

Microbial communities associated with juveniles of *Meloidogyne* spp. in soil

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Root-knot nematodes (*Meloidogyne* spp.) are one of the most damaging crop pathogens in the world. The newly-hatched juveniles of this obligate parasite have a free-living stage in the rhizosphere soil of the host plant where a high diversity of microbial species is present. Specific attachment of microbes to the cuticle of juveniles may play an ecological role, e. g. in transport of microbes through soil, microbial endophytic colonization or co-infection of roots, induction of plant defence systems, or microbial infection of the nematode. A better insight into nematode-microbe interactions might result in the discovery or improved application of biocontrol agents. The aim of this study was to assess by DNA-based techniques the species of bacteria and fungi that specifically attach to *Meloidogyne incognita* juveniles in

soil. Bacterial and fungal communities of arable soil and that of juveniles extracted from this soil were compared by PCR-DGGE fingerprints of 16S rRNA gene or ITS fragments, respectively. Numerous nematode-specific microbial ribotypes were identified which were abundant on the nematode surface but not in the surrounding soil. Some bands from Fungi, Bacillus, Alphaproteobacteria and Betaproteobacteria were consistently enriched on most replicate samples of juveniles. This was observed for four different races of *M. incognita*. In contrast, Pseudomonas, Actinobacteria, and Enterobacteria showed high variability among replicate juveniles and races, suggesting that species of these taxa were not specifically attaching to the nematode cuticle.