The genome, transcriptome, and proteome of the nematode *Steinernema carpocapsae*: evolutionary signatures of a pathogenic lifestyle

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The entomopathogenic nematode *Steinernema carpocapsae* has been widely used for the biological control of insect pests. It shares a symbiotic relationship with the bacterium *Xenorhabdus nematophila*, and is emerging as a genetic model to study symbiosis and pathogenesis. We obtained a high-quality draft of the nematode's genome comprising 84,613,633 bp in 347 scaffolds, with an N50 of 1.24 Mb. To improve annotation, we sequenced both short and long RNA and conducted shotgun proteomic analyses. *S. carpocapsae* shares orthologous genes with other parasitic nematodes that are absent in the free-living nematode *C. elegans*, it has ncRNA families that are enriched in parasites, and expresses proteins putatively associated with parasitism and pathogenesis, suggesting an active role for the nematode during the pathogenic process. Host and parasites might engage in a co-evolutionary arms-race dynamic with genes participating in their interaction showing signatures of positive selection. Our analyses indicate that the consequence of this arms race is better characterized by positive selection altering specific functions instead of just increasing the number of positively selected genes, adding a new perspective to these co-evolutionary theories. We identified a protein, ATAD-3, that suggests a relevant role for mitochondrial function in the evolution and mechanisms of nematode parasitism.

Global losses due to pests can vary from about 26 to 80% depending on the type of crop¹. Chemical pesticides are commonly used to fight this problem, however, they pose threats to humans, wildlife, and might have an adverse impact on soil fertility by killing beneficial microorganisms². Other strategies rely on biological control agents, but their use is not generalized because of their limited efficiency when compared to pesticides. Genetic improvements are possible, especially when genomic information of the biological agent is available³⁴. Entomopathogenic nematodes (EPNs) from the family of *Steinernematidae* have been commercialized in many countries as a

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Steinernema atode in the pathogenic process. In fact, a set of expanded gene families that are likely involved in parasitism that is more fragmented, with a much lower N50 (~0.3 Mb) and with the largest scaffold of 1.7 Mb (Table 2).

We obtained a coverage of 32-fold, considering a genome size of ~110 Mb estimated by both flow cytometry and read length of 334 bp at each fragment end. From a SOLiD shotgun library sequenced in half a lane of SOLiD, we obtained 3,340,915 total reads with an average length of 357 bp. From one 454 paired-end library, we obtained 2,784,713 total reads with an average length of 357 bp. From one 454 paired-end library, we obtained 3,340,915 total reads with an average length of 357 bp. From one 454 paired-end library, we obtained 2,784,713 total reads with an average length of 357 bp.

Table 1. Summary of sequencing data from Steinernema carpocapsae strain Breton, compared to the sequencing data of the strain All.11

| Strain | Source | Library type | Platform | No. of runs | No. of reads (Millions) | Average read length (bp) | Insert size (bp) |
|--------|--------|--------------|----------|-------------|------------------------|--------------------------|-----------------|
| Breton | DNA    | Shotgun      | 454 GS FLX | 3           | 33.41                  | 357                      | —               |
|        | DNA    | Paired-end   | 454 GS FLX | 2           | 27.85                  | 334                      | 8000            |
|        | RNA    | Shotgun      | SOLID 5500xl | ~Half lane | 24.94                  | 75                      | —               |
|        | RNA    | Shotgun cDNA | 454 GS FLX + | Half plate | 0.09                   | 288                      | —               |
|        | RNA    | Paired-end cDNA | Illumina MiSeq | 1 | 15.18                  | 201                      | —               |
|        | sRNA   | Shotgun      | Illumina HiSeq 2500 | 1 (6 tagged libraries) | 42.81 | 51 | — |
| All    | DNA    | Paired-end   | Illumina Genome Analyzer IIx | 1 | 85.76 | 75 | 400 |
|        | DNA    | Paired-end   | Illumina Genome Analyzer IIx | 1 | 103.09 | 100 | 350 |
|        | DNA    | Paired-end   | Illumina Genome Analyzer IIx | 1 | 131.59 | 100 | 1800 |
|        | RNA    | Paired-end cDNA | Illumina Genome Analyzer IIx | 4 (each from a different developmental stage) | 260.86 | 75 | 200 |

Results and Discussion

Genome sequencing. Total DNA was extracted from isolated nuclei from a near isogenic line (~96% of estimated homozygosity) of Steinernema carpocapsae strain Breton. The use of isolated nuclei reduces the amount of symbiont and mitochondrial DNA, and the isogenic line was generated to avoid the acknowledged problems posed by heterozygosity for accurate genome assembly.12 From one 454 shotgun library sequenced in three 454 FLX runs, we obtained 3,340,915 total reads with an average length of 357 bp. From one 454 paired-end library, with an insert size of 8 Kb, sequenced in two 454 FLX runs, we obtained 2,784,713 total reads with an average read length of 334 bp at each fragment end. From a SOLiD shotgun library sequenced in half a lane of SOLID 5500xl, we obtained 24,942,584 reads of 75 bp (Table 1). By combining these long, paired-end, and short reads, we obtained a coverage of 32-fold, considering a genome size of ~110 Mb estimated by both flow cytometry and genome assembly. The final draft consists of 84,613,633 base pairs in 347 scaffolds, with an N50 of 1.24 Mega bases.

We assessed the completeness of the genome by analysing 248 ultra-conserved core eukaryotic genes, obtaining 99.6% completeness considering partial genes and 99.2% for complete genes. These parameters indicated that our draft genome is of high quality, which gives us confidence in the genome annotation described below.

Genome annotation. From the repetitive elements, we identified 1,702 distinct retrotransposon sequences representing at least eight families. Four were long interspersed element (LINE) groups, Crl being the most abundant, and 588 were short interspersed elements (SINEs), of which 432 belong to the tRNA-RTE family. We identified only two long terminal repeats (LTRs): Gypsy and Pao. We also identified eight families of DNA transposons, comprising 1,202 sequences, of which hAT-Ac was the most abundant with 388 elements, followed by TcMar-Tc1, Merlin, and the rolling-circle Helitron (327, 106, and 105 elements, respectively).
et al. as in Dillman et al. 11, ab initio gene structures with C. elegans models, we only obtained 14,188 protein coding genes. This is lower than the previous predicted number of genes (28,313) for the strain “All” of the same species 11. In the previous study, the heterozygosity was not reduced to identify protein-coding genes in the assembled genome, we assigned specific weights to different types of evidence to generate consensus gene calls (see Material and Methods). The current genome sequence and annotation is available at www.genomevolution.org (ID 33774), and at the NCBI GenBank (BioProject ID# 39853).

We identified 16,333 protein-coding genes with an average length of 1,257 bp, an average exon length of 222.37 bp, and an average of six exons per gene. We also identified 6,708 alternative transcripts and 5,725 truncated genes (defined as predicted protein-coding genes missing a start codon). We verified the protein expression of 3,773 predicted genes through mass spectrometry analysis (see below and Supplementary Table S2). The total number of predicted genes in this study is much lower than the previously predicted number of genes (28,313) for the strain “All” of the same species 11. In the previous study, the heterozygosity was not reduced through the generation of an isogenic line, potentially negatively impacting on their genome assembly12. In addition, they performed gene prediction using Augustus 14 with parameters optimized only for Caenorhabditis elegans. However, these species diverged ~280 million years ago15, making it difficult to accurately predict genes in Steinernema by solely using C. elegans gene models. To overcome this bias, we combined predictions using Hidden Markov Models (HMM) trained on S. carpocapsae gene structures with ab initio predictions, along with HMM homology-based predictions using C. elegans genes and Brugia malayi gene predictions (all the predictions were obtained with Augustus14). Although B. malayi has the same estimated time of divergence from S. carpocapsae as C. elegans15, it is a parasite and therefore might share some homologous genes with S. carpocapsae that are not represented in C. elegans. However, the full strength of our approach is given by combining predictions using gene models from these species with ab initio predictions. When we used the same annotation strategy as in Dillman et al. 11 using C. elegans models, we only obtained 14,188 protein coding genes. This is lower than the previous study, and also lower to the one we obtained with our combined strategy, in which the number of predicted genes probably increased due to the inclusion of B. malayi models, along with the ab initio predictions.

| Strain  | Breton | All         |
|---------|--------|-------------|
| Sequencing depth | 32X    | 330X        |
| Estimated genome size in megabases (GSAssembler 2.7) | 111.3  | 85.6        |
| (Flow Cytometry) | ~110   | Not determined |
| Number of scaffolds | 347    | 1,578       |
| Total number of base pairs within assembled scaffolds | 84,613,633 | 86,127,942* |
| N50 Scaffold length (bp) | 1,245,171 | 299,566    |
| Largest scaffold (bp) | 8,793,593 | 1,722,607  |
| GC content of whole genome (%) | 45.67  | 45.53       |
| Repetitive sequences (%) | 6.99   | 7.46        |
| Proportion of genome that is coding (exonic) (%) | 19.72  | 38.8*       |
| Proportion of genome that is transcribed (exons + introns) (%) | 42.09  | 50.31*      |
| Number of putative coding genes | 16,333 | 28,313      |
| Number of non-coding RNAs | 1,317  | Not determined |
| Mean gene size (bp) | 2,681  | 2,030       |
| Mean coding sequence length per gene (bp) | 1,257  | 1,046*      |
| Average exon number per gene | 6      | 5           |
| Average gene exon length (bp) | 222.37 | 212         |
| Average gene intron length (bp) | 145.44 | 194         |
| GC content in coding regions (%) | 52.49  | 51.86       |
| Functionally annotated genes (according to BLAST2GO default parameters) | 10,395 (63.6%) | Not determined |

Table 2. Summary statistics of assembly and annotation of the genome of Steinernema carpocapsae strain Breton, compared to the assembly of the strain All11. *Calculated from version PRJNA202318.WBPS6 obtained from www.wormbase.org.

We collected RNA from pooled nematodes taken from all life cycle stages and subjected to various conditions (growing in larvae of two different insect species and on two different in vitro media, as described in Materials and Methods) in order to maximize the inclusion of condition-specific genes. We obtained 15,180,085 reads with an average length of 201 bp from an Illumina paired-end library on a MiSeq, and 92,231 reads with an average length of 288 bp from a 454 library on a partial 454 FLX + plate. After quality filtering, 94.93% of the reads mapped to the masked genome, suggesting a good reliability of the genome assembly. We performed genome-guided de novo assembly of the transcriptome that resulted in 21,457,711 bp of assembled transcripts (without introns). In order to identify protein-coding genes in the assembled genome, we assigned specific weights to different types of evidence to generate consensus gene calls (see Material and Methods). The current genome sequence and annotation is available at www.genomevolution.org (ID 33774), and at the NCBI GenBank (BioProject ID# 39853).

In summary, the use of an isogenic line (see Material and Methods), the combination of different sequencing platforms (Table 1), and an improved annotation strategy, resulted in a higher quality genome compared to a recent publication (Table 2). In any case, the studies used different strains of the nematode, and their goals were different, with Dillman et al. 10 focusing on comparing their genome to that of other species of Steinernema. In our study, we obtained a higher quality genome, included analyses of the proteome and small RNAs, and performed a genome-wide scan of positive selection.

The most abundant GO terms in predicted genes are shown in Fig. 1. Our analysis revealed 135 enriched GO terms in S. carpocapsae when compared to those in C. elegans (Fisher's exact test, FDR ≤ 0.05) (Supplementary Table S3). Many of these GO terms are involved in degradation, protein modification, binding and transport, and could
be associated to parasitism (reviewed in ref. 16). At least 22 GO terms are also enriched in at least two other pathogenic worms, but not in the free-living nematode *Pristionchus pacificus* (Table 3). Supplementary Table S4 shows the abundance of the different protein families in 10 different nematode genomes compared with the 30 most abundant families in *S. carpocapsae* (Supplementary Fig. S1). Most of the expanded families (16 out of 20) identified previously in the “All” strain of *S. carpocapsae* are also overrepresented in our strain (Breton). In addition, Peptidase S1 is also overrepresented in *S. carpocapsae* and other parasites (*Bursaphelenchus xylophilus*, *Meloidogyne hapla*, and *M. incognita*) compared to *C. elegans*. Integrase, enoyl-acyl-carrier-protein reductase (ENR) (IPR014358), retrotransposon pao, and pimelyl-acyl-carrier protein methyl ester esterase PFAM domains, are also overrepresented in some parasites, including *S. carpocapsae*.

Since *C. elegans* and *S. carpocapsae* are phylogenetically distant from one another, we found no evident macro-synteny. However, there are genes located in single chromosomes of *C. elegans* that match genes located in single scaffolds of *S. carpocapsae*. A similar result was obtained in a comparison with the *Brugia malayi* genome (version WS253) (Fig. 2 and Table 4), even though this genome is not of the same quality as that of *C. elegans*. This reinforces the idea that the use of *B. malayi* gene models in the annotation strategy is at least as good as the use of *C. elegans* models.

Beyond the protein-coding potential of the genome, we predicted non-coding RNA (ncRNA) using a variety of tools (see Materials and Methods), identifying 1,097 tRNAs, 40 rRNAs (15 5S rRNA, 1 5.8S rRNA and 24 8S rRNA), 38 micro-RNA hairpins and 146 other ncRNAs. Using the same annotation pipeline, we compared the abundance of each ncRNA family in parasitic (*Ascaris suum, Bursaphelenchus xylophilus, Brugia malayi, S. carpocapsae, M. incognita, M. hapla and Heterorhabditis bacteriophora*) and free-living (*Panagrellus redivivus, Pristionchus pacificus, C. remanei and C. elegans*) nematodes (Supplementary Table S5). By comparing the average number of elements in each family between parasitic and free-living nematodes, we derived a simple metric to decide if a family had a tendency to be enriched in one of the two lifestyles (see Materials and Methods). The families enriched in parasitic nematodes are, ACEA_U3 (a snoRNA), SeC (a tRNA), mir-100/mir-10, mir-227, mir-2b, mir-2444, and mir-4455 (microRNAs), all of which have at least twice the number of elements on average in the parasites (Supplementary Fig. S2). Although the correlation between these families and parasitism needs to be further investigated, this is a first indication that these ncRNA families might have a functional role in the pathogenic lifestyle.

To complement these bioinformatic predictions we performed small RNA-seq of *S. carpocapsae* with and without induction with insect hemolymph. We obtained a total of 42.8 million reads from 6 libraries. Less than 10% of the cleaned reads failed to map to the genome (see Materials and Methods), another indication that the genome assembly is very complete. We used two of the most popular tools to annotate known and novel microRNAs using small RNA sequencing data: miRDeep17 and ShortStack18. Both tools coincided in predicting 100 miRNAs, while

Figure 1. Enrichment analysis of GO terms in annotated sequences of *Steinernema carpocapsae*, in relation to those in *Caenorhabditis elegans*. 

![Enrichment analysis of GO terms](https://www.nature.com/scientificreports/)
miRDeep predicted an additional 162, and ShortStack 25 more, giving a total of 287 miRNA hairpins, each with a potential 5′ and 3′ mature product (Supplementary Table S6). These predictions followed an expected length distribution, with a dominant peak centred at 22 nucleotides. Of the sRNA sequencing reads of 20–24 nucleotides that mapped to the genome, 83% overlapped with the 287 miRNA hairpins (Supplementary Fig. S3). Interestingly, we detected a large number of novel miRNA genes, since only 25 out of the 287 predicted miRNA hairpins correspond to known miRNAs according to homology searches. Although the majority of the conserved miRNAs tend to have high expression in our experiments, half of the 20 most highly expressed miRNA predictions correspond to novel sequences (Supplementary Table S7). This confirms the great diversity of ncRNA genes that are species or

| GO-ID     | Term                                      | Sc | As | Bm | Bx | Di | Hb | Ll | Mh | Mi | Ov | Sr | Ts | #Sp |
|-----------|-------------------------------------------|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| GO:0005524 | ATP binding                               |    |    |    |    |    |    |    |    |    |    |    |    | 12  |
| GO:0003374 | translation initiation factor activity    |    |    |    |    |    |    |    |    |    |    |    |    | 11  |
| GO:0003964 | RNA-directed DNA polymerase activity      |    |    |    |    |    |    |    |    |    |    |    |    | 11  |
| GO:0006278 | RNA-dependent DNA replication             |    |    |    |    |    |    |    |    |    |    |    |    | 11  |
| GO:0015074 | DNA integration                           |    |    |    |    |    |    |    |    |    |    |    |    | 11  |
| GO:0034754 | cellular hormone metabolic process         |    |    |    |    |    |    |    |    |    |    |    |    | 9   |
| GO:0019915 | lipid storage                              |    |    |    |    |    |    |    |    |    |    |    |    | 7   |
| GO:0002824 | positive regulation of cell proliferation |    |    |    |    |    |    |    |    |    |    |    |    | 6   |
| GO:0004190 | aspartic-type endopeptidase activity      |    |    |    |    |    |    |    |    |    |    |    |    | 6   |
| GO:0006446 | regulation of translational initiation     |    |    |    |    |    |    |    |    |    |    |    |    | 4   |
| GO:0006744 | ubiquinone biosynthetic process            |    |    |    |    |    |    |    |    |    |    |    |    | 4   |
| GO:0008270 | zinc ion binding                           |    |    |    |    |    |    |    |    |    |    |    |    | 4   |
| GO:0045333 | cellular respiration                       |    |    |    |    |    |    |    |    |    |    |    |    | 4   |
| GO:0002824 | oxidation-reduction process                |    |    |    |    |    |    |    |    |    |    |    |    | 4   |
| GO:0006913 | nucleocytoplasmic transport                |    |    |    |    |    |    |    |    |    |    |    |    | 4   |
| GO:0015992 | proton transport                           |    |    |    |    |    |    |    |    |    |    |    |    | 3   |
| GO:0046339 | diacylglycerol metabolic process           |    |    |    |    |    |    |    |    |    |    |    |    | 3   |
| GO:0004180 | carboxypeptidase activity                  |    |    |    |    |    |    |    |    |    |    |    |    | 3   |
| GO:0006686 | intracellular protein transport            |    |    |    |    |    |    |    |    |    |    |    |    | 3   |
| GO:0009792 | embryo development ending in birth or egg hatching |    |    |    |    |    |    |    |    |    |    |    |    | 3   |
| GO:0006821 | chloride transport                         |    |    |    |    |    |    |    |    |    |    |    |    | 3   |
| GO:0004252 | serine-type endopeptidase activity         |    |    |    |    |    |    |    |    |    |    |    |    | 3   |

Table 3. Enriched GO terms in the genome of *Steinernema carpocapsae* and in at least two other pathogenic species but not in the free-living nematode *Pristionchus pacificus*, as compared to the free-living nematode *Caenorhabditis elegans*. Sc, *Steinernema carpocapsae*; As, *Ascaris suum*; Bm, *Brugia malayi*; Bx, *Bursaphelenchus xylophilus*; Di, *Dirofilaria immitis*; Hb, *Heterorhabditis bacteriophora*; Ll, *Loa loa*; Mh, *Meloidogyne hapla*; Mi, *M. incognita*; Ov, *Onchocerca volvulus*; Sr, *Strongyloides ratti*; Ts, *Taenia solium*. Up, enriched term in that species (and in *S. carpocapsae* but not in *P. pacificus*) as compared with *C. elegans*.

Figure 2. Schematic representation of shared sequences between *Steinernema carpocapsae* and (A) *Caenorhabditis elegans*, or (B) *Brugia malayi*, both based in HSPs (E-value < 1e-6).
lineage specific, and highlights the importance of using experimental data when annotating genomes, particularly for species that are distant to well annotated model organisms.

We were also interested to see if any of the microRNAs that we detected changed their expression in response to insect haemolymph. None of the miRNAs showed a significant decrease in expression, but five increased their expression after hemolymph induction (Supplementary Table S7 and Supplementary Fig. S4). These miRNAs were miR-84–3p, miR-84–5p, miR-31–3p, let-7–5p and Cluster_21397_3p (a new prediction with no similarity to known miRNAs). Interestingly, the induced miRNAs included miR-84 and let-7, members of the let-7 family of miRNAs that are important players during development. In *Caenorhabditis elegans*, double mutants of miR-84 and miR-48 (another let-7 family member) show a delayed moulting phenotype and accumulate a double cuticle19. This is interesting because *S. carpocapsae* infective juveniles have a double cuticle that is lost upon entering the insect host8. The up-regulation of miR-84 and let-7 could thus be involved in the moulting process, triggered by the contact with insect haemolymph.

Differentially expressed proteins. During infection, the nematodes first invade the insect intestine and then cross the intestinal wall by expressing putative effectors that facilitate parasite penetration to the hemocoel, where they continue to counteract insect defences10,20. Therefore, we were interested in comparing the soluble proteins from Infective Juveniles (IJs) induced with either insect intestines or insect hemolymph, against non-induced controls. We opted for a detection strategy combining shotgun proteomics strategy, with two-dimensional electrophoresis (2DE), and SDS-PAGE, that resulted in the identification of 7,527 proteins.

By eliminating duplicates (proteins that were detected more than once), we obtained 3,773 non-redundant proteins (Supplementary Table S2). Among the non-redundant proteins, 1,625 were expressed in the three conditions, 155 were only expressed under both hemolymph and intestine induction, and 349 were expressed in the control and one other condition. In addition, 489 proteins were exclusively expressed in nematodes induced with intestine, 510 in those induced with hemolymph, and 645 in the non-induced controls (Fig. 3). This suggests that specific activities occur at different stages during the pathogenic process. Proteins expressed specifically in the induced conditions, were associated with functional categories (GO terms) using Blast2GO (Supplementary Figs S5 and S6). We found four GO terms enriched among the 489 proteins expressed exclusively in the intestine-induced sample, 10 GO terms in the 510 proteins of the hemolymph-induced sample, and 8 GO terms in the 1,154 combined proteins from both induction conditions (Fisher’s exact test, p < 0.05); in all cases in relation to the untreated control (Supplementary Table S8). One of the differentially expressed proteins was a transthyretin-like protein (TLP). Unlike transthyretins, which are known for transporting thyroxine and related molecules, the function of TLPs is not well understood21. They seem to have a role in the uricase reaction pathway as 5-hydroxyisourate hydrolases22. Their abundance in parasitic nematodes and more specifically their expression during parasitic stages, suggests an involvement of TLPs in parasitism22,23. We also found other differentially expressed peptides in the parasitic stages of *S. carpocapsae* that, being found in other parasites, could be involved in the infective processes (Supplementary Table S2).

Proteases and excretory/secretory proteins. We found all types of proteases in the genome of *S. carpocapsae*. Proportions of most of them (Aspartic, Cysteine, and Threonine) are similar to the proportions found in free-living (*C. elegans*), necromeric (*P. pacificus*), and parasitic (*B. malayi, Strongyloides ratti*) nematodes. However, the amount of serine proteases in *S. carpocapsae* and *P. pacificus* genomes is higher than in other nematodes (39% and 33.2% of all proteases, respectively); while in *S. carpocapsae* the percentage of metalloproteases, although high (31%), is the lowest in the comparison (the highest is in the *Strongyloides ratti* genome with 52%).

Excretory/secretory (ES) products are complex mixtures of hundreds of different proteins that are thought to have important roles in the life cycle of a parasite and during host-parasite interactions8. A total of 1,421
Putative excreted proteins were predicted in the genome (see Methods), including various families of proteases, protease inhibitors, cuticular collagens, and C-type lectins, as well as putative signalling molecules such as warthog, ground and ground-like proteins (Supplementary Table S9). Some ES proteins are predicted to be involved in immuno-evasion; such as collagen25, whereas others play crucial roles in the suppression of host immune responses by mimicking host molecules, such as C-lectin26,27. Furthermore, C-lectins have been found to be upregulated in Ancylostoma ceylanicum at the onset of heavy blood feeding from the host28. We also found three putative copies of parasitic stage specific protein 1, a protein without known domains, which is present in several parasitic nematodes and is expressed during the transition to the parasitic lifestyle in Haemonchus contortus29. Other interesting putative secreted peptides in the S. carpocapsae genome were lipases, saposins, and transthyretin-like protein, all of which are expressed during early parasitic stages in H. contortus29. Serine proteases, including Sc-SP-1 and Sc-SP-3, can mediate the invasion or apoptosis of host cells10,20. Astacin metalloprotease is one of the effector molecules involved in tissue invasion of parasitic nematodes30. The family of papain-type aspartic and cysteine proteases are thought to have the same role in invertebrate digestion as trypsin in vertebrates31. Therefore, it is possible that the dependence of S. carpocapsae on aspartic protease activities is related to the digestion of nutrients. Cysteine proteases are involved in digestive processes or molting and cuticle renewal in free-living and parasitic nematodes32,33.

Orthologous proteins. We compared 7,724 orthologous groups of proteins among several species with different lifestyles. We found 318 orthologous groups that are absent in non-pathogenic species (Caenorhabditis angaria, C. remanei, C. briggsae, C. japonica, C. elegans, and Pristionchus pacificus) but present in S. carpocapsae and in at least another pathogenic nematode (Supplementary Table S10). The annotations of these orthologues revealed enrichment of protein functions with possible associations with parasitism, such as serine proteases and other terms related to degradation and binding (Table 5). We also found 134 additional groups from the orthoMCL-DB (version 5) database that are present in the genome of S. carpocapsae but not in the other tested species (Supplementary Table S11).

Positive selection. Because of the co-evolutionary arms-race relationship between hosts and their pathogens, genes involved in their interaction are expected to evolve under positive selection34, potentially resulting in specific genomic signatures associated with their lifestyles35. We used the branch-sites test of positive selection36,37 to analyse 2,034 orthologous genes in three species of Clade IV nematodes (as defined in ref. 38). This test is based on a maximum likelihood estimation of the nucleotide nonsynonymous and synonymous substitution rates. The ratio of nonsynonymous to synonymous rates (ω) can be used to identify purifying selection (ω < 1), neutral evolution (ω = 1), or positive selection (ω > 1), assessing the significance with a Likelihood Ratio Test (LRT)36. We found 83 genes with sites evolving under positive selection (ω > 1, LRT, p < 0.05; 14 of which had an FDR < 0.1) in S. carpocapsae (Table 6). Among the 83 genes, 23 GO terms were significantly enriched (Supplementary Table S12) when compared to the genes with no sites under positive selection (1,951 genes) (Fisher’s exact test, p < 0.01). Although we found more genes (95) with sites evolving under positive selection in the free-living nematode Panagrellus redivivus, there were no enriched GO terms among them (even with an alpha value of 0.05), indicating that the consequence of an arms-race relationship is better characterized by positive selection preferentially altering genes of specific functions than just increasing the number of positively
selected genes. Although we would need to increase the number of analysed genes to increase the power of these analyses, the initial results suggest a new perspective to the co-evolutionary arms-race theories. 

Phylogenetic analysis. To explore the phylogenetic relationships of *S. carpocapsae*, we reconstructed a phylogeny using 245 proteins from strictly 1-1 orthologous genes from nine nematode species. According to Blaxter et al.38, *Steinernema* is phylogenetically closer to *Strongyloides* than to *Caenorhabditis*, as inferred from a tree reconstructed using the small subunit ribosomal DNA (18S) sequences from 53 nematode species. A similar result was obtained in a more extensive analysis using 339 18S sequences39. However, Montiel et al.40 found *Steinernema* to be closer to *Caenorhabditis* than to *Strongyloides* using complete mtDNA sequences. Although this discrepancy may result from differential reproductive strategies and/or differential selective pressures acting on nuclear and mitochondrial genes40, an analysis of large subunit ribosomal DNA sequences (28S) also showed *Steinernema* to be closer to *Caenorhabditis* than to *Strongyloides* using complete mtDNA sequences. Although this discrepancy may result from differential reproductive strategies and/or differential selective pressures acting on nuclear and mitochondrial genes, an analysis of large subunit ribosomal DNA sequences (28S) also showed *Steinernema* to be closer to *Caenorhabditis* than to *Strongyloides*. Defining these relationships is relevant because if *Steinernema* is phylogenetically closer to *Strongyloides*, it could be used as a more general model for parasitism, with implications for human health. *Steinernema* is more tractable than *Strongyloides* because it does not require a vertebrate host to reproduce in the laboratory. Our new phylogenetic analysis supports *Steinernema* being closer to *Strongyloides* than to *Caenorhabditis* (Fig. 4). In addition, its basal position in relation to *Strongyloides*, gives support to the hypothesis that this vertebrate parasite originated by host shifting from an entomopathogenic ancestor12, in this case *Steinernema*.

Table 5. Enrichment of Gene Ontology (GO) terms of orthologs absent in non-pathogenic nematodes (*Caenorhabditis angaria, C. remanei, C. briggsae, C. japonica, C. elegans, and Pristionchus pacificus*) and present in *S. carpocapsae* and at least another parasitic nematode compared to *C. elegans* GO terms.

| GO-ID      | Term                                           | Category | FDR   | P-Value |
|------------|------------------------------------------------|----------|-------|---------|
| GO:0045449 | regulation of transcription, DNA-dependent     | P        | 4.30E-16 | 8.08E-20 |
| GO:0004252 | serine-type endopeptidase activity             | F        | 7.73E-15 | 2.90E-18 |
| GO:0005667 | transcription factor complex                    | C        | 8.03E-12 | 4.52E-15 |
| GO:0008236 | serine-type peptidase activity                 | F        | 1.25E-11 | 1.17E-14 |
| GO:0017171 | serine hydrolase activity                      | F        | 1.25E-11 | 1.17E-14 |
| GO:0045941 | positive regulation of transcription, DNA-dependent | P    | 2.16E-05 | 2.44E-08 |
| GO:0004175 | endopeptidase activity                         | F        | 1.78E-04 | 2.34E-07 |
| GO:0043234 | protein complex                                | C        | 3.18E-03 | 5.09E-06 |
| GO:0005515 | protein binding                                | F        | 3.18E-03 | 5.37E-06 |
| GO:0045935 | positive regulation of nucleobase-containing compound metabolic process | P | 4.95E-03 | 1.11E-05 |
| GO:0051254 | positive regulation of RNA metabolic process   | P        | 4.95E-03 | 1.11E-05 |
| GO:0051173 | positive regulation of nitrogen compound metabolic process | P   | 4.95E-03 | 1.11E-05 |
| GO:0008233 | peptidase activity                             | F        | 8.30E-03 | 2.02E-05 |
| GO:0003713 | transcription coactivator activity             | F        | 8.41E-03 | 2.21E-05 |
| GO:0010628 | positive regulation of gene expression         | P        | 1.00E-02 | 2.98E-05 |
| GO:0043170 | macromolecule metabolic process                | P        | 1.00E-02 | 3.02E-05 |
| GO:0070011 | peptidase activity, acting on L-amino acid peptides | F  | 1.01E-02 | 3.40E-05 |
| GO:0006508 | proteolysis                                    | P        | 1.01E-02 | 3.42E-05 |
| GO:0010557 | positive regulation of macromolecule biosynthetic process | P | 3.65E-02 | 1.49E-04 |
| GO:0045298 | tubulin complex                                | C        | 3.65E-02 | 1.58E-04 |
| GO:0033202 | DNA helicase complex                           | C        | 3.65E-02 | 1.58E-04 |
| GO:0031011 | Ino80 complex                                  | C        | 3.65E-02 | 1.58E-04 |
| GO:0097346 | INO80-type complex                             | C        | 3.65E-02 | 1.58E-04 |

Table 6. Genes with sites evolving under positive selection in *Steinernema carpocapsae* (Sc), *Panagrellus redivivus* (Pr), and *Strongyloides ratti* (Sr).

| Orthologue genes analysed by the Branch-site test | N = 2,034 |
|--------------------------------------------------|-----------|
| Tested branch                                    | Sc        | Pr       | Sr       |
| Genes with sites under positive selection (ω > 1, LRT, p < 0.05) | 83 (4.08%) | 95 (4.67%) | 8 (0.39%) |
| Average proportion of sites under positive selection per gene (s.d.) | 6.49% (0.067) | 7.47% (0.093) | 17.31% (0.187) |
Gene functions enriched at several levels. To assess how the pathogenic lifestyle is affecting specific gene functions at different levels, we compared the GO terms enriched in the genome of *S. carpocapsae* when compared to *C. elegans* (Supplementary Table S3), with those in differentially expressed proteins due to hemolymph or intestine induction (Supplementary Table S8), and with those in genes with putative sites evolving under positive selection (Supplementary Table S12). One GO term was enriched in the genome and in differentially expressed proteins (transcription factor activity – sequence-specific DNA binding); and two GO terms in both the genome and genes under positive selection (macromolecular complex and ribonucleoprotein complex). No GO terms were shared between the three analyses. However, one protein, ATAD-3 (ATPase family AAA domain-containing protein 3), is associated with 33 enriched GO terms in the annotated sequences, and two additional enriched GO terms from genes with evidence of positive selection (Supplementary Table S13). This protein is differentially expressed in nematodes induced with insect tissues (intestines) and presents amino acid sites evolving under positive selection. Functions or proteins shared between these analyses might reveal relevant effects of the pathogenic lifestyle in the genome. A deeper analysis of positive selection (i.e. including more orthologous genes or conducting population genetic analyses) could expand the number of shared genes, which should be good candidates for further studies. In this case we have identified a putative homolog of *C. elegans*’ ATAD-3. Its deficiency in *C. elegans* causes early larval arrest, gonadal dysfunction, and embryonic lethality. It is also associated with defects in organellar structure and mtDNA depletion42,43, suggesting that ATAD-3 is important for increased mitochondrial activity during the transition to later larval stages45. *S. carpocapsae* needs to go through developmental changes to establish itself in the insect body during the pathogenic process, which might explain the relevance of this, and probably other mitochondria-related genes, in nematode parasitism. For example, the defective mitochondrial respiration family member protein 1, with functions in regulation of growth rate, was differentially expressed in nematodes induced with insect tissues (hemolymph) and presented evidence of positive selection. Mitochondria have been identified as important contributors to the virulence of fungal pathogens44, and it has been previously hypothesised that differential selective constraints in mitochondrial genes might explain discrepancies between nuclear and mitochondrial gene phylogenies in nematodes40. In addition, depletion of ATAD-3 in *C. elegans* resulted in reduced intestinal fat storage42, and it would be interesting to explore if fat metabolism might also be relevant in nematode parasitism.

Conclusion

Our genomic analyses of *S. carpocapsae* confirm a role in pathogenicity beyond simply vectoring the symbiotic bacteria. *S. carpocapsae* shares orthologous genes with other parasitic nematodes that are absent in the free-living nematode *C. elegans*, it encodes ncRNA families that are enriched in parasites, and presents putative proteins associated with functions related to parasitism and pathogenesis. Until now, the best examples of positive selection in genes related to host-pathogen interactions were pathogen effectors and genes of the host immune and defence systems34. Our analyses indicate that positive selection can also alter genes belonging to other functional categories, such as metabolism and development, adding a new aspect to the arms-race co-evolutionary theories. Through a comprehensive analysis, we identified a protein, ATAD-3, suggesting a relevant role for mitochondria during the evolution of nematode parasitism that warrants further investigation. We provide additional evidence for the phylogenetically relatedness of *S. carpocapsae* to *Strongyloides*, making this high-quality genome valuable for comparative studies with potential implications for human health. Our genome also represents a useful resource to aid ongoing efforts towards the genetic improvement of entomopathogens as biological control agents as well as to better understand host-parasite interactions in nematodes.

Materials and Methods

Organisms, maintenance and storage. *Steinernema carpocapsae* strain Breton was obtained from Nelson Simões, and cultured using in vitro methods. Nematodes were grown using a modified protocol for mass production in artificial medium according to ref. 45, as well as in small-scale, on plates containing Fortified Lipid.
Agar (FLA) prepared with 1.6% TSB (nutrient broth), 1% vegetable oil, 1.2% bacteriological agar, and 5% yeast extract (modified from ref. 46). A near-isogenic line of *S. carpocapsae* strain Breton was generated by reproduction of single couples of brother and sister for 12 generations (F12). This produces ~96% homozygosis47.

**DNA isolation, sequencing and quality control.** Total genomic DNA was isolated from the nuclei48 using the phenol/chloroform extraction protocol described by Sambrook *et al.*49. Total DNA yield and integrity was measured with a 2100 Bioanalyzer (Agilent) using an Expert High Sensitivity DNA chip. Three high-quality libraries for Next Generation Sequencing (NGS) were prepared following manufacturer’s instructions. One shotgun 454 library was sequenced in three 454 FLX runs. One 454 paired-end library with 8-kb inserts was sequenced in two 454 FLX runs. Finally, a SOLiD shotgun library was tagged and sequenced, along with a different library (from other organisms), in a lane of SOLiD 5500xl, equivalent to half a lane of SOLiD sequencing. Low-quality sequences, base-calling duplicates and adapters were removed from all the sequence data (see below).

**Genomic assembly and filtering.** All DNA-sequence reads were filtered to remove contamination of the endosymbiotic bacteria *Xenorhabdus nematophila* (Xn). A genomic dataset was created by adding the published genome of Xn strain ATCC 19061 to the unpublished genome of the Xn strain isolated from the *S. carpocapsae* strain Breton nematodes, produced in our laboratory. The dataset was used for contamination screening and filtering using GS Assembler 2.7.

Raw standard flowgram format (sff) files coming from 454 platforms were assembled using GS Assembler 2.7 with the default trimming parameters. Basespace reads coming from the SOLiD platform using the Exact Call Chemistry Module (that allows conversion from colour to basespace) were filtered to remove PCR clonal repeats as well as reads with ambiguous bases. Subsequently, sequences were filtered based on Phred quality values. Bases below Phred18 were removed from 3’ ends and only reads longer than 20 bp were kept. Filtered data were assembled into contigs using GS Assembler 2.7, and joined into scaffolds using the paired-end data.

GC-content was estimated from the scaffolds using 10-kb non-overlapping sliding windows, and GC-bias was assessed based on a frequency distribution of these data. To evaluate the completeness of the genome assembly, we followed two strategies. RNA-seq sequences representing all different stages and diverse culture conditions of *S. carpocapsae* were mapped to the final assembly using Newbler (GS Reference Mapper v2.7). In addition, we analysed the completeness of 248 ultra-conserved core eukaryotic genes13. We expect a complete genome will contain a higher number of complete ultra-conserved genes.

**Estimation of genome size.** Genome size was estimated from the genomic assembly using GS Assembler 2.7 and corroborated through flow cytometry of the isolated cellular nuclei of *S. carpocapsae* using the nuclei of *C. elegans* strain N2 (genome size approx. 100 Mb10) as a size control. Nuclei were stained with CyStain® UV Ploidy (Partec 05-5001), and fluorescence was detected at λ ≤ 420 nm and quantified using a PARTECPAI (Partec, Germany) flow cytometer with a mercury lamp (100 W UV light).

**Assessment of repeat content.** Following genome assembly, repeats were identified using a combination of homology-based comparisons (using RepeatMasker51) and a de novo approach (using RepeatModeler52).

**Annotation of non-coding RNA.** Covariance models from Rfam53 were used to scan the genomes using Infernal software44. In addition, tRNAs were predicted using tRNAScan-SE55 and rRNAs were predicted using RNAmer56. Finally, microRNA precursor sequences (miRNA hairpins) were located using MapMi57, using all mature miRNA sequences from miRBase 2158 as input. MapMi results were filtered selecting only microRNA precursor sequences with score ≥ 420 nm and quantified using a PARTECPAI (Partec, Germany) flow cytometer with a mercury lamp (100 W UV light).

**RNA isolation, sequencing and assembly.** Total RNA was extracted from a pool of individuals from all lifecycle stages (eggs at different stages, L1, L2, L3, IJ, L4, and adults), cultured *in vivo* infecting *Galleria mellonella* and *Tenebrio molitor* larvae as described44, as well as all lifecycle stages cultured *in vitro* using the methods described in the Organisms, maintenance and storage section45,46. The final pool consisted of approximately 3 mg of individuals from each stage/condition. RNA was extracted using TRizol (Invitrogen) according to the manufacturer’s instructions with an additional step using Qiagen RNAeasy Mini Elute Clean up columns and buffers to clean and concentrate the RNA.

An Illumina paired-end library and a 454 library were generated for RNA-seq, which were run on a full plate of MiSeq and a partial plate of a 454 FLX +, respectively. RNA-seq reads were quality filtered and mapped to the repeat-masked genome using Newbler gmapper. Read alignments were provided to Trinity62 (r2013-02-25) as a coordinate-sorted bam file. Trinity was used to assemble the aligned reads. The Trinity-reconstructed transcripts were aligned and assembled using the PASA262 (r20130425 beta) pipeline.

For small RNA (sRNA) sequencing, nematodes were induced for 2 hour with hemolymph of *Galleria mellonella* and with buffer as control44. Nematodes were ground under liquid nitrogen and RNA was extracted with
Trizol according to the manufacturer’s instructions. Six sRNA-Seq tagged libraries were prepared from three replicates of each condition, which were run in an Illumina HiSeq lane.

**Processing small RNA sequencing results.** All sRNA-Seq libraries were 3′-adaptor trimmed using the reaper tool from Kraken66. After trimming, reads between 18 and 36 nucleotides were mapped to the genome using ShortStack 3.35, setting the maximum number of mismatches to 1, no stich, multi-mappers guided by unique-mappers and removing reads that mapped to more than 101 locations. The raw and processed sRNA-Seq results were deposited in GEO (http://www.ncbi.nlm.nih.gov/geo), under accession GSE85256.

**Predicting expressed microRNA loci with miRDeep and ShortStack.** When using ShortStack to annotate, we set the Dicer minimum and maximum size parameters to 18 and 36, minimum alignment coverage (mincov) to 5 and maximum distance to merge clusters (pad) to 50. To improve the predicted microRNA producing loci, we used MirDeep217. The mapper.pl and miRDeep2.pl modules were used to identify known and novel miRNAs. Reads between 18 and 36 nucleotides were used, with a maximum number of mismatches of 1, and 101 maximum number of locations for multi-mapping reads. The minimum alignment coverage (-a) was set to 5, the maximum number of precursors to analyze was set to 1000, and all the mature sequences from miRBase 21 were provided. Although both programs take small RNA sequencing reads mapped to a genome to predict microRNA loci, they produce slightly different results. They coincided in predicting 100 miRNAs, while miRDeep predicted an additional 162 and ShortStack 25 more.

**Differential expression analysis of microRNAs.** To focus the differential expression analysis on miRNAs, only reads in the 20–24 nucleotide range were considered. After mapping these to the genome, on average 83% fell within miRNA hairpin and 63% within mature miRNA coordinates. For miRNA quantification, the featureCounts function of the RsubeRead R package56 was used, asking for a minimum overlap of one nucleotide to any of the mature miRNA annotations. For differential expression analysis, the edgeR package was used57. miRNAs with less than 3 counts-per-million in at least 3 libraries were removed, leaving 302 out of the 574 annotated mature miRNAs. The trimmed mean of M-values was chosen as normalization method58. Gene expression dispersion was estimated with the function estimateGLMTagwiseDisp, which uses an empirical Bayes strategy57. Differentially expressed miRNAs were determined with a generalized linear model and gene-wise likelihood ratio tests. A False Discovery Rate threshold of 0.1 was selected to consider a miRNA to be significantly differentially expressed. According to this threshold, five miRNAs were overexpressed in response to hemolymph treatment and none were down regulated. Cluster_19164 was identified as miR-84 by a manual sequence search on the miRBase website58.

**Gene prediction and synteny.** The S. carpocapsae protein-coding gene set was inferred using de novo, homology- and evidence-based approaches (Supplementary Fig. S7). De novo gene prediction was performed on a repeat-masked genome using Augustus44. Training models were generated using hints from a compilation of S. carpocapsae gene structures (CEGMA13 v2.4.010312) predictions, PASA assemblies from our RNA-seq data, and 2,269 publicly available ESTs from GeneBank). The homology-based prediction was conducted with Augustus algorithms for C. elegans and Brugia malayi. Synteny was assessed on scaffolds >1 Mb using pairwise alignments with E-value < 10^-8 and homologous regions were visualized using CIRCOS60. Macro-synteny was analysed using the SynFind and SynMap tools from CoGe70,71.

**Functional annotation of coding genes.** Following the prediction of the protein-coding gene set, we conducted high-stringency BLASTp homology searches (E-value ≤ 10^-5) against the NCBI non-redundant protein database. Functional annotation was performed using Blast2GO72. Gene ontology categories were summarized and standardized to level 2 and level 3 terms, defined using the GOslim hierarchy73. For the secretion prediction, the signal peptide was predicted by SignalP 4.074 and Phobius75 employing both Hidden Markov Models and Neural Networks. Proteins were then filtered for the presence of transmembrane regions using THMMN76 and Phobious75. Subcellular localizations were identified using TargetP (>95% specificity)77 and WolfPSORT (score ≥ 30). Proteases and protease inhibitors were identified by homology searches to the MEROPS database79.

**Orthologous proteins.** Genes from different nematode species (Caenorhabditis angaria, C. briggsae, C. elegans, C. japonica, C. remanei, Pristionchus pacificus, Ascaris suum, Brugia malayi, Bursaphelenchus xylophilus, Heterorhabditis bacteriophora, Haemonchus contortus, Loa loa, Meloidogyne hapla, M. incognita, Onchocerca volvulus, Panagrellus redivivus, S. carpocapsae, Strongyloides ratti, Trichinella spiralis, and Wuchereria bancrofti) were assigned to OrthoMCL80 orthologous groups, and the presence or absence of groups was compared among the different species using ad hoc scripts from scriptome (http://archive.sysbio.harvard.edu/csb/resources/computational/scriptome/UNIX/).

**Additional bioinformatics analyses and use of software.** Data analysis was conducted in a UNIX environment or Microsoft Excel 2007 using standard commands. Bioinformatic scripts required to facilitate data analysis were designed using bash, GNU coreutils, Perl, and Python.

**Proteomic analysis. ** Sample preparation. Nematodes were induced as described64 with slight modifications. A pool of approximately 25,000 nematodes were induced with either hemolymph or intestine of Galleria mellonella. To obtain hemolymph we grinded G. mellonella larvae in liquid nitrogen, added a volume of cold
these time points we followed the infection process. At one hour to start traversing the intestine wall and at two hours, most of them were in the hemocoel. We included two additional time points for the nematodes to release the symbiotic bacteria. Nematodes without induction were used as a negative control. Nematodes were incubated in liquid nitrogen and suspended in lysis buffer (7 M urea, 2 M thiourea, 3% CHAPS) with trypsin inhibitor mix GE and sonicated at a frequency of 20 kHz. After centrifugation for 1 min at 16,000 rcf and 0.45 μm filter and supernatant was precipitated with a 2D Clean-up kit (GE Healthcare), resuspended in DeStreak solution (GE Healthcare Cat. No. 17600318), and quantified with the Bradford Method.

Protein sequences of all organisms were downloaded from WormBase (ftp.wormbase.org release WS241 29-Nov-2013). Orthologous genes for nine species were identified with OrthoMCL (v5). Protein-coding genes from those species were carbamidomethylation C (fixed), deamination NQ (variable), and oxidation M (variable).

Phylogenetic analysis. Protein sequences of all organisms were downloaded from WormBase (ftp.wormbase.org release WS241 29-Nov-2013). Orthologous genes for nine species were identified with OrthoMCL (v5). A total of 245 orthologous proteins were aligned with MUSCLE (v3.8.31) and Phylogenetically informative blocks were recovered with Gblocks and the best-fit evolutionary model for each aligned protein was predicted by ProtTest. MrBayes was used for phylogenetic reconstruction using concatenated alignments. Partitions were created by grouping proteins according to their best-fit model, i.e., each partition contained all the proteins evolving under the same model. A mixed model was applied to each partition, with different G, I, and F parameters andunlinking the model between partitions. To check for convergence, two runs with four chains each were performed. The analysis was run for 1,000,000 generations, and a burn-in of 25% was used. B. malayi and Ascaris suum were used to root the tree because these species were the most phylogenetically basal of the nine nematode species in the phylogenies obtained by both Blaxter et al. and Nadler et al.

Analysis of positive selection. We used protein-coding genes from Panagrellus redivivus, Strongyloides ratti and Steinernema carpocapsae, all nematodes from phylogenetic clade IV, according to Blaxter et al. All nucleic and amino acid sequences, except for H. bacteriophora, were downloaded from WormBase (ftp.wormbase.org) and Next ProtTest. MrBayes was used for phylogenetic reconstruction using concatenated alignments. Partitions were created by grouping proteins according to their best-fit model, i.e., each partition contained all the proteins evolving under the same model. A mixed model was applied to each partition, with different G, I, and F parameters and unlinking the model between partitions. To check for convergence, two runs with four chains each were performed. The analysis was run for 500,000 generations, and a burn-in of 25% was used. B. malayi and Ascaris suum were used to root the tree because these species were the most phylogenetically basal of the nine nematode species in the phylogenies obtained by both Blaxter et al. and Nadler et al.
org release WS241 29-Nov-2013). Orthologues proteins obtained with OrthoMCL (v5)\(^{30}\) were aligned with ClustalW2 (v2.1)\(^{37}\). After selecting phylogenetically informative sites with Gblocks\(^{41}\), and estimating the best-fit model with ProtTest\(^{46}\), we reconstructed a consensus phylogenetic tree with PhyML (v.3.0)\(^{48}\). A nucleotide alignment based on the complete amino acid alignment was obtained with SeqTrans (v1.4)\(^{39}\) to preserve codon homology. The tree and the nucleotide alignments of each orthogonal gene were used to assess signatures of natural selection with Codeml from the PAML package (v4.6)\(^{40}\), using the Branch-site model to identify genes with sites under positive selection. Annotation and functional enrichment in genes with positively selected sites were performed with Blast2GO\(^{72}\).

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Author Contributions

A.R.C., M.F.P., R.M., designed the study; M.F.P., H.E.R.A., L.C., conducted experiments; A.R.C., M.F.P., H.E.R.A., C.E.M.G., Y.-J.H., J.A.R.M., C.O.V., J.R.B.B., C.A.G., R.M., analysed data; N.Ch.H., N.S., R.M., contributed materials and reagents; A.R.C., M.F.P., R.M., wrote the paper, with contributions from H.E.R.A., Y.-J.H., C.O.V., J.R.B.B., C.A.G. All authors reviewed and approved the manuscript.

Additional Information

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