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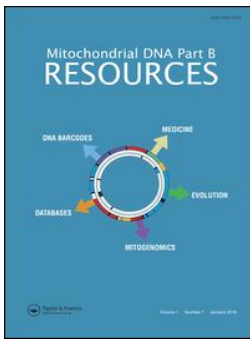
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## Complete mitochondrial genome of the Amur sculpin *Cottus szanaga* (Cottoidei: Cottidae)\*

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### ABSTRACT

The complete mitochondrial genome was sequenced in two individuals of the Amur sculpin *Cottus szanaga*. The genome sequences are 16,518 bp in size, and the gene arrangement, composition, and size are very similar to the other sculpin genomes published previously. The low level of sequence divergence detected between the genome of *C. szanaga* and the GenBank complete mitochondrial genome of the Cherskii's sculpin *Cottus czerskii* (KJ956027) may likely be due to recent divergence, historical hybridization, or presence of a new unrecognized taxonomic unit close to *C. szanaga* but erroneously identified as *C. czerskii*.

### ARTICLE HISTORY

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### KEYWORDS

Amur sculpin *Cottus szanaga*; Cherskii's sculpin *Cottus czerskii*; cottidae

The Amur sculpin *Cottus szanaga* Dybowski 1869 is a freshwater fish with wide distribution along the Amur River, as well as in some other rivers of the Sea of Japan and the Sea of Okhotsk basins, and north Sakhalin Island. Berg (1949) considered *C. szanaga* as a synonym of the spotted sculpin *C. poecilopus* Heckel. Later, based on morphological data, the validity of *C. szanaga* was proved (Shedko & Shedko 2003; Sideleva & Goto 2009). There are, however, no genetic data to confirm the species identity of *C. szanaga* or its relationship with other species belonging to the genus *Cottus*.

We have sequenced two complete mitochondrial (mt) genomes of *C. szanaga* (GenBank accession numbers KX762049 and KX762050) from the Sobolevka River (46° 27' 456 N, 137° 81' 247 E) and the Amgu River (45° 89' 100 N, 137° 25' 618 E), Primorsky krai, Russia, using primers designed with the program mitoPrimer\_V1 (Yang et al. 2011). The specimens are stored in the museum of the A. V. Zhirmunsky Institute of Marine Biology, Vladivostok, Russia ([www.museumimb.ru](http://www.museumimb.ru)) under accession numbers MIMB 33123 and MIMB 33124. The size of the genome is 16,518 bp and the gene arrangement, composition and size are very similar to the sculpin fish genomes published previously. There were 27 single nucleotides but no length differences between the haplotypes CSZID2 and CSZIF3; total sequence divergence ( $D_{xy}$ ) was  $0.0016 \pm 0.0003$ .

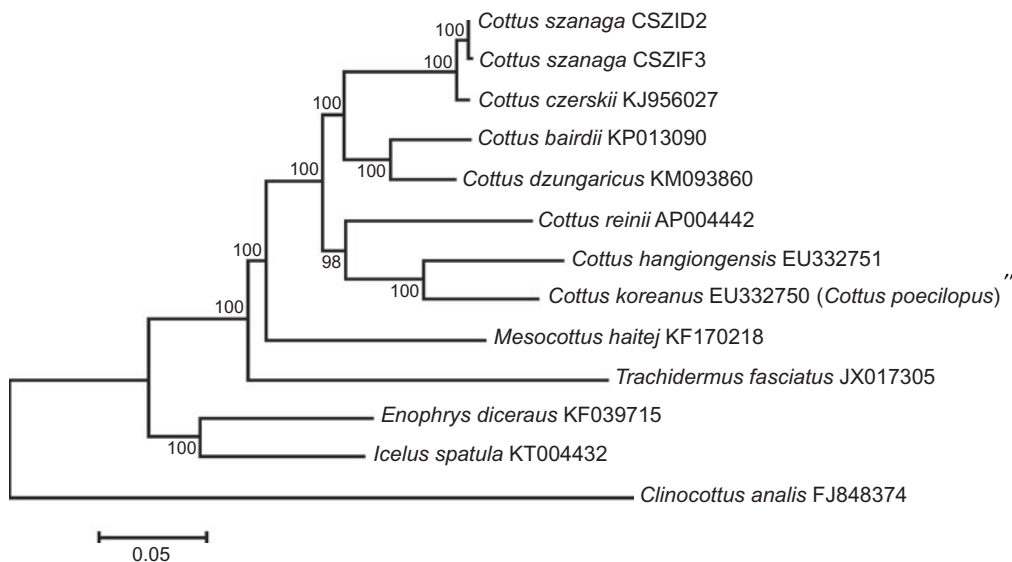
Comparison of the mt genomes now obtained with other complete mt genomes available in GenBank for the family Cottidae, including the genera *Cottus*, *Mesocottus*, *Trachidermus*, *Enophrys*, *Icelus* and *Clinocottus* reveal a close affinity of *C. szanaga* to other *Cottus* species (Figure 1) with a low level of sequence divergence between our specimens and the complete mitochondrial genome of Cherskii's sculpin *Cottus czerskii* ( $D_{xy} = 0.0135 \pm 0.0008$ ; Han et al. 2016). The average level of mt genome divergence ( $D_{xy}$ ) between six species within the genus *Cottus* (Figure 1) is  $0.0977 \pm 0.0015$ , which is significantly higher than the level of divergence between *C. szanaga* and *C. czerskii*. This discrepancy could suggest that *C. szanaga* and *C. czerskii* are not distinct biological species. There are however 223 single nucleotide and four indel differences between the *C. szanaga* and *C. czerskii* genomes, including a 17-bp insertion (CCCTTCGCCTCCCCCCC) located within the non-coding region at coordinates 7170–7186 (between tRNA-Asp and COX2). Interestingly, the same insertion is present in the mt genome of *C. hangiongensis* (EU332751; Figure 1), which makes it difficult to explain these differences by either sequencing mistakes and/or intraspecific variability. The low level of sequence divergence between *C. szanaga* and *C. czerskii* could be explained by recent divergence or historical hybridization, as has been found in other fishes including

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

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**Figure 1.** Maximum likelihood tree for the Amur sculpin *Cottus szanaga* specimens CSZID2 and CSZIF3, and GenBank representatives of the family Cottidae. The tree is constructed using whole mitogenome sequences and 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 GenBank species name for the accession number EU332750 is in parentheses.

sculpins (Baumsteiger et al. 2014); or due to the presence of a new unrecognized taxonomical unit close to *C. szanaga*, erroneously identified as *C. czerskii*. Obviously, more data from the nuclear genomes are necessary to draw a definite picture of the composition and relationship between the sculpins in eastern Asia.

### Disclosure statement

The funders had no role in the study's 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 that they have no financial interest or benefit from the direct applications of this research. The authors report that they have no conflict of interest.

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