

The Genes for Parasitism in the Parasitic Nematode *Strongyloides ratti*.

Supervisors

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Project description

Background. Nematodes are ubiquitous parasites of animals and plants – most wild animals are normally infected with them. Parasitic nematodes have a range of adaptations to their parasitic lifestyle. The within-host environment is a selection pressure on parasites.

Work in Viney's laboratory has now discovered several hundred genes / gene products that the rat parasite, *S. ratti*, uses only in its parasitic stages – we call these *parasitism genes* [1]. Among *S. ratti*'s parasitism genes astacin metallopeptidases and SCP/TAPS coding genes are prominent [2].

A key question of *parasitism genes* is whether they are under different selection pressures compared with other “housekeeping” genes. This project will study the (i) genetic diversity of *S. ratti*'s *parasitism genes* and (ii) seek evidence for the type of selection acting on these genes.

A highly complete assembly of the 35 Mbp *S. ratti* genome (and of other *Strongyloides* species) is now available [2]. This gives unrivalled genetic resources available for locus-specific genotyping and in-depth population genetics of wild *S. ratti* populations.

S. ratti is a common parasite. Two thirds of UK rats are infected; we have even isolated it from a run-over rat in Bristol's Whiteladies Road.

The Project Plan. The student will sample *S. ratti* populations from local rat-infested farms and from rat infestations attended by the City Council. This is a proven way of successfully obtaining *S. ratti*. These samples

will be genotyped at loci across the genome as well as at *parasitism gene* loci [2]. The genome-wide typing will be used to analyse the population genetic structure of the *S. ratti* populations. The locus-specific analyses will be analysed for evidence of selection.

The student will be able to develop the project in different ways depending on their interests, for example (i) focusing on loci of different functional classes, (ii) undertaking cross-species comparisons (there is a second species, *S. venezuelensis*, present in rats) and (iii) analysing the population genetics of other genomic features.

Understanding how selection is acting on *parasitism genes* is essential to understand the mode and tempo of evolution of parasites as they act and interact with their hosts.

1) Spinner *et al.* (2012) Characterisation of genes with a putative key role in the parasitic lifestyle of the nematode *Strongyloides ratti*. *Parasitology*, **139**, 1317-1328.

2) Hunt...25 others, Viney and Berriman (2015) The genomic basis of parasitism in the *Strongyloides* clade of nematodes. *Nature Genetics* (in review).