

1: [BMC Genomics](#). 2009 Jan 30;10:58.



**Sequence mining and transcript profiling to explore cyst nematode parasitism.**

[Eling AA](#), [Mitreva M](#), [Gai X](#), [Martin J](#), [Recknor J](#), [Davis EL](#), [Hussey RS](#), [Nettleton D](#), [McCarter JP](#), [Baum TJ](#).

Interdepartmental Genetics Program, Iowa State University, Ames, IA 50011, USA. axel.elling@yale.edu

**BACKGROUND:** Cyst nematodes are devastating plant parasites that become sedentary within plant roots and induce the transformation of normal plant cells into elaborate feeding cells with the help of secreted effectors, the parasitism proteins. These proteins are the translation products of parasitism genes and are secreted molecular tools that allow cyst nematodes to infect plants. **RESULTS:** We present here the expression patterns of all previously described parasitism genes of the soybean cyst nematode, *Heterodera glycines*, in all major life stages except the adult male. These insights were gained by analyzing our gene expression dataset from experiments using the Affymetrix Soybean Genome Array GeneChip, which contains probeset sequences for 6,860 genes derived from preparasitic and parasitic *H. glycines* life stages. Targeting the identification of additional *H. glycines* parasitism-associated genes, we isolated 633 genes encoding secretory proteins using algorithms to predict secretory signal peptides. Furthermore, because some of the known *H. glycines* parasitism proteins have strongest similarity to proteins of plants and microbes, we searched for predicted protein sequences that showed their highest similarities to plant or microbial proteins and identified 156 *H. glycines* genes, some of which also contained a signal peptide. Analyses of the expression profiles of these genes allowed the formulation of hypotheses about potential roles in parasitism. This is the first study combining sequence analyses of a substantial EST dataset with microarray expression data of all major life stages (except adult males) for the identification and characterization of putative parasitism-associated proteins in any parasitic nematode.

**CONCLUSION:** We have established an expression atlas for all known *H. glycines* parasitism genes. Furthermore, in an effort to identify additional *H. glycines* genes with putative functions in parasitism, we have reduced the currently known 6,860 *H. glycines* genes to a pool of 788 most promising candidate genes (including known parasitism genes) and documented their expression profiles. Using our approach to pre-select genes likely involved in parasitism now allows detailed functional analyses in a manner not feasible for larger numbers of genes. The generation of the candidate pool described here is an important enabling advance because it will significantly facilitate the unraveling of fascinating plant-animal interactions and deliver knowledge that can be transferred to other pathogen-host systems. Ultimately, the exploration of true parasitism genes verified from the gene pool delineated here will identify weaknesses in the nematode life cycle that can be exploited by novel anti-nematode efforts.

PMID: 19183474 [PubMed - in process]

PMCID: PMC2640417

**Related Articles**

- ▶ The parasitome of the phytonematode *Heterodera alvicens*. [Mol Plant Microbe Interact. 2003]
- ▶ Arabidopsis gene expression changes during cyst nematode parasitism revealed by statistical analyses of m [Plant J. 2003]
- ▶ Divergent evolution of arrested development in the dauer stage of *Caenorhabditis elegans* and the ii [Genome Biol. 2007]
- ▶ **Review** A model plant pathogen from the kingdom Animalia: *Heterodera glycines*, the [Annu Rev Phytopathol. 2006]
- ▶ **Review** Plant parasitic nematode proteins and the host parasite interaction. [Brief Funct Genomic Proteomic. 2007]

» See Reviews... | » See All...

**Recent Activity**

Turn Off Clear

- Sequence mining and transcript profiling to explore cyst nematode parasitism.