

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the aphid *Hormaphis betulae* (Mordvilko) (Hemiptera: Aphididae: Hormaphidinae)

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ABSTRACT

The complete mitochondrial genome of *Hormaphis betulae* has been sequenced and annotated, which is the first representation from the aphid subfamily Hormaphidinae. This mitogenome is 15 088 bp long with an A + T content of 82.2%, containing 37 genes arranged in the same order as the putative ancestral arrangement of insects and a control region. All protein-coding genes start with an ATN codon and terminate with a TAA codon or a single T residue. All the 22 tRNAs, ranging from 61 to 78 bp, have the typical clover-leaf structure except for *trnS* (AGN). The lengths of *rrnL* and *rrnS* genes are 1275 and 776 bp, respectively. The control region is 509 bp long and located between *rrnS* and *trnI*, including three domains: an AT-rich zone, a poly-thymidine stretch, and a stem-loop region. The phylogenetic tree supports *H. betulae* as the basal lineage within Aphididae.

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Aphids (Hemiptera: Aphidoidea) are an extraordinary insect group characterized by complicated life cycles, elaborate polyphenisms, gall formation, and harboring diverse endosymbionts. It comprises approximately 5000 species within three families, Adelgidae, Phylloxeridae, and Aphididae (24 subfamilies) (Blackman & Eastop, 2000; Favret, 2015; Remaudière & Remaudière, 1997). Up to now, seven complete and three nearly complete mitochondrial genomes of aphids have been reported, mostly from the subfamily Aphidinae (Thao et al., 2004; Wang et al., 2013, 2014; Zhang et al., 2014a–c). Herein, we present the complete mitochondrial genome of *Hormaphis betulae* (Mordvilko), the first species from the aphid subfamily Hormaphidinae.

Hormaphis betulae migrates between *Hamamelis japonica* and *Betula platyphylla* in Japan, producing conical pouch galls on the leaves of *H. japonica* (Aoki & Kurosu, 1991). In northern and central Europe and Siberia, it is anholocyclic on *Betula* spp. (Blackman & Eastop, 1994). The apterous exules on *Betula* are flat and circular, with a fringe of beam-like wax threads. *Hormaphis betulae* samples were collected on *Betula* sp. from Jilin, China (Ji'an City, Mt. Wunv, altitude 500 m) and deposited in the National Zoological Museum of China, Institute of Zoology, Chinese Academy of Sciences, Beijing, China (NZMC no. 15214).

The complete mitogenome of *H. betulae* was amplified and sequenced using a primer walking strategy and a combination of short and long PCRs. This genome is 15 088 bp long and is the shortest aphid mitogenome reported so far (GenBank accession no. KT875793). It includes 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and a control region.

Twenty-three genes are transcribed on the majority strand (J-strand), the remaining being located on the minority strand (N-strand). Gene order is identical to the inferred ancestral arrangement of insects (Boore, 1999). There are a total of 63 overlapped nucleotides between adjacent genes in 16 locations, ranging from 1 to 20 bp in length. Totally 161 bp intergenic spacers are present at 16 positions and the length of spacer is 1–46 bp.

The overall nucleotide composition of the *H. betulae* mitogenome is 45.3% A, 36.9% T, 11.7% C, and 6.1% G, with a strong bias towards A + T (82.2%). All PCGs initiate with a typical ATN codon. Eleven PCGs end with a conventional TAA stop codon, whereas *cox1* and *nad4* terminate with a single T residue.

The lengths of 22 tRNA genes range from 61 bp (*trnV*) to 78 bp (*trnH*). All tRNAs can be folded into a classic clover-leaf secondary structure except for *trnS* (AGN), of which the dihydrouridine (DHU) arm forms a simple loop. The *rrnL* gene is 1275 bp long with an A + T content of 84.2%, while the *rrnS* gene is 776 bp long with an A + T content of 83.0%. The control region spans 509 bp and is located between *rrnS* and *trnI*, with an A + T content of 82.3%. It consists of three domains: an AT-rich zone, a poly-thymidine stretch, and a stem-loop region. The unique repeat region between *trnE* and *trnF* found in some Aphidinae species is not present in *H. betulae* (Wang et al., 2013).

Phylogenetic tree was estimated using the maximum-likelihood (ML) method based on 13 PCGs. Aphidinae was recovered as monophyletic. *Hormaphis betulae* was positioned most basally within the clade of Aphididae (Figure 1).

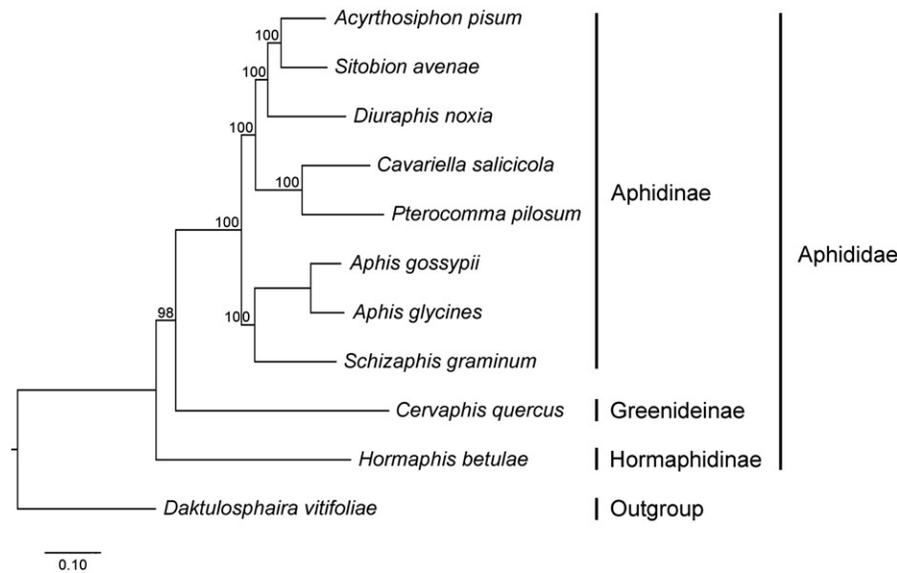


Figure 1. Phylogenetic tree resulting from the ML analysis. Bootstrap values are shown above the branches. GenBank accession numbers: *Acyrthosiphon pisum* (FJ411411), *Aphis glycines* (KC840675), *Aphis gossypii* (KJ669654), *Cavariella salicicola* (KC332935), *Cervaphis quercus* (KF254841), *Daktulosphaira vitifoliae* (DQ021446), *Diuraphis noxia* (KF636758), *Hormaphis betulae* (KT875793), *Pterocomma pilosum* (KC840676), *Schizaphis graminum* (AY531391), and *Sitobion avenae* (KJ742384).

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article. This work was supported by National Natural Sciences Foundation of China (Nos. 31430078 and 31402000), the Ministry of Science and Technology of the People's Republic of China (MOST Grant Nos. 2011FY120200 and 2013FY111200), and National Science Fund for Fostering Talents in Basic Research (No. J1210002).

References

- Aoki S, Kurosu U. (1991). Host alternation of *Hormaphis betulae* (Homoptera, Aphidoidea). *Jpn J Entomol* 59:164
- Blackman RL, Eastop VF. (1994). Aphids on the world's trees. An identification and information guide. Wallingford, UK: CAB International.
- Blackman RL, Eastop VF. (2000). Aphids on the world's crops. An identification and information guide, 2nd ed. Chichester, UK: Wiley.
- Boore JL. (1999). Animal mitochondrial genomes. *Nucleic Acids Res* 27:1767–80.
- Favret C. (2015). Aphid species file. Version 5.0/5.0. Available at: <http://Aphid.SpeciesFile.org> (Accessed 20 October 2015).
- Remaudière G, Remaudière M. (1997). Catalogue of the World's Aphididae. Homoptera Aphidoidea. Paris, France: Institut National de la Recherche Agronomique.
- Thao ML, Baumann L, Baumann P. (2004). Organization of the mitochondrial genomes of whiteflies, aphids, and psyllids (Hemiptera, Sternorrhyncha). *BMC Evol Biol* 4:25
- Wang Y, Huang XL, Qiao GX. (2013). Comparative analysis of mitochondrial genomes of five aphid species (Hemiptera: Aphididae) and phylogenetic implications. *PLoS One* 8:e77511
- Wang Y, Huang XL, Qiao GX. (2014). The complete mitochondrial genome of *Cervaphis quercus* (Insecta: Hemiptera: Aphididae: Greenideinae). *Insect Sci* 21:278–90.
- Zhang B, Ma C, Edwards O, Fuller S, Kang L. (2014a). The mitochondrial genome of the Russian wheat aphid *Diuraphis noxia*: Large repetitive sequences between *trnE* and *trnF* in aphids. *Gene* 533:253–60.
- Zhang B, Zheng J, Liang L, Fuller S, Ma CS. (2014b). The complete mitochondrial genome of *Sitobion avenae* (Hemiptera: Aphididae). *Mitochondrial DNA*. [Epub ahead of print].
- Zhang S, Luo J, Wang C, Lv L, Li C, Jiang W, Cui J, Rajput LB. (2014c). Complete mitochondrial genome of *Aphis gossypii* Glover (Hemiptera: Aphididae). *Mitochondrial DNA*. [Epub ahead of print].