


The complete mitochondrial genome of *Aphis gossypii* Glover, 1877 (Hemiptera: Aphididae) isolated from *Leonurus japonicus* in Korea

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ABSTRACT

We have determined the mitochondrial genome of *A. gossypii* isolated from *Leonurus japonicus* in Korea. The circular mitogenome of *A. gossypii* is 16,044 bp, including 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single control region of 797 bp. AT ratio is 83.8%. 88 SNPs and 4 INDELS (175 bp) were identified against mitogenome of *A. gossypii* isolated from cotton species. Especially, largest INDEL (170 bp) was in the control region. Phylogenetic trees show that four *A. gossypii* mitogenomes were clustered in one clade.

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Aphis gossypii Glover, 1877 is one of the typical aphids showing wide range of hosts, especially for agriculture and horticultural species (Ebert and Cartwright 1997). More than 200 species have been identified as its host plants (Spradbery and Dvorak 2013). Usually, their host specificity is tightly linked to its genetic background; however, 7-day artificial feeding can alter their host specificity from cotton to cucumber (Ma et al. 2019), indicating that the genetic background of *A. gossypii* isolated from different host species is valuable to understand characteristics of *A. gossypii*. Till now three mitogenomes of *A. gossypii* isolated from cotton (Zhang S et al. 2016), *Hibiscus syriacus* (Park, Jung, et al. 2019), and *Plantago asiatica* (Bae et al. 2020) have been sequenced. Here, we presented the complete mitogenome of *A. gossypii* isolated from *Leonurus japonicus* in Korea.

Similar to the previous studies in which complete genomes were rescued from the sample containing multiple organisms (Bae et al. 2020; Park, Xi, Park, Lee 2020; Park, Xi, Park, Nam, et al. 2020; Oh et al. in preparation), we sequenced and prepared the genomes from the *L. japonicus* sample with *A. gossypii* DNA (37.690627 N, 128.594893 E; InfoBoss Cyber Herbarium (IN); INH-00026) extracted using DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Sequencing library was constructed using Illumina TruSeq Nano DNA Library Preparation Kit (Illumina, San Diego, CA) following the manufacturer's recommendations with around 350-bp DNA fragments. 4.19 Gbp raw sequences obtained from Illumina NovaSeq6000 (Macrogen Inc., South Korea) were filtered by Trimmomatic v0.33 (Bolger et al. 2014), *de novo* assembled by Velvet v1.2.10 (Zerbino and Birney 2008). Gaps were closed with SOAPGapCloser v1.12

(Zhao et al. 2011), BWA v0.7.17, and SAMtools v1.9 (Li et al. 2009; Li 2013) under the environment of Genome Information System (GeIS; <http://geis.infoboss.co.kr/>). Geneious R11 11.1.5 (Biomatters Ltd, Auckland, New Zealand) was used to annotate mitogenome based on *A. gossypii* mitogenome (MN102349; Bae et al. 2020).

Aphis gossypii mitogenome (GenBank accession is MW013764) is 16,044 bp long, which is the second longest mitogenome among four available *A. gossypii* mitogenomes (Zhang S et al. 2016; Park Jung, et al. 2019; Bae et al. 2020). It contains 13 protein-coding genes, two rRNAs, and 22 tRNAs. Its nucleotide composition is AT-biased (A + T is 83.8%). Control region of 797 bp, which is longer than two *A. gossypii* mitogenomes (NC_024581 and MT430940), is found.

Eighty-eight single nucleotide polymorphisms (SNPs) and four insertions and deletions (INDELS) of which total length is 175 bp are identified against the mitogenome of *A. gossypii* isolated in cotton (NC_024581). Largest INDEL of which length is 170 bp is located in the control region, which is the most variable region in mitogenomes (Lee J et al. 2020; Zhang and Hewitt 1997). In addition, 35 SNPs and 4 INDELS (174 bp in total), 40 SNPs and 3 INDELS (3 bp) are identified against those isolated in *H. syriacus* (MN102349) and *P. asiatica* (MT430940), respectively. It is interesting that mitogenomes of *A. gossypii* isolated in *L. japonicus* and *P. asiatica* display the second lowest SNPs and significantly lowest total length of INDELS, indicating that control regions of both mitogenomes are similar to each other in comparison to the rest two mitogenomes.

Numbers of intraspecific variations identified against three previously sequenced mitogenomes are similar to those of

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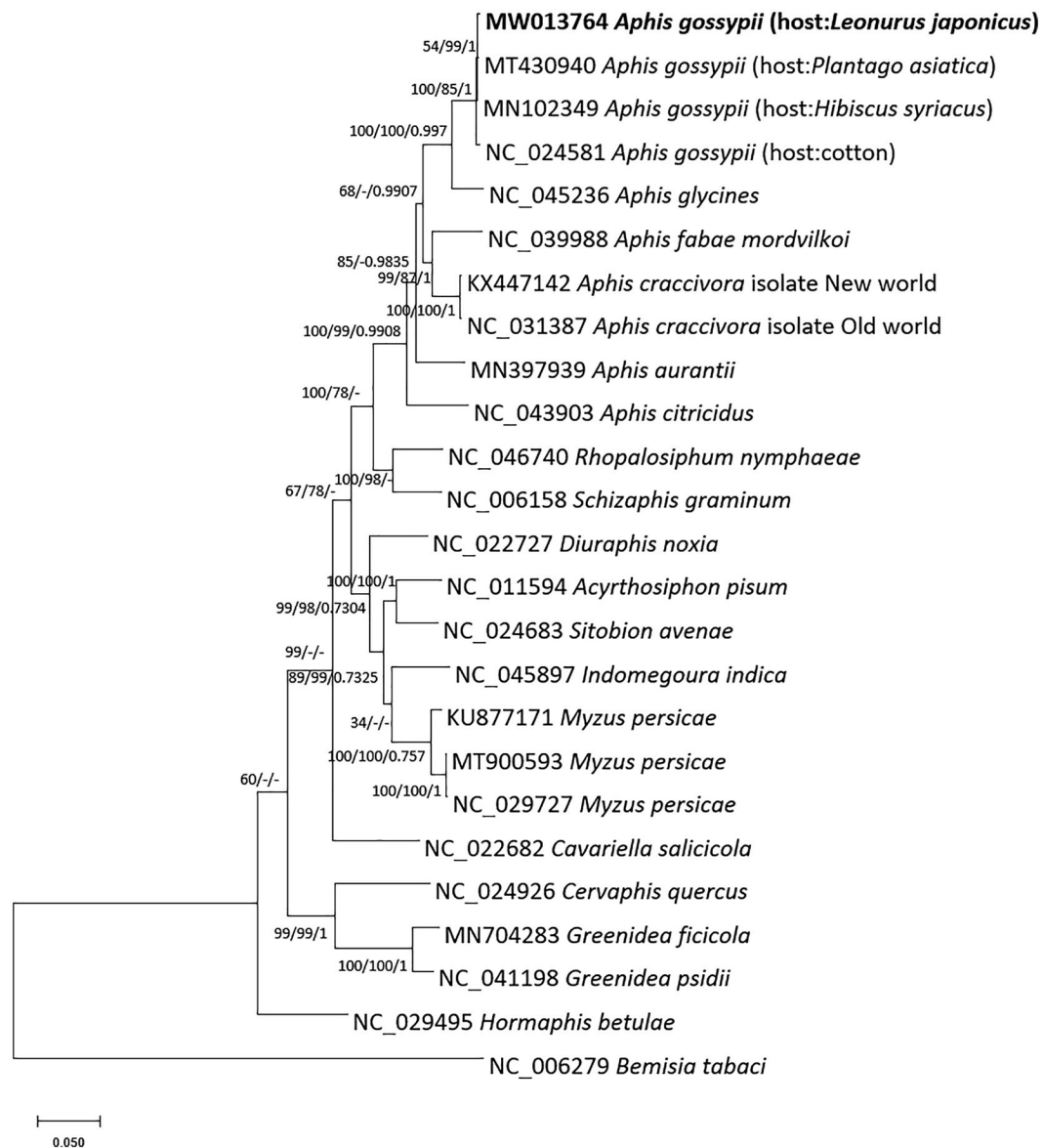


Figure 1. Maximum-likelihood (1000 bootstrap repeats), neighbor-joining (10,000 bootstrap repeats), and Bayesian Inference (1,100,000 generations) phylogenetic trees of 23 mitochondrial genomes of Aphididae and one outgroup: four *Aphis gossypii* (MW013764 in this study, MT430940 (Bae et al. 2020), MN102349 (Park J et al. 2019), and NC_024581 (Zhang S et al. 2016)), *Aphis glycines* (NC_045236; Song et al. 2019), *Aphis fabae mordvilkoii* (NC_039988; Voronova et al. 2020), *Aphis craccivora* (NC_031387 and KX447142; Sun et al. 2017), *Aphis aurantia* (MN397939; Wang Y et al. 2019), *Aphis citricidus* (NC_043903; Wei et al. 2019), *Schizaphis graminum* (NC_006158; Thao et al. 2004), *Rhopalosiphum nymphaeae* (NC_046740; Park, Kim, et al. 2020), *Diuraphis noxia* (NC_022727; De Jager et al. 2014), *Myzus persicae* (NC_029727, KU877171, and MT900593; Voronova et al. 2020; Cho et al., under revision), *Indomegoura indica* (NC_045897; Hong B et al. 2019), *Sitobion avenae* (NC_024683; Zhang B et al. 2016), *Acyrthosiphon pisum* (NC_011594), *Cavariella salicicola* (NC_022682; Wang Y et al. 2013), *Cervaphis quercus* (NC_024926; Wang Y et al. 2014), *Greenidea psidii* (NC_041198; Chen et al. 2019), *Greenidea ficicola* (MN704283; Liu et al. 2020), *Hormaphis betulae* (NC_029495; Li Y-Q et al. 2017), and *Bemisia tabaci* (NC_006279; Thao et al. 2004) as outgroup species. Phylogenetic tree was drawn based on the maximum-likelihood tree. The numbers above branches indicate bootstrap support values of maximum-likelihood, neighbor-joining, and Bayesian Inference phylogenetic trees, respectively.

Nilaparvata lugens (Choi et al. 2019; Park, Kwon, et al. 2019; Choi et al. 2020), *Laodelphax striatellus* (Park, Jung, et al. 2019; Seo, Jung, et al. 2019), and *Spodoptera frugiperda* (Seo, Lee, et al. 2019). However, they are smaller than those of *Chilo suppressalis* (Park, Xi, Kwon, et al. 2019) and are larger than those of *Alphitobius diaperinus* (Hong K-J et al. 2020) and *Hipparchia autonoe* (Lee Y-D et al. 2020).

We inferred the phylogenetic relationship of 25 Aphididae mitogenomes, including four *A. gossypii* mitogenomes with one outgroup species, *Bemisia tabaci* (Tay et al. 2016). Multiple sequence alignment was conducted by MAFFT v7.450 (Kato and Standley 2013). Bootstrapped maximum-likelihood, neighbor-joining, and Bayesian Inference trees

were constructed using MEGA X (Kumar et al. 2018) and MrBayes v3.2.7a (Ronquist et al. 2012) based on multiple alignment of 25 mitogenomes. The result shows that our mitogenome was clustered with the other three mitogenomes of *A. gossypii* well (Figure 1). However, there are many incongruencies among three different phylogenetic trees (Figure 1), which is similar to previous analyses (Park, Xi, Kim, et al. 2019; Bae et al. 2020). In addition, the clade containing four *A. gossypii* mitogenomes displays low supportive values of maximum-likelihood and neighbor-joining trees (Figure 1), requiring more phylogenetic analysis of *A. gossypii*. Our *A. gossypii* mitogenome can be used for understanding the potential relationship between host-specificity and

mitogenomes together, additional mitogenomes originated from different hosts.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

Mitochondrial genome sequence can be accessed via accession number MW013764 in GenBank of NCBI at <https://www.ncbi.nlm.nih.gov>. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA668988, SAMN16428189, and SRR12817477, respectively.

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