The Taranetz charr *Salvelinus taranetzi* was described by Kaganovsky (1955) from Lake Achchen in the Chukotka Peninsula, Russia. Originally described as a separate species, it was subsequently synonymized with Arctic charr *Salvelinus alpinus* taranetzi (Behnke 1984). However, Glubokovsky and Chereshnev (Glubokovsky and Chereshnev 1981; Chereshnev 1982) pointed out that *S. taranetzi* is different from *S. alpinus* and may be regarded as a separate species. However, there is still a lack of molecular data to prove this opinion (Oleinik et al. 2017). Most of the previous studies of *S. taranetzi* along with other charr are restricted to an analysis of only short fragments of few mitochondrial and nuclear genes (e.g. Osinov et al. 2017, and references therein).

We sequenced and described two complete mitochondrial genomes of *S. taranetzi* for the first time in this study, for further study and more precise phylogenetic analysis. Specimens of Taranetz charr were collected from Lake Achchen, Chukchi Peninsula (64°50′ N, 174°36′ W), and Lake Pekulineiskoe, Chukchi Peninsula (62°33′ N, 177°17′ E); one specimen was collected from the type locality. The fish specimens are stored in the collection of the Genetics Laboratory, National Scientific Center of Marine Biology FEB RAS, Vladivostok, Russia (www.imb.dvo.ru). Totally 5 pairs of primers were used (sequences are available upon request), which were designed based on public sequences available in GenBank for salmonid fishes. The sequenced fragments were de novo assembled into complete mitochondrial genome and annotated by comparing with published genome sequences of charr using Geneious R11 (http://www.geneious.com/).

The complete mitochondrial genome of *S. taranetzi* was 16,654 bp in length (GenBank accession numbers MK695630 and MK695631). The genome organization was identical to that of typical salmon mitochondrial genomes. Similar to *Salvelinus alpinus*, the overall base composition was 28.0% of A, 26.4% of T, 28.6% of C, and 17.0% of G with a slight A+T bias (54.5%). We detected 18 single-nucleotide and no length differences between the sequences MK695630 and MK695631; two substitutions were detected in the control region and 12S rRNA, other single-nucleotide substitutions were found in overall protein-coding sequences. The proportion of variable sites was highest for the NADH dehydrogenase subunit genes (55.6%). Total sequence divergence (*Dxy*) was 0.0011 ± 0.0002.

The comparison of mitochondrial genomes now obtained with mitochondrial genomes of related groups available in GenBank including genera *Salvelinus* (AF154851, KF974451, KJ746618, KJ746619, KT266870, KT266871, KU674351, KU674352, NC000860, NC036392, and NC037502), *Salmo* (AF1133701, and AM910409), and *Parahucho* (KJ816315, and KJ816316) pointed to the independent taxonomic status of *S. taranetzi* within the genus *Salvelinus* (Figure 1). The level of divergence (*Dxy*) between *S. taranetzi* and taxa within the phylogenetic group was in the range from 0.0095 ± 0.0006 to 0.0442 ± 0.0019. *Salvelinus taranetzi* specimens showed similar sequence divergence (0.0103 ± 0.0007 on average) from *S. malma malma*, *S. malma kuznetzovi*, *S. albus*, and *S. alpinus*. These values corresponded to the level of intraspecific
variability in the genus, and all charr taxa showed similar phylogenetic relationships to those found by Oleinik et al. (2015).

Disclosure statement

No potential conflict of interest was reported by the authors. The research on mitochondrial genome sequencing was conducted at the School of Natural Sciences, Far Eastern Federal University, Vladivostok, Russia. The data analysis and manuscript preparation were conducted at the National Scientific Center of Marine Biology, Vladivostok, Russia.

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