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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of blunt-snouted lenok *Brachymystax tumensis* (Salmoniformes, Salmonidae)

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Abstract

The complete mitochondrial genomes were sequenced in two individuals of blunt-snouted lenok *Brachymystax tumensis*. The sizes of the genomes in the two isolates were 16,754 and 16,836; the difference was due to variable number of repeat sequences within the control region. The gene arrangement, base composition, and size of the two sequenced genomes are very similar to the *B. lenok* and *B. lenok tsinlingensis* genomes previously published (JQ686730 and JQ686731). However, the level of divergence inferred from 12 protein-coding genes (3.48%) indicated clear species boundaries between the lenok species.

Keywords

*Brachymystax tumensis*, complete mitochondrial genome, lenok, salmonids

History

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Blunt-snouted lenok *Brachymystax tumensis* Mori is a representative of the family Salmonidae widely distributed in rivers of northern Eurasia. Until recently, the two common forms of lenok, blunt-snouted lenok *B. tumensis* and sharp-snouted lenok *B. lenok* (Pallas) were considered as a single species. Intermediate morphologies were detected indicating possible hybridization between the forms (Alekseev, 1983; Osinov et al. 1990; Shedko et al., 1996). New diagnostic morphological features (Shedko & Shedko 2003) along with ecological and genetic differences detected in the areas of sympatry have confirmed the species status of both forms and proved the presence of two lenok species, *B. tumensis* and *B. lenok* (Ma & Jiang, 2007; Osinov et al., 1990; Shedko et al., 1996). However, Ma et al. (2009) recently found no support for *B. tumensis* as an independent species in Tumen River and suggested that *B. tumensis* is a synonym of *B. lenok*.

We sequenced two complete mitochondrial genomes of *B. tumensis* (GenBank accession numbers KJ730524 and KJ730525) to enlarge the power of phylogenetic analysis of this complex salmonid group using primers previously developed for the Siberian taimen *Hucho taimen* (Balakirev et al., 2014) and primers designed for *B. tumensis* with the program mitoPrimer_V1 (Yang et al., 2011). Both approaches yielded identical sequences. The sizes of the genomes were different, 16,754 and 16,836 in the two isolates (Table 1) due to variable

<table>
<thead>
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<th>Gene</th>
<th>Strand</th>
<th>Position</th>
<th>Size</th>
</tr>
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<tbody>
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<td>D-loop</td>
<td>H</td>
<td>1–1093</td>
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<tr>
<td>tRNA-Phe</td>
<td>H</td>
<td>1094–1161</td>
<td>68</td>
</tr>
<tr>
<td>12S rRNA</td>
<td>H</td>
<td>1162–2109</td>
<td>948</td>
</tr>
<tr>
<td>tRNA-Val</td>
<td>H</td>
<td>2110–2181</td>
<td>72</td>
</tr>
<tr>
<td>16S rRNA</td>
<td>H</td>
<td>2182–3861</td>
<td>1680</td>
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<tr>
<td>tRNA-Leu</td>
<td>H</td>
<td>3862–3936</td>
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<tr>
<td>nad1</td>
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<td>972</td>
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<tr>
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<td>5125–6174</td>
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<td>tRNA-Cys</td>
<td>L</td>
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</table>

(continued)
number of repeat sequences within the control region (Si et al., 2012). The A + T base composition, 55.0% (55.3%) was higher than G + C, 45.0% (44.7%). There were 87 single nucleotide and one length differences between the haplotypes; total sequence divergence ($D_{xy}$) was 0.0051 ± 0.0006. The level of divergence between B. tumensis and both B. lenok and B. lenok tsinlingensis was however significantly higher, 0.0274 ± 0.0011 (inferred from complete mitochondrial genome) or 0.0348 ± 0.0017 (inferred from 12 protein-coding genes), indicating clear species boundaries between the lenok species.

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Declaration of interest

The authors report no conflict of interest. The authors alone are responsible for the content and writing of the paper.

References


