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MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of the endangered Sakhalin taimen
Parahucho perryi (Salmoniformes, Salmonidae)**

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Abstract

The complete mitochondrial genome sequence of *Parahucho perryi* has been obtained by the next generation sequencing, which contained 22 tRNA genes, 13 protein-coding genes, 2 rRNA genes and non-coding control region with the total length of 16,651 bp. The gene content, arrangement, codon usage and base composition of *P. perryi* mitogenome are identical to those observed in salmonids and most other teleost fishes. The sequence data could provide useful information for the studies on molecular systematics and conservation genetics.

KeywordsMitochondrial genome, *Parahucho*,
Salmonidae**History**

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Salmonid fishes (family Salmonidae) are widely distributed in the Northern Hemisphere. Currently there are 12 recognized genera in Salmonidae, and Sakhalin taimen *Parahucho perryi* is the only one extant species of the genus *Parahucho*. *Parahucho* is a distinct evolutionary lineage among other salmonid lineages and its origin was estimated to have occurred about 17–21 (Shedko et al., 2012, 2013), 22–25 (Osinov & Lebedev, 2004) or 27 (Crête-Lafrenière et al., 2012) MY ago. The anadromous and carnivorous Sakhalin taimen is distributed in the South of the Russian Far East (Maritime Province, Sakhalin, Southern Kuriles) and Northern Japan (Hokkaido). Wild populations of *P. perryi* have been steadily declining owing to habitat degradation and illegal fishing. The IUCN's (The International Union for the Conservation of Nature) Red List has classified Sakhalin taimen as critically endangered (CR) since 2006 (Rand, 2006).

According to NCBI Nucleotide Sequence Database (<http://www.ncbi.nlm.nih.gov>, accessed on 14 March 2013) the complete mitochondrial genomes of about 30 species and subspecies of Salmonidae were sequenced up to date. However, there is no mitogenome of *Parahucho* available until now. Therefore, we sequenced the complete mitochondrial genome of *P. perryi* in this study.

Mitochondrial DNA was purified from fresh liver by the alkaline extraction method (Palva & Palva, 1985) and used for

library construction and pyrosequencing using GS Junior Titanium chemistry according to the manufacturer's instructions (454 Life Sciences, A Roche Company, Branford, CT). The reads were assembled using GS De Novo Assembler (454 Life Sciences, A Roche Company, Branford, CT). The complete mitochondrial genome of *P. perryi* was generated with 16,651 bp in length and had been deposited in GenBank with an accession number of KC897653.

The mitochondrial genome of *P. perryi* contains a set of 13 protein-coding genes, 2 rRNA genes (12S and 16S), 22 tRNA genes and the control region (Table 1). Most of the genes were encoded on the heavy strand, with the exception of ND6 and eight tRNAs, which were encoded on the light strand. All the protein-coding genes begin with an ATG start codon except for *COI* and *ND4*, which start with GTG. Two types of complete stop codons were detected in open reading frames of *P. perryi*: TAA (*ND1*, *ND2*, *COI*, *ATPase8*, *ATPase6*, *COIII*, *ND4L* and *ND5*) and TAG (*ND6*). The four remaining genes had incomplete stop codon T (*COII*, *ND3*, *ND4* and *CYTB*) adjacent to a downstream tRNA gene. The 12S and 16S rRNA genes were located between the tRNA-Phe and tRNA-Leu (UUR) genes being separated by the tRNA-Val gene. The 22 tRNA genes varied from 67 to 75 bp in length, two tRNAs of which were determined for serine (UCN and AGY) and leucine (UUR and CUN) and one specific tRNA gene for the other amino acids. The control region was 988 bp long, which was close to lower limit of its length observed in salmonids (Wang et al., 2011).

The overall base composition of the novel mitogenome was estimated to be 28.47% of A, 28.75% of C, 16.55% of G and 26.23% of T, indicating an obvious bias against G commonly observed in salmonids and other fishes (Wang et al., 2011). The A + T base composition (54.70%) was higher than G + C (45.30%).

The gene content, arrangement, codon usage and base composition of *P. perryi* mitogenome are identical to those observed in salmonids and most other teleost fishes.

Table 1. Characteristics of the mitochondrial genome of the *Parahucho perryi*.

Gene	Strand	Position		Size (bp)	Codon	
		From	To		Start	Stop
Control region	H	1	988	988		
tRNA-Phe	H	989	1056	68		
12S rRNA	H	1057	2003	947		
tRNA-Val	H	2004	2075	72		
16S rRNA	H	2076	3753	1678		
tRNA-Leu (UUR)	H	3759	3833	75		
<i>ND1</i>	H	3834	4808	975	ATG	TAA
tRNA-Ile	H	4816	4887	72		
tRNA-Gln	L	4955	4885	71		
tRNA-Met	H	4955	5023	69		
<i>ND2</i>	H	5024	6073	1050	ATG	TAA
tRNA-Trp	H	6074	6145	72		
tRNA-Ala	L	6215	6147	69		
tRNA-Asn	L	6289	6217	73		
tRNA-Cys	L	6389	6323	67		
tRNA-Tyr	L	6460	6390	71		
<i>COI</i>	H	6462	8012	1551	GTG	TAA
tRNA-Ser (UCN)	L	8083	8013	71		
tRNA-Asp	H	8088	8161	74		
<i>COII</i>	H	8176	8866	691	ATG	T-
tRNA-Lys	H	8867	8940	74		
ATPase8	H	8942	9109	168	ATG	TAA
ATPase6	H	9100	9783	684	ATG	TAA
<i>COIII</i>	H	9783	10,568	786	ATG	TAA
tRNA-Gly	H	10,568	10,637	70		
<i>ND3</i>	H	10,638	10,986	349	ATG	T-
tRNA-Arg	H	10,987	11,056	70		
<i>ND4L</i>	H	11,057	11,353	297	ATG	TAA
<i>ND4</i>	H	11,347	12,727	1381	GTG	T-
tRNA-His	H	12,728	12,797	70		
tRNA-Ser (AGY)	H	12,798	12,866	69		
tRNA-Leu (CUN)	H	12,868	12,940	73		
<i>ND5</i>	H	12,941	14,779	1839	ATG	TAA
<i>ND6</i>	L	15,297	14,776	522	ATG	TAG
tRNA-Glu	L	15,366	15,298	69		
<i>Cytb</i>	H	15,370	16,510	1141	ATG	T-
tRNA-Thr	H	16,511	16,582	72		
tRNA-Pro	L	16,651	16,582	70		

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Declaration of interest

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