

## Mitochondrial genome of *Aphis gossypii* Glover cucumber biotype (Hemiptera: Aphididae)

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### ABSTRACT

The complete mitochondrial genome of *Aphis gossypii* Glover cucumber biotype was sequenced using traditional PCR amplification coupled with Sanger sequencing. The genome is 15,870 bp long, with 83.7% AT content (MW048625). The genome encodes 37 typical mitochondrial genes, including 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNAs, a repeat region of 784 bp, and a control region of 627 bp. The base composition of the genome is A (45.4%), T (38.3%), C (10.5%), and G (5.8%). An analysis of two biotypes *A. gossypii* mitogenomes identified 77 single nucleotide polymorphisms and 1 insertion and deletion.

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Cotton-melon aphid; mitogenome; cucumber biotype; cotton biotype; phylogenetic analysis


The *Aphis gossypii* Glover, 1877 is one of the most widely encountered insect pest in the agricultural flora and fauna. It often afflicts plants such as melon, marrow, zucchini, watermelon (*Cucurbitaceae*), cotton, okra, ornamental hibiscus from *Malvaceae* and potato, chili pepper, sweet pepper, eggplant from *Solanaceae* (Carletto et al. 2009). *Aphis gossypii* feeds on plant sap, which can eventually kill the plant and can also transmit several viruses (Webster et al. 2018).

To date, different host specialization types of aphids have evolved from which cucumber and cotton biotypes are prominently distributed (Zhang et al. 2018). Significant difference was recorded among different adaptive hosts of aphids. The biotype belonging to cotton cannot subsist in cucumber and similarly cucumber biotype cannot flourish normally in cotton crop (Wang et al. 2015). We have previously reported the mitochondrial genome of *A. gossypii* cotton biotype (Zhang et al. 2016). To investigate intra-specific variations and phylogenetic relationship of *A. gossypii* cucumber biotype, we determined the complete sequence of the mitochondrial genome of cucumber biotype. The extracted DNA of a single aphid (collected on cucumber, 36°3'43"N, 114°20'54"E) was used as a template for PCR. After sampling, the specimen (N201906) was stored in the State Key Laboratory of Cotton Biology, Institute of Cotton Research of Chinese Academy of Agricultural Sciences, Anyang, Henan Province, China. The cucumber biotype of *A. gossypii* was initially identified according to earlier reported studies (Wang et al. 2015). Primers were designed according to cotton biotype mitochondrial genome sequence (Supplementary Table 1), and

PCR products were sequenced in both directions. Then, we assembled the complete mitochondrial genome of *A. gossypii* cucumber biotype using Vector NTI 11.5.1. The online software MITOS2 (<http://mitos2.bioinf.uni-leipzig.de/index.py>) was used to annotate the splicing sequence of the mitochondrial genome of cucumber biotype (Torres et al. 2019) with *A. gossypii* mitochondrial genome as a reference (KJ669654; Zhang et al. 2016).

The mitochondrial genome of cucumber biotype is a circular molecule with a length of 15870 bp, which is 1 bp longer than the cotton biotype. The mitochondrial genome contains 13 protein coding genes, 2 ribosomal RNA genes, 22 tRNA genes, a control region of 627 bp, and a repeat region of 784 bp (Additional Table 2). The repeat region includes three 196-bp tandem repeats (near tRNA<sup>Glu</sup>) and one 189-bp copy of the anterior portion of the repeat unit. In general, the content of A+T in the mitochondrial genome of *A. gossypii* cucumber biotype was 83.7% (A = 45.4%; T = 38.3%; C = 10.5%; G = 5.8%). The A+T content was identical to that of cotton biotype (Zhang et al. 2016). Comparing the two biotypes of *A. gossypii* mitogenomes, 77 single nucleotide polymorphisms (SNPs) and 1 insertion and deletion (INDEL) were recognized. The 77 single nucleotide polymorphisms comprised of a molecular marker with 5 single nucleotide polymorphisms, which were stable and can be used to identify *A. gossypii* biotypes. These five poly nucleotides are located in the region of Cytb gene. The nucleotides present at the five polymorphic positions were T, A, A, T, and T in

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