The complete mitochondrial genome of the freshwater crab Potamiscus motuoensis (Decapoda: Brachyura: Potamoidea)

Songbo Wanga, Yifan Wangb, Yangjin Zhuoma, Ling Tongc, Zongheng Niea, Xinnan Jiaa, Chunchao Zhua, Xianmin Zhoua and Jieixin Zoua,e

aResearch lab of Freshwater Crustacean Decapoda and Paragonimus, School of Basic Medical Sciences, Nanchang University, Nanchang City, Jiangxi Province, People’s Republic of China; bInstitute of Pathogen Biology, Jiangxi Academy of Medical Sciences, Nanchang City, Jiangxi Province, People’s Republic of China; cLinzhi Municipal Center for Disease Control and Prevention, Linzhi City, Tibet Autonomous Region, China; dKey Laboratory of Poyang Lake Environment and Resource Utilization, Ministry of Education, Nanchang University, Nanchang City, Jiangxi Province, People’s Republic of China; eKey Laboratory of Freshwater Crustacean Decapoda and Paragonimus, School of Basic Medical Sciences, Nanchang University, Nanchang City, Jiangxi Province, People’s Republic of China

ABSTRACT

Potamiscus motuoensis is the only one freshwater crab species distributed in Yarlung Zangbo River Grand Canyon and its complete mitochondrial genome was obtained for the first time. The complete mitochondrial genome of P. motuoensis is 17,971 bp in length, including 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, and 1 control region. In addition, the mitogenome has 19 noncoding regions ranging from 1 to 1396 bp in length. The report of the mitochondrial genome will enrich the species diversity of Yarlung Zangbo River Grand Canyon and provide data support for further research.

ARTICLE HISTORY
Received 2 January 2020
Accepted 19 January 2020

KEYWORDS
Brachyuran; complete mitochondrial genome; phylogenetic; Potamiscus motuoensis

The species Potamiscus motuoensis (Crustacea: Malacostraca: Decapoda: Brachyura: Potamidae: Potamicus) is the only one freshwater crab species distributed in Yarlung Zangbo River Grand Canyon.

An adult specimen of P. motuoensis was collected from Zhu Village, Damu Town Medog County, Linzhi City, Tibet Autonomous Region, China in 2014 (N29.523009’/C3/C14/C14). The sample has been deposited in the Laboratory Specimen Library of Freshwater Crustacean Decapoda and Paragonimus, School of Basic Medical Sciences, Nanchang University, Nanchang, Jiangxi, China and National Parasite Germplasm Resources Specimen Library of China with a catalog number of NCUMCP4250. The sample was stored in 95% ethanol prior to extraction at room temperature before sequence analyses. Genomic DNA extraction, sequencing, gene annotation, and phylogenetic analyses were performed according to the method described by Plazzi et al. (Plazzi et al. 2013). The Bayesian Inference (BI) method was performed using MrBayes vers. 3.2 (Ronquist et al. 2012), with best model GTR + I + G selected by jModelTest vers.2.1.7. The maximum-likelihood (ML) method was performed using MEGA 6 (Tamura et al. 2013).

Potamiscus motuoensis (GenBank accession no. KY285013) has a full-length mitochondrial genome of 17,971 bp and shares the same 37 genes (13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes) and 1 control region (CR) as the typical metazoan mitochondrial genome. Among these genes, 26 are located in the H-strand and 11 are located in the L-strand. The mitochondrial genome composition of P. motuoensis is A (35.5%), C (19.1%), G (9.2%), and T (36.2%), with a high A + T bias.

The mitochondrial genome of P. motuoensis contains 13 protein-coding genes. Similar to other Brachyura mitochondrial genomes, 9 protein-coding genes are located in the H chain (COX1, COX2, COX3, ATP6, ATP8, ND2, ND3, ND6, and CYTb), and the remaining four are located in the L chain (ND1, ND4, ND4L, and ND5). The initiator codon of most protein-coding genes is ATN (ND4 is GTG), and the most frequent termination codon is TAA, containing incomplete termination codons TA and T and a rare termination codon TAG (ATP8). The A + T bias of the protein-coding gene is 69%. This bias is consistent with the genome.

The mitochondrial genome of P. motuoensis possesses 2 rRNA genes, 16S rRNA and 12S rRNA, which are located in the same L chain as other Brachyura mitochondrial genomes. The length of the 16S rRNA and 12S rRNA genes is 1294 bp and 859 bp, respectively; 16S rRNA is between tRNA^Leu(CUN) and tRNA^Gln, while 12S rRNA is between tRNA^Glu and the CR. Similar to other Brachyura mitochondrial genomes, P. motuoensis has 22 tRNAs in common and most tRNAs have a typical clover structure, with the exception of tRNA^Ser which lacks the dihydrouracil (DHU) arm (Ohtsu et al. 2002).

CONTACT Jieixin Zou (jzou@ncu.edu.cn) Research lab of Freshwater Crustacean Decapoda and Paragonimus, School of Basic Medical Sciences, Nanchang University, Nanchang City, Jiangxi Province, People’s Republic of China

# These authors have contributed equally to this work.

© 2020 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.
The 22 tRNA genes are between 60 and 71 bp in length. Additionally, there are certain base mismatches, including 35G-T mismatches, 3A-C mismatches, 2A-G mismatches, 2T-C mismatches, 2A-A mismatches, and 2T-T mismatches. The mitochondrial genome of *P. motuoensis* has 19 noncoding regions and is between 1 and 1396 bp in length. The CR of *P. motuoensis* has the typical characteristic of crustaceans; it is located in a typical crustacean position (between 12S rRNA and tRNAVal), is 859 bp in length and has a higher A + T bias than does the mitochondrial genome.

The phylogenetic position of *P. motuoensis* in mitogenome relative to other Brachyuran mitogenomes is determined by applying the BI and ML methods on 13 PCGs (Figure 1). The results were consistent with the current molecular classification and morphological classification (Segawa and Aotsuka 2005; Liang 2013; Ming et al. 2014; Tang et al. 2017), with other freshwater crab species of family Potamoidea forming a separate clade.

**Acknowledgment**

The authors thank Carrie E. Schweitzer for assistance with fossil time.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This work is supported by the National Natural Science Foundation of China [No. 81260257, 31560179], National Sharing Service Platform for Parasite Resources (TDRC-30), the Natural Science Foundation of Jiangxi Province [2017BAB214013], and the Nanchang University College Students’ Innovation and Entrepreneurship Training Program [No. 2018388] and Nanchang University’s Scientific Research Training Program (2019).

**ORCID**

Jiexin Zou  http://orcid.org/0000-0002-5549-2167

**References**

Liang G. 2013. Eight evidences about Hainan Island separated from Chinas Beibuwan Gulf with drifting and rotation. Acta Geol Sinica. 87: 73–76.

Ming TL, Schubart CD, Ahyong ST, Lj CY, Ae YC, Chan TY, Np KL, Chu KH. 2014. Evolutionary history of true crabs (Crustacea: Decapoda: Brachyura) and the origin of freshwater crabs. Mol Biol Evol. 31(5): 1173–1187.

Ohitsu K, Kawai G, Watanabe K. 2002. The minimal tRNA: unique structure of *Ascaris suum* mitochondrial tRNASerUCU having a short T arm and lacking the entire D arm. FEBS Letters. 514(1): 37–43.

Plazzi F, Ribani A, Passamonti M. 2013. The complete mitochondrial genome of *Solemya velum* (Mollusca: Bivalvia) and its relationships with Conchifera. BMC Genomics. 14(1): 409–409.

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 61(3): 539–542.

Segawa RD, Aotsuka T. 2005. The mitochondrial genome of the Japanese freshwater crab, *Geothelphusa dehaani* (Crustacea: Brachyura): evidence for its evolution via gene duplication. Gene. 355: 28–39.

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol. 30(12): 2725–2729.

Tang B-P, Xin Z-Z, Liu Y, Zhang D-Z, Wang Z-F, Zhang H-B, Chai X-Y, Zhou C-L, Liu Q-N. 2017. The complete mitochondrial genome of *Sesarmops sinensis* reveals gene rearrangements and phylogenetic relationships in Brachyura. PLoS One. 12(6): e0179800.