

MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome sequence of *Ptyas mucosus*

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ABSTRACT

The complete mitochondrial genome sequence of the *Ptyas mucosus* was sequenced and reported for the first time using muscle tissue. The total length is 17 151 bp and sequence analysis showed its structure is in accordance with other snakes. The complete mitochondrial genome contains 2 rRNA genes, 21 tRNA genes, 13 protein-coding genes (PCGs), 2 control regions and 1 putative origin of L-strand replication. The gene order and nucleotide composition of *P. mucosus* are very similar with *E. bimaculata*, *E. anomala* and *E. schrenckii*. A phylogenetic tree of mitochondrial genomes indicated *P. mucosus* had the most closely relationship with *E. bimaculata*, and formed a monophyletic group with *E. bimaculata*, *E. anomala* and *E. schrenckii*.

ARTICLE HISTORY

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KEYWORDS

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In this study, the complete mitochondrial genome sequence of *Ptyas mucosus* was sequenced and reported for the first time using muscle tissue obtained from a wild individual (preserved in Traditional Chinese Medicine Resources Laboratory of Heilongjiang University of Chinese Medicine) in Guangxi, China (E109°08'48.12", N25°20'38.54"). *P. mucosus* belongs to the family Colubridae, in China is mainly distributed in the south, with fierce personality and fast attack speed, preying on rodents, toads, frogs, lizards and other snakes. It can be used as medicine with effects of treating rheumatic arthritis and nameless pain. We hope this firstly sequenced *P. mucosus* mitogenome sequence will be conducive to further studies on molecular phylogeny, conservation biology and pharmacy.

The complete mitochondrial genome sequence of *P. mucosus* was deposited in GeneBank after accurately annotated with the accession number KT982276. Its total length is 17 151 bp and sequence analysis showed is in accordance with other snakes (Yan et al. 2016; Liu & Zhao 2015a, 2015b) which contains 2 rRNA genes, 21 tRNA genes, 13 protein-coding genes(PCGs), 2 control regions and 1 putative origin of L-strand replication (O_L) (Table 1). The total composition is 25.2% C, 35.8% A, 27.1% T and 11.9% G, and a strong A-T bias (54.4%) is found, which is identical to that of the typical vertebrate mitogenome (Mulcahy & Macey 2009; Jang & Hwang 2011).

As other vertebrates, most genes are encoded on the heavy strand except for ND6 and eight tRNA genes. ATG is the most commonly used start codon in *P. mucosus* mitochondrial PCG, while ND2 start with ATT and COX1 start with GTG. When it comes to stop codons, most of PCGs terminate with TAA except COX1 and ND6 gene terminate with AGA and AGG respectively. In addition, incomplete stop codons T are used in ND1, ND2, ND3, COX2, COX3 and Cytb. The length of

Table 1. Characteristics of the complete mitochondrial genome of *P. mucosus*.

Gene	Position			Base composition (%)				Codon		
	Form	To	Size(bp)	T	C	A	G	Start	stop	strand
tRNA-Phe	2	62	62	35.5	29.0	16.1	19.3			H
12s rRNA	63	989	927	37.8	19.4	17.5	25.3			H
tRNA-Val	990	1052	63	39.1	22.0	11.0	23.4			H
16s rRNA	1053	2535	1483	40.6	22.4	15.5	21.4			H
ND1	2536	3490	955	34.7	27.1	10.9	27.3	ATG	T-	H
CRII	3491	4597	1107	31.2	27.5	30.2	11.2			-
tRNA-Leu	4598	4670	73	39.7	23.2	15.0	21.9			H
tRNA-Gln	4672	4742	71	8.4	28.1	40.8	22.5			L
tRNA-Met	4744	4805	62	19.4	30.6	29.0	20.9			H
ND2	4806	5837	1032	40.1	25.8	7.5	26.4	ATT	T-	H
tRNA-Trp	5838	5900	65	36.9	24.6	15.3	23.0			H
tRNA-Ala	5903	5966	64	39.0	26.5	10.9	23.4			L
tRNA-Asn	5968	6040	73	32.8	21.9	17.8	27.3			L
O _L	6041	6075	35	25.7	17.1	31.4	25.7			-
tRNA-Cys	6076	6135	60	20.0	25.0	25.0	30.0			L
tRNA-Tyr	6136	6197	62	35.4	32.2	9.6	22.5			L
COX1	6199	7799	1602	30.2	29.8	15.5	24.0	GTG	AGA	H
tRNA-Ser	7790	7857	67	26.0	30.1	13.6	23.2			L
tRNA-Asp	7858	7920	63	26.0	30.1	13.6	23.2			H
COX2	7921	8605	685	35.4	24.5	14.8	25.1	ATG	T-	H
tRNA-Lys	8606	8668	63	31.7	33.3	19.0	15.8			H
ATP8	8670	8825	156	45.5	26.2	4.4	23.7	ATG	TAA	H
ATP6	8816	9496	681	36.7	30.8	8.8	23.6	ATG	TAA	H
COX3	9496	10279	784	34.0	26.4	13.9	25.6	ATG	T-	H
tRNA-Gly	10280	10340	61	37.7	26.2	14.7	21.3			H
ND3	10341	10683	343	36.1	30.3	9.9	23.6	ATG	T-	H
tRNA-Arg	10684	10747	64	35.9	26.5	15.6	21.8			H
ND4L	10748	11038	291	37.1	31.6	10.6	20.6	ATG	TAA	H
ND4	11038	12375	1338	34.7	27.8	10.0	27.2	ATG	TAA	H
tRNA-His	12377	12439	63	36.5	26.9	14.2	22.2			H
tRNA-Ser	12440	12493	54	27.7	18.5	18.5	35.1			H
tRNA-Leu	12494	12564	71	30.9	26.7	19.7	22.5			H
ND5	12565	14331	1767	38.8	27.0	9.5	24.5	ATG	TAA	H
ND6	14326	14824	498	51.4	17.6	4.4	26.35	ATG	AGG	L
tRNA-Glu	14834	14895	62	37.0	27.4	12.9	22.5			H
Cytb	14894	16010	1117	34.7	29.0	9.8	26.4	ATG	T-	L
tRNA-Thr	16011	16075	65	29.2	26.1	20.0	24.6			H
tRNA-Pro	16076	16136	61	32.7	26.2	11.4	29.5			L
CRI	16137	17151	1015	32.0	27.5	30.1	10.3			-
Total			17 151	27.1	25.2	35.8	11.9			

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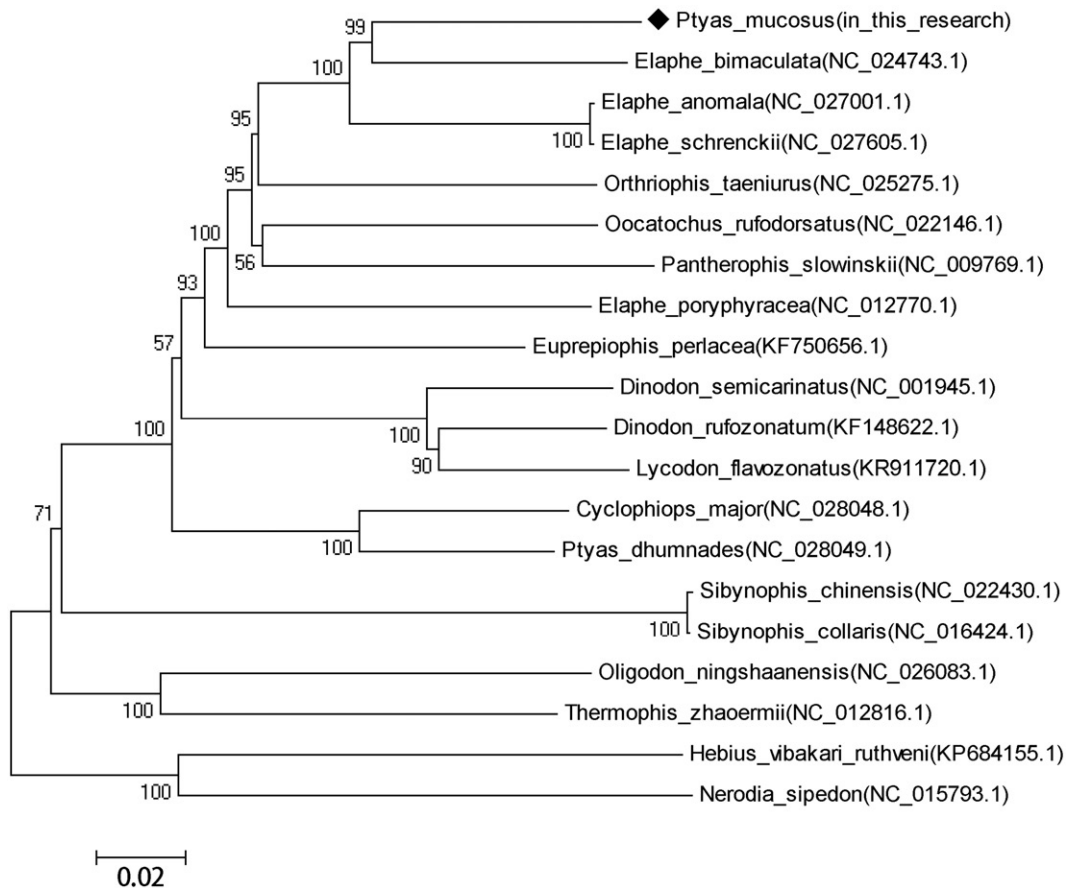


Figure 1. Phylogenetic tree of mitochondrial genomes analyses of 20 species snakes of Colubridae based on the NJ method.

12S rRNA gene and 16S rRNA gene are 927 bp and 1483 bp in length, respectively.

The mitochondrial genome sequence of *P. mucosus* contains two large non-coding regions (CRs; D-loop), which engaged in the processes of replication and transcription of mitochondrial DNA. CRI has 1015 bp, discovered between tRNA-Pro and tRNA-Phe, which is the typical position for CRI in vertebrate genomes. CRII is 1107 bp in length, located between ND1 and tRNA-Leu, which is different from some snakes (Li et al. 2014; Liu & Zhao 2015a, 2015b). The putative origin of L-strand replication (O_L) with length of 35 bp, which located between tRNA-Asn and tRNA-Cys, is similar to most vertebrates (Su et al. 2007).

A phylogenetic tree (Figure 1) of mitochondrial genomes analyses of 20 species snakes of Colubridae was made based on the NJ method, *P. mucosus* has the most closely relationship with *E. bimaculata*, and formed a monophyletic group with *E. bimaculata*, *E. anomala* and *E. schrenckii*.

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Declaration of interest

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