Complete mitochondrial genome of Rhus gall aphid Meitanaphis microgalls (Hemiptera: Aphididae: Eriosomatinae)

Yu-Kang Liang, Jun Wen and Zhu-Mei Ren

School of Life Science, Shanxi University, Taiyuan, Shanxi, China; Department of Botany, MRC-166, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

ABSTRACT

We sequenced the complete mitochondrial genome of the Chinese Rhus gall aphid Meitanaphis microgalls (Hemiptera: Aphididae: Eriosomatinae; Fordini) by the genome skimming method on an Illumina platform. The assembled mitogenome is 16,191 bp in length with a very high A + T content of 84.3%. This genome consists of 13 protein-coding genes, 22 tRNAs, 2 rRNAs, and a control region. All the protein-coding genes have a typical ATN initiation codon and TAA termination codon except COX1 and ND4 with a single T as stop codon. The trRNAs ranged in size from 59 to 77 bp and formed a clover-leaf secondary structure except trRNA-Ser (AGN). We constructed the phylogenetic relationship of Fordini aphids including all the Rhus gall aphids, and the ML tree showed that M. microgalls grouped with M. elongallis as its sister group.

Rhus gall aphids feed on the developing shoots or leaves of Rhus species to induce galls, which are economically very important in China (Zhang et al. 1999; Ren et al. 2013). This group was formerly placed in the subtribe Melaphidina within Fordini (Insecta: Aphididae: Eriosomatinae) (Heie 1980; Blackman and Eastop 1984), and later raised to tribe Melaphidini (Zhang et al. 1999; Heie and Wegierek 2009). Favret (2019) currently put them in the tribe Fordini without subtribal recognition. To date, it has been reported that there are six genera and 12 species, among which Meitanaphis microgalls is narrowly distributed in the limited area of the Qinling mountains in China (Xiang 1980).

In this study, we sequenced the complete mitochondrial genome of Meitanaphis microgalls (GenBank accession no. MK948431), the samples of which were obtained from a gall collected on Rhus potaninii Maxim in Hanzhong, Shaanxi, China, in 2017. All the aphid individuals from a Rhus aphid gall are parthenogenetic, and we deposited some individuals from the same gall as the voucher specimen at School of Life Science, Shanxi University, China (voucher no. A4540).

We extracted the genomic DNA of Meitanaphis microgalls using the DNeasy extraction kit (QIAGEN, Valencia, CA) and sent it to the Genomic Sequencing and Analysis Co. (Majorbio, Shanghai, China) for library construction and sequencing by the shotgun genome skimming method on an Illumina NextSeq 500 platform (Zimmer and Wen 2015). The mitogenome sequence of M. microgalls was assembled and annotated using the two species of the eastern Asian genus Meitanaphis (GenBank accession no. MF043989 and MF043982) as the reference genomes. We also finished the de novo assembly using Spades v. 3.7.1 (Bankevich et al. 2012) and kmers 21, 33, 55, 77, and 99.

The complete mitochondrial sequence of M. microgalls is a closed-circular molecule of 16,191 bp in length, which contains 13 protein-coding genes (PCGs, COX1-COX3, ATP6, ATP8, ND1-ND6, ND4L, Cytb), 22 tRNA genes, 2 rRNA genes, and one control region. The gene order is identical to the inferred ancestral arrangement of insects (Clary and Wolstenholme 1985). The overall nucleotide composition of the M. microgalls mitogenome is 39.6% T, 10.0% C, 44.8% A and 5.7% G, with a strong bias towards A + T (84.3%). Excluding stop codons, the A + T content of the concatenated PCGs is 83.2%. All PCGs are initiated by the canonical start codon ATN. Five genes (ATP6, ND1 and ND3-ND5) start with ATT, three genes (COX3, ND4L and Cytb) start with ATG, and the five remaining genes start with ATA. Eleven PCGs are terminated with the typical stop codon TAA, whereas COX1 and ND4 end with a single T. The 22 typical tRNAs range from 59 to 77 bp in length, and all except trnS display the typical clover-leaf secondary structure, which we predicted with trRNAscan-SE v2.0 (Lowe and Chan 2016). The truncated secondary structure with the loss of dihydrouridine (DHU) arm occurs in trnS (AGN), which is common in insect mitogenomes (Wolstenholme 1992).

We used the maximum-likelihood method to construct a phylogenetic tree of the Fordini, including Meitanaphis microgalls using 13 PCG genes and two rRNA genes (Figure 1) (Stamatakis 2014). The ML tree showed that M. microgalls is much closer to M. elongallis to form a sister group. Whereas, the other species M. flavogallis grouped with
Kaburagia species. Thus, the relationships between the two genera still need to be further examined by adding the samples and genes.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This study was partially supported by the National Natural Science Foundation of China [31870366, 31170359], Shanxi International Science and Technology Cooperation Project (2018), the National High Technology Research and Development '863' Program [2014AA021802], the Hundred-Talent Project in Shanxi Province, Shanxi Scholarship Council of China [2013-020], and the Laboratory of Analytical Biology of the National Museum of Natural History and the Endowment Grants Program of Smithsonian Institution.

**References**

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19:455–477.

Blackman RL, Eastop VF. 1984. Aphids on the world’s crops: an identification guide. Chichester: John Wiley & Sons.

Clary DO, Wolstenholme DR. 1985. The mitochondrial DNA molecular of Drosophila yakuba: nucleotide sequence, gene organization, and genetic code. J Mol Evol. 22:252–271.

Favret C. 2019. Aphid species file. Version 5.0/5.0; [accessed 2019 Mar 27]. http://Aphid.SpeciesFile.org.

Heie OE. 1980. The Aphidoidea of Fennoscandia and Denmark. I. Fauna Entomol Scand. 9:1–236.

Heie OE, Wegierek P. 2009. Diagnoses of the higher taxa of Aphidomorpha (Hemiptera: Sternorrhyncha). Redia. 92:261–269.

Lowe TM, Chan PP. 2016. trRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. Nucleic Acids Res. 44:W54–W57.

Ren ZM, Zhong Y, Kurosu U, Aoki S, Ma EB, von Dohlen CD, Wen J. 2013. Historical biogeography of eastern Asian–eastern North American disjunct Melaphidia aphids (Homoptera: Aphididae: Eriosomatinae) on Rhus hosts (Anacardiaceae). Mol Phylogenet Evol. 69:1146–1158.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30:1312–1313.

Wolstenholme DR. 1992. Animal mitochondrial DNA: structure and evolution. Int Rev Cytol. 141:173–216.

Xiang H. 1980. Studies of Chinese Gall-nut aphids on Rhus potaninii Maxim. Entomotaxonomia. 2:303–313.

Zhang GX, Qiao GX, Zhong TS, Zhang WY. 1999. Fauna sinica insecta. Homoptera: Mindaridae and Pemphigidae, vol. 14. Beijing: Science Press.

Zimmer EA, Wen J. 2015. Using nuclear gene data for plant phylogenetics: progress and prospects II. Next-gen approaches. J Syystem Evol. 53:371–379.