

The genome of *Strongyloides* spp. gives insights into protein families with a putative role in nematode parasitism

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SUMMARY

Parasitic nematodes are important and abundant parasites adapted to live a parasitic lifestyle, with these adaptations all aimed at facilitating their survival and reproduction in their hosts. The recently sequenced genomes of four *Strongyloides* species, gastrointestinal parasites of humans and other animals, alongside transcriptomic and proteomic analysis of free-living and parasitic stages of their life cycles have revealed a number of protein families with a putative role in their parasitism. Many of these protein families have also been associated with parasitism in other parasitic nematode species, suggesting that these proteins may play a fundamental role in nematode parasitism more generally. Here, we review key protein families that have a putative role in *Strongyloides*' parasitism – acetylcholinesterases, astacins, aspartic proteases, prolyl oligopeptidases, proteinase inhibitors (trypsin inhibitors and cystatins), SCP/TAPS and transthyretin-like proteins – and the evidence for their key, yet diverse, roles in the parasitic lifestyle.

Key words: *Strongyloides*, helminths, acetylcholinesterases, astacins, aspartic proteases, prolyl oligopeptidases, proteinase inhibitors, SCP/TAPS, transthyretin-like proteins.

INTRODUCTION

The genomes of four *Strongyloides* species (*S. ratti*, *S. stercoralis*, *S. papillosus* and *S. venezuelensis*), and two closely related species from the same evolutionary clade, the parasite *Parastrongyloides trichosuri* and the free-living species *Rhabditophanes* sp. have recently been sequenced. The genomes of each of these six species have been formed into 42–60 Mb assemblies, with each containing 12 451–18 457 genes (Hunt *et al.* 2016). The genomes of *S. ratti*, *S. stercoralis* and *P. trichosuri* each comprises two autosomes and an X chromosome (Bolla and Roberts, 1968; Hammond and Robinson, 1994), while in *S. papillosus* and *S. venezuelensis* chromosomes I and X have fused (Albertson *et al.* 1979; Hino *et al.* 2014); *Rhabditophanes* sp. has five chromosomes (Hunt *et al.* 2016). All six genomes are AT rich, with GC values ranging from 21 to 25% in the four *Strongyloides* spp. to 31 and 32% in *P. trichosuri* and *Rhabditophanes*, respectively (Hunt *et al.* 2016). The genomes have been assembled to a high-quality – the reference genome *S. ratti* into single scaffolds for each of the two autosomes, and the X chromosome assembled into ten scaffolds. The high-quality assembly of these genomes makes the *Strongyloides* species an excellent model in which to understand nematode genomics. For *Strongyloides* spp., the parasitic and free-living

adult female stages of their life cycle are genetically identical because the parasitic female reproduces by a genetically mitotic parthenogenesis (Viney, 1994). The differences between the parasitic and free-living adult stages are therefore due solely to differences in expression of genes of the *Strongyloides* genome. Because the parasitic and free-living adult stages are genetically identical, the genes and proteins upregulated in the parasitic stage, compared with the free-living stage can be directly attributed to a putative role in parasitism. Most parasitic nematode species do not have genetically identical parasitic and free-living adult stages. *Strongyloides* therefore offers a uniquely tractable system to study the genetic basis of nematode parasitism.

Specific gene and protein families are upregulated at different stages of the *Strongyloides* life cycle when compared with other life cycle stages (Fig. 1) (Hunt *et al.* 2016). Comparisons of the transcriptome and proteome of parasitic females with the transcriptome and proteome of free-living adult female stages of the *Strongyloides* life cycle have revealed genes and proteins upregulated in the parasitic female, with a putative role in parasitism (Hunt *et al.* 2016). Genes encoding two protein families – astacins and SCP/TAPS – are the most commonly upregulated gene families in the transcriptome of the parasitic adult female, when compared with the genetically identical free-living female adult stage of the life cycle. Together the astacins and SCP/TAPS gene families account for 19% of all of the genes

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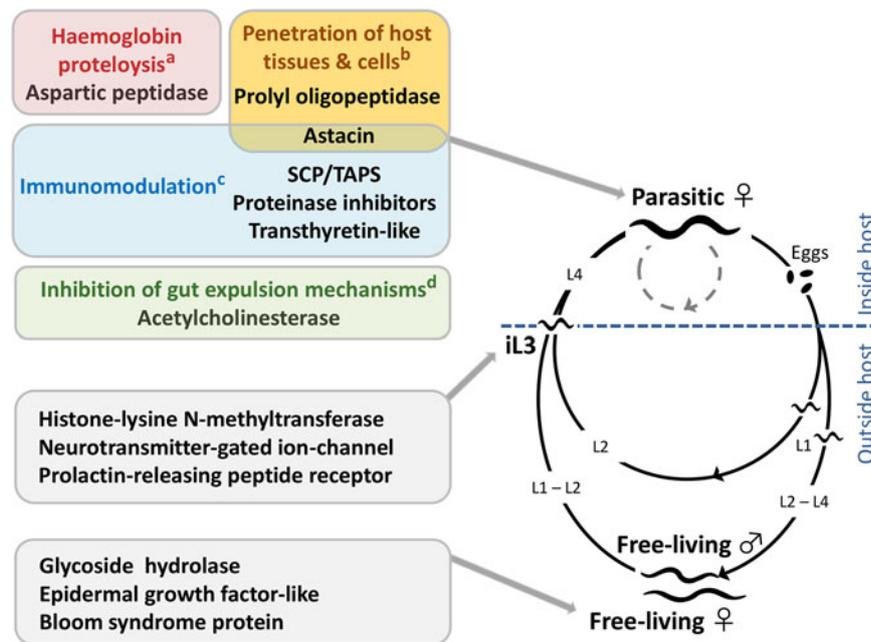


Fig. 1. The *Strongyloides* life cycle and the protein families associated with the parasitic adult female, free-living adult female and third stage infective larvae (iL3), and their putative roles in nematode parasitism. The coloured boxes represent the different putative roles of protein families in parasitism, including haemoglobin proteolysis (red), penetration of host tissues and cells (orange), immunomodulation (blue) and inhibition of gut expulsion mechanisms (green). These putative roles are based on empirical evidence of proteins from parasitic nematodes and other parasites. Mostly, protein families are associated with a single putative role, apart from astacins where there is evidence for roles of astacin proteins in host tissue penetration and immunomodulation. Little is known about the role of these protein families and further investigation may reveal that other protein families also have multiple roles in parasitism. Adapted from Hunt *et al.* (2016). ^aBrindley *et al.* (2001); Williamson *et al.* (2002); Sharma *et al.* (2005); ^bMcKerrow *et al.* (1990); Grellier *et al.* (2001); Bastos *et al.* (2005); Williamson *et al.* (2006); ^cMoyle *et al.* (1994); Zang *et al.* (1999); Culley *et al.* (2000); Dainichi *et al.* (2001); Manoury *et al.* (2001); Pfaff *et al.* (2002); Del Valle *et al.* (2003); Asojo *et al.* (2005); Sun *et al.* (2013); Lin *et al.* (2016); ^dLee (1970, 1996); Selkirk *et al.* (2005).

significantly upregulated in parasitic females. An expansion in the number of the astacin and SCP/TAPS genes in *Strongyloides* and *Parastrongyloides*, when compared with a range of nematode species, coincides with the evolution of parasitism in the *Strongyloides-Parastrongyloides-Rhabditophanes* clade of nematodes, further highlighting their likely role in parasitism. A detailed analysis of the astacin and SCP/TAPS protein families in *Strongyloides* spp. has recently been published (Hunt *et al.* 2016). Several other gene and protein families, including acetylcholinesterases (AChE), aspartic proteases (APs), prolyl oligopeptidases (POP), proteinase inhibitors (trypsin-inhibitors and cystatins) and transthyretin-like proteins (TLP), are also commonly upregulated in the proteome and transcriptome of the parasitic female suggesting that these proteins also have a putative role in *Strongyloides* parasitism (Fig. 2). Many of these protein families with a putative role in *Strongyloides* parasitism are also expressed and sometimes secreted by the parasitic stage of the life cycles of many other species of parasitic nematodes, further suggesting these families more a general role in nematode parasitism. For example, AChEs, astacins, APs, prolyl

endopeptidases, proteinase inhibitors, SCP/TAPS and TLP proteins have all been associated with parasitism in parasitic species including nematodes (Lee, 1996; Williamson *et al.* 2002, 2006; Knox, 2007; Asojo, 2011; Fajtová *et al.* 2015; Lin *et al.* 2016). Possible roles of the protein families upregulated in parasitic females, compared with the free-living stage, are summarized in Fig. 1. These roles are based on evidence for these protein families in other parasite species, as discussed for each protein family, below.

While identification of protein families with putatively important roles in nematode parasitism is a major advance, understanding the specific role that they each play in parasitism is still a substantial challenge. Many of these protein families also occur in a diverse range of nematode species, including free-living nematode species, as well as a diverse range of non-nematode taxa. The members of a given protein family have likely evolved diverse functions which may include conserved roles important for a range of species and life cycle stages, as well as more specialized roles specific to nematode parasitism. Uncovering the roles of these proteins will be essential for understanding parasitism by

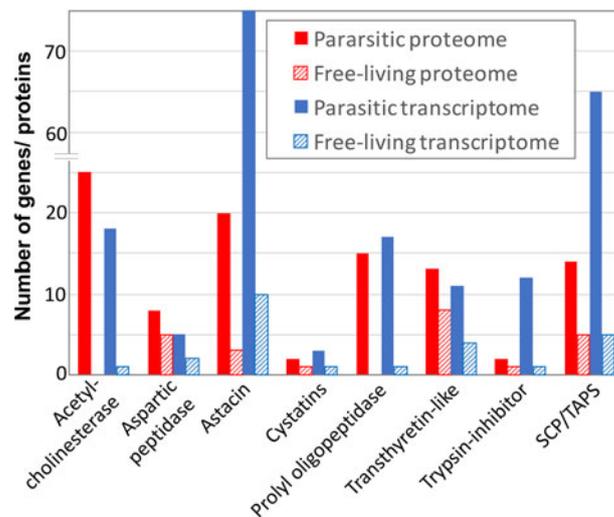


Fig. 2. Key gene and protein families with a putative role in parasitism showing the number of genes/ proteins in each family that are significantly upregulated in the proteome and transcriptome of parasitic adult females compared to free-living adult females of *S. ratti*.

nematodes. Understanding the role of these proteins is also important for identifying and developing drugs and other treatments to control nematode populations. Here, we consider in turn key protein families that have a putative role in parasitism in *Strongyloides* – AChEs, astacins, APs prolyl endopeptidases, proteinase inhibitors (trypsin inhibitors and cystatins), SCP/TAPS and TLPs (Table 1). Identification of these key protein families is based on the genomic, transcriptomic and proteomic data presented by Hunt *et al.* (2016). We consider the possible roles of these proteins in nematode parasitism and we present new analyses of these protein families, expanding on this recently published work.

PROTEIN FAMILIES WITH A PUTATIVE ROLE IN PARASITISM

Proteinases

Parasites secrete proteinases and peptidases into their environment that will act on both host- and nematode-derived proteins (Tort *et al.* 1999). Proteinases and peptidases make up a significant proportion of genes upregulated in the parasitic adult female stage of the *S. ratti* and *S. stercoralis* life cycle (Hunt *et al.* 2016). The majority of these proteinases and peptidases can be categorized into key protein families. Here we discuss the largest of these families that are associated with a putative role in *Strongyloides* parasitism: astacins, APs and POPs.

Astacins. Astacins are zinc-metalloproteinases that require the binding of zinc in their active site for catalytic activity. They are found in diverse taxa, ranging from bacteria to mammals and have been associated with a range of functions including

digestion in the crayfish (after whom they are named, *Astacus astacus*) and a bone-inducing factor (e.g. bone morphogenic protein) in vertebrates (Wang *et al.* 1988; Bond and Beynon, 1995). In nematodes, astacins have been best characterized in *Caenorhabditis elegans* where they have roles in cuticle biosynthesis, moulting and hatching (Hishida *et al.* 1996; Suzuki *et al.* 2004; Davis *et al.* 2004; Novelli *et al.* 2006). Nematode cuticles are predominantly made up of collagens, and astacins play a key role in cuticle biosynthesis where they are involved in processing collagen molecules for cuticle formation (Page and Winter, 2003; Stepek *et al.* 2015). Astacins play these roles in both free-living and parasitic species and life cycle stages. However, many of the astacins coded for by the genomes of parasitic species are differentially expressed across the life cycle, suggesting that in parasitic species they have wider roles too. For example, specific sets of astacin coding genes are upregulated in infective larval stages and adult parasitic stages compared with other parasitic and free-living stages of the *Strongyloides* life cycle, suggesting astacins have also evolved roles specific to the parasitic lifestyle. The role of astacins in parasitic stages has been best characterized for infective larval stages where the gene expression and protein secretion of astacins has been reported in many parasitic nematodes, including *Haemonchus contortus* (Gamble *et al.* 1996), *Onchocerca volvulus* (Borchert *et al.* 2007), *Ancylostoma caninum* (Williamson *et al.* 2006), *Dictyocaulus viviparus* (Cantacessi *et al.* 2011), *Teladorsagia circumcincta* (Menon *et al.* 2012), *S. ratti* and *S. stercoralis* (Hunt *et al.* 2016). Most of the evidence for the role of astacins in nematode parasitism points to them functioning in infective larvae penetrating host skin and in subsequent tissue invasion

Table 1. Summary of the genes encoding the key protein families with a putative role in parasitism in *Strongyloides*.

Species	Protein family	Total no. of genes in the genome	No. of genes upregulated in parasitic stage	No. of genes upregulated in free-living stage	Fold change range (log ₂ FC) ^a
<i>S. ratti</i>	Acetylcholinesterase	24	17	1	2.06–10.01
	Astacin	184	106	10	2.34–12.00
	SCP/TAPS	89	63	5	2.75–12.93
	Trypsin-like inhibitor	18	11	1	1.17–11.24
	Transthyretin-like	40	13	4	2.12–12.61
	Prolyl oligopeptidase	23	17	1	1.02–10.86
	Aspartic protease	53	6	6	1.87–9.81
<i>S. stercoralis</i>	Acetylcholinesterase	28	24	0	3.80–12.98
	Astacin	237	146	13	2.02–17.32
	SCP/TAPS	113	64	8	1.85–14.25
	Trypsin-like inhibitor	17	10	2	3.88–13.60
	Transthyretin-like	52	20	4	3.28–17.94
	Prolyl oligopeptidase	17	11	2	2.66–13.88
<i>Rhabditophanes</i>	Aspartic protease	53	15	2	3.28–12.71
	Acetylcholinesterase	2			
	Astacin	36			
	SCP/TAPS	12			
	Trypsin-like inhibitor	31			
	Transthyretin-like	34			
<i>C. elegans</i>	Prolyl oligopeptidase	8			
	Aspartic protease	33			
	Acetylcholinesterase	4			
	Astacin	40			
	SCP/TAPS	36			
	Transthyretin-like	59			
	Prolyl oligopeptidase	6			
	Aspartic peptidase	18			

^a FC – Fold change. Values represent the range of log₂ fold change values for expression in the parasitic female compared with the free-living adult female transcriptome.

(Williamson *et al.* 2006). For example, the astacin *Ac*-MTP-1 occurs in secretory granules of the glandular oesophagus of L3s of the dog hookworm, *A. caninum* suggesting that it plays a role in host infection. Recombinant *Ac*-MTP-1 protein (expressed in a baculovirus/insect cell system) was able to digest a range of connective tissues, including collagen and inhibition of *Ac*-MTP-1 function with either antiserum or the metalloprotease inhibitors EDTA and 1,10-phenanthroline greatly reduced tissue penetration by infective larvae (Williamson *et al.* 2006). Similarly, a role of the *S. stercoralis* secreted astacin, Ss40, also has tissue degradation properties (McKerrow *et al.* 1990; Brindley *et al.* 1995).

In the genomes of *Strongyloides* spp. and *Parastrongyloides* the astacin gene family has expanded to some 184–387 astacin coding genes per species, shown by comparison with eight other species (*Trichinella spiralis*, *Trichuris muris*, *Ascaris suum*, *Brugia malayi*, *Bursaphelenchus xylophilus*, *Meloidogyne hapla*, *Necator americanus*, *C. elegans* – spanning four evolutionary clades). The astacin coding gene family is the single most upregulated gene family in *S. ratti* and *S. stercoralis* parasitic adult females compared with both free-living adult

females and infective third-stage larvae (iL3s) (Hunt *et al.* 2016). The *Strongyloides* parasitic females reside in the mucosa of the small intestine, but rather little is known about the role of astacins at this life cycle stage. Many of the astacins expressed by parasitic females are likely to be secreted based on the prediction of a signal peptide (Hunt *et al.* 2016), and the identification of astacins in the secretome of *Strongyloides* parasitic females (Brindley *et al.* 1995; Soblik *et al.* 2011; Hunt *et al.* 2016). The secretion of these proteins into their host implies that their target substrate is external to the nematode. Because astacins have key roles in tissue degradation in larvae infecting hosts, it is probable that their role in the gut of their host is also involved in tissue degradation. One possibility is that astacins are required to break down the mucosa through which the parasitic females burrow, presumably feeding as they do so. A second, non-mutually exclusive, possibility is that astacins may have evolved a role in immunomodulation, where their proteolytic role may be directed against protein components of the host immune response. Astacins present in the secretome of the hookworm *N. americanus* are believed to be responsible for proteolysis of eotaxin, a potent

eosinophil chemo-attractant (Culley *et al.* 2000). Further investigation is required to ascertain if astacins have a similar role in immunomodulation by *Strongyloides* and other parasitic nematode species (Maizels and Yazdanbakhsh, 2003).

Aspartic proteases. AP, characterized by the presence of aspartic acid residues in their active site clefts, have been identified in a diverse range of organisms (Dash *et al.* 2003). In parasitic nematodes, such as *H. contortus*, *A. caninum* and *N. americanus*, they are thought to play a role in the digestion of host haemoglobin (Brindley *et al.* 2001; Williamson *et al.* 2002; Jolodar *et al.* 2004; Sharma *et al.* 2005; Balasubramanian *et al.* 2012). Genes encoding APs are upregulated in the parasitic adult female of *S. ratti* and *S. stercoralis* compared to free-living adult female stage (Hunt *et al.* 2016). At this stage of the *Strongyloides* life cycle, parasitic adults inhabit the host's intestine, an environment that unlikely requires degradation of haemoglobin. Previously, ten AP genes had been identified in *S. ratti* (Mello *et al.* 2009). Using the recently sequenced *S. ratti* and *S. stercoralis* genome data, we have found that there are in fact a total of 53 genes encoding proteins containing an AP domain (InterPro domain IPR021109). Twelve and 17 of these genes are differentially expressed in the parasitic and free-living *S. ratti* adult females (six upregulated in parasitic and six upregulated in free-living females) and *S. stercoralis*, respectively (15 upregulated in parasitic females and two in free-living females). This indicates that different sets of AP genes are expressed at different stages of the life cycle in *Strongyloides*, possibly reflecting the diversification of APs in parasitic and free-living adults. Two paralogous *S. ratti* APs, ASP-2A and ASP-2B, which are highly expressed in parasitic and free-living females, respectively, have previously been described (Mello *et al.* 2009) and molecular modelling of these suggests that they have maintained specificity for similar substrates but differ in their electrostatic charge. These differences may be an adaptation to the differences in environmental conditions encountered by parasitic and free-living stages of the life cycle (Mello *et al.* 2009).

Many of the *S. ratti* and *S. stercoralis* genes that code for a protein with an AP domain and are not differentially expressed between parasitic and free-living adult females are associated with retrotransposons. Specifically, in *S. ratti* and *S. stercoralis* most of the genes coding for gene products with AP domains typically are associated with retroviruses and retrotransposons including ribonuclease H-like domain, peptidase A2A, zinc finger CCHC-type domain and intergrase catalytic core domains (Table 2). Retroviral-like and retrotransposon-associated APs are homodimeric, and an AP residue located on each molecule come together to form

the active site cleft (Koelsch *et al.* 1994). The predicted folding structure of retroviral-like APs of platyhelminth and of *Leishmania* retroviral-like aspartic peptidase have a quaternary structure similar to that of HIV (Santos *et al.* 2013; Wang *et al.* 2015). Because the AP inhibitors currently used as treatment against HIV (e.g. nelfinavir) have also been shown to inhibit the activity of *Leishmania* and *Trypanosoma* retroviral-like APs (Santos *et al.* 2013), AP inhibitors offer a potential control treatment for nematode parasites.

Prolyl oligopeptidases (POPs). POP (also known as prolyl endopeptidase or PEP) enzymes are 70–80 kDa in size and belong to the S9 family of serine peptidases that cleave peptides at internal proline residues (Gass and Khosla, 2007). A common feature of POP enzymes is that they only cleave peptides up to 30 residues in length, such as neurotransmitters and hormones (Camargo *et al.* 1979). In *S. ratti* and *S. stercoralis* there are 23 and 17 genes, respectively, predicted to code for a POP, based on the predicted presence of a peptidase S9 prolyl oligopeptidase domain (Pfam ID PF00326). Of these genes, 18 and 11 are upregulated in the parasitic female transcriptome, compared with the free-living transcriptome for *S. ratti* and *S. stercoralis*, respectively. Several of these upregulated POPs have the greatest differential levels of expression between parasitic and free-living stages (Table 1). The role of POPs in parasitism is best characterized in *Trypanosoma*, *Leishmania* and *Schistosoma* (Bastos *et al.* 2013). For example, the *T. cruzi* POP, Tc80, is thought to have a role in facilitating entry of the trypanosomes into the mammalian host cells (Grellier *et al.* 2001; Bastos *et al.* 2005). In *Schistosoma*, POPs are also important in parasitism, shown by *in vitro* experiments where recombinant *S. mansoni* POP, smPOP, cleaves small host-derived peptides such as the vasoregulatory hormones angiotensin I and bradykinin. This suggests a possible role of POPs in modulating the host vascular system (Fajtová *et al.* 2015). Less is known about the role of POPs in nematodes, and especially in parasitic species.

We have identified genes predicted to encode a peptidase S9 prolyl oligopeptidase domain (Pfam ID PF00326) in 14 nematode species (four *Strongyloides* spp., *Parastrongyloides*, *Rhabditophanes* and eight species, as above), with between 5 and 18 such genes in each of the eight other species. In the *C. elegans* genome, we identified six genes that are predicted to encode a POP, but the function of POPs in *C. elegans* and other nematodes is not understood. In, the *Strongyloides*–*Parastrongyloides*–*Rhabditophanes* clade each species had 8–23 POP. Genes encoding POPs have previously been associated with parasitism based on genomic, transcriptomic and proteomic data of parasitic nematode

Table 2. Domain combinations for the genes encoding an aspartic peptidase domain in *S. rattii* and *S. stercoralis*. Both species have a total of 53 aspartic peptidase coding genes.

Domain combinations	<i>S. rattii</i>	<i>S. stercoralis</i>
Aspartic peptidase domain	15	15
Integrase, catalytic core domain – PAN-1 domain – Apple-like domain – Ribonuclease H-like domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	0	1
Integrase, catalytic core domain – Peptidase A2A, retrovirus, catalytic domain – Ribonuclease H-like domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	0	1
Integrase, catalytic core domain – Ribonuclease H-like domain – Aspartic peptidase domain-containing protein	0	1
Peptidase A2A – retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	0	3
Retroviral aspartyl protease domain – Aspartic peptidase domain-containing protein	0	1
Reverse transcriptase domain – Integrase catalytic core domain – Ribonuclease H-like domain – Retroviral aspartyl protease domain – Aspartic peptidase domain-containing protein	1	0
Reverse transcriptase domain – Aspartic peptidase domain-containing protein	2	2
Reverse transcriptase domain – Integrase catalytic core domain – Ribonuclease H-like domain – Aspartic peptidase domain-containing protein	8	4
Reverse transcriptase domain – Integrase catalytic core domain – Ribonuclease H-like domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	1	1
Reverse transcriptase domain – Integrase catalytic core domain – Ribonuclease H-like domain – Peptidase A2A, retrovirus RVP subgroup domain – AT hook-like family – Aspartic peptidase domain-containing protein	1	0
Reverse transcriptase domain – Integrase catalytic core domain – Zinc finger, CCHC-type domain – Peptidase A2A, retrovirus, catalytic domain – Ribonuclease H-like domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	3	1
Reverse transcriptase domain – Integrase catalytic core domain – Zinc finger, CCHC-type domain – Protein of unknown function DUF1759 family – Ribonuclease H-like domain – Aspartic peptidase domain-containing protein	1	0
Reverse transcriptase domain – Integrase catalytic core domain – Zinc finger, CCHC-type domain – Ribonuclease H-like domain – Aspartic peptidase domain-containing protein	9	5
Reverse transcriptase domain – Peptidase A2A – retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	2	0
Reverse transcriptase domain – Zinc finger, CCHC-type domain – Aspartic peptidase domain-containing protein	2	1
Reverse transcriptase domain – Zinc finger, CCHC-type domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	1	0
Reverse transcriptase domain – Integrase catalytic core domain – Ribonuclease H-like domain – AT hook-like family – Aspartic peptidase domain-containing protein	3	1
Reverse transcriptase domain – Integrase, catalytic core domain – Peptidase A2A, retrovirus, catalytic domain – Ribonuclease H-like domain – Aspartic peptidase domain-containing protein	0	1
Reverse transcriptase domain – Integrase, catalytic core domain – Zinc finger, CCHC-type domain – Ribonuclease H-like domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	0	1
Reverse transcriptase domain – Peptidase A2A, retrovirus, catalytic domain – Aspartic peptidase domain-containing protein	0	2
Reverse transcriptase domain – Retroviral aspartyl protease domain – Aspartic peptidase domain-containing protein	0	1
Reverse transcriptase domain – Zinc finger, CCHC-type domain – Peptidase A2A, retrovirus, catalytic domain – Aspartic peptidase domain-containing protein	0	1
Reverse transcriptase domain – Zinc finger, CCHC-type domain – Peptidase A2A, retrovirus, catalytic domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	0	1
Reverse transcriptase domain – Zinc finger, CCHC-type domain – Ribonuclease H-like domain – Aspartic peptidase domain-containing protein	0	1
Thioredoxin-like fold domain – Aspartic peptidase domain-containing protein	0	1
Zinc finger, CCHC-type domain – Aspartic peptidase domain-containing protein	2	2
Zinc finger, CCHC-type domain – Aspartic peptidase, DD11-type domain – Aspartic peptidase domain-containing protein	0	1
Zinc finger, CCHC-type domain – Peptidase A2A, retrovirus RVP subgroup domain – Aspartic peptidase domain-containing protein	2	1
Zinc finger, CCHC-type domain – Peptidase A2A, retrovirus, catalytic domain – Aspartic peptidase domain-containing protein	0	3

species including *S. ratti* (Soblik *et al.* 2011; Hunt *et al.* 2016), *S. stercoralis*, *P. trichosuri*, *Dirofilaria immitis* (Mitreva *et al.* 2004) and *T. muris* (Mitreva *et al.* 2011). The presence of a β -propeller domain (InterPro domain IPR004106) has been associated with genes encoding a POP-domain in parasitic species (*S. ratti*, *P. trichosuri* and *D. immitis*) (Mitreva *et al.* 2004). The β -propeller domain is associated with ligand binding, oxidoreductase and hydrolase (Chen *et al.* 2011) and, more generally, β -propeller domains are thought to exclude larger peptides from the POP active site, thus protecting them from proteolysis in the cytosol (Fülöp *et al.* 1998). Among the *S. ratti* and *S. stercoralis* POPs, 21 and 14, respectively, are predicted to contain a β -propeller domain, most of which (15 of 16 and all 11 in *S. ratti* and *S. stercoralis*, respectively) are upregulated in the parasitic female stage when compared to free-living adult females. A β -propeller domain has also been identified in the *Schistosoma* smPOP (Fajtová *et al.* 2015) and Tc80 of *T. brucei*. It is not known if POPs with a β -propeller have a specific role in parasitism and, if so, what this role is.

Proteinase inhibitors

Proteinases are an important component of the host immune defence against parasites. There is strong evidence that proteinase inhibitors are secreted by parasitic nematodes to counteract attack by host proteinases, therefore providing the parasite with protection from the effects of the host digestive system and the immune response (Knox, 2007). Proteinase inhibitors are secreted by hematophagous parasites to facilitate feeding within the host environment – for example *A. caninum* secretes the anticoagulant proteinase inhibitors anticoagulant peptide (AcAP) and hookworm platelet inhibitor (HPI) (Cappello *et al.* 1995; Stassens *et al.* 1996; Del Valle *et al.* 2003). In *Strongyloides* proteinase inhibitors including trypsin inhibitors and cystatins are upregulated in the transcriptome and proteome of parasitic females, compared with free-living adult females. These proteinase inhibitors potentially have a role in parasitism in *Strongyloides*, possibly modulating the host immune response.

Proteinase inhibitors can be categorized into two classes based on their interaction with a target proteinases: (i) irreversible high-binding interactions and (ii) reversible interactions (Rawlings *et al.* 2004; Knox, 2007). Proteinase inhibitors that irreversibly interact with their targets are endopeptidases and include the serine proteinase inhibitors (serpins) and the nematode-specific smapins family. Serpins are found in a diverse range of animals, plants and viruses (Irving, 2000) and are the largest known family of proteinase inhibitors (Law *et al.* 2006; Rawlings *et al.* 2010). The serpins are named after their most common function

which is to inhibit serine proteases. However, some serpins also inhibit other proteases such as caspases and cysteine proteases (Ray *et al.* 1992; Irving *et al.* 2002), or have non-inhibitory roles such as hormone transporters in inflammation (Pemberton *et al.* 1988). Serpins interact with their target substrate *via* conformational change which inhibits the protease (Huntington *et al.* 2000). This involves a scissile bond on a reactive-site loop near the C-terminus that traps the protease. The protease cleaves this loop but remains attached to the serpin via an active site serine. In this process the structure of the protease is disrupted and becomes susceptible to degradation (Huntington *et al.* 2000; Zang and Maizels, 2001). Because these inhibitors act irreversibly and can only inhibit a protease once they are often referred to as ‘suicide’ or ‘single use’ inhibitors (Law *et al.* 2006).

Little is known about the role of serpins in nematode parasitism. The *B. malayi* serpin Bm-SPN-2 is expressed in the blood-dwelling microfilariae stage. Screening of potential target mammalian serine proteinases revealed that Bm-SPN-2 inhibits human neutrophil-derived proteinases cathepsin G and elastase (Zang *et al.* 1999). Similarly, the serpin *Anisakis simplex* serpin (ANISERP) also inhibits cathepsin G, as well as the human blood clotting serine protease thrombin and the digestive serine protease trypsin (Valdivieso *et al.* 2015). In *S. ratti*, and *S. stercoralis* there are 12 and 10 genes, respectively, encoding serpins belonging to the trypsin-inhibitor protein family which are significantly upregulated in the parasitic female transcriptome when compared to the free-living female transcriptome. These genes have some of the highest relative differences in expression levels suggesting they have an important role in parasitism. Further investigation is required to identify the targets of *Strongyloides* serpins and if the target is host-derived.

The second type of proteinase inhibitor are those that reversibly interact with their targets, characterized by binding to the active site of a protease with high affinity. These proteinase inhibitors are commonly found in the secretome of parasitic nematodes (Knox, 2007). For example, cystatins are a subfamily of the cysteine proteinase inhibitors, which reversibly block the active site of a target cysteine protease. In parasitic nematodes there is evidence that cystatins play a role in the modulation of the host anti-nematode response (Hartmann *et al.* 2002; Maizels and Yazdanbakhsh, 2003), including antigen presentation, T cell responses and nitric oxide production (Dainichi *et al.* 2001; Manoury *et al.* 2001; Pfaff *et al.* 2002; Shaw *et al.* 2003; Knox, 2007). For example, in *Heligmosomoides polygyrus*, a recombinant cystatin protein is able to modulate differentiation and activation of bone-marrow-derived CD11c⁺ dendritic cells (Sun *et al.* 2013). In the

host antigen-presenting cells there are two key pathways involving cystatins (cysteine protease-dependent degradation of proteins to antigenic peptides, and the presentation of the MHC class II complex to T cells, which is partly regulated by cysteine proteases that cleave the MHC class II associated invariant chain), and these pathways are potential targets for parasite-derived cystatins to modulate the host immune response (Hartmann and Lucius, 2003). Using the genome and transcriptome data for *S. ratti* and *S. stercoralis* (Hunt *et al.* 2016) we have identified three *S. ratti* genes and one *S. stercoralis* gene encoding cystatin proteins which are upregulated in parasitic females compared with free-living adult females suggesting they have an important role in the parasitic life style. The *Strongyloides* upregulated cystatin-encoding genes were identified by the predicted presence of a cystatin domain (InterPro domain IPR000010), but they otherwise have no significant sequence homology with known nematode cystatins. Further investigation is required into these *Strongyloides* proteins to identify if they represent a novel group of immunomodulators.

SCP/TAPS

The sperm-coating protein (SCP)-like extracellular proteins, also known as SCP/Tpx-1/Ag5/PR-1/Sc7 (SCP/TAPS) belong to the cysteine-rich secretory proteins (CRISP) superfamily of proteins. The SCP/TAPS are characterized by the presence of one or two cysteine-rich secretory proteins, antigen 5, and pathogenesis-related 1 proteins (CAP) domains (InterPro domain IPR014044, Pfam ID PF00188). These proteins are found in a diverse range of organisms, including parasitic nematodes, where they are also known by various other names including the venom allergen-like (VAL) (Hewitson *et al.* 2011) and *Ancylostoma*-secreted proteins (ASP) (Asojo, 2011). In *S. ratti* and *S. stercoralis*, the SCP/TAPS are the second most commonly upregulated protein family in the adult female parasitic female after the astacins (Hunt *et al.* 2016) and are secreted by the parasitic female stage (Soblik *et al.* 2011; Hunt *et al.* 2016).

The first reported nematode SCP/TAPS protein was *Ac*-ASP-1 identified in the secretome of *A. caninum* infective larvae (Hawdon *et al.* 1996). SCP/TAPS have since been identified in the secretome of a range of parasitic nematodes suggesting they have an important role in parasitism (Cantacessi and Gasser, 2012). The role of SCP/TAPS in parasitism is poorly understood. The best example for a role of SCP/TAPS in nematode parasitism is in hookworms, where there is evidence for a role in immunomodulation. Specifically, in *A. caninum*, the SCP/TAPS protein known as neutrophil inhibitory factor inhibits neutrophil adhesion to vascular endothelial

cells *in vitro* by selective binding to the integrin CD11b/CD18, thus inhibiting neutrophil function and the release of hydrogen peroxide from activated neutrophils (Moyle *et al.* 1994). Secondly, HPI, inhibits *in vitro* platelet aggregation and adhesion by impeding the function of cell surface integrins (Del Valle *et al.* 2003). In *N. americanus*, the SCP/TAPS protein, *Na*-ASP-2, has structural and charge similarities to CC-chemokines, which are involved in inducing the migration of immune cells such as monocytes and dendritic cells (Asojo *et al.* 2005).

Among four *Strongyloides* spp. a total of 89–205 genes are predicted to encode SCP/TAPS coding proteins. Comparing these to eight outgroup species (as above), there is an expansion of the SCP/TAPS coding gene family in *Strongyloides* and *Parastrongyloides* but not in *Rhabditophanes* suggesting an expansion of SCP/TAPS protein coding genes coincided with the evolution of parasitism in the *Strongyloides* clade (Hunt *et al.* 2016). Interestingly, as for the astacin gene family, the SCP/TAPS gene family is also expanded in *N. americanus* (Tang *et al.* 2014; Schwarz *et al.* 2015) but phylogenetic analysis suggests that the hookworm expansion of the number of SCP/TAPS coding genes is independent to that of the *Strongyloides*–*Parastrongyloides* clade (Hunt *et al.* 2016).

Transthyretin-like proteins (TLP)

TLP have some of the highest relative levels of gene expression in *S. ratti* and *S. stercoralis* adult parasitic females, compared with that of free-living adult females (Table 1) (Hunt *et al.* 2016). This protein family, also sometimes referred to as transthyretin-like (TTL or TTR-like) proteins, is only found in nematodes and is distinct from the transthyretin-related proteins (TRPs, and sometimes also referred to as TLPs) which are found across a wide range of prokaryotic and eukaryotic taxa (Sauer-Eriksson *et al.* 2009). The TLPs are distantly related to TTRs, plasma proteins in vertebrates that transport thyroid hormones (Power *et al.* 2000), though only a low level of sequence homology has been found among the TTRs, TRPs and TLPs. TRPs, along with uricase and 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazole (OHCU) decarboxylase, have been associated with a role in the oxidation of uric acid to allantoin (Ramazzina *et al.* 2006), however, less is known about the role of TLPs. TLPs were originally discovered in *C. elegans* (Sonnhammer and Durbin, 1997) where the TLP, TTR-52, is involved in the recognition and subsequent engulfment of apoptotic cells. Expression of TTR-52 fluorescent protein constructs and *C. elegans* mutant analysis has shown that TTR-52 aggregates around apoptotic cells and binds to surface-exposed phosphatidylserine, a known 'eat me' signal for apoptotic cells. TTR-52 also binds to

the CED-1 phagocyte receptor, acting as a bridging molecule to mediate phagocytosis of apoptotic cells (Wang *et al.* 2010). Similarly, the TTRs in vertebrates also have a binding role, together suggesting that binding to molecules could be a conserved role of TLPs, although the target molecules they have evolved to bind to may have diverged among different taxa. One can envisage that in parasitic nematodes, binding of host molecules is likely to be an important function in a parasitic lifestyle.

The TLPs have been identified in the secretome, and are upregulated in the transcriptome, of parasitic stages for a number of nematode species including *A. caninum* (Mulvenna *et al.* 2009), *B. malayi* (Hewitson *et al.* 2008), *A. suum* (Wang *et al.* 2013), *H. contortus* (Schwarz *et al.* 2013), *Radopholus similis* (Jacob *et al.* 2007) and *Litomosoides sigmodontis* (Armstrong *et al.* 2014). This suggests that TLPs are universally important in nematode parasitism. Little is known about the role of TLPs in nematodes other than *C. elegans*, and it is not known if the TLPs associated with nematode parasitism have a similar molecular-binding role. The plant parasite nematode *Meloidogyne javanica* secretes the TLP protein MjTTL5. Yeast two-hybrid protein–protein interaction screens have revealed that MjTTL5 interacts with the *Arabidopsis thaliana* protein ferredoxin: thioredoxin reductase catalytic subunit (AtFTRc), the expression of which is induced by infection with *M. javanica*. The AtFTRc protein is an important component of the host antioxidant system that is deployed by plants as part of their infection defence mechanism. It is hypothesized that MjTTL5 causes a conformational change in AtFTRc that results in the reduction of reactive oxygen species in the host, enhancing nematode parasitism (Lin *et al.* 2016). MjTTL5 is the best characterized parasitic nematode TLP to date. More research is required to identify the binding targets, if any, of TLPs in parasitic nematodes that infect animals. This is particularly important because TLPs are potentially interesting as a vaccine or drug target because they only occur in nematodes, thereby facilitating chemotherapeutic specificity.

Acetylcholinesterases

Cholinesterases are serine esterases that preferentially hydrolyse choline esters, and are members of a large family of related esterases and lipases which share a core arrangement of eight beta sheets connected by alpha helices (the alpha/beta hydrolase fold) (Ollis *et al.* 1992). Vertebrate cholinesterases can be distinguished by their substrate specificity; for example, AChE hydrolyses acetylcholine (ACh), the major excitatory neurotransmitter, which is common to most animals, including nematodes (Selkirk *et al.* 2005). A key feature of AChEs is

that the catalytic triad (S200, H440, E327, numbering based on the *Torpedo californica* enzyme) is located at the base of a 20 angstrom-deep narrow gorge which extends halfway into the enzyme (Sussman *et al.* 1991). The gorge is lined by the rings of 14 aromatic residues; most of which can be assigned functional roles. Of these, W84 is critical for enzymatic activity, as both it and F330 form part of the ‘anionic’ (choline) binding site, which orients the substrate in the active site.

ACh controls motor activities such as locomotion, feeding and excretion in nematodes (Seegerberg and Stretton, 1993; Rand and Nonet, 1997), and thus AChE plays a crucial role in regulation. Among nematodes, AChE coding genes have been most thoroughly characterized in the free-living nematode *C. elegans*, which has four AChE coding genes: *ace-1–4*. Homozygous mutants of individual *ace* loci result in slight defects in locomotion, or have no phenotypic effect. However, *ace-1–2* double-mutant worms are severely uncoordinated, and *ace-1–3* triple mutants have a lethal phenotype, suggesting that although the *ace* genes have essential functions and are required for viability it is possible that *ace-1* and *ace-2* can assume the function normally carried out by *ace-3* (Culotti *et al.* 1981; Johnson *et al.* 1981, 1988; Kolson and Russell, 1985). Green fluorescent protein (GFP) localization studies of the *ace-1–3* products show that each gene has a distinct pattern of expression, though with some areas where expression is overlapping (Culetto *et al.* 1999; Combes *et al.* 2000). There is little evidence of expression for *ace-4* and it is likely to code for a redundant protein.

Neuromuscular AChEs of parasitic nematodes are much more ill-defined. In addition to expression of neuromuscular AChEs, many parasitic nematodes release variants of these enzymes from specialized secretory glands (Ogilvie *et al.* 1973), and this property appears to be restricted to parasitic nematodes which colonize mucosal surfaces (Selkirk *et al.* 2005). These secretory enzymes have been best characterized in *Nippostrongylus brasiliensis* and *D. viviparus*. *N. brasiliensis* secretes three distinct AChEs encoded by separate genes (Hussein *et al.* 1999, 2000, 2002). Two secreted AChEs from *D. viviparus* have been characterized (Lazari *et al.* 2003), although this parasite secretes variants which may be encoded by additional genes (McKeand *et al.* 1994). All of the secreted AChEs take the form of hydrophilic monomers, and analysis of substrate specificity and sensitivity to inhibitors indicates that they can all be classified as true AChEs (Selkirk *et al.* 2005). The rationale for secretion of multiple forms is unclear, since they display similar substrate specificities and pH optima.

The exact role of AChEs in nematode parasitism is still unclear. In mammals, ACh is a key neurotransmitter involved in the regulation of gut peristalsis. It

is likely that parasitic nematodes secrete AChE in order to neutralize host cholinergic signalling, with this signalling normally promoting physiological responses (smooth muscle contraction, mucus and fluid secretion by goblet cells and enterocytes, and effects on the immune system) which contribute to parasite expulsion (Selkirk *et al.* 2005). For example, it has been proposed that *N. brasiliensis*' release of AChE into the host gut reduces local intestinal wall spasm and reduces peristalsis, thus providing a more stable environment for *N. brasiliensis* to inhabit (Lee, 1970, 1996). Parasitic nematode-derived AChE may inhibit the release of host intestinal mucus. ACh is also involved in inflammatory immune responses (Wang *et al.* 2003; Tracey, 2009) and has recently been shown to act as a co-stimulatory signalling molecule for CD4⁺ T cell activation and cytokine production in mice during *N. brasiliensis* infection (Darby *et al.* 2015). The host anti-nematode immune response is therefore also a potential target of parasitic-nematode derived AChEs.

Strongyloides ratti and *S. stercoralis* have 24 and 28 AChE coding genes, respectively, of which 17 and 24 were upregulated in the adult parasitic female stage (whereas only 1 and 0 were comparatively upregulated in the free-living female) (Table 1, Fig. 2.). We have resolved the phylogeny of AChE genes in 14 nematode species, including four *Strongyloides* species, *P. trichosuri* and *Rhabditophanes* sp. (from the same evolutionary clade) and eight outgroup species (as above) encompassing four further nematode clades (Fig. 3). AChEs coding genes were identified by the presence of a predicted cholinesterase protein domain (InterPro domain IPR000997) and the phylogeny was determined using the method described by Hunt *et al.* (2016). The phylogeny shows an expansion of the cholinesterase gene family in *Strongyloides* and *Parastrongyloides* compared with the other nematode species (Fig. 3). The expanded cholinesterase-like genes are all predicted to encode proteins with truncated C-termini, characteristic of secreted AChEs. The number of these genes in *Strongyloides* and *Parastrongyloides* are remarkable: 178 genes between 5 *Strongyloides* and *Parastrongyloides* species, with 80 representatives for *P. trichosuri* alone.

The expansion of the AChE family has not occurred in the closely related free-living nematode *Rhabditophanes*, which only possess two AChE coding genes. Many of the genes in the expanded AChE gene family are upregulated in the parasitic stage of *S. ratti* and *S. stercoralis* suggesting that, like the astacins and SCP/TAPS, the expansion of the AChE coding gene family has coincided with the evolution of parasitism in the *Strongyloides*–*Parastrongyloides*–*Rhabditophanes* clade and has a role in parasitism. All *Strongyloides* and *Parastrongyloides* species were observed to possess one

sequence encoding a protein closely related to *C. elegans* ACE-1, ACE-2 and ACE-3/4, respectively. The nematode sequences which cluster with *C. elegans* ACE-1 show features characteristic of this enzyme and tailed forms in general. The sequences, which cluster with ACE-2 show similar conservation of the key amino acids required for disulphide bonds, the catalytic triad, and generally thirteen of the fourteen aromatic residues, which line the active site gorge. A key feature of these predicted proteins is that many have a hydrophobic C-terminus with signals for peptide cleavage and GPI addition, analogous to *C. elegans* ACE-2. The same is true of the sequences which cluster with ACE-3/ACE-4, and key residues are particularly well conserved in this group. In summary, most parasitic nematodes examined appear to mirror *C. elegans* in possessing genes for one tailed and two hydrophobic AChEs, and in all likelihood these represent neuromuscular enzymes which perform analogous functions to their *C. elegans* counterparts. In comparison to the AChE coding genes that have expanded in *Strongyloides* and *Parastrongyloides*, the expression of the *S. ratti* and *S. stercoralis* AChE coding genes most closely related to the *C. elegans ace 1–4* genes were not upregulated in the parasitic or free-living stages of the *Strongyloides* life cycle (Fig. 3).

We classified the members of the *Strongyloides*–*Parastrongyloides* expanded cholinesterase-like gene family into eight groups, based on the phylogeny shown in Fig. 3. The vast majority have cysteine residues in the correct position to form the three intramolecular disulphide bonds, and features of the active site gorge characteristic of cholinesterases. However, closer examination reveals that almost all of the predicted proteins are likely to be enzymatically inactive, with the exception of those in group 1. The group 1 predicted protein sequences possess the necessary key residues for AChE activity. Groups 2, 3 and 4 lack S200 or have modifications around this residue that would render the enzymes inactive. The consensus sequence around the active site serine in cholinesterases is FGESAG. Mutation of S200 generates loss of activity (Gibney *et al.* 1990; Shafferman *et al.* 1992), and mutation of E199 reduces it. Most *Parastrongyloides* genes in group 2 also lack E327, approximately half of the sequences in group 3 lack H440, and mutations of these residues also render AChEs inactive (Radić *et al.* 1992; Shafferman *et al.* 1992). Almost all group 6 sequences are predicted to retain F330 in the choline-binding site, but show altered residues around S200: many sequences predict the consensus FGTSSG rather than FGESAG, which would likely severely reduce catalytic efficiency (Radić *et al.* 1992). Group 5 sequences show relatively poor conservation of active site gorge aromatic residues. All group 6 predicted sequences have a W84Y substitution. W84 is considered a signature of

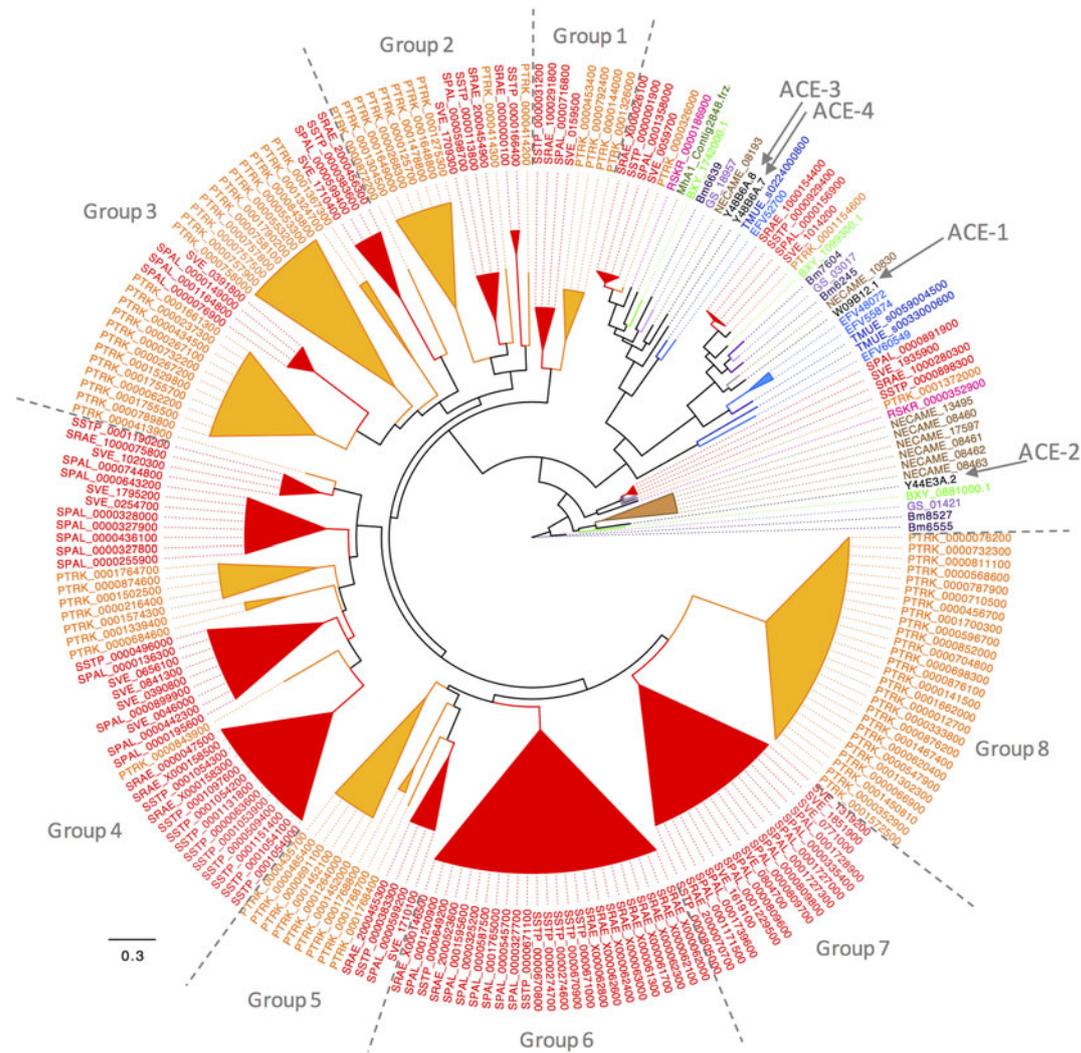


Fig. 3. The phylogeny of acetylcholinesterases from 14 nematode species including four *Strongyloides* species (red) and two species, *Parastrongyloides* (orange) and *Rhabditophanes* (pink), from the same evolutionary clade as *Strongyloides*. The four acetylcholinesterases, ACE 1–4, in the *C. elegans* genome are marked on the phylogeny. Acetylcholinesterases from *Strongyloides* and *Parastrongyloides* were categorized into eight distinct groups based on clustering in the phylogeny. The scale bar represents the number of amino acid substitutions. The phylogeny also includes genes predicted to encode acetylcholinesterases for eight further species of nematode including *Caenorhabditis elegans* (black), *Necator americanus* (brown), *Bursaphelenchus xylophilus* (light green), *Trichinella spiralis* (light blue), *Trichuris muris* (blue), *Brugia malayi* (navy blue), *Ascaris suum* (purple), and *Meloidogyne hapla* (dark green).

cholinesterases, as the quaternary nitrogen groups of the substrate are stabilized by cation–aromatic interactions. Nevertheless, cholinesterases substituted with smaller aromatic residues such as tyrosine and phenylalanine at this site retain activity, albeit reduced several-fold (Ordentlich *et al.* 1995; Loewenstein-Lichtenstein *et al.* 1996). Proteomic analysis has identified twenty cholinesterase-like sequences in the secretome of adult female parasitic *S. ratti*, none of which were present in secreted products of free-living adult females (Hunt *et al.* 2016). Of these, only SRAE_1000291800 from group 1 is predicted to encode an active AChE. Ten of the sequences are from group 6: of these, five have the sequence FGTSSG and five have FGTGTG around

the active site serine and are thus most likely enzymatically inactive. The other secreted proteins are from groups 2, 4 and 5.

The presence of large numbers of these genes in the genomes of *Strongyloides* and *Parastrongyloides*, that these genes are transcribed and (from *S. ratti* and *S. stercoralis*, data) specifically in the parasitic female stage, and (from *S. ratti* proteomic data) that many result in proteins, sits oddly with most of these not coding for functional cholinesterases. It is possible that these proteins could have quite different, perhaps novel, roles. It is notable that cholinesterases are thought to have a wider variety of non-enzymatic roles, such as in cellular differentiation, adhesion and morphogenesis (Grisaru *et al.*

1999; Johnson *et al.* 1988), and such roles might be compatible with how *Strongyloides* exploits host mucosal tissue during its parasitic phase.

DISCUSSION

The continued advances in next generation sequencing have led to a great increase in the number of sequenced parasitic nematode genomes that are available. These data, along with high quality data on the transcriptomes and proteomes of different life cycle stages of parasitic nematodes has enabled predictions of genes and proteins with possible roles in parasitism. We have discussed the protein families with a putative role in parasitism based on evidence that these proteins are upregulated in the transcriptome and proteome of the parasitic stage of the life cycle, compared with the genetically identical free-living stage. Some of these protein families are now under further investigation as potential vaccine targets against nematode infection, including members of the astacin (Nisbet *et al.* 2013; Page *et al.* 2014), SCP/TAPS (Goud *et al.* 2005), AP (Loukas *et al.* 2005) and cystatin (Arumugam *et al.* 2014) protein families. Proteins with a role in parasitism are also key targets for the development of anthelmintic drugs (Page *et al.* 2014), and as immunomodulatory drugs for autoimmune disease such as asthma and colitis (Wilson *et al.* 2010; Whelan *et al.* 2012; Maizels *et al.* 2014).

There are still big gaps in our knowledge. Our understanding of the role played by many of these proteins in the parasitic nematode lifestyle, and their targets, if any, within the host are still largely unknown. With the exception of the TLP family, which is only found in nematodes, many of the protein families likely to play an important role in nematode parasitism have been identified across a diverse array of nematode and non-nematode taxa. In many cases, these protein families have a diversity of roles. For example, the SCP/TAPS are not only found in nematodes, but also in plants and animals, where they have been implicated in plant pathogen defence, as components of insect and snake venom, in sperm maturation and male reproduction in insects and mammals, and the development of fibrosis (Cantacessi *et al.* 2009). Thus, identifying the family to which a protein belongs is not necessarily informative about the roles that they might have in nematode parasitism. The proteins involved in nematode parasitism may have evolved new functions, which may be novel to a particular species, genus or clade of parasitic nematodes.

Many *Strongyloides* proteins/genes, especially for the protein families discussed here, have the greatest expression in the parasitic stage, compared with the free-living stage, and these proteins are key candidates for proteins involved in parasitism. Of these proteins, many are likely to be secreted into their host based on

the prediction of a signal peptide domain in their protein sequence and the presence of these proteins in the secretome (Hunt *et al.* 2016). The secretion of these proteins is important because proteins that have a role in parasitism are likely to interact directly with their host, for example interacting with components of the host's immune system or other host molecules that are in close association with the parasite in its within-host niche (Hewitson *et al.* 2009). Secreted proteins that are highly expressed in parasitic females compared with free-living females, therefore offer the best candidates for further investigation into their role in parasitism.

Empirical studies are now required to investigate the role, if any, that these *Strongyloides* proteins have in parasitism. For example, measuring the effect of parasite proteins on immune responses will identify if a protein has immunomodulatory properties (McSorley *et al.* 2013). Another avenue of research that will be important for uncovering the functions and roles of parasite proteins, is transgenic studies. Transgenic techniques have been established in few parasitic nematode species. Recent developments in transgenic techniques for *S. ratti* and *S. stercoralis* will now enable the expression patterns of proteins involved in parasitism to be investigated (Li *et al.* 2011; Shao *et al.* 2012; Lok, this issue). *Strongyloides* spp. therefore offer exciting opportunities to further explore the role of protein families with a putative role in parasitism. Furthermore, the potential application of knock-down and knock-in techniques for parasitic nematodes, which are especially available for *Strongyloides* (Lok, this issue; Ward, 2015), will provide important tools for exploring the function and importance of these proteins in parasitism.

Comparison of the genetically identical parasitic and free-living stages of *Strongyloides* offers a powerful tool to study nematode parasitism. However, when comparing these two life cycle stages it is also important to consider the other phenotypic differences that exist between parasitic and free-living *Strongyloides* adult nematodes, which will also be determined by differential gene expression. In addition to their considerable differences in lifestyle, i.e. parasitic *vs.* free-living, they also differ in their longevity, morphology and method of reproduction. Parasitic adults live for around a month in the gut of their host and this is extended up to a year in immunocompromised hosts. By comparison free-living adults are short-lived and survive for around 5–6 days as adults. Parasitic adults are approximately 2 mm long, twice the size of free-living females which also differ in their oesophagus and gut morphology (Gardner *et al.* 2004, 2006). Unlike parasitic females which reproduce asexually by mitotic parthenogenesis, free-living females reproduce sexually (Viney, 1994). The protein and gene families that are differentially expressed between parasitic and free-living females may

therefore also represent differences in longevity, morphology and reproductive strategy.

Here, we have compared the acetylcholinesterase protein families across 14 nematode species including four *Strongyloides* species, and in a previous study (Hunt *et al.* 2016) we compared the astacin and SCP/TAPS protein families across the same 14 species. These comparisons have revealed that the *Strongyloides* and *Parastrongyloides* nematodes have undergone a massive expansion of genes encoding protein families with a putative role in parasitism, compared to most other parasitic nematode species spanning four nematode clades. The exception is *N. americanus* which also has a greater number of both astacins and SCP/TAPS genes, though phylogenetic analysis indicates that these possible gene family expansions are independent to the expansions observed in *Strongyloides* and *Parastrongyloides* (Hunt *et al.* 2016). Future studies including greater numbers of parasitic and free-living nematode species are needed to identify if a similar phenomenon of major expansions of gene families with a putative role in parasitism has occurred in parasitic nematode species more widely. Within *Strongyloides* the high level of sequence similarity of genes within a given expanded gene family indicates that these genes have probably arisen through tandem duplication (Hunt *et al.* 2016). Many of these genes are also physically clustered in the genome, often located in a region at the end of chromosome II suggesting this particular region has been subject to multiple tandem duplication events, where genes from different gene families with a putative role in parasitism have duplicated. The clustering of these genes could imply that they are under selective pressures to maintain close proximity. For example, genes in the same region of a chromosome may share regulatory elements or allow accessibility to certain transcription factors (Lercher *et al.* 2003).

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