

1: [Science](#). 2007 Sep 21;317(5845):1756-60.



Draft genome of the filarial nematode parasite Brugia malayi.

[Ghedini E](#), [Wang S](#), [Spiro D](#), [Caler E](#), [Zhao Q](#), [Crabtree J](#), [Allen JE](#), [Delcher AL](#), [Guiliano DB](#), [Miranda-Saavedra D](#), [Anghioli SV](#), [Creasy T](#), [Amedeo P](#), [Haas B](#), [El-Sayed NM](#), [Wortman JR](#), [Feldblyum T](#), [Tallon L](#), [Schatz M](#), [Shumway M](#), [Koo H](#), [Salzberg SL](#), [Schobel S](#), [Perteau M](#), [Pop M](#), [White O](#), [Barton GJ](#), [Carlow CK](#), [Crawford MJ](#), [Daub J](#), [Dimmic MW](#), [Estes CF](#), [Foster JM](#), [Ganatra M](#), [Gregory WF](#), [Johnson NM](#), [Jin J](#), [Komuniecki R](#), [Korf I](#), [Kumar S](#), [Laney S](#), [Li BW](#), [Li W](#), [Lindblom TH](#), [Lustigman S](#), [Ma D](#), [Maina CV](#), [Martin DM](#), [McCarter JP](#), [McReynolds L](#), [Mitreva M](#), [Nutman TB](#), [Parkinson J](#), [Peregrin-Alvarez JM](#), [Poole C](#), [Ren Q](#), [Saunders L](#), [Sluder AE](#), [Smith K](#), [Stanke M](#), [Unnasch TR](#), [Ware J](#), [Wei AD](#), [Weil G](#), [Williams DJ](#), [Zhang Y](#), [Williams SA](#), [Fraser-Liggett C](#), [Slatko B](#), [Blaxter ML](#), [Scott AL](#).

Division of Infectious Diseases, University of Pittsburgh School of Medicine, Pittsburgh, PA 15261, USA. GhedinE@dom.pitt.edu

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.

PMID: 17885136 [PubMed - indexed for MEDLINE]

Related Articles

- ▶ The filarial genome project: analysis of the nuclear, mitochondrial and endosymbiont gene [Int J Parasitol. 2000]
- ▶ Conservation of long-range synteny and microsynteny between the genomes of two distantly [Genome Biol. 2002]
- ▶ Construction of bacterial artificial chromosome libraries from the parasitic nematode *Brugia malayi* [Int J Parasitol. 2004]
- ▶ Sequencing and analysis of a 63 kb bacterial artificial chromosome insert from the *Wolbachia* [Int J Parasitol. 2002]
- ▶ Mining predicted essential genes of *Brugia malayi* for nematode drug targets. [PLoS ONE. 2007]

» See all Related Articles...