3. THE REPERTOIRE OF CELL WALL MODIFYING PROTEINS OF THE ROOT-KNOT NEMATODE MELOIDOGYNE CHITWOODI

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Meloidogyne chitwoodi, a root-knot nematode from temperate climate zones, has a wide range of host plants, including monocotyledons and dicotyledons. During invasion of the roots of a host plant the nematode is faced with the plant cell wall – a highly organized network of polysaccharides, proteins and aromatic compounds. To study the genes expressed in these initial phases of nematode-plant interaction we have undertaken an EST project with the pre-parasitic stage of this nematode species. A full-length cDNA library was constructed of water-hatched second-stage M. chitwoodi juveniles. Approximately, 4,000 5'-end expressed sequence tags were produced by randomly sequencing clones from this cDNA library. Sets with a significant homology to proteins involved in cell wall modification were selected to generate full-length cDNA sequences. Among these candidates we found sequences encoding β-1,4-endoglucanases, putative cellulose binding proteins in various configurations, pectate lyases, exo-polygalacturonases, xylanases and expansins. In situ hybridisation localised the transcripts of these genes in the subventral esophageal glands of preparasitic second-stage juveniles of M. chitwoodi. These results show that i) random sequencing of a cDNA library is a powerful method to identify genes involved in parasitism in relatively unexplored nematode species, and ii) the repertoire of cell wall modifying proteins identified in this project is the most elaborate found in a plant-parasitic nematode species so far.