



Mitochondrial DNA Part B Resources

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Complete mitochondrial genomes of Baikal oilfishes (Perciformes: Cottoidei), earth's deepest-swimming freshwater fishes

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ABSTRACT

Sculpins are predominantly benthic sit-and-wait predators that inhabit marine and freshwaters of the Northern Hemisphere. In striking contrast to riverine relatives, sculpins endemic to Lake Baikal have diversified in both form and function, with multiple taxa having adaptations for pelagic and bathyal niches within the world's deepest lake. Baikal Oilfishes (*Comephorus* spp.) represent a highly apomorphic taxon with unique skeletal morphology, soft anatomy, and reproductive ecology. Selection for novel behavior and life history may be evident in genes responsible for organismal energy balance, including those encoding subunits of the electron transport chain. Complete mitochondrial genomes were sequenced for the Big Baikal Oilfish (*Comephorus baicalensis*) and Little Baikal Oilfish (*Comephorus dybowskii*). Mitochondrial genomes encode genes essential for electron transport, and data provided here will complement ongoing investigations of genome-to-phenome maps for teleost respiration and metabolism. Phylogenetic analyses including oilfish mitogenomes and all publicly available cottoid representative sequences are largely concordant with previous studies.

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Introduction

The Big Baikal Oilfish (*Comephorus baicalensis*; Pallas 1776) and Little Baikal Oilfish (*Comephorus dybowskii*; Korotneff 1904) are known locally as Golomyanka, which is derived from the old Russian word "Golomen," meaning "open sea, far from shore." This corresponds well with the species' pelagic habits within Lake Baikal, as oilfishes undergo diel migration to the bottom of the world's only oxygenated bathyal (>1800 m) freshwater ecosystem (Sideleva 2003). Both species are distinguished from stream-dwelling relatives by extraordinarily high lipid content (≤40%), reduced dermal pigmentation and retinal development, elongated fins and skull bones, and viviparity. Like all freshwater sculpins, oilfishes lack a gas bladder, but high proportional body fat enables evolutionary specialization on a pelagic life history. Such adaptations may have facilitated oilfishes becoming the dominant vertebrate taxa within Lake Baikal, both in terms of biomass and abundance (Sideleva 2003; Teterina et al. 2010). Oilfishes support a substantial local fishery, and they comprise the primary food item of the Nerpa, a Baikal endemic seal. *Comephorus baicalensis* is distinguished from *C. dybowskii* by having greater total length, greater proportional orbit length, shorter proportional pectoral fins, and smaller cephalic pore chambers (Taliev 1955).

Life at great depth is subject to relatively uncommon selective forces, including extraordinary hydrostatic pressure, which may disrupt homeostasis. In species that utilize environments varying greatly in hydrostatic pressure, gene products must exhibit functional plasticity in order to maintain homeostasis. Considering that *Comephorus* species are known to migrate vertically through the Baikal water column, we hypothesize that the genome sequences of *Comephorus* species will reveal important information regarding adaptation to hydrostatic plasticity in vertebrates. In order to explore genome-to-phenome maps for Oilfish physiology and morphology, we present the first complete mitochondrial genome sequences for *C. baicalensis* and *C. dybowskii*.

Data generation

Whole genomic DNA was isolated from fin clips collected from two specimens for each species, and voucher material was retained at the Sandel Laboratory of Aquatic Evolution at UWA. Mitochondrial genomes were generated using traditional Sanger sequencing at the Limnological Institute of the Russian Academy of Sciences and sequencing-by-synthesis on

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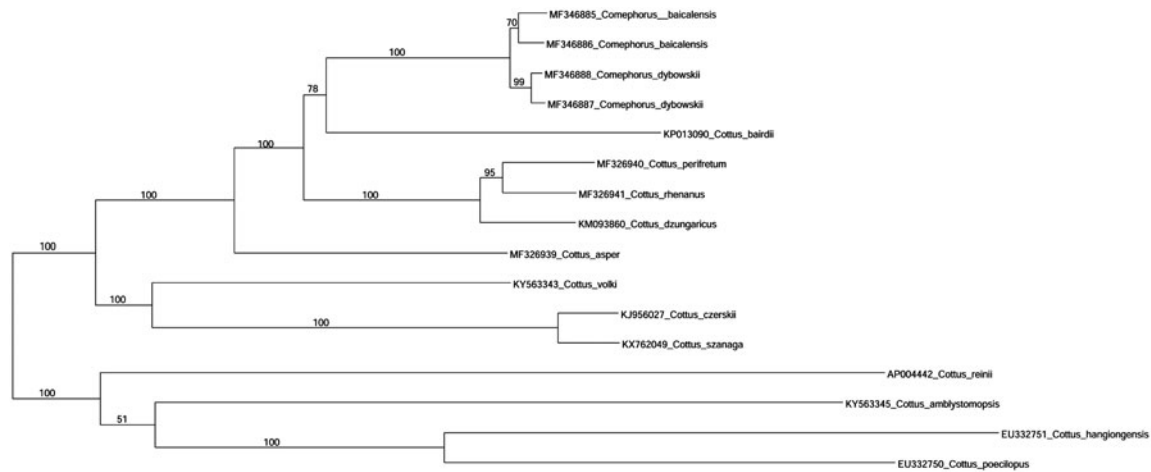


Figure 1. Interspecific phylogeny inferred under the maximum-likelihood (GTR + G + I) optimality criterion (Nei and Kumar 2000). Support values represent the proportion of 500 bootstrap replicates in which the associated taxa clustered together. Evolutionary analyses were conducted in MEGA6 (Tamura et al. 2013).

illumina HiSeq at the UAB Heflin Center for Genomic Sciences. Sanger reads were trimmed and aligned with Bioedit 7.0.0 (Hall 2005), and HiSeq reads were assembled using MITObim 1.7 (Hahn et al. 2013) on the CHEAHA central computing resource at the University of Alabama at Birmingham. The mitochondrial genome of *Cottus poecilopus* (GenBank accession EU332750) was used as a reference sequence. A multiple alignment was conducted with MAFFT version 7 (Katoh and Standley 2013) and validated by eye with Bioedit.

Phylogenetic analysis

MEGA 6 was used to select the optimum nucleotide substitution model and conduct a maximum-likelihood phylogenetic analysis (Tamura et al. 2013; Figure 1). Minimum evolution and neighbour-joining trees resulted in the same tree topology as the maximum-likelihood tree. With the exception of the taxa added in this paper, phylogenetic analyses revealed the same tree topologies reported in recent studies of *Cottus* mitochondrial genomes (Balakirev et al. 2016; Han et al. 2016; Swanburg et al. 2016; Fast et al. 2017).

Disclosure statement

No potential conflict of interest was reported by the authors.

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