The complete mitochondrial genome and phylogenetic analysis of *Amusium pleuronectes*

Lijie Yao\(^{a,b}\), Hongwei Yu\(^a\), Yaran Liu\(^a\), Yuehuan Zhang\(^c\) and Yuli Li\(^{a,b}\)

\(^a\)MOE Key Laboratory of Marine Genetics and Breeding, College of Marine Life Sciences, Ocean University of China, Qingdao, China; \(^b\)Laboratory for Marine Biology and Biotechnology, Pilot National Laboratory for Marine Science and Technology, Qingdao, China; \(^c\)Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China

**ABSTRACT**

*Amusium pleuronectes*, commonly known as the Asian moon scallop, is widely distributed in Indo-Pacific coastal areas (Minchin 2003) and characterized by beautiful two-colored shells. Except for high economic value, the Asian moon scallop is often used as a biological monitor to evaluate the impact of human activities on the marine environment (Siriprom and Lim suwan 2009). However, genetic information for this species remains scarce. Recently, complete mitogenome has been considered as an effective tool for phylogeny and phylogeography studies (Curole and Kocher 1999; Saccone et al. 1999). In this study, we report the sequencing and assembly of the complete mitogenome of *A. pleuronectes*, which is the first mitogenome of the genus *Amusium*.

The example of *A. pleuronectes* was derived from Tung Ping Chau Bay near Tung Chung village (Guangdong province, China; 22.4907\(^{\circ}\)N, 114.5801\(^{\circ}\)E) at a depth of 7–8m. All soft tissues were preserved in liquid nitrogen after sampling. Total DNA was extracted using the phenol/chloroform/isooamy alcohol method (Sambrook et al. 1989). The DNA sample was deposited at the Key Laboratory of Marine Genetics and Breeding (Ministry of Education), Ocean University of China (Specimen code: OUC-MGB-2018-AP-08). Whole genomic sequencing of the individual sample was performed using the Illumina NovaSeq 6000 sequencing platform. The mitogenome of *A. pleuronectes* was de novo assembled using NOVOPlasty (Dierckxsens et al. 2017), gene information of which was retrieved by the MITOS software (Bernt et al. 2013).

The complete circular mitogenome of *A. pleuronectes* was 18,044 bp in length. Thirteen protein-coding genes (PCGs), 2 ribosomal RNA genes, and 21 transfer RNA genes were annotated. The 13 conserved PCGs were cytochrome oxidase subunit (I, II, and III), NADH dehydrogenase subunit (1, 2, 3, 4, 5, 6, and 4L), and ATP synthase subunit (6, and 8), which was similar to the reported mitochon- discharge genomes of most marine bivalves. Phylogenetic analysis reveals that within the family Pectinidae, the genus *Amusium* is closely related to the genus *Argopecten*. The mitogenome of *A. pleuronectes* provides a valuable resource for further advancing the understanding of bivalve phylogeny and evolution.
previous studies (Serb 2016; Smedley et al. 2019). The A. pleuronectes mitogenome provides a valuable resource for further advancing our understanding of bivalve phylogeny and evolution.

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

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Data availability statement
The data that support the findings of this study are openly available in GeneBank at [https://www.ncbi.nlm.nih.gov/nuccore/MT419374.1/], reference number [Accession number: MT419374].

References
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Figure 1. The phylogenetic tree of A. pleuronectes and 13 other bivalves based on complete mitochondrial genomes. The accession numbers of downloaded sequences are as follows: Argopecten irradians concentricus (KT161259.1), Argopecten irradians irradians (NC_012977.1), Argopecten irradians (NC_009687.1), Argopecten ventricosus (KT161261.1), Argopecten purpuratus (NC_027943.1), Crassadoma gigantea (MH016739.1), Azumapecten farreri (NC_012138.1), Mizuhopecten yessoensis (NC_009081.1), Mimachlamys nobilis (NC_011608.1), Mimachlamys senatoria (NC_022416.1), Placopesten magellanicus (NC_007234.1), Crassostrea gigas (NC_001276.1), and Limnoperna fortunei (NC_028706.1).