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Comparative genomics of nematodes

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Recent transcriptome and genome projects have dramatically expanded the biological data available across the phylum Nematoda. Here we summarize analyses of these sequences, which have revealed multiple unexpected results. Despite a uniform body plan, nematodes are more diverse at the molecular level than was previously recognized, with many species- and group-specific novel genes. In the genus *Caenorhabditis*, changes in chromosome arrangement, particularly local inversions, are also rapid, with breakpoints occurring at 50-fold the rate in vertebrates. Tylenchid plant parasitic nematode genomes contain several genes closely related to genes in bacteria, implicating horizontal gene transfer events in the origins of plant parasitism. Functional genomics techniques are also moving from *Caenorhabditis elegans* to application throughout the phylum. Soon, eight more draft nematode genome sequences will be available. This unique resource will underpin both molecular understanding of these most abundant metazoan organisms and aid in the examination of the dynamics of genome evolution in animals.

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