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Abstract  Plant-parasitic nematodes are important and cosmopolitan pathogens of crops. Here, we describe the generation and analysis of 1928 expressed sequence tags (ESTs) of a splice-leader 1 (SL1) library from mixed life stages of the root-lesion nematode Pratylenchus penetrans. The ESTs were grouped into 420 clusters and classified by function using the Gene Ontology (GO) hierarchy and the Kyoto KEGG database. Approximately 80% of all translated clusters show homology to Caenorhabditis elegans proteins, and 37% of the C. elegans gene homologs had confirmed phenotypes as assessed by RNA interference tests. Use of an SL1 approach, while ensuring the cloning of the 5' ends of mRNAs, has demonstrated bias toward short transcripts. Putative nematode-specific and Pratylenchus -specific genes were identified, and their implications for nematode control strategies are discussed.

Electronic Supplementary Material  Supplementary material is available in the online version of this article at http://dx.doi.org/10.1007/s00438-004-1054-0

Keywords  Pratylenchus - Expressed sequence tags (ESTs) - Comparative genomics - Gene expression - Parasite

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Introduction

Nematodes are the most pervasive pests in the world, and although the number of species is steadily increasing, the control of nematodes is still a challenge. Understanding the secretome of root nematodes is crucial for developing effective control strategies. In this study, we aim to characterize the secretome of the root-knot nematode, *Pratylenchus penetrans*, by analyzing its transcriptome.

Methods

We used a combination of cDNA cloning and large-scale gene expression analysis to identify genes involved in nematode-host interactions. This approach allowed us to identify genes that are specific to *P. penetrans* and those that are shared with other parasitic nematodes.

Results

Our analysis revealed that *P. penetrans* has a diverse secretome, with genes encoding proteins involved in various cellular processes, such as signal transduction, defense, and host cell invasion. We also identified genes that are specific to *P. penetrans* and may be involved in the unique pathogenicity of this nematode.

Discussion

The findings from this study will provide a valuable resource for understanding the molecular basis of nematode parasitism and for developing novel control strategies. Further research is needed to validate the identified genes and to understand their role in nematode biology and pathogenesis.

Conclusion

In conclusion, our study provides insights into the secretome of the root-knot nematode, *Pratylenchus penetrans*, and identifies potential targets for the development of effective control strategies. Further research is needed to validate these findings and to understand the molecular mechanisms of nematode parasitism.