

The complete mitochondrial genome of *Phlaeoba infumata* (Orthoptera: Acrididae)

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ABSTRACT

Phlaeoba infumata belongs to Acrididae, Orthoptera. The complete mitochondrial genome of *P. infumata* is 15,642 bp in length, and its arrangement was identical to the *Locusta migratoria* mitogenome, and contained 13 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes and a A+T-rich region. Using the 13 PCGs and two rRNA of *P. infumata*, together with 10 other close-related and two outgroup species, we constructed Bayesian inference (BI) phylogenetic tree to validate the mitogenome sequences of *P. infumata*.

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KEYWORDS

Mitogenome; *Phlaeoba infumata*; phylogeny

Phlaeoba infumata belongs to Acrididae, Orthoptera. *Phlaeoba* which is a large genus of Acrididae distribute all over the world. 12 species of the genus are known at present. Among them, eight species are found in China, and distribute mainly in the south of China (Wei & Zheng 2005). The specimen of

P. infumata was collected from Xing'an County (Guangxi, China) in 2006, and was now deposited in Molecular and Evolutionary Lab in Shaanxi Normal University in China. The PCR amplifications were performed following the study of Liu et al. (2006). The Staden Package 1.7 was used for the

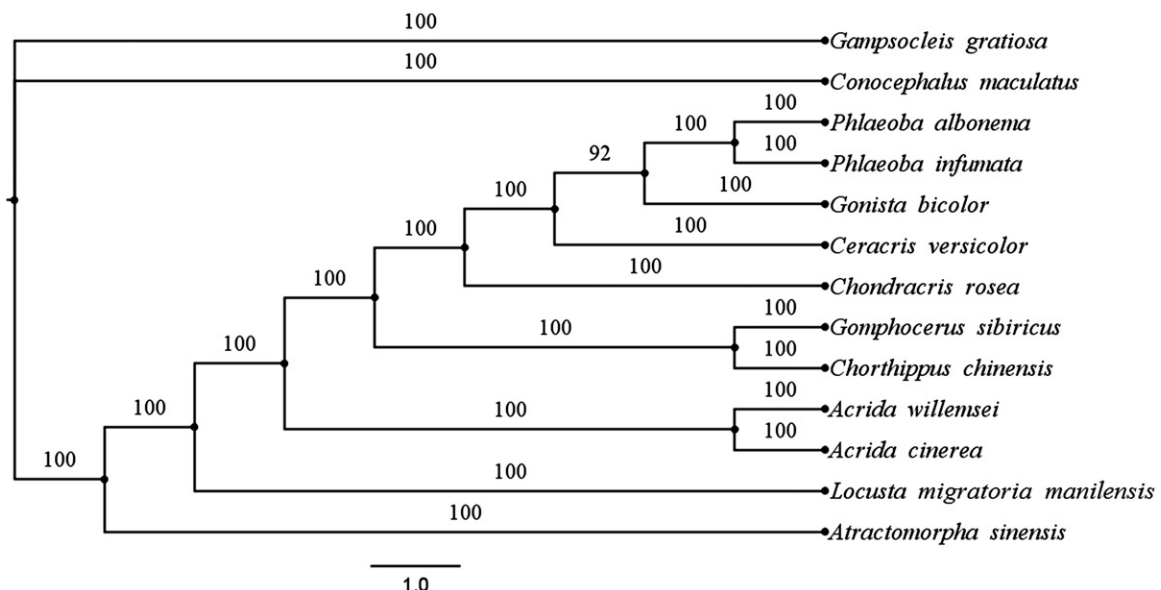




Figure 1. The BI phylogenetic tree of *Phlaeoba infumata* and other 12 species including 10 close-related species and two outgroup species based on mitochondrial PCGs and rRNAs concatenated dataset. GenBank accession nos.: *Phlaeoba albonema* NC_011827.1; *Atractomorpha sinensis* NC_011824.1; *Locusta migratoria manilensis* NC_014891.1; *Chondracris rosea* NC_019993.1; *Acrida willemsei* NC_011303.1; *Gomphocerus sibiricus* NC_021103.1; *Chorthippus chinensis* NC_011095.1; *Acrida cinerea* NC_014887.1; *Conocephalus maculatus* NC_016696.1; *Ceracris versicolor* KJ188251.1; *Gampsocleis gratiosa* EU527333.1; *Gonista bicolor* NC_029205.1

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mitogenome assembly and annotation (Staden et al. 2000). The 17 tRNA genes were predicted using online software tRNAscan-SE 1.21 (Lowe & Eddy 1997), the remaining five tRNAs, two rRNA, 13 protein-coding genes (PCGs) and a A + T-rich region were identified and annotated by sequence alignment with *Locusta migratoria* mitogenome sequences (GenBank accession no. X80245.1).

The complete mitogenome of *P. infumata* is 15,642 bp in length and has been deposited in GenBank (accession no. KU866166). It consists of 13 PCGs, 22 tRNA genes, two rRNA genes and one A + T-rich region, and its arrangement was identical to the *L. migratoria* mitogenome. The overall base composition of the whole mitochondrial genome was A (42.61%), T (31.32%), G (10.84%) and C (15.23%) with an AT bias of 73.93%. The A + T-rich region is as long as 744 bp and contains the highest A + T content (83.07%). The length of tRNA genes ranged from 65 bp to 71 bp. The start codons of all PCGs were typical ATN except COI which started with CTT, and the stop codons of all the 13 PCGs were complete (TAA or TAG) except ND5 which ended with an incomplete stop codon (TA). The *rrnL* and *rrnS* genes are 1315 bp and 824 bp in length, respectively.

To furthermore validate the mitogenome of *P. infumata*, the phylogenetic analysis was performed using MrBayes 3.2.2 based on concatenated mitogenome dataset (PCGs and rRNAs) of *P. infumata* in this study (Ronquist & Huelsenbeck 2003), and together with other 12 species from GenBank,

including 10 close-related species and two ensiferan outgroup species (Figure 1).

Disclosure statement

The authors report no conflicts of interest.

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