

2016

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Recommended Citation

Gaughan, Sarah; Johnson, Robin; Wang, Jun; Wachholtz, Michael; Steffensen, Kirk; King, Timothy; and Lu, Guoqing, "The complete mitochondrial genome of the silver chub, *Macrhybopsis storeriana*" (2016).

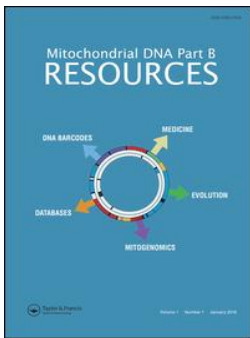
Biology Faculty Publications. 169.

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Mitochondrial DNA Part B Resources

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

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To cite this article: Sarah Gaughan, Robin Johnson, Jun Wang, Michael Wachholtz, Kirk Steffensen, Timothy King & Guoqing Lu (2016) The complete mitochondrial genome of the silver chub, *Macrhybopsis storeriana*, Mitochondrial DNA Part B, 1:1, 789-790, DOI: [10.1080/23802359.2016.1197053](https://doi.org/10.1080/23802359.2016.1197053)

To link to this article: <https://doi.org/10.1080/23802359.2016.1197053>



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Published online: 12 Nov 2016.



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The complete mitochondrial genome of the silver chub, *Macrhybopsis storeriana*

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ABSTRACT

The complete mitochondrial genome of the silver chub *M. storeriana* was determined to be 16,709 bp and contained 22 tRNA genes, 2 rRNA genes and one control region. The whole genome base composition was 30.3% A, 28% T, 25.5% C and 16.2% G. This complete mitochondrial genome provides essential molecular markers for resolving phylogeny and aiding future conservation efforts.

ARTICLE HISTORY

Received 18 March 2016
Revised 19 May 2016
Accepted 31 May 2016

KEYWORDS

Macrhybopsis storeriana;
mitochondrial; genome; next
generation sequencing

Macrhybopsis chubs are a genus of the Leuciscinae subfamily consisting of small-bodied fishes that are typically obligate river species (Galat et al. 2005). The silver chub, *M. storeriana*, has been listed as Vulnerable (N3) in Canada due to anthropogenic disturbances such as eutrophication and baitfish harvesting (Boyko & Staton 2010). Conservation efforts have been complicated due to a wide variety of habitat utilization (Starrett 1950, Klutho 1983, Luttrell et al. 2002). The differences in habitat usage suggest that the taxonomy of the chubs may not have been fully resolved, which makes identifying populations that are susceptible to anthropogenic disturbances difficult.

Previous molecular studies have been unable to resolve the phylogeny of *Macrhybopsis* chubs with singular mitochondrial markers (Nagle & Simons 2012). Here, we report the complete mitogenome of the silver chub, *M. storeriana*. The silver chub was collected from a channelized section of the Missouri River along Nebraska's eastern border (42°19'07.8"N 96°22'41.6"W) and is part of the ichthyology collection at the University of Kansas Biodiversity Institute (KUI 41379). This mitogenome will establish a solid basis to resolve phylogenetic confusion within this genus and may aid future conservation measures.

Genomic DNA was extracted and purified from fin tissue using the Qiagen DNeasy Blood and Tissue Kit (Hilden,

Germany) for Genotyping by Sequencing (GBS). PCR free libraries were constructed with a TruSeq PCR Free library protocol and sequenced using an Illumina NextSeq500 (San Diego, CA) at the USGS Leetown Science Facility. Sequences were assembled using Velvet (Zerbino & Birney 2008), aligned with Mega 6.06 (Tamura et al. 2013) and annotated with MitoFish (Iwasaki et al. 2013). DOGMA was used to verify annotation and identify start and stop codons (Wyman et al. 2004).

The total length of the silver chub's mitogenome was 16,709 bp (GenBank Accession No. KX139438). The mitogenome consisted of 22 tRNA genes, 2 rRNA genes and one control region. Fourteen of the tRNA genes were encoded on the heavy (H) strand along with all of the protein-coding genes except NADH dehydrogenase subunit 6. The whole genome base composition was 30.3% A, 28% T, 25.5% C and 16.2% G. The putative control region was located between tRNA^{Pro} and tRNA^{Phe} and was 1056 bp long.

To investigate the position of *M. storeriana* within Leuciscinae, a maximum likelihood tree based on fourteen complete mitochondrial genomes was constructed using MEGA6 under the GTR+G+I model with 500 bootstrap replicates (Pattengale et al. 2010, Tamura et al. 2013) (Figure 1). This maximum likelihood tree phylogenetically positioned *M. storeriana* as a sister clade to the Notropin clade supporting previous morphological phylogenetic analysis (Cavender & Coburn 1992).

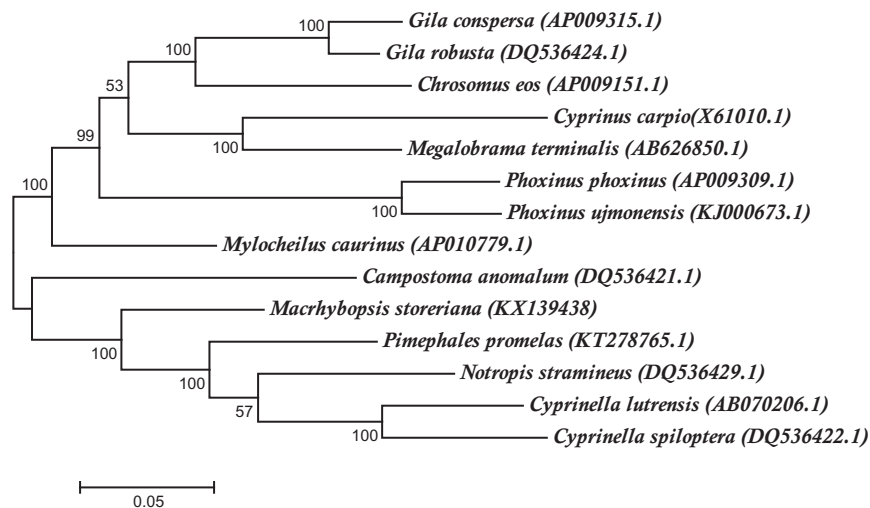


Figure 1. Phylogenetic tree generated using a maximum likelihood method and a general time reversal model based on fourteen complete mitochondrial genomes. The GenBank accession number is listed next to each species within the tree.

Disclosure statement

The authors report no conflict of interest. The authors are solely responsible for the content and writing of this manuscript. Use of trade, product, or firm names does not imply endorsement by the U.S. Government.

Funding

This study was supported through funding from the University of Nebraska Omaha Graduate Research and Creative Activity (GRACA), UCRCA, Office of Graduate Studies Rhoden Fellowship and the Department of Biology.

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