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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 1. Characteristics of the mitochondrial genome of *B. tumensis* (isolates Bt257 and Bikin).

Gene	Bt257			Bikin		
	Strand	Position	Size	Strand*	Position	Size
D-loop	H	1–1093	1093	H	1–1175	1175
tRNA-Phe	H	1094–1161	68	H	1176–1243	68
12S rRNA	H	1162–2109	948	H	1244–2191	948
tRNA-Val	H	2110–2181	72	H	2192–2263	72
16S rRNA	H	2182–3861	1680	H	2264–3943	1680
tRNA-Leu	H	3862–3936	75	H	3944–4018	75
nad1	H	3937–4908	972	H	4019–4990	971
tRNA-Ile	H	4917–4988	72	H	4999–5070	72
tRNA-Gln	L	4986–5056	71	L	5068–5138	71
tRNA-Met2	H	5056–5124	69	H	5138–5206	69
nad2	H	5125–6174	1050	H	5207–6256	1050
tRNA-Trp	H	6176–6247	72	H	6258–6329	72
tRNA-Ala	L	6250–6318	69	L	6332–6400	69
tRNA-Asn	L	6320–6392	73	L	6402–6474	73
Oril	L	6393–6426	34	L	6475–6508	34
tRNA-Cys	L	6427–6493	67	L	6509–6575	67

(continued)

Table 1. Continued

Gene	Bt257			Bikin		
	Strand	Position	Size	Strand*	Position	Size
tRNA-Tyr	L	6494–6564	71	L	6576–6646	71
cox1	H	6566–8116	1551	H	6648–8198	1551
tRNA-Ser	L	8117–8187	71	L	8199–8269	71
tRNA-Asp	H	8192–8265	74	H	8274–8347	74
cox2	H	8280–8970	691	H	8362–9052	691
tRNA-Leu	H	8971–9044	74	H	9053–9126	74
atp8	H	9046–9213	168	H	9128–9295	168
atp6	H	9204–9887	684	H	9286–9969	684
cox3	H	9887–10,672	786	H	9969–10,754	786
tRNA-Gly	H	10,672–10,741	70	H	10,754–10,823	70
nad3	H	10,742–11,090	349	H	10,824–11,172	349
tRNA-Arg	H	11,091–11,160	70	H	11,173–11,242	70
nad4l	H	11,161–11,457	297	H	11,243–11,539	297
nad4	H	11,451–12,831	1381	H	11,533–12,913	1381
tRNA-His	H	12,832–12,900	69	H	12,914–12,982	69
tRNA-Ser	H	12,901–12,969	69	H	12,983–13,051	69
tRNA-Leu	H	12,971–13,043	73	H	13,053–13,125	73
nad5	H	13,044–14,882	1839	H	13,126–14,964	1839
nad6	L	14,879–15,400	522	L	14,961–15,482	522
tRNA-Glu	L	15,401–15,469	69	L	15,483–15,551	69
Cob	H	15,473–16,613	1141	H	15,555–16,695	1141
tRNA-Thr	H	16,614–16,685	72	H	16,696–16,767	72
tRNA-Pro	L	16,685–16,754	70	L	16,767–16,836	70

*H and L refer to genes located in the heavy strand and light strand, respectively.

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.

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