Potato cyst nematode genomics

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The potato cyst nematodes (PCN) cause damage valued at £50 million in the UK each year. The white species of PCN, *Globodera pallida* causes particular problems to farmers as there are few commercially viable cultivars that have high levels of resistance against it. Problems caused by *G. pallida* are not limited to the UK; this pathogen is spreading across the EU and has recently been discovered in the Ukraine and Idaho, two of the largest potato growing regions in the world. In a completely novel approach, the genome of *G. pallida* is being sequenced in order to help the search for novel control strategies against this pathogen.

The genome sequencing project, a £1.7 million BBSRC-funded grant, will be run by a consortium consisting of SCRI, Leeds University, Rothamsted Research and the Wellcome Trust Sanger Institute. The sequence will emerge over the next three years and bioinformatic analysis and annotation will allow all the genes present in the nematode to be identified. Each of the partners in the project will use the information from the genome sequence to underpin functional studies on various aspects of the biology of *G. pallida*. At SCRI the focus will be on understanding how the nematode invades plants and establishes the complex feeding structures that provide it with the nutrients required for development to the adult stage. Understanding how the host plant recognises the nematode in a resistant interaction will be another important area for future studies.

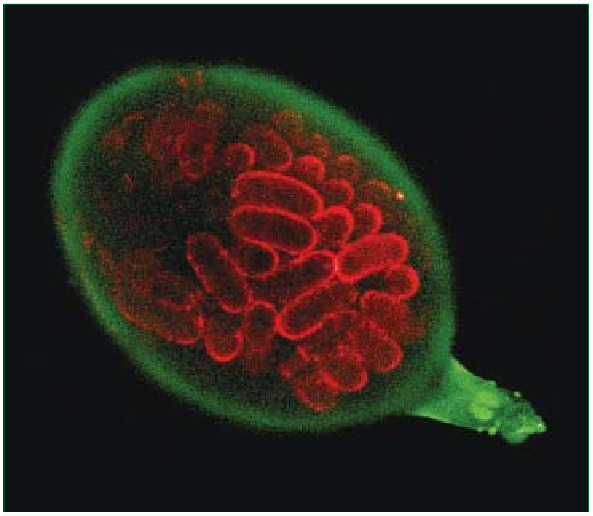

Figure 1 A cyst of *G. pallida* (green) with eggs (red) containing the next generation of juvenile nematodes.

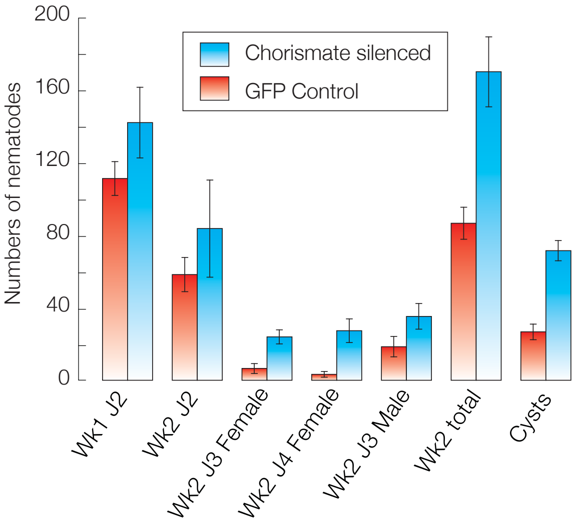

Figure 2 Numbers of nematodes developing on plants after exposure to double stranded RNA targeting chorismate mutase (red bars) or a control gene (GFP – blue bars).

The identification and functional characterisation of proteins secreted from nematode gland cells into the plant is of key importance to both these areas. Much of our previous work in this area has focused on characterisation of a secreted chorismate mutase which is thought to be important in plant–nematode interactions. Silencing this gene using RNA interference reduces the ability of the nematodes to infect plants (Figure 2) and the effect is most pronounced on nematodes that develop into adult females. This is important as sex is determined by food source in *G. pallida;* nematodes that develop on a large healthy feeding site can become female while those that obtain less food become male. This implies that the chorismate mutase either helps induce the formation of the feeding site or that it protects it from defence responses of the host. The latter possibility is currently being investigated in more detail. The genome sequence of *G. pallida* will revolutionise work in this area, providing a full list of candidate genes that may play a role in the parasitic process that can be fed into functional testing programmes.

Genome sequencing is now underway for two other plant parasitic nematodes as well other nematodes that parasitise humans or that are of veterinary importance. The availability of these sequences and the *G. pallida* sequence will allow comparative studies that will reveal the evolutionary relationships of these nematodes and that will shed light on what is required to become a parasite of an animal or of a plant.

Although there will be numerous scientific benefits from this project, the main goal is to provide novel strategies for the sustainable management of PCN. Information from the project will help identify new genes or nematode-specific enzyme pathways that can serve as targets for novel nematicides. The project will help develop a better understanding of interactions of PCN with its natural enemies that will aid identification and development of effective biocontrol isolates. Finally, improved pest management tools will come from a better understanding of biologically important phenomena such as dormancy and virulence characteristics.