

COMPARATIVE GENOMICS OF GENE EXPRESSION IN PARASITIC AND FREE-LIVING NEMATODES.

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Molecular characterization of parasites, as well as the development of new techniques for control, can benefit from genomic approaches. As an entrée to characterizing parasitic nematode genomes, we have generated 196,500 expressed sequence tags (ESTs) from 26 nematode species as of April 2003. A key goal of our bioinformatic analysis is to organize this large dataset uniformly across multiple species in a manner that allows simple access by the community of nematologists. We will report on the progress of parasitic EST analysis including: creation of NemaGene clusters to reduce sequence redundancy, identification of common and rare represented genes, identification of stage-specific expression, functional classification based on Gene Ontology assignments, biochemical pathway identification using KEGG, and identification of genes orthologues in *C. elegans* and other nematodes. All sequences are publicly available at www.ncbi.nlm.nih.gov/dbEST. Projects details, NemaGene sequences and a list of collaborators are available at www.nematode.net. The project is funded by grants NIH-NIAID-46593 and NSF-0077503.