



Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

Complete mitochondrial genome of the Belligerent sculpin *Megalocottus platycephalus* (Cottoidei: Cottidae)

Evgeniy S. Balakirev, Alexandra Yu. Kravchenko, Eleonora V. Cherepkova,
Pavel A. Saveliev, Alexander A. Semenchko & Francisco J. Ayala

To cite this article: Evgeniy S. Balakirev, Alexandra Yu. Kravchenko, Eleonora V. Cherepkova, Pavel A. Saveliev, Alexander A. Semenchko & Francisco J. Ayala (2019) Complete mitochondrial genome of the Belligerent sculpin *Megalocottus platycephalus* (Cottoidei: Cottidae), *Mitochondrial DNA Part B*, 4:2, 2980-2981, DOI: [10.1080/23802359.2019.1664348](https://doi.org/10.1080/23802359.2019.1664348)

To link to this article: <https://doi.org/10.1080/23802359.2019.1664348>



© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 12 Sep 2019.



Submit your article to this journal [↗](#)



Article views: 28



View related articles [↗](#)



View Crossmark data [↗](#)

Complete mitochondrial genome of the Belligerent sculpin *Megalocottus platycephalus* (Cottoidei: Cottidae)

Evgeniy S. Balakirev^{a,b}, Alexandra Yu. Kravchenko^a, Eleonora V. Cherepkova^c, Pavel A. Saveliev^a, Alexander A. Semenenko^c and Francisco J. Ayala^{d,e}

^aNational Scientific Center of Marine Biology, Far Eastern Branch, Russian Academy of Sciences, Vladivostok, Russia; ^bSchool of Biomedicine, Far Eastern Federal University, Vladivostok, Russia; ^cSchool of Natural Sciences, Far Eastern Federal University, Vladivostok, Russia; ^dRussian Academy of Science, Moscow, Russia; ^eFar Eastern Federal University, Vladivostok, Russia

ABSTRACT

The complete mitochondrial (mt) genome was sequenced in two specimens of the Belligerent sculpin *Megalocottus platycephalus* by high-throughput sequencing technology (Ion S5 platform). The sequences are 16,673 bp in size, and the gene arrangement, composition, and size are very similar to the other sculpin mt genomes published previously. Comparison of the two *M. platycephalus* mt genomes now obtained with other complete mt genomes available in GenBank reveals an affinity to the sculpin fishes from the genus *Myoxocephalus*. The intergeneric difference between the *Megalocottus* and *Myoxocephalus* is 0.0757 ± 0.0019 , which is significantly less than the corresponding value, 0.1240 ± 0.0120 , obtained previously for the sculpin fishes based on the *COI* barcoding marker.

ARTICLE HISTORY

Received 5 July 2019
Accepted 31 July 2019



KEYWORDS

Mitochondrial genome; phylogenetic relationships; Belligerent sculpin *Megalocottus platycephalus*; genetic divergence; Cottidae

The Belligerent sculpin *Megalocottus platycephalus* (Pallas) has a wide distribution in the North Pacific including the Sea of Japan, the Sea of Okhotsk, the Bering Sea, and the Chukchi Sea (e.g., Fedorov et al. 2003; Mecklenburg et al. 2016). The taxonomical status of *M. platycephalus* is uncertain. It has been considered as a monotypic species, polytypic species including two subspecies, *M. platycephalus platycephalus* and *M. platycephalus taeniopterus*, or as two separate species, *M. platycephalus* and *M. taeniopterus* (review in Radchenko and Petrovskaya 2019). Using the *COI*, cytochrome b, and 16S rRNA nucleotide sequences, Radchenko and Petrovskaya (2019) revealed the samples of *M. platycephalus* from the different seas form separate groups, with low level of intergroup divergence (p -distances $< 1\%$). The authors suggested the geographical groups correspond to the southern *M. platycephalus taeniopterus* and northern *M. platycephalus platycephalus* subspecies. To increase the power of phylogenetic analysis of this complex fish group we have sequenced two complete mitochondrial (mt) genomes of *M. platycephalus* (GenBank accession numbers MK936041 and MK936042) from the Sea of Japan, Djigit bay, Kluchi River (27.07.2017, 44.7948°N 136.3413°E, MPL3-17 and MPL5-17). The fish specimens are stored at the museum of the A. V. Zhirmunsky National Scientific Center of Marine Biology, Vladivostok, Russia (www.museumimb.ru) under accession number MIMB 38000.

The genomic DNA was extracted using the KingFisher Flex System and a set of reagents MagMAX DNA Multi-Sample Kit (ThermoFisher Scientific). The complete mt genomes were amplified in five overlapping fragments using the Phusion High-Fidelity DNA Polymerase (ThermoFisher Scientific). Libraries were prepared using Ion Plus Fragment Library Kit and unique adapters (Ion Xpress) with pre-fragmentation on the focused ultrasonicator Covaris M220. Ready libraries were sequenced on the Ion S5 sequencing platform (ThermoFisher Scientific) at the Far Eastern Federal University (Vladivostok, Russia). The complete mt genomes obtained were initially annotated using the MitoFish Web Server (Iwasaki et al. 2013) and further manually adjusted with MEGA 7 (Kumar et al. 2016) by comparisons with mt genomes of other sculpin fishes.

The *M. platycephalus* mt genomes (120× coverage) are 16,673 bp in size; the gene arrangement, composition, and size are very similar to the sculpin fish genomes published previously. There are 47 single nucleotide differences between the two genomes; total sequence divergence (D_{xy}) is 0.0028 ± 0.0004 . Comparison of the two mt genomes now obtained with other complete mt genomes available in GenBank for the genera *Myoxocephalus*, *Enophrys*, *Icelus*, *Gymnocanthus*, *Mesocottus*, and *Trachidermus* reveals an affinity of *M. platycephalus* to the sculpin fishes of the genus *Myoxocephalus* (Figure 1). The difference (D_{xy}) between *M. platycephalus* and *Myoxocephalus polyacanthocephalus* +

CONTACT Francisco J. Ayala  fjaya2018@gmail.com  Russian Academy of Science, 14 Leninsky Prospect, Moscow 119991, Russia; Far Eastern Federal University, 8 Sukhanova st., Vladivostok 690950, Russia

The research on mitochondrial genome sequencing was conducted at the Far Eastern Federal University, Vladivostok, Russia. The data analysis and manuscript preparation were conducted at the National Scientific Center of Marine Biology, Vladivostok, Russia.

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

