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Intestinal Transcriptomes of Nematodes: Comparison of the Parasites *Ascaris suum* and *Haemonchus contortus* with the Free-living *Caenorhabditis elegans*.

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BACKGROUND: The nematode intestine is a major organ responsible for nutrient digestion and absorption; it is also involved in many other processes, such as reproduction, innate immunity, stress responses, and aging. The importance of the intestine as a target for the control of parasitic nematodes has been demonstrated. However, the lack of detailed knowledge on the molecular and cellular functions of the intestine and the level of its conservation across nematodes has impeded breakthroughs in this application. **METHODS AND FINDINGS:** As part of an extensive effort to investigate various transcribed genomes from *Ascaris suum* and *Haemonchus contortus*, we generated a large collection of intestinal sequences from parasitic nematodes by identifying 3,121 *A. suum* and 1,755 *H. contortus* genes expressed in the adult intestine through the generation of expressed sequence tags. Cross-species comparisons to the intestine of the free-living *C. elegans* revealed substantial diversification in the adult intestinal transcriptomes among these species, suggesting lineage- or species-specific adaptations during nematode evolution. In contrast, significant conservation of the intestinal gene repertoires was also evident, despite the evolutionary distance of approximately 350 million years separating them. A group of 241 intestinal protein families (IntFam-241), each containing members from all three species, was identified based on sequence similarities. These conserved proteins accounted for approximately 20% of the sampled intestinal transcriptomes from the three nematodes and are proposed to represent conserved core functions in the nematode intestine. Functional characterizations of the IntFam-241 suggested important roles in molecular functions such as protein kinases and proteases, and biological pathways of carbohydrate metabolism, energy metabolism, and translation. Conservation in the core protein families was further explored by extrapolating observable RNA interference phenotypes in *C. elegans* to their parasitic counterparts. **CONCLUSIONS:** Our study has provided novel insights into the nematode intestine and lays foundations for further comparative studies on biology, parasitism, and evolution within the phylum Nematoda.

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