**Analysis of parasitic and pseudo-parasitic nematode genomes**

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Nematodes are a phylum of worms found on all seven continents. The most well-known nematode is the model organism *Caenorhabditis elegans*, but nematodes encompass over ten million other species with greatly diverse body structures, lifecycles, and inhabited ecosystems. A small but important subset of nematodes are parasites that infect 1.5 billion human beings, their companion animals, or food crops. In humans, the most debilitating parasitic nematodes are hookworms, which feed on human blood and cause debility comparable to that caused by malaria. Another blood-feeding nematode related to hookworms is *Haemonchus contortus*, the most harmful parasite of sheep and goats worldwide. In collaboration with others, my laboratory uses nematode genomics both to understand how nematodes evolved to parasitize humans and to identify possible cures for nematode parasitism. This work has so far identified one possible subunit of a hookworm vaccine; we are now pursuing a multisubunit vaccine that will work against both hookworms and *Haemonchus*. Meanwhile, we are developing the nematode *Rhabditella axei* as a model for how the ancestors of hookworms and *Haemonchus* evolved from being free-living nematodes to mammalian parasites. *R. axei* is a primarily free-living nematode, but it sporadically infects humans and other animals (which has led to its being called a "pseudoparasite"), and it is one of the closest free-living relatives of hookworms and *Haemonchus*. An African strain of *R. axei* can survive and reproduce at 31ºC, and this resistance is genetically dominant to weaker heat-resistance in European *R. axei*. We have analyzed a third-generation genome sequence for European *R. axei* and begun using it to map heat-resistance genes incrossed from African *R. axei*. Our current hypothesis is that identifying such heat-resistance genes will elucidate one mechanism that allowed nematodes to parasitize warm-bodied mammals.