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MITOGENOME ANNOUNCEMENT

# Complete mitochondrial genome of the white char *Salvelinus albus* (Salmoniformes, Salmonidae)

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**Abstract**

The complete mitochondrial genome was sequenced in two individuals of white char *Salvelinus albus*. The genome sequences are 16 653 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 *S. albus* and the GenBank complete mitochondrial genomes of the Northern Dolly Varden char *S. malma* (KJ746618) and the Arctic char *S. alpinus* (AF154851) may likely be due to recent divergence of the species and/or historical hybridization and interspecific replacement of mtDNA.

**Keywords**

Arctic char *S. alpinus*, complete mitochondrial genome, hybridization, mtDNA introgression, Northern Dolly Varden char *S. malma*, salmonids, white char *Salvelinus albus*

**History**

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The white char *Salvelinus albus* Glubokovsky is an endemic of the Kamchatka River, Russia (Glubokovsky, 1977). The species status of the white char was supported with morphological (Glubokovsky, 1995; Parensky et al., 2004; Romanov et al., 2011; Viktorovskii, 1978) and karyological (Frolov, 2001) data. However, genetic markers including allozymes, myogens, mitochondrial DNA, nuclear ribosomal DNA, ITS sequences, and microsatellites failed to confirm the identity of *S. albus* (review in Salmenkova & Omelchenko, 2013).

We have sequenced two complete mitochondrial (mt) genomes of *S. albus* (GenBank accession numbers KT266870 and KT266871) from the Azabachye lake creek (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 16 653 bp and the gene arrangement, composition, and size are very similar to the salmonid fish genomes published previously. The overall base composition was 28.0% for A, 26.4% for T, 17.0% for G, and 28.6% for C. The 54.4% A + T base composition was higher than G + C, 45.6%. There were no any nucleotide differences between the two isolates (SA1 and SA2) studied.

The comparison of mt genomes now obtained with other complete mt genomes available in GenBank for the family Salmonidae including genera *Salvelinus*, *Parahucho*, *Salmo*, *Hucho*, and *Brachymystax* (Figure 1) reveals a close affinity of *S. albus* to other *Salvelinus* species with a very low level of sequence divergence ($D_{xy} = 0.0020 \pm 0.0003$) between our specimens SA1 and SA2 and the complete mt genome of the Northern Dolly Varden char *S. malma* (KJ746618; Balakirev et al., 2014) (Figure 1). The divergence was higher ($D_{xy} = 0.0079 \pm 0.0006$) between *S. albus* and *S. alpinus* (AF154851; Doiron et al., 2002), but still too low for considering them as separate species. The low level of sequence divergence among *S. albus*, *S. malma*, and *S. alpinus* could be explained by recent divergence and/or historical hybridization and interspecific replacement of mtDNA, as it has been found for other char species (e.g., Bernatchez et al. 1995; Shedko et al. 2007).

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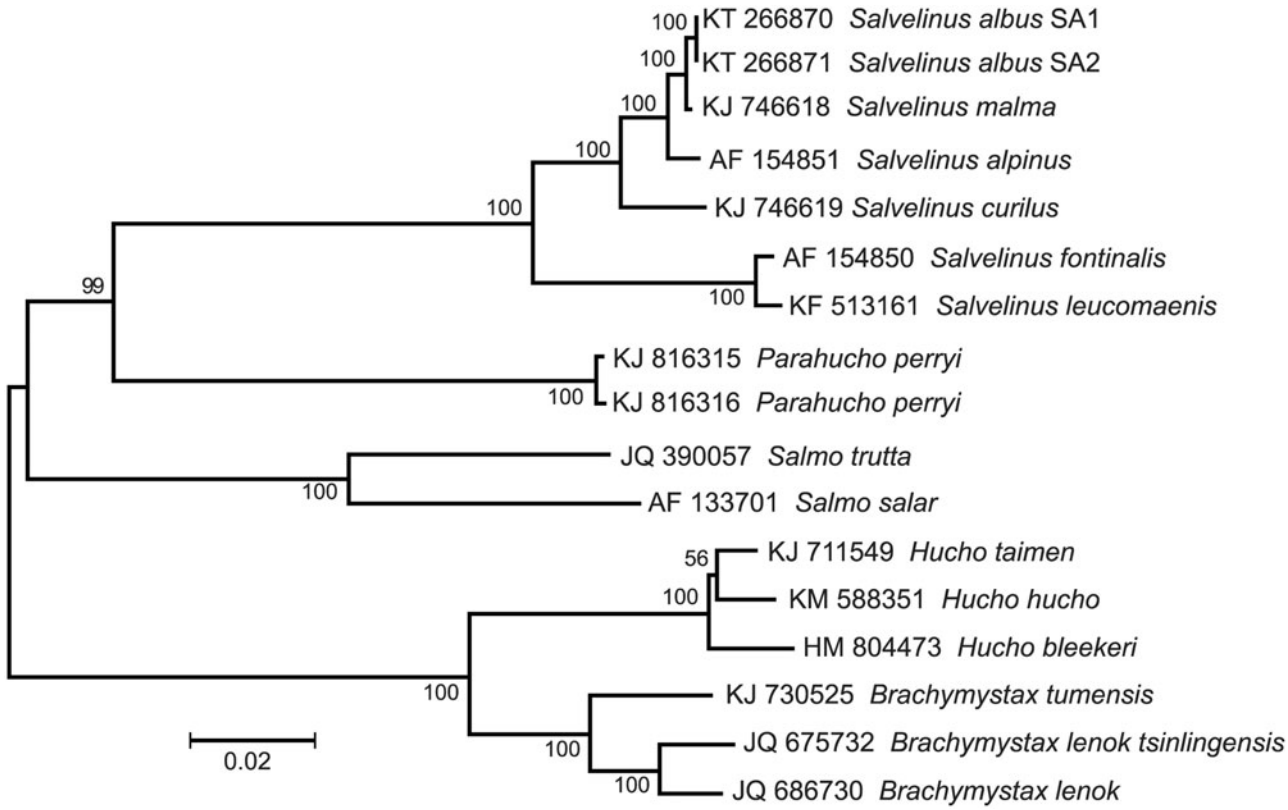


Figure 1. Maximum likelihood tree based on 12 protein-coding genes (11 026 bp) for the *Salvelinus albus* specimens SA1 and SA2, and the GenBank representatives of the family Salmonidae. The tree is based on the General Time Reversible + gamma + invariant sites (GTR + G+I) model of nucleotide substitution. The numbers at the nodes are bootstrap percent probability values based on 1000 replications.

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## Declaration of interest

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

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