

MITOGENOME ANNOUNCEMENT

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## The complete mitochondrial genome of the endangered Chinese black-necked pond turtle, *Mauremys nigricans*

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### ABSTRACT

The complete mitochondrial genome of the endangered Chinese black-necked pond turtle, *Mauremys nigricans*, was determined in this study. The mitogenome was 16 779 bp in length, and the GC content was 39.07%. The genomes encoded 37 genes typically found in other vertebrates. In the control region, three CSBs were identified, followed by long tandem repeats of (ATATCATATT)<sub>10</sub> (ATATC)(ATATATC)<sub>7</sub>(TA)<sub>102</sub>. The mitochondrial genome sequence would be useful for the phylogenetic and conservation studies of Asian endangered turtles.

### ARTICLE HISTORY

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### KEYWORDS

Chinese black-necked pond turtle; *Mauremys nigricans*; mitochondrial genome

The Chinese black-necked pond turtle, *Mauremys nigricans*, is native to the southern region of China, and listed in Appendix III of CITES and as endangered in the IUCN red list of threatened species (Asian Turtle Trade Working Group 2000). It is close to *M. reevesii* in appearance. But the two lateral keels are not obvious, and red color appears on the head, neck and limbs in male individuals, which are distinctive characters from *M. reevesii* (Shi 2008).

A wild living male turtle was caught by a local farmer and conserved in Guangdong province, China. The nails of the specimen were used to extract genomic DNA. A library was constructed and sequenced using Illumina HiSeq2500. Mitochondrial reads were captured from high quality data by blasting to the mitochondrial sequences of other *Mauremys* species. The complete mitochondrial genome was assembled and the arrangement and characterization of the genome were determined using the program DOGMA, UT Austin (Wyman et al. 2004; <http://dogma.cccb.utexas.edu/>) and tRNA scan-SE 1.21, Santa Cruz, CA (Schattner et al. 2005; [http://lowelab.ucsc.edu/tRNA\\_Scan-SE](http://lowelab.ucsc.edu/tRNA_Scan-SE)).

The complete mitogenome is 16 779 bp in size, and the GC content is 39.07%. Thirty-seven genes are encoded in the genome, of which 13 genes are protein-coding, 2 genes are rRNA and 22 genes are tRNA. The control region is 1253 bp in length, containing three conserved sequence boxes (CSB1, CSB2 and CSB3), and a long tandem repeat (VNTR). The VNTR is 358 bp long, consisting of 10 repeats of (ATATCATATT), 1 (ATATC), 7 repeats of (ATATATC) and 102 repeats of (TA).

A maximum likelihood (ML) analyses (Figure 1) were conducted with congeneric species distributed in Asia using

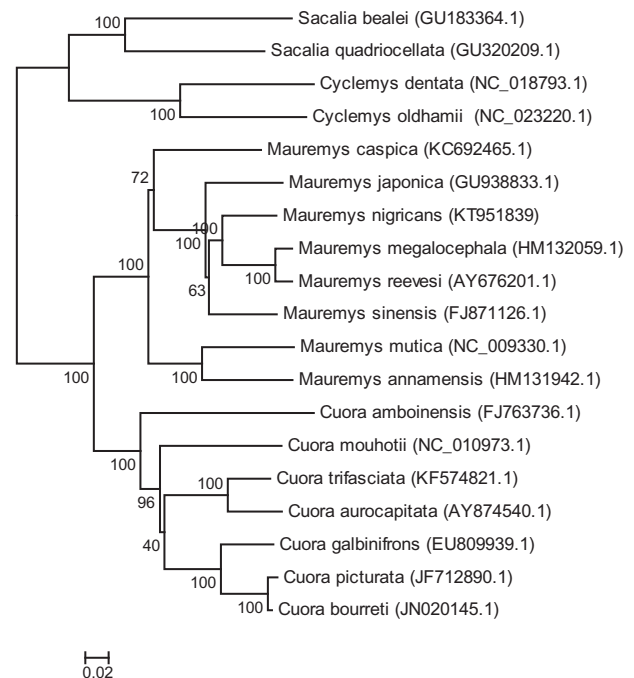


Figure 1. Phylogenetic analysis (ML topology) of *M. nigricans* based on the whole mitochondrial genome sequences. Numbers at each node represent the bootstrap value for ML analysis.

RAxML8.1.5 software, Lausanne, Switzerland (Stamatakis 2006). The reconstructed phylogeny indicated the *M. nigricans* was close to the *M. reevesii* and *M. sinensis*. The barcoding sequence, a 650-bp region of COI gene, which was used for species identification in many animals (Hebert et al. 2003;

Reid et al. 2011), was analyzed using MEGA version 6, Philadelphia, PA (Tamura et al. 2013). The Kimura 2-parameter (K2P) distance of this specimen to the voucher specimen (MVZ 130463; Parham et al. 2001) is 0.002, and 0.025 to *M. reevesii* (FJ469674), with which the two close species could be distinguished.

### Nucleotide sequence accession number

The complete mitochondrial genome of *M. nigricans* has been assigned Genbank accession number KT951839.

### Disclosure statement

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