Analysis and functional classification of transcripts from the nematode Meloidogyne incognita.


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BACKGROUND: Plant parasitic nematodes are major pathogens of most crops. Molecular characterization of these species as well as the development of new techniques for control can benefit from genomic approaches. As an entrée to characterizing plant parasitic nematode genomes, we analyzed 5,700 expressed sequence tags (ESTs) from second-stage larvae (L2) of the root-knot nematode Meloidogyne incognita. RESULTS: From these, 1,625 EST clusters were formed and classified by function using the Gene Ontology (GO) hierarchy and the Kyoto KEGG database. L2 larvae, which represent the infective stage of the life cycle before plant invasion, express a diverse array of ligand-binding proteins and abundant cytoskeletal proteins. L2 are structurally similar to Caenorhabditis elegans dauer larva and the presence of transcripts encoding glyoxylate pathway enzymes in the M. incognita clusters suggests that root-knot nematode larvae metabolize lipid stores while in search of a host. Homology to other species was observed in 79% of translated cluster sequences, with the C. elegans genome providing more information than any other source. In addition to identifying putative nematode-specific and Tylenchida-specific genes, sequencing revealed previously uncharacterized horizontal gene transfer candidates in Meloidogyne with high identity to rhizobacterial genes including homologs of nodL acetyltransferase and novel cellulases. CONCLUSIONS: With sequencing from plant parasitic nematodes accelerating, the approaches to transcript characterization described here can be applied to more extensive datasets and also provide a foundation for more complex genome analyses.

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