The complete mitochondrial genome of Aphis gossypii Glover, 1877 (Hemiptera: Aphididae) isolated from Plantago asiatica in Korea

Yoonhyuk Bae\textsuperscript{a,b*}, Jongsun Park\textsuperscript{a,b*} and Wonhoon Lee\textsuperscript{c}

\textsuperscript{a}InfoBoss Inc., Seoul, Republic of Korea; \textsuperscript{b}InfoBoss Research Center, Seoul, Republic of Korea; \textsuperscript{c}Department of Plant Medicine and Institute of Agriculture & Life Science, Gyeongsang National University, Jinju, Republic of Korea

\textbf{ABSTRACT}

We have determined mitochondrial genome of \textit{A. gossypii} isolated from \textit{Plantago asiatica} in Korea. The circular mitogenome of \textit{A. gossypii} is 16,045 bp including 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single control region of 798 bp. Its AT ratio is 83.8\%. In comparison this mitogenome to Chinese and Korean \textit{A. gossypii} mitogenomes, 66 single nucleotide polymorphisms (SNPs) and 176 insertions and deletions (INDELs) and 11 SNPs and 173 INDELs are identified, respectively, presenting similar level to those of \textit{Nilaparvata lugens}, \textit{Laodelphax striatellus}, and \textit{Spodoptera frugiperda} and lower than that of \textit{Chilo suppressalis}.

\textit{Aphis gossypii} Glover, 1877 is widely distributed polyphagous and popular pest species to agriculture and horticultural species with influencing mortality of crops and transmitting virus (Ebert and Cartwright 1997). It results that biological control programs for managing Aphid populations has been utilized in Europe, Russia, and Korea (Gilkeson and Klein 1981; Vuong et al. 2001). More than 200 species including \textit{Plantago asiatica} (Inaizumi 1970) have been identified as host plants of \textit{A. gossypii} (CABI 2014).

Like previous study that mitogenome of \textit{Ophiocordycipitaceae sp.} was rescued from the \textit{Riciaria speculum} sample (Park et al. 2020), we sequenced the DNA (37°45′74″N, 126°94′84″E; InfoBoss Cyber Herbarium (IN); IBS-000016) prepared from the \textit{P. asiatica} sample with \textit{A. gossypii} extracted using DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). The sample of \textit{A. gossypii} isolated from \textit{P. asiatica} was identified based on its morphological features. Raw sequences obtained from Illumina HiSeqX (Macrogen Inc., South Korea) were filtered by Trimmomatic 0.33 (Bolger et al. 2014), \textit{de novo} assembled by Velvet 1.2.10 (Zerbino and Birney 2008). Gaps were closed with SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17, and SAMtools 1.9 (Li et al. 2009; Li 2013). These works were conducted under the environment of the 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 Korean \textit{A. gossypii} mitogenome (MNN934399; Park Jonghyun et al. 2019).

\textit{A. gossypii} mitogenome (GenBank accession is MT430940) is 16,045 bp long, which is the longer than those of Chinese and Korean \textit{A. gossypii} (Zhang et al. 2016; Park et al. 2019) containing 13 protein-coding genes, two rRNAs, and 22 tRNAs. Its nucleotide composition is AT-biased (A+T is 83.8\%). Control region of 784 bp, which is also longer than two \textit{A. gossypii} mitogenomes, is found.

Sixty-six single nucleotide polymorphisms (SNPs) and 176 insertions and deletions (INDELs) and 11 SNPs and 173 INDELs are identified against those of Chinese and Korean \textit{A. gossypii}, respectively. These numbers of sequence variations are similar to those of \textit{Nilaparvata lugens} (Choi et al. 2019; Park, Kwon, et al. 2019; Choi et al. 2020), \textit{Laodelphax striatellus} (Park, Jung, et al. 2019; Seo, Jung, et al. 2019), and \textit{Spodoptera frugiperda} (Seo, Lee, et al. 2019). It is smaller than that of \textit{Chilo suppressalis} (Park, Xi, et al. 2019). One of the possible reasons why our mitogenome is much different from the remaining two mitogenomes, specifically control region, can be a different host plant like the cases of \textit{Acrithysiphon pisum} (Peccoud et al. 2009) and \textit{Aphis glycine} (Park et al., in preparation).

We inferred the phylogenetic relationship of 23 mitogenomes, including three \textit{A. gossypii} mitogenomes, with one outgroup species, \textit{Bemisia tabaci} (Tay et al. 2016). Multiple sequence alignment was conducted by MAFFT 7.450 (Katoh and Standley 2013). Bootstrapped maximum likelihood, neighbor joining, and Bayesian Inference trees were constructed using MEGA X (Kumar et al. 2018) based on multiple alignment of mitogenomes. The result shows that \textit{Aphis} genus was clearly clustered with the rest genera in Aphidinae, but conspicuously, three phylogenetic trees showed incongruent topology of Aphidinae clade (Figure 1).

\textbf{CONTACT} Jongsun Park (starfr@infoboss.co.kr) Infoboss Inc., Seoul, Republic of Korea; Wonhoon Lee (wonhoon@gnu.ac.kr) Department of Plant Medicine and Institute of Agriculture & Life Science, Gyeongsang National University, Jinju, Republic of Korea

\textsuperscript{*}Indicates co-first authors.

\textcopyright{} 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
Taken together, our mitogenome is helpful to understand intraspecific mitogenome variations of *A. gossypii* as well as phylogenetic relationship among Aphidinae species.

**Disclosure statement**

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

**Funding**

This study was carried out with the support of InfoBoss Research Grant [IBG-0008]. This study was also supported by Research of Animal and Plant Quarantine Agency of South Korea Fund (PQ20180B008-SP).

**ORCID**

Jongsun Park [http://orcid.org/0000-0003-0786-4701](http://orcid.org/0000-0003-0786-4701)

**Data availability statement**

The mitochondrial genomes in this study can be accessed via the NCBI GenBank accession number, MT430940.

**References**

Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics. 30(15):2114–2120.

CABI. (2014). Invasive species compendium. Xcscconsulting.Com.Au:4066. [https://doi.org/10.1094/pdis](https://doi.org/10.1094/pdis)

Choi NJ, Lee B-C, Park J, Park J. 2019. The complete mitochondrial genome of *Nilaparvata lugens* (Stål, 1854) captured in China (Hemiptera: Delphacidae): investigation of intraspecies variations between countries. Mitochondrial DNA Part B. 4(1):1677–1678.

Choi NJ, Lee B-C, Park J, Park J. 2020. The complete mitochondrial genome of *Nilaparvata lugens* (Stål, 1854) captured in Guangxi province, China (Hemiptera: Delphacidae): identification of the origin of *N. lugens* migrated to Korea. Mitochondrial DNA Part B. 5(2):1960–1961.

Ebert T, Cartwright B. 1997. Biology and ecology of *Aphis gossypii* Glover (Homoptera: aphididae). Southwestern Entomol. 22(1):116–153.

Gilkeson L, Klein M. 1981. A guide to the biological control of greenhouse aphids. the University of Wisconsin, Madison: Ark Project.

Inaizumi M. 1970. Primary host plants for *Aphis gossypii* Glover, and its landing on secondary host plants. Jpn J Appl Entomol Zool. 14(1):29–38.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, 1000 Genome Project Data Processing Subgroup 2009. The sequence alignment/map format and SAMtools. Bioinformatics. 25(15):2078–2079.

Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint arXiv:13033997.

Park J, Jung JK, Ho Koh Y, Park J, Seo BY. 2019. The complete mitochondrial genome of *Laodelphax striatellus* (Fallén, 1826) (Hemiptera: Delphacidae) collected in a mid-Western part of Korean peninsula. Mitochondrial DNA Part B. 4(2):2229–2230.

Park J, Xi H, Kim Y, Park J, Lee W. 2019. The complete mitochondrial genome of *Aphis gossypii* Glover, 1877 (Hemiptera: Aphididae) collected in Korean peninsula. Mitochondrial DNA Part B. 4(2):3007–3009.
Park J, Kwon W, Park J, Kim H-J, Lee B-C, Kim Y, Choi NJ. 2019. The complete mitochondrial genome of *Nilaparvata lugens* (stål, 1854) captured in Korea (Hemiptera: Delphacidae). Mitochondrial DNA Part B. 4(1):1674–1676.

Park J, Xi H, Kim Y, Park J, Lee W. 2019. The complete mitochondrial genome of *Aphis gossypii* Glover, 1877 (Hemiptera: Aphididae) collected in Korean peninsula. Mitochondrial DNA Part B. 4(2):3007–3009.

Park J, Xi H, Kwon W, Park C-G, Lee W. 2019. The complete mitochondrial genome sequence of Korean *Chilo suppressalis* (Walker, 1863)(Lepidoptera: Crambidae). Mitochondrial DNA Part B. 4(1):850–851.

Park J, Xi H, Park J, Lee W. 2020. The complete mitochondrial genome of fungal endosymbiont, Ophiocordycipitaceae sp., isolated from *Ricania speculum* (Hemiptera: Rcaniidae). Mitochondrial DNA Part B. 5(2):1888–1889.

Park et al., In-depth investigation of intraspecific variations on mitochondrial genomes of *Aphis glycines* Matsumura (Hemiptera:Aphididae) from the publicly available NGS raw reads, in preparation.

Peccoud J, Ollivier A, Plantegenest M, Simon J-C. 2009. A continuum of genetic divergence from sympatric host races to species in the pea aphid complex. Proc National Acad Sci. 106(18):7495–7500.

Seo BY, Jung JK, Ho Koh Y, Park J. 2019. The complete mitochondrial genome of *Laodelphax striatellus* (Fallén, 1826) (Hemiptera: Delphacidae) collected in a southern part of Korean peninsula. Mitochondrial DNA Part B. 4(2):2242–2243.

Seo BY, Lee G-S, Park J, Xi H, Lee H, Lee J, Park J, Lee W. 2019. The complete mitochondrial genome of the fall armyworm, *Spodoptera frugiperda* Smith, 1797 (Lepidoptera; Noctuidae), firstly collected in Korea. Mitochondrial DNA Part B. 4(2):3918–3920.

Tay W, Elfeiky S, Court L, Gordon K, De Barro P. 2016. Complete mitochondrial DNA genome of *Bemisia tabaci* cryptic pest species complex Asia I (Hemiptera: Aleyrodidae). Mitochondrial DNA A DNA Mapp Seq Anal. 27(2):972–973.

Vuong PT, Kim J, Song Y. 2001. The seasonal occurrence of the two aphid species, *Myzus persicae* and *Aphis gossypii*, and their natural enemies on vegetable crops in Chinju, Korea. J Asia-Pac Entomol. 4(1):41–44.

Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. 18(5):821–829.

Zhang S, Luo J, Wang C, Lv L, Li C, Jiang W, Cui J, Rajput LB. 2016. Complete mitochondrial genome of *Aphis gossypii* Glover (Hemiptera: Aphididae). Mitochondrial DNA A DNA Mapp Seq Anal. 27(2):854–855.

Zhao Q-Y, Wang Y, Kong Y-M, Luo D, Li X, Hao P. 2011. Optimizing de novo transcriptome assembly from short-read RNA-Seq data: a comparative study. BMC Bioinformatics. 12(Suppl 14):S2.