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Evgeniy S. Balakirev, N. S. Romanov & Francisco J. Ayala

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Complete mitochondrial genome of the yellow-spotted grayling *Thymallus flavomaculatus* (Salmoniformes, Salmonidae)*

Evgeniy S. Balakirev, N. S. Romanov and Francisco J. Ayala

A. V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch, Russian Academy of Science, Vladivostok, Russia; Far Eastern Federal University, Vladivostok, Russia

**ABSTRACT**

The complete mitochondrial genome was sequenced in two individuals of yellow-spotted grayling *Thymallus flavomaculatus*. The genome sequences are 16,659 bp in size, and the gene arrangement, composition and size are very similar to the salmonid fish genomes published previously. The low level of sequence divergence detected between the genome of *Th. flavomaculatus* and the GenBank complete mitochondrial genomes of the *Th. yaluensis* (KJ866484) and *Th. grubii* (KF649073) may likely be due to recent divergence of the species and/or historical hybridization and interspecific replacement of mtDNA.

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The yellow-spotted grayling *Thymallus flavomaculatus* Knizhin et al. (2006) had been described first form the Maksimovka river of the Japan Sea drainage (Shedko 2001), and then as a subspecies of the Amur grayling *Th. grubii* Dybowski (Knizhin et al. 2006). Bogutskaya et al. (2008) considered the yellow-spotted grayling as a separate species distributed in the lower reach of the Amur River as well as some other rivers of Sea of Japan and Sea of Okhotsk basins. Close relationships were detected between *Th. flavomaculatus* and *Th. grubii* based on two mitochondrial markers, COI and CytB (Shedko et al. 2013). However, the complete mitochondrial genome of *Th. flavomaculatus* had not yet been sequenced.

We have sequenced two complete mitochondrial (mt) genomes of yellow-spotted grayling *Th. flavomaculatus* (GenBank accession nos. KU674353 and KU674354) from the Muli River, Khabarovsk Territory, Russia (50°00’10.44"N, 139°51’24.48"E), using primers designed with the program mitoPrimer_V1 (Yang et al. 2011). The fish specimens are stored at the museum of the A. V. Zhirmunsky Institute of Marine Biology, Vladivostok, Russia (www.museumimb.ru) under accession numbers TF163 and TF165. The size of the genome is 16,659 bp and the gene arrangement, composition, and size are very similar to the salmonid fish genomes published previously. There were 17 single nucleotide and no any length differences between the TF163 and TF165 haplotypes; the total sequence divergence (*Dxy*) was 0.0010 ± 0.0002.

The comparison of mt genomes now obtained with other complete mt genomes available in GenBank for the family Salmonidae including genera Thymallus, Prosopium and Coregonus reveals a close affinity of *Th. flavomaculatus* to other *Thymallus* species (Figure 1). Low level of sequence divergence is detected between our specimens TF163 and TF165 and the complete mt genomes of the *Th. yaluensis* (*Dxy* = 0.0161 ± 0.0009) and *Th. grubii* (*Dxy* = 0.0213 ± 0.0010). The level of divergence inferred from the 12 protein-coding genes (excluding ND6) is slightly higher: *Dxy* = 0.0206 ± 0.0012 and *Dxy* = 0.0281 ± 0.0014 between our specimens and *Th. yaluensis* and *Th. grubii*, respectively. Low divergence is also detected between other Thymallus species: *Th. burejensis* and *Th. tugarinae* (*Dxy* = 0.0072 ± 0.0007), *Th. mertensi* and *Th. arcticus* (*Dxy* = 0.0092 ± 0.0007), *Th. yaluensis* and *Th. grubii* (*Dxy* = 0.0181 ± 0.0010), and between three Coregonus species.


Thus, low level of mt genome divergence is not rare for the *Thymallus* and *Coregonus* species and could be explained by recent divergence and/or hybridization and interspecific replacement of mtDNA, as it has been found for other salmonids (e.g., Bernatchez et al. 1995).

**Disclosure statement**

The funders had no role in the study design, data collection and analysis, decision to publish, or preparation of the manuscript. The authors alone are responsible for the content and writing of the paper.

The authors declare no financial interest or benefit from the direct applications of this research. The authors report that they have no conflicts of interest.

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**References**

Bernatchez L, Glémet H, Wilson CC, Danzmann R. 1995. Introgression and fixation of Arctic char (*Salvelinus alpinus*) mitochondrial genome in an allopatric population of brook trout (*Salvelinus fontinalis*). Can J Fish Aquat Sci. 52:179–185.

Bogutskaya NG, Naseka AM, Shedko SV, Vasil’eva ED, Chereshnev IA. 2008. The fishes of the Amur river: updated check-list and zoogeography. Ichthyol Explor Freshwaters. 19:301–366.

Knizhin IB, Antonov AL, Weiss SJ. 2006. A new subspecies of the Amur grayling *Thymallus grubii flavomaculatus* ssp. nova (Thymallidae). J Ichthyol. 46:555–562.

Shedko SV. 2001. A list of Cyclostomata and freshwater fish from the coast of Primorye. In: Makarchenko EA, Kholin SK, editors. Vladimir Ya. Levanidov’s Biennial Memorial Meetings, no. 1. Vladivostok: Dalnauka. p. 229–249.

Shedko SV, Miroshnichenko IL, Nemkova GA. 2013. Phylogeny of salmonids (Salmoniformes: Salmonidae) and its molecular dating: analysis of mtDNA data. Russ J Genet. 49:623–637.

Yang CH, Chang HW, Ho CH, Chou YC, Chuang LY. 2011. Conserved PCR primer set designing for closely-related species to complete mitochondrial genome sequencing using a sliding window-based PSO algorithm. PLoS One. 6:e17729.