Littlemouth flounder (*Pseudopleuronectes herzensteini*; Jordan & Snyder 1901) is an economically important cold-water fish, belonging to *Pleuronectiformes* (family *Pleuronectidae*). *P. herzensteini* inhabits in East Sea of Korea, Northwest Pacific, Yellow Sea, inland Sea of Japan, and Kuril Islands (FishBase 2021). In South Korea, the annual catch has increased since 1990s (KOSIS 2021). Previous reports on *P. herzensteini* have mainly focused on ecological characteristics (Takahashi et al. 1995; Han and Kim 1999; Lee et al. 2006; Shimoda et al. 2006; Kobayashi et al. 2015) and the studies on genetic information have scarcely been reported. Thus, here we focused on the complete mitochondrial DNA (mtDNA) sequence of *P. herzensteini* and identified gene distribution, gene sequences, transfer RNA (tRNA) information, and phylogenetic relationships. This is the first study reporting the complete mitochondrial genome sequence of *P. herzensteini*.

The complete mitochondrial genome of *Pseudopleuronectes herzensteini* is 16,719 bp long and contains 13 mitochondrial protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and a putative control region between tRNA-P and tRNA-F distinguished by a single short noncoding region. Phylogenetic analysis using PCGs confirmed that this mtDNA sequence belongs to the family *Pleuronectidae*. This is the first study reporting the complete mitochondrial genome sequence of *P. herzensteini*.
tRNA-C, tRNA-Y, tRNA-S2, tRNA-E, and tRNA-P), other 15 tRNA genes were encoded on the positive strand. The D-arm loop structure in the tRNA-C and tRNA-S1 was not observed; however, the rest tRNAs retained the standard cloverleaf structure in the predicted secondary structure.

Small rRNA with a 949 bp length was located in between tRNA-F and tRNA-V, whereas large rRNA was located in between tRNA-V and tRNA-L2 and had a length of 1716 bp. The putative control region was 1016 bp long and located in between tRNA-P and tRNA-F. The gene order was accorded with P. yokohamae (Zheng et al. 2016).

Several nucleotide sequences of PCGs from other related species, divided by family level for comparison with P. herzensteini, were collected from NCBI and Acipenseridae was utilized as an out-group. The phylogenetic tree was constructed using the MEGA 11 software (Tamura et al. 2021). The P. herzensteini was classified with P. yokohamae belonging to Pleuronectidae (Figure 1). Furthermore, P. herzensteini was gathered with Pleuronectidae not Paralichthyidae and Bothidae. The results of the present study evidence that the flounder analyzed in this study belongs to P. herzensteini.

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Author contributions
Jun Young Chae, Moo-Sang Kim, and Hyung-Ho Lee conceived the original idea. Jun Young Chae carried out the experiments. Jun Young Chae wrote the manuscript with support by Moo-Sang Kim and Hyung-Ho Lee. Tae-Wook Kang and JinHo Kim performed data analysis, and Dong-Gyun Kim provided specimen. All authors agree to be accountable for all aspects of the work.

Disclosure statement
The authors report no conflict of interest.

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Data availability statement
The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov/ under the accession no. ON127848. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA821835, SRR18558256, and SAMN27124384, respectively.

References
Bernt M, Braband A, Schierwater B, Stadler PF. 2013. Genetic aspects of mitochondrial genome evolution. Mol Phylogenet Evol. 69(2):328–338.
Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319.
FishBase. 2021. Fish information. https://www.fishbase.de/Summary/SpeciesSummary.php?ID=8556&AT=littlemouth+flounder
Han KH, Kim YU. 1999. Eggs development and morphology of larvae of the flounder, Limanda herzensteini. Korean J Ichthyol. 11(1):86–93.
Johnson M, Zaretskaya I, Raytselis I, Merezhuk Y, McGinnis S, Madden TL. 2008. NCBI BLAST: a better web interface. Nucleic Acids Res. 36(Web Server issue):W5–W9.
Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12):1647–1649.
Kobayashi Y, Takatsu T, Yamaguchi H, Joh M. 2015. Comparisons of diet and nutritional conditions in Pseudopleuronectes herzensteini juveniles between two nursery grounds off northern Hokkaido, Japan. Fish Sci. 81(3):463–472.
[KOSIS] Korean Statistical Information Service. 2021. Fishery production survey. www.Kosis.kr.
Lee SI, Park KY, Kim YS, Park HW, Yand JH, Choi SH. 2006. Age and growth of brown sole Pleuronectes herzensteini (Jordan et Snyder) in the East Sea of Korea. Korean J Ichthyol. 18(4):355–362.
Shimoda K, Itaya K, Murooka M, Hoshino N. 2006. Features and cohort analysis of brown sole Pleuronectes herzensteini population in northern Hokkaido, Japan. Sci Rep Hokkaido Fish Res Inst. 71:43–54.
Takahashi T, Hayakawa Y, Kamiharako T, Nakatani T, Takatsu T. 1995. Age and growth of brown sole Pleuronectes herzensteini in the coastal waters of western Aomori Prefecture, Japan. Fish Sci. 61(6):893–897.
Tamura K, Stecher G, Kumar S. 2021. MEGA11: molecular evolutionary genetics analysis version 11. Mol Biol Evol. 38(7):3022–3027.
Ward RD, Zemlak TS, Innes BH, Last PR, Hebert PD. 2005. DNA barcoding Australia’s fish species. Philos Trans R Soc Lond B Biol Sci. 360(1462):1847–1857.
Zheng F, Liu H, Zhang Y, Wang Q, Wang B. 2016. Complete mitochondrial genome of the Pseudopleuronectes yokohamae (Pleuronectiformes: Pleuronectidae). Mitochondrial DNA A DNA Mapp Seq Anal. 27(6):4347–4348.