

MITOGENOME ANNOUNCEMENT

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Sequencing and analysis of mitochondrial genome of *Elaphe carinata* (Reptilia, Squamata, Colubridae)

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ABSTRACT

The complete mitochondrial genome of *Elaphe carinata* was sequenced and analysed using muscle tissue for the first time. The genome is 17 154 bp in length. The complete mitochondrial genome contains 22 tRNA genes, 13 protein-coding genes (PCGs), two rRNA genes, two control regions (CRI and CRII) and one putative origin of L-strand replication. The gene order and nucleotide composition of *E. carinata* are very similar with *E. davidi*, *E. schrenckii*, *E. anomala* and *E. bimaculata*. A phylogenetic tree of mitochondrial genomes analyses of 16 species snakes of Colubridae was made based on the Neighbour-Joining (NJ) method, *E. carinata* has the most closely relationship with *E. davidi*, while *E. poryphyracea* and *Euprepiophis perlacea* are special species.

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Elaphe carinata belonging to genus *Elaphe* of family Colubridae, is a large, ferocious and non-toxic snake, in China is mainly distributed in the south. It can be used for the treatment of epilepsy, pharyngitis, scrofula, scabies and other symptoms. In this study, complete mitochondrial genome of the *E. carinata* was sequenced and analysed 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 Yunnan, China. GenBank accession number KU180459 will be shown after the manuscript is accepted.

Organization of the complete mitochondrial genome sequence of *E. carinata* is shown in Table 1. Its total length is 17 154 bp. It consists of 13 protein-coding genes (PCGs), two rRNA genes, 22 tRNA genes, two control regions (CRI and CRII) and one putative origin of L-strand replication, which is similar to that of other reported snakes (Jang & Hwang 2011; Yan et al. 2014), especially to that of *E. davidi* (KM401547.1), *E. schrenckii* (KM888955.1), *E. anomala* (KM900218.1) and *E. bimaculata* (KM065513.1). As other vertebrates, most of these genes are coded on the heavy strand except for eight tRNA genes and ND6. The total composition is 25.2% C, 35.8% A, 27.0% T and 12.0% G with an obvious AT bias (62.8%), which is identical to that of other typical vertebrate mitogenomes (Mulcahy & Macey 2009; Jang & Hwang 2011).

As reported in other snakes. Except for ND2 (ATT) and COXI (GTG), the other 11 PCGs use ATG as start codon. When it comes to stop codons, eight PCGs end with the complete stop codon: TAA (ATP8, ATP6, ND4L, ND4 and ND5), TAG (ND2), AGA (COXI), AGG (ND6), while incomplete stop codons T are used in other five PCGs (ND1, ND3, COX2, COX3

Table 1. Gene organization of the complete mitochondrial genome of *E. carinata*.

Gene	Position		Size (bp)	Base composition (%)				Codon		
	Form	T _o		T	C	A	G	Start	Stop	Strand
tRNA-Phe	2	62	62	29.0	19.4	35.5	16.1			H
12s rRNA	63	989	927	19.4	25.4	37.8	17.5			H
tRNA-Val	990	1052	63	25.4	22.2	39.7	11.1			H
16s rRNA	1053	2535	1483	22.3	21.3	40.7	14.4			H
ND1	2536	3490	955	27.1	27.3	34.7	10.9	ATG	T-	H
tRNA-Ile	3491	3556	66	16.7	28.8	27.3	27.3			H
CRII	3557	4598	1042	32.1	27.5	30.0	10.4			-
tRNA-Leu	4599	4671	73	27.0	22.0	39.7	15.1			H
tRNA-Gln	4673	4743	71	28.2	22.5	40.8	8.5			L
tRNA-Met	4745	4806	62	19.4	30.6	29.0	21.0			H
ND2	4807	5838	1032	25.9	26.5	40.1	7.6	ATT	TAG	H
tRNA-Trp	5837	5901	65	24.6	23.1	36.9	15.4			H
tRNA-Ala	5904	5968	65	26.2	24.6	38.5	10.8			L
tRNA-Asn	5969	6041	73	21.9	27.4	32.9	17.8			L
O _L	6042	6076	35	25.7	17.1	31.4	25.7			-
tRNA-Cys	6077	6136	60	25.0	30.0	20.0	25.0			L
tRNA-Tyr	6137	6198	62	32.3	22.6	35.4	9.6			L
COX1	6200	7801	1602	30.0	24.0	30.4	15.6	GTG	AGA	H
tRNA-Ser	7792	7858	67	32.8	23.9	28.4	14.9			L
tRNA-Asp	7859	7921	63	30.2	22.2	30.2	17.5			H
COX2	7922	8606	685	24.5	25.1	35.4	14.8	ATG	T-	H
tRNA-Lys	8607	8669	63	33.3	15.9	31.7	19.0			H
ATP8	8671	8826	156	26.3	23.7	45.5	4.5	ATG	TAA	H
ATP6	8817	9497	681	30.8	23.6	36.7	8.8	ATG	TAA	H
COX3	9497	10 280	784	26.4	25.6	34.1	13.9	ATG	T-	H
tRNA-Gly	10 281	10 341	61	26.2	21.3	37.7	14.8			H
ND3	10 342	10 684	343	30.3	23.6	36.2	9.9	ATG	T-	H
tRNA-Arg	10 685	10 748	64	26.6	21.9	36.0	15.6			H
ND4L	10 749	11 039	291	31.6	20.6	37.1	10.7	ATG	TAA	H
ND4	11 039	12 376	1338	27.9	27.3	34.8	10.1	ATG	TAA	H
tRNA-His	12 378	12 440	63	27.0	22.2	36.5	14.3			H
tRNA-Ser	12 441	12 494	54	18.5	35.1	27.8	18.5			H
tRNA-Leu	12 495	12 565	71	26.8	22.5	31.0	19.7			H
ND5	12 566	14 332	1767	27.0	24.5	38.8	9.6	ATG	TAA	H
ND6	14 328	14 828	501	17.8	26.5	51.3	4.4	ATG	AGG	H
tRNA-Glu	14 834	14 896	62	27.4	22.6	37.1	12.9			L
Cytb	14 895	16 011	1117	29.0	26.4	34.7	9.8	ATG	T-	H
tRNA-Thr	16 012	16 076	65	26.2	24.6	29.2	20.0			H
tRNA-Pro	16 077	16 137	61	26.2	29.5	32.8	11.5			L
CRI	16 138	17 154	1017	32.0	27.5	30.2	10.3			-
Total			17 154	27.0	25.2	35.8	12.0			

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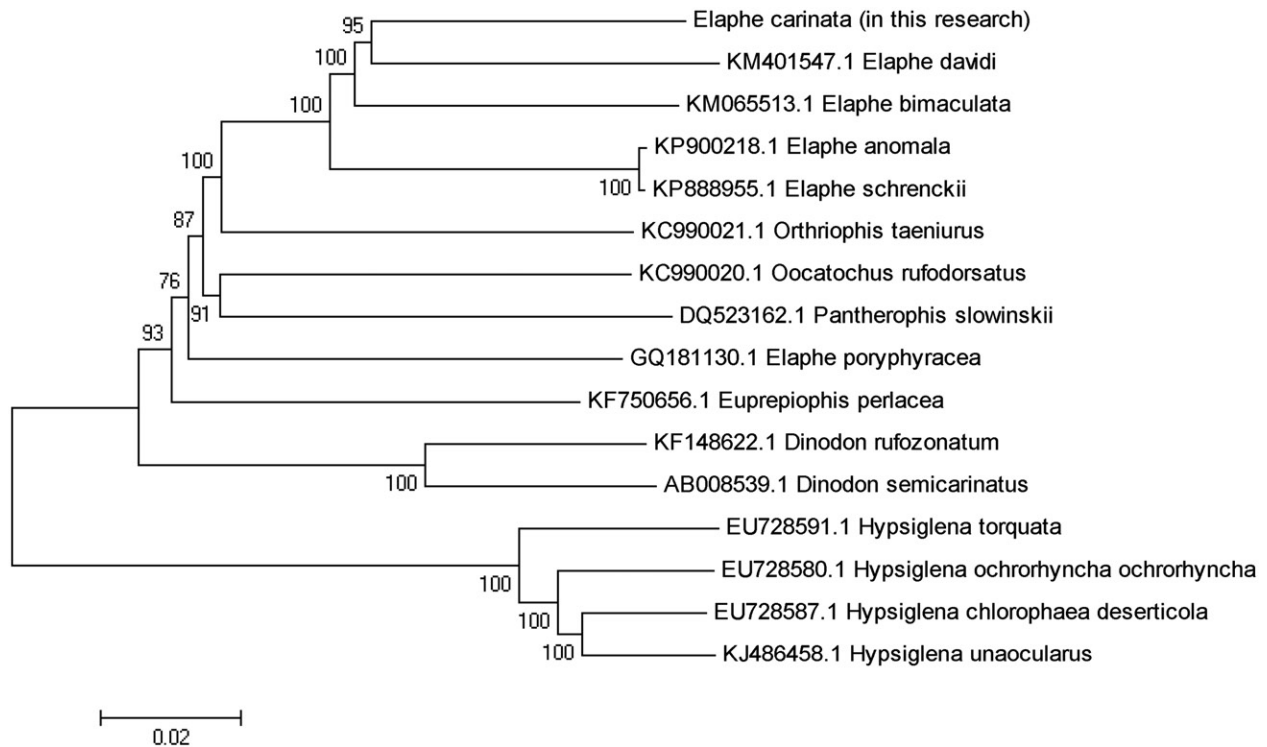


Figure 1. Phylogenetic tree of mitochondrial genomes analyses of 16 species snakes of Colubridae based on the NJ method.

and Cytb), which may be completed by posttranscriptional poly-adenylation (Boore 2001).

The mitogenome of *E. carinata* contains two CRs, surrounded by tRNA-Pro and tRNA-Phe (CRI), and by tRNA-Ile and tRNA-Leu (CRII), respectively. CRI has 1017 bp and CRII has 1042 bp in length, which is identical to that of other typical vertebrate mitogenomes (Li et al. 2014; Liu et al. 2015a, 2015b). The 22 tRNA genes are interspersed along the whole genome. The sequence length of the 12S rRNA and 16S rRNA are 927 and 1483 bp, respectively. The putative origin of L-strand replication (O_L) is 35 bp in length, located between tRNA-Asn and tRNA-Cys, which is similar to most vertebrates (Su et al. 2007; Liu et al. 2015a, 2015b).

A phylogenetic tree (Figure 1) of mitochondrial genomes analyses of 16 species snakes of Colubridae was made based on the NJ method, *E. carinata* has the most closely relationship with *E. davidi* and formed a monophyletic group with *E. davidi*, *E. schrenckii*, *E. anomala* and *E. bimaculata*, meanwhile *E. poryphyracea* and *Euprepiophis perlacea* are special species.

We hoped that this firstly sequenced and analysis of mitochondrial genome of *E. carinata* will be conducive to further studies on population genetics, molecular phylogeny and pharmacy of this species.

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Disclosure statement

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

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