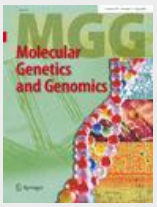

A survey of SL1-spliced transcripts from the root-lesion nematode *Pratylenchus penetrans*

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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-PCR 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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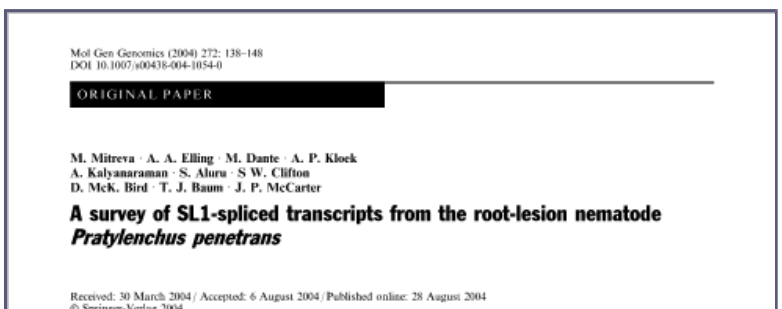
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ORIGINAL PAPER

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Referenced by
3 newer articles
1. Jacob, Joachim (2008) Exploring the transcriptome of the burrowing nematode Radopholus similis . *Molecular Genetics and Genomics* [CrossRef]
2. Vanholme, Bartel (2006) Detection of putative secreted proteins in the plant-parasitic nematode Heterodera schachtii. *Parasitology Research* 98(5) [CrossRef]
3. ROZE, ERWIN (2007) Mining the secretome of the root-knot nematode Meloidogyne chitwoodi for candidate parasitism genes. *Molecular Plant Pathology* 0(0) [CrossRef]

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Introduction

Nematodes are the most prevalent animals in the world (Boucher and Lambshead 1994). Although the roundworm body plan is broadly conserved (Bird and Bird 1991), different species exhibit unique life cycle adaptations, including parasitism of plants, insects and vertebrates (Blaxter and Bird 1997). Phylogenetic analysis (Blaxter et al. 1998) has shown parasitism to be phylum-wide, with multiple independent evolutionary origins (Blaxter 2003). To date, plant parasitism has been observed for members of three nematode clades (Blaxter et al. 1998). Species of Clade IV, which includes the tylenchid nematodes, are especially devastating to agricultural production (Koenning et al. 1999) and a significant effort has been made to generate expressed sequence tags (ESTs) from the Tylenchida. To date, approximately 100,000 sequences have been deposited in NCBI's GenBank, mainly from the root-knot (*Meloidogyne* spp.) and cyst (*Heterodera* and *Globodera* spp.) nematodes (McCarter et al. 2000, 2003a, 2003b; Popeijus et al. 2000a; Dautova et al. 2001b; Parkinson et al. 2003; Wylie et al. 2003). These genera establish elaborate long-term feeding sites within host roots. By contrast, root-lesion nematodes (genus *Pratylenchus*) are migratory plant endoparasites (Zunke 1990b). They have a wide host range, suggesting that *Pratylenchus* is a less specialized (i.e., more primitive) form of plant-parasite, possibly representing an evolutionary intermediate between the very specialized sedentary endoparasites and