In animal evolution, hybridization is a useful means of inducing genetic and epigenetic alterations leading to increased diversity and speciation (Barton 2001). Animal mitochondrial DNA (mtDNA) is almost exclusively inherited from the mother (White et al. 2008); however, Luo et al. said they found mtDNA parental inheritance in three families (Luo et al. 2018). There is no report of the complete genome of this hybrid fish Salvelinus fontinalis (♀) × Salvelinus malma sp. (♂) was sequenced. It was 16,623-nucleotide in length and consisted of 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes, and 2 non-coding regions (L-strand replication origin and control region), showing conserved gene arrangement with most vertebrates. The phylogenetic tree showed the hybrid salmon to be one of the Salvelinus and the relationships of S. fontinalis were closer. The complete mitochondrial genome sequence of S. fontinalis (♀) × S. malma sp. (♂) provided an important dataset for a better understanding of the mitogenomic diversities and evolution in salmon fish as well as novel genetic markers for studying population genetics and species identification.

The complete mitogenome of the hybrid fish S. fontinalis (♀) × S. malma sp. (♂) was 16,623 bp in length. The genomic organization was identical to those of typical vertebrate mitochondrial genomes, including 2 rRNA genes, 13 protein-coding genes, 22 tRNA genes, a light-strand replication origin (OL), and a putative control region (CR). The overall base composition was 28.3% of A, 28.4% of T, 26.5% of G, and 16.8% of C, and 16.8% of G with a slight A + T bias (54.8%) like other vertebrate mitochondrial genomes. The features mentioned above were accordant with typical Salvelinus fish mitogenome.

For the 13 protein-coding genes, 12 genes started with ATG while only COI started with GTG. Five genes shared the termination codon TAA (COI, ATPase8, ND1, NDS, and ND4L), one with TAG (ND6), the remaining with incomplete stop codon (COII, COIII, ND2, ND3, ND4, ATPase6, and Cytb). This feature was common among vertebrate mitochondrial protein-coding genes. Salvelinus fontinalis (♀) × S. malma sp. (♂) had two non-coding regions, the L-strand replication origin region (36 bp) was located between tRNA-Asn and tRNA-Cys, and the control region (962 bp) located within the tRNA-Pro and tRNA-Phe. Eight tRNA (tRNA-Ser, tRNA-Pro, tRNA-Glu, tRNA-Tyr, tRNA-Cys, tRNA-Asn, tRNA-Ala, and tRNA-Gln) and the ND6 gene were encoded on the L-strand, the others were encoded on the H-strand. This feature is similar to other fish mitochondrial genes. The complete mitogenome sequence had 16s RNA (1678 bp) and 12s RNA (946 bp), which were located between tRNA-Phe and tRNA-Leu and separated by tRNA-Val gene. The location is same with most vertebrates that have high conservation.
To determine the taxonomic status of the hybrid salmon, we reconstructed the phylogeny of this salmon stock with other natural populations in salmon based on the entire mitogenome sequences. The phylogenetic tree showed the hybrid salmon to be one of the *Salvelinus* and the closer relationship with *S. fontinalis* other than *S. malma* sp. (Figure 1). The phylogeny was reconstructed based on the General Time Reversible + gamma sites (GTR + G) model of nucleotide substitution using Mega7 (Kumar et al. 2016). The complete mitochondrial genome sequence of the *S. fontinalis* (♂) × *S. malma* sp. (♀) hybrid provided an important dataset for a better understanding of the mitogenomic diversities and evolution in salmon fish as well as novel genetic markers for studying population genetics and species identification.

![Figure 1](image)

**Figure 1.** Maximum likelihood tree for the *S. fontinalis* (♂) *S. malma* sp. (♀), 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 sites (GTR + G) model of nucleotide substitution. The numbers at the nodes are bootstrap percent probability values based on 1000 replications.

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