

Complete mitochondrial genome of *Oncorhynchus masou formosanus* (Jordan & Oshima, 1919) (Pisces, Salmonidae)

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ABSTRACT

We describe the complete mitochondrial genome sequence of *Oncorhynchus masou formosanus*, which is a critically endangered landlocked salmon of Taiwan by using next-generation sequencing. The circle genome (16,653 bp) has the typical vertebrate mitochondrial gene arrangement, consisting of 13 protein-coding genes, 22 tRNA genes, two rRNA genes and a non-coding control region. The overall base composition of *O. m. formosanus* is 28.6% for A, 26.8% for T, 16.5% for G and 28.1% for C, with a slight AT bias of 55.4%.

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The landlocked salmon of Taiwan, *Oncorhynchus masou formosanus* (Jordan & Oshima 1919), was listed as Critically Endangered by the IUCN in 1996 (Kottelat 1996), which only distributed in the upstream of Dajia River (Hsu et al. 2010). The total number of *O. m. formosanus* has increased from 200 to around 3000 through the efforts of repopulation and habitat recovery (Chung et al. 2008). Since the species status of *O. m. formosanus* is conflict (Numachi et al. 1990; Gwo et al. 2008) and the characteristics of landlocked and southernmost distribution of salmonids has been considered, mitochondrial genome may provide additional reference to not only conservation issue, but also taxonomy and phylogeography study.

Here, we determined the complete mitochondrial genome sequence with all genes annotated of *O. m. formosanus* that was deposited in GenBank with accession number KU523579. The two specimens of *O. m. formosanus* were used in this study, one was from wild environment and another was cultivated individual of Hatchery and Conservation Center of Formosa Salmon, Shei-Pa National Park. The number of collection licenses is 103020–103033. The mtDNAs were extracted and prepared according to manufacturer's instructions of Illumina MiSeq platform (Illumina Inc., San Diego, CA). The paired-end sequencing reads (250 bases) of mitochondrial genome were assembled by CLC Genomics Workbench version 5.5.1 (CLC-bio, Aarhus, Denmark). The annotation of protein-coding genes and rRNA genes were determined by online software MitoAnnotator (Iwasaki et al. 2013). To elucidate the phylogenetic relationship between *O. m. formosanus* and other closely related species, 16 mitochondrial genomes were used for phylogenetic analysis. The complete mitochondrial genome sequences of 15 other species are downloaded

from GenBank and the names and GenBank accession numbers of these species are as follows: *O. mykiss* (NC_001717), *O. tshawytscha* (NC_002980), *O. clarkia henshawi* (NC_006897), *O. nerka* (NC_008615), *O. masou ishikawae* (NC_008746), *O. masou masou* (NC_008747), *O. masou Biwa* (NC_009262), *O. kisutch* (NC_009263), *Salmo trutta trutta* (NC_010007), *O. gorbusha* (NC_010959), *O. keta* (NC_017838), *Brachymystax lenok* (NC_018341), *B. lenok tsinlingensis* (NC_018342), *S. trutta* (NC_024032) and *O. mykiss* x *S. salar* (NC_026537).

The complete mitochondrial genomes of these two specimens were identical (16,653 bp in length) which consists of 13 protein-coding genes, 22 tRNA genes, two rRNA genes and one control region (CR). The arrangement of all genes was identical to that of other Cypriniformes (Yang et al. 2013). Most of the genes are encoded on the heavy strand (H-strand), except for the eight tRNA genes (tRNA-Gln, –Ala, –Asn, –Cys, –Tyr, –Ser, –Glu and –Pro) and one protein-coding gene (ND6). Its overall base composition is 28.6% for A, 26.8% for T, 16.5% for G and 28.1% for C, with relatively lower of GC and AT bias of 55.4%.

Multiple alignments of 16 mitochondrial genomes were performed using CLC Genomics Workbench with progressive alignment algorithm (Feng & Doolittle 1987). The phylogenetic tree from maximum-likelihood was reconstructed using MEGA6 (Tamura et al. 2013) (Figure 1). To obtain the confident supports, one thousand bootstrap replicates were set for the analysis. Phylogenetic analysis showed that *O. m. formosanus* shared the same cluster with other *O. masou* subspecies. *Oncorhynchus m. formosanus* may diverge earlier than *O. masou ishikawae* and *O. masou masou* but later than *O. masou Biwa*. We expect that the present result will help to elucidate

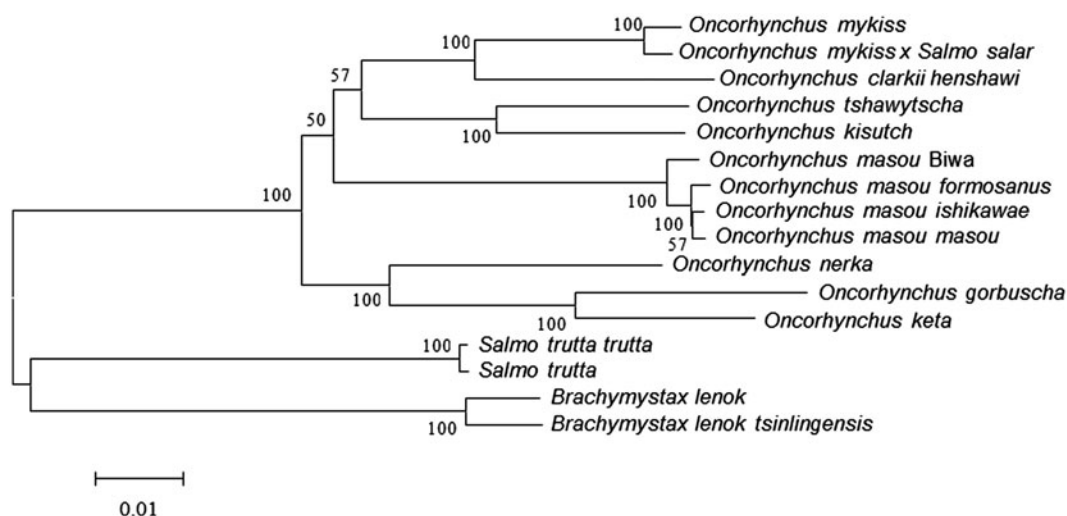


Figure 1. Phylogeny based on the complete mitochondrial genomes by MEGA6 with 1000 bootstrap replications. The maximum-likelihood tree is drawn to scale.

the taxonomic status of *O. m. formosanus* and contribute to the conservation.

Disclosure statement

The authors declare no competing interests in the preparation and execution of this manuscript. The authors are solely responsible for its content.

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