

## MITOGENOME ANNOUNCEMENT

Complete sequence and gene organization of the mitochondrial genome of *Podocnemis unifilis* (Pleurodira: Podocnemididae)Xuming Zhou<sup>1,2</sup>, Ling Wang<sup>3</sup>, Liu-Wang Nie<sup>3</sup>, and Ming Li<sup>1</sup><sup>1</sup>Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing, China, <sup>2</sup>University of Chinese Academy of Sciences, Beijing, China, and <sup>3</sup>Life Science College, Anhui Normal University, Wuhu, Anhui, China

## Abstract

The mitochondrial genome of *Podocnemis unifilis* (Pleurodira: Podocnemididae) is 16,493 bp in length, which contains 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs, and a control region. The A+T content of the overall base composition of H-strand is 61.7% (T: 27.7%, C: 25.5%, A: 34.0%, G: 12.8%). ATP6, ATP8, CO3, ND4-6 and Cyt *b* genes begin with ATG as start codon, ND1, ND2 and ND4L begin with ATT, CO1 starts with GTG, CO2 starts with ATA, ND3 starts with ATC. ATP6, CO2, ND4L and ND5 genes are terminated with TAA as stop codon, ND1, ND2, ND3, ND6 and CO1 end with TAG, and the other four protein-coding genes end with an incomplete stop codon (a single stop nucleotide T or TA). A long unit repeat region is found in the control region.

## Keywords

Mitochondrial, Podocnemididae, *Podocnemis unifilis*

## History

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According to the traditional classification based on morphology, Testudines was divided into two reciprocally monophyletic clades, Cryptodira and Pleurodira. In Pleurodira, there are three families (Chelidae, Pelomedusidae and Podocnemididae), and approximately 81 species (Rhodin et al., 2010), representing a quarter of total species diversity in turtles. The Yellow-spotted river turtle (*Podocnemis unifilis*) belonged to Podocnemididae, which represents an important economic and cultural resource for habitants in regions of South America (Mittermeier, 1978). Unfortunately, anthropogenic over exploitation and habitat destruction has caused drastic population declines in this species (Escalona & Fa, 1998; Thorbjarnarson et al., 1997) and it is classified as Vulnerable by the IUCN Red Data Book (IUCN, 1994). Comparing with Cryptodira, Pleurodira has seldom sources of sequence information for complete mitochondrial genomes and in particular, there was only three published complete mitochondrial genomes from this clade (Wang et al., 2012; Zardoya & Meyer, 1998). Therefore, the genomic information of Pleurodira is too scarce to explain its phylogenetic relationships and evolutionary history.

The samples of *P. unifilis* were obtained from the specimen storeroom of College of Life Sciences in Anhui Normal University, and preserved at  $-20^{\circ}\text{C}$  before DNA extraction. Total genomic DNA was extracted from the tissues using with the proteinase K method (Sambrook & Russell, 2001) and dissolved in TE buffer. The extracted DNA was diluted 10 times stored at  $-20^{\circ}\text{C}$  until use as a template for PCR (polymerase chain reactions) amplification.

Based on the mitochondrial genome sequences of *Pelomedusa subrufa* (GenBank accession numbers: AF039066), *Chelonia mydas* (GenBank accession numbers: AB012104) and *Manuremys reevesii* (GenBank accession numbers: AY676201), the primers for conserved mtDNA (12S rRNA, 16S rRNA, ND1-2, CO1 and Cyt *b*) were designed for PCR and sequencing. The remained parts of the mitochondrial genome were amplified used primer walking.

The organization of mitochondrial genome is shown in Table 1. The complete mtDNA was 16,493 bp in length and contains 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNAs genes, and a large noncoding region (control region). The overall base composition of H-strand was as follows: T (27.7%), C (25.5%), A (34.0%), G (12.8%), and the A + T content (61.7%). Within the mitochondrial genome of *P. unifilis*, there were 11 reading frame overlaps (ND1 gene and tRNA-*Ile* share one nucleotide; tRNA-*Ile* and tRNA-*Gln* share one nucleotide; tRNA-*Gln* and tRNA-*Met* share one nucleotide; ND2 and tRNA-*Trp* share two nucleotides; CO2 and tRNA-*Lys* share one nucleotide; ATP6 and CO3 share eight nucleotides; ND3 and tRNA-*Arg* share two nucleotides; ND4L and ND4 share seven nucleotides; tRNA-*Ser* (AGY) and tRNA-*Leu* (CUN) share one nucleotide; tRNA-*Leu* (CUN) and ND5 share one nucleotide and Cyt *b* and tRNA-*Thr* share one nucleotide). ATP6, ATP8, CO3, ND4-6 and Cyt *b* genes began with ATG as start codon, ND1, ND2 and ND4L began with ATT, CO1 started with GTG, CO2 started with ATA, ND3 started with ATC. ATP6, CO2, ND4L and ND5 genes are terminated with TAA as stop codon, ND1, ND2, ND3, ND6 and CO1 ended with TAG, and the other four protein-coding genes ended with an incomplete stop codon (a single stop nucleotide T or TA). The non-coding regions include a control region (D-loop) and twelve intergenic spacers (range from 1 to 8 bp). The control regions are 985 bp in length, and the A + T content of this region was 74.8% (A: 33.9%, C: 15.7%, G: 9.6%, T: 40.9%).

Table 1. Location of organization in the mtDNA of yellow-spotted river turtle.

Gene/region	Start position	Stop position	Spacer (+) Overlap (–)	Size (bp)	Start codon	Stop codon	Strand
tRNA <sup>Phe</sup>	1	69		69			H
12SrRNA	70	1027		958			H
tRNA <sup>Val</sup>	1028	1098		71			H
16SrRNA	1099	2695		1597			H
tRNA <sup>Leu(UR)</sup>	2696	2771		76			H
ND1	2772	3743	–1	972	ATT	TAG	H
tRNA <sup>Ile</sup>	3743	3812	–1	70			H
tRNA <sup>Gln</sup>	3812	3882	–1	71			L
tRNA <sup>Met</sup>	3882	3950		69			H
ND2	3951	4994	–2	1044	ATT	TAG	H
tRNA <sup>Trp</sup>	4993	5063	2	71			H
tRNA <sup>Ala</sup>	5066	5134	2	69			L
tRNA <sup>Asn</sup>	5137	5209	8	73			L
tRNA <sup>Cys</sup>	5218	5284	1	67			L
tRNA <sup>Tyr</sup>	5286	5356	1	71			L
CO1	5358	6908	2	1551	GTG	TAG	H
tRNA <sup>Ser(UCN)</sup>	6911	6981	8	71			L
tRNA <sup>Asp</sup>	6990	7057		68			H
CO2	7058	7741	–1	684	ATA	TAA	H
tRNA <sup>Lys</sup>	7741	7811	3	71			H
ATP8	7815	7974		159	ATG	T	H
ATP6	7973	8662	–8	690	ATG	TAA	H
CO3	8655	9438		784	ATG	TA	H
tRNA <sup>Gly</sup>	9439	9507		69			H
ND3	9508	9858		351	ATC	TAG	H
tRNA <sup>Arg</sup>	9857	9923	1	67			H
ND4L	9925	10,221	–7	297	ATT	TAA	H
ND4	10,215	11,595		1381	ATG	T	H
tRNA <sup>His</sup>	11,596	11,665		70			H
tRNA <sup>Ser(AGN)</sup>	11,666	11,726	–1	61			H
tRNA <sup>Leu(CUN)</sup>	11,726	11,798	–1	73			H
ND5	11,802	13,613	8	1812	ATG	TAA	H
ND6	13,632	14,156		525	ATG	TAG	L
tRNA <sup>Glu</sup>	14,157	14,224	3	68			L
Cytb	14,228	15,367	–1	1141	ATG	T	H
tRNA <sup>Thr</sup>	15,367	15,438	1	72			H
tRNA <sup>Pro</sup>	15,440	15,508		69			L
Control region	15,509	16,493		985			H

### Nucleotide sequence accession number

The complete genome sequence of *P. unifilis* has been assigned GenBank accession number JF802204.

### Declaration of interest

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

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