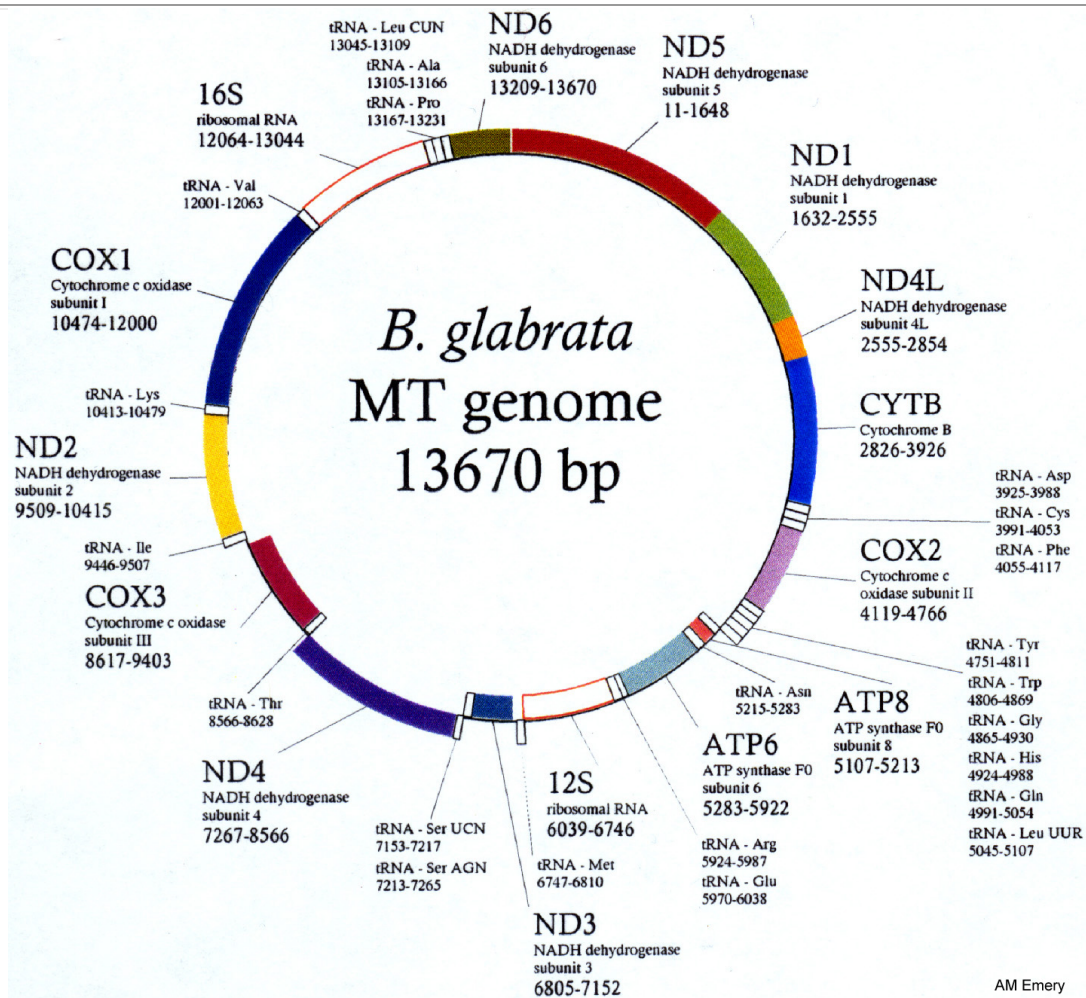


Biomphalaria glabrata GENOME INITIATIVE



Full-length mitochondrial genome sequence of *Biomphalaria glabrata*

The complete mitochondrial genome (13,670 nt) of *Biomphalaria glabrata* was characterized from M-line and NHM 1742 strains in a collaborative effort between the University of New Mexico (USA) and the Natural History Museum (UK). The sequences are available from GenBank (AY380567 and AY380531, respectively), the information is also available from the Genome database (NC_005439).



The circular mt genome (13670 bp) is displayed above. The 13 protein coding genes are displayed as solid, colored blocks. Genes encoded on the plus strand are displayed outside the circle; those on the minus strand are displayed inside the circle. RNAs are displayed as open blocks - transfer RNAs (22 in number) with a black outline, the 2 ribosomal RNAs with a red outline. Numbers below the genes refer to position in the genome (bp).

Literature reference

DeJong, R.J., Emery A.M., Adema, C.M. (2004). The mitochondrial genome of *Biomphalaria glabrata* (gastropoda, basommatophora), intermediate host of *Schistosoma mansoni*. Journal of Parasitology, 90:991-996 PMID: 15562597 DOI: 10.1645/GE-284R