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MITOGENOME ANNOUNCEMENT

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Complete mitochondrial genome of the stone char *Salvelinus kuznetzovi* (Salmoniformes, Salmonidae)*

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ABSTRACT

The complete mitochondrial genome was sequenced in two individuals of stone char *Salvelinus kuznetzovi*. The genome sequences are 16,654 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. kuznetzovi* and the GenBank complete mitochondrial genomes of the white char *S. albus* (KT266870 and KT266871), the Northern Dolly Varden char *S. malma* (KJ746618) and the Arctic char *S. alpinus* (AF154851) may likely be due to recent divergence and/or historical hybridization and interspecific replacement of mtDNA.

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Arctic char *S. alpinus*; Northern Dolly Varden char *S. malma*; salmonids; stone char *Salvelinus kuznetzovi*; white char S. albus

The stone char *Salvelinus kuznetzovi* (Taranetz 1933) is an endemic of the Kamchatka River with uncertain taxonomic status. Savvaitova and Maksimov (1970) included *S. kuznetzovi* in the *S. alpinus complex*. Glubokovsky (1995) based on morphological data suggested that *S. kuznetzivi* represents a resident form of the white char *S. albus*. However, Sheiko and Fedorov (2000) as well as Bogutskaya and Naseka (2004) considered the stone char as a separate species. No genetic data are available to confirm the species identity of *S. kuznetzovi*.

We have sequenced two complete mitochondrial (mt) genomes of *S. kuznetzovi* (GenBank accession nos. KU674351 and KU674352) from the Azabachye lake creek, Kamchatka, Russia (56°08′30″N, 161°48′00″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 nos. SK1 and SK2. The size of the genome is 16,654 bp and the gene arrangement, composition and size are very similar to the salmonid fish genomes published previously. There were four single nucleotides and no any length differences between the haplotypes SK1 and SK2; the total sequence divergence (D_{xy}) was 0.0002 ± 0.0001.

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* reveals a close affinity of *S. kuznetzovi* to other *Salvelinus* species (Figure 1) with a very low level of sequence divergence between our specimens (SK1 and SK2) and the complete mt genome of the white char *S. albus* ($D_{xy} = 0.0010 \pm 0.0003$; Balakirev et al. 2015) and the Northern Dolly Varden char *S. malma* ($D_{xy} = 0.0023 \pm 0.0003$; Balakirev et al. 2016). The divergence was higher ($D_{xy} = 0.0079 \pm 0.0006$) between *S. kuznetzovi* and *S. alpinus* ($D_{xy} = 0.0090 \pm 0.0010$; Doiron et al. 2002), but still too low for considering them as separate species. The low level of sequence divergence among *S. kuznetzovi*, *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).

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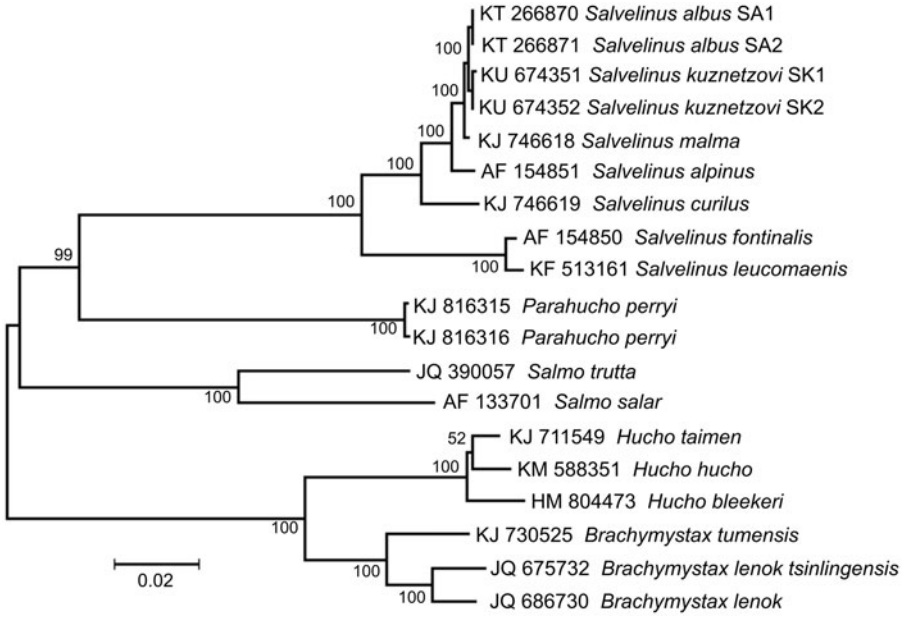

Figure 1. Maximum likelihood tree for the stone char *Salvelinus kuznetzovi* specimens SK1 and SK2, and the GenBank representatives of the family Salmonidae. The tree is constructed using whole mitogenome sequences. The tree is based on the General Time Reversible + gamma + invariant sites (GTR + G + I) model of nucleotide substitution. The numbers at the nodes are bootstrap percent probability values based on 1000 replications.

Disclosure statement

The funders had no role in 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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