MITOCHONDRIAL DNA PART B
2022, VOL. 7, NO. 1, 84–86
https://doi.org/10.1080/23802359.2021.2008839

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MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome of *Uroleucon erigeronense* (Thomas, 1878) (Hemiptera: Aphididae)

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ABSTRACT

We have sequenced mitochondrial genome of *Uroleucon erigeronense* (Thomas, 1878) isolated from *Erigeron canadensis* in Korea. The circular mitogenome of *U. erigeronense* is 15,691 bp long including 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNAs, and a single control region of 968 bp. AT ratio is 84.2%. Additional phylogenetic studies of aphid mitogenomes are required due to the inconsistency found in the three phylogenetic trees.

ARTICLE HISTORY
Received 2 September 2021
Accepted 15 November 2021

KEYWORDS
Aphididae; *Erigeron canadensis*; Mitochondrial genome; *Uroleucon erigeronense*

The genus *Uroleucon* Mordvilko, 1914 (Hemiptera: Aphididae) consisting of more than 200 species is distributed worldwidely (Nafría et al. 2007). *Uroleucon erigeronense* (Thomas, 1878) belonging to the subgenus *Lambersius* Olive, 1965, which is one of five subgenera of *Uroleucon*, was introduced to Europe (Blackman and Eastop 2006) and Australia recently (Brumley and Watson 2017). *U. erigeronense* usually feeds on the *Erigeron* species; but its host range was revealed widely including another Asteraceae plant species, such as *Dieteria canescens* (Pursh) A.Gray and *Ericameria nauseosa* (Pall. ex Pursh) G.L.Nesom & G.I.Baird (Jensen et al. 2010). In Korea, *U. erigeronense* is already considered a native species (Park, An, et al. 2020). Here, we presented the complete mitogenome of *U. erigeronense* isolated from *Erigeron canadensis* in Korea as the first mitogenome of *Uroleucon* genus.

Like the previous studies that complete organelle genomes were rescued from the sample contains multiple organisms (Bae et al. 2020; Park, Xi, Park, Lee 2020; Park, Xi, Park, Nam, et al. 2020; Choi et al. 2021; Park, Lee, et al. 2021; Park, Xi, Kim, et al. 2021; Park, Xi, Park 2021), we sequenced the DNA (37.529708 N, 126.842867E; InfoBoss Cyber Herbarium (IN); IB-30034; Contact person: Jongsun Park, starflr@infoboss.co.kr) prepared from the *E. canadensis* sample with *U. erigeronense* extracted using DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). 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 GapCloser v1.12 (Zhao et al. 2011), BWA v0.7.17, and SAMtools v1.9 (Li et al. 2009; Li 2013) in the environment of Genome Information System (GelS; http://geis.infoboss.co.kr/), which utilized in previous insect mitogenome studies (Han et al. 2017; Park, Jung, et al. 2019; Park, Park, et al. 2019; Lee et al. 2020; Park, Xi, et al. 2020; Jung et al. 2021; Park and Park 2021). Geneious Prime® 2020.2.4 (Biomatters Ltd, Auckland, New Zealand) was used to annotate mitogenome based on *Sitobion avenae* (Fabricius, 1775) mitogenome (GenBank accession: KJ742384; Zhang et al. 2016).

U. erigeronense mitogenome (GenBank accession: MZ695840) is 15,691 bp long, which is longer than *S. avenae* mitogenome (Zhang et al. 2016). It contains 13 protein-coding genes, two ribosomal RNAs, and 22 transfer RNAs, which is a typical configuration of the aphid mitogenomes (Cameron 2014; Boore 1999). Its nucleotide composition is AT-biased (A + T ratio: 84.2%). Control region is 968 bp long, which is longer than *S. avenae* mitogenome (430 bp in length). It is the major reason that *U. erigeronense* mitogenome is longer than *S. avenae* mitogenome. Most of aphid mitogenomes contain another repeat region between *tRNA-Glu* and *NAD5* (Lee et al. 2019; Park, Xi, et al. 2019; Park, Kim, et al. 2020). The second repeat region of *U. erigeronense* mitogenome is 245 bp long, which is shorter than that of *S. avenae* (261 bp).

Thirty Aphididae mitogenomes which are representative mitogenome for each species including *U. erigeronense* mitogenome with one outgroup species, *Daktulosphaira vitifoliae* (Fitch, 1856) (Hemiptera: Phylloxeridae), were aligned by MAFFT v7.450 (Katoh and Standley 2013) for conducting phylogenetic analysis of the Maximum-Likelihood (ML) with 1,000 bootstrap repeats and the Neighbor-Joining (NJ) with 10,000 bootstrap repeats by MEGA X (Kumar et al. 2018) and Bayisean inferrence (BI) with GTR model with gamma rates and 1,100,000 generations for Monte Carlo algorithm by MrBayes v3.2.6 (Ronquist et al. 2012). Three phylogenetic

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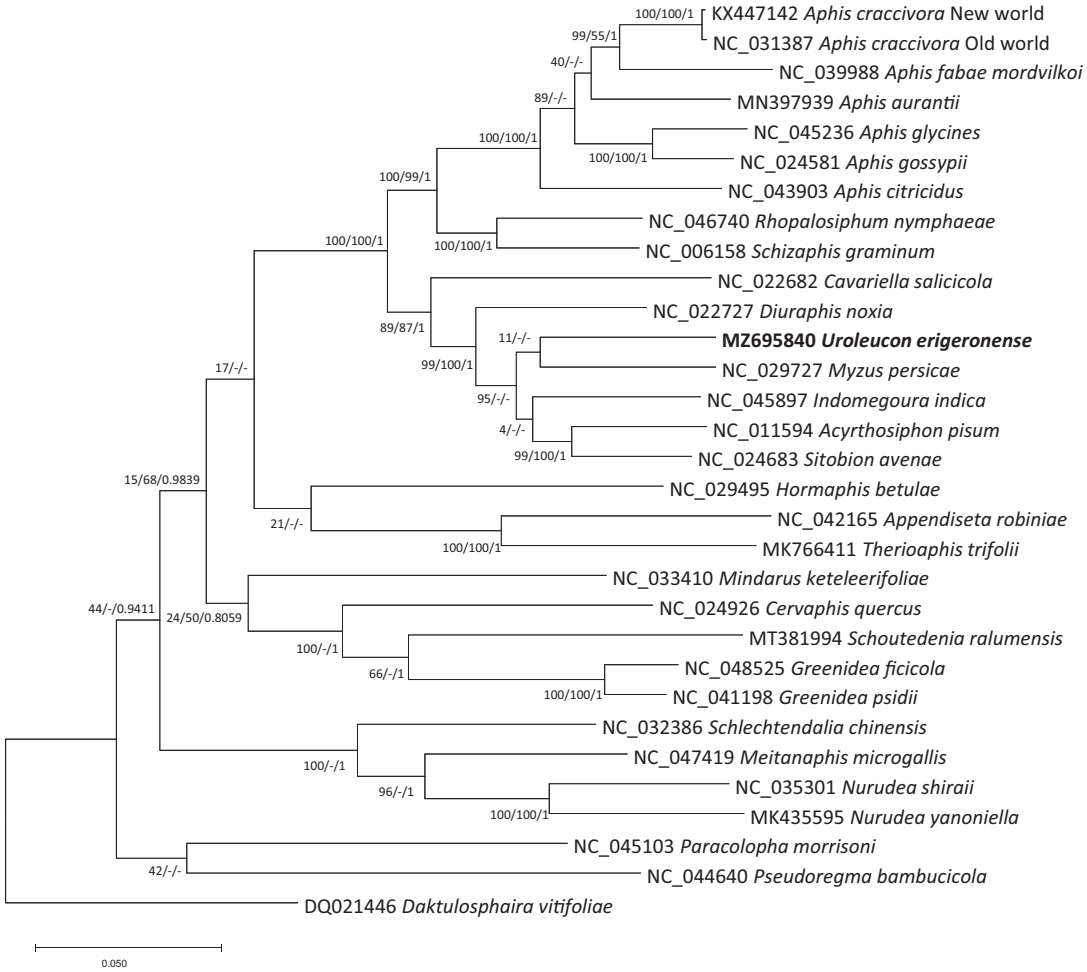

Figure 1. Maximum-Likelihood, Neighbor-Joining, and Bayesian inference phylogenetic trees of 31 mitochondrial genomes of Aphididae and one outgroup species, *D. vitifoliae*. Phylogenetic tree was drawn based on Maximum-Likelihood tree. The numbers above branches indicate supportive values of Maximum-Likelihood and Bayesian inference phylogenetic trees, respectively.

trees displayed the incongruency of topology of the clade containing to *U. erigeronense*: the ML tree presented that *U. erigeronense* was clustered with *Myzus persicae* (Sulzer, 1776) with very low supportive values (Figure 1); while NJ and BI trees exhibited that *U. erigeronense* was clustered with *Acrythosiphon pisum* (Harris, 1776) and *S. avernae* mitogenomes with high supportive values, congruent to the molecular phylogeny of nuclear and mitochondrial marker sequences (Moran et al. 1999). Moreover, additional clades displaying incongruence among three trees were also found (Figure 1), indicating that additional studies for clarifying phylogenetic tree of aphid species are required. Taken together, the *U. erigeronense* mitogenome sequence addresses the further questions to understand phylogenetic relationship and mitogenome characteristics in tribe Macrosiphini in near future.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This study was carried out with the support of InfoBoss Research Grant [IBG-0008].

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Data availability statement

The mitochondrial genomes in this study can be accessed via the NCBI GenBank accession number, MZ695840. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA756639, SAMN20893750, and SRR15558516, respectively.

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