

MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of the Asian tapirs
(*Tapirus indicus*): the only extant Tapiridae species in the old world**

Yuttamol Muangkram^{1,2}, Worawidh Wajjwalku², Nongnid Kaolim², Waradee Buddhakosai³, Sumate Kamolnorrath⁴, Boripat Siriaronrat⁴, Wanlaya Tipkantha⁴, Khwanruean Dongsard⁵, Umaporn Maikaew⁶, and Saowaphang Sanannu⁷

¹The Graduate School, Kasetsart University, Jatujak, Bangkok, Thailand, ²Faculty of Veterinary Medicine, Kasetsart University, Nakhon Pathom, Thailand, ³Interdisciplinary Graduate Program in Genetic Engineering, Kasetsart University, Jatujak, Bangkok, Thailand, ⁴Bureau of Conservation, Research and Education, Zoological Park Organization, Dusit, Bangkok, Thailand, ⁵Chiang Mai Zoo, Muang, Chiang Mai, Thailand, ⁶Khao Kheow Open Zoo, Sriracha, Chonburi, Thailand, and ⁷Dusit Zoo, Dusit, Bangkok, Thailand

Abstract

Asian tapir (*Tapirus indicus*) is categorized as Endangered on the 2008 IUCN red list. The first full-length mitochondrial DNA (mtDNA) sequence of Asian tapir is 16,717 bp in length. Base composition shows 34.6% A, 27.2% T, 25.8% C and 12.3% G. Highest polymorphic site is on the control region as typical for many species.

Keywords

Malayan tapir, mitochondrial DNA, Perissodactyla, Thailand

History

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The Asian or Malayan tapir (*Tapirus indicus* Desmarest, 1819) is categorized as Endangered on the 2008 IUCN red list (Lynam et al., 2008). It is the only extant tapir found in Southeast Asia (Thailand, Myanmar, Malaysia and Indonesia) that is isolated from the other three species found in Neotropical America (Carter, 1984). In this study, three Asian tapirs were randomly selected from three haplotype: Ti-1, Ti-2, and Ti-3 (Muangkram et al., 2013) from Zoological Park Organization of Thailand. DNA was extracted (Nelson & Krawetz, 1992) and amplified using seventeen primer pairs (Maikaew et al., 2007; Muangkram et al., 2013; Ward et al., 1999) (Supplementary Table 1). PCR was performed at 95 °C for 3 min, followed by 35 cycles at 95 °C for 30 s, 30 s at 50–59 °C, 60 s at 72 °C and final incubation at 72 °C for 10 min. PCR products were purified with the Gel

Elution kit (GeneMark, Taipei, Taiwan) according to the manufacturer's instruction. DNA sequencing results were provided by 1st BASE Laboratories in Malaysia. The sequences were aligned using CLUSTALW (Thompson et al., 1994) and calculated using DnaSP v5 (Librado & Rozas, 2009). The complete mitochondrial DNA (mtDNA) sequence of three Asian tapirs in this study was deposited in GenBank under accession numbers KJ417808–KJ417810.

The first complete mtDNA sequence of *Tapirus indicus* is 16,717 bp in length (all three haplotypes) with base composition of 34.63% A, 25.84% C, 12.29% G and 27.24% T. It is circular double-stranded structure and consists of 13 protein-coding genes, 12S rRNA, 16S rRNA, 22 tRNA genes, the origin of replication (O_L), and control region (CR) (Table 1). Most of the

Table 1. Composition of the complete mitochondrial genome sequence of the Asian tapir (*Tapirus indicus*) showing heavy (H) and light (L) strand is total 16,717 bp in length. The baseline gene sequence corresponds to GenBank accession no. KJ417808 (this study).

Gene/element	Strand	Start	Stop	Size (bp)	Start codon	Stop codon	GC%	Anti-codon	Intergenic nucleotides**
<i>tRNA-Phe</i>	H	1	68	68			36.76	GAA	0
<i>12S rRNA</i>	H	69	1037	969			39.32		0
<i>tRNA-Val</i>	H	1038	1104	67			34.33	TAC	0
<i>16S rRNA</i>	H	1105	2685	1581			36.50		0
<i>tRNA-Leu UUR</i>	H	2686	2760	75			41.33	TAA	2
<i>ND1</i>	H	2763	3719	957	ATG	TAA	39.81		–1
<i>tRNA-Ile</i>	H	3719	3787	69			28.99	GAT	–3
<i>tRNA-Gln</i>	L	3785	3857	73			36.99	TTG	2

(continued)

Table 1. Continued

Gene/element	Strand	Start	Stop	Size (bp)	Start codon	Stop codon	GC%	Anti-codon	Intergenic nucleotides**
<i>tRNA-Met</i>	H	3860	3928	69			47.83	CAT	0
<i>ND2</i>	H	3929	4970	1042	ATA	Taa*	35.99		0
<i>tRNA-Trp</i>	H	4971	5038	68			37.31	TCA	5
<i>tRNA-Ala</i>	L	5044	5112	69			37.68	TGC	1
<i>tRNA-Asn</i>	L	5114	5186	73			41.10	GTT	0
<i>O_L</i>	H	5187	5221	35			57.14		-3
<i>tRNA-Cys</i>	L	5219	5284	66			42.42	GCA	0
<i>tRNA-Tyr</i>	L	5285	5350	66			39.39	GTA	1
<i>COI</i>	H	5352	6896	1545	ATG	TAA	38.90		-3
<i>tRNA-Ser UCN</i>	L	6894	6962	69			43.48	TGA	8
<i>tRNA-Asp</i>	H	6971	7037	67			25.37	GTC	0
<i>COII</i>	H	7038	7721	684	ATG	TAA	37.43		3
<i>tRNA-Lys</i>	H	7725	7792	68			29.41	TTT	1
<i>ATP8</i>	H	7794	7997	204	ATG	TAA	28.43		-43
<i>ATP6</i>	H	7955	8635	681	ATG	TAA	38.62		-1
<i>COIII</i>	H	8635	9418	784	ATG	Taa*	41.45		0
<i>tRNA-Gly</i>	H	9419	9487	69			33.33	TCC	0
<i>ND3</i>	H	9488	9833	346	ATA	Taa*	38.73		1
<i>tRNA-Arg</i>	H	9835	9902	68			22.06	TCG	0
<i>ND4L</i>	H	9903	10,199	297	ATG	TAA	35.02		-7
<i>ND4</i>	H	10,193	11,570	1378	ATG	Taa*	37.16		0
<i>tRNA-His</i>	H	11,571	11,639	69			23.19	GTG	0
<i>tRNA-Ser AGY</i>	H	11,640	11,698	59			38.98	GCT	0
<i>tRNA-Leu CUN</i>	H	11,699	11,768	70			32.86	TAG	0
<i>ND5</i>	H	11,769	13,589	1821	ATA	TAA	38.50		-17
<i>ND6</i>	L	13,573	14,100	528	ATG	TAA	36.93		0
<i>tRNA-Glu</i>	L	14,101	14,169	69			34.78	TTC	5
<i>CYTB</i>	H	14,175	15,314	1140	ATG	AGA	41.75		0
<i>tRNA-Thr</i>	H	15,315	15,382	68			44.12	TGT	1
<i>tRNA-Pro</i>	L	15,384	15,449	66			40.30	TGG	0
CR									
ETAS domain	H	15,450	15,755	306			31.70		0
Central domain	H	15,756	16,070	315			44.44		0
CSB domain	H	16,071	16,717	647			40.03		0

*The Taa indicates the incomplete stop codon completed by the additional of 3' A residue formed stop codon by post-transcriptional polyadenylation.
 ***(+) positive value indicates gap nucleotide, (-) negative value indicates overlapped nucleotides, and (0) zero indicates no intergenic nucleotide between two adjacent genes.

protein-coding genes start with an ATG codon, except *ND2*, *ND3* and *ND5* that start with an ATA codon. The stop with a TAA codon represents a typical codon, except for one gene, *CYTB*, which has an AGA codon. The incomplete stop codon (Taa) is discovered in some genes including *COIII*, *ND2*, *ND3* and *ND4*. It is a created stop codon by the additional of a 3' A residue in post-transcriptional polyadenylation process (Ojala et al., 1981). The 22 *tRNA* genes vary in length from 59 bp of *tRNA-Ser AGY* to 75 bp of *tRNA-Leu UUR* (68.4 ± 3.1 bp). The anti-codon of all tRNA genes among *Perissodactyla* species shows a similar anti-codon pattern to the Asian tapir.

The *O_L* of our old world Tapiridae species forms the 35 bp stable stem-loop secondary structure matched well with the representative new world Tapiridae species, the Brazilian tapir. This replication element is located within WANCY region that seen in other vertebrate species (Seutin et al., 1994). The CR is bound by *tRNA-Pro* and *tRNA-Phe* sized 1268 bp in length. The long repetitive motif 5'-(CACACGTATACG CATA)₁₈-3' is located on CSB domain.

Among three haplotypes of Asian tapir revealed twelve polymorphic sites with transitional substitution. Nucleotide diversity was 0.00048 ± 0.00015 . Only two non-synonymous substitutions were identified: (1) position 7221 on *COII* (Glu-GAA ← → Lys-AAA), and (2) position 14,884 on *CYTB* (Ser-TCA ← → Lys-TTA). CR contained the highest variation (0.39%).

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Declaration of interest

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

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Supplementary material available online
Supplementary Table 1

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