities offered by an integrated approach to weed control, it is expected that weed pressure will increase. A literature review was conducted to assess the plant host status of common or hard to control weeds with regard to propagation or maintenance of plant-parasitic nematode populations and diseases. To limit the search, a list was compiled of the 35 most common and difficult to control weed species in The Netherlands.

Commonly occurring weed species such as chickweed, couch grass, and goosefoot species are relevant, as well as highly persistent or difficult to control weeds. Examples include species that have developed resistance to certain herbicides, but also weeds that spread easily and quickly, such as nutgrass.

Weed species differ in host plant status and thus their effect on populations of plant-parasitic nematodes. Weed infestation with certain species can reduce the effectiveness of measures against a given nematode species and, in specific cases, even completely negate them. Integrated approaches dealing with high weed pressure should take into account the host plant status of weeds for control of plant-parasitic nematodes.

Poster 38

Biodiversity of soilborne nematodes on non-productive fields

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As part of research into the occurrence of soilborne nematodes in non-productive agriculture areas, nine localities were selected in 2025 in the western part of the Czech Republic (Central Bohemia Region and Vysočina Region). Five of the sites were fallow land used for bee pasture, two were stripes of bee pasture situated in the middle of conventional production fields, and three were grassy strips along watercourses. Soil samples (depth approx. 15 cm) were taken at all these sites; control soil samples were also taken from conventionally farmed fields in the immediate vicinity of non-productive areas at each site. From 100 g of collected soil, the complete soil nematode fauna was extracted, the number of individuals was determined, and 100 specimens were identified to genus. Based on the data obtained, the Maturity Index was calculated for each site and compared with the Maturity Index value determined for the conventional control variant.

The results showed Maturity Index values ranging from around 2.0 for both non-productive and conventional areas, indicating a moderately stable soil ecosystem. In the case of grass strips, greater biodiversity was found in the adjacent control areas.

The research was funded by the Czech Ministry of Agriculture project number QL25020080.

Occurrence of phytoparasitic nematodes in the Karlštejn vineyard (Czech Republic)

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As part of the initial phase of research into biological methods of protecting grapevines against significant harmful organisms, soil samples were taken at the Karlštejn wine research station (Central Bohemia Region), Czech Republic. A motorized soil drill 50 cm long and 10 cm wide was used to collect the soil. In this way, 20 soil samples were taken from soil profile up to depth of 50 cm in a 15-year-old vineyard, and phytoparasitic nematodes were extracted from the obtained soil using the Baermann method. In all samples, the phytoparasitic nematode genera *Rotylenchus* and *Helicotylenchus* predominated. A smaller number of nematodes of the genera *Pratylenchus*, *Ditylenchus*, and *Aphelenchoides* were also found. In addition to the omnivorous genera *Mesodorylaimus* and *Eudorylaimus*, nematodes of the genus *Xiphinema*, specifically *Xiphinema vuittenezi*, were found among the nematodes of the order Dorylaimida.

The research was funded by the Czech Ministry of Agriculture project number QL26010031.

WEDNESDAY 3 JUNE

Parallel session 08

08:30 — 10:00 GMT+2

Lamoraalzaal

Parallel session 8: Soil microbe/nematode interactions (I)

Chair: Lisa Van Sluijs & Stefan Geisen

8:30-8:48 hrs Hans Helder

On the remarkably broad global distribution of fungal nematode antagonists

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Plant-parasitic nematodes can be suppressed by antagonistic representatives of the local soil microbiome. Although fungal nematode antagonists are regularly detected in soils worldwide, their global distribution has not been documented systematically. We mined a global fungal dataset comprising nearly 28,000 samples from 484 studies. We showed that 83% of the soil samples harbored ³ 1 nematode antagonist. Most of the common nematode antagonists barely show any biogeography. This observation underlines their enormous ecological flexibility. Within a selection of the six most common antagonistic taxa across all biomes, three were also most prevalent in croplands. Except for *Chaetomium globosum*, the most frequently detected antagonistic fungi belonged to a single fungal order, Hypocreales. These common and widespread nematode antagonists parasitize representatives of fungi and insects as well. We also investigated the commonness and the global distribution of microbial antagonists that are applied as biological control agents. *Purpureocillium lilacinum*, *Metacordyceps chlamydosporium* and *Trichoderma harzianum* were detected in 6 - 23% of the cropland samples and occurred on all continents. Insights in the prevalence and the distribution of specific and non-specific nematode antagonists at a global scale, might contribute to the exploration of the nematode-suppressive potential that is more widespread than often assumed.

8:48-9:06 hrs Chia-Han Chen

Interactions between symbiotic rhizobia and root-knot nematodes:

early signaling shapes parasitism outcomes

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Legumes can be simultaneously infected by symbiotic rhizobia and parasitic root-knot nematodes (RKN). RKN are highly destructive and typically suppress nodulation and nitrogen fixation, whereas rhizobia can reduce nematode parasitism, though the underlying mechanisms remain unclear. Our previous work examining how nodulation and nitrogen fixation influence RKN infection showed that rhizobia-mediated suppression of parasitism requires functional early nodulation genes in *Medicago truncatula*, indicating either an effect of nitrogen fixation or early symbiotic signaling on RKN parasitism. Here, we investigated the effect of rhizobial strains differing in nodulation and nitrogen fixation on RKN parasitism. This included poorly nodulating mutants of *Sinorhizobium meliloti*, field-sampled strains and well nodulating strains of *S. meliloti* and *S. medicae*. We found that rhizobia impacts were strongly strain-specific: only well-nodulating strains significantly reduced gall formation and egg production, and the antagonism effects were localized rather than systemic. Moreover, staggered co-inoculation experiments revealed that inoculating rhizobia one day or even eight hours before RKN infection markedly blocked RKN entry into roots and reduced gall formation, while simultaneously modulating the induction of antioxidants that support plant defence against RKN. These findings suggest that early signaling in the root during co-infection of *M. truncatula* with rhizobia and RKN largely explains the antagonism of rhizobia on parasitism.

9:06-9:24 hrs Samad Ashrafi

Endophytic nematode antagonistic fungi – an extended plant defence against plant parasitic nematodes

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We have described several nematode egg-parasitic fungi with dual functionality, acting as nematode antagonists, while colonising host plants endophytically. Representatives of *Niesslia gamsii*, *Laburnicola nematophila*, *Polydomus karssenii* and *Polyphilus sieberi* were isolated from eggs of *Heterodera filipjevi* and demonstrated to antagonise eggs of other plant parasitic nematodes, including *H. schachtii* and *Meloidogyne hapla*. In greenhouse trials, *N. gamsii* and *P. karssenii* significantly reduced *M. hapla* reproduction on tomato. Co-inoculation studies further showed that these fungi induce host plant defence upon nematode attack and suppressed invasion of *H. filipjevi* and *Pratylenchus thornei* in wheat by limiting nematode penetration.

Here, a novel function of a potentially new pleosporalean fungus, strain 55, is discussed. Microscopic observations revealed that in addition to direct parasitism, the fungus colonised nematodes at different developmental stages within the roots system. The fungus established endophytically and subsequently entered developing juveniles, causing pronounced discolouration of the body cavity. Cross-sections of root samples infected with nematodes further showed fungal colonisation of females and cysts within the root cortex, including their egg contents. These observations support our hypothesis that the endophytic nematode antagonistic fungi can act as an extended plant defence mechanism targeting nematodes during their establishment and development inside host roots.

9:24-9:42 hrs Seema Aslam

Rhizospheric *Bacillus subtilis* and *Bacillus stercoris* suppress *Heterodera schachtii* and promote *Arabidopsis thaliana* growth

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Cyst nematodes such as *Heterodera schachtii* are major pathogens of many economically important crops. Plant growth-promoting rhizobacteria (PGPR) offer a promising control strategy, because they can simultaneously enhance plant growth and suppress nematodes. Our study investigated the biocontrol potential of seven rhizobacterial isolates (SC11, SW33, SW44, SW53, SW69, SW73, and SW83) against *H. schachtii*. In vitro assays showed that both living bacterial cells (LBC) and cell-free supernatants (CFS) significantly increased mortality of infective juveniles (J2) compared with the control ($p < 0.05$), with LBC of SW44 and SW73 and CFS of SW33 causing the highest J2 mortality, up to about 48% and 64%, respectively. In planta nematode infection assays with *Arabidopsis thaliana* confirmed the strong biocontrol effects of these isolates, as all treatments reduced *H. schachtii* parasitism, and SW83 in particular decreased the number of developed females by around 69% and the total nematode population by roughly 58%. The isolates also reduced J2 invasion into roots by up to 46% (SC11), and the development of invaded J2 into adults was significantly curtailed in SW33 (about 26%), SW73 (about 34%), and SW83 (about 36%), accompanied by a reduction in female size of 12% (SC11) to 18% (SW44 and SW83). Several isolates additionally promoted plant growth, with SW33, SW53, SW69, and SW73 significantly improving growth parameters. 16S rRNA gene sequencing assigned SC11, SW33, and SW53 to *Bacillus subtilis* and SW44, SW69, SW73, and SW83 to *Bacillus stercoris*. All

isolates produced biofilm and siderophores, while SW44, SW73, and SW83 secreted chitinase, SW33 produced hydrogen cyanide, and SW33 and SW44 solubilized phosphate. This study demonstrates that *Bacillus* isolates can effectively suppress *H. schachtii* both *in vitro* and in planta and highlights their potential as components of integrated nematode management, providing the first evidence for antagonistic activity of *B. stercoris* against a plant-parasitic nematode.

9:42-10:00 hrs Veronica Casey

Two Can Play: Investigating the Root-Knot Nematode and Bacterial Wilt Disease Complex

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Disease complexes threaten plant health when multiple pathogens amplify disease severity beyond infection by one pathogen alone. Two globally distributed pathogens that form a disease complex are root-knot nematodes (RKNs; *Meloidogyne* spp.) and bacterial wilt disease (*Ralstonia* spp.). In the roots, RKNs travel intercellularly to reach the vascular cylinder and establish a permanent feeding site. *Ralstonia* spp. enter the roots through wounds or natural openings, colonize xylem vessels, multiply rapidly and produce a thick biofilm, blocking upstream water flow and leading to wilting in infected plants. However, the exact mechanism of interaction between RKNs and *Ralstonia* remains unknown. Based on the pathogens' lifestyles, we hypothesize that *Ralstonia* spp. interact with RKNs by attaching to the nematode cuticle, entering through nematode-induced wounds, and colonizing the *de novo* xylem around the RKN feeding site. We tested the role of nematode-induced wounds through greenhouse and controlled environment plant experiments utilizing RKN susceptible and resistant tomato plants. Additionally, we utilized confocal microscopy to visualize if an mCherry-tagged *Ralstonia* strain attaches to RKN juveniles or congregates within the galls formed after RKN infection. Our results will provide insight into the mechanisms underlying disease complexes and further illuminate cross-kingdom interactions between plants, bacteria, and animals.

Parallel session 09

08:30 — 10:00 GMT+2

Abdijzaal

Parallel session 9: Management – Distribution

Chair: Raquel Campos Herrera & Pella Brinkman

8:30-8:48 hrs Sevilhan Mennan

Distribution, population density and species identification of root-knot nematodes in vegetable-growing areas in Türkiye*

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Accurate species identification is a fundamental prerequisite for the effective management of root-knot nematodes (RKN; *Meloidogyne* spp.), which collectively parasitize more than 3,000 host plant species, with vegetables being among the most susceptible crops. To assess the distribution, infestation rate, population density, and species composition of RKN, surveys were conducted during the 2024 and 2025 growing seasons in major summer vegetables as tomato, cucumber, eggplant, watermelon, okra, pepper, and melon growing areas of six northwestern provinces of Türkiye (İstanbul, Çanakkale, Balıkesir, Edirne, Kırklareli, and Bursa). Soil samples were collected from infested fields to determine the population density of second-stage juveniles (J2), while infected root samples were obtained for species identification. Nematode populations were multiplied from single females, and species identification was performed using polyacrylamide gel electrophoresis (PAGE) based on esterase phenotypes. Of the 103 fields surveyed, 20 (19.41%) were found to be infested with RKN. Tomato fields exhibited the highest infestation rate, followed by eggplant and watermelon. The J2 density in 100 ml of soil ranged from 2 to 203, as determined by counting the J2s in the soil. Mixed-species populations were detected in only two infested fields, consisting of *M. arenaria* + *M. javanica* and *M. incognita* + *M. javanica*. Overall, three RKN species—*M. incognita*, *M. arenaria*, and *M. javanica*—were identified as the predominant species in the surveyed regions.

8:48-9:06 hrs Grace Mohoanatso Tefu

Evaluation of soil physical and chemical properties that are associated with root-knot nematodes from bush tea (*Athrixia phylicoides*) plants harvested in three provinces.

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Bush tea is an important herbal beverage in Southern Africa with health benefits, cultural value, and potential for economic development. Recent surveys across three bush tea (*Athrixia phylicoides*) growing regions in South Africa identified *Meloidogyne* and *Helicotylenchus* as the most prevalent nematode genera. This study aimed at evaluating soil physico-chemical properties that were associated with root-knot nematodes on bush tea. Soil and root samples were collected from the wild in Mpumalanga (MPU), Limpopo (LIM) and KwaZulu Natal (KZN) in 20 localities in summer (Nov 2024-January 2025). Soil was analysed for physical and chemical properties while nematodes were extracted from the roots. The results showed significant differences ($p \leq 0.001$) in PPN populations between LIM, KZN and MPU. Root-knot nematodes were significantly lower in KZN compared to LIM and MPU. No significant differences were observed for *Helicotylenchus* sp. The lower *Meloidogyne* numbers may be associated with high zinc, phosphorus and organic matter content. Understanding these soil nematode relationships provide a foundation for developing soil based nematode management strategies, including maintaining P, K and Zn inputs, while promoting the application of organic amendments to reduce root-knot nematode pressure. Understanding how soil properties affect the growth of bush tea will also be helpful both for wild harvesting and possible cultivation of this health tea.

9:06-9:24 hrs Julija Polanšek

Spatial distribution and morphological characteristics of nematode species *Xiphinema index* in Slovenian vineyards

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This study examines the morphology and spatial distribution of the nematode *Xiphinema index* in Slovenian vineyards and its role as a vector of Grapevine fanleaf virus (GFLV). Understanding the population structure and spatial dynamics of *X. index* is essential for developing sustainable management strategies to limit virus transmission in vineyards.

The morphology and spatial distribution of *X. index* populations were analysed using systematically collected soil samples from vineyard rhizospheres. Population density patterns and factors influencing nematode abundance and dispersal were assessed.

Preliminary results indicate a patchy and uneven distribution of *X. index* within vineyards, likely influenced by soil properties, root distribution, moisture conditions, and mechanical transfer via equipment, human activity, or animals. Differences among vineyards further highlight the impact of biotic and abiotic factors on nematode distribution.

This research provides an overview of the relationship between morphological diversity and spatial distribution of *X. index* populations and the occurrence of GFLV symptoms. The findings offer valuable insights for the development of environmentally sustainable vineyard management strategies, enabling targeted interventions to control nematode populations and reduce virus spread.

9:24-9:42 hrs Nancy Ntidi

Exploring nematology through grain production systems in South Africa

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1 ARC-Grain Crops Institute, Private Bag X 1251, Potchefstroom, 2520, South Africa

2 ARC-Institute for Tropical and Subtropical Crops, Private Bag X11208, Mbombela, 1200, South Africa

Limited information exists for SA conditions with regard to the effect of soil-borne pests for grain crops. The current trend of increasing crop production under conservation agriculture practices furthermore accentuates the importance of soil-borne pests, since little is known in this regard. Survey was conducted in two provinces during 2022/23 growing season to investigate the diversity and occurrence of nematodes and soil-borne diseases in fields of the 'n_e_w_e_r_a' farmers. Substantial and significant ($P < .001$) variation existed among fields sampled with significantly higher populations of plant-parasitic nematodes (PPN) in the 2nd sampling phase compared to the first sampling. The nematode data for soil samples shows very little difference, however, the beneficial nematodes have high populations while compared to the PPN for the 1st sampling. The co-inertia analyses indicated that in the first sampling the nematode soil status in relation with soil parameters the Criconemoides positively correlated with %Sand, Ca% & pH, while the fungivores correlates with the percentage of silt. The second sampling revealed that *Rotylenchulus* and *Pratylenchus* are positively related with %sand and K% Om, Ca and Fu are positively related with Ca, Mg, %Silt, while Criconemoides positively correlated with pH and Ca but less strong as the 1st sampling.

9:42-10:00 hrs Raquel Campos-Herrera

Integrating entomopathogenic nematodes and symbiotic bacteria into next-generation vineyard pest management: efficacy, new products, and soil health indicators

Campos-Herrera, R.¹, Vicente-Díez, I.^{1,2}, Blanco-Pérez, R.¹, Carpentero, E.¹, Dueñas-Hernani, J.¹, González-Trujillo, M.M.¹, Vaquero-Jiménez, E.¹, Álvarez-Ortega, S.³

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Viticulture faces multiple biotic threats, including fungal pathogens (e.g., *Botrytis cinerea*, *Armillaria mellea*), insect pests (e.g., *Lobesia botrana*, *Philaenus spumarius*), and soil-borne nematodes (e.g., *Meloidogyne incognita*). Conventional control strategies rely on short-lived agrochemicals, raising environmental concerns and prompting the development of sustainable alternatives. Historically, entomopathogenic nematodes (EPNs; *Steinernema* and *Heterorhabditis*) have been largely overlooked in vineyard pest management. However, recent evidence demonstrates their versatility above and below ground, positioning EPNs as a viable biotool in this agroecosystem. Infective juveniles (IJs), symbiotic bacteria (*Xenorhabdus*, *Photorhabdus*), and their secondary metabolites provide multiple functions. Aerial EPN-IJ applications effectively suppress *L. botrana* under optimal conditions (sunset, 15–25 °C), and IJs remain compatible with *P. spumarius* foam. Bacterial supernatants and ferments exhibit potent antifungal activity against *B. cinerea* and *A. mellea*, nematocidal effects on *Meloidogyne incognita*, and deter moth oviposition and feeding. Laboratory assays also confirm 24h-aerial survival of *X. nematophila*, also preventing herbivory-induced fruit damage. Additionally, grape cluster treatment with EPNs, bacteria, and by-products did not compromise must quality. Finally, EPN abundance correlates with soil health, with higher activity under organic management practices. These findings set EPNs-bacteria-by products as innovative biotools for integrated, eco-friendly viticulture, combining effective pest suppression with bioindicators of soil quality.

Parallel session 10

08:30 — 10:00 GMT+2

Room 522

Parallel session 10: Smart technologies (I)

Chair: Qing Xue & Jaap-Jan Willig

8:30-8:48 hrs Jenna Ross

Transforming slug control in the UK

McDonald, K¹, Allen-Stevens, T²., Veys, C³., Blacker, C⁴., Chalmers, C⁵., Griffiths, S⁶., Walters, K⁷., and Ross, J.L¹

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⁷Insect Biology and Ecology Harper Adams University Edgmond, Newport, Shropshire, TF10 8NB

Slugs are a major pest, severely decreasing crop yields globally, with *Deroceras reticulatum*, the grey field slug, being one of the most widespread and pestiferous. In the United Kingdom (UK), it is estimated that without adequate control in wheat and oilseed rape crops, slugs cause losses of £43.5 million annually. The current slug control method used by farmers in the UK is iron phosphate pellets, with alternative biocontrol also available in the form of slug parasitic nematodes (*Phasmarhabditis* genus) but these are cost prohibitive at scale. The nematode, once applied, enters through the mantle of the slug and infects the slug host, causing feeding inhibition with subsequent mortality between 4-21days after infection. The SLIMERS (Strategies Leading to Improved Management and Resilience against Slugs) project aimed to break down cost barriers of aforementioned nematode based biocontrol products, and reduce reliance on chemical pellet usage, through the development of an autonomous solution using AI powered slug detection smart map system via multispectral imagery together with a spot spray application of nematodes. This novel approach has the ability to work alongside other platforms for improved slug monitoring,

forecasting and precision application of nematode-based products, thus decreasing losses due to slug damage, and increasing yields of arable crops.

8:48-9:06 hrs Jule Steinert

X-ray computed tomography for imaging root system alterations induced by *Meloidogyne incognita*

Steinert, J.¹, Hallmann, J.², Schmidt, J.H.², Zandantsetseg, K.¹, and Gerth, S.¹

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Root-knot nematodes of the genus *Meloidogyne*, including *Meloidogyne incognita*, are globally distributed plant parasites causing significant yield losses in many crops. Traditional nematode assessment relies on manual, time-consuming, and destructive procedures, limiting objectivity and scalability. This study evaluates X-ray computed tomography (CT) as an imaging approach to detect nematode-induced changes in root architecture and establish a methodological basis for simplified infestation assessment.

Tomato plants were used as a model system and inoculated with defined densities of *M. incognita*. 40 plants were cultivated under controlled climate conditions and divided into five experimental groups, including a non-inoculated control and a non-irradiated control to account for potential effects arising from the irradiation using CT. Over eight weeks, plants were scanned twice weekly using CT. Image data were analyzed for root volume, total root length, and number of root tips.

Initial feasibility experiments show that nematode-induced root galls can be clearly visualized using CT. Ongoing time-series analyses aim to determine whether quantitative root parameters correlate with nematode density and whether infestation can be detected before aboveground symptoms appear. These results demonstrate the potential of CT as an innovative imaging method for automated applications, such as resistance screening and phenotypic characterization of plant–nematode interactions.

9:06-9:24 hrs Bob Klein Lankhorst

New automated and AI driven Potato Cyst Nematode analysis with LIFE Monitor

Klein Lankhorst, B., Den Hartog, P.R., Rodrigues, L.F.S., Wang, Q., Van den Berg, J., Li, K., Groen, E., Morfidou, K., Mendez, F.

Antonie B.V., Uitmeentsestraat 19, 6987CX Giesbeek, the Netherlands

Life Monitor is a combination of advanced hardware and software designed to automate morphological analyses of nematodes through the integration of robotics and artificial

intelligence. The system is designed to rapidly image particles sized between 50 and 1500 micrometers in nematode suspensions. These images are processed through a purpose-made neural network where nematodes are isolated from other particles and further identified. Technological development follows two trajectories: (1) the quantification and identification of free-living soil nematodes to calculate Nematode Based Indices, indicating biodiversity and ecosystem health; and (2) the detection, quantification, and viability distinction of plant parasitic nematodes including cysts and cyst contents. Development of the neural network is ongoing at all levels from order to species, with evidence of successful species-level classification shown in several trials. When Life Monitor is combined with automated extraction equipment, nematode analyses can potentially be fully automated. Life Monitor provides a rapid and scalable approach to nematode monitoring, offering reliable insights to support evidence-based soil management.

9:24-9:42 hrs Alexandros Dritsoulas

Optimization of Sugar Flotation-Based and qPCR Methods for Reliable Detection of Root-Knot Nematode eggs in soil

Dritsoulas, A., Bui, H. X., and Desaegeer, J.

Department of Entomology and Nematology, Gulf Coast Research and Education Center, University of Florida, Wimauma, FL, USA

Root-knot nematode (*Meloidogyne* spp.) infestations are among the most economically significant plant-parasitic nematode problems globally, while accurate detection and quantification of their egg stage in soil remain key challenges for nematode diagnostics and management. The current project has developed an integrated framework that improves both physical extraction and molecular detection of nematode eggs from soil. The research focuses on refining sugar flotation-based extraction methods, including classical sucrose centrifugation and the mini-FLOTAC technique (an apparatus for diagnosing animal parasite eggs), across different soil types and environmental conditions to enhance consistency and sensitivity, particularly at low population densities. In parallel, a quantitative PCR (qPCR) assay has been developed and optimized for the sensitive and specific detection and quantification of root-knot nematode eggs following soil extraction. By linking optimized egg recovery protocols with molecular quantification, the project seeks to establish a standardized and scalable diagnostic pipeline for soil-borne root-knot nematodes, capable of predicting their population dynamics. Ultimately, this work aims to provide researchers and practitioners with reliable tools to improve nematode monitoring and support more informed management decisions.

9:42-10:00 hrs Ziad Matar

Combined automated imaging and morphology based identification enable accurate and scalable plant-parasitic nematode diagnosis

Matar, Z.¹, Kurfürst, V.¹, Kolarik, M.¹, Cervenka, A.¹, Tanahashi, K.¹, Issa, H.¹, Verheijen, G.¹, Wigman, A.¹, Brandt, S.², Brinkman, P.², Molendijk, L.², Janissen, R.¹

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²Wageningen University & Research | Field Crops, Edelhertweg 1, 8219 PH Lelystad, The Netherlands

Plant-parasitic nematode (PPN) infections of agricultural crops destroy ~12% of annual global food production, causing a yearly economic loss of ~US\$ 160 billion threatening global food security. For infested crop systems, PPN species identification is crucial for effective pest management. The current standard of manual PPN identification by expert nematologists is globally limited by their capacity and faces a shrinking pool of qualified nematologists, highlighting the need for scalable solutions. We developed an automated end-to-end diagnostics system combining automated imaging (NEMASCOPE™) with taxonomy-guided computer vision AI for fast and accurate PPN species identification. We evaluated the system's performance on Root-knot nematode (RKN) identification accuracy across several *Meloidogyne* species that are among the most economically damaging plant-parasitic nematodes, using naturally infested field samples containing *M. chitwoodi*. Compared with manual identification, the AI-based approach for the present *M. chitwoodi* in a field sample achieved an accuracy on species-level prediction of ~96%, essentially matching manual expert performance. Our platform thus demonstrates expert-level accuracy for PPN identification and offers a scalable, industry-ready solution to address the global shortage of nematologist expertise and enables evidence-based pest nematode advice & management

Plenary session 3

10:30 — 12:30 GMT+2

Lamoraalzaal

Plenary session 3

Chair: Tina Kyndt

10:30-11:00 hrs Chris Bell (INVITED SPEAKER)

Do parasites exploit mutualistic interactions?

Chris Bell

Faculty of Biological Sciences, University of Leeds, Willow Terrace, LS29JT, Leeds, United Kingdom

Plants exist within complex below-ground communities where roots simultaneously interact with mutualists, such as arbuscular mycorrhizal fungi, and parasites, such as plant-parasitic nematodes. Despite their contrasting ecological roles, both symbionts depend on the same host resource pools to sustain growth and reproduction, raising the question of whether parasites may exploit plant responses that evolved to support ancient mutualistic interactions.

Viewing complex root-associated interactions through a resource-economics framework highlights how host investment strategies can influence both resistance and tolerance, with consequences that extend beyond any single interaction. Enhanced nutrition from mutualistic partners may benefit other co-colonising symbionts when multiple consumers draw upon shared, unrestricted host resources. These perspectives highlight disparities between fixed “mutualist” and “parasite” classification of symbionts and instead emphasise that overall outcomes for the host plant emerge from dynamic ecological contexts; what may be directly good for the plant may be indirectly good for the parasite.

11:00-11:20 hrs Mieke Daneel

Nematode community dynamics in regenerative and conventional potato-based cropping systems

De Kock J.¹, Matlala L.², Mohlala R.³, Tefu G.³, Guga I.³, Du Preez G.C.¹ and Daneel M.S.^{1,3},

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³ARC-Tropical Subtropical Crops, Private Bag X11208, Nelspruit 1200.

Regenerative agriculture (RA) is an emerging approach that emphasizes soil health and ecosystem function, with potential to enhance natural pest suppression, including plant-parasitic nematodes (PPNs). This study evaluated PPN and free-living nematode (FLN) community dynamics in regenerative and conventional cropping systems focusing on potatoes as the main cash crop. The trial was conducted over two years at four sites near Lichtenburg, South Africa. Two sites followed a RA focussed crop rotation system, while the other two adhered to conventional practices. Soil samples were collected seasonally from GPS-designated points and analysed for nematode populations and environmental parameters. Each season, a different crop was planted on each of the fields to reflect typical rotational practices. Genera-level nematode responses were primarily driven by crop identity (PERMANOVA and SIMPER), with susceptible hosts markedly increasing nematode abundance underscoring the pivotal role of crop selection in managing nematode pressure within potato-based cropping systems.

Among free-living nematodes, 22 genera/families were observed, with Cephalobidae being the most frequent family. Metabolic footprint (NINJA) indicated nutrient-depleted and degraded soils in all sampling intervals and fields irrespective of the practice. More time is probably needed to change the free-living nematode community into a more structured community.

11:20-11:40 hrs Xue Qing

Root phenomics resolve the interaction soil nematode and plant

Xue Qing^{1*}, Yincui Ren¹, Shouyang Liu², Hongmei Li¹

¹Department of Plant Pathology, Nanjing Agricultural University, Nanjing, China

²Academy for Advanced Interdisciplinary Studies, Nanjing Agricultural University, Nanjing, China

Nematodes are microscopic in size and their activities occur underground, making them difficult to monitor directly. As a result, current studies on nematode ecology and nematode-plant interactions face limitations in accuracy. We developed a high-throughput root phenotyping facility capable of continuously monitoring root traits. The system accommodates 160 individual root boxes. Each box is automatically loaded, and both shoot and root images are captured within approximately 20 seconds, enabling a complete imaging cycle of all plants up to 24 times per day. This platform measures more than 20 root parameters, including root-knot counts, vertical root distribution, branching patterns, and growth rates derived from time-series image analysis. These traits can be further linked to plant stress-response mechanisms, with the potential to elucidate underlying pathways through molecular plant biology approaches. Thus, the system provides a precise and dynamic means to assess the impact of nematodes on soil biology and plant development. We demonstrate the utility of this platform through three representative applications in our

laboratory: (1) high-throughput screening for nematode-suppressive soils and the identification of potential biocontrol agents; (2) investigation of soil nematode population dynamics integrated with community metagenomic analysis; and (3) study of the interactions between free-living nematodes and tomato plants.

11:40-11:50 hrs Short Break

11:50-12:10 hrs Marion Sesia

Evaluation of deep learning-based counting approaches for the automatic quantification of plant-parasitic nematodes

Marion Sesia^{1,2}, Nicolas Mariette¹, Eric Grenier², Laurent Folcher¹, And Nicolas Parisey²

¹French Agency for Food, Environmental and Occupational Health and Safety (ANSES), Plant Health Laboratory, Nematology Unit, Le Rheu, France

²IGEPP, INRAE, Institut Agro, Univ Rennes, Le Rheu, France

Plant-parasitic nematodes pose a threat to agriculture, requiring regular monitoring of their populations. Manual larval counting under a binocular microscope, the method commonly used for pest surveillance, is time-consuming and subject to both inter and intra-operator variability. This study investigates the automation of this task (on *Globodera pallida* and *Meloidogyne fallax*) through computer vision with deep learning, comparing four models: three convolutional neural networks (CNN) equipped respectively with regression heads (ResNet18), density heads (CSRNet), and detection heads (YOLOv8), and one Transformer (RF-DETR) with a detection head. Models were trained on images of live larvae acquired in the laboratory. For *G. pallida*, RF-DETR outperformed the other approaches, achieving a relative RMSE of 0.113 (average error of 11.3%) compared to ~0.22 for the CNNs. In contrast, for *M. fallax*, performance was significantly lower (relative RMSE: 0.693, average error of 69.3%), mainly due to information loss during image acquisition, related to larval sedimentation issues. These results confirm an increasingly marked trend in deep learning, where Transformer-based models outperform CNNs. Additionally, the performance of RF-DETR, particularly on *Meloidogyne*, highlights the need to adapt image acquisition protocols for each species and to expand the training dataset to further improve the model.

12:10-12:30 hrs Julia Truch (Nominated by YNN)

The telomere-to-telomere genome of *Xiphinema index* reshuffles the epigenetic toolkit dogma in nematodes

Julia Truch^{1*}, Karine Robbe-Sermesant^{1*}, Arthur Péré^{1*}, Dominique Colinet¹, Corinne Rancurel¹, Elodie Drula², Martine Da Rocha¹, Laetitia Perfus-Barbeoch¹, Ercan Seçkin¹, Ulysse Julien-Portier¹, Céline Lopez-Roques³, Carole Iampietro³, Marie Gislard³, Roxane Boyer³, Léo Luvisutto³, Daniel Esmenjaud¹, Etienne GJ Danchin^{1*c} & Cyril Van Ghelder^{1*c}

* equal contributions

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The plant parasitic nematode *Xiphinema index* transmits the Grapevine Fanleaf Virus (GFLV) causing a devastating grapevine degeneration in vineyards worldwide. Here we produced the first high-quality T2T genome for *X. index* as a representative of the Dorylaimida, for which no T2T reference genome was available so far. We identified the first horizontal gene transfer originating from plants reported in the nematode phylum. Most importantly, we detected three canonical DNA (cytosine-5)methyltransferase 1 (DNMT1) and one complete gene encoding for the chromatin remodeler alpha-thalassemia mental retardation X-linked (ATRX). Both were supposedly absent in their complete form in nematodes so far. Our work revealed that canonical DNMT1 and ATRX are restricted to the most basal nematode clades. This suggests that a major reshuffling of the epigenetic machinery occurred during nematode evolution. Furthermore, we showed that (i) the presence of these pivotal epigenetic actors is concomitant with a clear DNA methylation at CpGs in *X. index* and, (ii) observed a genomewide association between the level of CpG methylation, chromatin accessibility at TSS and gene expression. Here, we unveil a nematode genome mimicking the vertebrate epigenetic dogma. These findings will provide a key resource for plant-nematode parasitic interactions and virus-vector research and foster further evolutionary and epigenetic studies contributing to deepen our understanding of the gene regulation.

THURSDAY 4 JUNE

Parallel session 11

08:30 — 10:00 GMT+2

Lamoraalzaal

Parallel session 11: Management - Non-chemical control of nematodes

Chair: Misghina Teklu & Rik Peters

8:30-8:48 hrs Francis Kawalya

Suitability of brassica cover crops for partial biofumigation against potato cyst nematodes under glasshouse conditions.

Francis Kawalya¹, Simon Edwards¹, Joe Roberts¹, Roy Neilson², Matthew Back¹

¹ Agriculture & Environment Department, Harper Adams University, Newport, TF10 8NB, UK.

² Ecological Sciences, James Hutton Institute Invergowrie Dundee DD2 5DA, Scotland, UK.

Potato cyst nematodes (PCN), *Globodera rostochiensis* and *G. pallida*, are important pests affecting potato production. In the UK, growers incur annual losses of around £31 million due to yield reduction and management costs, while increasing restrictions on nematicide use have prompted a shift towards integrated pest management (IPM) strategies. One promising IPM approach is partial biofumigation using brassica cover crops. Brassicas release glucosinolates (GSLs) from their roots, which are converted to biocidal compounds, such as isothiocyanates, that impact PCN egg viability. Two glasshouse studies investigated the suitability of 19 oilseed radish (*Raphanus sativus*), and 8 Indian mustard (*Brassica juncea*) varieties for partial biofumigation against PCN over a period of 12 weeks. Oilseed radish varieties reduced the PCN viability by 14-43 % and 7- 43% whereas varieties of Indian mustard caused reductions of 4-48% and 8-31% in experiment 1 and 2, respectively. Results indicate that specific varieties were suited for partial biofumigation based on PCN viability reduction, root biomass and root glucosinolate concentration. To optimise partial biofumigation, further experiments have been undertaken to determine whether root development and GSL production can be increased, GSL release from brassica roots can be enhanced, and myrosinase activity in the soil can be increased.

8:48-9:06 hrs Lindsay Schulz

Toxic effects of *Solanum sisymbriifolium* on *Globodera pallida*

Schulz, L, and Dandurand, L.M.

Department of Entomology, Plant Pathology and Nematology, University of Idaho, Moscow, ID 83844-2329

The regulated pest of potato, *Globodera pallida*, was first discovered in Idaho in 2006. This specialized plant parasitic nematode can cause up to 80% yield loss on susceptible potatoes. Idaho producers cannot grow potatoes in infested fields resulting in millions of dollars of economic loss. *Solanum sisymbriifolium*, a trap crop for *G. pallida*, has been demonstrated to decrease *G. pallida* populations by 99% when in rotation with potato. Potentially toxic, this research focuses on identifying and purifying toxic compounds from *S. sisymbriifolium* and determining their impact on *G. pallida*. Secondary metabolites of *S. sisymbriifolium* were extracted with various solvents. Extracts with high levels of solamargine significantly reduced *G. pallida* hatch and viability. Lastly, exposure of *G. pallida* to volatiles from *S. sisymbriifolium* roots significantly reduced reproduction of the nematode by 50%. Overall, *Solanum sisymbriifolium* appears to produce compounds toxic to *G. pallida* that may provide novel control strategies for *G. pallida*.

9:06-9:24 hrs Farzana Haque Tumpa

**L-Threonic Acid as Key Bioactive Degradation Compounds of Dehydroascorbic Acid
Conferring Nematicidal Activity and Induced Resistance in Rice**

Tumpa, F. H., Degroote, E., Mangelinckx, S., Chavan, S. N., Ahmad, Y., Kyndt, T.

Department of Plant Pathology, Faculty of Agriculture, Bangladesh Agricultural University,
Mymensingh-2202, Bangladesh.

Dehydroascorbic acid (DHA), the oxidized form of ascorbic acid, exhibits nematicidal activity and induces systemic resistance in rice against the root-knot nematode *Meloidogyne graminicola*. Both *in planta* and in aqueous solutions, DHA undergoes gradual degradation through distinct chemical and metabolic pathways, generating multiple degradation compounds that may contribute to its bioactivity. Progressive degradation of DHA results in the formation of 2,3-diketogulonic acid, oxalic acid, hydrogen peroxide, and L-threonic acid (TA). Among these compounds, TA displayed strong nematicidal activity and emerged as the most effective DHA biodegradation compound in reducing nematode infection. Rice seedlings treated with TA via foliar spray, seed treatment, or soil drenching exhibited significantly reduced gall formation and nematode populations without any adverse effects on plant growth. TA treatment triggered reactive oxygen species accumulation and modulated defense-associated phytohormone profiles, indicating activation of plant immune responses. Transcriptomic analysis of foliar TA-treated plants revealed rapid induction of defense-related pathways in shoots, followed by delayed but robust activation in roots. Collectively, these findings identify TA as a dual-action degradation compound of DHA that holds nematicidal and resistance-inducing activity in rice.

9:24-9:42 hrs Alejandro Expósito Creo

**From lab to field: Can zoophytophagous miridae insects and commercial algae extracts
formulates induce resistance against root-knot nematodes in vegetable crops?**

Expósito, A; Fullana, AM; Cendra, M; Roig, I; Sorribas FJ; Giné A.

Department of Agri-Food Engineering and Biotechnology. Universitat Politècnica de Catalunya, BarcelonaTech, Esteve Terradas 8, Castelldefels, 08860 Barcelona, Spain

Pot and field experiments were conducted to evaluate the efficacy of *Macrolophus pygmaeus*, *Nesidiocoris tenuis*, and Vacciplant® and Primtal® algae extracts as plant-resistance inducers against *Meloidogyne incognita* (Mi) in nine horticultural crops (tomato, eggplant, pepper, cucumber, zucchini, watermelon, lettuce, chard, and bean). In pots, plants were inoculated with 1 J2 Mi/cm³ of soil one day after plant treatment or exposure to miridae. Both LOX and PR1 gene expression was assessed at 0 and 7 days after nematode inoculation (DANI) and nematode infectivity and reproduction at the end of the experiments. Field experiment was done in Mi-infested plots ranging between 1,5 and 55 J2 Mi/cm³ of soil. Plant treatments and exposure to miridae was done as in pot experiments and galling index (GI), nematode reproduction and crop yield were assessed. In pots, all crops showed significant reduction on nematode infectivity and reproduction with at least one inducer. Gene expression varied regarding inducer, crop and DANI combination without a consistent model. In field, only *N. tenuis* reduced both GI (22%) and reproduction (63%) in eggplant, and none of them influenced crop yield. These results demonstrate that inducer efficacy is highly crop-specific and highlights the challenge of translating pot success to field conditions.

9:42-10:00 hrs Islam Darwish

A novel bioactive product containing *Steinernema feltiae* and *Pseudomonas ogorae* for the management of the cabbage root fly (*Delia radicum*) and enhancement of plant health

Islam Ahmed Abdelalim Darwish¹, Daniel P. Martins², David Ryan¹, Thomais Kakouli- Duarte¹

¹Molecular Ecology and Nematode Research Group, enviroCORE, Department of AppliedScience, South East Technological University, Kilkenny Road Campus, R93 V960 Carlow, Ireland.

²School of Computer Science and Electronic Engineering, University of Essex, Colchester CO4 3SQ, UK.

The cabbage root fly (*Delia radicum*) is a major threat for Brassica crops in Europe, Asia, and North America. This study focused on developing an alginate-based formulation comprised of an Irish strain of the entomopathogenic nematode *Steinernema feltiae* SB12(1) and the plant growth-promoting rhizobacteria *Pseudomonas ogorae* F113 *gfp* to provide pest control and plant health enhancement. These organisms have been shown to be compatible in a previous project, while in the present study they displayed further strong synergistic interaction. Greenhouse experiments using 7-week-old cabbage seedlings showed that the encapsulated nematodes were effective in controlling second-instar cabbage root fly larvae, causing 100% mortality at 5 and 10 days post-infestation. Co-encapsulation reduced the root

damage caused by larvae and improved plant survival compared to treatment using nematodes only. Cabbage roots were able to reestablish and significant root and shoot length increases were observed. Furthermore, the encapsulated bacteria successfully colonised and established in the rhizosphere and root tissues, as confirmed by re-isolation 2 weeks post-treatment. Currently, molecular communication analyses applying graph theory approaches are being conducted for further investigation on the interaction between the biological components to improve the developed bioactive product.

Parallel session 12

08:30 — 10:00 GMT+2

Abdijzaal

Parallel session 12: Effector biology and host manipulation (I)

Chair: Stephanie Jaubert & Anika Damm

8:30-8:48 hrs Anna Dickinson

Spatiotemporal Coordination of Effector Expression in *Heterodera schachtii* by Sensing Compartmentalised Host-derived Signals

Dickinson, A.¹, Damm, A.¹, Hardege, I.², Eves-van den Akker, S¹.

¹The Crop Science Centre, Department of Plant Sciences, University of Cambridge, Cambridge CB2 3EA, United Kingdom

²Department of Zoology, University of Cambridge, Cambridge CB2 3EA, United Kingdom

Pathogens must detect a variety of host-derived signals because triggering the profound biological changes indispensable for infection is costly if mistimed. The beet cyst nematode, *Heterodera schachtii*, responds to macerated whole-root systems, termed root extract, by upregulating two master transcriptional regulators of effectors in the gland cells: SUGR-1 regulates early-stage effectors for destructive migration through the cortex, whereas DGR-1 regulates later-stage effectors for feeding site establishment in the vascular cylinder. Given that root extract does not induce metacarpus pumping of *H. schachtii*, external perception is likely linked to transcriptional activation of *sugr-1* and *dgr-1* in the gland cells via an internal signalling pathway. Indeed, extract-induced upregulation of *sugr-1*, but not *dgr-1*, is gated by glutamatergic neuronal signalling. The discovery of different internal signalling pathways for SUGR-1 and DGR-1, in combination with the requirement to activate SUGR-1 in the cortex and DGR-1 in the vascular cylinder, suggests that they must respond to distinct root signals. Consistent with this, diffusate from the *A. thaliana* Casparian strip mutant *myb36/sgn3*, which is enriched in vascular signals, upregulates *dgr-1*, but not *sugr-1*, compared to Col-0. Taken together, these data indicate that *H. schachtii* responds to compartmentalised host-derived signals to appropriately regulate effector expression during infection.

8:48-9:06 hrs Jianlong Zhao

The Meloidogyne incognita Effector Minc10750 Hijacks Plant Chitinase to Suppress Immunity and Promote Parasitism

Rui Liu, D.U.Nilunda Madhusanka, Yuqing Lai, Tong Qin, Jian Ling, Zhenchuan Mao and Jianlong Zhao

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Root-knot nematodes (RKNs, *Meloidogyne* spp.) are among the most destructive soil-borne pathogens, relying on secreted effector proteins to overcome host immunity. Here, we show that Minc10750, a specific effector of *M. incognita*, is identified as a key virulence factor that directly targets plant chitinase ChiB. Minc10750 transcripts accumulate in the subventral esophageal glands of pre-parasitic juveniles and are highly induced during early infection. Functional assays demonstrate that silencing Minc10750 reduces nematode infection, whereas transgenic expression enhances infection in host plants. Genetic evidence establishes ChiB as a positive regulator of immunity, restricting nematode parasitism across multiple plant species. Overexpression of ChiB enhances defense responses, including mitogen-activated protein kinase (MAPK) signaling and reactive oxygen species (ROS) burst, whereas these responses are compromised in ChiB mutants and suppressed by Minc10750. Transcriptome profiling further shows that ChiB modulates defense-associated transcription factors, reinforcing its central role in plant immunity. These findings show that a RKN effector hijacks a host chitinase and directs it to proteasome-mediated degradation. This reveals a new mechanism of plant-nematode interaction and suggests a promising target for durable resistance engineering.

9:06-9:24 hrs Junior Lusu Kika

Unmasking Root-Knot Nematode Parasitism: From Life-Stage-Specific Transcriptomics to the Core Effectorome

Kika, J.L.¹, Sonawala, U.¹, Eves-van den Akker, S.¹, Derevnina, L.¹

¹ Crop Science Centre, Department of Plant Sciences, University of Cambridge

Root-knot nematodes (RKN; *Meloidogyne* spp.) cause substantial agricultural losses worldwide. Successful parasitism relies on the secretion of effectors that suppress host immunity and reprogram plant physiology. These effectors are primarily produced in the oesophageal gland cells and delivered via a stylet; however, only a limited number have been identified and functionally characterised, with most studies focusing on pre-parasitic or late parasitic stages. To address this gap, we performed a comprehensive transcriptomic analysis of the *M. enterolobii*–sweet potato pathosystem, generating life-stage-specific RNA-seq profiles at 36 hours post-infection (hpi) and at 3-, 5-, and 7-days post-infection (dpi). Preliminary analyses reveal distinct transcriptional reprogramming across infection stages, with enrichment of predicted secreted protein genes and partial overlap between stages, particularly at 5- and 7-dpi. These data provide a temporal framework for investigating effector gene deployment during early parasitism. In parallel, efforts on oesophageal gland cell isolation and sequencing are underway to enable spatially resolved transcriptomics of effector-producing tissues, improving effector candidate resolution. Comparative effectoromics across *Meloidogyne* species will further support identification of conserved

virulence strategies. Together, these advances will be presented to demonstrate how integrating temporal, spatial, and comparative analyses provides new insights into effector biology and the molecular basis of RKN parasitism.

9:24-9:42 hrs Shahid Siddique

Fake it to make It: Peptide hormone mimicry and small effectors in root-knot nematodes

Shahid Siddique

Department of Entomology and Nematology, University of California, Davis, CA, 95616

Root-knot nematodes (*Meloidogyne* spp.) are obligate plant endoparasites that cause severe yield losses worldwide by reprogramming host developmental and immune pathways. A key component of this reprogramming is the secretion of small-sized effector molecules that mimic endogenous plant signals. To systematically identify such effectors, we established integrated genomics- and proteomics-based pipelines combining genome mining, secretome prediction, and mass spectrometry-based proteomic analyses of nematode proteome. These approaches enabled the identification of multiple classes of low-molecular weight effector candidates. In parallel, we specifically investigate peptide hormone mimics, with a strong focus on sulfated peptides that resemble endogenous plant signaling molecules. At ESN, I will present updates on the functional characterization of some of these effectors, including their expression dynamics during infection, their contribution to nematode parasitism, and emerging insights into their perception by plant receptors. In addition, I will highlight new candidate small effector molecules uncovered through our genomics-proteomics pipeline. Together, these findings advance our understanding of peptide hormone mimicry as a virulence strategy and provide new perspectives for developing targeted control strategies against plant-parasitic nematodes.

9:42-10:00 hrs Jasper Chippendale

Identification and characterisation of proteins present in the gelatinous matrix of *Meloidogyne incognita* egg masses

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Root-knot nematodes cause extensive damage to crops throughout the world. The most damaging species is *Meloidogyne incognita*, which has a very broad host range and is

present primarily in tropics/subtropics. Eggs of *M. incognita* are laid directly into a gelatinous matrix (GelM) which is thought to protect eggs from environmental stresses.

To identify components of this structure we have undertaken a proteomic analysis of the GelM; this analysis revealed the presence of a number of abundant proteins including vitellogenins – known to be associated with eggs in other nematode species – as well as a range of novel secreted proteins which were highly and specifically upregulated at the adult female life stage, consistent with a role in the GelM. Among these proteins are two families of novel small peptides that may interact with bacterial cell walls as well as a GH25 lysozyme, known for its ability to degrade cell wall components. The GH25 gene bears high homology to lysozymes in cellular slime moulds, rotifers and bacteria suggesting potential origin through horizontal gene transfer.

This work shows that the *M. incognita* GelM may contain proteins that allow the nematode to modulate the bacteria present in its environment and thus protect eggs from predation.

Parallel session 13

08:30 — 10:00 GMT+2

Room 522

Parallel session 13: Nematodes as bioindicators

Chair: Gerard Korthals

8:30-8:48 hrs Lilian Atira

Ecological impacts of recovered nitrogen from manure (RENURE) products in commercial farms using nematode diversity as a bioindicator of soil health

Atira, S.L., Germaine, K., and Kakouli-Duarte, T.

Molecular Ecology and Nematode Research Group, enviroCORE

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Recycling-derived fertilisers (RDFs), including recovered nitrogen from manure (ReNure), provide a sustainable alternative to synthetic fertilisers. To encourage their use, it is crucial to understand their environmental impacts. Two Belgian field trials, involving potatoes and maize, used nematodes as bioindicators to evaluate the impacts of ReNure products on soil health. Morphological and molecular methods were used to assess nematode abundance and diversity as key indicators. Treatments included pig urine (PU), ammonium sulphate (AS), and liquid pig manure (LF). The positive controls were synthetic fertiliser (S) and farmer's practice (synthetic + cattle slurry) (FP), while unfertilised (U) plots were the negative control. Potato trial results indicated that nematode diversity remained unaffected by fertiliser type, although nematode abundance increased significantly in fertilised soils. Soils treated with LF had the lowest nematode abundance and differed from those with PU and S but not AS. In the maize trial, the nematode abundance was highest under AS fertilisation, and differed from U, S, and PU. Further analysis will clarify the impact of RDFs on nematode diversity in maize and will be discussed. These results suggest that RDF fertilisation does not disrupt soil nematode communities.

8:48-9:06 hrs Thomais Kabouli-Duarte

An ecological sustainability assessment of recycling derived fertilisers using nematodes as environmental indicators

Atira, L., Karpinska, A., and Kakouli-Duarte, T.

Molecular Ecology and Nematode Research Group, enviroCORE, Department of Applied Science, South East Technological University, Carlow R93 V960, Ireland

Soil is the primary reservoir of essential nutrients for plant growth. Conventionally, farmers apply soil nutrients in the form of synthetic mineral fertilisers. These materials are unsustainable, subject to geopolitical turmoil and expensive to the farmers. At the same time, excess nutrients are being lost in the form of organic waste. The ReNu2Farm and ReNu2Cycle projects aim to help mitigate this and provide viable alternatives, by applying circular economy principles in the development of recycling derived fertilisers (RDF) from organic waste. Crucial part of RDF development is their ecological impact assessment and nematodes have been utilised for this purpose. A sustainability analysis was subsequently carried out on the performance of RDF in the ReNu2Farm project. Struvite RDF supported a highly complex, structured and resilient soil food web. Ammonium sulphate RDF had an ecological advantage compared to the chemical fertiliser CAN. The conventional CAN resulted in a degraded and simplified soil food web, while the RDF fertilised soils resulted in mature, structured and self-regulating systems. Therefore, it is concluded that both RDF, struvite and ammonium sulphate, strongly maintained the ecological integrity of agricultural soils, which is one of the core principles of ecological sustainability. Interreg-NWE is acknowledged for supporting these projects.

9:06-9:24 hrs Negin Ebrahimi

Biogeographic region, land-use and management intensity shape nematode communities

Ebrahimi, N.^{1,2}, Valvekens, L.¹, de Sutter, N.¹, Haegeman, A.¹, Rodríguez Seijo, A.³, Fernández-Calviño, D.³, Kundel, D.⁴, Wassermann, T.⁴, Fließbach, A.⁴, Schrader, S.⁵, van Capelle, C.⁵, Bind, D.A.⁶, Álvaro-Fuentes, J.⁷, Zusevica, A.⁸, Sánchez-Navarro, V.⁹, Zornoza, R.⁹, and Waeyenberge, L.¹

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⁹Sustainable Use, Management, and Reclamation of Soil and Water Research Group, Department of Agricultural Engineering, Universidad Politécnica de Cartagena, Paseo Alfonso XIII 48, 30203 Cartagena, Spain

Soil nematode communities play a key role in terrestrial ecosystems and respond sensitively to environmental change. Within the EU Soil Mission project BIOserviceS-101112374, we assessed how biogeographic region, land-use and management intensity influence soil nematode communities. Nematodes were extracted from 770 samples across 25 locations covering five biogeographic regions (Alpine, Atlantic, Boreal, Continental and Mediterranean), seven land-uses (urban, industrial, agricultural, forest, mining, semi-natural and wetland) and three management intensities. Communities were characterised to genus level using DNA metabarcoding of nematode extracts targeting a 490 bp fragment of the 18S rRNA gene (V6-V8), and sequenced on Illumina NextSeq. Reads were quality-filtered and taxonomically assigned using an in-house curated nematode reference database. Our analysis revealed that Shannon diversity differed among biogeographic regions, with Mediterranean communities showing lower to intermediate diversity compared with other regions, depending on land-use. Across regions, diversity varied consistently with land-use, with semi-natural, urban and wetland soils generally exhibiting higher diversity. Management intensity influenced diversity in a region- and land-use-dependent manner, with lower intensity sites generally supporting higher diversity. Communities were dominated by bacterivores and herbivores, whereas omnivores and predators were scarce, and fungivores showed the strongest regional variation. These shifts likely affect ecosystem functions and services.

9:24-9:42 hrs Alejandra Vieyra-Ramirez

Nematode diversity and soil health: insights from a study on an Irish built environment

Alejandra Vieyra-Ramírez¹, Lisa Moran², Cara Daly³, Zeta Dooly⁴, Thomais Kakouli-Duarte¹

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Soil health is defined as the ability of the soil to sustain its biodiversity and productivity, and to provide environmental services in terrestrial ecosystems. The study of nematode diversity and nematode community structure is an extensively used approach to assess soil health, as soil biodiversity is a fundamental factor in the capacity of the soil to provide ecosystem

services. However, the assessment of soil health using nematodes as bioindicators is not as widespread in built environments (i.e. public gardens) as in other habitats. In this study, nematode diversity and community composition are being studied in Mount Congreve Gardens, Co. Waterford, Ireland. Established in the 1960s, the gardens comprise a 70-acre planted woodland, and a 4-acre walled garden with a unique collection of exotic to Ireland plants. A combination of morphological and DNA metabarcoding methods to identify nematodes and the following use of Nematode-Based Indices reveal a complex nematode diversity landscape inside the Gardens. Preliminary results indicate variability in the soil health status in different locations inside the Gardens and demonstrate the usefulness of nematode-based soil health assessments for built environments that provide cultural and other ecosystem services.

9:42-10:00 hrs Gerhard Du Preez

Inoculation Potential and Functional Roles of Compost Nematodes in Soil Ecosystems

Griesel, T.¹, Daneel, M.^{1, 2}, and Du Preez, G.¹

¹Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa

²Agricultural Research Council – Tropical and Subtropical Crops, Nelspruit, South Africa

Johnson Su compost is promoted as a biological inoculant in agricultural soil, yet evidence for their long-term establishment and functional benefits remains limited. We asked whether mature Johnson Su compost can (i) establish beneficial nematode communities in soil and (ii) measurably influence soil food-web functioning after application. Compost nematode community development was quantified over 13 months in Johnson Su bioreactors after which nematode inoculation potential was tested in a repeated soybean greenhouse pot experiment. Treatments included root-zone incorporation and surface broadcasting (sterilised and non-sterilised), and an unamended control. Nematode and general soil and plant health indicators were compared across treatments using inferential and multivariate analyses. Mature compost contained diverse free-living assemblages, including the common compost taxa *Butlerius*, *Cuticularia*, *Ditylenchus*, *Diplogasteriana*, and *Mononchoides*. However, following application, soil communities showed little evidence of sustained compost-derived nematode populations. Instead, taxa converged toward resident assemblages, shaped by compost amendment type. Also, nematode functional metrics signalled that root-zone incorporation of non-sterilised compost strengthened soil ecosystem functioning with significantly greater fungal-dominated decomposition and more structured, mature, and suppressive food webs. These patterns indicate that Johnson Su compost enhances soil health mainly by stimulating resident trophic interactions rather than through long-term establishment of compost-borne taxa.

Plenary session 4

10:30 — 12:30 GMT+2

Lamoraalzaal

Plenary session 4

Chair: Catherine Lilley

10:30-11:00 hrs Sara Sánchez Moreno (INVITED SPEAKER)

Nematode indicators of past, present and future environmental threats

Sánchez-Moreno, S.

¹ Dpt. of Biodiversity and Evolutionary Biology, National Museum of Natural Sciences (MNCN-CSIC), José Gutiérrez Abascal 2, 28006 Madrid, Spain.

Soil nematodes have long been used as bioindicators of soil conditions in a wide range of agricultural systems and natural ecosystems worldwide. Over recent decades, the impacts of intensive agricultural practices —such as chemical fertilization and pest control, tillage, and reduced crop diversity— have been assessed in comparison with alternative practices, including organic amendments, biological control, and direct sowing, through the study of soil nematode communities. The effects of these disturbances on soil functions (e.g. nutrient cycling) and ecosystem services (e.g. pest control) are inferred using appropriate sets of nematode-based indices (NBIs). In recent times, new anthropogenic impacts, from microplastics to climate change, threaten natural and agricultural systems at global level. More recently, emerging anthropogenic pressures, ranging from microplastics to climate change, threaten natural and agricultural systems at a global scale. In addition to NBIs, functional traits —such as body size, population age and sex structure, and resistance-related adaptations— are increasingly recognized as indicators of anthropogenic environmental stress on soil nematode communities and may serve as valuable bioindicators of human impacts on the biosphere.

11:00-11:20 hrs Olivera Topalovic

Microbe-mediated contribution of host plants and soil nematodes to the parasitism and survival of root-knot nematodes

Topalović, O.^{1,2,3}, Geisen, S.³, Vestergård, M.⁴, Grenier, E.¹, Ekelund, F.²

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Microbial role in the life cycle of phytonematodes is important but underexplored. Using amplicon sequencing of the 16S rRNA gene and ITS region, we showed that the parasitism of root-knot nematodes is followed by a restructuring of the microbiomes in the galls (“gallobiome”) and rhizosphere, and that these changes depend on the plant host. For instance, bacterial genus *Flavobacterium* was depleted in the galls of *Meloidogyne incognita* across several plant species compared to the healthy roots, while *Devosia* and *Rhizobium* were enriched in the gallobiome on tomato and cucumber. Moreover, the shared presence of several bacterial taxa in the gallobiomes of all tested plant species suggests a similar composition of the nematode-facilitating microbial taxa independently of the host. The diversity of fungi, on the other hand, was reduced in both the galls and rhizosphere of all nematode inoculated plants. We further show that survival of root-knot nematodes in soil also depends on other nematode groups that likely indirectly affect the composition of their microbes. Thus, we argue that deciphering the complex and life cycle-stage dependent interactions between microbes and phytonematodes both in soil and *in planta* would result in a more successful control of phytonematodes *in situ*.

11:20-11:40 hrs Leendert Molendijk

Integrated Nematode Management as a part of Integrated Crop Management: Six years of onsite research in arable farming; proving the principle

Molendijk, L.P.G , Visser J.M., Wesselink, M.

Wageningen University and Research | Field Crops, Edelhertweg 1 , 8219 PH, Lelystad, The Netherlands

The call for a reduction in the use of crop protection agents requires a system shift. Integrated Crop Management (ICM) is a field-based approach that integrates multiple disciplines to develop site-specific crop protection strategies, with Integrated Nematode Management (INM) as one of the components.

ICM starts with an inventory of existing and expected bottlenecks taking into account crop choice, soil type and region. Based on this analysis, available measures within the five ICM pillars are examined: crop rotation in space and time, variety selection and cultivation practices, soil management, targeted control and monitoring/evaluation. This structured process/approach enables the selection of effective, site-specific strategies.

In 2020, a field trial was initiated at the Wageningen University & Research location in Vredepeel (sandy soil), comparing the ICM approach with a reference system reflecting current farming practices. The INM approach, as part of the ICM-strategy, enabled effective nematode control with the complete elimination of nematicides.

Crop yields and economic returns were lower during this transition phase, nematode populations remained well controlled. Strategic crop rotation and careful variety selection proved essential.

These results highlight INM as a successful and robust element of sustainable arable farming.

11:40-11:50 hrs Short Break

11:50-12:10 hrs Stephanie Jaubert

Plant-parasitic nematode microRNAs hack plant AGO1 to induce host cell reprogramming

Ange Dussutour¹, Yara Nouredine¹, Martine da Rocha¹, Oussama Yahmi¹, Abile T¹. Mohammed, Karine Mulet¹, Pauline Foubert¹, Ann Po Cheng², Jérôme Zervudacki³, Ercan Seçkin¹, Michael Quentin¹, Pierre Abad¹, Lionel Navarro³, Arne Weiberg², Bruno Favery¹ and Stephanie Jaubert¹

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Root-knot nematodes of the *Meloidogyne* induce the formation of galls by triggering the dedifferentiation of parenchyma cells into specialized giant, polynucleated, and hypermetabolic feeding cells that serve as nutrient sinks essential for their life cycle. This dramatic reprogramming of root cells is driven by *Meloidogyne* effectors secreted that manipulate host defense and gene expression. Cross-kingdom RNA interference (RNAi) has emerged as a novel mode of communication, involving the exchange of small non-coding RNAs (sRNAs) that hijack RNA silencing pathways. Whether *Meloidogyne*-secreted sncRNAs contribute to root cell reprogramming remains unknown. To investigate this, we performed Argonaute 1 (AGO1) immunoprecipitation from infected roots, followed by small RNA sequencing. We identified nine *Meloidogyne*-secreted miRNAs associated with *Solanum lycopersicum* AGO1. Similar experiments in *Medicago truncatula* and *Arabidopsis thaliana* revealed two conserved miRNAs, previously reported to be excreted through extracellular vesicles by animal parasitic nematodes. Using degradome sequencing, RNA sequencing, and computational target prediction, we identified putative plant targets of these nematode-derived miRNAs. Using degradome sequencing, RNA sequencing, and computational target prediction algorithms, we identified the putative plant targets of these nematode secreted miRNAs. Characterizing these secreted sncRNAs opens new perspectives on plant-RKN molecular dialogue and offers potential strategies for developing novel pest management approaches.

12:10-12:30 hrs Tim Thoden

Potential for reduced performance and plant-parasitic nematode resistance development in modern nematicides

Thoden, T.C¹, Radakovic, Z.², Stamatas, Y³., Wiles, J.A.⁴

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The risk of resistance development in plant-parasitic nematodes has historically been considered low, with few cases documented beyond controlled laboratory studies. This has been largely attributed to the relatively short soil persistence of earlier nematicides, including carbamates, organophosphates, and soil fumigants, which limited the duration of plant-parasitic nematode exposure under field conditions. Over the past decade, several novel nematicides with new modes of action, such as fluopyram, fluazaindolizine, and cyclobutrifluram have been introduced around the world, with soil persistence differing among compounds and influenced by soil type. Recently, isolated cases of reduced sensitivity or possible resistance of root-knot nematodes to fluopyram have been reported from intensively managed systems, including golf courses and greenhouse vegetable production. In this study, we investigate (1) the potential for resistance development to fluazaindolizine under controlled laboratory selection and (2) field-based observations of changes in root-knot nematode sensitivity to fluopyram. Together, these findings provide insight into resistance risk associated with modern nematicides and highlight the importance of proactive resistance monitoring and management.

Parallel Session 14

14:00 — 15:30 GMT+2

Lamoraalzaal

Parallel session 14: Ecology - there is more than nematodes

Chair: Thomais Kakouli-Duarte & Gerhard Du Preeze

14:00-14:18 hrs Simon Groen

Gradients in belowground herbivory may drive geographic clines in plant root defenses

Godinez-Vidal, D., Jansen R. P. Santos, J.R.P., Romero, A.N., Mostafavi, F., Roberts, P.A., Huynh, B.L., and Groen, S.C.

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The longstanding biotic interactions hypothesis predicts that plants from lower latitudes experience stronger herbivore pressure and should thus invest in more potent defenses. However, the evidence is mixed and highly skewed towards aboveground tissues. To address knowledge gaps regarding belowground herbivory, we studied phenotypic variation in root defense against *Meloidogyne* root-knot nematodes (RKNs), which attack a wide variety of plants. RKN activity is influenced by temperature and typically higher at lower latitudes. Strikingly, a latitudinal cline in plant defense against RKNs was visible in all monocot and dicot plant species analyzed, with generally lower nematode fitness on low-latitude plants. Among the plant species in our dataset was *Arabidopsis thaliana*, which produces glucosinolates as defensive chemicals. Across European *Arabidopsis* accessions we identified heritable latitudinal clines in levels of certain glucosinolates. In particular, long-chain aliphatic glucosinolate levels were higher in low-latitude accessions and negatively correlated with RKN fitness. In addition, RKNs imposed fitness costs on plants that varied in magnitude depending on root long-chain aliphatic glucosinolate accumulation. To summarize, we find patterns consistent with the biotic interactions hypothesis: more intense nematode herbivory may have contributed to the evolution of more effective chemical defenses in roots of plants from lower latitudes.

14:18-14:36 hrs Sigal Brown Miyar

Re-evaluating Root Lesion Nematode Disease in Pepper: The *Pratylenchus capsici*–Microbiome Disease Complex, Their Interactions, and Temperature-Driven Dynamics

Sigal Brown Miyara¹, Abraham Gamliel², Patricia Bucki¹, Svetlana Duvrinin³, Noa Sela⁴, Xue Qing⁵, Marina Benichis² and Abebe Aseffa^{1,6}

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Rising soil temperatures associated with climate change are expected to alter rhizosphere microbial communities, with important consequences for plant–nematode interactions. Here, we investigated temperature-mediated changes in root- and rhizosphere-associated microbial communities in pepper (*Capsicum annuum*) in response to infection by the root lesion nematode *Pratylenchus capsici*, using high-throughput metabarcoding. Pepper plants were grown under controlled soil temperatures of 25°C, 30°C, and 33°C, and root tissues and rhizosphere soils were sampled separately. Fungal and bacterial communities were characterized using ITS and 16S rRNA gene sequencing, respectively. In parallel, nematode communities were analyzed using nematode-specific primers to assess plant-parasitic and free-living nematode assemblages. Distinct microbial assemblages were observed between roots and soils across temperatures. Root-associated fungi were dominated by *Rhizophagus*, with *Olpidium* consistently enriched in roots and showing higher abundance at 25°C. Co-occurrence analysis revealed an asymmetric interaction in which *Pratylenchus* was negatively affected by *Olpidium* occurrence. Soil fungal communities were more diverse, dominated by *Aspergillus*, *Penicillium*, *Fusarium*, and *Rhizophagus*, showing minimal temperature effects. Root-associated bacteria were dominated by rhizobia and *Pseudomonas*, with moderate abundances of other genera, while soil bacterial communities were more diverse, with *Bacillus* as the most prominent genus. Overall, increasing soil temperature reshapes microbial communities in a compartment-specific manner, and asymmetric nematode–fungus interactions may modulate disease development. These findings provide a foundation for climate-smart, microbiome-informed management of root lesion nematodes in pepper.

14:36-14:54 hrs Dorota Porazinska

Limited Impact of Gopher Tortoise Activity on Nematode Diversity

Rachel M. Shepherd^{1,2}, Eli M. S. Gendron², Philip G. Hahn², Marcus A. Lashley³, Dorota L. Porazinska²

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Keystone species and ecosystem engineers maintain biodiversity by creating ecological niches that support a wide range of organisms. The gopher tortoise (*Gopherus polyphemus*) is a well-known example in the longleaf pine sandhill ecosystems of southeastern United States. Although its positive effect on aboveground biodiversity is well documented, its impact on belowground biodiversity remains unclear. Additionally, it is unknown whether these effects vary across intact vs. human-altered ecosystems.

To address these questions, we conducted an observational study in Florida, examining two microhabitats shaped by gopher tortoise activity: burrowing sites vs. foraging areas across intact sandhills and degraded pastures. Collected soil samples were analyzed for nematode, microbial, and plant communities, as well as soil biogeochemistry.

Gopher tortoise activities significantly affected only bacterial-feeding nematodes with their diversity being lower in burrowing than foraging areas. Vegetation type did not play a key role, as degraded pastures supported diversity levels comparable to sandhills. However, the size of gopher tortoise effects varied by vegetation type with more pronounced impacts in pastures than sandhills. Gopher tortoise activities did not explain compositional shifts. Instead, biotic drivers, such as the diversity of microbial and plants communities shaped nematode communities in sandhills, whereas abiotic factors played a larger role in pastures.

14:54-15:12 hrs Mihail Kantor

Spatiotemporal dynamics of vector-mediated transmission of beech leaf nematode populations

Kantor, M.¹, Berry, L.¹, Consoli, E.¹, Lyndby, N.¹ and Kantor, C.²

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Beech leaf disease (BLD) has spread more rapidly than any other disease caused by plantparasitic nematodes. Yet, current knowledge on how the beech-leaf nematode, *Litylenchus crenatae*(Lc), are transmitted locally and long distances are limited. This study investigated potential vectors associated with BLD and characterized seasonal population dynamics of the beech leaf nematode, including biotic and abiotic factors. The biotic factors included arthropods and birds, and results indicated that both could be possible vectors for transmission of the beech leaf nematode, as Lc were found to survive the gastrointestinal tract of caterpillars and were also present on bird feet. Nematode abundance was quantified over time over a three-year period to assess temporal trends in population dispersal, while candidate vectors were examined for nematode presence using morphological and molecular approaches. Local scale results dispersal showed that abiotic factors, such as wind

and rain, can spread the nematodes as far as 300 feet away from the closest infected tree. These findings provide new insights into the spatiotemporal biology of the beech leaf nematode and can help identify possible pathways for disease spread. Improved understanding of BLD vectors and population dynamics will inform disease monitoring, risk assessment, and the development of effective management strategies.

15:12-15:30 hrs Rosana Salazar-García

How management impacts plant-parasitic nematode communities in Mediterranean olive groves in the face of increasing desertification derived from global change

Salazar-García, R.¹, Palomares-Rius, J.E.¹, Cantalapiedra-Navarrete, C.¹, Valenzuela-Polo, V.², García-Velázquez, A.¹, Criado-Navarro, I.¹, Castillo, P.¹ and Archidona-Yuste, A.¹

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Olive groves are the core of Mediterranean agroecosystems, both culturally and economically. However, this transitional ecosystem between arid and temperate climates faces dual threats: plant-parasitic nematodes (PPNs), which pose significant challenges for sustainable management, and increasing desertification driven by global change. Adapting nematode management practices to these changing conditions is fundamental for maintaining the long-term viability of Mediterranean olive agriculture. This study examined how PPN communities are shaped by local environmental conditions and management practices across the Mediterranean Basin. A total of 51 olive groves were surveyed resulting in 306 samples distributed across five major olive-producing countries: Greece, Italy, Morocco, Portugal, and Spain. Data from PPN communities, environmental variables (climate and soil properties), management practices, and their chemical and biological agricultural residues were integrated through extensive statistical analyses, including regression models, variation partitioning, and structural equation models (SEMs).

Results demonstrate that management strategies significantly mitigate diversity loss caused by desertification. This finding highlights the critical role of agricultural practices in preserving soil health and nematode community diversity under global change, offering practical pathways for sustainable pest management in aridifying croplands. The study provides evidence that appropriate management can buffer Mediterranean olive groves against the mounting pressures of global change.

Parallel Session 15

14:00 — 15:30 GMT+2

Abdijzaal

Parallel session 15: Genomes and Genomics

Chair: Mark Sterken & Pallavi Shakya

14:00-14:18 hrs Lucy Jimenez

CNeGmA: A lineage-aware framework for assessing genome completeness in nematodes

Jiménez, L.^{*1}, Tran, V.², Ebersberger, I.², Philipp H., S.¹

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Accurate genome completeness is essential for understanding nematode biology, genome evolution, adaptation, and functional diversity. However, its estimation remains challenging due to extreme phylogenetic diversity, rapid sequence evolution, and frequent gene duplication and loss. Existing frameworks often underestimate completeness in early-diverging and non-model nematodes because their reference databases are phylogenetically biased.

To address this limitation, we introduce **CNeGmA (Complete Nematode Genome Assembly)**, a lineage-aware framework specifically designed for evaluating genome completeness in nematodes using a comprehensive, phylum-wide reference gene set. CNeGmA is built on a curated orthology dataset from 128 nematode species spanning all major clades. Importantly, includes both single-copy and multicopy orthologs to capture nematode-specific gene-family evolution. Completeness is estimated by querying protein sequences against our nematode-wide core reference, using direct ortholog detection and feature-architecture similarity, and computing completeness metrics to identify conserved gene families.

With CNeGmA, we show that lineage-aware orthology improves completeness estimates for early-branching and non-model nematodes compared to traditional approaches such as BUSCO, expanding phylogenetic coverage from 79 to 128 species. By prioritizing evolutionary context over universal metrics, CNeGmA offers a more biologically informative framework for assessing genome quality and establishes a robust foundation for future genomic and transcriptomic analyses in nematodes.

14:18-14:36 hrs Vidyasagar Sathuvalli

Genome Announcement: Draft Genome for Stubby Root Nematode *Paratrichodorus allius*

Sathuvalli, V.¹, Golightly, H.^{1.}, Danchin, E.², Wram, C.³

¹Oregon State University

²French national research institute for agriculture, food & environment

³USDA-ARS

Stubby root nematodes (SRNS) belonging to *Paratrichodorus* and *Trichodorus* genera are the vectors for tobacco rattle virus (TRV), the causal agent of Corky Ringspot (CRS) disease in potato. There are few genomic resources for SRNs, limiting the study of SRN genetic diversity and potential implications for pathogenicity to crop plants. We generated a contig-level genome assembly for *Paratrichodorus allius*, the most common SRN in the potato-growing region of the Pacific Northwest of USA using PacBio HiFi reads. The assembly has a BUSCO completeness score of 67.3%, a contig N50 of 366KB, 2403 total number of contigs, and a total length of 275226805bp. Kmer analysis suggests the genome may be triploid or tetraploid. There was only 0.4% alignment of Illumina 100bp single RNA reads from SRNs to the HiFi assembly, suggesting possible issues with contig construction due to highly repetitive genome content or alternatively, greater genetic diversity of SRNs in the PNW than previously anticipated. Additionally, with a BUSCO duplicate score of 47%, it is possible that many contaminating contigs remain even after contamination filtering with BlobTools. Developing genome resource for SRN is challenging and understanding of SRN is essential for effective control of CRS in potato.

14:36-14:54 hrs David Kihoro Sirengo

Genome sequencing and analysis of the plant-parasitic nematode *Xiphinema americanum* and its endosymbiont *Candidatus Xiphinematobacter*

Sirengo, D.K.¹, Sevigny, J.L.³, MacDonald, E.³, Thomas, W.K.³, Zasada, I.A.⁴, Yin, Y.², and Powers, T.O.¹

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Dagger nematodes in the *Xiphinema americanum* group are globally distributed plant-parasitic nematodes of economic importance due to their role as vectors of quarantinable plant viruses. Despite their significance, genomic resources for this genus remain limited because of their complex biology and difficulties in culture. In this study, PacBio HiFi long-read sequencing was performed on four *Xiphinema americanum* individuals and one pooled sample from a population originally collected from a raspberry field in Washington State and

maintained on sudangrass. High molecular weight DNA was extracted, amplified, and sequenced, followed by genome assembly and quality assessment using standard metrics. Assemblies were dominated by nematode host sequences and bacterial contigs corresponding primarily to the obligate endosymbiont *Candidatus* Xiphinematobacter, which accounted for more than 90% of bacterial reads in most samples. De novo assembly of symbiont reads produced a circular genome of approximately 917 kb, consistent with reduced intracellular bacterial genomes and supporting a vertically transmitted and evolutionarily stable symbiosis. Although whole-genome amplification favored recovery of mitochondrial and symbiont DNA, sufficient nuclear reads were obtained to initiate a draft *X. americanum* genome estimated at 250 to 300 Mb. One individual has been re-sequenced to improve coverage, and host-focused binning and annotation are in progress.

14:54-15:12 hrs Ercan Seçkin

Whole-genome detection and origin identification of orphan genes in root-knot nematodes

Seçkin E.^{1,2}, Colinet D.¹, Bailly-Bechet M.¹, Seassau A.¹, Bottini S.¹, Sarti E.², Danchin E.G.J.¹

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Genes lacking homologs in other species, known as orphan genes, are widespread and often functionally important. Their presence can result either from extreme divergence of ancestral genes or from *de novo* emergence out of non-genic regions, and distinguishing between these origins remains challenging. Root-knot nematodes (*Meloidogyne*) provide an important system to study orphan gene evolution as many of their genes involved in plant parasitism have no homologs outside the genus, and several species have undergone whole-genome duplications. Here, we present a pipeline to identify orphan genes and infer their evolutionary origins. The pipeline first performs comparative homology searches to detect putative orphan orthogroups, then verifies their expression and translation with transcriptomic and proteomic data. Ancestral sequences for each orphan orthogroup are reconstructed and aligned to closely related species, complemented by synteny analyses, to discriminate between divergent and *de novo* origins. Using our pipeline, we find that 18% of *Meloidogyne* genes are orphans and at least 20% of these orphans have emerged *de novo*, while at least 25% result from high divergence. We also showed that orphan proteins in this genus are short, often extracellular, and enriched in signal peptides—features consistent with known effectors. Finally, we highlighted the limitations of characterising orphan proteins in the absence of homologs.

Parallel Session 16

14:00 — 15:30 GMT+2

Room 522

Parallel session 16: Effector biology and host manipulation (II)

Chair: Sebastian Eves-van den Akker & Madalena Mendonça Silva

14:00-14:18 hrs Madalena Mendonça Silva

A transcription factor-duet works in concert to regulate gene expression across the life cycle of the pinewood nematode, *Bursaphelenchus xylophilus*

Mendonça, M¹., Xia, C²., Vicente, C. S. L.¹., Eves-van den Akker, S²., Espada, M.¹

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The migratory endoparasitic pinewood nematode (PWN), *Bursaphelenchus xylophilus*, is responsible for pine wilt disease, causing economic and ecological losses in forest ecosystems. Understanding the molecular mechanisms regulating PWN parasitism-related genes may lead to new sustainable solutions. Using PWN transcriptomic datasets from the pre-parasitic/parasitic stages and the pharyngeal gland cells (GC), an *in-silico* analysis identified 7 candidate transcription factors (TF) highly expressed in the GC with their spatial expression confirmed by *in situ* hybridisation. Two TFs, *BXY_079* and *BXY_022*, each encoding zinc finger domains, were successfully RNAi-knockdown. Transcriptomic data from silenced *BXY_079* and *BXY_022*, analysed with PWN life cycle, showed that these TFs work simultaneously by repressing male- related genes while activating genes expressed during the J3 and D3 stages. Additionally, *BXY_079* activates parasitism-related highly expressed genes in the J2 stage, mainly encoding lytic functions such as secreted peptidases and glycoside hydrolases, potentially related with nematode feeding and migration during host interaction. *BXY_022*, alone, represses the expression of several genes related to the reproduction system, such as major sperm and cytosolic motility proteins, particularly in the adult male stage. Overall, both TFs work together, non-redundantly, to regulate gene expression across the life cycle, while individually regulating diverse and distinct gene sets.

14:18-14:36 hrs Beth Molloy

Identification and screening of development-altering effector candidates in *Heterodera schachtii*.

Molloy, B.¹, Abraham, J.¹, Shin, D. S.¹, Long, J.¹, Ahmad, M.¹, Pellegrin, C.¹, Senatori, B.¹, Kranse, O. P.¹, Sperling, A.¹, Damm, A.¹, Derevnina, L.¹, Vieira, P.², Thorpe, P. J.³, Maier, T.⁴, Baum, T.⁴, Eves-van den Akker, S.¹

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During parasitism, plant-parasitic nematodes (PPNs) secrete effectors from pharyngeal gland cells, eliciting profound changes in host biology to suppress immunity and establish a plant-derived feeding organ. Despite their importance in parasitism, the identities and functions of few effectors are known and effector prediction remains a bottleneck for the field, particularly for those involved in feeding site formation.

Here we advance techniques for gland cell isolation and transcriptional analysis to define 269 high-confidence homologs of PPN effectors, and 448 novel predicted effectors with high gland-cell expression. Using this predicted “effectorome”, we provide a systems-level understanding of the deployment and evolution of PPN effectors and select 80 novel effector candidates to be screened for development-altering functions in *Arabidopsis* using our custom phenotyping platform. Preliminary screening reveals 50 % of candidates exhibited a potential growth or developmental phenotype, and the most promising 16 were selected for further characterisation.

Our effector discovery pipeline has allowed us to predict novel effector genes and identify effectors potentially involved in feeding site formation for *in planta* screening and downstream characterisation. The robust identification of plant-parasitic nematode effectoromes and subsequent identification of novel effector functions will underpin our understanding of nematode pathology and inform strategies for crop protection.

14:36-14:54 hrs Sylvain Chéreau

Metabolomic to help for deployment of alternatives control solutions against *Heterodera carotae*

Sylvain Chéreau, Sylvain Fournet, Catherine Porte & Josselin Montarry.

INRAE IGEPP, Domaine de la Motte, 35653 Le Rheu, France

Heterodera carotae is an obligate plant-parasitic cyst nematode. Without protection, its development on carrots is responsible for yield losses of up to 80%. Since 2018, phytosanitary control methods (via chemical soil fumigation) have been banned in France, severely impacting carrot production across entire production areas. Capable of parasitizing only the genus *Daucus*, *H. carotae* has developed strategies to recognize its host plant by perceiving the chemical signals it emits through its roots. This specificity has led to the development of a "suicide hatching" strategy, which involves fooling the nematode on the presence of its host plant, whose effectiveness has already been demonstrated. However, its widespread deployment across production areas is hampered, by the difficulty of producing sufficient quantities of root exudates. Identifying the molecule(s) recognized by this nematode could help overcome this obstacle. To this end, the ECLODERA project relies on combining two complementary approaches to metabolomic (by LC-HRMS) analysis of root exudates: 1) the analysis of exudates collected at different phenological stages., and 2) the analysis of exudates from 15 different Apiaceae varieties. The results obtained have allowed the identification of a candidate molecule. To confirm this structure, bio-guided fractionation approaches (via UHPLC) are being carried out.

14:54-15:12 hrs Anika Damm

From host signals to parasitism: two antagonistic transcription factors orchestrate sequential effector deployment

Damm, A.¹, Pellegrin, C.¹, Sperling, A. L.¹, Jezierska-Suwinska, A. G.¹, Dickinson, A.¹, Desikan, P.¹, Xia, C.¹, Wei, S.¹, Molloy, B.¹, Harpum, G.¹, Shin, D. S.¹, Long, J.¹, Brett, P.², Moura de Souza, V. H.¹, Kranse, O. P.¹, Euler, M.³, Grundler, F. M. W.³, Vieira, P.⁴, Mejias, J.⁵, Kumar, A.⁵, Masonbrink, R. E.⁶, Maier, T. R.⁵, Baum, T. J.⁵, Eves-van den Akker, S.¹

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Pathogens secrete discrete and sequential waves of effectors to manipulate their host. However, the regulators and signals that shape this sophisticated trans-kingdom dialogue are poorly understood. Here, we show that a pair of transcription factors in the plant-parasitic

cyst nematodes are stimulated by discrete plant signals termed effectostimulins: small, host-specific molecules that vary in natural populations. We demonstrate that these effectostimulin-activated transcription factors work both antagonistically but yet in concert to determine parasitism in the beet cyst nematode *Heterodera schachtii*. The nuclear hormone receptor SUGR-1 activates early-stage effector expression required for plant invasion. Its homologue, DGR-1, acts as a dual-functional switch that “switches off” SUGR-activated early-stage effectors, and “switches on” the next wave of later-stage effectors associated with biotrophic establishment in the host. Together, DGR-1 and SUGR-1 control nearly one half of all

H. schachtii effectors expressed before feeding site formation, and over one fifth of effectors of any kind. Importantly, given that knockdown of *sugr-1* reduces root penetration by 80%, blocking the regulators of effector deployment may open novel and generalisable control mechanisms to pathogens that secrete effectors.

15:12-15:30 hrs Ryoji Shinya

Decoding volatile sex pheromone communication in plant-parasitic nematodes: insights from *Bursaphelenchus xylophilus*

Shinya R.

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Despite their enormous ecological and agricultural impact, little is known about how plant-parasitic nematodes use chemical signals to coordinate reproduction and behavior. Pheromone research in nematodes has primarily focused on water-soluble ascarosides, leaving the existence and biological roles of volatile pheromones largely unexplored. Here, we show that the plant-parasitic nematode *Bursaphelenchus xylophilus* relies on volatile sex pheromones to regulate reproductive behavior. By combining chemical identification, behavioral assays, neuronal ablation, and ultrastructural reconstruction of sensory neurons, we identify the volatile sex pheromones and dissect the neural basis of their perception, including the key amphid neurons responsible for detection. In parallel, we have established a genetically tractable *Bursaphelenchus okinawaensis* as an experimental system to apply genetic and molecular approaches for identifying pheromone receptors. Our results reveal a previously unexplored mode of chemical communication in plant-parasitic nematodes and provide a new framework for comparative and evolutionary studies of chemosensory systems. Furthermore, these findings open new possibilities for developing novel control strategies based on the manipulation of chemical communication.

Parallel session 17

14:00 — 15:30 GMT+2

Room 532

Parallel session 17: Chemical control of nematodes

Chair: Tim Thoden & Johan Deseager

14:00-14:18 hrs Giovambattista Depietra

Tymirium® technology: advancing protection of high-value crops against plant-parasitic nematodes

Depietra, G.¹, Carter G.¹, Mugnier, JY¹, Wallis, E.¹, Kurtz, B.³, Viri, V.³, Fontes, J.³, Harlow, P.¹, Perez, T.¹, Schiano di Cola, C.¹, Thacker, U.¹, Simmons, J.⁴, Drakopoulos, D.³, Morath, J.³, Ridolfi, M.³, Gaberthueel, M.², Ivacic, D.², Lemos, A.²

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Plant-parasitic nematodes, particularly root-knot (Meloidogyne) and lesion nematodes (Pratylenchus), pose significant threats to global production of key crops. Managing these destructive pests presents complex challenges due to their persistent nature and the high-value status of the relevant crops. TYMIRIUM® technology introduces an innovative approach through its dual nematicide-fungicide action. Field trials across diverse agricultural zones have shown that TYMIRIUM® technology systemically and movement through the soils provides additional benefits with activity against key soil-borne fungal diseases, highlighting its crucial role in sustainable production of high-value crops while promoting long-term soil health and ecosystem balance. To visualise the product's exceptional performance in reducing nematode populations, we used high-end imaging technology "making the invisible visible". This advanced visualisation reveals the comprehensive protection provided by TYMIRIUM® technology, from root systems to above-ground plant parts, offering growers a reliable solution for integrated pest management in modern agriculture.

14:18-14:36 hrs John Wiles

The Benefits of Nematicide MoA Classification - Work of the IRAC International Working Group on Nematodes

Wiles, J.A.¹, Braun, C.A.⁴, Collienne, U.⁴, Crossthwaite, A.⁵, Daum, J.³, Dos Santos, F.L.³, Ebbenga, D.⁷, Fudali-Alves, S.⁶, Gaberthueel, M.⁵, Huggins, J.³, Lovato, B.², Nauen, R.⁴, Riga, E.⁶ & Thoden, T.C.¹

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⁶ FMC Corporation, USA

⁷ Valent BioSciences, USA.

In Europe, the need for effective tools to manage plant-parasitic nematodes has increased substantially in recent years, attracting attention from growers, regulators, and industry stakeholders. This presentation highlights the activities of the IRAC International Nematode Working Group, which has a global mandate to develop and maintain a Mode of Action (MoA) Classification Scheme for nematicides, analogous to those used for insecticides, fungicides, and herbicides. The Nematicide MoA Classification Scheme encompasses a wide range of nematode control agents, including conventional chemical nematicides, soil fumigants, and biological products with demonstrated nematicidal activity. MoA group codes begin with the letter “N,” denoting nematicide or nematode control agent. Examples of current groupings include carbamates (Group N-1A), organophosphates (Group N-1B), avermectins such as abamectin (Group N-2), pyridinylmethyl benzamides and phenethyl pyridineamides including fluopyram and cyclobutirfluram (Group N-3). Compounds with unknown modes of action are classified as Group N-UN, such as fluazaindolizine, fumigants as N-UNX, and bionematicides as N-UNB, N-UNF, or N-UNE. The scheme is regularly reviewed and updated based on new scientific evidence submitted to the Working Group, ensuring accurate classification. The classification supports informed product labelling and enables effective resistance and integrated nematode management strategies. Updates are available on <https://irac-online.org/>.

14:36-14:54 hrs Zoran Radakovic

Residual efficacy and soil health compatibility of 2 modern nematicides in 4 different soils from Sicily.

Dhama, A.¹, Thun, W.¹, Radakovic, Z.S.¹, Wiles, J.A.², Thoden, T.C.¹.

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Root-knot nematodes (*Meloidogyne spp.*) pose a major threat to vegetable production worldwide. This study evaluated the efficacy of Salibro™ nematicide (fluazaindolizine,

Reklemel™ active) and Velum Prime® (fluopyram) in suppressing *Meloidogyne javanica* in four contrasting Sicilian soil from four different farms. Soil samples were collected, characterized for physical and chemical properties, and used to establish pot trials under controlled greenhouse conditions. Cucumber plants (*Cucumis sativus*, AUDAX F1) were inoculated with *M. javanica* eggs, treated with the nematicides, and monitored across six time points (T0–T5) with 2 weeks gap between each time point. Key parameters included nematode reproduction (Pf/Pi), galling index, plant growth metrics, and free-living (non-plant-parasitic) nematode (FLN) community dynamics; the latter assessed via the NINJA ecological index tool. Salibro and Velum Prime consistently suppressed *Meloidogyne javanica* populations across all soils, even at T5 time point showing reliable duration for crop protection. FLN profiling revealed that Salibro had minimal impact on soil food web indices, while Velum Prime led to a strong decline in key FLN groups and ecological stability indicators such as the Structure and Maturity Indices. These results affirm the potential of Salibro™ as a selective nematicide suitable for Mediterranean horticultural systems.

14:54-15:12 hrs Yannis Stamatias

Reklemel™ active: a novel tool for integrated nematode management – key learnings from the development in southern europe

Yannis Stamatias¹, Tim Thoden², John Wiles³ and Antonino Fenio⁴

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Across Europe, plant-parasitic nematodes remain a major threat to crop production, causing substantial yield losses across diverse agricultural systems. Reklemel™ active (fluazaindolizine) is a proprietary, soil-applied nematicide developed by Corteva Agriscience to address this challenge, providing excellent control of root-knot nematodes and protection against several other economically important plant-parasitic species across a wide range of crops. Remarkably, Reklemel™ active demonstrates exceptional compatibility with beneficial soil organisms, including free-living nematodes and key microbial groups essential for soil health, enabling effective plant-parasitic nematode management while supporting the biological integrity of the soil ecosystem. Development of Reklemel™ active began more than a decade ago and was supported by an extensive global research program, with more than 4,500 field studies conducted across varying soil types, climates, and crop–nematode complexes to rigorously evaluate performance under real-world conditions. In 2025, the commercial formulation Salibro™ 500SC, containing Reklemel™ active, received an emergency use authorization in Italy for solanaceous and cucurbit vegetable crops affected

by root-knot nematodes. This presentation will highlight the key biological attributes of this novel nematicide and share field efficacy results from Southern Europe, demonstrating its value as a new and highly selective tool for sustainable nematode management in modern European agricultural systems.

Workshop 5: Education Nematology Future Proof

16:00 — 17:15 GMT+2

Lamoraalzaal

Building a resilient future for Nematology education

Chairs and presenters: Wim Bert, Evelyn Heese, Paige Hickman, Jet Vervoort and Aska Goverse

This workshop explores nematology education's evolving landscape, highlighting existing programs and their related sustainability challenges. Join our interactive session to share your knowledge, identify collaborative opportunities and help define the shared goals that will sustain our discipline for the next generation.

Workshop 6: Young Nematologist Network

16:00 — 17:15 GMT+2

Abdijzaal

“Knot” what we expected: Extracting value from negative results

Chairs: Clarissa Hiltl and Anika Damm

Presenters: Florian Grundler, Godelieve Gheysen and Sebastian-Eves van den Akker

Research rarely goes as planned yet we often don't talk about it. Negative and unexpected results are just as valuable for the field but receive little to no attention. We invited leading experts in the field to share their stories, with the opportunity to ask questions.

Workshop 7: Community resources - digitalization of collections and biobanks

16:00 — 17:15 GMT+2

Room 522

The future of nematode identification and collection digitalization

Chairs: Nicole Viaene

Presenters: Simon "Niels" Groen and Negin Ebrahimi

The workshop will feature presentations about ongoing developments in image-based digitalization and sequencing efforts of nematode collections as part of open science initiatives. Workshop participants will exchange ideas on how to bring this information

together and coordinate efforts to make such initiatives as useful and available as possible for the community.

Workshop 8: Addressing fundamental research questions together

16:00 — 17:15 GMT+2

Workshop Room 531

Presenters: Hans Helder and Geert Smant

Identifying fundamental nematological questions with intrinsically low chances of external support, and exploring options for community efforts to address them (by invitation)

Poster session 2

17:15 — 18:15 GMT+2

Lounge 1

Poster session 2

Poster 39

Observations on the nematocidal activity of vanillin and caffeine on *Meloidogyne incognita*

Rosso, L.C.¹, Colagiero, M.¹, Ciancio, A.¹, Pentimone, I.¹, Novy, ²

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Two products, available in large amounts and considered safe because of use in the food industry, were investigated. *In vitro* nematocidal assays were performed to test wood-derived vanillin (4-hydroxy-3-methoxybenzaldehyde) or caffeine (1,3,7-trimethylxanthine) vs second stage juveniles (J2) and eggs of *Meloidogyne incognita*. Vanillin showed high death rates of J2 when immersed in 1.0·10³ ppm and 2.0·10³ ppm solutions (mortalities = 39.7% and 96.4%, respectively), significantly different from tap water controls (p<0.001). No effect was observed, however, on eggs hatching after one week incubation at 26°C, at the same concentrations. Germination of tomato exposed to vanillin at 2·10³ ppm showed not significant inhibition. In other assays, eggs were tested *in vitro* with caffeine solutions ranging from 0.3·10³ to 1.27·10⁴ ppm. Data showed a dose-dependent reduction of hatching, with no hatching at 7.5·10³ ppm and higher concentrations (DL50=2.5·10³ ppm). Highest J2 mortality (100%) was observed at 1.27·10⁴ ppm (DL50=1.4·10³ ppm). Incubation at 2.0·10³ or 4.0·10³ ppm allowed embryo development but the J2 could not exit eggs, significantly lowering hatching (p<0.001). Research partially funded by the EU, Project CropSafe (GA 101209410).

Poster 40

Comparative nematocidal activity of *Artemisia annua* Essential Oils (EOs) from different geographical origins against *Meloidogyne incognita*

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The current study evaluated and compared the nematocidal activity of two *Artemisia annua* essential oils (EOs), differing in geographical origin and extraction method, against infective second-stage juveniles (J2s) of *Meloidogyne incognita* using *in vitro* assays.

J2s were exposed for 24 and 48 h to 2000-4000 µg ml⁻¹ concentrations of both laboratory-extracted and commercial EOs of *A. annua*, in an orbital incubator set at 25°C and 70 RPM.

After 24 h, exposure to 2000 µg ml⁻¹ of the commercial EO caused 48% mortality of *M. incognita* J2s, whereas the laboratory-extracted EO induced only 12% mortality under the same conditions.

The chemical profiles of both *A. annua* EOs was assessed by GC–MS analyses and compared. The main compounds of *A. annua*, 1,8-cineole and camphor, were present in both EOs, but with different percentage. Thus, different mortality percentages suggested that the variation in the chemical compositions of the two *A. annua* EOs is due to geographical location and methods of extraction on the activity of EOs. Despite increasing interest in EOs as nematocides, little information is available on their underlying molecular modes of action. The expression profiles of several genes in *M. incognita* following exposure to both EOs will be discussed.

Poster 41

Development of RT-qPCR method for detection and distinction of live and dead pinewood nematode *Bursaphelenchus xylophilus*, and *B. mucronatus*, in wood.

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The quarantine nematode *Bursaphelenchus xylophilus* is a causal agent of the pine wilt disease. The lack of precision in early detection of this nematode in the vector insect and wood may have significant consequences for the future in the newly infested forest stands. Identification, allowing the distinction between live and dead PWN individuals, is particularly important during routine border phytosanitary inspections of wood and wooden packaging imported into the European Union. If dead nematodes remain in the wood after successful thermal treatment, the routine-DNA-based molecular analysis may yield false positive results. A better approach is to analyze the presence of the nematode RNA, as it degrades rapidly after the animal death.

Our study was conducted using an RT-qPCR assay to differentiate live and dead individuals of the pine wood nematode. The nonpathogenic nematode *B. mucronatus* was also included in the diagnostic tests. Before the experiments universal forward and reverse primers and specific TagMan probes were developed for both *B. xylophilus* and *B. mucronatus*. RT-qPCR enabled precise identification and differentiation of these nematode species. The probe designed for *B. xylophilus* only amplified RNA from the tested populations of this species.

Similar results were observed for the probe designed for *B. mucronatus*. None of the designed specific probes detected DNA from these nematode species (i.e., untreated wood or ineffective treatment). Furthermore, these probes did not detect DNA and RNA from other *xylophilus* nematode species – *B. fraudulentus* and *B. populi*, closely related to the quarantine pine wood nematode. The analyses were performed with RNA isolated from individual nematodes at various developmental stages or from larger populations.

The reported study has demonstrated that the newly developed molecular technique, RT-qPCR, is a reliable tool for distinction between *B. xylophilus* and *B. mucronatus*, and between their live and dead individuals.

Poster 42

How native nematode communities could limit the invasion by *Meloidogyne graminicola* in soil for cereal crops

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The occurrence in Italy of the rice root-knot nematode *Meloidogyne graminicola* constitutes an emerging threat in Europe. In this context, our study focused on biological invasions in agroecosystems, more specifically the possible threat posed by this nematode to cereal crops in France. *Meloidogyne graminicola* has a wide host range, including wheat, an economically important crop in France. Understanding its competitive interactions with native plant-parasitic nematode (PPN) communities is crucial to identify risk indicators of soil resistance. We carried out two bioassays under controlled conditions with two populations of *M. graminicola*, one from Italy and one from Borneo, inoculated onto soft wheat in soil from Brittany. Interactions with the native PPN community were monitored 35 and 85 days after inoculation at two inoculum levels. Results showed that the endoparasite *Pratylenchus fallax* was an effective competitor and a potential resistance indicator of soil, limiting *M. graminicola* in roots. Ectoparasites like Dolichodoridae and Tylenchidae also contributed by restricting the access to roots for *M. graminicola*. This work illustrates that the functional diversity of PPN communities in France could constitute a biotic filter to *M. graminicola* invasion.

Poster 43

Guardians from the grass; Harnessing fungal endophytes to suppress plant parasitic nematodes of potatoes

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The fungal endophyte, *Epichloë* spp., forms symbiotic relationships with a wide range of cool-season grasses and has been shown to enhance host plant resistance to various biotic and abiotic stresses, through the production of secondary metabolites that influence both micro and macro-organisms within the rhizosphere. Additionally, *Epichloë* spp. have been used in New Zealand and Australia to manage several insect pests, including the African black beetle (*Heteronychus arator*). Although research on nematode interactions remains limited, preliminary studies suggest that endophyte-infected grasses can influence nematode populations. This study aims to identify *Epichloë* infected grass lines that exhibit the greatest suppression on potato cyst nematodes (*G. pallida*) and stubby root nematodes (*Trichodorus* and *Paratrichodorus* spp.). Screening-based assays will be conducted to identify strains/species of *Epichloë* which have the greatest nematode suppression. Metabolites released from each type will be analysed to determine both chemical composition and the quantities present. This process includes growing endophyte grasses for 120 days and analysing different plant tissues for the metabolite quantities present. Following this, nematodes will be subjected to endophyte metabolites, and the mortality and hatch rates assessed. The most promising strains will be subject to further studies and assessment.

Poster 44

Native Mediterranean Entomopathogenic Nematodes and Their Microbiota: Implications for Sustainable Pest Management

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Entomopathogenic nematodes (EPNs) are effective biological control agents, but their field performance may depend on environmental adaptation and interactions with associated microbiota. This research investigates bacterial communities linked to native EPNs from Mediterranean agroecosystems in southeast Spain, with the aim of determining how microbial partners contribute to nematode virulence, persistence, and stress tolerance under semi-arid conditions. Field surveys were carried out in citrus, olive, and stone fruit orchards, and native EPN isolates were recovered using *Galleria mellonella* and *Tenebrio molitor* baiting. Molecular identification indicates the presence of three dominant species: *Steinernema feltiae*, *S. carpocapsae*, and *Heterorhabditis bacteriophora*. High-throughput 16S rRNA amplicon sequencing is being used to characterise EPN-associated microbiota and

assess species-specific bacterial signatures. Preliminary observations suggest diverse bacterial assemblages, frequently including related to *Pseudomonas*, *Bacillus* and Enterobacteriaceae-related taxa. Functional prediction and comparative microbiome analysis are underway to explore pathways potentially involved in toxin production, oxidative stress defence and secondary metabolite biosynthesis. Bioassays are ongoing to evaluate EPN efficacy against *Ceratitidis capitata* and *Drosophila suzukii*. Expected outcomes include identifying microbiota patterns associated with enhanced biocontrol performance and resilience, supporting microbiota-informed IPM strategies.

Poster 45

Vegetable pathogenicity, nematicide susceptibility, and cold tolerance of banana-burrowing nematode, *Radopholus similis*

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Banana-burrowing nematodes cause severe damage to bananas, anthuriums, and other crops in tropical and subtropical regions but have not yet invaded Japan. In preparation for their potential introduction, we investigated the parasitism of the banana-burrowing nematode, *Radopholus similis*, on eight vegetables and other plant species and its susceptibility to three nematicides in Japan. Low-temperature exposure tests were conducted to simulate overwintering conditions. The results indicated that the nematode reproduced well in seven of the eight vegetable species, including groundnut, soybean, tomato, and aubergine, suggesting that it could cause considerable agricultural damage if introduced into Japan. *R. similis* exhibited higher susceptibility to fosthiazate than the southern root-knot nematode. These findings suggested that fosthiazate is an effective control agent. In the low-temperature exposure test, survival rates gradually declined between 5–10°C, sharply decreased at 0°C, and reached zero at –5°C. Although this species cannot survive freezing temperatures, it has the potential to overwinter in warm regions of Japan where soil temperatures around 15–20 cm below ground do not fall below 0°C.

Poster 46

Screening Potato Cultivars and Breeding Clones for *H1*-Mediated Resistance to *Globodera rostochiensis* in China

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Potato cyst nematodes (PCN), particularly *Globodera rostochiensis*, are soilborne quarantine pests that threaten potato production and seed potato trade. In southwestern China, occurrences of *G. rostochiensis* have been reported, yet the resistance of local potato cultivars and breeding clones remains poorly characterized. In this study, 50 major potato cultivars and 132 breeding clones from southwestern and northern China were evaluated for resistance to *G. rostochiensis* using H1-linked molecular markers (57R and TG689) and greenhouse bioassays. Thirteen cultivars and 35 breeding clones were found to carry the *H1* gene, of which seven cultivars and 13 clones exhibited high resistance, with no cysts detected in the rhizosphere soil. Representative highly resistant cultivars included Yunshu 505, Xuanshu 5, Huishu 15, Huishu 19, Yunshu 202, Yunshu 304, and Zhongshu 20. This study identified resistant cultivars for immediate integration into China's comprehensive potato cyst nematode management strategy while also facilitating the screening of breeding clones for resistance to *G. rostochiensis*.

Poster 47

Suppressive activity of food wastes on the root knot nematode *Meloidogyne incognita*

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Wasted bread (WB) and spent coffee grounds (SCG), raw or bioprocessed with enzymatic treatments and fermentation with the lactic acid bacteria *Lactiplantibacillus plantarum* H64 and the fungus *Trichoderma asperellum* (H64TAWB and TASCG respectively), have been evaluated for their suppressiveness to *Meloidogyne incognita* on potato tomatoes. A natural soil was amended with the test materials at doses corresponding to 3,000 kg ha⁻¹ of organic carbon. The amended soil was placed in 100 ml pots, 18 replicates for each treatment, considering untreated soil, either infested or uninfested, as controls. After two weeks, tomato seedlings were transplanted and inoculated with 350 *M. incognita* J2. The experiments were conducted in a growth chamber at 25°C. After 7 and 14 days, galls and corresponding portions of uninfected roots were collected from six plants for each treatment for transcriptomic analysis. At the end of the nematode life cycle, a decrease of infestation was observed in terms of number of galls, egg masses and nematodes, particularly with bioprocessed amendments. In particular, the treatments with WB and H64TAWB induced an approximately 80% decrease in number of eggs/g roots as an effect of

root biomass stimulation, while the treatments with SCG and TASCG were found to be phytotoxic.

Poster 48

Modulation of volatile organic compound production in *Purpureocillium lilacinum* by chitosan and its impact on the plant–nematode interaction

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Volatile organic compounds (VOCs) emitted by nematophagous fungi play an important role in the orientation of plant-parasitic nematodes due to their high volatility and diffusion in soil environments. In this study, the temporal dynamics of VOCs production were evaluated in two strains of *Purpureocillium lilacinum* grown in liquid medium (Czapek Dox) and on a solid substrate (rice) supplemented with chitosan (1 mg/mL). In liquid medium, oxime-, methoxy-phenyl- was the predominant compound in all treatments (RP%= 52.59). Chitosan stimulated the production of additional VOCs (SR14: 6; SR38: 7; SR14–SR38: 7), and increased the relative percentage of 1-octen-3-ol and 3-octanone. On rice, VOCs production was higher during the exponential growth phase (10 d), with profiles varying according to the presence of chitosan.

Additionally, the VOCs profiles of *P. lilacinum* applied with chitosan was analyzed in a bioassay (Magenta box) using tomato seedlings inoculated with *Meloidogyne incognita*. Chitosan altered the VOCs profiles in all treatments, with a significant increase in volatilome complexity observed in the combined strain treatment (SR14+SR38). This effect was associated with the inhibition of nematode-related VOCs. Overall, chitosan modulates VOCs production by *P. lilacinum* across different systems, increasing volatilome complexity and potentially interfering with phytoparasitic nematode orientation mechanisms.

Poster 49

Preliminary results of the effects of cover crop root extracts on the plant parasitic *Meloidogyne incognita* and the bacteriophagous *Panagrellus redivivus* nematodes

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Root-knot nematodes (*Meloidogyne* spp.) cause significant damage to many crops and their control remains a challenging task even today. Nowadays, the use of cover crops is one of the key elements of regenerative agriculture. Cover crops can reduce the damage and population of *Meloidogyne*, however, less attention has been paid to their effects and mode of actions on non-target beneficial nematodes. We examined the effects of fresh and dry root extracts derived from four cover crops (rye, radish, red clover, and hairy vetch) on the plant-parasitic (*M. incognita*) and the bacteriophagous nematode (*P. redivivus*) in area choice, and mortality tests.

Dry extract of hairy vetch from 1%, dry extract of radish from 0.5%, and 5% extract of rye and red clover showed mortality rates of over 90% in the case of *M. incognita*. All root extracts had repellent effect on *M. incognita*. In the case of *P. redivivus*, only a 5% root extract of the plants had a lethal effect, but it was never as strong as that observed for *M. incognita*. A 5% radish root extract was the only one to show significant toxicity. Both dry and fresh extracts of each plant had an attractive effect on *P. redivivus*.

Poster 50

Legume species with potential use as cover crops for root-knot nematode management in greenhouse tomato cultivation

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The use of legume cover crops in agroecosystems has gained increasing relevance due to their role in increasing soil health, and selected legume-rhizobia associations have been shown to reduce galling by root-knot nematodes (*Meloidogyne* spp.). As part of the RHIPL project (<https://doi.org/10.54499/2023.17906.ICDT>), we propose the integration of legume cover crops in tomato cultivation in RKN-infested greenhouses could reduce nematode pressure on the main crop. This study aimed to identify legume species with potential as cover crops in greenhouse tomato cultivation, aimed to provide control of root-knot nematodes (*Meloidogyne* spp.). A survey of indigenous legume species was conducted in commercial tomato greenhouses, and their roots were analysed for the presence of rhizobial

nodules and nematode-induced galls. Then, a stepwise review of ca. 50 commercially available legume species was carried out, documenting their susceptibility to *Meloidogyne* spp. and other diseases, their ability to nodulate with a range of rhizobia, and their compatibility with the agronomic conditions of greenhouse cultivation. A shortlist of promising legume species was produced, including species from the genera *Medicago* and *Vicia*. Results on preliminary testing in pot trials will be presented and discussed.

Poster 51

The IPM-POPILLIA *Vademecum*: Entomopathogenic Nematodes for the Sustainable Control of *Popillia japonica*

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Popillia japonica is a major invasive pest threatening European agriculture. Within the Horizon 2020 project IPM-POPILLIA, a comprehensive *Vademecum* was developed to support national plant protection services and growers the implementation of integrated pest management (IPM) strategies against *P. japonica*. This guide provides an overview of surveillance tools, adult control techniques, larval management options, and an optimized timeline of interventions for field applications.

One of the key strategies described in the *Vademecum* is the biological control of soil-dwelling larvae using autochthonous strains of the entomopathogenic nematode *Heterorhabditis bacteriophora*. Field trials demonstrated that these native isolates achieve high larval mortality and good persistence in treated soils, making them particularly suitable for both preventive and curative applications. Moreover, no negative effects on non-target soil fauna were observed.

Nematode treatments are integrated with innovative monitoring methods, such as AI-based traps, and complementary control methods, including attract-and-kill systems using long-lasting insecticide-treated nets, targeted acetamiprid applications on host plants, and the use of kaolin clay as a repellent. The *Vademecum* defines the optimal timing and combination of these tools to counteract the population of this pest. This integrated and biologically based approach provides a sustainable framework for the long-term management of *P. japonica* in Europe.

Poster 52

Identification of Conserved Anthelmintic Targets in Nematodes Using an Orthology-Based Pipeline

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Parasitic nematodes impose significant burdens on human health and agriculture; however, the development of anthelmintics is hindered by the limited number of validated drug targets. Previous comparative genomics and single-species screens characterized nematode genomic diversity but failed to integrate cross-species gene conservation with druggability criteria to identify drug targets effective across multiple nematode species. Here, we present a computational pipeline that accounts for paralogous gene redundancy and combines comparative genomics, phylogenetic coverage analysis, and domain-level druggability assessment to prioritize candidate drug targets in parasitic nematodes. Applied to genome-scale orthogroup inference across 90 helminth genomes, this approach identifies gene families enriched for essential biological processes in nematodes, including proteolysis and signaling pathways. By distinguishing stable core gene functions from lineage-specific expansions, our method emphasizes gene families present at low copy number, reducing redundancy among paralogous genes. We further support the prioritization of candidate drug target gene families through protein network analysis, which reveals that these families form network communities with major hubs independently confirmed as essential by RNAi and mutant studies. We are currently conducting CRISPR knockout experiments on selected candidates to verify their essentiality. Collectively, these findings establish an evolution-informed strategy for discovering anthelmintic targets across phylogenetically diverse nematode species.

Poster 53

Development of essential oil-based smart Nematicidal formulates by means of plasma processing

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The treatment of the essential oils (EOs) with plasma is a mature and environmentally sustainable technology for the production of biocidal formulations. In this study, EOs from *Allium sativum*, *Cinnamomum zeylanicum* and *Ruta graveolens* previously *in vitro* proven for their toxicity to the infective stages of the root-knot nematode *Meloidogyne incognita*, were encapsulated into composite films deposited on zeolites by means of the Plasma Deposition (AA-APPD) technique for an *in vivo* evaluation of their nematicidal activity. Infested soil was amended with zeolites loaded with the three EOs both uncoated and coated with a 100 or 200 nm film, and distributed into 1 L pots, which were maintained for two weeks in a greenhouse at 26 °C, providing five replicates for each treatment. Subsequently, a one-month-old tomato seedling was transplanted into each pot and allowed to grow for 50 days. The EO-loaded zeolites coated with barrier films showed a consistently higher nematicidal activity compared to both the uncoated EO-loaded zeolites and the pure EOs, as indicating that coating acted as a barrier improving the stability of the volatile compounds and

allowing their gradual diffusion into the soil and a consequent prolonged nematode suppression.

Poster 54

Assessment of cereal cultivars susceptibility to *Heterodera avenae*

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Cereals are crops grown worldwide, and they are an important component of food security. However, the production is threatened by yield loss due to infection of cereal cyst nematodes (CCNs), especially *Heterodera avenae*. Cultivation of resistant cultivars is the only sustainable, cost-effective, and environmentally safe method to reduce populations of CCNs in the soil and counteract yield losses. Current Swedish marketed oat and spring wheat cultivars lack resistance to *H. avenae* with one exception, a resistant fodder oat cultivar, cv. Nemesis. Generally, there is a lack of knowledge regarding resistance in the modern genetic material. The aim of this study was to investigate susceptibility of several cereal crops towards *H. avenae*. Twenty cultivars of winter wheat, winter rye, spring wheat, spring barley and oats were tested in an outdoor experiment (September 2024-August 2025). Seedlings were grown in naturally infested soil with *H. avenae* in PVC tubes. Plants were harvested at the end of the experiment, roots were washed, cysts extracted from 100 gram soil/tube, and the number of cysts calculated in soil and on roots. Grain and straw weights were measured. We will present the results of nematode densities and yield of each cultivar.

Poster 55

Impact of organic compounds from *Serendipita* spp. on sugar beet growth and defence responses against cyst nematode *Heterodera schachtii*.

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Several EU strategies aim to reduce pesticide use, increasing the need for effective biological alternatives in agriculture. At the same time, climate change is expected to intensify environmental stress through more frequent extreme weather events. *Serendipita indica* has shown potential to promote plant growth under unfavourable conditions and suppress pathogens in various crops. Therefore, *S. indica* and *S. williamsii*, the latter native to temperate climates, were evaluated for their effects on plant growth and *Heterodera schachtii* infestation in sugar beet. Glasshouse experiments were conducted using preparation of dead fungal mycelium, including additional control fungi with comparable or

contrasting biological properties. All fungal treatments significantly reduced nematode infestation, whereas plant growth responses varied markedly among treatments. Plants treated with *Aspergillus nidulans* and *Saccharomyces cerevisiae* produced significantly higher biomass than other variants but also exhibited pronounced drought symptoms despite equal irrigation. To assess potential defence-related effects, the expression of defence-associated genes was analysed by qPCR. Several fungi significantly altered the expression of *PR1*, *PR2*, and *RB004820*, indicating interactions with plant defence pathways. Overall, all fungal treatments influenced plant growth and nematode infection; however, some variants are unsuitable for agricultural use due to the unexpected induction of water stress under non-stress conditions.

Poster 56

Contrasting outcomes of arbuscular mycorrhizal fungi in *Solanum*: genetic drivers of resistance and susceptibility to plant-parasitic nematodes

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Plant-parasitic nematodes threaten crop establishment and productivity across the globe thus, sustainable approaches are needed to mitigate their impact. Arbuscular mycorrhizal fungi (AMF) are plant-mutualistic fungi that can impact plant resistance to nematodes, however their effects can be variable. Here, we found that AMF colonisation of tomato increases resistance to both *Meloidogyne incognita* and *Globodera pallida*, whereas colonisation of potato by the same fungi increased host susceptibility to both nematodes. Given the contrasting results observed from two crops from within the same genus we conducted RNA seq to identify potential resistance/susceptibility genes that are differentially regulated in tomato and potato during AMF colonisation. We assessed the effects of knockout lines of selected genes of interest to understand the mechanisms underpinning mycorrhizal-induced resistance (MIR) or susceptibility (MIS). Additionally, we assessed a range of different *Solanum* species to determine the incidence of MIR or MIS throughout the genus and where the shift may have occurred. Forward-looking, our data will inform predictions of MIR or MIS based on the presence of differing mechanisms within the host, directing breeding for induced resistance rather than induced susceptibility in wider crops.

Poster 57

The resistance response of the *Mi-1.2* gene against *Meloidogyne luci* isolates at high temperatures

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The *Mi-1.2* gene in tomato confers resistance against several root-knot nematode species including *Meloidogyne luci*. However, temperature is one of the main factors affecting the resistance mediated by this gene. The study was conducted to screen the resistance responses of homozygous resistant (*MiMi*) cultivar Brownny and heterozygous resistant (*MiMi*) cultivar Seval for *Mi-1.2* gene against *M. luci* (2 avirulent and 1 virulent) and *M. incognita* (1 avirulent) isolates in high temperature (32°C). In the high-temperature treatment, the plants were kept at 32°C for 48 hours after nematode inoculation and then placed in a climate chamber at 24°C for 8 weeks. The reproduction (number of egg masses and eggs) of *M. incognita* and *M. luci* isolates on resistant cultivars significantly increased in the high temperature. In both temperatures, the reproduction index (RI=number of eggs in the resistant plant/number of eggs in the susceptible plant x 100) of *M. luci* isolates is lower on Brownny than on Seval. In contrast to Brownny, the resistance response of Seval against avirulent isolates of *M. incognita* and *M. luci* was lost (RI>10) in the high temperature. The cultivar Seval was more resistant to avirulent isolates of *M. luci* than *M. incognita* in high temperature.

Poster 58

‘Better late than never: increased infectivity of late hatching *Heterodera schachtii* is linked to physiological and gene expression differences’

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It is estimated that, of the 4100 plant-parasitic nematode species, there is at least one able to parasitise most major angiosperm clades. Among these, the cyst nematodes are of particular agricultural relevance, where the second stage juvenile (J2) hatches from the cyst in response to host-derived cues, locates the host root, and invades. While it is widely known that eggs from a given pool of cysts will hatch over a period of days, it is currently unclear whether and how these nematode hatching dynamics impact nematode morphology, physiology, gene expression, and infectivity.

To isolate hatching date from time since hatching, we analysed *Heterodera schachtii* J2s emerging on days 4, “early”, and day 9, “late”, each at one week post hatching. We found that hatching time significantly influences nematode infectivity. Late hatchers show significantly higher rates of root penetration and feeding site establishment than early hatchers. This is correlated with, and perhaps driven by, faster internal fat reserve depletion

and stronger upregulation of parasitism-associated genes in later hatching compared to early hatching. Taken together, these data show that J2s which hatch later tend to be more infective than those which hatch earlier at the same absolute age.

Poster 59

Characterisation of Long Intergenic Non-Coding RNA in the parasitism of *Bursaphelenchus xylophilus*.

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The migratory endoparasitic nematode, *Bursaphelenchus xylophilus* (pinewood nematode, PWN), is an EU quarantine A2-listed organism that causes major conifer forestry losses worldwide. Long non-coding RNAs (lncRNA) (>200 bp) can be involved in nematode virulence regulation, development and pathogenesis, due to their function as key regulators of different transcriptional processes. To characterise PWN lncRNAs expression and understand their potential function in parasitism, we performed RNA-seq analysis of the PWN-lncRNA libraries in interaction with the susceptible host extract, *Pinus pinaster*. *In silico* analysis identified 925 novel lncRNAs, from which, 300 were differentially expressed during the host interaction. From those, 35 are long intergenic non-coding RNA (lincRNA), a class of ncRNAs, which were significantly upregulated ($\log_2FC > 2$; $p < 0.0001$) during host interaction. Co-expression analysis of the differential up-regulated lincRNAs predicted associations targeting: i) validated gland cell-expressed genes related to parasitism, such as Saposin B-type; ii) *Bursaphelenchus*-specific genes (unknown protein domain); iii) homeobox (involved in gene regulation) and iv) elongation of fatty acids (involved in metabolic pathways). Future studies combining functional characterisation will elucidate the roles of lincRNAs in the biology and pathogenicity of PWN, providing new candidates for nematode control strategies.

Poster 60

Effector Discovery in *Meloidogyne chitwoodi* Using Gland-Specific Transcriptomics

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The Columbia root-knot nematode (CRKN), *Meloidogyne chitwoodi*, parasitizes potato roots and tubers, resulting in significant economic losses in potato production. CRKN parasitism depends in part on secreted effector proteins that modify host cellular functions and suppress host defenses. Understanding the identity and function of these effectors is critical for developing new, sustainable approaches to CRKN management. Because nematode effectors are primarily produced in the esophageal glands, we generated the first gland-specific transcriptome for CRKN. This approach revealed a set of proteins with gland-specific expression. Gland localization of selected candidates was validated by in situ hybridization. Transcript abundance profiling across developmental stages showed that many of these genes are highly expressed in pre-parasitic second-stage juveniles (J2s), consistent with a role during the initiation of host infection. Functional analysis further demonstrated that transgenic plants ectopically expressing a candidate effector, *McGland26*, were more susceptible to CRKN infection, supporting its contribution to parasitism. Interestingly, *McGland26* expression did not significantly alter host immune responses, indicating that it likely promotes infection through mechanisms other than defense suppression. Overall, our findings demonstrate that integrating gland-specific transcriptomics with high-quality genome resources and stringent selection criteria improves effector identification and advances our understanding of CRKN–potato interactions.

Poster 61

Decoding the Mechanisms by which Nematodes Perceive and Locate Host Roots

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Plant parasitic nematodes are obligate parasites that are only able to survive and reproduce following successful infection of host species. Thus, once the juveniles hatch, they need to efficiently locate and infect roots before their residual lipid reserves are depleted. Numerous host root-derived compounds have been demonstrated to elicit chemotaxis responses, however, there is little data describing the receptors that recognise these host cues and the downstream signalling pathways that facilitate the precise host-finding and root invasion behaviours of nematodes.

This work aims to elucidate key components involved in recognising host-derived signals and understand how they integrate into the nematode's neural network. Genes of interest were identified from transcriptomic analysis of three diverse plant-parasitic nematode species: *Globodera pallida*, *Meloidogyne incognita* and *Radopholus similis* in response to root exudates from economically significant crop species. Both conserved and species-specific responses are being investigated by RNAi knockdown and behavioural assays. Localisation of

expression in sensory neurons and integration into neural networks are being explored via *in situ* hybridisation assays and immunolocalisation is being used to determine neurotransmitters with potential involvement in the responses. Elucidating the key signalling pathways behind host-finding in plant-parasitic nematodes offers the potential for identifying novel targets for control.

Poster 62

“What’s on the Menu?” Metabolic Dynamics of Root-Knot Nematode Feeding Sites Across Host Plants

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Root-knot nematodes are economically important pests causing huge yield losses across agricultural production systems, significantly impacting crop productivity and farmers' income. These nematodes induce and maintain highly metabolically active feeding sites in the roots of the host plants, which serve as their sole source of nutrients throughout their life cycle. This sustained host-parasite interaction is governed by sophisticated molecular and physiological dynamics. The parasite depends on the host for essential nutrients and energy required for its survival, growth, and reproduction. In response, the host activates immune responses and metabolic pathways to combat the infection. This metabolic complexity has profound implications to the severity of infection and disease symptoms. However, the specific dietary requirements of nematodes remain largely unexplored. The study aims to fill this knowledge gap by looking into the metabolite profiles of infected host tissues in different host-pathogen systems, including tomato, cucumber, and beans. We will also profile the metabolites of the nematode temporally, covering all major parasitic stages. Our goal is to identify metabolites with consistent changes across various host plants. This study will pave the way for a comprehensive understanding of the metabolic dynamics in host-parasite interactions, potentially leading to more effective nematode management and control strategies.

Poster 63

Parasitic Nematode Responses to Root-Emitted VOCs of *Brassica nigra*

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Parasitic nematodes play an important role in pest regulation and contribute to sustainable agricultural systems. This study investigated the behavioral responses of three nematode species—*Phasmarhabditis papillosa*, *Oscheius myriophilus*, and *Oscheius onirici*—to volatile organic compounds (VOCs) emitted by *Brassica nigra* roots under herbivore attack. Five VOCs were tested across varying concentrations and temperatures to evaluate their effects on nematode movement. Benzonitrile emerged as a strong attractant for *O. myriophilus* and *O. onirici*, whereas phenylethyl isothiocyanate exhibited toxic effects, suppressing nematode activity and causing mortality. Other compounds, including dimethyl sulfide and dimethyl disulfide, induced moderate attraction depending on species and temperature. Overall, these findings demonstrate that root-emitted VOCs significantly influence nematode behavior and may be leveraged to enhance biocontrol strategies as environmentally sustainable alternatives to chemical pesticides.

Poster 64

The *Candida quercitrusa* strain Cq-C08 induces plant resistance to root-knot nematodes

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Root-knot nematodes (RKNs), belonging to the genus *Meloidogyne*, are plant-parasitic nematodes with a broad host range, causing substantial economic losses annually. The selection and utilization of novel biological control resources are crucial for managing RKNs diseases. This study isolated *Candida quercitrusa* Cq-C08 from rhizosphere soil, and a series of experiments confirmed that the fermentation broth had a lethal rate of 100% against *M. incognita* J2s within 12 hours and exhibited a significant repellent effect on the nematodes. In pot and plot tests, the strain Cq-C08 achieved a control effect over 50% against *M. incognita* and significantly promoted cucumber (*Cucumis sativus*, Zhongnong No.6, China) growth. Inoculation experiments confirmed that the Cq-C08 strain could activate key immune signaling pathways of salicylic acid (SA) and jasmonic acid (JA). Split-root tests showed significant induced resistance of cucumber to *M. incognita* by 32.3%. Comparative transcriptome analysis confirmed that strain Cq-C08 could regulate the host's basal immune response and oxidative burst response through SA, JA, and ethylene (ET) signaling pathways, and alter secondary metabolism, activating the synthesis of cucurbitacin and auxins, which promotes plant immune regulation and growth. These results prove that *C. quercitrusa* Cq-C08 has high control effects against *M. incognita* and the potential to be developed into a biological control product against root-knot nematodes.

Poster 65

Effect of substrate type on the development and reproduction of *Meloidogyne* spp. in tomato crop under controlled conditions

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Root-knot nematodes from the genus *Meloidogyne* are among the most important pest groups, causing economically significant yield losses in crops worldwide. Their damage potential is influenced by soil type and texture, which affect *Meloidogyne* hatching, movement, and root penetration. An experiment was conducted at NEVAL's experimental fields to compare the suitability of different substrate types for *Meloidogyne* development and reproduction in tomato pots under controlled conditions. In the trial, seven substrates were evaluated across different assessments periods: natural soil (sandy loam), commercial substrate, silica sand, coconut fibre, and mixtures of silica sand with coconut fibre, silica sand with commercial substrate, and natural soil with silica sand. Each treatment included eight plants (56 plants in total), previously inoculated with 300 eggs and second-stage (J2) juveniles of *Meloidogyne* spp. per 100 cm³ of soil. Plant damage caused by *Meloidogyne* infection was assessed using plant and root length, root galling (Zeck scale), root weight and the number of juveniles per 100 cm³ of soil. At the end of the trial, significant differences were observed among treatments, with tomato plants grown in natural soil (sandy loam) showing the most severe damage due to *Meloidogyne* infection, whereas those grown in commercial substrate showed lower damage.

Poster 66

***Globodera rostochiensis* overcomes *Solanum vernei* derived resistances via balancing selection**

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The potato cyst nematode *Globodera rostochiensis* reduces potato yield worldwide. Currently, agriculture relies on resistant cultivars as the primary approach for *G. rostochiensis* management. However, virulent *G. rostochiensis* populations were reported to overcome used resistances. The mechanisms underlying the emergence of virulence are currently unknown.

We found *G. rostochiensis* populations virulent on resistances derived from *S. vernei* via the VT(n)62.33.3 breeding line. Using genetic analysis, we determined that emerging virulence was caused by selection on existing genotypes. Initial analyses indicate that virulence on *S. vernei*-derived resistances is associated with a hyperdivergent genomic locus. This locus was

associated with virulence in diverse *G. rostochiensis* genotypes. Furthermore, the locus exhibited high variability between populations.

As of now, we cannot determine the exact cause of virulence. Although it is clear that virulence was selected or emerged from standing genetic variation, it is unclear whether virulence indeed has a single genomic origin. Currently, controlled selection experiments are underway to further pinpoint the genetic origin. The information presented here might ultimately lead to the development of diagnostic systems and calls for the deployment of novel resistance in commercial cultivars.

Poster 67

Cover cropping in a Vinho Verde vineyard increases soil health and grapevine yield

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In the Vinho Verde region of Northern Portugal, viticulture represents a valuable socioeconomic and cultural heritage but faces sustainability challenges. Cover cropping is proposed to restore soil ecological balance after progressive degradation due to intensification. In the scope of the Strengths4WineChain project (NORTE2030-FEDER-0178610), our objective was to evaluate the impact of cover cropping on soil biodiversity and functions, and relate these to grapevine production. A trial was conducted in a Vinho Verde vineyard to evaluate effects of six commercial seed mixtures (with distinct composition of perennials and annuals), a spontaneous vegetation control, and tilled soil (farmer practice). We analysed the nematode community as indicators of soil ecological quality, as well as vegetation cover, soil agroecological performance, and grapevine production. The perennial mixtures and spontaneous vegetation promoted a more mature and structured soil food web, with a greater abundance of higher trophic groups, and achieved the best agroecological quality. Inter-rows with higher structure footprint and good plant cover resulted in significant increases in grape yield and pruning weight, whereas tillage negatively affected soil health. Therefore, the adoption of diverse perennial cover crop mixtures or the maintenance of spontaneous vegetation cover were the most promising strategies for increased vineyard sustainability.

Poster 68

Extreme survival records in dry condition for *Ditylenchus dipsaci* in anhydrobiosis form

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The IMOTEP project (Infection in Microgravity of Plant-parasitic TELLuric Organisms Project) initiated by ANSES and INRAE aims to assess the risk of plant-parasitic nematodes for agriculture in space. In the framework of this project, we have tested the resistance to extreme temperatures of the nematode *Ditylenchus dipsaci*, a species known to be capable of anhydrobiosis. With dehydrated state and minimal metabolic activity, anhydrobiosis is likely the most efficient survival form in the animal kingdom. For this purpose, nematodes were exposed in dry conditions to eight temperatures ranging from -196°C to +120°C for three durations: 5, 15, and 45 minutes. Exposure to low temperatures had no effect on survival compared to controls. Conversely, high temperatures were lethal for nematodes after 45 minutes at 80°C. However, some individuals survived to an exposure of 5 minutes to an average temperature of 109°C, including 2 minutes at 120°C. To our knowledge, the survival of *D. dipsaci* at such high temperatures had not been observed until now and therefore constitutes a new record for this species. Our study thus suggests that *D. dipsaci* is a good candidate to test the resistance to space exposure, capacity previously reported in another thermophilic animal, the tardigrade *Milnesium tardigradum*.

Poster 69

Species and distribution of frog-parasitic nematodes, with a focus on the genus *Rhabdias*, in the Kinki region of central Japan

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Amphibian populations in Japan have been declining in recent years due to habitat loss caused by land development and forest abandonment. This study was performed to promote biodiversity conservation by clarifying the current poorly documented diversity and ecology of parasitic nematodes in Japan that impact their populations. Although 17 frog species have been recorded in Shiga Prefecture, information regarding frog-parasitic nematodes is limited. We investigated the species composition and distribution of these nematodes in the Kinki region of Central Japan. Five nematode species, belonging to four genera, were identified. One of these species, *Rhabdias* sp., was collected from faeces from a Japanese pond frog (*Pelophylax nigromaculatus*) in Kyoto Prefecture and examined in detail. To our knowledge, this is the first report of a *Rhabdias* species in Japan. Ecological observations have revealed that this *Rhabdias* species is ovoviviparous and produces one to five offspring within a maternal body. The larvae emerge from the mother within one day of hatching, indicating a highly distinctive reproductive strategy among frog-parasitic nematodes. This strategy may confer the adaptive advantage of rapid repetitive reproduction. Rearing experiments are currently underway to assess the influence of nematode infection on growth and development among adult frogs and larvae.

Poster 70

***Bursaphelenchus mucronatus* pathogenicity under climate change: A weak pathogen or an emerging threat?**

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Previous studies suggested that *Bursaphelenchus mucronatus* can be pathogenic in stressed pine trees. Projected climate change, with increasing temperatures and drought events, may alter host susceptibility and nematode reproduction within trees. In this work, *B. mucronatus* pathogenicity was evaluated in *Pinus pinaster* and *P. pinea* under different temperatures and water availability conditions. Two-to three-years-old seedlings were inoculated with 3,000 nematodes and exposed to two temperatures (25°C, 30°C) and two water regimes (water-stressed, watered). Wilting symptoms and soil moisture content were monitored for 40 days, and nematodes quantified per gram/dry wood at the end of assay. *Pinus pinea* remained asymptomatic with no nematode reproduction, suggesting a high level of resistance. In *P. pinaster*, at 25°C, no symptoms and no nematode reproduction were detected. At 30°C under watered conditions, seedlings remained asymptomatic but nematode reproduction was observed. At 30°C under water-stressed conditions, wilting symptoms and high nematode reproduction were detected. These results indicate that *B. mucronatus* act as a weak pathogen under non-stress conditions and can be a potential threat to pine forestry areas under climate change scenarios.

Poster 71

Characterization of a population of *Aphelenchoides* from rice in Iran

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The rice white tip nematode, *Aphelenchoides besseyi*, is one of the main pests on this culture and has been considered one of the emerging nematode species of significant phytosanitary and economic importance.

Recently, Subbotin et al. 2020 proposed a reclassification of *A. besseyi* into *Aphelenchoides besseyi* sensu stricto, *Aphelenchoides oryzae*, and *Aphelenchoides pseudobesseyi*. But most of the studies after the reclassification keep the old classification, even if an update of *A. besseyi* sensu lato, regarding to geographic distribution and host ranges, is needed to confirm the occurrence of cryptic species.

During a nematology survey in northern Iran, a population morphologically identical to *A. besseyi* was recovered. *Aphelenchoides besseyi* was already reported in rice fields in northern parts of Iran of the country, including Guilan province. Specimens of *A. besseyi* s. l. used in the present study were extracted from infected rice plants collected in Guilan. Nematodes were identified based on morphological characters, and molecular and phylogenetic analyses by using 18S rRNA, 28S rRNA genes, ITS and partial COI. Phylogenetic relationships were also inferred, and the clustering of the Iranian population will be discussed.

Poster 72

Nematode Diversity and soil properties in North Italian Vineyards

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In 2024-2025, a comprehensive survey was conducted in Northern Italy to investigate the occurrence of plant parasitic (PPNs) and free-living nematodes (FLN) associated with *Vitis vinifera* vineyards. This study aimed to evaluate the influence of soil structure, climate change and nematode community diversity across fourteen vineyards in Northern Italy. Forty-nine soil samples were collected, and nematode species and genera were identified. Approximately 4300 soil nematodes were recovered, and 18 nematode genera were identified at morphological level. Relationships between soil variables, nematode taxa, and biodiversity indices were evaluated across sites. Edaphic factor such as pH, EC, texture, and nutrient content were recorded, while ecological indices (trophic groups, Maturity, Enrichment, Structure and Plant Parasitic Indexes) were determined using the NINJA framework. Nematode assemblages differed among vineyards, with shifts in the relative dominance of bacterivore and plant parasitic nematodes across sites. Among PPNs, *Xiphinema*, *Helicotylenchus*, *Pratylenchus*, *Tylenchorhynchus*, *Tylenchus*, and *Mesocriconema* abundantly occurred, while *Meloidogyne* and *Zygotylenchus* at low abundance, but

Trichodorus, *Paratylenchus* and *Heterodera* sporadically occurred. The assemblage observed is consistent with the typical nematode community reported for vineyard soils. The correlation between soil parameters and nematofauna will be presented. Molecular analysis is in progress to characterize plant parasitic nematode communities.

Poster 73

Long-read DNA sequencing technology to map effects of cover-crops on nematode antagonists

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With the increased prohibition of nematicides, sustainable management methods of plant-parasitic nematodes is becoming increasingly important. In this study, we assessed the effects of cover crop treatments on nematode antagonists against a background of different nematode infestation levels by *Meloidogyne fallax*. Our results show that all cover crop treatments significantly affect the microbiome. We find that out of all cover crops, oil seed radish seems to have the largest effect on both nematode antagonists and the microbiome composition as a whole. Specifically, we find that *Pseudomonas fluorescens*, *Pseudomonas putida* and *Plectosphaerella plurivora* are significantly more abundant in the presence of oil seed radish. Our study indicates that the effects of cover crops on the soil microbiome are largely consistent across different experimental fields and types of nematode infestation, as evidenced by the similarity between our findings and those of a previous study conducted under comparable field conditions.

Poster 74

Identifying the molecular mechanisms behind the thermosensitivity of nematode resistance in tomato

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With climate change causing warmer summers and milder winters, tropical root-knot nematode species are emerging more frequently in northern Europe. Furthermore, the major tomato resistance (R) gene *Mi-1.2*, providing effective resistance to these tropical *Meloidogyne* species, stops working at soil temperatures above 28°C. This double problem

causes an urgent demand for heat-stable alternatives. However, the reason for *Mi-1.2* thermosensitivity remains unclear. Heat stress causes a complex response in plants, and there is a crosstalk between heat stress adaptation and immunity regulation. Since thermostable R-genes do exist, immunity is not downregulated altogether under high temperature conditions, but thermosensitivity is the result of a more intricate mechanism. *Mi-1.2*, encoding for a Nucleotide-binding Leucine-rich Repeat (NLR) receptor, is as such an ideal model to study the effects of elevated temperature on plant defence against nematodes. By comparing *Mi-1.2* with close homologs and other NLRs showing differences in thermostability, we were able to elucidate molecular signatures that may determine the thermostability of nematode R-genes. For functional testing and validation, we developed an in-planta assay to screen NLR thermostability in both an elicitor-dependent or independent manner. Using this structure-informed approach, we aim to reveal the potential thermosensitive steps in the NLR activation pathway.

Poster 75

Investigating the role of melatonin in tomato plants against root-knot nematode infection

Reyhaneh Kordi and Mohammad Reza Atighi

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Root-knot nematodes (RKN) are obligate plant parasites that can infect a broad range of mono- and dicotyledons. Among strategies to control plant-parasitic nematodes, plant defence elicitors represent a viable and environmentally friendly management approach. Melatonin is a signalling molecule that contributes to physiological processes, helping plants to cope with biotic and abiotic stresses. However, its role in plant defence against nematodes has not yet been investigated. The expression of melatonin biosynthesis genes in RKN-induced galls on tomato plants was investigated, and their expression profiles indicated their involvement in defence processes. Foliar application of 100 μ M melatonin to tomato plants significantly decreased the number of galls and nematodes. Biochemical assays showed that the activity of defence-related enzymes peaked two days after melatonin treatment. Concurrently, the expression of genes linked to the jasmonic acid (JA) pathway was significantly upregulated two days after melatonin treatment, indicating the contribution of the JA pathway in resistance induction. Moreover, mutants deficient in the JA pathway including *jai1-1* and *def1* failed to exhibit melatonin-mediated resistance. A functional study of the melatonin biosynthesis pathway showed that CRISPR/Cas9-mediated gene knockout of one of the key genes in the melatonin biosynthesis pathway, SNAT, conferred lower susceptibility to RKN infection.

Poster 76

Comparison of the parasitisation of *Thrips tabaci* by *Steinernema feltiae* and *S. carpocapsae* in clay mineral and liquid-core capsule formulations.

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Although entomopathogenic nematodes (EPNs) have been studied for thrips control, their practical use remains limited. A novel liquid-core formulation, patented in 2021, may improve handling and persistence in soil, but its performance relative to the standard clay mineral formulation remains unclear. This study compared parasitisation rates of *Steinernema feltiae* and *Steinernema carpocapsae* applied in both formulations at recommended concentrations. EPNs were applied to quartz sand in experimental cups, after which 10 *Thrips tabaci* pupae were introduced per cup. White-trap experiments were additionally used to assess EPN reproduction within and emergence from thrips pupae. No significant differences were observed between EPN species, formulations, or concentrations. At recommended application rates of 50–200 infective juveniles/cm², mean parasitisation reached only 10%. Although EPN reproduction within thrips pupae was confirmed, overall efficacy was low, likely due to limited habitat overlap between nematodes and thrips. These results indicate that EPNs alone are insufficient for effective thrips control. However, previous studies suggest that combining EPNs with other biological control agents, such as *Hypoaspis miles* or *Orius laevigatus*, can enhance control efficacy and broaden the pest spectrum.

FRIDAY 5 JUNE

Parallel Session 18

09:30 — 11:00 GMT+2

Lamoraalzaal

Parallel session 18: Soil microbe/nematode interactions (II)

Chair: Sigal Brown Miyana & Olivera Topalovic

9:30-9:48 hrs Sabine De Graauw

The exobiome: the composition of (advantageous) microbial communities on the cuticle of plant-parasitic nematodes

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A pathogen or pest often interacts with a broader network of organisms than exclusively with its host. During infection, pathogenic agents also interact with (other) microorganisms. We hypothesize that juveniles of plant-parasitic nematodes (PPN) carry bacterial and fungal propagules acquired during migration through soil. These juveniles may transfer such propagules to host plants, where they could influence plant infection. Such an exobiome needs to be studied to fully comprehend pathogenesis, persistence, transmission, and evolution of pathogenic agents, yet remains poorly understood.

We will discuss the composition of microbial propagules present on the surface of PPNs. So far, this topic has received little attention and has only been studied in soil suspensions and for few PPN species. Moreover, the exobiome of cyst nematodes has not yet been studied. Here, we present a novel experimental setup and methodology to isolate and characterize nematode exobiomes. Using this approach, bacterial and fungal propagules will be identified by sequencing full-length 16S rDNA for bacteria and the ITS1 and ITS2 regions for fungi, allowing identification to species level. Combined with high-throughput sequencing, this methodology will be used to compare exobiomes of several root-knot and cyst nematode species in natural soils.

9:48-10:06 hrs Benius Tukahirwa

Modulating soil microbiome with cover crops to suppress the root knot nematode *Meloidogyne chitwoodi* on potato

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Emerging root knot nematodes (RKN) are difficult to control and a major concern in potato production. Cover cropping can condition soil microbiomes and promote soil suppressiveness against these RKN. However, limited knowledge of cover crops which stimulate and enrich native beneficial soil microbiota to promote soil suppressiveness limits effective use of cover cropping to manage RKN in potato production. We conducted greenhouse trials with field soils collected from different agricultural fields to evaluate the potential of different cover crops to modulate RKN-suppressive soil microbiomes. Soil microbiomes conditioned by some cover crops significantly suppressed invasion and reproduction of the quarantine root knot nematode *Meloidogyne chitwoodi* on potato. In particular, microbiomes conditioned by crotalaria (*Crotalaria juncea*), phacelia (*Phacelia tanacetifolia*) and nasturtium (*Tropaeolum majus*) consistently suppressed *M. chitwoodi* invasion and reproduction across the field soils. Crotalaria modulated the most suppressive soil microbiome, reducing nematode root invasion and reproduction by up to 60% and 81%, respectively compared to non-conditioned fallow soil. Among glucosinolate (GLS)-rich plants tested, nasturtium containing glucotropaeolin as the main GLS conditioned the most suppressive microbiome. We will use 16S rRNA and ITS amplicon sequencing to analyze microbial communities and identify beneficial microbiota enriched by the cover crops. This study provides new insights on potential cover crops which can be used to modulate nematode-suppressive soil microbiomes. This could provide a sustainable alternative for management of the quarantine root knot nematode *M. chitwoodi* in potato production.

10:06-10:24 hrs Sulaiman Abdulsalam

Plant-Plant Interactions Shaped Microbiome-Mediated Suppression of Root-Knot Nematodes in Cowpea–Maize and Cover Crop Systems

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Abstract: Root-knot nematodes limit cowpea yields for smallholders. Sustainable alternatives to chemical nematicides are needed. This study tested whether rhizosphere microbiomes, shaped by plant interactions in cowpea–maize and cowpea–cover crop systems, can suppress nematode invasion and reproduction when transferred to new cowpea plants. In mesh-partitioned pots, cowpea rhizosphere microbiomes were

conditioned by pairing with maize or cover crops. Pairings with cowpea or bulk soil were controls. Following conditioning, microbiomes were extracted and used to inoculate sterile seedlings. Standardised assays with *Meloidogyne incognita* and *M. enterolobii* were then used to assess nematode invasion and reproduction. Compared to bulk soil microbiome, microbiome treatments significantly reduced juvenile penetration by up to 20%, egg counts by over 45%, and galling. Suppression was strongest in maize-, phacelia-, and crotalaria-conditioned microbiomes. Effects on plant biomass varied by treatment. Although overall microbial abundance was similar, suppressive treatments provided greater nematode protection, showing that microbiome composition, not density alone, drives suppression. Thus, plant-plant interactions can support suppressiveness of the cowpea rhizosphere microbiome against root-knot nematodes. The study supports microbiome strategies, integrated with intercropping and cover crops, for sustainable nematode management in cowpea systems.

10:24-10:42 hrs Ana García-Velázquez

From conventional to regenerative agriculture: unlocking soil's natural defence against plant-parasitic nematodes

García-Velázquez, A.¹, Archidona-Yuste, A.¹, Cantalapiedra-Navarrete, C.¹, Salazar-García, R.¹, Criado-Navarro, I.¹, Font, F.², Castillo, P.¹ and Palomares-Rius, J.E.¹

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Plant-parasitic nematodes represent a persistent agricultural challenge, with management efficacy often constrained by limited understanding of soil suppressiveness mechanisms. This study evaluated whether basal soil suppressiveness differed across management systems in Mediterranean woody crops by comparing regenerative groves, conventional groves, and adjacent natural vegetation as ecological references. Our objectives were to (i) assess differences in soil suppressiveness and (ii) identify biological and physicochemical factors associated with suppressiveness. Soil samples were subjected to two complementary *Meloidogyne incognita* bioassays: a) nematode reproduction on tomato plants; and b) egg-bait bioassay quantifying fungal parasitism. Parasitic fungi were isolated and molecularly identified. Microbial community composition and abundance, alongside physicochemical properties, were characterized. Regenerative management significantly enhanced suppressiveness compared to conventional systems. Basal soil suppressiveness operated through distinct microbial patterns: bacterial abundance correlated with reduced nematode reproduction, while fungal abundance promoted egg parasitism. Metabarcoding revealed distinct bacterial composition between regenerative and conventional systems, whereas fungal communities remained similar between agricultural managements. These results demonstrate that regenerative practices can restore soil suppressiveness by

promoting antagonistic microbial communities, supporting conservation biological control as sustainable approach in Mediterranean perennial crops.

10:42-11:00 hrs Carlos Gutiérrez Gutiérrez

VITISBIOTA: Exploring the interaction between the microbiome and nematode activity in vineyards infested by the virus vector nematode *Xiphinema index* and the root-knot nematodes (*Meloidogyne* spp.) in Portugal

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Portugal is a producer of wines of excellence and any factor compromising the sustainability of the vineyards is of great economic concern. Plant-parasitic nematodes (PPNs) are a notorious threat to grapevine health worldwide that affects yield production and crop

quality, being responsible for significant economic losses due to grapevine damage. In particular, the virus vector *Xiphinema index* and RKNs (*Meloidogyne* spp.) are primary plant pathogens present in Portuguese vineyards.

The progressive withdrawal of chemical nematicides due to their negative impact on environmental and human health highlights the urgent need for sustainable alternative control strategies. The grapevine rhizosphere and root endosphere contain diverse microbial communities with the capacity to suppress soilborne pathogens, and specific plant–microbe associations may contribute to natural PPN suppression.

The main goal of VITISBIOTA is to elucidate the structure and functions of the microbial community associated with the grapevine root system, including both the root endosphere and the rhizosphere soil, in vineyards infested by the virus vector nematode *X. index* and RKNs (*Meloidogyne* spp.), and its potential role in the life cycle of these plant-pathogens. Part of the originality of VITISBIOTA is to apply new integrative approaches for exploring the microbiome and its interaction with nematode activity, in order to design new bacteria-dependent biocontrol strategies.

Parallel Session 19

09:30 — 11:00 GMT+2

Abdijzaal

Parallel session 19: Management - Host Plants /Interactions

Chair: Wim Wesemael & Inga Zasada

9:30-9:48 hrs Zohaib Ahmad

Population dynamics and thermal requirements of *Meloidogyne* spp. on selected Brassicaceae cover crops.

Ahmad, Z; Expósito, A; Fullana, AM; Serrano, L; Sorribas, FJ; Giné, A.

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Brassicaceae crops can be used as a root-knot nematode control method through biofumigation and also as trap crop if the nematode does not reproduce on them when incorporated into the soil. The best candidate plant species would be those that are less conducive to nematode reproduction, whose growth is less affected by increasing nematode density at sowing (P_i), and in which nematodes require more stringent thermal requirements to reproduce. Then, pot experiments were conducted to determine the impact of P_i (0-16 J2/cm³) on final population densities, and plant ecophysiology and productivity of *Brassica carinata*, *Brassica juncea* and *Sinapis alba*. Thermal requirements of *M. incognita* (M_i) and *M. javanica* (M_j) from inoculation to female laying eggs (FLE) and life cycle completion (LCC) were also determined. All plant species were poor and tolerant hosts to root-knot nematodes due to low values of population dynamic parameters (a , M and E) and the negligible effect on plant ecophysiology and productivity at increasing P_i . Thermal requirements of M_i and M_j did not differ between plant species. Consequently, all these plant species could be used as cover crops to suppress nematode reproduction without the P_i , commonly found in field conditions, significantly affecting biomass production for biofumigation.

9:48-10:06 hrs Pella Brinkman

Host plant status of crops to *Paratrichodorus anemones*

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The increasing withdrawal of nematicides calls for other means to manage problems. Recently, *Paratrichodorus anemones* has been found a problem in the cultivation of lily and onion. Information on the host plant status of different cash and cover crops that are grown in rotation with lily and onion is scarce. However, this information is needed to design a clever crop rotation.

We performed a field experiment on a sandy soil with a known infestation of *P. anemones*. In the first year, we created a density range of the nematode. In the second year, we grew a range of cash crops and cover crops. In springtime and at the end of the growing season, all fields were sampled for nematodes, yielding initial and final population densities of *P. anemones*. Seinhorst population dynamics curves were fitted to the data to estimate maximum multiplication rate and maximum population density.

The crops showed differences in both maximum multiplication rate and in maximum population density. The combination of the values of both parameters can be used to estimate nematode densities at the end of a growing season. The collected information will be added to www.Best4Soil.eu, aiding farmers to make sound choices for their crop rotation.

10:06-10:24 hrs Johan Desaegeer

Summer Cover Crops for Nematode Management in Florida vegetables: A Five-Year Field Study

Desaegeer, J., Jacobs, D., Bui, H., and Carter, J.

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Root-knot nematodes (*Meloidogyne* spp.) are major constraints to vegetable production in Florida and one of the main reasons for the continued use of soil fumigants. A five-year field study was conducted to evaluate sunn hemp (*Crotalaria juncea*), sorghum-sudangrass (*Sorghum x drummondii*), cowpea (*Vigna unguiculata*) and sunflower (*Helianthus annuus*) as summer cover crops, both in monoculture and biculture, for their potential to suppress root-knot nematodes and improve subsequent tomato and squash production. Cover crops were grown for approximately 80 days and then mowed and incorporated into the soil. Shortly after cover crop incorporation, raised plastic-mulch vegetable beds with drip irrigation were formed, and tomatoes (*Solanum lycopersicum*) and squash (*Cucurbita pepo*) were planted. No fumigants or nematicides were applied during the entire study period. Cover crop growth varied by year depending on environmental conditions, with bicultures generally offering greater resilience and reliability in terms of biomass production. Sorghum sudangrass and sunn hemp reduced root-knot nematodes but increased lesion nematodes (*Pratylenchus*

spp.), while the opposite was noted for the weed fallow and sunflower cover crop. All cover crop treatments improved tomato yields compared to the weedy fallow control.

10:24-10:42 hrs Israel Ikoyi

Nematode Response to Microbial Inoculant Application and Sward Diversification in Grassland Soils

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Intensively-managed grasslands depend on high chemical inputs, negatively affecting soil biodiversity and long-term sustainability. Sward diversification and application of microbial inoculants are potential strategies to enhance soil health, nutrient cycling and reduction in fertilizer dependency. Here, we investigated the impact of microbial inoculants and sward composition on nematode faunal assemblage in grassland soils.

A field experiment was established comprising three main sward types: perennial ryegrass monoculture, grass clover mix, and multi-species sward comprising of six plants species. Microbial inoculants targeting nutrient solubilization were applied, alongside uninoculated controls. Soil samples were collected post-application to extract nematodes using the Oostenbrink elutriator. Nematodes were identified, assigned to trophic groups and nematode-based indices were calculated to assess soil food web conditions.

Results showed that sward diversification significantly influenced nematode community composition, with multi-species swards supporting higher abundances of omnivorous and predatory nematodes compared to monocultures, suggesting a more structured and stable food web. The application of microbial inoculants resulted in an increase in cp1 bacterivore, reflecting a localized enrichment effect and stimulated microbial turnover.

Our findings suggest that while microbial inoculants can transiently stimulate specific soil biological activity, sward diversification plays a more dominant role in establishing a complex and resilient soil food web.

Parallel session 20

09:30 — 11:00 GMT+2

Room 522

Parallel session 20: Plant-nematode ecology

Chair: Sara Sánchez Moreno & Mihail Kantor

9:30-9:48 hrs Renáta Petrikovszki

Microscale habitat exploration of *Gaillardia* blanket flower for free-living nematodes

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In the rhizosphere, research has so far focused primarily on the diversity of microorganisms. Free-living nematodes are a neglected group in this respect. Our study aimed to fill this gap. Blanket flower (*Gaillardia* spp.) was chosen as model plant, because it is getting to become invasive plant in Hungary. Therefore, its effect on soil organisms may be a hot spot in the future. At five sampling times in 2024 and 2025, five *Gaillardia* plants were removed with roots and root ball in Kiskunság National Park. Four microhabitats were separated: wall of the planting hole, bulk soil, rhizoplane soil, and root. Free-living nematodes were extracted using a modified Baermann funnel for one week. The number of individuals and their feeding groups (identification to genera level) were determined, and nematological indices were calculated. The structural and functional diversity of free-living nematodes generally differed significantly depending on microhabitats and sampling times.

9:48-10:06 hrs Addisie Belay Mulusew

Plant parasitic nematodes of ginger (*Zingiber officinale* Rosc.) in Southern Ethiopia

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Ginger is a widely cultivated and economically important spice in Ethiopia, but its productivity is hindered by plant parasitic nematodes (PPNs). However, information on PPNs associated with ginger cultivation in Ethiopia have been limited. To address this gap, a survey was conducted across eight districts in southern Ethiopia during the 2022 cropping season. In total, 330 soil and ginger rhizomes with roots samples were collected. Nematodes were characterized based on morphological characteristics and molecular analysis. Six PPN genera were identified: *Meloidogyne*, *Scutellonema*, *Helicotylenchus*, *Rotylenchulus*, *Crossonema* and *Mesocriconema*. *Meloidogyne* was the most dominant genus, occurring in 86% of fields with densities of 102–368 J2 per 100 ml of soil and a frequency of occurrence of 20–92%. It was also the only genus recovered from ginger rhizomes, with densities reaching up to 1158 J2 per 10 g rhizome with roots at 100% frequency of occurrence. Other genera (*Rotylenchulus*, *Scutellonema*, *Helicotylenchus*) with densities up to 72, 108, and 116 individuals per 100 ml soil respectively. Molecular analysis confirmed seven species of PPNs: *Meloidogyne incognita*, *Meloidogyne javanica*, *Scutellonema paralabiatum*, *Helicotylenchus dihystra*, *Helicotylenchus* sp., *Rotylenchulus borealis*, *Mesocriconema sphaerocephalum* and *Crossonema civellae*. Notably, *Rotylenchulus borealis* and *Scutellonema paralabiatum* are reported for the first time from ginger in Ethiopia. These findings provide a scientific basis for monitoring and managing PPNs effectively, thereby supporting the sustainable production of ginger in the region.

10:06-10:24 hrs Yohannes Moges Ferede

Diversity and Molecular Characterisation of Plant-Parasitic Nematodes Associated with Wheat (*Triticum aestivum* L.) in Ethiopia

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Ethiopia, with a rapidly growing population of approximately 135 million, faces increasing food-security challenges. Wheat (*Triticum aestivum* L.) is a strategic crop central to national self-sufficiency goals, yet its production is increasingly constrained by biotic factors, notably plant-parasitic nematodes (PPNs). At population densities exceeding 2,000–4,000 nematodes kg⁻¹ soil, yield losses caused by *Pratylenchus thornei* or *Heterodera* spp. can

reach 40–85%, as reported from major wheat-producing regions worldwide. Field surveys conducted in major Ethiopian wheat-growing areas in 2024 assessed the diversity, distribution, and molecular identity of wheat-associated PPNs. Community analysis revealed *Helicotylenchus* and *Rotylenchulus* as the most prevalent genera, followed by *Pratylenchus*. Molecular characterisation using the D2–D3 regions of 28S rDNA, ITS rDNA, and mitochondrial COI and/or Nad5 sequences confirmed the presence of *Pratylenchus thornei*, *Rotylenchulus parvus*, *Merlinius brevidens*, and *Meloidogyne javanica*. *Pratylenchus* populations were most abundant at Wudget and Adazer, with prominence values of 454 and 312, respectively, while *Rotylenchulus* showed a high prominence value of 1521 at Adazer. Possible virus-vector nematodes of the genera *Paratrichodorus* and *Longidorus* were also detected. Ongoing resistance screening of 50 wheat germplasms will support a genome-wide association study, while future studies will examine population dynamics and damage thresholds to guide management applications.

10:24-10:42 hrs April Lyn Leonar

Context-dependent responses of nematode food webs in oak plant-soil feedbacks

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Soil biota is intimately connected to plant health and adaptation under climate change by enhancing nutrient and water availability. While most plant-soil feedback studies emphasize microbial communities as key drivers, the integration of higher trophic levels remains less explored. In particular, nematodes represent a wide range of trophic groups in the soil community, including plant parasites, bacterial and fungal feeders, predators and omnivores, providing an integrative indicator of both direct and indirect belowground influences on tree health.

This study examines how soil biota influence oak growth under drought stress and their potential to regulate belowground herbivores such as root-lesion and root-knot nematodes. Using *Quercus robur*, a foundation tree species of European forests, we manipulated soil biotic complexity under greenhouse conditions and inoculated plant-parasitic nematodes to assess ecosystem functioning. Preliminary analyses suggest that while tree biomass showed no significant treatment effects, drought stress amplified functional differences in nematode diversity between sterilized soils and soil biota treatments. These patterns were strongly sitespecific including contrasting microbial activity responses highlighting context-dependent community assembly. These initial findings suggest interactions between soil

biota complexity, environmental stress, and local edaphic conditions that warrant further investigation.

10:42-11:00 hrs Anne Sophie Van Bruggen

***Meloidogyne enterolobii* outbreaks in potted ornamental plants in the Netherlands; measures and action plan.**

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The tropical root-knot nematode *Meloidogyne enterolobii* is an European Union (EU) quarantine organism since April 2022, affecting several important agricultural crops, including tomato, pepper, cucumber and potato. The nematode is polyphagous and has a high damage potential due to its ability to overcome resistance genes against other similar tropical *Meloidogyne* species.

M. enterolobii has been intercepted many times in the EU on various plant species, as *Ficus microcarpa*, *Zelkova*, *Sageretia*, and *Gardenia* all originating from China, *Syngonium*, *Liriope* and *Portulacaria* from other countries. In 2023 *M. enterolobii* was found in the Netherlands in several greenhouses mostly in *Ficus microcarpa* originating from China. Eradication was confirmed by the end of 2023.

In July 2025 *M. enterolobii* was detected again, this time in ornamental *Chrysalidocarpus lutescens* originating from El Salvador. Remarkably, no root-knot symptoms on infested plants were observed. Import inspections for *C. lutescens* from all origins were intensified.

Measures included destruction of all infested lots and plants within the same watering system, as well as cleaning and disinfection of the production site. These measures have greatly impacted affected companies and show the importance of phytosanitary sound production systems in the country of origin to prevent import of infested plant material.

Parallel Session 21

11:20 — 12:32 GMT+2

Lamoraalzaal

Parallel session 21: Plant resistance to nematodes (II)

Chair: Shahid Siddique & Juan Emilio Palomares-Rius

11:20-11:38 hrs Christopher Tom

Long-term genetic analysis of resistance to *Pratylenchus* spp. and *Meloidogyne* spp. in sugarcane germplasm

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Parasitic nematodes in sugarcane cause significant yield losses, costing the Australian sugar industry \$82million annually. Currently, there are no known commercial varieties resistant to *Pratylenchus* spp. or *Meloidogyne* spp. Management options are limited, as nematode populations can rebound within 10-12 months after break crops or nematicide application.

This study analyses a long-term phenotypic dataset generated by Sugar Research Australia's (SRA) Variety Development Program. The dataset includes resistance scores for 1,545 lines screened for root-lesion nematode since 2011, and 1,169 lines screened for root-knot nematode since 2012, with all data collected from glasshouse conditions. Resistance data will be analyzed using linear mixed models with factor analytic variance structures, within a multi-environment (MET) framework, enabling assessment of varietal performance and stability across years. The outputs from the MET will be used in a selection index, to help simplify varietal decision making.

This project will identify nematode resistance within existing germplasm and highlight elite cultivars for use in breeding programs. Additionally, detecting commercial cultivars with resistance to *Pratylenchus* spp. or *Meloidogyne* spp. would facilitate better varietal selection for nematode-affected paddocks.

11:38-11:56 hrs Jan Henrik Schmidt

Resistance of open-pollinated cucurbit rootstocks to *Meloidogyne* spp. for organic cucumber production

Schmidt, J.H., Brumlop, S., Nagel, C., Arti, A., Bacanovic-Sisic, J.

Julius Kühn Institute

Organic growers in Germany prefer using cucumbers grafted on cucurbit rootstocks due to higher expected yields and stronger resistance root-knot nematodes (RKN). Some organic growers' organisations recommend the use of open-pollinated varieties and rootstocks, which are not available in Germany (only hybrids). We aimed to detect homozygous rootstock lines from Cucurbitaceae with strong resistance/tolerance to RKNs. In four experiments, 3-5 cucumber varieties, and up to 20 cucurbit lines of *Cucurbita ficifolia* (F₃) and *C. moschata* (F₅₋₆) were inoculated with *M. hapla* and *M. incognita* and their reproduction potential assessed. In a fifth experiment, 3 common varieties of cucumber, zucchini, melon, and cucurbit were tested for their resistance to *M. chitwoodi*. Cucumber varieties showed diverging resistance response towards *M. hapla* while all cucurbits were resistant towards this nematode. In contrast, all genotypes were susceptible towards *M. incognita*. Cucumber and zucchini varieties were susceptible to *M. chitwoodi*, while the cucurbit variety "Butternut Waltham" and the melon varieties "Blacktrail" and "Sugar Baby" did not reproduce this nematode. We showed that Cucurbitaceae rootstocks are useful for cucumber production in *M. hapla* infested soils. Although, *M. hapla* is currently the dominant RKN in Germany, more efforts to find *M. incognita* resistant cucurbit germplasm are needed.

11:56-12:14 hrs Daan Langendoen

Poor Hatching: an alternative resistance strategy against Potato Cyst Nematodes?

Daan Langendoen^{1,2}, Kelly Wieldraaijer¹, Atharv Ambekar³, Hilde Room¹, Anna Winiarczyk¹, Casper van Schaik², Martijn Zwinderman¹, Mark Sterken¹, Aska Goverse¹

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Potato cyst nematodes (PCN), *Globodera pallida* and *G. rostochiensis*, are among the most damaging pests in potato cultivation. These biotrophic, sedentary endoparasites synchronize their life cycle with that of their host, remaining dormant in soil as cysts until exposed to hatching factors such as Solanoeclipin A from potato root exudates. As the durability of resistance genes becomes increasingly debated, alternative strategies for nematode management should be explored. Traditionally, trap crops that stimulate hatching have been used to reduce PCN populations by inducing juvenile emergence and subsequent destruction of the host before nematode reproduction. However, we hypothesize that reduced hatching may also confer resistance by limiting nematode establishment. To investigate this, hatching assays and SolA quantification were conducted on root exudates from 20 potato cultivars to assess variation in hatching potential. Four

cultivars differing in resistance to *G. rostochiensis* and hatching capacity were selected for a pot experiment using three inoculum types: cysts, eggs, and second-stage juveniles (J2). Nematode propagation was evaluated through Pf/Pi ratios, cyst counts, and cyst contents. Results demonstrate that poor hatching cultivars exhibit significantly enhanced resistance. Specifically, PCN propagation (Pf/Pi) was 37% lower when inoculated with eggs compared to J2 in poor hatching potato cultivars, whereas no significant differences were observed in good hatching potato cultivars. Additionally, poor hatching cultivars showed increased cyst counts when inoculated with J2 and reduced cyst content when inoculated with cysts. These findings support the hypothesis that reduced hatching can serve as an alternative resistance mechanism against PCN. Future research will focus on bulked segregant analysis of a segregating population to identify genetic loci associated with hatching suppression. Further hatching assays on cysts propagated on poor hatching cultivars will assess the durability and heritability of this resistance trait.

Parallel Session 22

11:20 — 12:32 GMT+2

Abdijzaal

Parallel session 22: Smart technologies (II)

Chair: Andre Bertran

11:20-11:38 hrs Leidy Rusinque

Recombinase polymerase amplification-based: rapid and sensitive detection of the rice root-knot nematode *Meloidogyne graminicola* and screening of *M. oryzae*

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Meloidogyne graminicola (*Mg*), also known as the rice root-knot nematode (RRKN), is a devastating pest in rice production, leading to significant yield losses in affected regions. The identification of *Mg* is challenging and typically relies on the observation of hook-like galls on rice roots. However, once rice is infected and shows these symptoms, it becomes difficult to successfully reduce the population. Therefore, rapid and accurate detection is critical for *Mg* management, but while conventional methods are laborious and depend on specific developmental stages, modern molecular tools though more sensitive and specific still demand time and specialized equipment, limiting routine diagnostics. In this study, a Recombinase Polymerase Amplification (RPA) assay, was developed for the rapid and accurate detection of *Mg* targeting a Sequence Characterised Amplified Region (SCAR). This optimized RPA assay -TwistAmp Basic and TwistAmp exo (TwistDx, Cambridge, UK) - successfully screened *M. oryzae* and identified *Mg* directly from crude extracts of second-stage juveniles (J2), eliminating the need for complex DNA extraction steps. Using a dilution series of crude nematode extracts combined with real-time fluorescent detection, this RPA assay achieved an accurate result within eight minutes, successfully identifying a single

juvenile (J2) of *Mg* in mixed populations containing non-target species at ratios as low as 1:9. Additionally, *M. oryzae* amplified with a significant delay (14 minutes) and remained below the baseline (50 dRn), allowing a clear distinction from *Mg* and serving as initial screening of this species. This ultra-fast, sensitive, and user-friendly method presents a game-changing tool for early and on-site detection of *Mg*, paving the way for more effective nematode management strategies in rice cultivation.

11:38-11:56 hrs Peter Den Hartog

Cyst Monitor™: Automated Potato Cyst Nematode Quantification and Identification

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A potato infestation by potato cyst nematodes (PCN) is identified when PCN cysts containing viable eggs and/or juveniles are found at a sampling location. Diagnosis methods widely used in commercial labs are labour-intensive, costly and based on estimates derived from subsamples. The Cyst Monitor is a new development to automate and accelerate PCN analyses through the combination of light-microscopy, advanced robotics and artificial intelligence. Cysts are first extracted, optionally counted and imaged. Then the cysts are crushed and the juveniles and eggs are suspended in a liquid. This suspension can then be completely imaged and analysed without the need to subsample or extrapolate. The goal for the Cyst Monitor is to enable PCN diagnosis through 1) imaging and counting all individuals in a cyst nematode suspension; 2) identifying PCN eggs and stage II juveniles in mixtures possibly containing eggs and larvae of other cyst nematode species; and 3) estimating the viability of PCN juveniles and eggs. The automation setup enables continuous testing for up to 540 samples without human input. Cyst Monitor will provide a rapid, reliable, affordable and scalable approach to worldwide PCN monitoring and control. We will present the status and latest results of the developed technology.

11:56-12:14 hrs Kerry McDonald-Howard

Transforming slug control in the UK

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Slugs are a major pest, severely decreasing crop yields globally, with *Deroceras reticulatum*, the grey field slug, being one of the most widespread and pestiferous. In the United Kingdom (UK), it is estimated that without adequate control in wheat and oilseed rape crops, slugs cause losses of £43.5 million annually. The current slug control method used by farmers in the UK is iron phosphate pellets, with alternative biocontrol also available in the form of slug parasitic nematodes (*Phasmarhabditis* genus) but these are cost prohibitive at scale. The nematode, once applied, enters through the mantle of the slug and infects the slug host, causing feeding inhibition with subsequent mortality between 4-21days after infection. The SLIMERS (Strategies Leading to Improved Management and Resilience against Slugs) project aimed to break down cost barriers of aforementioned nematode based biocontrol products, and reduce reliance on chemical pellet usage, through the development of an autonomous solution using AI powered slug detection smart map system via multispectral imagery together with a spot spray application of nematodes. This novel approach has the ability to work alongside other platforms for improved slug monitoring, forecasting and precision application of nematode-based products, thus decreasing losses due to slug damage, and increasing yields of arable crops.

Parallel session 23

11:20 — 12:32 GMT+2

Room 522

Parallel session 23: Non-chemical control of nematodes

Chair: Lirette Taning & Johannes Hallmann

11:20-11:38 hrs Ronald Manjoro

Utilising chitin and chitosan soil amendments to reduce potato cyst nematode populations in fallow soil.

Ronald Manjoro¹, Tom Pope, Joe Roberts¹, Matthew Back¹

Harper Adams University

Potato cyst nematodes (PCN) cause substantial yield losses worldwide and are difficult to manage due to limited nematicides, market preferences for susceptible potato cultivars and the ease of spread in contaminated soil. Environmentally sustainable alternatives, such as chitinous amendments, are promising strategies for reducing PCN between potato rotations. To evaluate the suppressiveness of chitin and chitosan amendments on PCN, a 3-month glasshouse experiment was conducted, in which PCN-infested field soil (*Globodera pallida*) was amended with different concentrations of chitin, chitosan, and a combination of both amendments at sequential rates of 0, 1.5, 3, and 6%. The underlying mechanisms involved in PCN suppression were determined through chitinase and protease assays. The overall viability of the cysts and fitness of the second-stage juveniles were evaluated through hatching and infection assays. Chitin and combined amendments stimulated high enzyme activity, but these effects were insignificant in chitosan treatments. The viability of PCN eggs was reduced by up to 18% and infectivity by 38% in the highest chitin dose. Chitosan amendments similarly reduced nematode viability across all doses when compared to the control. Combined treatments showed intermediate, potentially synergistic effects on nematode suppression. This study demonstrates the effectiveness of chitinous amendments in fallow soil.

11:38-11:56 hrs Misghina Goitom Teklu

The efficacy of Bionematicides to key plant-parasitic nematodes

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The success of achieving food resilience in the European zone, was largely due to the use of plant-protection products. In this line although synthetic nematicides played a significant role, there were obvious environmental and human health concerns associated with their use. In recent decades, sustainability has become a central focus of agricultural practices. Initiatives like the European Green Deal and the 'Farm to Fork' strategy aim to create food production systems fair, healthy, and environmentally sustainable. Consequently, several synthetic nematicides are being phased out in the European Union. Recently, oxamyl has been withdrawn from the market since 2023 in The Netherlands and is listed as a candidate for substitution (CfS) within the European Union directive (EC1107/2009). This has left farmers with limited options to combat key and major plant-parasitic nematodes. In the EU funded SAGROPIA project, 3 Bionematicides of different Technology Readiness Levels (TRL) were evaluated for their efficacy and potential in replacing CfS in climate-controlled pot experiments. The tested Bionematicides were of microbial, or plant extract origin and their efficacy were evaluated on two important raw crops potato and sugar beet. Detailed results of the efficacy and potential practical use of those Bionematicides will be presented and discussed.

11:56-12:14 hrs Johnny Visser

Growing potato as a catch crop in late summer to control Potato Cyst Nematodes

Visser, J. H. M. and Molendijk, L. P. G.

Wageningen University and Research | Field Crops, Edelhertweg 1 , 8219 PH, Lelystad, The Netherlands

Growing potato as a catch crop to control potato cyst nematodes (PCN) has been known for a long time. In the Netherlands, this measure is officially recognized by the Dutch Plant Protection Service, but only permitted when performed in spring, based on the assumption that in the second half of summer dormancy could prevent hatching, causing ineffectiveness.

The efficacy of growing potato as a catch crop in late summer was investigated in greenhouse, mesocosm and field experiments. The effects of planting time cultivation duration and location on hatching were studied. Late-season implementation of potato as a catch crop also proved to be very effective for control of PCN.

It is mandatory to destroy the catch crop within forty days after planting by application of the herbicide glyphosate. Field trials have been conducted to test alternative methods for destruction of the catch crop. Some of the tested mechanical techniques proved to be highly effective, with results comparable to those achieved with glyphosate.

Based on these results, also late summer cultivation of potato as a catch crop has been approved by the Dutch Plant Protection Service as an official measure for controlling PCN.

12:14-12:32 hrs Lirette Taning

Effectiveness of (biological) agents against plant-parasitic nematodes under field conditions in tree nurseries

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In Flanders, Belgium, tree nurseries play a key role in ornamental horticulture, and surveys have shown widespread infestations, especially by *Pratylenchus* species, causing significant economic losses. Although chemical nematicides are effective, their environmental and health risks have driven interest in biological and alternative control agents. This study assessed the field performance of several biological compounds and commercial products, including *Paenibacillus polymyxa*, melon cold peeling extract (mCOPE), dehydroascorbic acid (DHA), piperonylic acid (PA), Fytosave (COS-OGA), Nemguard, Nefast, KREG-Xt, Nemathorin, and Vydate. Trials were conducted in naturally infested tree nurseries on beech (*Fagus sylvatica*) and cherry (*Prunus avium*) using randomized block designs over one- and two-year periods. Nematode populations and plant growth were monitored. Results showed variable efficacy. DHA and mCOPE significantly reduced *Pratylenchus* populations in some beech fields, while Fytosave and Nefast improved plant growth and reduced certain nematodes in cherry trials. Laboratory assays confirmed the nematicidal effects of DHA and PA. However, field effectiveness was inconsistent, influenced by environmental conditions and application factors. Most biological agents did not harm beneficial nematodes or plant growth, indicating their potential role in integrated nematode management strategies.