


## The complete mitochondrial genome and phylogenetic analysis of the dwarf surf clam *Mulinia lateralis*

Jing Liu<sup>a\*</sup>, Qifan Zeng<sup>a,b\*</sup>, Hao Wang<sup>a</sup>, Mingxuan Teng<sup>a</sup>, Ximing Guo<sup>c</sup>, Zhenmin Bao<sup>a,d</sup> and Shi Wang<sup>a,b</sup> 

<sup>a</sup>MOE Key Laboratory of Marine Genetics and Breeding, College of Marine Life Sciences, Ocean University of China, Qingdao, Shandong, China; <sup>b</sup>Laboratory for Marine Biology and Biotechnology, Pilot National Laboratory for Marine Science and Technology, Qingdao, Shandong, China; <sup>c</sup>Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, Rutgers University, Port Norris, New Jersey, USA; <sup>d</sup>Laboratory for Marine Fisheries Science and Food Production Processes, Pilot National Laboratory for Marine Science and Technology, Qingdao, Shandong, China

### ABSTRACT

*Mulinia lateralis* (Say, 1822) is a species of the bivalve family Mactridae and represents a promising model species for molluscan research. In this study, the complete mitochondrial genome (mitogenome) of *M. lateralis* was sequenced and assembled for the first time. The 21,668 bp mitogenome contained 13 protein-coding genes, 2 rRNAs, 22 tRNA genes, and an AT-rich region. The overall AT content (69.56%) was higher than GC content (30.44%). Phylogenetic analysis supported that *M. lateralis* belongs to the family Mactridae. The mitochondrial genome of *M. lateralis* provides a valuable resource for further understanding the phylogeny of the family Mactridae and for functional studies of molluscan mitochondrial genes.

### ARTICLE HISTORY

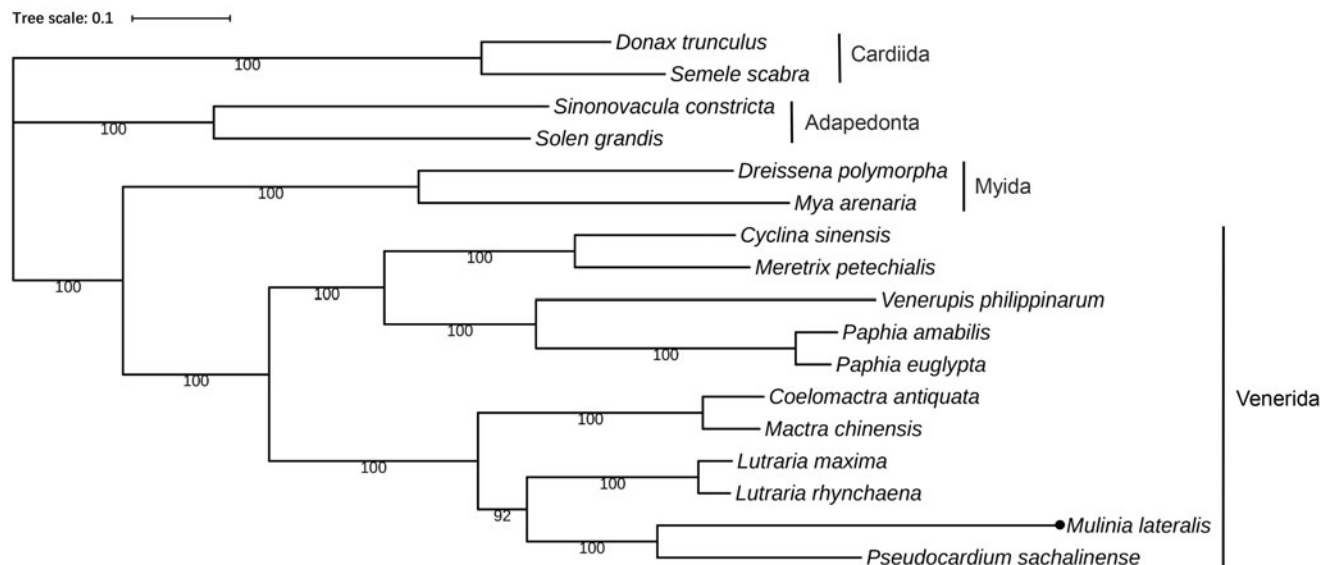
Received 12 November 2019  
Accepted 23 November 2019

### KEYWORDS



*Mulinia lateralis*; Bivalvia; mitochondrial genome; phylogenetic analysis

*Mulinia lateralis*, commonly known as the dwarf surf clam or coot clam, is a small bivalve mollusk that naturally distributes along the coast of Western Atlantic (Walker and Tenore 1984). Due to its small body size (10–20 mm), short generation time (2–3 months) and ease of culture and

maintenance, *M. lateralis* has long been considered as a promising model organism for genetic and transgenic studies in mollusks (Calabrese 1969; Guo and Allen 1994; Lu et al. 1996). Despite its value in molluscan research, omics-scale resources are still limited for this species (Rice et al. 1993;



**Figure 1.** Maximum-likelihood tree of *M. lateralis* and 16 other mollusks based on the protein sequences of 12 protein coding genes. Numbers at each node indicate the bootstrap supporting values. The accession numbers for all species are as follows: *Donax trunculus* (NC\_035985.1), *Semele scabra* (NC\_018374.1), *Sinonovacula constricta* (EU880278.1), *Solen grandis* (HQ703012.1), *Dreissena polymorpha* (KY091877.1), *Mya arenaria* (NC\_024738.1), *Coelomactra antiquata* (JN692486.1), *Mactra chinensis* (NC\_025510.1), *Cyclina sinensis* (KU097333.1), *Meretrix petechialis* (NC\_012767.1), *Venerupis philippinarum* (AB065374.1), *Paphia amabilis* (NC\_016889.1), *Paphia euglypta* (GU269271.1), *Lutraria maxima* (MF784266), *Lutraria rhynchaena* (HG799089), *Pseudocardium sachalinense* (MG431821).

**CONTACT** Shi Wang  [swang@ouc.edu.cn](mailto:swang@ouc.edu.cn)  MOE Key Laboratory of Marine Genetics and Breeding, College of Marine Life Sciences, Ocean University of China, 5 Yushan Road, Qingdao 266003, Shandong, China

\*These authors contributed equally to this work.

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License (<http://creativecommons.org/licenses/by-nc/4.0/>), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Park and Foighil 2000). In this study, the complete mitogenome of *M. lateralis* was sequenced and assembled, which represents the first mitogenome for the genus *Mulinia* of the bivalve family Mactridae.

An adult male *M. lateralis* derived from a wild population collected from Delaware Bay, New Jersey, United States, was used for this study. All soft tissues without the hepatopancreas were dissected and frozen in liquid nitrogen immediately after sampling. Total DNA was extracted using phenol/chloroform/isoamyl 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-ML-08). Whole-genome sequencing was performed by Frasergen (Wuhan, China). The mitogenome of *M. lateralis* was *de novo* assembled using NOVOPlasty (Dierckxsens et al. 2017).

The complete circular mitochondrial genome of *M. lateralis* is 21,668 bp in length with high AT nucleotide content (30.87% A, 38.69% T, 18.94% G, and 11.50% C). Thirteen protein-coding genes, two ribosomal RNA genes, and twenty-two transfer RNA genes were annotated by MITOS (Bernt et al. 2013). The 13 conserved protein-coding genes were *cox* (*I*, *II*, and *III*), *nad* (*1*, *2*, *3*, *4*, *5*, *6*, and *4L*), *atp* (*6*, and *8*), and *cob* as in Venerida (Xu et al. 2012; Dong et al. 2016; Fernandez-Perez et al. 2017; Zhong et al. 2017). The sequence has been deposited in GenBank under accession number MN326303.

The phylogenetic analysis was carried out using maximum-likelihood (ML) method based on the concatenated amino acid sequences of mitochondrial protein-coding genes. As indicated by the tree, *M. lateralis* formed a clade with other species of the bivalve family Mactridae (Figure 1), which provides strong evidence that *M. lateralis* belongs to the Mactridae family.

## Disclosure statement

The authors report no conflict of interest.

## Funding

We acknowledge the grant support from the Fundamental Research Funds for the Central Universities [201762001] and the Major basic

research projects of Shandong Natural Science Foundation [ZR2018ZA0748].

## ORCID

Shi Wang  <http://orcid.org/0000-0002-9571-9864>

## References

- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved *de novo* metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69(2): 313–319.
- Calabrese A. 1969. *Mulinia lateralis*: molluscan fruit fly? *Proc Natl Shellfisheries Assoc.* 59:65–66.
- Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: *de novo* assembly of organelle genomes from whole genome data. *Nucleic Acids Res.* 45(4):e18.
- Dong PZ, Ma GY, Chang LY, Zhu Y, Tian XX. 2016. The complete mitochondrial genome of *Cyclina sinensis* (Veneroidea: Veneridae). *Mitochondrial DNA.* 1(1):173–174.
- Fernandez-Perez J, Nanton A, Ruiz-Ruano FJ, Camacho JPM, Mendez J. 2017. First complete female mitochondrial genome in four bivalve species genus *Donax* and their phylogenetic relationships within the Veneroidea order. *PLoS One.* 12(9):e0184464.
- Guo XM, Allen SK. 1994. Sex determination and polyploid gigantism in the dwarf surfclam (*Mulinia lateralis* Say). *Genetics.* 138(4): 1199–1206.
- Lu J, Chen TT, Allen SK, Matsubara T, Burns JC. 1996. Production of transgenic dwarf surfclams, *Mulinia lateralis*, with pantropic retroviral vectors. *Proc Natl Acad Sci USA.* 93(8):3482–3486.
- Park J, Foighil DO. 2000. Sphaeriid and corbiculid clams represent separate heterodont bivalve radiations into freshwater environments. *Mol Phylogenet Evol.* 14(1):75–88.
- Rice EL, Roddick D, Singh RK. 1993. A comparison of molluscan (Bivalvia) phylogenies based on palaeontological and molecular data. *Mol Marine Biol Biotechnol.* 2(3):137–146.
- Sambrook J, Fritsch EF, Maniatis T. 1989. *Molecular cloning: a laboratory manual.* New York (NY): Cold Spring Harbor Lab Press.
- Walker RL, Tenore KR. 1984. Growth and production of the dwarf surf clam *Mulinia lateralis* (Say 1822) in a Georgia estuary. *Gulf and Caribbean Res.* 7(4):357–363.
- Xu XD, Wu XY, Yu ZN. 2012. Comparative studies of the complete mitochondrial genomes of four Paphia clams and reconsideration of subgenus Neotapes (Bivalvia: Veneridae). *Gene.* 494(1):17–23.
- Zhong SP, Zhao YF, Wang XF, Song ZF, Zhang Q. 2017. The complete mitochondrial genome of *Lutraria maxima* Jonas (Veneroidea: Mactridae). *Mitochondrial DNA.* 2(2):709–710.