

The complete mitochondrial genome of *Artemia persimilis* Piccinelli and Prosdocimi, 1968 (Crustacea: Anostraca)

Xuekai Han^{a*}, Lahm Tashi^{b*}, Liying Sui^a, Guishuang Wang^b, Gusang Deji^c and Chi Zhang^b

^aAsian Regional Artemia Reference Center, Tianjin University of Science and Technology, Tianjin, China; ^bInstitute of Fisheries Science, Tibet Academy of Agricultural and Animal Husbandry Sciences, Lhasa, P. R. China; ^cTibet Academy of Agricultural and Animal Husbandry Sciences, Lhasa, P. R. China

ABSTRACT

In the study, we report the complete mitochondrial genome of *Artemia persimilis* Piccinelli and Prosdocimi, 1968 for the first time. The mitochondrial genome of *A. persimilis* is 15,436 bp in length, with the typical structure of 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs) and 2 ribosomal RNA genes, and a non-coding control region (CR). Phylogenetic analysis showed that *A. persimilis* was at the basal position among the bisexual *Artemia* species, which revealed that *A. persimilis* is likely to be an ancestral clade. The present study could provide effective resources for population genetics study, as well as germplasm conservation in *Artemia*.

ARTICLE HISTORY

Received 16 September 2021
Accepted 26 January 2022

KEYWORDS

Artemia persimilis;
mitochondrial genome;
phylogenetic relationship

Introduction

Artemia is not only one of the most important live food items used in larval aquaculture, but also an ideal laboratory model organism for scientific research. As a small crustacean, *Artemia* have a widely distribution all over the world, mainly in hypersaline environments, and play an important biological regulatory role in salt field ecosystem. The genus *Artemia* is generally considered to contain seven bisexual species as well as some parthenogenetic *Artemia* populations with different polyploidy types (Asem et al. 2010). However, their generic taxonomy is not universally accepted, especially in relation to *Artemia tibetiana* and *Artemia urmiana*. Mitochondrial DNA are widely used to study the molecular ecology of animals because it is convenient and economical, comparison of the mitochondrial genomes will permit examination of evolution and relationships between species. At present the complete mitochondrial genome of four bisexual species (*Artemia franciscana*, *A. urmiana*, *A. tibetiana* and *Artemia sinica*) is already known (Valverde et al. 1994; Zhang et al. 2013; Asem et al. 2019). But for another bisexual species *Artemia persimilis* Piccinelli and Prosdocimi, 1968, a species endemic to the South American and geographically restricted to Argentina and Chile (Sainz Escudero et al. 2021), the complete mitochondrial genome has not been reported and characterized. Herein, we reported the complete mitochondrial genome sequence of *A. persimilis*, and we performed a phylogenetic analysis to study the evolutionary relationships of *A. persimilis* with other *Artemia* species. We expect that the present result will facilitate the further

investigations of phylogenetic relationship, taxonomic resolution and phylogeography of the *Artemia* species.

Materials and methods

The cysts of *A. persimilis* Piccinelli and Prosdocimi, 1968 was collected from Bahia Blanca, Argentina (**latitude** –62.1338 and **longitude** –38.8385). The specimen was deposited at the Asian Regional Artemia Reference Center (Tianjin University of Science and Technology, China) (Liying Sui, suily@tust.edu.cn) under the voucher number 1807. The genomic DNA was extracted from cysts according to the instructions of TIANGEN@TIANamp Genomic DNA Kit (Tianjin, China). Then the high quality gDNA was sequenced using Illumina Novaseq6000 platform with 350 bp insert size. The complete mitochondrial genome was assembled using SPAdes v.3.5.0 (<http://cab.spbu.ru/software/spades/>) with *A. franciscana* (GenBank accession number: X69067) as reference. The reference mitochondrial map and BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) were used for gene annotation. The tRNA genes were predicted using the ARWEN (<http://mbio-serv2.mbioekol.lu.se/ARWEN/>) and tRNAscan-SE 2.0 (<http://lowelab.ucsc.edu/tRNAscan-SE/>) online software.

Results and discussion

The complete mitochondrial genome of *A. persimilis* Piccinelli and Prosdocimi, 1968 (Genbank accession number: MZ199176) is 15,436 bp in length, with the typical structure

CONTACT Chi Zhang  zc0891@163.com  Institute of Fisheries Science, Tibet Academy of Agricultural and Animal Husbandry Sciences, Lhasa 850002, P. R. China

*The first two authors, Xuekai Han and Tashi Lahm, contributed equally to this study.

© 2022 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 License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

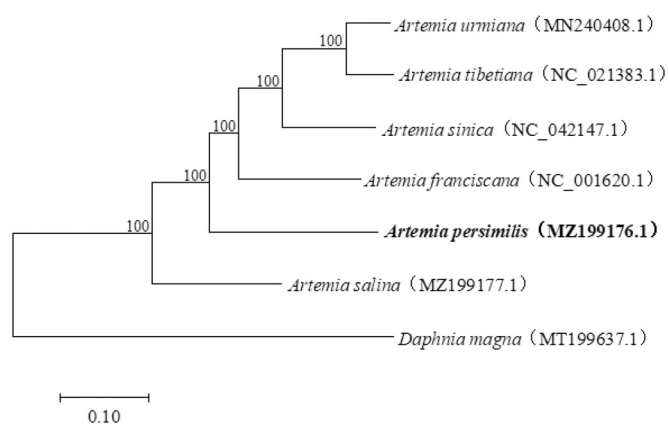


Figure 1. Phylogenetic tree showing the relationship among *A. persimilis* and other species from the *Artemia*. The numbers on each node are the bootstrap support values. *Daphnia magna* was selected as an outgroup.

of 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs) and 2 ribosomal RNA genes, and a non-coding control region (CR). The base composition is 25.70% A, 24.00% C, 20.07% G, and 30.23% T, with an A+T content of 55.93%. Just six PCGs (*cox1*, *atp6*, *cox3*, *cytb*, *nd1* and *nd2*) began with the common ATG start codon. Stop codons included TAA (*cox3*, *nd2*, *atp8*, *atp6*, *nd3* and *cytb*) and TAG (*nd1*, *nd4* and *nd6*). There are 4 genes ended with the incomplete stop codon T (*cox1*, *cox2*, *nd4* and *nd5*). The 12S rRNA and 16S rRNA were separated by the *trnV*. The length of *rrnL* and *rrnS* is 1148 bp and 711 bp, respectively. The 22 tRNA genes size varies from 61 to 67 bp, respectively.

Combined with the complete mitochondrial genome sequences of four bisexual *Artemia* species as well as dieocious *Artemia salina* from GenBank, a phylogenetic tree was constructed by Maximum-likelihood (ML) method with the Kimura 2-parameter model using the software MEGA 7.0 (Kumar et al. 2016), so as to infer the phylogenetic relationships among *Artemia* species. The phylogenetic tree showed that *A. persimilis* was at the basal position among the bisexual *Artemia* species, which revealed that *A. persimilis* is likely to be an ancestral clade (Figure 1). The mitochondrial genome sequence of *A. persimilis* reported here provide a useful genetic resource for population genetics and evolutionary studies in *Artemia*.

Acknowledgements

The authors thank Artemia Reference Center (Ghent University, Belgium) for assistance with specimen collection.

This study was funded by the Projects of Agricultural intelligence introduction of Tibet (2020WZ006) and the National Science Foundation of Tianjin (18JCQNJC78500).

Ethics statement

The study protocol was approved by the Committee on the Ethics of Animal Experiments of Tianjin University of Science and Technology.

Author contributions statement

Chi Zhang supervised the project. Xuekai Han and Tashi Lahm conceived and designed the study. Liying Sui and Guishuang Wang guided data analysis and interpretation. Xuekai Han performed experiments and drafted the manuscript. GUSANG Deji revised it critically for intellectual content. All authors approved the final version of the manuscript.

Disclosure statement

The authors declare that they have no conflict of interest.

Funding

This study was funded by the Projects of Agricultural intelligence introduction of Tibet [2020WZ006] and Error! Hyperlink reference not valid. [18JCQNJC78500].

Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>, reference number MZ199176. The associated BioProject, SRA, and BioSample numbers are PRJNA749897, SRR15292985, and SAMN20424866, respectively.

References

- Asem A, Li WD, Pei-Zheng Wang PZ, Eimanifar A, Shen CY, De Vos S, Van Stappen G. 2019. The complete mitochondrial genome of *Artemiasinica* Cai, 1989 (Crustacea: Anostraca) using next-generation sequencing. *Mitochondrial DNA Part B*. 4(1):746–747.
- Asem A, Rastegar-Pouyani N, De los Rios P. 2010. The genus *Artemia* Leach, 1819 (Crustacea: Branchiopoda): true and false taxonomical descriptions. *Lat Am J Aquat Res*. 38:501–506.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Bio Evol*. 33(7): 1870–1874.
- Sainz Escudero L, López Estrada EK, Rodríguez Flores PC, García París M. 2021. Settling taxonomic and nomenclatural problems in brine shrimps, *Artemia* (Crustacea: Branchiopoda: Anostraca), by integrating mitogenomics, marker discordances and nomenclature rules. *Peer J*. 9: e10865.
- Valverde J, Batuecas B, Moratilla C, Marco R, Garesse R. 1994. The complete mitochondrial DNA sequence of the Crustacean *Artemia franciscana*. *J Mol Evol*. 39(4):400–408.
- Zhang HX, Luo QB, Sun J, Liu F, Wu G, Yu J, Wang WW. 2013. Mitochondrial genome sequences of *Artemia tibetiana* and *Artemia urmiana*: assessing molecular changes for high plateau adaptation. *Sci China Life Sci*. 56(5):440–452.