Draft genome of the filarial nematode parasite Brugia malayi.


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Parasitic nematodes that cause elephantiasis and river blindness threaten hundreds of millions of people in the developing world. We have sequenced the approximately 90 megabase (Mb) genome of the human filarial parasite Brugia malayi and predict approximately 11,500 protein coding genes in 71 Mb of robustly assembled sequence. Comparative analysis with the free-living, model nematode Caenorhabditis elegans revealed that, despite these genes having maintained little conservation of local synteny during approximately 350 million years of evolution, they largely remain in linkage on chromosomal units. More than 100 conserved operons were identified. Analysis of the predicted proteome provides evidence for adaptations of B. malayi to niches in its human and vector hosts and insights into the molecular basis of a mutualistic relationship with its Wolbachia endosymbiont. These findings offer a foundation for rational drug design.

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