

MITOGENOME ANNOUNCEMENT

**Mitochondrial genome of the neotropical Parnell's mustached bat
Pteronotus parnellii (*Pteronotus*, Mormoopidae)**Chunyong Yin¹ and Chao Shi^{2,3}

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Abstract

We reported complete mitochondrial genome of neotropical Parnell's mustached bat *Pteronotus parnellii* (16,564 bp in length). Its mitochondrial genome consisted of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and 1 control region. The base composition of mtDNA was A (33.1%), G (13.7%), C (27.3%), T (25.9%), and the percentage of A and T (59.0%) was higher than G and C. All the genes in *P. parnellii* were distributed on the H-strand, except for the *ND6* subunit gene and 10 tRNA genes, which were encoded on the L-strand. The new sequenced mitochondrial genome will contribute to our understanding of the systematic evolution in the bats.

Keywords

Genome, mitochondrion, Parnell's mustached bat (*Pteronotus parnellii*)

History

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Bats are the only mammals capable of sustained flight and one of the few mammals that echolocate. Mustached bat exhibits "constant frequency" echolocation and is the only New World species to use high-duty cycle echolocation (Clare et al., 2013). In the present study, the complete mtDNA of neotropical Parnell's mustached *P. parnellii* was reported (GenBank accession number KF752590), for which we added second published data from *P. rubiginosus* (NC_022425; Botero-Castro et al., 2013) in genus *Pteronotus* and family Mormoopidae.

This mitochondrial genome sequence share 91% sequence identity with *P. rubiginosus*, but only about 80% similarity with mitochondrial genomes of other families sequenced so far. We annotated *P. parnellii* by blast against with previous published bats mitochondrion genomes of this genus *P. rubiginosus* (NC_022425; Botero-Castro et al., 2013), and also species from other families, *Rhinolophus luctus* (JN986580; Xu et al., 2012) and *Eptesicus serotinus* (NC_022474; Nam et al., 2013). This complete mtDNA sequence of *P. parnellii* (16,564 bp in length) had 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA) and 1 control region. The total lengths of

the 13 protein-coding genes are 11,413 bp and they encode 3792 amino acids. Ten of the 13 protein-coding genes regard ATG as the start codon, while *ND2*, *ND3* and *ND5* utilize ATA, respectively (Table 1). Eight of the 13 protein-coding genes use TAA as stop codons. The *ND2* and *COX1* stop with TAG, *Cytb* and *ND4* ends with AGA, and *COX3* use T as an incomplete stop codon, which was presumably completed as TAA.

The 22 tRNA genes range in size from 60 bp in tRNA-Ser to 76 bp in tRNA-Leu. And 21 tRNA genes of *P. parnellii* could be fold into typical cloverleaf secondary structure except the tRNA-Ser where the dihydrouridine (DHU) arm is lacking. The OL region (H-strand replication origin) is located between tRNA-Asn and tRNA-Cys. The 12S and 16S rRNA genes were 961 and 1563 bp in size, respectively. These ribosomal subunit genes are located between the tRNA-Phe and tRNA-Leu genes and are further separated by the tRNA-Val gene. The control region of the *P. parnellii* mtDNA is 1131 bp long. In all, this new reported *P. parnellii* will provide new insights into bats evolution of genus *Pteronotus* and family Mormoopidae.

Table 1. Characteristics of *P. parnellii* mitochondrial genome.

Gene	Position		Intervals	Size (bp)	Base composition (%)				Codons	Strand
	From	To			A	C	G	T		
tRNA-Phe	1	69	0	69	42.0	17.4	17.4	23.2		H
12S rRNA	70	1030	1	961	36.2	22.3	17.3	24.2		H
tRNA-Val	1032	1100	8	69	39.1	21.7	13.1	26.1		H
16S rRNA	1109	2671	0	1563	36.3	22.7	17.5	23.5		H
tRNA-Leu	2672	2747	2	76	28.9	22.4	17.1	31.6		H
<i>ND1</i>	2750	3706	-1	957	33.6	30.1	11.7	24.6	ATG TAA	H
tRNA-Ile	3706	3774	-3	69	39.1	14.5	17.4	29.0		H
tRNA-Gln	3772	3844	0	73	26.0	13.7	26.0	34.3		L
tRNA-Met	3845	3913	0	69	29.0	26.1	18.8	26.1		H
<i>ND2</i>	3914	4957	-2	1044	36.5	31.0	9.2	23.3	ATA TAG	H
tRNA-Trp	4956	5024	2	69	39.1	17.4	16.0	27.5		H
tRNA-Ala	5027	5095	1	69	27.6	11.6	24.6	36.2		L
tRNA-Asn	5097	5169	0	73	26.0	13.7	26.0	34.3		L
OL	5170	5202	0	33	33.3	24.2	27.3	15.2		L
tRNA-Cys	5203	5268	0	66	27.3	19.7	22.7	30.3		L
tRNA-Tyr	5269	5335	1	67	31.3	16.4	23.9	28.4		L
<i>COX1</i>	5337	6881	-3	1545	27.2	25.6	17.1	30.1	ATG TAG	H
tRNA-Ser	6883	6951	7	69	26.1	15.9	23.2	34.8		L
tRNA-Asp	6959	7026	0	68	38.2	14.8	11.7	35.3		H
<i>COX2</i>	7027	7710	3	684	32.5	27.6	13.7	26.2	ATG TAA	H
tRNA-Lys	7714	7781	1	68	35.3	19.1	16.2	29.4		H
<i>ATP8</i>	7783	7986	-43	204	35.8	31.9	6.8	25.5	ATG TAA	H
<i>ATP6</i>	7944	8624	-1	681	30.4	30.7	11.4	27.5	ATG TAA	H
<i>COX3</i>	8624	9407	0	784	27.7	29.6	14.8	27.9	ATG T- -	H
tRNA-Gly	9408	9477	0	70	37.1	20.0	12.9	30.0		H
<i>ND3</i>	9478	9825	0	348	30.7	30.2	13.2	25.9	ATA TAA	H
tRNA-Arg	9826	9894	0	69	43.5	13.0	10.2	33.3		H
<i>ND4L</i>	9895	10,191	-7	297	31.3	25.9	12.5	30.3	ATG TAA	H
<i>ND4</i>	10,185	11,564	-5	1380	33.0	28.2	11.1	27.7	ATG AGA	H
tRNA-His	11,560	11,627	0	68	44.1	14.7	10.3	30.9		H
tRNA-Ser	11,628	11,687	0	60	35.0	26.7	15.0	23.3		H
tRNA-Leu	11,688	11,757	0	70	38.6	14.3	20.0	27.1		H
<i>ND5</i>	11,758	13,578	-17	1821	34.2	29.9	10.9	25.0	ATA TAA	H
<i>ND6</i>	13,562	14,089	0	528	17.1	8.7	33.9	40.3	ATG TAA	L
tRNA-Glu	14,090	14,157	4	68	29.4	11.8	20.6	38.2		L
<i>Cytb</i>	14,162	15,301	0	1140	30.1	30.2	13.8	25.9	ATG AGA	H
tRNA-Thr	15,302	15,368	-1	67	31.3	22.4	22.4	23.9		H
tRNA-Pro	15,368	15,433	0	66	22.7	13.7	31.8	31.8		L
D-loop	15,434	16,564	0	1131	31.6	25.4	17.1	25.9		H

Declaration of interest

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

References

- Botero-Castro F, Tilak MK, Justy F, Catzeflis F, Delsuc F, Douzery EJ. (2013). Next-generation sequencing and phylogenetic signal of complete mitochondrial genomes for resolving the evolutionary history of leaf-nosed bats (phyllostomidae). *Mol Phylogenet Evol* 69:728–39.
- Clare EL, Adams AM, Maya-Simões AZ, Eger JL, Hebert PDN, Fenton MB. (2013). Diversification and reproductive isolation: cryptic species in the only New World high-duty cycle bat, *Pteronotus parnellii*. *BMC Evol Biol* 13:26.
- Nam TW, Yoon KB, Cho JY, Park YC. (2013). Complete mitochondrial genome of the serotine bat (*Eptesicus serotinus*) in Korea. *Mitochondrial DNA*. [Epub ahead of print]. doi: 10.3109/19401736.2013.819503.
- Xu H, Yuan Y, He Q, Wu Q, Yan Q, Wang Q. (2012). Complete mitochondrial genome sequences of two Chiroptera species (*Rhinolophus luctus* and *Hipposideros armiger*). *Mitochondrial DNA* 23:327–8.