

The complete mitochondrial genome of *Eutrichosiphum pasaniae* (Okajima, 1908) (Hemiptera: Aphididae: Greenideinae)

Cailling Li^{a,b}, Liyun Jiang^a, Xiaolu Zhang^{a,c}, Jing Chen^a and Gexia Qiao^{a,c}

^aKey Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China; ^bInstitutes of Physical Science and Information Technology, Anhui University, Hefei, China; ^cCollege of Life Sciences, University of Chinese Academy of Sciences, Beijing, China

ABSTRACT

In this study, we sequenced the complete mitochondrial genome of *Eutrichosiphum pasaniae* through Illumina platform. The circular mitogenome is 16,500 bp in length and composed of 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes (rRNAs), a large control region and a special repeat region. The nucleotide composition of whole mitogenome is strongly AT-biased (85.5%). All PCGs start with ATN and end with TAA except for *cox1* which terminates with an incomplete stop codon T. All tRNAs have a typical clover-leaf secondary structure except for *trnS* (AGN). The lengths of *rrnL*, *rrnS* and control region are 1276, 774 and 996 bp, respectively. The repeat region with a length of 909 bp is located between *trnE* and *trnF* and consists of 4.1 repeat units. The phylogenetic tree supports the sister relationship of *Eutrichosiphum pasaniae* and *Greenidea psidii*.

ARTICLE HISTORY

Received 15 September 2020
Accepted 28 September 2020

KEYWORDS

Mitogenome; aphid; repeat region; phylogeny

The aphid species *Eutrichosiphum pasaniae* (Okajima, 1908) (Hemiptera: Aphididae: Greenideinae) distributes in eastern and southeastern Asia and mainly feeds on leaves and young shoots of the plants of *Lithocarpus* and *Castanopsis* (Blackman and Eastop 2020). In the present study, we sequenced the complete mitochondrial genome of *E. pasaniae* through the Illumina platform. The *E. pasaniae* samples were collected from *Castanopsis uraiana* in Daren Township, Taiwan, China (22.3750°N, 120.8592°E) and deposited in the National Zoological Museum of China, Institute of Zoology, Chinese Academy of Science, Beijing, China (NZMC no. 39256).

The circular mitochondrial genome of *E. pasaniae* is 16,500 bp long (GenBank accession number MT883997) and includes 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), 2 ribosomal RNA genes (rRNAs), a control region and a special repeat region between *trnE* and *trnF*. The gene order is identical to the inferred ancestral arrangement of insects (Clary and Wolstenholme 1985). The majority strand contains 9 PCGs and 14 tRNAs, while the remaining genes are located on the minority strand. The overall nucleotide composition of *E. pasaniae* mitogenome is 46.6% A, 38.9% T, 5.5% G and 9.1% C, which is strongly AT-biased (85.5%). In the whole mitogenome, there are 21 intergenic spacers ranging from 1 to 51 bp and 8 gene overlapping regions ranging from 1 to 20 bp.

Thirteen PCGs are initiated by the standard ATN and ended with TAA except for *cox1*, which uses an incomplete stop codon T. The tRNA genes range from 62 to 73 bp in length and are predicted to possess a classical clover-leaf secondary structure except for *trnS* (AGN), the dihydrouridine (DHU) arm of which forms a simple loop. The lengths of *rrnL* and *rrnS* genes are 1276 and 774 bp, with an A + T content of 85.3 and 83.8%, respectively. The control region is 996 bp long and located between *rrnS* and *trnI*, with an A + T content of 92.2%. A large repeat region is present between *trnE* and *trnF*, which is unique and species-specific in aphids (Wang et al. 2015). The repeat region is 909 bp long with an A + T content of 87.6% and consists of a 222-bp repeat unit which is repeated 4.1 times.

To perform the phylogenetic analysis, we used the whole mitogenome sequences of *E. pasaniae* and 24 other aphid species. The maximum-likelihood phylogenetic tree was constructed with RAxML v8.2.10 (Stamatakis 2014). The subfamily Greenideinae was monophyletic and *E. pasaniae* was placed as a sister to *Greenidea psidii* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the author(s).

CONTACT Gexia Qiao  qiaogx@ioz.ac.cn; Jing Chen  chenjing@ioz.ac.cn  Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, No. 1 Beichen West Road, Chaoyang District, Beijing 100101, China

© 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.

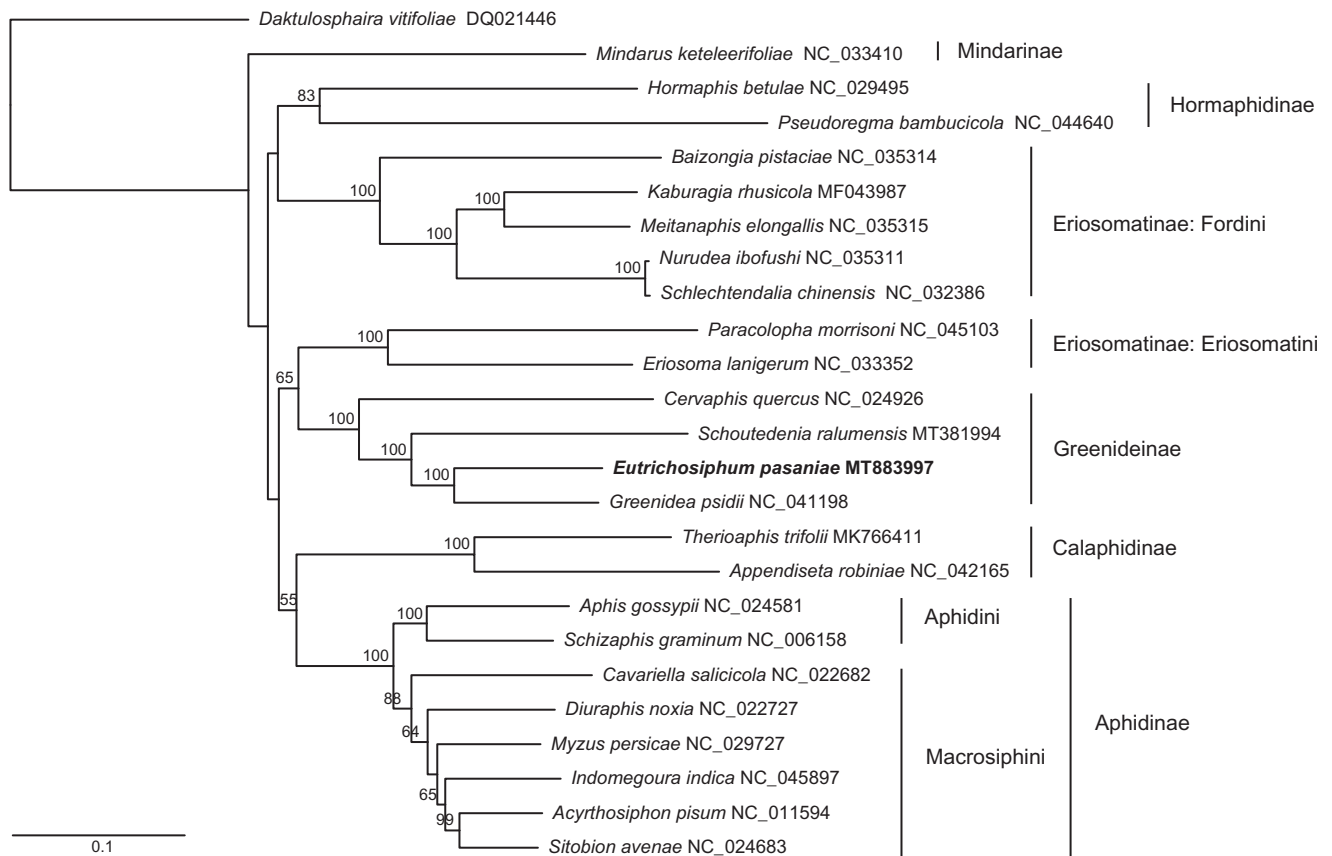


Figure 1. The maximum-likelihood tree of *Eutrichosiphum pasaniae* and 24 other aphid species based on whole mitogenomes. Numbers above the branches indicate bootstrap values (>50%).

Funding

This work was supported by the National Natural Science Foundation of China [Nos. [31620103916](#) and [31772492](#)], the Strategic Priority Research Program of the Chinese Academy of Sciences [No. [XDA19050303](#)], the Youth Innovation Promotion Association of Chinese Academy of Sciences [No. [2020087](#)], and the Second Tibetan Plateau Scientific Expedition and Research (STEP) program [No. [2019QZKK0601](#)].

Data availability statement

The data that support the findings of this study are openly available in Dryad at <https://doi.org/10.5061/dryad.zkh189388>.

References

- Blackman RL, Eastop VF. 2020. Aphids on the world's plants; [accessed 2020 Sep 4]. <http://www.aphidsonworldsplants.info/>.
- Clary DO, Wolstenholme DR. 1985. The mitochondrial DNA molecular of *Drosophila yakuba*: nucleotide sequence, gene organization, and genetic code. *J Mol Evol.* 22(3):252–271.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30(9): 1312–1313.
- Wang Y, Chen J, Jiang LY, Qiao GX. 2015. Hemipteran mitochondrial genomes: features, structures and implications for phylogeny. *Int J Mol Sci.* 16(6):12382–12404.