Asopinae (Insecta: Heteroptera: Pentatomomorpha: Pentatomidae) is a subfamily of Pentatomidae, which is a large predatory stink bug that usually feeds on the larvae of various Coleoptera, Lepidoptera and Hemiptera. To date, all the pentatomid mitogenomes (mt-genomes) are from Pentatominae and Podopinae, which limits our understanding of the diversity and phylogeny of Pentatomidae (Wang et al. 2017). Herein, we report and analyze the complete mt-genome of Picromerus griseus, which is commonly used in biological control strategies. Adults specimens of P. griseus were collected from Baoshan City (25.3° N, 98.8° E), Yunnan Province, China, on 15 August 2015. Both the voucher specimens and remaining genomic DNA were deposited in the Institute of Entomology, Shanxi Agricultural University.

The complete mt-genome of P. griseus is a double-stranded circular molecule that is 16,338 bp long (GenBank accession number: MF805778) and contains 37 typical mitochondrial genes: 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), the large and small ribosomal RNA unit genes (rrnL and rrnS) and a control region. The genome size, gene arrangement, A + T content, codon usage and secondary structures of 22 transfer RNA genes of the P. griseus mitogenome were similar to those of other sequenced pentatomoinds. Bayesian analyses performed using the mitogenomes of P. griseus and its relatives, including 14 taxa, confirmed the reasonable placement of P. griseus. Ten PCGs share the same termination codon of TAA, two PCGs (ND5 and ND6) end with TAG and COII is terminated with a single T.

The 22 tRNAs range from 61 to 76 bp, and all have a typical cloverleaf secondary structure except trnS-Ser (GCT) and trnV-Val (TAC), which lack a dihydrouridine arm. The rrnL has a length of 1302 bp with an A + T content of 75.73%, while rrnS has a length of 807 bp with an A + T content of 75.22%, and they are separated from each other by trnV-Val. The D loop region is located between the 12S rRNA and trnI-Ile with a total length of 1521 bp.

Phylogenetic analyses of 14 superfamly Pentatomoidea species and two superfamly Coreoidea species were conducted using Bayesian inference on 14 nucleotide sequences of 13 mitochondrial PCGs, resulting in a tree topology (Figure 1). Bayesian analyses were conducted using GPU MrBayes (Zhou et al. 2011) under the GTR + I + G model estimated by PartitionFinder v1.1.0 (Lanfear et al. 2012). Each family formed a monophyletic cluster with a high degree of bootstrap support. In Pentatomidae, the species G. rubrolineata, which belongs to the subfamily Podopinae, was separated from two other subfamilies. Although P. griseus was from the subfamily Asopinae, this species mixed with species from the subfamily Pentatominae. This suggested that Pentatominae might not be monophyletic or that Asopinae was more closely related with Pentatominae. Because mt-genome sequences are limited, the sequencing of more mt-genomes is needed to adequately resolve the subfamily relationships within Pentatomidae, and more mt-genome sequences are required to resolve the family relationships within Pentatomoidea. Therefore, further studies are needed to resolve the family relationships within Pentatomidae.
are needed to sequence more species from Asopinae and other subfamilies, which will enhance our understanding of the molecular phylogeny in Pentatomidae. This is the first sequenced complete mt-genome from the subfamily Asopinae, and the mitogenomic data of *P. griseus* will help to better understand the population genetics and evolution of Pentatomoidea.

**Disclosure statement**

The authors report no conflict of interest and are responsible for the content and writing of the paper.

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