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Microbiome analysis of malacopathogenic nematodes suggests no evidence of a single bacterial symbiont responsible for gastropod mortality

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Nematodes and bacteria are prevalent in soil ecosystems, and some have evolved symbiotic relationships. In some cases, symbionts carry out highly specialised functions: a prime example being entomopathogenic nematodes (EPNs), which vector bacteria (Xenorhabdus or Photorhabdus) into insect hosts, killing them to provide a food source for the nematodes. It is thought that the commercially available malacopathogenic (kills slugs and snails) biocontrol nematode Phasmarhabditis hermaphrodita vectors a bacterium (Moraxella osloensis) into slugs to kill them. To investigate this further we used a metagenomic approach to profile the bacteria present in the commercial strain of P. hermaphrodita, a wild strain of P. hermaphrodita and two other Phasmarhabditis species (P. californica and P. neopapillosa), after they had killed their slug host (Deroceras invadens). We show that these nematodes do not exclusively associate with one bacterium but a range of species, with members of the phyla Pseudomonadota, Bacillota, Actinobacteriota and Bacteroidota the most prevalent. The commercial strain of P. hermaphrodita had the least diverse bacterial community. Furthermore, we found that the bacterium P. hermaphrodita has been cultured on for 25 years is not the expected species M. osloensis but is actually Psychrobacter spp. and the only strain of the Phasmarhabditis species to associate with Psychrobacter spp. was the commercial strain of P. hermaphrodita. In summary, we found no evidence to show that P. hermaphrodita rely exclusively on one bacterium to cause host mortality but found variable and diverse bacterial communities associated with these nematodes in their slug hosts.

Keywords: Metagenomics, Nematodes, gastropod, Symbiosis, biocontrol, Bacteria, 16S / 18S ribosomal RNA gene analysis

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