



Mitochondrial DNA Part A

DNA Mapping, Sequencing, and Analysis


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MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of the Yellow-bellied Tit
Parus venustulus (Passeriformes, Paridae)**

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Abstract

The circular mitochondrial genome of Yellow-bellied Tit *Parus venustulus* is 16,778 bp in length, containing 13 protein-coding genes (PCGs), 2 ribosomal RNA genes, 22 transfer RNA (tRNA) genes, and a putative control region. All of the genes are encoded on the H-strand, except for one PCG (*nad6*) gene and eight tRNA genes (*tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA^{Ser}(UCN)*, *tRNA^{Pro}* and *tRNA^{Glu}*). All of these PCGs are initiated with ATG, except for *cox1*, which began with GTG, while stopped by six types of stop codons. All tRNA genes have the potential to fold into typical clover-leaf structure, with exception of the *tRNA^{Ser}(AGY)* which lacks the DHU stem.

Keywords

Complete mitochondrial genome, *parus venustulus*, passeriformes

History

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The Yellow-bellied Tit *Parus venustulus* is endemic to China, and has no subspecies differentiation (Gao, 2006). The *P. venustulus* is a small widespread passerine species of montane habitats across central and eastern China (MacKinnon et al., 2000). Unlike the majority of the other well-studied *Parus* species, which are residential, the relatively little-studied *P. venustulus* is migratory (Wei et al., 2011). In this study, the *P. venustulus* (code FJHB090) was collected from Yangxin County, Huangshi City, Hubei Province, China, in 2004. The total genomic DNA was extracted from the muscle tissue with standard phenol/chloroform methods

(Yang et al., 2010). Twelve PCR and sequencing primers were designed based on avian mtDNA primers with minor changes (Sorenson, 2003). Purified PCR fragments were directly sequenced by Shenzhen Huada Gene Technology Co., Ltd (Shenzhen, China) using primer-walking method. The Staden Package 1.7 (Staden et al., 2000) was used for sequence assembly and annotation. Identification of most tRNA genes was verified using the program tRNAscan-SE 1.21 (Lowe & Eddy, 1997). The remaining tRNAs, protein-coding genes, rRNA genes and a control region were identified by sequence comparison with other

Table 1. Mitochondrial genome characteristics of *P. venustulus*.

Gene	Position		Size (bp)	Nucleotide	Codon			Inter-genic nucleotides	Strand
	From	To			Amino acid	Initiation	Stop		
<i>tRNA^{Phe}</i>	1	72	72				0	H	
<i>12S rRNA</i>	73	1058	986				0	H	
<i>tRNA^{Val}</i>	1059	1128	70				0	H	
<i>16S rRNA</i>	1129	2728	1600				0	H	
<i>tRNA^{Leu}(UUR)</i>	2729	2803	75				0	H	
<i>nad1</i>	2812	3789	978		326	ATG	AGA	+8	H
<i>tRNA^{Ile}</i>	3801	3871	71				+11	H	
<i>tRNA^{Gln}</i>	3876	3946	71				+4	L	
<i>tRNA^{Met}</i>	3946	4014	69				-1	H	
<i>nad2</i>	4015	5054	1040		346	ATG	TA	0	H
<i>tRNA^{Trp}</i>	5055	5125	71				0	H	
<i>tRNA^{Ala}</i>	5127	5195	69				+1	L	
<i>tRNA^{Asn}</i>	5206	5278	73				+10	L	

(continued)

Table 1. Continued

Gene	Position		Size (bp)	Nucleotide	Codon			Inter-genic nucleotides	Strand
	From	To			Amino acid	Initiation	Stop		
<i>tRNA^{Cys}</i>	5279	5345	67				0	L	
<i>tRNA^{Tyr}</i>	5345	5415	71				-1	L	
<i>cox1</i>	5417	6967	1551		517	GTG	AGG	+1	H
<i>tRNA^{Ser}(UCN)</i>	6959	7033	75				-9	L	
<i>tRNA^{Asp}</i>	7038	7106	69				+4	H	
<i>cox2</i>	7117	7800	684		228	ATG	TAA	+10	H
<i>tRNA^{Lys}</i>	7802	7872	71				+1	H	
<i>atp8</i>	7874	8041	168		56	ATG	TAA	+1	H
<i>atp6</i>	8032	8715	684		228	ATG	TAA	-10	H
<i>cox3</i>	8718	9501	784		261	ATG	T	+2	H
<i>tRNA^{Gly}</i>	9502	9569	68				0	H	
<i>nad3</i>	9570	9920	351		117	ATG	TAG	0	H
<i>tRNA^{Arg}</i>	9923	9992	70				+2	H	
<i>nad4l</i>	9994	10,290	297		99	ATG	TAA	+1	H
<i>nad4</i>	10,284	11,661	1378		459	ATG	T	-7	H
<i>tRNA^{His}</i>	11,662	11,732	71				0	H	
<i>tRNA^{Ser}(AGY)</i>	11,733	11,798	66				0	H	
<i>tRNA^{Leu}(CUN)</i>	11,799	11,869	71				0	H	
<i>nad5</i>	11,870	13,687	1818		606	ATG	AGA	0	H
<i>cytb</i>	13,698	14,840	1143		381	ATG	TAA	+10	H
<i>tRNA^{Thr}</i>	14,845	14,913	69				+4	H	
<i>tRNA^{Pro}</i>	14,923	14,992	70				+9	L	
<i>nad6</i>	14,998	15,516	519		173	ATG	TAG	+5	L
<i>tRNA^{Glu}</i>	15,518	15,589	72				+1	L	
Control region	15,590	16,778	1189				0	N/A	

available Passeriformes mitochondrial sequences. The complete mitochondrial genome of *P. venustus* (GenBank Accession No. KP313823) was determined to be 16,778 bp, containing 13 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, and a putative control region. The organization and gene order of *P. venustus* mitochondrial genome (Table 1) are similar to those of other Passeriformes (Yang et al., 2010). The overall A + T content of *P. venustus* mitochondrial genome is 51.8%. Most of the mitochondrial genes were encoded on the H-strand, while one protein-coding gene (*nad6*) and eight tRNA genes (*tRNA^{Gln}*, *tRNA^{Ala}*, *tRNA^{Asn}*, *tRNA^{Cys}*, *tRNA^{Tyr}*, *tRNA^{Ser}(UCN)*, *tRNA^{Pro}* and *tRNA^{Glu}*) were located on the L-strand. All PCGs are initiated with ATG, except for *cox1*, which began with GTG, while stopped by six types of stop codons, AGA for *nad1* and *nad5*; AGG for *cox1*; TAA for *cox2*, *atp8*, *atp6*, *nad4l* and *cytb*; TAG for *nad3* and *nad6*; TA for *nad2* and T for *cox3* and *nad4*. The two rRNA genes, 986 bp in *12S rRNA* and 1600 bp in *16S rRNA*, are located between *tRNA^{Phe}* and *tRNA^{Leu}(UUR)* and separated by *tRNA^{Val}* gene. All tRNA genes, ranging from 66 to 75 bp in size, can fold into a typical cloverleaf secondary structure, with exception of the *tRNA^{Ser}(AGY)* which lacks the DHU stem. Between *tRNA^{Glu}* and *tRNA^{Phe}* genes, a putative control region was detected, in the size of 1189 bp.

Declaration of interest

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