

Mitochondrial DNA Part B Resources

ISSN: (Print) (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

The complete mitochondrial genome of *Mactra chinensis* (Bivalvia: Macridae)

Hongtao Nie & Yuri Ph. Kartavtsev

To cite this article: Hongtao Nie & Yuri Ph. Kartavtsev (2021) The complete mitochondrial genome of *Mactra chinensis* (Bivalvia: Macridae), Mitochondrial DNA Part B, 6:10, 2812-2815, DOI: [10.1080/23802359.2021.1970635](https://doi.org/10.1080/23802359.2021.1970635)

To link to this article: <https://doi.org/10.1080/23802359.2021.1970635>



© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



[View supplementary material](#)



Published online: 31 Aug 2021.



[Submit your article to this journal](#)



Article views: 205



[View related articles](#)



[View Crossmark data](#)

The complete mitochondrial genome of *Mactra chinensis* (Bivalvia: Macridae)

Hongtao Nie^a and Yuri Ph. Kartavtsev^b

^aLaboratory of Engineering and Technology Research, Center of Shellfish Breeding in Liaoning Province, College of Fisheries and Life Science, Dalian Ocean University, Dalian, China; ^bLaboratory of Molecular Systematic, A.V. Zhirmunsky National Scientific Center of Marine Biology, Russian Academy of Sciences, Vladivostok, Russia

ABSTRACT

The structure and composition of the mitogenome of a bivalve mollusk, denoted as *Mactra* sp. (MT780813), has been obtained. The genome has a variable organization: it includes 12 protein-coding genes, 28 tRNAs, and two rRNA genes. Its content is sufficiently different from that of nearest specimen, accessed from GenBank, supposedly belonging to the other gender. All genes are encoded on the “+”-strand. All protein-coding genes are initiated with ATG codon. Analysis confirms the close topological position of the GenBank *Mactra chinensis* (KJ754823) and our *M. sp.* specimen on gene tree. Above data suggesting female- vs. male-type mitogenomes or cryptic species presence.

ARTICLE HISTORY

Received 20 April 2021
Accepted 15 August 2021

KEYWORDS

Mitogenome; structure; phylogenetic analysis; bivalve mollusk; *Mactra*

Introduction

Bivalve mollusk the Chinese surf clam, *Mactra chinensis* Philippi, 1846, is one of the commercially valuable species of the family Macridae (Bivalvia: Venerida; WoRMS, <http://www.marinespecies.org/aphia.php?p=taxdetails&id=367847>; Ni et al. 2012; Shen et al. 2014). The species is a typical member of benthic communities distributed in boreal nearshore sandy habitats, usually at a depth of 7–10 m (Scarlato 1976). Its range extends to the West Pacific: from the Kuril Islands to coastal waters of the Sea of Japan and off the Korean Peninsula down to the Yellow Sea (Scarlato 1976). *Mactra chinensis* has appeared to vary in shell color pattern between the southern and northern parts of the species range: in China and South Korea waters, its shells are colored yellowish, without brown rays, while in the Russian part of the Sea of Japan, shells have a typical brown-and-grayish pattern with brown and violet purple rays (Scarlato 1976; Lutaenko and Noseworthy 2012). Bivalve mollusks of the order Venerida, including *M. chinensis* and many other members of Bivalvia, were subjected to a comparative molecular phylogenetic analysis by sequences of certain mitochondrial genes, nuclear loci, and complete mitogenome (Theologidis et al. 2008; Ni et al. 2012; Shen et al. 2014; Fernández-Pérez et al. 2017; Reunov et al. 2019). Several studies have revealed a number of taxonomic issues at the species, genus, and family levels. Mitogenome has been described for many bivalve species and appeared to be very variable in size, structure, and even order of genes (Yuan et al. 2013; Shen et al. 2014; Fernández-Pérez et al. 2017). Many bivalves show a phenomenon of





double uniparental inheritance (DUI) of single mtDNA genes and whole mitogenome in females (F) and males (M) causing their drastic divergence (Zouros et al. 1994; Skibinski et al. 1994; Theologidis et al. 2008; Fernández-Pérez et al. 2017 etc.).


The aim of the present work was to study the mitogenome of one *Mactra* specimen, whose shell originally was not identified exactly and was referred to as *Mactra* sp., and also to clarify its species name, investigate the mitogenome composition of this organism, and show its place among a few relatives from the genera *Mactra*, *Colomacra*, and *Lutraria* using literature sources.

Materials and methods

The mitogenome of *Mactra* sp. (GenBank accession no. MT780813, voucher no. WB-F) was obtained by Illumina sequencing technology (Novaseq 6000, USA) and assembled in SPAdes v. 3.11.0. (Bankevich et al. 2012) using the adductor muscle specimen from the sampled individual in Shahekou District, Dalian, China (sex was not determined for this mollusk due to empty gonads at the sampling time). The original mitogenome annotation was obtained from a sequencing laboratory: Huitong Biotechnology, Shenzhen, China. The voucher specimen was collected by the College of Fisheries and Life Science, Dalian Ocean University, #52 Heishijiao Street, Shahekou District, Dalian, Liaoning 116023, China.

The produced consensus sequence of the complete genome was annotated using the MITOS Web Server (Bernt et al.

CONTACT Yuri Ph. Kartavtsev  yuri.kartavtsev48@hotmail.com  Laboratory of Molecular Systematic, A.V. Zhirmunsky National Scientific Center of Marine Biology, Russian Academy of Sciences, Vladivostok, Russia; Hongtao Nie  hntnie@dlo.edu.cn  Laboratory of Engineering and Technology Research, Center of Shellfish Breeding in Liaoning Province, College of Fisheries and Life Science, Dalian Ocean University, Dalian, China

 Supplemental data for this article is available online at <https://doi.org/10.1080/23802359.2021.1970635>.

© 2021 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.

2013). The mitogenome map was built with GeSeq software (Tillich et al. 2017). The nucleotide sequences were aligned by Muscle or ClustalW for the whole mitogenome or separately for protein-coding genes (PCGs) as implemented in MEGA-X (Kumar et al. 2018). At the next step, two substitution models, TrN + G + I or HKY + G + I, were determined as best fit and used for neighbor-joining, maximum likelihood, and maximum parsimony (NJ, ML, and MP, respectively) reconstructions of gene trees for phylogenetic analysis; these two models were applied, respectively, for NJ and ML. For building gene trees, the MEGA-X software was used. For estimating the node's support, the default settings and bootstrapping mode with $n=1000$ replications were applied. NJ (Figure 1) and other trees (not shown) were built on 12 PCGs sequences of seven mitochondrial genomes. The outgroup, where necessary, was *Lutraria* whose representatives belong to a different subfamily.

Results and discussion

The mitogenome annotation of the *Mactra* sp. MT780813 specimen was characterized as circular molecular with obvious deviations from the mitochondrial gene order typical of vertebrates and depauperate in this and some other features from the closest specimen in the GenBank (<https://www.ncbi.nlm.nih.gov/>), as shown by BLAST searches on 27 June 2020 and 22 August 2020. It was found belonging to *M. chinensis* KJ754823 (identified as female's mitogenome, F; Fernández-Pérez et al. 2017). MITOS detected the following content for the *Mactra* sp. MT780813 specimen: 12 PCGs, two D-loops or Control Regions (CR), 12S rRNA, and 16S rRNA, 27 tRNAs including two tRNA-Leu's, tRNA-Ser's, and tRNA-Asn's, and also four tRNA-Phe's (Figure 1(A)). No ATPase 8 known for some bivalves (Shen et al. 2014) were found in this genome. Each of the four copies of tRNA-Phe was accompanied by the 189bp non-coding region, hence, representing tandem repeats (Figure 1(A)). As follows from Supplementary Table 1 data, tRNA gene numbers and NCR, noncoding regions sharply differ in two compared sequences; tRNA gene numbers are 27 for MT780813 (this paper) and 20 for KJ754823 (Shen et al. 2014). Three NCR have been listed in our specimen, while no one mentioned KJ754823 (Supplementary Table 1). However, for PCGs the overall diversity is reasonably big too, as illustrated in the paper and indicated by the composition bias calculated for seven sequences in the analysis (Figure 1(B)). There are also the tandem repeats as noted above.

The mitogenome of *Mactra* sp. MT780813 was 17,802bp in length with the above-noted complement of genes and structural elements, which differed from the earlier described mitogenome sequence KJ754823 (Shen et al. 2014). The overall base composition was $41.2 \pm 0.51\%$ T (the values presented hereafter are mean \pm standard error), $13.4 \pm 0.51\%$ C, $23.1 \pm 0.51\%$ A, and $22.2 \pm 0.51\%$ G. By this composition, this mitogenome did not differ from the sequence KJ754823 by Shen et al. (2014), $F=1.015$, $p>0.39$. All 12 PCGs started with the ATG initiation codon. A few atypical starts and stop codons were also found as well as in many other fish and

shellfish taxa (Kartavtsev et al. 2007; Shen et al. 2014; Li et al. 2014; Turanov et al. 2019; Zheng et al. 2019).

In order to investigate the phylogenetic position of *Mactra* sp. MT780813 among the nearest relatives, NJ, ML, and MP phylogenetic analyses were carried out on the basis of complete mitogenome sequences from a few nearest relatives from the family Mactridae and two species from another subfamily as an outgroup (Figure 1(B)). As shown in Figure 1(B), *Mactra* sp. MT780813 is more closely related to the specimen *M. chinensis* KJ754823. However, the two *Mactra* sequences potentially have large distance scores (e.g. 0.181 for composition bias), in accordance with the pattern provided in the NJ tree (Figure 1(B)). Congruent tree topology was obtained for all three reconstructions, that is, NJ, ML, and MP-trees (the two latter are not shown). The topology for the Mactridae representatives in Figure 1(B) well matches the wider comparison of F-mitogenome sequences of bivalves (Fernández-Pérez et al. 2017). Thus, judging by the known interspecies differences for the other two species representing this genus, with a p -distance score equal to 0.073–0.083 (Shen et al. 2014), we can conclude that the specimen of *Mactra* sp. MT780813 probably belonged to the species *M. chinensis* of M-type (male genome). The alternative of different sex lines representation in the source specimens due to DUI is differences occurred in the hidden taxa that might be specified as an unknown taxon (*Mactra* sp.) different from typical *M. chinensis*. As is well known, M-type is highly divergent from F-type in many bivalve mollusks (Theologidis et al. 2008). In several bivalve mollusks, differences between the M- and F-type sequences in p -distance for the 16S rRNA and *cyt b* genes averaged at 0.366 ± 0.038 and 0.507 ± 0.044 , respectively (Theologidis et al. 2008). While for the two representatives of the nearest genera of Mactridae, *M. chinensis* and *Colomacra* (*Mactra*) *antiquate* (MolluscaBase, 2020), the p -distance score between M- and F-type reached 0.0953 ± 0.0023 and 0.0949 ± 0.0016 , respectively, or even greater depending on sequence assemblage (mitogenome, estimates based on our and GenBank data). Cryptic species among *Colomacra* (*Mactra*) *antiquata* (Ni et al. 2012; Yuan et al. 2013; Shen et al. 2014) and *Mactra* (Reunov et al. 2019) were considered, but there was no clarification about the DUI point. As noted in the introduction, such bivalve taxa as Mytilidae, Veneridae, etc., that exhibiting the DUI phenomenon of mtDNA inheritance, may have a level of F- vs. M-type intraspecies divergence (Zouros et al. 1994; Skibinski et al. 1994; Theologidis et al. 2008; Fernández-Pérez et al. 2017) higher than the divergence typical for different species. The assembly artifacts and Labs' made mistakes if sequencing made in different conditions may possibly cause such an obscure conclusion. However, in our case the most natural and highly probable are two reasons: (i) the gender differences that have been established earlier for the relatives of these mollusks' (Theologidis et al. 2008; Fernández-Pérez et al. 2017) because source tissues (adductor muscle) are same for two compared sequences, MT780813 (this paper) and KJ754823 (Shen et al. 2014) or (ii) differences occurred in the hidden taxa that might be specified by *Mactra* sp. MT780813 vs. *M. chinensis* KJ754823. By the orthodox viewpoint the adductor specimen from *Mactra* sp. MT780813 must be F-type. However, the

Thus, despite the probability of the existence of cryptic taxa, accurate sex determination, homogenous gender representation, and the comparison of a voucher collection of specimens are the ultimate requirement for phylogenetic reconstructions and taxonomic identification, as exemplified elsewhere (Fernández-Pérez et al. 2017), including individual-based assessment of the F- vs. M-type mtDNA difference. This will be the aim of the next research by our team.

Acknowledgments

The authors thank E. P. Shvetsov for MS proofreading. We also grateful to Dr. S. V. Turanov for help with MS editing at earlier stages.

Disclosure statement

The authors have no conflicts of interest to declare. The authors are solely responsible for the content and the writing of this paper.

Funding

This research was supported by the Ministry of Science and Higher Education of the Russian Federation in the framework of the federal project no. 13.1902.21.0012 'Basic problems in the research and conservation of deep-water ecosystems...' (agreement no. 075-15-2020-796), by the 'Liaoning BaiQianWan Talents Program', and by the Modern Agro-industry Technology Research System [CARS-49].

Data availability statement

The mitogenome of *Mactra* sp. can be obtained from GenBank under accession no. MT780813. The voucher specimen was collected and stored by the College of Fisheries and Life Science, Dalian Ocean University, #52, Heishijiao Street, Shahekou District, Dalian, Liaoning 116023, China. It is deposited at this institution, as a specimen with voucher no. WB-F and curated at the Lab by person Nie, Hongtao (Tel. +86-0411-84763083; e-mail: htnie@dlo.edu.cn). The associated BioProject, SRA, and Bio-Sample numbers are PRJNA745510, SUB9992288, and SAMN20168722, respectively. Also, data from the paper are available on web-page: (13) (PDF) Complete mitochondrial genome of *Mactra chinensis* (Bivalvia: Macridae) (researchgate.net).

References

- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol.* 19(5):455–477.
- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsche G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69(2): 313–319.
- Fernández-Pérez J, Nantón A, Ruiz-Ruano FJ, Camacho JPM, Méndez J. 2017. First complete female mitochondrial genome in four bivalve species genus *Donax* and their phylogenetic relationships within the Veneroida order. *PLoS One.* 12(9):e0184464.
- Kartavtsev YP, Jung S-O, Lee Y-M, Byeon H-K, Lee J-S. 2007. Complete mitochondrial genome of the bullhead torrent catfish, *Liobagrus obesus* (Siluriformes, Amblycipididae): genome description and phylogenetic considerations inferred from the Cyt b and 16S rRNA genes. *Gene.* 396(1):13–27.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol.* 35(6):1547–1549.
- Kyriakou E, Kravariti L, Vasilopoulos T, Zouros E, Rodakis GC. 2015. A protein binding site in the M mitochondrial genome of *Mytilus galloprovincialis* may be responsible for its paternal transmission. *Gene.* 562(1):83–94. doi:10.1016/j.gene.2015.02.047.
- Li H, Zhang J, Li H, Gao X, He C. 2014. Development and characterization of 13 polymorphic microsatellite markers for the Chinese surf clam (*Mactra chinensis*) through Illumina paired-end sequencing. *Conservation Genet Resour.* 6(4):877–879.
- Lutaenko KA, Noseworthy RG. 2012. Catalogue of the living Bivalvia of the continental coast of the Sea of Japan (East Sea). Vladivostok (Russia): Dalnauka; p. 247.
- MolluscaBase. 2020. *Mactra chinensis* Philippi, 1846. Brussels (Belgium): LifeWatch; Accessed 2020 September 18]. <http://www.marinespecies.org/aphia.php?p=taxdetails&id=367847>
- Ni L, Li Q, Kong L, Huang S, Li L. 2012. DNA barcoding and phylogeny in the family Macridae (Bivalvia: Heterodonta): evidence for cryptic species. *Biochem Syst Ecol.* 44:164–172.
- Reunov AA, Lutaenko KA, Zakharov EV. 2019. Genetic divergence in bivalve mollusk *Mactra chinensis* related with disproportional heteromorphism in male gametes. *Proc Russ Acad Sci.* 455(5):1–4.
- Scarlato OA. 1976. Bivalve mollusks – Bivalvia. In: Animals and plants of Peter the Great Bay. Moscow (Russia): Nauka. p. 95–107.
- Schwartz JH. 2021. Evolution, systematics, and the unnatural history of mitochondrial DNA. *Mitochondrial DNA A DNA Mapp Seq Anal.* 32(4): 126–151. doi:10.1080/24701394.2021.1899165.
- Shen X, Meng XP, Chu KH, Zhao NN, Tian M, Liang M, Hao J. 2014. Comparative mitogenomic analysis reveals cryptic species: a case study in Macridae (Mollusca: Bivalvia). *Comp Biochem Physiol Part D Genomics Proteomics.* 12:1–9.
- Skibinski DOF, Gallagher C, Beynon CM. 1994. Mitochondrial DNA inheritance. *Nature.* 368(6474):817–818.
- Theologidis I, Fodelianakis S, Gaspar MB, Zouros E. 2008. Doubly uniparental inheritance (DUI) of mitochondrial DNA in *Donax trunculus* (Bivalvia: Donacidae) and the problem of its sporadic detection in Bivalvia. *Evolution.* 62(4):959–970.
- Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq - versatile and accurate annotation of organelle genomes. *Nucleic Acids Res.* 45(W1):W6–W11.
- Turanov SV, Rutenko OA, Kartavtsev YP. 2019. Complete mitochondrial genome of *Stichaeus grigorjewi* Herzenstein, 1890 (Zoarcales: Stichaeidae). *Mitochondrial DNA Part B.* 4(1):899–901.
- Yuan Y, Kong L, Li Q. 2013. Mitogenome evidence for the existence of cryptic species in *Coelomacra antiquata*. *Genes Genom.* 35(6): 693–701.
- Zheng Y, Chen Y, Chen P. 2019. The complete mitochondrial genome of an eelpout *Lycodes ygreknotatus* (Teleostei: Zoarcidae). *Mitochondrial DNA Part B.* 4(1):616–617.
- Zouros E, Ball AO, Saavedra C, Freeman KR. 1994. Mitochondrial DNA inheritance. *Nature.* 368(6474):818.