

Complete mitochondrial genome of the Korean endemic springtail *Homidia koreana* Lee & Lee, 1981 (Collembola: Entomobryidae)

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ABSTRACT

The Korean endemic springtail *Homidia koreana* Lee & Lee, 1981 is popular in the leaf litter of various forests of South Korea, probably widely distributed throughout the Korean Peninsula. The complete mitochondrial genome of *H. koreana* was sequenced, assembled, and annotated. The mitochondrial genome of *H. koreana* consists of a circular DNA molecule of 14,846 bp, with 68.4% AT content. It comprises 13 protein-coding genes (PCGs), 22 transfer (tRNA) genes, and 2 ribosomal RNA (rRNA) genes. The molecular phylogenetic relationships estimated using MrBayes 3.2 revealed that *H. koreana* was closely related to *Homidia socia* Denis, 1929, both of which belong to the genus *Homidia*.

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Entomobryomorpha; complete mitogenome; next-generation sequencing; phylogenetic analysis

Collembola are wingless and entognathous hexapods with Diplura and Protura, and comprise a taxonomic group of the same rank as the class Insecta in the phylum Arthropoda. They are probably the most abundant of all soil-dwelling arthropods and have the widest distribution of any hexapod group, occurring throughout the world, including Antarctica. There are about 9300 published species worldwide (Bellinger et al. 1996–2021).



The genus *Homidia* Börner, 1906 which belongs to the family Entomobryidae is widely distributed in East Asia, especially China, Japan, and Korea. To date, 70 species in this genus have been recorded all over the world (Pan and Yang 2019), 18 of them from Korea (Kang and Park 2010, 2012). The Korean endemic springtail *Homidia koreana* Lee and Lee 1981 was first described with specimens collected from litter sample of pine trees in Mt. Namgosan (Jeonju, Republic of Korea; Collection no. 79-33-1, 78-10-1) (Lee and Lee 1981). This species is popular in the leaf litter of various forests of South Korea, probably widely distributed throughout the Korean Peninsula. Mitochondrial DNA sequences can be used to estimate phylogenetic relationships. Regarding complete mitogenomes of *Homidia*, information on only one species, *Homidia socia* Denis, 1929, was recorded so far (Wu and Chen 2019). In the present study, the mitochondrial genome of *H. koreana* was sequenced, assembled, and annotated, and its molecular characteristics were described. The result of sequencing and analysis of the mitochondrial genome structure of *H. koreana* will contribute to providing more evidence for the identification and phylogenetic study of this group.

The individuals of *H. koreana* were collected in Jinan, South Korea (35°40'38" N, 127°26'38" E) on 17th May 2021.

The voucher specimen was deposited and, preserved at Insect Collection in Department of Biology Education, Jeonbuk National University, Jeonju (Kyung-Hwa Park, pkhsyst@jbnu.ac.kr) under the voucher number '158-En-HK.' Total genomic DNA was prepared from a single specimen using QIAamp DNA Mini Kit (Qiagen, Hilden, Germany). The sequencing library is prepared by random fragmentation of the genomic DNA, followed by 5' and 3' adapter ligation using Illumina TruSeq DNA Nano Library Prep Kit (Illumina Inc., San Diego, CA, USA). The paired-end (2 × 150 bp) sequencing was performed using the Illumina HiSeq-X platform (San Diego, CA, USA) at Macrogen Inc. (Seoul, Korea). De novo assembly of raw reads sequences was performed by various k-mer lengths using SPAdes version 3.13.0 (Bankevich et al. 2012). The *trnI* gene (tRNA-Ile) of mitogenome was used as a seed sequence for the assembly. Mitochondrial-related contigs were assembled into one contig as a circular molecule. The annotation of mitochondrial genomes was performed using the MitoZ version 2.3 (Meng et al. 2019) and manual curation based on BLAST searches in the NCBI database.

The complete mitochondrial genome of *H. koreana* is a closed circular molecule of 14,846 bp and contained 13 protein-coding genes (PCGs), 22 transfer RNA genes, and 2 ribosomal RNA genes. The overall nucleotide composition was 33.2% A, 12.1% C, 19.5% G, and 35.2% T, indicating an obvious A + T bias (68.4%) as typically found in hexapod mitogenomes. A 441-bp of the non-coding region was located at the junction between *trnQ* and *trnI*.

Among the 13 PCGs, four start codons were found: ATA (*nad4l*, *nad6*, *nad1*), ATC (*cox1*, *atp8*), ATG (*nad2*, *atp6*, *cox3*,

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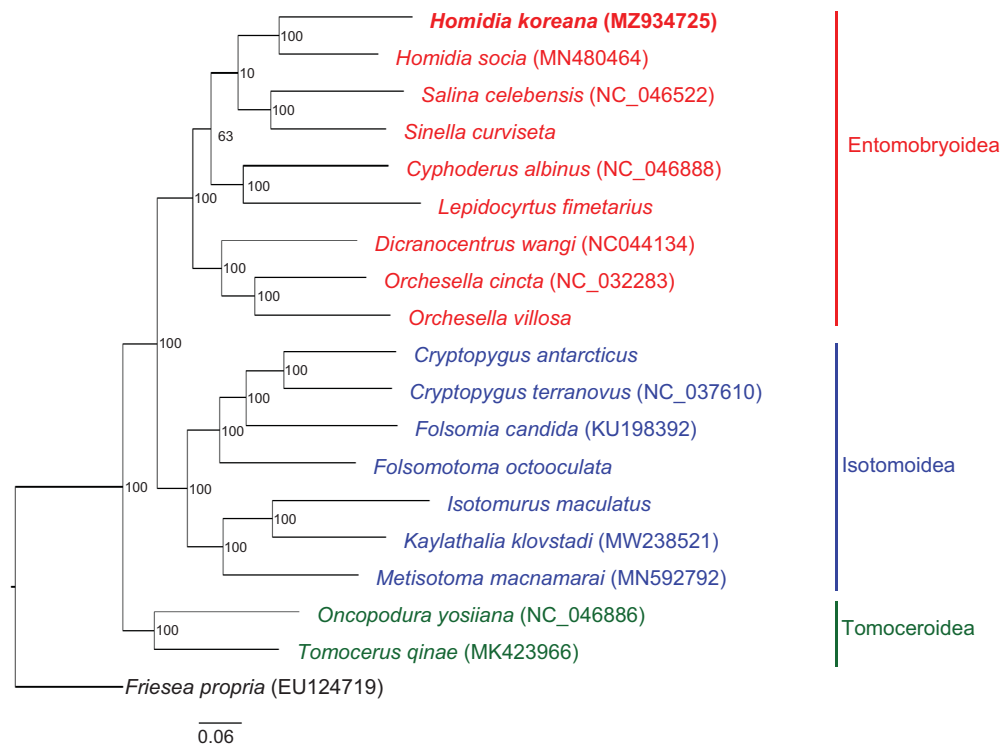


Figure 1. Bayesian inference (100,000 generations) tree showing phylogenetic relationships among 18 Entomobryomorpha species was constructed based on 13 mitochondrial protein-coding genes sequences. A Poduromorpha, *Friesea propria* was used as outgroup. *Homidia koreana* in bold is the result obtained in this study. Posterior probability is shown at nodes.

nad4, *cytb*), and ATT (*cox2*, *nad3*, *nad5*). The PCGs had a 'TAA' stop codon (*nad2*, *cox1*, *atp8*, *atp6*, *nad4l*, *nad6*, *cytb*, *nad1*) or a 'TAG' stop codon (*cox2*, *nad3*, *nad5*); however, *cox3*, and *nad4* did not.

To explore the evolutionary relationships and phylogenetic position of *H. koreana*, we selected the mitochondrial DNA sequences of 19 Collembola species (18 Entomobryomorpha as ingroup and one Poduromorpha as outgroup). *Friesea propria* Greenslade & Fanciulli, 2020 (in Carapelli et al. 2020) was used as an outgroup. The nucleotide sequences from each PCG were aligned using MAFFT v.7.450 (Katoh and Standley 2013). Then concatenate the aligned sequences into a dataset. Phylogenetic trees (Bayesian inference tree) were reconstructed using MrBayes 3.2 (Ronquist et al. 2012) with the GTR+I+ Γ model run with four chains for 10^5 generations, with a sampling of one tree/1000 iterations and 25% of burn-in. The result showed that all the superfamilies formed monophyletic groups respectively (Figure 1). *H. koreana* was closely related to *H. socia*, both of which belong to the genus *Homidia*.

Disclosure statement

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

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov>) under the accession no. MZ934725. The associated BioProject, Bio-sample, SRA numbers are PRJNA756712, SAMN22346667 and SRR16368306.

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