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A transcriptomic analysis of the phylum Nematoda.

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The phylum Nematoda occupies a huge range of ecological niches, from free-living microbivores to human parasites. We analyzed the genomic biology of the phylum using 265,494 expressed-sequence tag sequences, corresponding to 93,645 putative genes, from 30 species, including 28 parasites. From 35% to 70% of each species' genes had significant similarity to proteins from the model nematode *Caenorhabditis elegans*. More than half of the putative genes were unique to the phylum, and 23% were unique to the species from which they were derived. We have not yet come close to exhausting the genomic diversity of the phylum. We identified more than 2,600 different known protein domains, some of which had differential abundances between major taxonomic groups of nematodes. We also defined 4,228 nematode-specific protein families from nematode-restricted genes: this class of genes probably underpins species- and higher-level taxonomic disparity. Nematode-specific families are particularly interesting as drug and vaccine targets.

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