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 of this aphid from China and added novel mtDNA data to this bamboo pest.

In January 2019, numerous aphids were sampled from the *Bambusa multiplex*, 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 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 (S-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<sup>(GCT)</sup>-Ser. For two rRNAs, the *rrnL* (1284 bp) presented between tRNA<sup>(TAG)</sup>-Leu and tRNA-Val and the *rrnS* (758 bp) between tRNA-Val and D-loop region. The D-loop region (727 bp) with 96.4% A + T content was placed between *rrnS* and tRNA-Ile.

**CONTACT** Xiang Nong, nongx2008@163.com, Department of Parasitology, College of Veterinary Medicine, Sichuan Agricultural University, Chengdu 611130, China; authors contributed equally to this work.

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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 phylogeneric 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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**References**

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 313–319.

Cameron SL. 2014. Insect mitochondrial genomics: implications for evolution and phylogeny. Annu Rev Entomol. 59(1):95–117.

De Mandal S, Chhakchhuak L, Gurusubramanian G, Kumar NS. 2014. Mitochondrial markers for identification and phylogenetic studies in insects—a review. DNA Barcodes. 2(1):1–9.

Fukatsu T, Shibao H, Nikoh N, Aoki S. 2001. Genetically distinct populations in an Asian soldier-producing aphid, Pseudoregma bambucicola (Homoptera: Aphididae), identified by DNA fingerprinting and molecular phylogenetic analysis. Mol Phylogenet Evol. 18(3):423–433.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. Nucleic Acids Res. 41(13):e129.

Ijichi N, Shibao H, Miura T, Matsumoto T, Fukatsu T. 2004. Soldier differentiation during embryogenesis of a social aphid, Pseudoregma bambucicola. Entomol Sci. 7(2):143–155.

Li YQ, Chen J, Qiao GX. 2017. Complete mitochondrial genome of the aphid Hormaphis betulae (Mordvilko) (Hemiptera: Aphididae). Mitochondrial DNA B. 28(2):265–266.

Marquina D, Andersson AF, Ronquist F. 2019. New mitochondrial primers for metabarcoding of insects, designed and evaluated using in silico methods. Mol Ecol Resour. 19(1):90–104.

Nong X, Zhong SN, Chen L, Yang YJ, Xie Y, Luo CB, Fu C, Yu H, Liang Z. 2019. Genetic differentiation of populations of Pseudoregma bambucicola based on mtDNA cytb gene sequences. Mitochondrial DNA B. 4(1):1803–1807.

Nong X, Zhong SN, Li SM, Yang YJ, Liang Z, Xie Y. 2019. Genetic differentiation of Pseudoregma bambucicola population based on mtDNA COII gene. Saudi J Biol Sci. 26(5):1032–1036.

Nong X, Zeng X, Yang Y, Liang Z, Tang M, Liao L, Luo C. 2017. Morphological observation and characterization of the Pseudoregma bambucicola with the scanning electron microscope. Saudi J Biol Sci. 24(7):1626–1630.

Wang Y, Huang XL, Qiao GX. 2013. Comparative analysis of mitochondrial genomes of five aphid species (Hemiptera: Aphididae) and phylogenetic implications. PLoS One. 8(10):e77511.

Zhang H, Deng J, Liu Q, Huang X. 2019. The mitochondrial genome of a social aphid, Pseudoregma bambucicola (Hemiptera: Aphididae: Hormaphidinae). Mitochondrial DNA B Resour. 4(2):2100–2101.

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.