Complete mitochondrial genome of the MacClelland’s Coral Snake *Sinomicrurus macclellandi* (Reinhardt, 1844) (Serpentes: Elapidae)

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**ABSTRACT**

We report the complete mitochondrial genome (mitogenome) sequence of the MacClelland’s Coral Snake *Sinomicrurus macclellandi* (Reinhardt, 1844). The sequence was determined by shotgun sequencing. The mitogenome of *S. macclellandi* is 17,120 bp in length and contains 13 protein-coding genes (PCGs), 22 tRNA genes, two ribosome RNA genes, and two noncoding regions. Most genes of *S. macclellandi* were distributed on the H-strand, except for the ND6 subunit gene and eight tRNA genes which were encoded on the L-strand. The phylogenetic tree of *S. macclellandi* and 12 other related species was built. The DNA data presented here will be useful to study the evolutionary relationships and genetic diversity of *S. macclellandi*.

*Sinomicrurus* Slowinski, Boundy, and Lawson, 2001 is a group of small to medium-sized Asian coral snakes (Slowinski et al. 2001; Zhao, 2006). In recent years, two more new species, *S. houi* Wang, Peng, and Huang, 2018, *S. peinani* Liu et al. 2020, were described (Peng et al. 2018; Liu et al. 2020). The number of species of *Sinomicrurus* now is seven. None complete mitochondrial genome was reported about this genus. *S. macclellandi* is widely distributed in China and India (Zhao et al. 1998; Zhao 2006; Uetz et al. 2020). In this study, we determined and described the mitogenome of *S. macclellandi* in order to obtain basic mitochondrial genetic information about this species.

The specimen of *S. macclellandi* was collected from Tianzhushan Town (30°40′44″ N, 116°28′32″ E, 40 m a. s. l.) Qianshan County, Anhui Province, China. The sampling site is located in the southeast of Dabie Mountains. Muscle tissues were removed and immediately preserved in 75% ethanol. Total genomic DNA was extracted from muscle using a Qiagen DNEasy blood and tissue extraction kit (Qiagen Inc., Valencia, CA). This specimen and total genomic DNA were preserved and deposited in the Museum of Huangshan University (Voucher number: HS2020001).

The complete mitogenome of *S. macclellandi* (Genbank accession number MT547176) was sequenced to be 17,120 bp which consisted of 13 typical vertebrate protein-coding genes (PCGs), two ribosome RNA genes, 22 transfer RNA (tRNA) genes, and two noncoding regions, which is similar to the typical mtDNA of other vertebrates (Boore 1999; Sorenson et al. 1999). The annotation was predicted by the MITOS (Bernt et al. 2013), and the locations of protein-coding genes were corrected by comparing with the homologous genes of other closely related species. Most of the *S. macclellandi* mitochondrial genes are encoded on the H-strand except for the ND6 gene and eight tRNA genes, which are encoded on the L-strand. The overall base composition of the entire genome was as follows: A (33.0%), T (26.7%), G (12.5%), and C (27.8%), the overall GC content is 40.3% reflected a typical sequence feature of the vertebrate mitogenome. The 12S rRNA (927 bp) and 16S rRNA (1476 bp), are located between the tRNA-Phe and ND1 gene and separated by the tRNA-Val gene. Two noncoding control regions (D-loop) of the *S. macclellandi* mitogenome in size are 1008 bp and 996 bp, respectively.

In order to validate the new determined sequence, whole mitochondrial genome sequence of the *S. macclellandi* and together with other 12 related species from GeneBank to perform phylogenetic analysis. These species were as follows: *Naja atra*, *N. atra*, *N. naja*, *N. kaouthia*, *Ophiophagus hannah*, *Bungarus fasciatus*, *B. multicinctus*, *Laticauda semifasciata*, *L. laticaudata*, *L. colubrine*, *Micrurus fulvius*, *Sinomicrurus macclellandi*, *Deinagkistrodon acutus*. A maximum-likelihood (ML) tree was constructed based on the dataset by online tool RAxML (Kozlov et al. 2019). The phylogenetic analysis result shows that *S. macclellandi* is sister to *Micrurus fulvius* and resides within the clade representing the family Elapidae (Figure 1). The new determined mitogenome sequences
could meet the demands. It will enable improved environmental DNA and understanding of some evolution issues.

Disclosure statement
No potential conflict of interest was reported by the author(s).

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Data availability statement
The data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MT547176.

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Figure 1. A maximum–likelihood (ML) tree of the Sinomicrurus macclellandi in this study and other 12 related species was constructed based on the dataset of the whole mitochondrial genome by online tool RAxML. The numbers above the branch meant bootstrap value. The analyzed species and corresponding NCBI accession number as follows: Naja atra (EU913475), N. atra (EU921898), N. naja (DQ343648), N. kaouthia (LC431744), Ophiophagus hannah (EU921899), Bungarus fasciatus (EU579523), B. multicinctus (EU579522), Laticauda semifasciata (KY496325), L. laticaudata (KY496323), L. colubrina (KY496324), Micrurus fulvius (GU045453), Sinomicrurus macclellandi (MT547176), and Deinagkistrodon acutus (MK450437).
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