The mitochondrial genome of *Platencyrtus parkeri* Feriere (Hymenoptera: Encyrtidae)

Yan-Zhou Zhang\(^{a,b}\), Mei Xiong\(^{b,c}\), Qing-Song Zhou\(^b\), Gong-Cheng Jiang\(^a\) and Chao-Dong Zhu\(^{a,b,c}\)

\(^a\)Jiangsu Key Laboratory of Biofunctional Molecule, School of Life Sciences, Chemistry & Chemical Engineering, Jiangsu Second Normal University, Nanjing, China; \(^b\)Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China; \(^c\)University of Chinese Academy of Sciences (UCAS), Beijing, China

**ABSTRACT**

The mitochondrial genome of the *Platencyrtus parkeri* Feriere (Hymenoptera: Encyrtidae) was obtained via next-generation sequencing. The assembled mitogenome is 13,393 bp in length, which contains 33 classical eukaryotic mitochondrial genes with three tRNA genes and rrnS gene missing. All the 13 PCGs begin with typical ATN codons. The 19 detected tRNAs range from 58 to 70 bp in length with typical cloverleaf structure except for trnS1, whose dihydrouridine (DHU) arm forms a simple loop. Meanwhile, they have six tRNAs inserted between nad2 and nad3 compared with *Encyrtus infelix*. Phylogenetic analysis highly supported the monophyly of Pteromalidae. Eupelmidae and Encyrtidae have a close relationship. Within Encyrtidae, *Platencyrtus parkeri* Feriere and *Encyrtus infelix* are close to each other.

*Nipponaclerda biwakoensis* (Kuwana) (Hemiptera: Acleridae) is a main injurious pest on *Phragmites australis* in East Asia (Xu and Wang 2010; Noyes 2019) and now is invaded into southern Louisiana, USA (Knight et al. 2018). *Platencyrtus parkeri* Feriere (Hymenoptera: Encyrtidae) is one of the important parasitoids (Xu and Wang 2010; Noyes 2019), which show high host specificity to *N. biwakoensis* (unpublished data). As a gregarious endoparasitoid of *N. biwakoensis*, *Platencyrtus parkeri* might be very useful to biocontrol the population density of *Nipponaclerda biwakoensis* in the future. So far as we know, little knowledge on their genetic information is available. Here, we present the mitochondrial genome of *P. parkeri* Feriere.

Specimen of *P. parkeri* Feriere (Voucher number: XM19002) was reared from *N. biwakoensis* collected in Ningbo, Zhejiang. Voucher specimens of this study were deposited in the Institute of Zoology, Chinese Academy of Sciences (IZCAS). The total mitochondrial genome of *P. parkeri* Feriere was obtained through next-generation sequencing. The extracted DNA mixture was applied for library construction by the usage of Illumina TruSeq® DNA PCR-Free HT Kit, and sequenced by the platform of Illumina HiSeq sequencer (150 bp paired-end). The mitochondrial genome of *P. parkeri* Feriere was assembled based on Illumina short reads with NOVOPlasy v2.7.0 (Dierckxsens et al. 2017) using COI sequence as the initial seed. The whole mitochondrial genome annotation was annotated by Mitos WebServer (http://mitos2.bioinf.uni-leipzig.de/index.py) under the invertebrate mitochondrial code (Bernt et al. 2013). Transfer RNA (tRNA) genes were confirmed by online ARWEN (http://130.235.46.10/ARWEN/) (Laslett and Canback 2008). The GenBank accession number of *P. parkeri* is MN296710.

The mitogenome sequence of *P. parkeri* Feriere was 13,393 bp in length with an A+T content of 82.3%. It consists of 13 protein-coding genes (PCGs), 19 transfer RNAs (tRNAs), and one partial 16 ribosomal RNAs (rRNAs). Three tRNAs, 12S rRNA, and control region were missing. All 13 PCGs were initiated by typical ATN codons (eight ATT and five ATG). Ten genes use TAA as terminal stop, one gene stop with TAG, two genes have incomplete stop codon. All of the 19 tRNA genes, ranging from 58 to 70 bp, have a typical cloverleaf structure except for trnS1, whose dihydrouridine (DHU) arm forms a simple loop. The absence of the DHU arm in trnS1 was found in the mitochondrial genomes existed in most insects (Wolstenholme 1992). The rml gene is 837 bp, with an average A+T content of 85.2%. Additionally, 22 intergenic spacers (234 bp in total) and 5 overlapping regions (19 bp in total) are dispersed throughout the genome. The inversion of six PCGs (including nad3, cox3, atp6, atp8, cox2 and cox1) has also been found in *P. parkeri* which consisted of other chalcidoidea (Oliveira et al. 2008). Besides, they also have six tRNAs inserted between nad2 and nad3 compared with *Encyrtus infelix* (Xiong et al. 2019).

**CONTACT** Yan-Zhou Zhang zhangyz@ioz.ac.cn

Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, 1 Beichen West Road, Chaoyang District, Beijing, 100101, PR China

© 2019 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 mitogenomic sequences of 22 chalcidoid species were used to reconstruct the phylogeny of Chalcidoidea. Two species from superfamily Proctotrupoidea (Vanhornia eucnemidaraum and Pelecinus polyturator) were chosen as outgroup. Phylogenetic analyses based on 13 PCGs were incomplete PCGs in some species that were identified using MrBayes (Ronquist et al. 2012). The nodes of bayesian inference phylogeny tree with high support value are shown in Figure 1. Generally, Mymaridae was always at the basal position within Chalcidoidea (Sharkey et al. 2012; Heraty et al. 2013). The monophyly of Encyrtidae was strongly supported, showing a sister relationship with Eupelmidae (Xiong et al. 2019).

Disclosure statement

No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of the paper, and report no conflicts of interest.

Funding

This work was supported by the National Natural Science Foundation of China under Grant [No.31572296, No.31872269].

References

Bernt M, Donath A, Juhling F, Externbrink F, Florentz C, Fritzsch G, Putz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69:313–319.
Dierckxsens N, Mardulpyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45:e18.
Heraty JM, Burks RA, Cruaud A, Gibson GAP, Liljeblad J, Munro J, Rasplus JY, Delvare G, Jansta P, Gumovsky A, et al. 2013. A phylogenetic analysis of the megadiverse Chalcidoidea (Hymenoptera). Cladistics. 29:466–542.
Knight IA, Wilson BE, Gill M, Aviles L, Cronin JT, Nyman JA, Schneider SA, Diaz R. 2018. Invasion of *Nipponaclerda biwakoensis* (Hemiptera: Aclerdidae) and *Phragmites australis* die-back in southern Louisiana, USA. Biol Invasions. 20:2739–2744.
Laslett D, Canback B. 2008. ARWEN: a program to detect tRNA genes in metazoan mitochondrial nucleotide sequences. Bioinformatics. 24:172–175.
Noyes JS. 2019. Universal Chalcidoidea Database. World Wide Web electronic publication. [accessed 2019 March 1]. http://www.nhm.ac.uk/chalcidooids.
Oliveira D, Raychoudhury R, Lavrov DV, Werren JH. 2008. Rapidly evolving mitochondrial genome and directional selection in mitochondrial genes in the parasitic wasp *Nasonia* (Hymenoptera: Pteromalidae). Mol Biol Evol. 25:2167–2180.
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. 61:539–542.
Sharkey MJ, Carpenter JM, Vilhelmsen L, Heraty J, Liljeblad J, Dowling AP, Schulmeister S, Murray D, Deans AR, Ronquist F, et al. 2012. Phylogenetic relationships among superfamilies of Hymenoptera. Cladistics. 28:80–112.

Wolstenholme DR. 1992. Animal mitochondrial DNA: structure and evolution. Int Rev Cytol. 141:173.

Xiong M, Zhou QS, Zhang YZ. 2019. The complete mitochondrial genome of Encyrtus infelix (Hymenoptera: Encyrtidae). Mitochondrial DNA Part B. 4:114–115.

Xu ZH, Wang M. 2010. Two genera of Cheiloneurini (Hymenoptera: Encyrtidae) newly recorded from China with descriptions of two new species. Insect Sci. 10:149–153.