






Complete mitochondrial genomes of two scaphopod molluscs

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ABSTRACT

Complete mitochondrial genomes were determined for two scaphopod molluscs: the dentaliid *Antalis entalis* and an unidentified Antarctic gadilid. Both genomes are complete except, in *Gadilida* sp. indet., a short stretch of *nad5* was undetermined and *trnR* could not be annotated. Organization of the *Gadilida* sp. genome is nearly identical to that previously reported for the gadilid *Siphonodentalium* whereas *trnK*, *nad5*, *trnD*, *nad4*, and *nad4l* are transposed to the opposite strand in the previously published *Graptacme* genome relative to that of *Antalis*. Phylogenetic analysis of the 13 protein-coding and 2 rRNA genes recovered Scaphopoda, Gadilida, and Dentaliida monophyletic with maximal support.

ARTICLE HISTORY

Received 24 July 2019
Accepted 3 August 2019

KEYWORDS

Scaphopoda; Dentaliida;
Gadilida; Mollusca;
Antalis entalis

Scaphopoda is a clade of burrowing marine molluscs characterized by tubular shells and anterior feeding tentacles called captacula (Reynolds and Steiner 2008). Phylogenomic analyses have shown that Scaphopoda forms a clade with Gastropoda and Bivalvia, but relationships among these three remain unclear (Kocot et al. 2011; Smith et al. 2011). The ~600 extant species of scaphopods are divided into Dentaliida and Gadilida (e.g., Steiner and Dreyer 2003), but the taxonomy within these groups needs revision. Such work is hindered by limited molecular resources for the group. In particular, just one mitochondrial (mt) genome is available from each of the two major lineages. Here, we present annotated mt genomes for an additional representative of each scaphopod lineage in order to provide additional resources for evolutionary studies of this group.

Adult *Antalis entalis* were collected off Roscoff, France at 25 m. The mt genome of an unidentified species of *Gadilida* was obtained from an environmental sample collected from the Weddell Sea, Antarctica (75°44'45.132" S, 31°15'12.708" W) at 587 m. The shell of the *Antalis* specimen used and a second specimen from the same locality were deposited in the Alabama Museum of Natural History (ALMNH accessions 21272 and 21273, respectively). DNA was extracted using CTAB + phenol/chloroform. For *Antalis*, DNA was sent to the Genomic Services Lab at Hudson Alpha for Illumina PCR-free library preparation and sequencing using 1/2 lane of a HiSeq X. For *Gadilida* sp., an Illumina Nextera library was prepared and sent to Macrogen for sequencing on a HiSeq 4000 using ~1/24 lane.

Assembly was performed with Spades 3.12.0 (Bankevich et al. 2012). This did not yield a complete mt genome for *Antalis*, so Norgal (Al-Nakeeb et al. 2017) was used. Assembled mt genomes were annotated using MITOS 2 (Bernt et al. 2013) with the invertebrate genetic code. The assembled *Antalis* (NCBI MN098312) and *Gadilida* sp. (NCBI MN104231) mt genomes are 14,836 bp and 13,789 bp, respectively. Both appear complete except, in *Gadilida* sp., part of *nad5* is undetermined and *trnR* could not be annotated. Aside from differences in the relative positions of *trnA*, *trnH*, and possibly *trnR*, the *Gadilida* sp. mt genome organization is identical to that of *Siphonodentalium lobatum* (Dreyer and Steiner 2004). Organization of the *Antalis* mt genome was similar to that of *Graptacme eborea* (Boore et al. 2004) except *trnK*, *nad5*, *trnD*, *nad4*, and *nad4l* are transposed to the minus strand in *Graptacme* relative to *Antalis*.

The 13 protein-coding and 2 rRNA genes were aligned with MAFFT 7.407 (Katoh and Standley 2013) using the 'auto' option. Alignments were trimmed with Gblocks 0.91 b (Castresana 2000) using relaxed settings and concatenated. Maximum likelihood analysis of the partitioned matrix was performed in RAxML 8.2.4 (Stamatakis 2014) using the GTR + GAMMA model with rapid bootstrapping. A *cox1* tree including all publicly available scaphopod sequences was also reconstructed using this approach, but this failed to provide an unambiguous identification for *Gadilida* sp. (data not shown). Phylogenetic analysis of 15 mt genes recovered Scaphopoda, Dentaliida, and *Gadilida* monophyletic with maximal support (Figure 1).

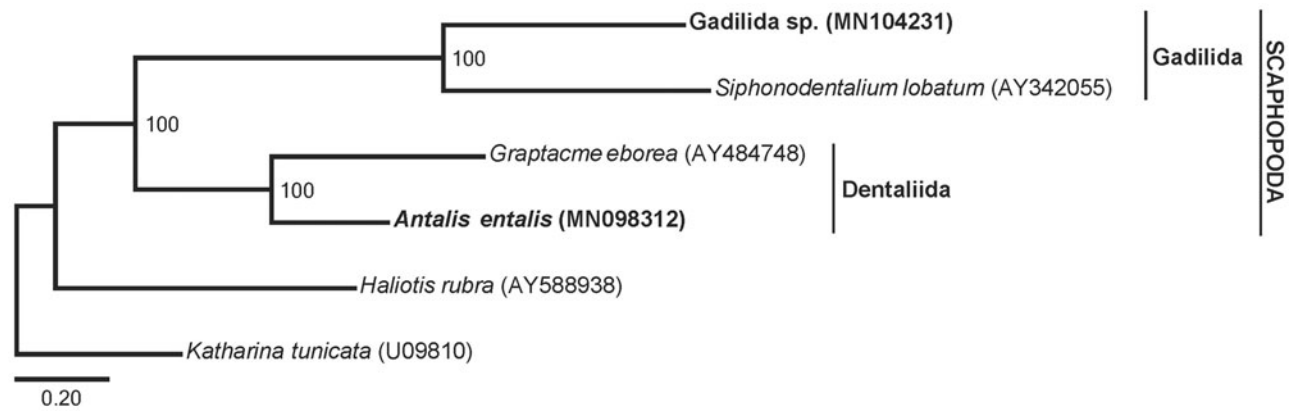


Figure 1. Maximum likelihood tree showing relationships among scaphopod species with sequenced mitochondrial genomes. Bootstrap support values are shown at each node. Scale bar indicates substitutions per site. Newly sequenced taxa are listed in bold.

Disclosure statement

No potential conflict of interest was reported by the authors.

Acknowledgements

The authors thank the staff and administration of Station Biologique de Roscoff for assistance in collecting specimens of *Antalis entalis* and the British Antarctic Survey for sharing samples used for mt genome sequencing of *Gadilida* sp.

Funding

This work was supported by University of Alabama College of Arts and Sciences and Department of Biological Sciences start-up funds to KMK. Sampling of *Antalis entalis* was supported by ASSEMBLE (Association of European Marine Biological Laboratories) grant no. [835 SBR-1] to TW.

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