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.