The first complete mitochondrial genome of Antigona lamellaris (Schumacher, 1817) (Veneroida: Veneridae)

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ABSTRACT
Venus clams (Veneridae) including Antigona lamellaris are commercially important fishery resources by their dominance in local benthic communities. However, despite their great diversity, the phylogenetic and taxonomic relationships in venus clams remain poorly understood. In this study, we report the first complete mitochondrial genome of A. lamellaris. The mitogenome has 17,532 base pairs (67.9% A + T content) and is made up of a total of 37 genes (13 protein-coding, 22 transfer RNAs and 2 ribosomal RNAs), plus a putative control region. This study will provide useful molecular resources for clarifying taxonomic and phylogenetic confusion in venus clams.
understanding the phylogenetic and taxonomic classification in venus clams.

**Disclosure statement**

The authors declare that they have no conflict of interest.

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/) under the accession no. MT254059. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA701318, SRR13684237, and SAMN17862031, respectively.

**Figure 1.** Phylogenetic tree of 13 species in family Veneridae. The complete mitogenomes were downloaded from GenBank and the phylogenetic tree based on the concatenated nucleotide sequences of 13 mitochondrial PCGs was constructed by maximum-likelihood method with 100 bootstrap replicates. The bootstrap values were labeled at each branch node, Macridiscus melanaegis and Macridiscus multifarius were chosen to be outgroup species.

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