The complete mitochondrial genome of western painted turtle, Chrysemys picta bellii (Chrysemys, Emydidae)

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of western painted turtle, *Chrysemys picta bellii* (*Chrysemys*, Emydidae)

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Abstract

In this study, we report the complete mitochondrial genome sequence of western painted turtle, *Chrysemys picta bellii*. The genome is found to be 16,875 bp in length and has a base composition of A (34.4%), G (13.0%), C (26.0%), and T (26.6%). Similar to other turtles, it contains a typically conserved structure including 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 control region (D-loop). Most of the genes are encoded on H-strand, except for the eight tRNA and *ND6* genes. All protein-coding genes start with an ATN codon except for *COX1* and *ND4*, which initiate with GTG instead, and terminate with the typical stop codon (TAA/TAG) or a single T (T-) or an unexpected codon of AGG. The complete mitochondrial genome sequence provided here would be useful for further phylogenetic analysis and conservation genetic studies in *C. p. bellii*.

Keywords

C. picta bellii, genome, mitochondrion, western painted turtle

History

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The painted turtle, *Chrysemys picta*, has been recognized as a continentally distributed species with a wide range from southern Canada to extreme northern Mexico of North America (Conant & Collins, 1991; Iverson, 1992). Currently, four subspecies are recognized for this species, including *C. p. bellii*, *C. p. dorsalis*, *C. p. marginata*, and *C. p. picta* (Bishop & Schmidt, 1931). However, only the mitochondrial genome of *C. p. picta* was reported previously (AF069423; Mindell et al., 1999). Here, using the CLC Genomic Workbench v3.6 (2010), we assembled and analyzed the mitochondrial genome of western painted turtle (GenBank accession no. KF874616), *C. p. bellii*, one of the most widespread, abundant, and well-studied turtles, with the Illumina sequencing data released by Shaffer et al. (2013). This mitochondrial sequence reported here added a new genetic resource for the family Emydidae and would contribute to better understand population genetics and dynamic evolution of *C. p. bellii*.

The complete mitochondrial genome sequence of *C. p. bellii* had 16,875 bp in length and contained a total of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (*12S rRNA* and *16S rRNA*), and 1 non-coding control region (D-loop). Most of these genes are encoded on the H-strand except for the *ND6* subunit gene and 8 tRNA genes (Table 1). The overall base composition was A (34.4%) > T (26.6%) > C (26.0%) > G (13.0%), with an AT bias of 61.0%. Further comparison with earlier reported turtle mitochondrial genomes revealed that gene synteny was conserved

Table 1. List of genes encoded by *Chrysemys picta bellii* mitochondrial genome.

	Position			Base composition (%)						
Gene	From	To	Size (bp)	A	C	G	T	Start codon	Stop codon	Strand
$tRNA^{Phe}$	1	70	70	37.1	22.9	18.6	21.4			H
12S rRNA	71	1038	968	37.7	24.0	17.0	21.3			H
$tRNA^{Val}$	1039	1107	69	43.5	18.8	11.6	26.1			H
16S rRNA	1109	2722	1614	39.9	22.2	16.5	21.4			H
$tRNA^{Leu}$	2724	2799	76	27.6	26.3	22.4	23.7			H
ND1	2800	3771	972	32.5	27.9	10.8	28.8	ATA	TAG	H
$tRNA^{Ile}$	3771	3841	71	28.2	21.1	23.9	26.8			H
$tRNA^{Gln}$	3841	3912	72	23.6	9.7	26.4	40.3			L
$tRNA^{Met}$	3912	3980	69	31.9	26.1	14.5	27.5			H
ND2	3981	5021	1041	37.9	30.0	8.1	24.0	ATA	TAG	H

(*continued*)

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Table 1. Continued.

Gene	Position		Size (bp)	Base composition (%)				Start codon	Stop codon	Strand
	From	To		A	C	G	T			
tRNA^{Trp}	5020	5094	75	36.0	24.0	18.7	21.3			H
tRNA^{Ala}	5096	5164	69	36.2	11.6	17.4	34.8			L
tRNA^{Asn}	5166	5238	73	26.0	16.5	26.0	31.5			L
tRNA^{Cys}	5264	5329	66	27.3	16.7	24.2	31.8			L
tRNA^{Tyr}	5330	5400	71	21.1	15.5	28.2	35.2			L
COX1	5402	6949	1548	29.6	24.5	16.3	29.6	GTG	AGG	H
tRNA^{Ser}	6941	7011	71	26.8	15.5	26.7	31.0			L
tRNA^{Asp}	7014	7083	70	37.1	15.7	12.9	34.3			H
COX2	7084	7770	687	34.6	25.3	13.6	26.5	ATG	TAA	H
tRNA^{Lys}	7772	7842	71	33.8	19.7	21.1	25.4			H
ATP8	7844	8032	189	39.7	27.5	5.8	27.0	ATG	TAA	H
ATP6	8002	8685	684	32.9	30.0	10.5	26.6	ATG	TAA	H
COX3	8685	9468	784	30.0	27.2	14.9	27.9	ATG	T– –	H
tRNA^{Gly}	9469	9537	69	39.1	16.0	11.6	33.3			H
ND3	9538	9887	349	30.6	26.1	13.2	30.1	ATA	T– –	H
tRNA^{Arg}	9888	9957	70	34.3	21.4	17.1	27.2			H
ND4L	9958	10,254	297	31.0	26.9	10.4	31.7	ATG	TAA	H
ND4	10,248	11,628	1381	34.8	28.9	10.5	25.8	GTG	T– –	H
tRNA^{His}	11,629	11,698	70	41.4	15.7	12.9	30.0			H
tRNA^{Ser}	11,699	11,763	65	32.3	24.6	16.9	26.2			H
tRNA^{Leu}	11,764	11,835	72	36.1	16.7	18.0	29.2			H
ND5	11,836	13,644	1809	33.5	27.2	11.4	27.9	ATG	TAG	H
ND6	13,807	14,331	525	13.9	8.4	32.7	45.0	ATG	AGG	L
tRNA^{Glu}	14,332	14,399	68	33.8	13.2	16.2	36.8			L
CytB	14,403	15,542	1140	31.2	30.4	11.0	27.4	ATG	TAA	H
tRNA^{Thr}	15,547	15,621	75	36.0	21.3	13.3	29.4			H
tRNA^{Pro}	15,622	15,691	70	28.6	12.9	27.1	31.4			L
D-loop	15,692	16,875	1184	33.6	18.3	13.2	34.9			H

among them (Chen et al., 2013; Jung et al., 2006; Russell & Beckenbach, 2008; Shin et al., 2013).

The 13 identified protein-coding genes were 11,406 bp in length and encoded 3791 amino acids in total. Of them, eight initiated with ATG, while *ND1*, *ND2*, and *ND3* used ATA as the start codon, and *COX1* and *ND4* started with GTG. Five protein-coding genes ended with TAA, whereas, *ND1*, *ND2*, and *ND5* terminated with TAG, and *COX1* and *ND6* stopped with AGG. Incomplete stop codons (T-) were observed in *COX3*, *ND3*, and *ND4*.

The 22 tRNA genes of *C. p. bellii* range in size from 65 bp (*tRNA*^{Ser}) to 76 bp (*tRNA*^{Leu}). Of them, 21 could fold into typical cloverleaf secondary structure except for *tRNA*^{Ser}. The two rRNA genes, *12S* and *16S rRNA*, were 968 bp and 1614 bp in length, respectively. They were located between the *tRNA*^{Phe} and *tRNA*^{Leu} genes and further separated by *tRNA*^{Val}. The control region of *C. p. bellii* mtDNA was 1184 bp long and located between *tRNA*^{Pro} and *tRNA*^{Phe}.

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Declaration of interest

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