

Complete mitochondrial genome of the Kamchatka grayling *Thymallus mertensii* (Salmoniformes, Salmonidae)

Evgeniy S. Balakirev^{1,2,3}, Nikolai S. Romanov², and Francisco J. Ayala¹

¹Department of Ecology and Evolutionary Biology, University of California, Irvine, 321 Steinhaus Hall, Irvine, CA, USA, ²A. V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch, Russian Academy of Science, Vladivostok, Russia, and ³Far Eastern Federal University, School of Natural Sciences, Vladivostok, Russia

Abstract

The complete mitochondrial genome was sequenced in two individuals of the Kamchatka grayling *Thymallus mertensii*. The genome sequences are 16 662 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 (0.92%) detected between the genome of *T. mertensii* and the GenBank complete mitochondrial genomes of the Arctic grayling *T. arcticus* (FJ872559) may likely be due to recent divergence of the species and/or historical hybridization and interspecific replacement of mtDNA.

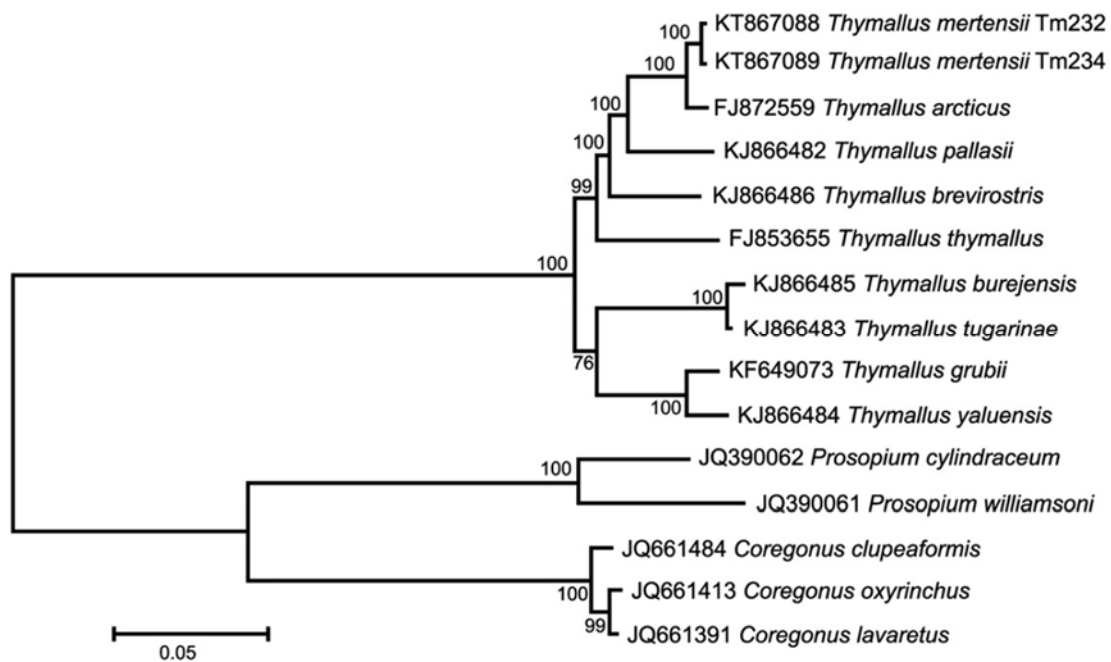


Figure 1. Maximum likelihood tree based on 12 protein-coding genes (excluding ND6) for the *Thymallus mertensii* specimens Tm232 and Tm234, and the GenBank representatives of the family Salmonidae. The tree is based on the General Time Reversible+gamma+invariant sites (GTR+G+I) model of nucleotide substitution. The numbers at the nodes are bootstrap percent probability values based on 1000 replications.

The Kamchatka grayling *T. mertensii* Valenciennes has wide distribution in freshwaters of the northeast Asia including the Kamchatka Peninsula, eastern part of the Magadan region, and up to south of the Chukchi Peninsula. The species status of the Kamchatka grayling was supported with morphological data (review in Bogutskaya & Naseka 2004). However, no genetic data are available to confirm the species identity of *T. mertensii*.

We have sequenced two complete mitochondrial (mt) genomes of *T. mertensii* (GenBank accession nos, KT867088 and KT867089) from Ozernaya River (eastern Kamchatka, Russia) to increase the power of phylogenetic analysis of this complex salmonid group, using primers designed with the program mitoPrimer_V1 (Yang et al., 2011). The size of the genome is 16 662 bp and the gene arrangement, composition, and size are very similar to the salmonid fish genomes published previously (Balakirev et al., 2015). The overall base composition was 28.2% A, 27.4% T, 17.1% G and 27.3% C. The 55.6% A+T base composition was higher than G+C, 44.4%. There were 12 single nucleotide differences between the Tm232 and Tm234 isolates; total sequence divergence (D_{xy}) was 0.0007 ± 0.0002 .

The comparison of the mt genomes now obtained with other complete mt genomes available in GenBank for the family Salmonidae, including the genera *Thymallus*, *Prosopium*, and *Coregonus* (Figure 1), reveals a close affinity of *T. mertensii* to other *Thymallus* species. There is a low level of sequence divergence ($D_{xy} = 0.0092 \pm 0.0006$) between our specimens Tm232 and Tm234 and the complete mt genome of the Arctic grayling *T. arcticus* (FJ872559) (Figure 1). The level of divergence between *T. mertensii* and *T. arcticus* inferred from the 12 protein-coding genes (excluding ND6) was higher ($D_{xy} = 0.0115 \pm 0.0010$), but still too low for considering them as separate species. Low divergence is also detected between other *Thymallus* species, *T. burejensis* and *T. tugarinae* ($D_{xy} = 0.0073 \pm 0.0008$) and three *Coregonus* species ($D_{xy} = 0.0120 \pm 0.0009$) (Figure 1). The low level of sequence divergence between *T. mertensii* and *T. arcticus* and other *Thymallus* and *Coregonus* species could be explained by recent divergence and/or hybridization and interspecific replacement of mtDNA, as it has been found for other salmonids (Balakirev et al., 2013; Bernatchez et al., 1995; Shedko et al., 2007).

Acknowledgements

The authors thank Elena Balakireva for encouragement and help.

Declaration of interest

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the paper. The work on mitochondrial genome sequencing was supported by Bren Professor Funds at the University of California Irvine to Francisco J Ayala. The analysis of the data was supported by the Russian Science Foundation (RSF; Grant No. 14-50-00034) to Evgeniy S. Balakirev.

References

- Balakirev ES, Romanov NS, Mikheev PB, Ayala FJ. (2013). Mitochondrial DNA variation and introgression in Siberian taimen *Hucho taimen*. *PLoS One* 8: e71147.
- Balakirev ES, Parensky VA, Kovalev MY, Ayala FJ. (2015). Complete mitochondrial genome of the white char *Salvelinus albus* (Salmoniformes, Salmonidae). Mitochondrial DNA. [Epub ahead of print]. doi: 10.3109/19401736.2015.1079890.
- Bernatchez L, Gle´met H, Wilson CC, Danzmann R. (1995). Introgression and fixation of Arctic charr (*Salvelinus alpinus*) mitochondrial genome in an allopatric population of brook trout (*Salvelinus fontinalis*). *Can J Fish Aquat Sci* 52:179–85.
- Bogutskaya NG, Naseka AM. (2004). Catalogue of Agnathans and fishes of fresh and brackish waters of Russia with comments on their nomenclature and taxonomy. Moscow: Izdatelstvo KMK Scientific Association Press, Ltd. p 389.
- Shedko SV, Ginatulina LK, Miroshnichenko IL, Nemkova GA. (2007). Phylogeography of mitochondrial DNA in South Asian Dolly Varden char *Salvelinus curilis* (Pallas, 1814) (Salmoniformes, Salmonidae): Mediated gene introgression? *Russ J Genet* 43:165–76.
- 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.

Correspondenc: Francisco J. Ayala, Department of Ecology and Evolutionary Biology, University of California, Irvine, 321 Steinhaus Hall, Irvine, CA 92697-2525, USA. Tel: +1 949 824 8293. Fax: +1 949 824 2474. E-mail: fjayala@uci.edu