



## Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <http://www.tandfonline.com/loi/tmdn20>

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To cite this article: Evgeniy S. Balakirev, N. S. Romanov & Francisco J. Ayala (2016) Complete mitochondrial genome of the yellow-spotted grayling *Thymallus flavomaculatus* (Salmoniformes, Salmonidae), *Mitochondrial DNA Part B*, 1:1, 318-319

To link to this article: <http://dx.doi.org/10.1080/23802359.2016.1166081>



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Published online: 19 Apr 2016.



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

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### 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.

### ARTICLE HISTORY

Received 1 March 2016  
Accepted 11 March 2016

### KEYWORDS



Amur grayling *Th. grubii*;  
*Th. yaluensis*; salmonids;  
yellow-spotted grayling  
*Thymallus flavomaculatus*

The yellow-spotted grayling *Thymallus flavomaculatus* Knizhin et al. (2006) had been described first from 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](http://www.museumimb.ru)) under accession numbers Tf163 and Tf165. The size of the

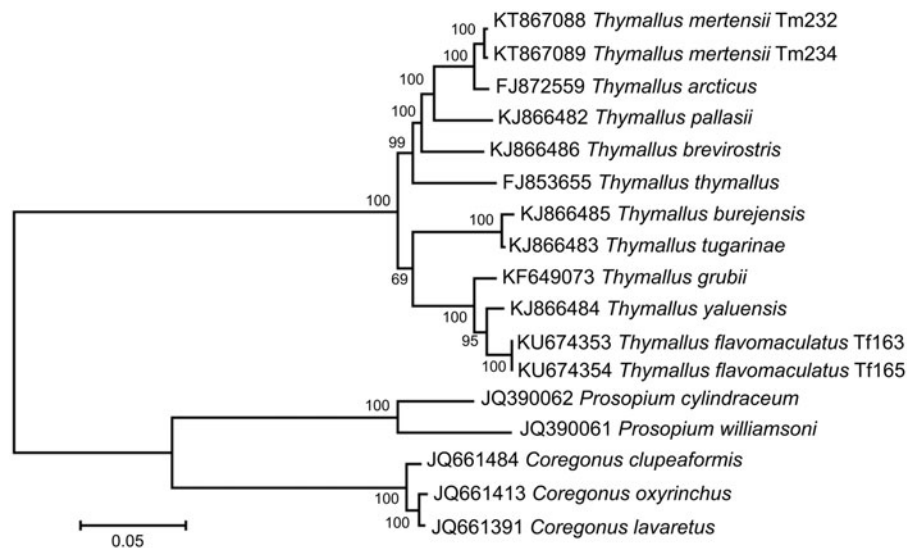
genome is 16,659 bp and the gene arrangement, composition, and size are very similar to the salmonid fish genomes published previously. There were 17 single nucleotide and no any length differences between the Tf163 and Tf165 haplotypes; the total sequence divergence ( $D_{xy}$ ) was  $0.0010 \pm 0.0002$ .

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* ( $D_{xy} = 0.0161 \pm 0.0009$ ) and *Th. grubii* ( $D_{xy} = 0.0213 \pm 0.0010$ ). The level of divergence inferred from the 12 protein-coding genes (excluding *ND6*) is slightly higher:  $D_{xy} = 0.0206 \pm 0.0012$  and  $D_{xy} = 0.0281 \pm 0.0014$  between our specimens and *Th. yaluensis* and *Th. grubii*, respectively. Low divergence is also detected between other *Thymallus* species: *Th. burejensis* and *Th. tugarinae* ( $D_{xy} = 0.0072 \pm 0.0007$ ), *Th. mertensii* and *Th. arcticus* ( $D_{xy} = 0.0092 \pm 0.0007$ ), *Th. yaluensis* and *Th. grubii* ( $D_{xy} = 0.0181 \pm 0.0010$ ), and between three *Coregonus* species

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\*The research on mitochondrial genome sequencing was conducted in the Department of Ecology and Evolutionary Biology, University of California, Irvine, USA. The data analysis was conducted at the A. V. Zhirmunsky Institute of Marine Biology, Vladivostok, Russia.

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**Figure 1.** Maximum likelihood tree for the yellow-spotted grayling *Thymallus flavomaculatus* specimens Tf163 and Tf165, and the GenBank representatives of the family Salmonidae. The tree is constructed using whole mitogenome sequences. The tree is based on the General Time Reversible + gamma + invariant sites (GTR + G + I) model of nucleotide substitution. The numbers at the nodes are bootstrap percent probability values based on 1000 replications.

( $D_{xy} = 0.0120 \pm 0.0009$ ) (Figure 1). 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.

### Funding statement

This work was supported by the Bren Professor Funds at the University of California, Irvine, USA (mitochondrial genome sequencing); and Russian Science Foundation under Grant number 14-50-00034 (data analysis).

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