

Analysis of Complete Mitochondrial Genomes of Three *Gadus chalcogrammus* Specimens (Teleostei; Gadiformes; Gadidae) from Korea and Japan

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Received : March 23, 2022

Revised : March 29, 2022

Accepted : April 12, 2022

Mitochondrial genomes of three specimens of *Gadus chalcogrammus* Pallas 1,814 from Korea and Japan were completely analyzed by the primer walking method. They were 16,570~16,571 bp in length, each comprising 13 protein-coding genes, two ribosomal RNA genes, and 22 transfer RNA genes. Their gene orders were identical to those of conspecific specimens, but exhibited unique haplotypes. In the phylogenetic tree, the juvenile Korean and adult Japanese specimens were separated from the dominant clade composed of specimens from Japan, Korea, the Bering Sea, and the Arctic, including the adult Korean specimen.

Keywords: *Gadus chalcogrammus*, Japan, Korea, Mitochondrial genome, Phylogeny

The walleye pollock, *Gadus chalcogrammus* Pallas 1,814 (Teleostei; Gadiformes; Gadidae) is a demersal fish widely distributed in the North Pacific Ocean (Froese and Pauly, 2019). The species lives between depths of 50~500 m and forms an intermediate key component of the marine food web as both a predator and prey items (Funamoto, 2018). Although its population has dramatically declined in the last two decades, uncertainty in its genetic information limits our understanding of its population structure.

Three specimens of *G. chalcogrammus* from Korea, of different ages (juvenile and adult), and Japan (adult) were collected at Goesong in Korea (from 38°18'00"N, 128°35'00"E) and Otobe in Japan (41°57'44"N, 139°50'47"E). The voucher specimens were deposited at the aquatic animal collection of the Department of Marine Bioscience, Gangneung-Wonju National University (Gangneung, South Korea) under voucher numbers, KGB01, KGC01, and JO01. Genomic DNA was extracted from fin tissues according

to Asahida et al. (1996) and deposited at the aquatic animal collection of the Department of Marine Bioscience. Their meta-genomes were amplified through two independent and overlapping PCR runs, and the PCR products were directly sequenced using a set of 39~41 primers. The sequence data that support the findings of this study are openly available in GenBank (<https://www.ncbi.nlm.nih.gov/>) under the accession numbers MW288641-MW288643.

All complete mitogenome sequences of 27 specimens of *G. chalcogrammus* were retrieved from GenBank. They were aligned and refined manually to correct obvious misalignments. The nucleotide matrix of 13 protein-coding genes (PCGs) (11,410 bp), two ribosomal RNA (rRNA) genes (2,623 bp), and 22 transfer RNA (tRNA) genes (1,536 bp) excluding non-coding regions were used to reconstruct a phylogenetic tree with MEGA7 (Kumar et al., 2016) for maximum likelihood (ML) analysis. Tree support was evaluated

by bootstrapping (1,000 replications).

The three complete mitogenomes of *G. chalcogrammus* in this study were circular molecules of 16,570~16,571 bp in length, consisting of 13 PCGs, two rRNA genes, and 22 tRNA genes. Their gene orders were identical not only to conspecific specimens (Yanagimoto et al., 2004; Sim et al., 2018) but also to those of typical vertebrates. They exhibited unique haplotypes by showing genetic distance of 0.0008-0.0048 among all *G. chalcogrammus* available in GenBank across all mitogenome sequences.

In the ML tree, *Gadus* species formed a strongly supported monophyletic group, and the three specimens from Korea and Japan formed a monophyletic group with conspecific specimens in GenBank (Fig. 1). Within the *G. chalcogrammus* lineage, the juvenile Korean (KGB01) and adult Japanese (JN01) specimens formed a distinct clade with one of conspecific specimens in GenBank and separated from the dominant clade composed of specimens from Japan, Korea, and the Bering Sea, and the Arctic, including the adult Korean specimen (KGC01). The mitogenome

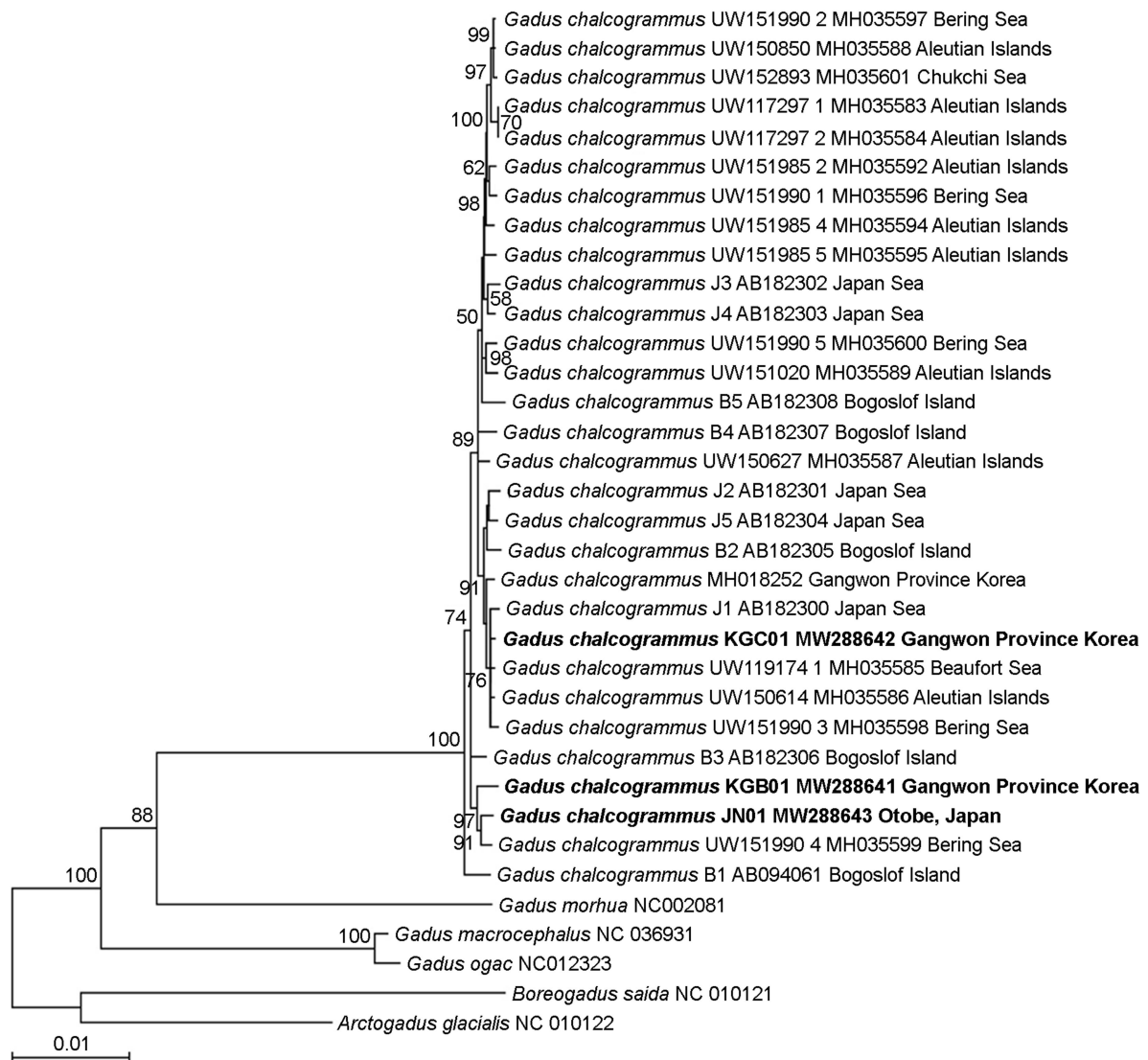


Fig. 1. Bayesian inference of phylogeny based on complete mitochondrial genomes from the species belonging to the genus Gauds (Teleostei; Gadiformes; Gadidae). The matrix included the three codon positions of the 12 protein-coding genes and two ribosomal RNA and 22 transfer RNA genes. Posterior probability value above 0.90 is indicated at each node. The three specimens of *Gadus chalcogrammus* analyzed in this study were shown in bold.

information in this study will provide baseline data for population structure, effective management, and recovery plan of a valuable fisheries resource, *G. chalcogrammus*.

Acknowledgements

This work was supported from the project 'Walleye pollock stock management based on marine information and communication technology'; 'Long-term change of structure and function in marine ecosystems of Korea' funded by the Ministry of Oceans and Fisheries; 'the Marine Biotechnology Program [20170488]' funded by the Ministry of Oceans and Fisheries, Korea; and supported by grants from the National Marine.

National Marine Biodiversity Institute of Korea [2022M00400]. We are grateful to professor Yasunori Sakurai and Jun Yamamoto who is professor in Hokkaido University for valuable comment and providing Walleye pollock samples.

Competing Interests

The authors declare no conflicts of interest.

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