Characterization of the complete mitochondrial genome of *Tripetaloceroides tonkinensis* (Orthoptera: Tetrigoidea) from China and its phylogenetic analysis

Rong-Jiao Zhang, Lei Xin and Wei-An Deng

School of Chemistry and Bioengineering, Hechi University, Yizhou, PR China; Ministry of Education, Key Laboratory of Ecology of Rare and Endangered Species and Environmental Protection (Guangxi Normal University), Guilin, PR China; Guangxi Key Laboratory of Rare and Endangered Animal Ecology, Guangxi Normal University, Guilin, PR China; College of Life Sciences, Guangxi Normal University, Guilin, PR China

**ABSTRACT**

The mitochondrial genome (mitogenome) of the *Tripetaloceroides tonkinensis* (Orthoptera: Tetrigoidea) was sequenced and annotated. The complete mitogenome has a length of 16,696 bp and consists of 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and a A+T-rich region. Thirteen PCGs started with typical ATN codon and ended with complete stop codons (five with TAG, eight with TAA). The overall nucleotide composition was 42.7% A, 10.34% G, 25.87% T, and 21.08% C. The phylogenetic trees in the current study confirmed that *T. tonkinensis* was clustered with other Tetrigoidea species, and the study would improve our understanding for the mitogenomes of Tetrigoidea.

**KEYWORDS**

Tetrigidae; Tripetalocerinae; *Tripetaloceroides tonkinensis*; mitogenome; phylogenetic analysis

**ARTICLE HISTORY**

Received 22 March 2021
Accepted 28 May 2021

**CONTACT**

Wei-An Deng, dengwei5899@163.com, Ministry of Education, Key Laboratory of Ecology of Rare and Endangered Species and Environmental Protection (Guangxi Normal University), Guilin, PR China

**ARTICLE INFORMATION**

MITOCHONDRIAL DNA PART B

MITOGENOME ANNOUNCEMENT

2021, VOL. 6, NO. 7, 1990–1991

https://doi.org/10.1080/23802359.2021.1938724

© 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 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.
as monophyletic with strong support (posterior probability, PP = 1). *T. tonkinensis* split off earliest from the other taxa, was positioned as a sister group to the remaining Tetrigoidea (PP = 1), suggesting that it is the earliest species within Tetrigoidea.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This work was supported by the National Natural Science Foundation of China [31900351, 31960111], Guangxi Natural Science Foundation [2020GXNSFBA159032], Young Teachers’ Basic Ability Improvement Program of Guangxi Colleges and Universities [2019KY0641], High-level Scientific Research Program for the Talent of Hechi University [2019GCC009] and High level Innovation Team and Outstanding Scholars Program of Guangxi Colleges and Universities.

**ORCID**

Rong-Jiao Zhang [http://orcid.org/0000-0001-5545-856X](http://orcid.org/0000-0001-5545-856X)

Wei-An Deng [http://orcid.org/0000-0002-8023-2498](http://orcid.org/0000-0002-8023-2498)

**Data availability statement**

The data that support the findings of this study are openly available in National Center for Biotechnology Information at [https://www.ncbi.nlm.nih.gov/nuccore](https://www.ncbi.nlm.nih.gov/nuccore), Reference no. MW770353.

**References**

Anderson S, Bankier AT, Barrell BG, de Bruijn MH, Coulson AR, Drouin J, Eperon IC, Nierlich DP, Roe BA, Sanger F, et al. 1981. Sequence and organization of the human mitochondrial genome. Nature. 290(5806): 457–465.

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 313–319.

Deng WA. 2016. Taxonomic study of Tetrigoidea from China [Ph.D. dissertation]. Wuhan: Huazhong Agricultural University.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12): 1647–1649.

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.

Storozhenko SY. 2013. Review of the subfamily Tripetalocerinae Bolivar, 1887 (Orthoptera: Tetrigidae). Zootaxa. 3718(2):158–170.