

Mitochondrial korean species 2021

by Sapto Andriyono

Submission date: 09-Jan-2023 05:12PM (UTC+0800)

Submission ID: 1990128704

File name: ndemic_species_Cobitis_hankugensis_Kim_Park_Son_Nalbant_2003.pdf (1.23M)

Word count: 1627

Character count: 9160



Mitochondrial DNA Part B Resources



ISSN: (Print) (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

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 & Hyun-Woo Kim

To cite this article: Soo Rin Lee, Eun-Bi Kim, Yunji Go, Yuan Kang, Md. Jobaidul Alam, Kyung Su Kim, Sapto Andriyono & Hyun-Woo Kim (2022) The complete mitochondrial genome of the Korean endemic species *Cobitis hankugensis* (Kim, Park, Son & Nalbant, 2003), *Mitochondrial DNA Part B*, 7:1, 21-22, DOI: [10.1080/23802359.2021.2005496](https://doi.org/10.1080/23802359.2021.2005496)

To link to this article: <https://doi.org/10.1080/23802359.2021.2005496>



4

© 2021 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 10 Dec 2021.



Submit your article to this journal [↗](#)



Article views: 939







View related articles [↗](#)



View Crossmark data [↗](#)

Full Terms & Conditions of access and use can be found at
<https://www.tandfonline.com/action/journalInformation?journalCode=tmdn20>

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

Soo Rin Lee^a , Eun-Bi Kim^a , Yunji Go^b, Yuan Kang^b, Md. Jobaidul Alam^c , Kyung Su Kim^d, Sapto Andriyono^f and Hyun-Woo Kim^{b,e} 

^aIndustry 4.0 Convergence Bionics Engineering, Pukyong National University, Busan, Republic of Korea; ^bDepartment of Marine Biology, Pukyong National University, Busan, Republic of Korea; ^cDepartment of Fisheries, Ministry of Fisheries and Livestock, Dhaka Bangladesh; ^dGyeongsangnam-do Freshwater Fish Research Center, Miryang, Republic of Korea; ^eMarine Integrated Biomedical Technology center, The National Key Research Institutes in Universities, Busan, Republic of Korea; ^fFisheries and Marine Faculty, C Campus Jl, Universitas Airlangga, Surabaya, Indonesia

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 Gyriinocheilidae 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.

ARTICLE HISTORY

Received 30 September 2021
Accepted 6 November 2021

KEYWORDS

Next generation sequencing; *Cobitis hankugensis*; mitochondrial genome; Cobitidae

Fish in the family Cobitidae are widely distributed in the Palearctic region (Šlechtová et al. 2008). Among 146 species currently reported in the family, 17 species (5 genera) are known in Korean rivers (Kim 2009). As one of endemic species in Korean peninsula, *Cobitis hankugensis* (Kim, Park, Son & Nalbant, 2003) mainly inhabits in Nakdong River and Hyongsan River as well as their tributaries. Due to the morphological similarity, *C. hankugensis* often confused with its relatives, including *C. tenia* and *C. sinensis* (Kim 2009). In particular, interspecific hybridization between *C. hankugensis* and its relative, *Iksokimia longicorpa* has been detected (Perdices et al. 2016; Kwan et al. 2019). Besides, many foreign species in the genus have been introduced for their aquaculture. Therefore, it is urgent to secure the native genetic resources of cobitid fish in Korea for its sustainability.

Cobitis hankugensis were collected from a tributary of Nakdong River, South Korea (N35°32'20.96", E128°6'27.73") in 2018. The mitochondrial DNA was isolated using the commercial mitochondrial isolation kit (Abcam, USA). Species identification was conducted by the morphological characteristics (Kim et al. 2003; Kim 2009) and its nucleotide sequence identity of COI region (99.02%) with the reference sequence of *C. hankugensis* (EU670772) in the database. The specimen and its DNA are stored at the Marine Biodiversity Institute of Korea (<https://www.mabik.re.kr/html/en/>, Ha Yeun Song, and hysong@mabik.re.kr) under the number MABIK GR00004770.

For the high-throughput sequencing, the mitochondrial DNA was sheared by Covaris M220 Focused-Ultrasonicator (Covaris Inc., USA), which was further used for constructing a library using the TruSeq[®] RNA library preparation kit V2 (Illumina, USA). The constructed library was sequenced by the Illumina MiSeq sequencing platform. After removal of the low-quality reads and adapter region, the trimmed reads were assembled and annotated by using Geneious Prime 2021.0.3 (<https://www.geneious.com>) under the default parameter settings. The secondary structures of 22 tRNAs were predicted by the tRNA-Scan-SE online software (Lowe and Chan 2016).

The complete circular mitogenome of *C. hankugensis* (MZ339224) was 16,657 bp in length, which encoded the 13 protein-coding genes (PCGs), two ribosomal RNA genes, 22 tRNA genes, and a control region. The overall AT and GC contents were 57.84% and 42.16%, respectively, which is similar to other freshwater fish taxa. Except for ND6 gene and eight tRNAs (Gln, Ala, Asn, Cys, Tyr, Ser, Glu, Pro), a total of 12 PCGs, two ribosomal RNAs, and 14 tRNAs were located on the heavy strand (H-strand). The control region (929 bp) was identified between tRNA-*Pro* and tRNA-*Phe*. Twelve PCGs were started with typical initiation codon (ATG), except for COX1 (GTG). Transcription of six PCGs were predicted to be terminated with the typical stop codons (TAA), while the incomplete termination codons (T—TA—) were identified in

CONTACT Hyun-Woo Kim  kimhw@pknu.ac.kr  Department of Marine Biology, Pukyong National University, Busan 48513, Republic of Korea

© 2021 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.

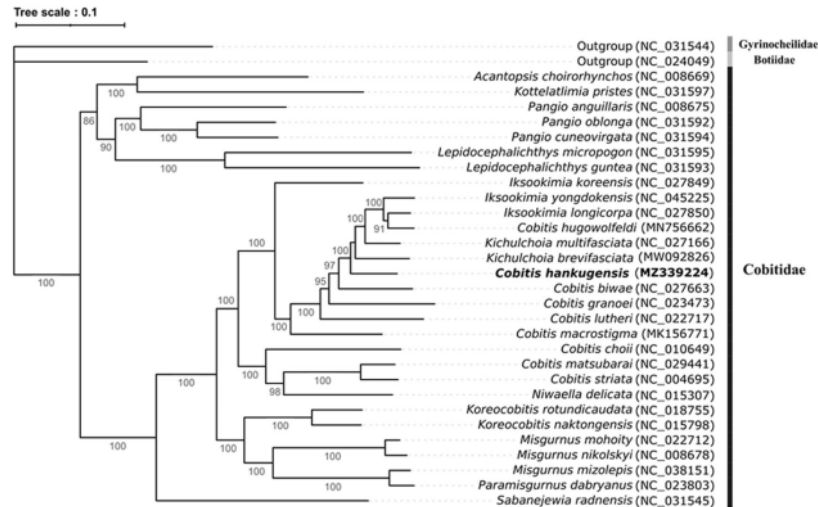


Figure 1. Phylogenetic relationship of *Cobitis hankugensis* in the family Cobitidae.

six PCGs including COX2, COX3, ND2, ND3, ND4, and Cytb genes.

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 *Gyrinocheilus pennocki* (NC_031544) and Botiidae *Leptobotia microphthalmia* (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 (Kato 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.

Funding

This research was supported by Pukyong National University Development Project Research Fund (Philosopher of Next Generation), 2020.

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.

References

- Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Brief Bioinform.* 20(4):1160–1166.
- Kim I-S. 2009. A Review of the Spined Loaches. Family Cobitidae (Cypriniformes) in Korea. *Korean J Ichthyol.* 21:7–28.
- Kim IS, Park JY, Son YM, Nalbant TT. 2003. A review of the loaches, genus *Cobitis* (Teleostomi: Cobitidae) from Korea, with the description of a new species *Cobitis hankugensis*. *Korean J Ichthyol.* 15:1–11.
- Kwan Y-S, Kim D, Ko M-H, Lee W-O, Won Y-J. 2018. Multi-locus phylogenetic analyses support the monophyly and the Miocene diversification of *Iksookimia* (Teleostei: Cypriniformes: Cobitidae). *Syst Biodivers.* 16(1):81–88.
- Kwan YS, Ko MH, Jeon YS, Kim HJ, Won YJ. 2019. Bidirectional mitochondrial introgression between Korean cobitid fish mediated by hybridogenetic hybrids. *Ecol Evol.* 9(3):1244–1254.
- Lowe TM, Chan PP. 2016. tRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. *Nucleic Acids Res.* 44(W1):W54–W57.
- Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, Von Haeseler A, Lanfear R. 2020. IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. *Mol Biol Evol.* 37(5):1530–1534.
- Perdices A, Bohlen J, Šlechtová V, Doadrio I. 2016. Molecular evidence for multiple origins of the European spined loaches (Teleostei, Cobitidae). *PloS One.* 11(1):e0144628.
- Šlechtová V, Bohlen J, Perdices A. 2008. Molecular phylogeny of the freshwater fish family Cobitidae (Cypriniformes: Teleostei): delimitation of genera, mitochondrial introgression and evolution of sexual dimorphism. *Mol Phylogenet Evol.* 47(2):812–831.

Mitochondrial korean species 2021

ORIGINALITY REPORT

7%

SIMILARITY INDEX

0%

INTERNET SOURCES

7%

PUBLICATIONS

0%

STUDENT PAPERS

PRIMARY SOURCES

- 1 Jeung Il Kim. "Gene expression in mixed type liposarcoma", *Pathology*, 4/1/2006 1%

Publication
- 2 Mingming Bao, Xiujie Zhang, Congxin Xie, Shiming Wan, Lingang Cai, Qiong Zhou. " The complete mitochondrial genome of (Cypriniformes: Cyprinidae) ", *Mitochondrial DNA*, 2014 1%

Publication
- 3 Peng Yu, Li Zhou, Wen-Tao Yang, Li-jun Miao, Zhi Li, Xiao-Juan Zhang, Yang Wang, Jian-Fang Gui. "Comparative mitogenome analyses uncover mitogenome features and phylogenetic implications of the subfamily Cobitinae", *BMC Genomics*, 2021 1%

Publication
- 4 Richard R. Rosenkranz, Kate Ridley, Justin M. Guagliano, Sara K. Rosenkranz. "Physical activity capability, opportunity, motivation and behavior in youth settings: theoretical framework to guide physical activity leader 1%

interventions", International Review of Sport and Exercise Psychology, 2021

Publication

5

In - Su Choi, Martin F. Wojciechowski, Kelly P. Steele, Sarah G. Hunter, Tracey A. Ruhlman, Robert K. Jansen. " Born in the mitochondrion and raised in the nucleus: evolution of a novel tandem repeat family in (Fabaceae) ", The Plant Journal, 2022

Publication

1 %

6

Yan - Kuo Sun, Yong - Jie Chen, Yu Cai, Qi Li et al. "Insights into the evolutionary history and epidemiological characteristics of the emerging lineage 1 porcine reproductive and respiratory syndrome viruses in China", Transboundary and Emerging Diseases, 2020

Publication

1 %

7

Ray Keren, Raphaël Méheust, Joanne M. Santini, Alex Thomas, Jacob West-Roberts, Jillian F. Banfield, Lisa Alvarez-Cohen. "Global genomic analysis of microbial biotransformation of arsenic highlights the importance of arsenic methylation in environmental and human microbiomes", Computational and Structural Biotechnology Journal, 2022

Publication

1 %

8

Keun-Yong Kim, In-Chul Bang. "Phylogeny and speciation time estimation of two Koreocobitis species (Teleostei; Cypriniformes; Cobitidae) endemic to Korea inferred from their complete mitogenomic sequences", Genes & Genomics, 2012

Publication

1 %

Exclude quotes On

Exclude matches Off

Exclude bibliography On

Mitochondrial korean species 2021

GRADEMARK REPORT

FINAL GRADE

/100

GENERAL COMMENTS

Instructor

PAGE 1

PAGE 2

PAGE 3
