

The complete mitochondrial genome of the bamboo aphid *Pseudoregma bambucicola* and its phylogenetic position

Xiang Nong^{a,b*}, Lidan Wang^{c*}, Yunjian Liu^{c*}, Shengnan Zhong^{a,b,d}, Xiaobo Yu^{a,b} and Yue Xie^c

^aBamboo Diseases and Pest control and Resources Development Key Laboratory of Sichuan Province, Leshan, China; ^bCollege of Life Science, Leshan Normal University, Leshan, China; ^cDepartment of Parasitology, College of Veterinary Medicine, Sichuan Agricultural University, Chengdu, China; ^dCollege of Food and Biological Engineering, Xihua University, Chengdu, China

ABSTRACT

The bamboo aphid, *Pseudoregma bambucicola*, is a terrible insect pest of bamboos. Herein, the complete mitochondrial genome of a representative of this aphid from China was determined through next generation sequencing platform. The whole genome was 16,651 bp in size and encoded 13 protein-coding genes, 22 tRNA genes, and two rRNA genes. The phylogeny showed that two Chinese isolates of *P. bambucicola* clustered together and formed a monophyletic relationship with *Hormaphis betulae* in Hormaphidinae, supporting their species validity among the family Aphididae. The cumulative mitochondrial DNA data should contribute to a better understanding of the phylogenetic relationship of this aphid species.

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The bamboo aphid, *Pseudoregma bambucicola* (Takahashi 1921), is a parthenogenic insect pest of bamboos that is widely distributed throughout the warmer regions of eastern Asia. This aphid infests all parts of *Bambusa* bamboo including stems, branches, twigs, leaves, and shoots and develops into large and high-density colonies that impair bamboo growth and even cause death (Fukatsu et al. 2001; Ijichi et al. 2004; Nong et al. 2019). Although until now there has been significant advance of knowledge about the ecology, behavior and chemical control of *P. bambucicola*, it is still existing major gaps in the understanding of this aphid pest, especially in genetics and molecular epidemiology because of lacking suitable genetic markers (Nong et al. 2017, 2019). Mitochondrial DNA (mtDNA) is proven to be a valuable source of molecular markers and has been widely used for genetics and molecular identification of many insect pests including plant aphids (Cameron 2014; De Mandal et al. 2014; Marquina et al. 2019). Here, we reported the complete mitochondrial genome sequence of a representative *P. bambucicola* from the Sichuan Province, China and added novel mtDNA data to this bamboo pest.

In January 2019, numerous aphids were sampled from the *Bambusa multiplexcv*, which plants in Leshan city (28°89'N, 103°15'E), Sichuan province, China. After morphological identification, the aphid specimens ($n = 100$) were identified as *P. bambucicola* according to the taxonomic key of Sakata (1991) and the molecular confirmation by amplification and sequencing of the mitochondrial cytochrome b (*Cytb*) gene

(Nong et al. 2019). Ten aphids were pooled for mtDNA extraction, and the remaining were fixed in 5% formalin solution and archived in the Insect Museum of Bamboo Diseases and Pest control and Resources Development Key Laboratory of Sichuan Province, China, under voucher number NX2019_12. The mtDNA was sequenced using the Illumina HiSeq platform (BGI, Shenzhen, China). The genome was assembled using MITObim (Hahn et al. 2013), and gene annotation was achieved using MITOS (Bernt et al. 2013). The genome sequence has been deposited in GenBank under accession number: MN820984.

The complete mitochondrial genome of *P. bambucicola* is 16,651 bp in size and encoded 13 protein-coding genes (PCGs), 22 tRNA genes (tRNAs), and two rRNA genes (rRNAs). Nine PCGs and 15 tRNAs were located on the forward strand (J-strand), whereas the remaining genes were transcribed on the reverse strand (N-strand), similar patterns found in other aphids (Wang et al. 2013; Li et al. 2017; Zhang et al. 2019). Among the 13 PCGs, except the *nad4* deduced to use an incomplete stop codon 'T', the rest were predicted to use the typical TAA or TAG as the stop codons. The sizes of tRNAs ranged from 52 bp (tRNA-Cys) to 73 bp (tRNA-Lys) and all had a typical clover-leaf like secondary structure, except for tRNA-Cys and tRNA^(GCT)-Ser. For two rRNAs, the *rnrL* (1284 bp) presented between tRNA^(TAG)-Leu and tRNA-Val and the *rnrS* (758 bp) between tRNA-Val and D-loop region. The D-loop region (727 bp) with 96.4% A+T content was placed between *rnrS* and tRNA-Ile.

CONTACT Xiang Nong  nongx2008@163.com  Bamboo Diseases and Pest control and Resources Development Key Laboratory of Sichuan Province, Leshan 614000, China; College of Life Science, Leshan Normal University, Leshan 614000, China; Yue Xie  xyue1985@gmail.com  Department of Parasitology, College of Veterinary Medicine, Sichuan Agricultural University, Chengdu 611130, China

*Authors have contributed equally to this work.

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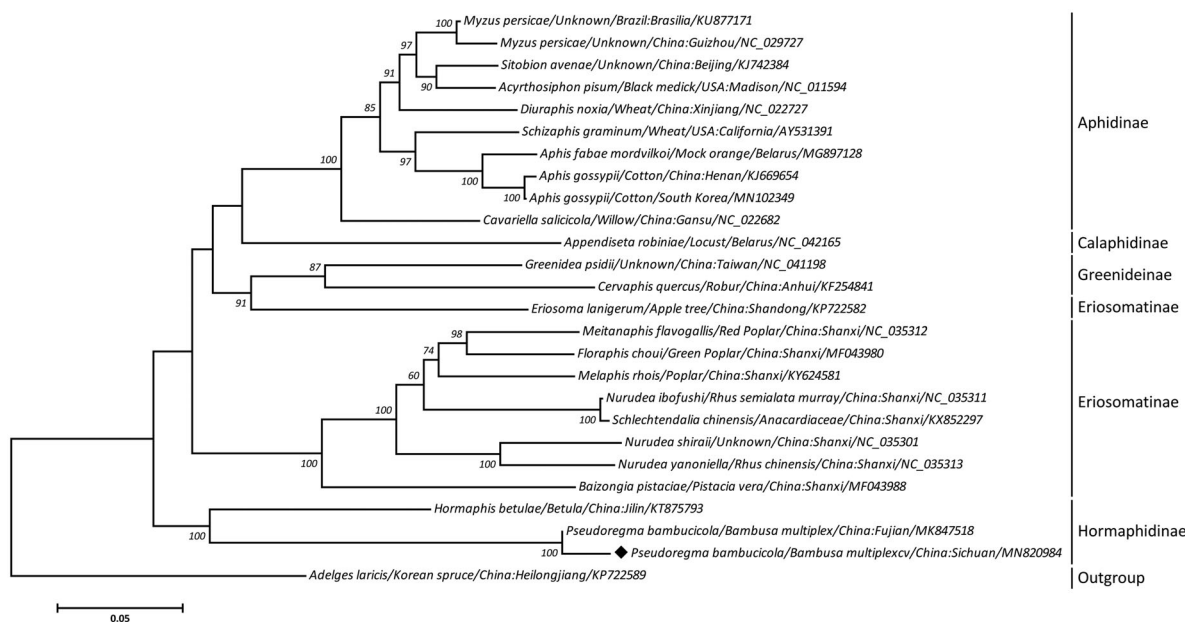


Figure 1. Maximum-likelihood (ML) tree inferred from concatenated amino-acid sequences of 13 mitochondrial protein-coding genes of *P. bambucicola* and other related insect aphids, utilizing MtArt model with 100,000 bootstrap replications (<50% support not shown). The solid black diamond represents the species in this study.

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

Disclosure statement

No potential conflict of interest was reported by the authors.

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