Mitochondrial genome of *Hormaphis betulae* and its comparative analysis with *Pseudoregma bambucicola* (Hemiptera: Hormaphidinae)

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**ABSTRACT**

*Hormaphis betulae* (Hemiptera: Hormaphidinae) is a common aphid of birch plants. Here, the complete mitochondrial genome sequence of a representative of this aphid from China was determined using next generation sequencing platform. The genome was 15,129 bp in length and encoded 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes. The phylogeny revealed that two Chinese isolates of *H. betulae* clustered together and formed a monophyletic relationship with *Pseudoregma bambucicola* in the subfamily Hormaphidinae, supporting their species validity in Aphididae. The cumulative mitochondrial DNA data provides a better understanding of the phylogenetic relationship of this species in plant aphids.

**KEYWORDS**

Mitochondrial genome; *Hormaphis betulae*; aphids; phylogeny

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and the rrnS (776 bp) between tRNA-Val and D-loop region, consistent with those of P. bambucicola (Nong et al. 2019). The D-loop region (551 bp) with 83.1% A + T content was located between rrnS and tRNA-Ile.

A maximum-likelihood (ML) phylogeny was reconstructed on the basis of a concatenated amino acid sequence of 13 protein-coding genes from 26 aphid species, using Adelges laricis as outgroup. This phylogeneric tree showed that two Chinese isolates of H. betulae clustered together and formed a branch that was monophyletic with P. bambucicola in the subfamily Hormaphidinae, with 100% bootstrap confidence, supporting their species validity among the family Aphididae (Figure 1). In addition, each subfamily of Aphidinae, Calaphidinae, Greenideinae, Eriosomatinae or Hormaphidinae within this topology formed a monophyletic group in Aphididae, which were consistent with the results of recent molecular studies (Li et al. 2017; Nong et al. 2019; Zhang et al. 2019). Taken together, the complete mtDNA of H. betulae sequenced here added a novel marker resource for genetic and evolutionary biological studies of this birch pest.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Figure 1. Inferred maximum likelihood (ML) tree based on concatenated amino-acid sequences of 13 mitochondrial protein-coding genes of H. betulae and other related aphid species, using MtArt + I + G model with 10,000 bootstrap replications (<50% support not shown). The black dot represents the species in this study.