



# The mitochondrial genome of *Melampus bidentatus* (Say, 1822; Panpulmonata, Ellobioidea)

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## Background

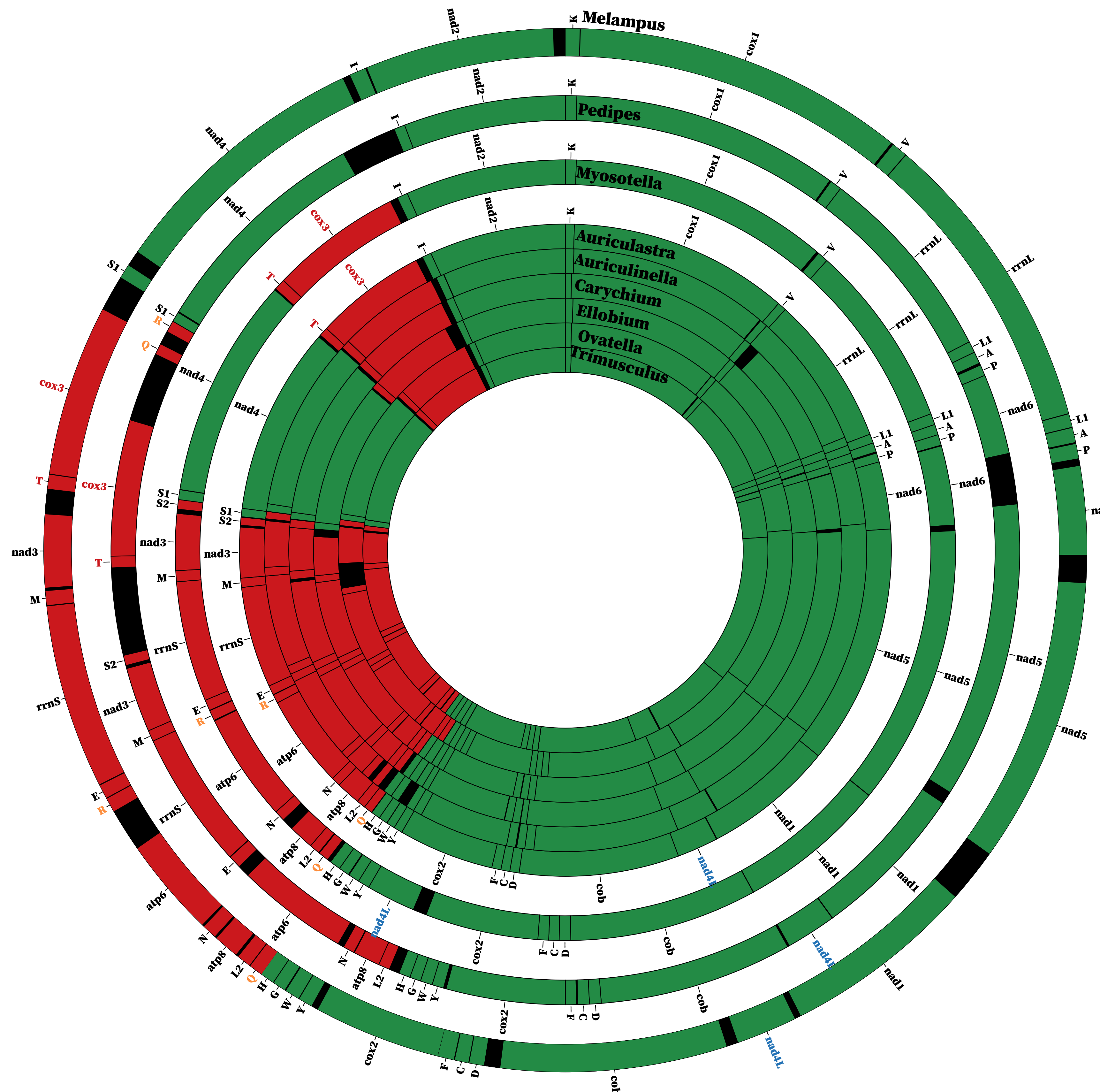
The snail *Melampus bidentatus* is an important component of the salt marsh communities along the North American Atlantic Coast, the Gulf of Mexico and the Caribbean. *M. bidentatus* has recently been found to be a complex of three species with mostly disjunct distribution ranges.

## Methods

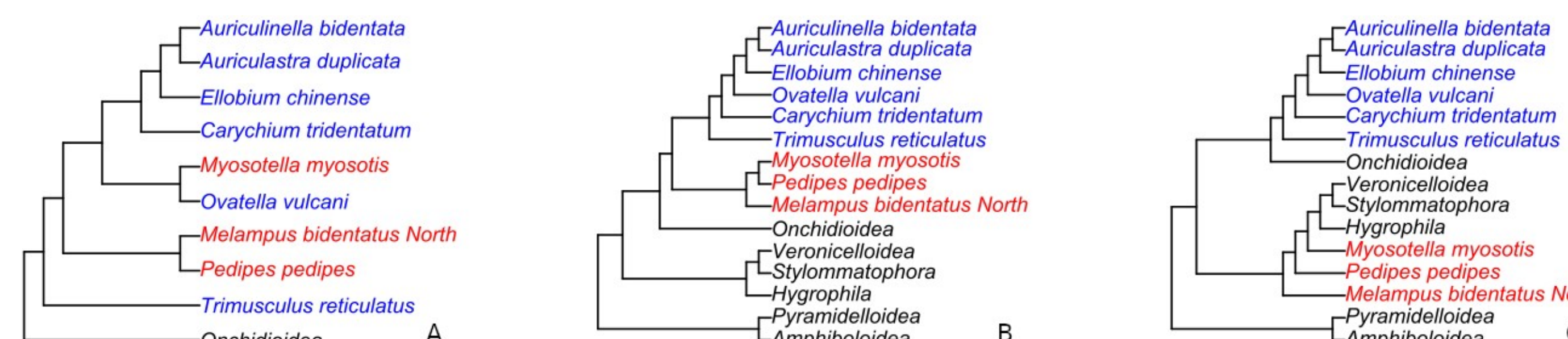
The mitochondrial genome of *M. bidentatus* North was assembled from Illumina short read data using NovoPlasty and annotated on the MITOS webserver.

Trees were created by using protein coding genes and rRNA of this and other mitochondrial genomes that were downloaded from Genbank. Sequences were aligned with MAFFT and trees were calculated with IQTree and MrBayes.

→ Fig. 2: Three simplified trees using species for which we have mitochondrial genomes. Blue: Ellobioidea with a possibly ancestral gene order; Red: Ellobioidea with derived gene orders; Black: groups outside the Ellobioidea. A: Tree based on Romero et al. (2016); B) based on mitochondrial nucleotide sequences; C) based on mitochondrial amino acid sequences.



↑Fig. 1: The mitochondrial genomes of *M. bidentatus* and other members of the Ellobioidea. Species with derived gene orders are on the outside. Genes coded on the forwards strand in green, those on the reverse strand in red. Deviations in gene order in *Melampus* and *Pedipes*: red labels; in *Pedipes* alone: orange labels; in *Myosotella*: blue labels.



## The mitochondrial genome

- Size: 14668 bp
- 36 genes (24 on forward strand, 12 on reverse strand)
- All genes coded on the reverse strand are grouped together
- 13 protein coding genes, 2 rRNAs, 21 tRNAs
- One tRNA gene (S2) that is usually present in Pulmonates is missing.

## Gene order changes & phylogeny

*M. bidentatus* is one of three species (Fig. 1, the outer three rings; the other species being *Pedipes pedipes* and *Myosotella myosotis*) with known mitogenome (out of nine) within the Ellobioidea, whose gene order deviates from a possibly ancestral gene order that is very frequent in many Panpulmonate groups. These three species are consistently recovered outside the rest of Ellobioidea (Fig. 2B & C), which is not supported by other phylogenetic & morphological studies (Fig. 2A).