The complete mitochondrial genome of the mealy plum aphid, *Hyalopterus pruni* (Hemiptera: Aphididae)

Yanxin Liang, Zhenyong Du, Fan Song and Jia He

**ABSTRACT**

This study completes the sequencing and annotation of the mitochondrial genome (mitogenome) of *Hyalopterus pruni* (Hemiptera: Aphididae) by using the high-throughput sequencing. The mitogenome is a typical circular DNA of 15,410 bp with 86.2% A+T content, and consists of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes, a repeat region between tRNA-Glu and tRNA-Phe, and a control region. The gene order follows the putative ancestral arrangements of insect mitogenome. All 13 protein-coding genes start with codon ATN and terminate with TAA or a single T. All tRNA genes have typical clover-leaf structure except for tRNA-Ser^{AGN}. The control region is 638 bp in length with 86.0% A+T content. The phylogenetic tree supports the monophyly of Aphidini and Macrosiphini in Aphidinae and the sister relationship between *Hyalopterus pruni* and *Schizaphis graminum*.

Mitochondrial genome; Aphididae; *Hyalopterus pruni*

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respectively. The control region was rich in A + T (86.0%) and 638 bp in length. There is a repeat region between tRNA-Glu and tRNA-Phe in H. pruni with 2 tandem repeats, which is an interesting feature and reported in aphid mitogenomes several times (Wang et al. 2014; Wang et al. 2015).

Phylogenetic analysis was generated by the maximum-likelihood (ML) method based on 16 aphid mitogenome sequences (Figure 1). The result supports the monophyly of Hormaphidinae, Eriosomatinae, Greenideinae, and Aphidinae. Meanwhile, the monophyly of Aphidini and Macrosiphini in Aphidinae are well recovered with high support values. The sister relationship between H. pruni and Schizaphis graminum is also highly supported.

**Disclosure statement**

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

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**Data availability statement**

The mitogenome and raw sequencing data in this study are available in GenBank (https://www.ncbi.nlm.nih.gov/) under the accession numbers of MT898422 and PRJNA663207.

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