

## The complete mitochondrial genome of *Fruhstorferiola huayinensis* (Orthoptera: Catantopidae)

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### ABSTRACT

The complete mitochondrial genome of *Fruhstorferiola huayinensis* is 16 227 bp in length, and consisted of 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes and a control region. In control region, a tRNA<sup>leu</sup>-like sequence was identified. Additionally, a 259 bp long tandem repeat was identified in the control region. Using the 13 PCGs and 2 rRNA of *F. huayinensis*, together with 14 other close-related and 2 outgroup species, we constructed BI phylogenetic tree to verify the accuracy and utility of new determined mitogenome sequences.

### ARTICLE HISTORY

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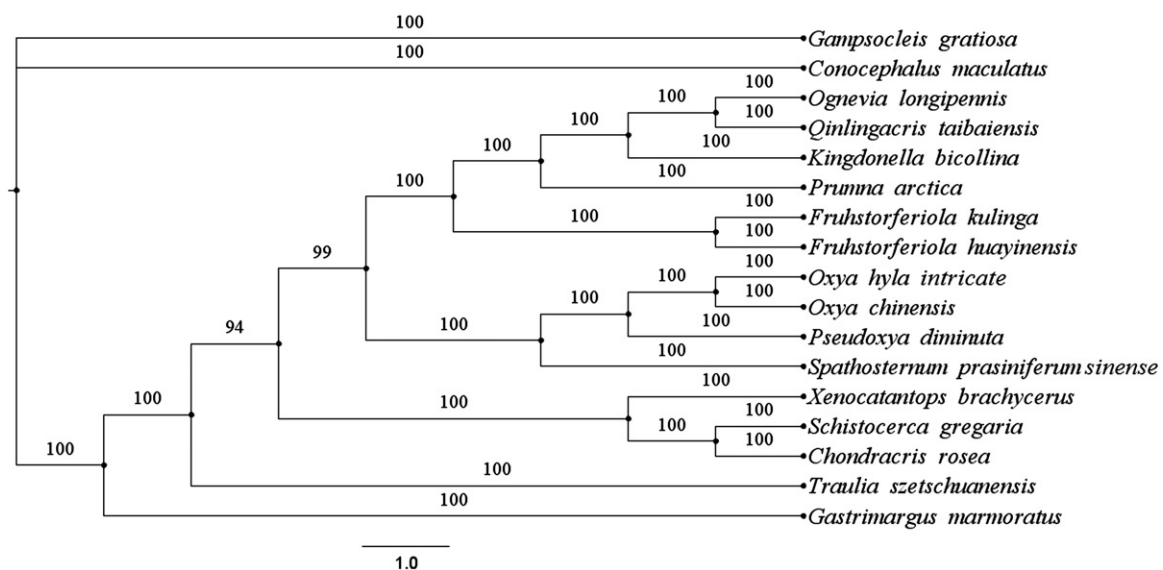
### KEYWORDS

*Fruhstorferiola huayinensis*;  
mitogenome; phylogeny

*Fruhstorferiola huayinensis* belongs to Catantopidae, Orthoptera. Eight species of the genus *Fruhstorferiola* are reported so far, and distributed mainly in China (Feng et al. 2004). The specimen of *F. huayinensis* was collected from Xi'an (Shaanxi, China) in September 2015, and was now deposited in Molecular and Evolutionary Lab in Shaanxi Normal University. The total DNA was isolated from the leg muscle of the specimen using the phenol-chloroform extraction method (Zhou et al. 2010). Orthoptera universal mitochondrial primers were used to

amplify and sequence the mitochondrial genome (mitogenome) of *F. huayinensis* (Liu et al. 2006). The Staden Package 1.7 was used for the mitogenome assembly and annotation (Staden et al. 2000). tRNA genes were predicted using online software tRNAScan-SE 1.21 (Lowe & Eddy 1997).

The complete mitogenome of *F. huayinensis* is 16 227 bp in length and has been deposited in GenBank (accession no. KU668856), and its arrangement was identical to the *L. migratoria* mitogenome (GenBank accession no. X80245.1).



**Figure 1.** The Bayesian inference phylogenetic tree based on mitochondrial PCGs and rRNAs concatenated dataset. GenBank accession numbers: *Chondracris rosea* NC\_019993.1; *Fruhstorferiola kulinga* NC\_026716.1; *Gastrimargus marmoratus* EU527334.1; *Kingdonella bicollina* NC\_023920.1; *Ognevia longipennis* NC\_013701.1; *Oxya chinensis* NC\_010219.1; *Oxya hyla intricate* KP313875.1; *Prumna arctica* GU294758.1; *Pseudoxya diminuta* NC\_025765.1; *Qinlingacris taibaiensis* NC\_027187.1; *Schistocerca gregaria* NC\_013240.1; *Spathosternum prasiniferum sinense* KM588074.1; *Traulia szetschuanensis* EU914849.1; *Xenocatantops brachycerus* NC\_021609.1; *Conocephalus maculatus* NC\_016696.1; *Gampsocleis gratiosa* EU527333.1.

It comprises 13 PCGs, 22 tRNA genes, 2 rRNA genes and one A + T-rich region which could also be termed as control region. However, a tRNA<sup>Ile</sup>-like sequence which is 111 bp in length was identified in the control region, the assumed tRNA<sup>Ile</sup> could be folded into cloverleaf secondary structures but with an intron which is 40 bp in length inserted in the anticodon loop.

The overall base composition of the whole mitochondrial genome was A (43%), T (32.63%), G (10.28%) and C (14.09%) with an AT bias of 75.63%, as generally reported in other orthopteran mitogenomes. The start codons of all PCGs were typical ATN except COI which started with TAT, and the stop codons of all the 13 PCGs were complete (TAA or TAG). *IrRNA* and *srRNA* genes are 1312 bp and 834 bp in length separately, and the control region is as long as 1365 bp. In *srRNA* gene and control region, a 259 bp long tandem repeat was identified using Tandem Repeats Finder 4.07b (Benson 1999), and was repeated 2.9 times in the surveyed individual.

To furthermore validate the new determined sequences and annotations, the concatenated mitogenome dataset (PCGs and rRNAs) of *F. huayinensis* in this study, and together with other 16 species from GenBank, including 14 species from Catantopidae and two ensiferan outgroup species were used to perform phylogenetic analysis (Figure 1).

## Disclosure statement

The authors report no conflicts of interest.

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## References

- Benson G. 1999. Tandem repeats finder: a program to analyze DNA sequences. *Nucleic Acids Res.* 27:573–580.
- Feng L, Sun J, Fu P. 2004. Comparative studies on the male genitalia of the genus *Fruhstorferiola* (Orthoptera, Aderidae). *J Nat Sci Hunan Norm Univ.* 27:79–83 (in Chinese with an English abstract).
- Liu N, Hu J, Huang Y. 2006. Amplification of grasshoppers complete mitochondrial genomes using long PCR. *Chin J Zool.* 41:61–65 (in Chinese with an English abstract).
- Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25:955–964.
- Staden R, Beal KF, Bonfield JK. 2000. The Staden package, 1998. *Methods Mol Biol.* 132:115–130.
- Zhou Z, Ye H, Huang Y, Shi F. 2010. The phylogeny of Orthoptera inferred from mtDNA and description of *Elimaea cheni* (Tettigoniidae: Phaneropterinae) mitogenome. *J Genet Genomics.* 37:315–324.