Title
Complete mitochondrial genome of Sakhalin taimen Parahucho perryi (Salmoniformes, Salmonidae) without two frame-disrupting indels in the ND4 gene

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of Siberian taimen, *Hucho taimen* not introgressed by the lenok subspecies, *Brachymystax lenok* and *B. lenok tsinlingensis*

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Abstract

The complete mitochondrial genomes were sequenced in two individuals of Siberian taimen *Hucho taimen*. The sizes of the genomes were 16,833 and 16,914 in the two isolates, representing two haplotype groups previously detected. The gene arrangement, base composition, and size of the two sequenced genomes are very similar to the *H. taimen* genome previously published (HQ897271), but did not contain introgressed fragments from two subspecies of lenok, *Brachymystax lenok* and *B. l. tsinlingensis*.

Keywords

Brachymystax lenok, *Brachymystax lenok tsinlingensis*, complete mitochondrial genome, *Hucho taimen*, hybridization, introgression, salmonids

History

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Siberian taimen *Hucho taimen* (Pallas, 1773) is the largest representative of the family Salmonidae in rivers of northern Eurasia. The species has drastically declined in abundance throughout its range and it is now included as an Endangered species in the Mongolian, Russian, and Chinese red lists. The aquaculture of *H. taimen* is under intensive development and artificial intergeneric hybrids between *H. taimen* and lenok *Brachymystax lenok* have been reported (Xu et al., 2009, 2010, 2011). Previously, we sequenced a portion (8141 bp) of the mitochondrial (mt) genome in 28 specimens of *H. taimen* from six localities in the Amur River basin (Balakirev et al., 2013). A comparison of the data with the GenBank *H. taimen* mt genome (Wang et al., 2011; HQ897271) revealed significant differences between them in spite of the fact that the fish specimens come from neighboring geographical areas. We found (Balakirev et al., 2013) that the GenBank sequence (Wang et al., 2011; HQ897271) contained two introgressed fragments from two lenok subspecies, *B. lenok* (JQ686730) and *B. lenok tsinlingensis* (JQ686731) (Si et al., 2012). This observation motivated us to sequence the complete mitochondrial genome of *H. taimen* showing no sign of modern introgression with lenok subspecies.

We sequenced two complete mitochondrial genomes of *H. taimen* (GenBank accession numbers KJ711549 and KJ711550) using primers of Wang et al. (2011) and primers obtained with the program mitoPrimer_V1 (Yang et al., 2011). Both approaches yielded identical sequences. The complete genome sequences were 16,833 and 16,914 in the two isolates (Table 1) due to variable number of repeat sequences within the control region (Wang et al., 2011). The gene arrangement, composition, and sizes were very similar to the *H. taimen* genome

Table 1. Characteristics of the mitochondrial genome of *Hucho taimen* (isolates Ht9 and Ht16).

	Ht9			Ht16		
Gene	Strand*	Position	Size	Strand*	Position	Size
Control region	H	1–1257	1257	H	1–1175	1175
tRNA-Phe	H	1258–1325	68	H	1176–1243	68
12S rRNA	H	1326–2272	947	H	1244–2190	947
tRNA-Val	H	2273–2344	72	H	2191–2262	72
16S rRNA	H	2345–4024	1680	H	2263–3942	1680
tRNA-Leu	H	4025–4099	75	H	3943–4017	75
nad1	H	4100–5071	972	H	4018–4989	972
tRNA-Ile	H	5080–5151	72	H	4998–5069	72
tRNA-Gln	L	5149–5219	71	L	5067–5137	71
tRNA-Met2	H	5219–5287	69	H	5137–5205	69
nad2	H	5288–6337	1050	H	5206–6255	1050
tRNA-Trp	H	6336–6406	71	H	6254–6325	72
tRNA-Ala	L	6409–6477	69	L	6328–6396	69
tRNA-Asn	L	6479–6551	73	L	6398–6470	73
Oril	L	6552–6586	35	L	6471–6505	35
tRNA-Cys	L	6587–6653	67	L	6506–6572	67
tRNA-Tyr	L	6654–6724	71	L	6573–6643	71
cox1	H	6726–8276	1551	H	6645–8195	1551
tRNA-Ser	L	8277–8347	71	L	8196–8266	71
tRNA-Asp	H	8352–8425	74	H	8271–8344	74
cox2	H	8440–9130	691	H	8359–9049	691
tRNA-Leu	H	9131–9204	74	H	9050–9123	74
atp8	H	9206–9373	168	H	9125–9292	168
atp6	H	9364–10,047	684	H	9283–9966	684
cox3	H	10,047–10,832	786	H	9966–10,751	786

(*continued*)

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Table 1. Continued

	Ht9			Ht16		
Gene	Strand*	Position	Size	Strand*	Position	Size
tRNA-Gly	H	10,832–10,901	70	H	10,751–10,820	70
nad3	H	10,902–11,250	349	H	10,821–11,169	349
tRNA-Arg	H	11,251–11,320	70	H	11,170–11,239	70
nad4l	H	11,321–11,617	297	H	11,240–11,536	297
nad4	H	11,611–12,991	1381	H	11,530–12,910	1381
tRNA-His	H	12,992–13,060	69	H	12,911–12,979	69
tRNA-Ser	H	13,061–13,129	69	H	12,980–13,048	69
tRNA-Leu	H	13,131–13,203	73	H	13,050–13,122	73
nad5	H	13,204–15,042	1839	H	13,123–14,961	1839
nad6	L	15,039–15,560	522	L	14,958–15,479	522
tRNA-Glu	L	15,561–15,629	69	L	15,480–15,548	69
Cob	H	15,633–16,773	1141	H	15,552–16,692	1141
tRNA-Thr	H	16,774–16,845	72	H	16,693–16,764	72
tRNA-Pro	L	16,845–16,914	70	L	16,764–16,833	70

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

previously published (HQ897271), but did not contain the introgressed fragments from the two subspecies of lenok, *B. lenok* and *B. l. tsinlingensis*. The overall base composition, including protein, tRNA, and rRNA genes (or, in parentheses, only the 13 protein-coding genes) was 28.0% (26.6%) for A, 26.7% (28.1%) for T, 16.6% (14.9%) for G, and 28.8% (30.3%) for C. The A + T base composition, 54.6% (54.8%) was higher than G + C, 45.4% (45.2%). There were 26 single nucleotide and two length differences between the Ht9 and Ht16 haplotypes; total sequence divergence (D_{xy}) was 0.0015 ± 0.0003. A slightly higher D_{xy} value (0.0021 ± 0.0005) was previously obtained on the partial mt genome sequences (8141 bp) (Balakirev et al., 2013).

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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. This study was supported by Bren Professor Funds at the University of California Irvine to Francisco J. Ayala and Evgeniy S. Balakirev.

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