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Abstract

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The canine hookworm genome: Analysis and classification of *Ancylostoma caninum* survey sequences [☆]

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Abstract

Hookworms infect nearly a billion people. The *Ancylostoma caninum* hookworm of canids is a model for studying human infections and information from its genome coupled with functional genomics and proteomics can accelerate progress towards hookworm control. As a step towards a full-scale *A. caninum* genome project, we generated 104,000 genome survey sequences (GSSs) and determined the genome size of the canine hookworm. GSSs assembled into 57.6 Mb of unique sequence from a genome that we estimate by flow cytometry of isolated nuclei to be 347 ± 1.2 Mb, substantially larger than other Rhabditina species. Gene finding identified 5538 genes in the GSS assembly, for a total of 9113 non-redundant *A. caninum* genes when EST sequences are also considered. Functional classifications of many of the 70% of genes with homology to genes in other species are provided based on gene ontology and KEGG associations and secreted and membrane-bound proteins are also identified.

Keywords: Hookworm; *Ancylostoma caninum*; Genome survey sequences; Expressed sequence tags; Genome; Comparative genomics

Abbreviations: BLAST, basic local alignment search tool; EST, expressed sequence tags; GSS, genome survey sequence; GO, gene ontology; KEGG, Kyoto encyclopedia of genes and genomes

Article Outline

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