


The complete mitochondrial DNA sequence of *Heterochaerus australis* (Acoela, Convolutidae)

Bin Li^{a,b}, Meijie Liao^{a,b} , Miao Kong^{a,b}, Yingeng Wang^{a,b}, Xiaojun Rong^{a,b}, Zheng Zhang^{a,b} and Yongxiang Yu^{a,b}

^aYellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Qingdao, China; ^bQingdao National Laboratory for Marine Science and Technology, Laboratory for Marine Fisheries Science and Food Production Processes, Qingdao, China

ABSTRACT

One complete mitochondrial genomes (mitogenomes) was determined for *Heterochaerus australis* (Acoela, Convolutidae). Its mitochondrial genome size was 13,885 bp. The sequence contains 2 ribosomal RNA genes (*rnl* and *rns*), 20 tRNA genes, and 12 protein-coding genes (PCGs). The A+T content of the complete mitochondrial genome sequence was 70.8%. The base composition showed a tendency of high AT. The resulted maximum likelihood (ML) tree supported that Acoela had a distant relationship with other orders of Turbellaria and the Xenacoelomorpha.

ARTICLE HISTORY

Received 29 June 2020
Accepted 11 July 2020

KEYWORDS

Heterochaerus australis;
Acoela;
Xenacoelomorpha;
mitogenome

The taxonomic status of Acoela of Turbellaria is controversial. Some researchers believe that the Acoela belongs to Deuterostomia and should be removed from the Platyhelminthes and combined with the *Xenoturbella japonica* to form the Phylum Xenacoelomorpha (Philippe et al. 2011; Cinar 2014). Jondelius et al. (2011) interpreted the initial grouping of the Acoela and tunicates as a classical example of long-branch attraction (LBA). This is of particular relevance for Acoela species, which already demonstrate a very rapid rate of nucleotide substitution compared to other metazoans, leaving them vulnerable to LBA (Robertson et al. 2017). Here, we sequenced the mitochondrial genomes (mitogenomes) of

Heterochaerus australis from *Apostichopus japonicus* breeding pond, and it has been indicated to be a new enemy species. In order to provide theoretical basis and scientific guidance for the taxonomic status of Acoela, mitochondrial gene composition, biological evolution, and molecular identification were studied.

Heterochaerus australis was collected from Dalian, Liaoning Province of China (39.22N, 122.18E) in 2019 from sea cucumber culture ponds. The specimen was deposited into Fishery Barcode Data Base of China (YSF-ZW-4634). Total DNA was extracted using Omega Mollusk DNA Kit. The genome was sequenced by BGISEQ-500 method. The type of sequencing

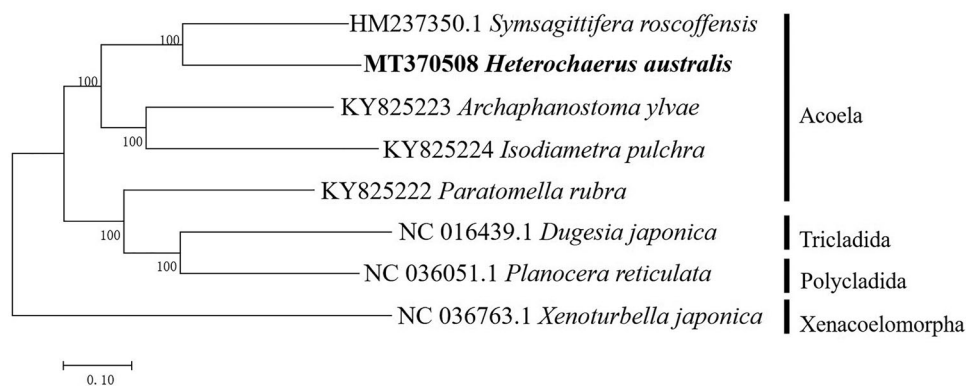


Figure 1. Phylogenetic trees based on the concatenated nucleic acid of 12 protein-coding genes. The branch lengths are determined with ML analysis. *Heterochaerus australis* is shown in bold. Numbers above or below branches denote bootstrap percentages (1000 replicates). Genbank accession numbers are shown for published sequences.

was PE100 and the length of the inserted fragment was 250 bp. The remaining reads were assembled using NOVOplasty. ORF Finder (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>) and BLASTx were used to determine the protein-coding genes (PCGs) using the invertebrate mitochondrial genetic code. The positions of transfer RNA (tRNA) genes were localized by ARWEN (Laslett and Canbäck 2008) and DOGMA (Wyman et al. 2004) using the invertebrate mitochondrial genetic code and the default search mode.

The complete mitogenome sequences was 13,885 bp in length and has been deposited in the GenBank (Accession No. MT370508). The complete mitogenome contained 2 ribosomal RNA genes (*rrnL* and *rrnS*), 20 tRNA genes, and 12 protein-coding genes (PCGs). The A + T content of the complete mitochondrial genome sequence was 70.8%. The base composition showed a tendency of high AT. This phenomenon also appears in other species of Acoela (Mwinyi et al. 2010; Robertson et al. 2017).

A maximum likelihood phylogenetic tree of 7 species of Turbellaria and 1 species of Xenacoelomorpha was constructed based on the concatenated nucleic acid of 12 PCGs (Figure 1). In Acoela, only one species (*P. rubra*) clustered with other orders of Turbellaria, while the other four species (*A. ylvae*, *I. pulchra*, *H. australis*, *S. roscoffensis*) clustered into a single cluster, showing a distant relationship with other turbellarian. But *X. japonica* of Xenacoelomorpha is a separate branch.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This work was supported by the National Key R&D Program of China [2018YFD0901603], Agriculture Seed Improvement Project of Shandong

Province [2017LZGC010], and Central Public-interest Scientific Institution Basal Research Fund, CAFS [2020TD40].

ORCID

Meijie Liao  <http://orcid.org/0000-0002-9478-359X>

Data availability statement

The data that support the findings of this study are openly available in NCBI GenBank (<https://www.ncbi.nlm.nih.gov/>) with reference number [MT370508].

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