Anthelmintic resistance is a growing threat to nematode control worldwide. Much of what we know about the genetic basis of resistance is based on experiments with the model nematode *Caenorhabditis elegans*, but this information does not always directly translate into parasitic species of interest. Moreover, relatively little is known about how the genetic basis of resistance varies across nematode species. For example, macrocyclic lactones such as ivermectin act on *C. elegans* mainly through glutamate-gated chloride channels located in the amphids, and most known resistance-related mutations disrupt amphid development, hindering nematodes' ability to sense physical and chemical environments, but these mechanisms do not seem to be relevant in any of the gastro-intestinal nematodes of livestock for which ivermectin resistance has been investigated. To address this, we plan to investigate ivermectin resistance in a more diverse panel of free-living nematode species, including *Oscheius tipulae* (*CEW1*), *Panagrellus redivivus* (*PS1163*), *Pristionchus pacificus* (PS312) and a new wild isolate (cf *Rabditis terricola* – to be confirmed with Sanger sequencing), alongside *C. elegans* (N2) as a control. For each of the other species, we optimised culture methods to maximise survival. Dose-response conditions were established to determine the lowest ivermectin concentration at which no wild-type worms survived. These optimised conditions will support future EMS mutagenesis and the characterisation of resistant lines. Developing controlled, multi-species systems will allow direct comparison of anthelmintic resistance across species, help extend experimental work beyond current nematode models and hopefully generate new insights into ivermectin resistance in parasitic species.

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