

Mitochondrial DNA Part B Resources

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

Complete mitochondrial genome of the Volk's sculpin *Cottus volki* (Cottoidei: Cottidae)

Evgeniy S. Balakirev, Pavel A. Saveliev & Francisco J. Ayala

To cite this article: Evgeniy S. Balakirev, Pavel A. Saveliev & Francisco J. Ayala (2017) Complete mitochondrial genome of the Volk's sculpin *Cottus volki* (Cottoidei: Cottidae), *Mitochondrial DNA Part B*, 2:1, 185-186, DOI: [10.1080/23802359.2017.1307705](https://doi.org/10.1080/23802359.2017.1307705)

To link to this article: <http://dx.doi.org/10.1080/23802359.2017.1307705>



© 2017 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



Published online: 29 Mar 2017.



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



View related articles [↗](#)



View Crossmark data [↗](#)

Full Terms & Conditions of access and use can be found at
<http://www.tandfonline.com/action/journalInformation?journalCode=tmdn20>

Complete mitochondrial genome of the Volk's sculpin *Cottus volki* (Cottoidei: Cottidae)

Evgeniy S. Balakirev^{a,b,c}, Pavel A. Saveliev^b and Francisco J. Ayala^a

^aDepartment of Ecology and Evolutionary Biology, University of California, Irvine, CA, USA; ^bA.V. Zhirmunsky Institute of Marine Biology, National Scientific Center of Marine Biology, Far Eastern Branch, Russian Academy of Sciences, Vladivostok, Russia; ^cSchool of Natural Sciences, Far Eastern Federal University, Vladivostok, Russia

ABSTRACT

The complete mitochondrial genome was sequenced in two individuals of the Volk's sculpin *Cottus volki*. The genome sequences are 16,519 and 16,536 bp in size, and the gene arrangement, composition, and size are very similar to the other sculpin mitochondrial genomes published previously. The difference between the two genomes studied is relatively high, 3.42%, which is 30% of the average interspecific divergence (8.76%) detected between seven *Cottus* species from the GenBank database. The data are consistent with the sedentary lifestyle in *C. volki*, limiting gene flow even between neighbouring rivers.

ARTICLE HISTORY

Received 7 March 2017
Accepted 14 March 2017

KEYWORDS

Volk's sculpin *Cottus volki*;
intraspecific divergence;
sedentary lifestyle; Cottidae

The Volk's sculpin *Cottus volki* Taranetz 1933 is a freshwater fish inhabiting the Sea of Japan's inland coastal rivers (Taranets 1933; Shedko 2001). Berg (1949) as well as Sideleva (2002) has considered *C. volki* to be a subspecies of the spotted sculpin *C. poecilopus* Haeckel. Later, based on the short mitochondrial (mt) sequences (control region) and morphology, the validity of *C. volki* was established (Shedko & Miroshnichenko 2007; Yokoyama et al. 2008; Sideleva & Goto 2009). However, the complete mt genome of *C. volki* had not yet been sequenced to confirm the species identity and to clarify its relationships with the other species belonging to the genus *Cottus*.

We have sequenced two complete mt genomes of *C. volki* (GenBank accession numbers KY563343 and KY563344) from the Alekseevka river (43° 65' 08 N; 133°51' 44 E) and Zerkal'naya river (44° 26' 77 N; 135° 27' 60 E), Primorsky krai, Russia, using primers designed with the program mitoPrimer_V1 (Yang et al. 2011). The fish specimens are stored at the museum of the A. V. Zhirmunsky Institute of Marine Biology, National Scientific Center of Marine Biology, Vladivostok, Russia (www.museumimb.ru) under accession numbers MIMB 33260 and MIMB 33261. The mt genome sequences are 16,519 and 16,536 bp in size; the gene arrangement, composition, and size are very similar to the

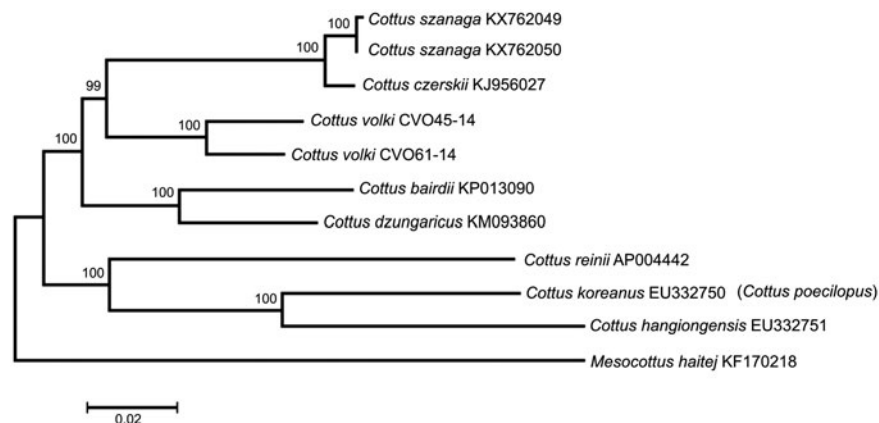


Figure 1. Maximum-likelihood tree for the Volk's sculpin *C. volki* specimens CV045-14 and CV061-14, and GenBank representatives of the family Cottidae. The tree is constructed using whole mitogenome sequences. The tree is based on the General Time Reversible + gamma + invariant sites (GTR + G + I) model of nucleotide substitution. The numbers at the nodes are bootstrap per cent probability values based on 1000 replications. The GenBank species name for the accession number EU332750 is in parentheses.

sculpin fish genomes published previously. There are 564 single nucleotide and 14 length differences (some involving more than one bp) between the two haplotypes of CVO45 and CVO61; total sequence divergence (D_{xy}) is 0.0342 ± 0.0014 .

Comparison of the two mt genomes now obtained with other complete mt genomes available in GenBank for the genera *Cottus* and *Mesocottus* reveals a close affinity of *C. volki* to the cluster of *C. czerskii* + *C. szanaga* within the genus *Cottus* (Figure 1). The difference (D_{xy}) between *C. volki* and the cluster *C. czerskii* + *C. szanaga* is 0.0707 ± 0.0012 , which is in close agreement with the average divergence between the *Cottus* species from the GenBank database (0.0846 ± 0.0014).

The difference between the two *C. volki* mt genomes now studied is relatively high, 3.42%, which is only 2.56 times less (30% of it) than the average interspecific divergence, 8.46%, detected between all seven *Cottus* mt genomes available in GenBank, including *C. bairdii*, *C. czerskii*, *C. dzungaricus*, *C. hangiongensis*, *C. koreanus*, *C. reinii*, and *C. szanaga*. The data are consistent with the sedentary lifestyle of *C. volki*, limiting gene flow even between neighbouring rivers (Kolpakov 2011).

Acknowledgements

This work was supported by the Bren Professor Funds at the University of California, Irvine, USA (mitochondrial genome sequencing); and the Russian Science Foundation, Russia, Grant number 14-50-00034 (data analysis and manuscript preparation).

The research on mitochondrial genome sequencing was conducted at the Department of Ecology and Evolutionary Biology, University of California, Irvine, United States of America. The data analysis and manuscript preparation were conducted at the A. V. Zhirmunsky Institute of Marine Biology, National Scientific Center of Marine Biology, Vladivostok, Russia.

Disclosure statement

The funders had no role in study design, data collection, data analysis, decision to publish, or preparation of the manuscript. The authors alone are responsible for the content and writing of the paper.

Funding

This work was supported by the Bren Professor Funds at the University of California, Irvine, USA (mitochondrial genome sequencing); and the Russian Science Foundation, Russia, Grant number 14-50-00034 (data analysis and manuscript preparation).

References

- Berg LS. 1949. Freshwater Fish of the USSR and adjacent countries. Moscow: Akad. Nauk SSSR.
- Kolpakov EV. 2011. Biology of Volk's sculpin *Cottus volki* (Cottidae) from the Serebryanka river (central Primor'e). *J Ichthyol.* 51:178–186.
- Shedko SV. 2001. A list of Cyclostomata and freshwater fish from the coast of Primorye. In: Vladimir Ya. Levanidov's Biennial Memorial Meetings. Issue 1. Vladivostok: Dal'nauka; p. 229–249.
- Shedko SV, Miroshnichenko IL. 2007. Phylogenetic relationships of sculpin *Cottus volki* Taranetz, 1933 (Scorpaeniformes, Cottidae) according to the results of analysis of control region of mitochondrial DNA. *J Ichthyol.* 47:21–25.
- Sideleva VG. 2002. Order XIII. Scorpaeniformes. Suborder Cottoidei. In: Atlas of freshwater fishes of Russia. vol. 2. Moscow: Nauka; p. 144–214.
- Sideleva VG, Goto A. 2009. Species status and redescription of three species of the group *Cottus poecilopus* (Cottidae) from Eurasia. *J Ichthyol.* 49:599–613.
- Taranets AY. 1933. On some new freshwater fishes from Dal'nevostochnyi Krai. *Dokl Akad Nauk. SSSR.* 2:83–85.
- Yang CH, Chang HW, Ho CH, Chou YC, Chuang LY. 2011. Conserved PCR primer set designing for closely-related species to complete mitochondrial genome sequencing using a sliding window-based PSO algorithm. *PLoS One.* 6:e17729.
- Yokoyama R, Sideleva VG, Shedko SV, Goto A. 2008. Broad-scale phylogeography of the Palearctic freshwater fish *Cottus poecilopus* complex (Pisces: Cottidae). *Mol Phylogeny Evol.* 48:1244–1251.