The complete mitochondrial genome of the Korean endemic species Cobitis hankugensis (Kim, Park, Son & Nalbant, 2003)

Soo Rin Lee, Eun-Bi Kim, Yunji Go, Yuan Kang, Md. Jobaidul Alam, Kyung Su Kim, Sapto Andriyono and Hyun-Woo Kim.

ABSTRACT
As one of efforts to conserve a genetic resource of the endemic cobitid species in the Korean peninsula, the complete mitogenome of Cobitis hankugensis (Kim, Park, Son & Nalbant, 2003) was determined using Illumina MiSeq system. The circular mitogenome was 16,557 bp length and encoded 13 protein-coding genes (PCGs), two ribosomal RNA genes, 22 tRNA genes, and a control region. Only the COX1 gene was identified with an aberrant initiation codon GTG and an incomplete termination codon (T—/TA—) was identified in six PCGs including COX2, COX3, ND2, ND3, ND4, and Cytb genes. Phylogenetic analysis using 30 mitochondrial genomes belonging to Cobitidae, Botiidae, and Gyrinocheilidae showed that the highest identity (92.38%) with Kichulchoia brevifasciata (NC_027166). The complete mitogenome of C. hankugensis, an endemic species in Korea, will provide fundamental data on the evolutionary relationship of Cobitidae species.

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In order to confirm the evolutionary relationship of C. hankugensis with its relatives, total of 31 complete mitochondrial genomes were obtained from the GenBank database (https://www.ncbi.nlm.nih.gov/genbank/) and a phylogenetic tree was constructed (Figure 1). Two sister species, Gyrinocheilidae Gyminocheilus pennnocki (NC_031544) and Botiidae Leptobotia microphthalmalma (NC_024049) were selected as outgroup members. The nucleotide sequences of 13 PCGs were aligned by using MAFFT v7.48 with the L-INS-I algorithm (Katoh et al. 2019). The Maximum likelihood (ML) phylogenetic analysis was performed with 1,000 bootstrap replicates based on the GTR$+$F$+$R4 model in the IQ-TREE2 package version 2.1.3 (Minh et al. 2020). As a result, C. hankugensis showed the highest nucleotide sequence identity (92.38%) with Kichulchoia brevifasciata (NC_027166) followed by the Cobitis biwae (91.08%, NC_027663) (Figure 1). This result strongly supported the previous biogeographical analysis of cobitid species, in which those species have been evolved in South subdistrict (Kwan et al. 2018).

A phylogenetic tree was based on the complete mitogenomes in the family Cobitidae using the IQ-TREE2 package version 2.1.3 by Maximum likelihood (ML) algorithm. Number at each node indicates bootstrap replications. The GenBank accession numbers were shown followed by each species scientific name.

Disclosure statement
The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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Figure 1. Phylogenetic relationship of Cobitis hankugensis in the family Cobitidae.

ORCID
Soo Rin Lee http://orcid.org/0000-0002-6443-855X
Eun-Bi Kim http://orcid.org/0000-0002-2075-2109
Md. Jobaidul Alam http://orcid.org/0000-0002-3594-8147
Hyun-Woo Kim http://orcid.org/0000-0003-1357-5893

Data availability statement
The mitogenome data that support the findings of this study are available in GenBank of NCBI at: https://www.ncbi.nlm.nih.gov/nuccore/MZ339224. Associated accession numbers BioProject: PRJNA732999, BioSample: SAMN19357315, and SRA: SRR14663551 are available.

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