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Funding Source: MU Monsanto Undergraduate Research Fellowship

Functional characterization of the candidate nematode parasitism gene 2DO1

Nematode secreted proteins originating from esophageal gland cells are injected through the stylet directly into root tissues to facilitate plant parasitism. Microaspiration of soybean cyst nematode (SCN; *Heterodera glycines*) gland cell contents for cDNA library construction and in situ hybridization have identified more than 60 candidate parasitism genes encoding proteins containing a signal peptide and expressed specifically within gland cells. One of the candidate parasitism genes, Hg2DO1, encodes a 186 amino acid protein with a signal peptide and is specifically expressed in the dorsal gland of SCN. Hg2DO1 is a pioneer gene with no homology to any other sequences present in databases. We have determined the genomic structure of the Hg2DO1 gene and isolated both genomic DNA and corresponding cDNA sequences from the closely related nematode, *Heterodera schachtii*, for comparative analysis. Quantitative real-time PCR will be used to determine the expression pattern of Hg2DO1 throughout various stages of the nematode life cycle. For functional analysis of Hg2DO1, overexpression and RNAi constructs were generated and used to transform *Arabidopsis* and soybean hairy roots. These plants are being assessed for phenotypes and effects on parasitism, respectively. These studies will provide important insight into the mechanism of pathogenesis by this important pathogen of soybean.