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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the aquatic coralsnake *Micrurus surinamensis* (Reptilia, Serpentes, Elapidae)

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ABSTRACT

In this study, we report the first complete mitochondrial genome sequence of the Aquatic Coralsnake *Micrurus surinamensis*. The mitochondrial genome lengthis 17,375 bp, comprising 13 protein-coding genes, 2 rRNA (12S and 16S) and 22 tRNA, as well as two typical control regions. Phylogenetic analysis based upon 13 protein-coding genes showed clusters based on terrestrial and marine species.

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Micrurus is a genus of New World coralsnakes that includes 84 species at present. *Micrurus surinamensis* is the only aquatic species, with a distinct venom composition owing to its peculiar diet of fish (Aird and Silva Jr 2016; Silva Jr et al. 2018). The venom is rich in three-finger toxins (3FTxs) and presents high neurotoxic activity (Aird et al. 2017).

From a specimen of *M. surinamensis* of Altamira (Pará – Brazil; 3°20′14″N and 51°48′16″E) collected on 9 June 2014, we extracted total DNA using the chloroform–phenol protocol (Sambrook et al. 1989). The specimen is deposited in the herpetological collection of the Center for Biological Studies and Research of PUC-Goiás (CEPB 8984). Sequencing was performed using the Illumina MiSeq platform (309 × 2-bp reads). A paired-end library was prepared using a TruSeq DNA PCR-Free LT Sample Prep Kit (Illumina). The assembly was constructed using NOVOPlasty in 'mitochondrial' mode (Dierckxsens et al. 2017). Genome annotation was performed using MITOS webserver (Bernt et al. 2013) and the phylogenetic analysis was performed using 13 mitochondrial protein-coding genes. These genes were aligned individually using MAFFT v. 7 (Katoh and Standley 2013). Alignment files were concatenated into a single matrix using Sequence Matrix software (Vaidya et al. 2011). Informative sites were extracted from this matrix using GBlocks v. 0.91 (Cruickshank 2000) and were used as input for jModelTest v. 2.1.10 (Darriba et al. 2012) to test the best-fitting evolutionary model for phylogeny estimation, based on the Akaike Information Criterion (AIC). Bayesian inference approach using MrBayes v. 3.2 software with 30,000,000 generations in MCMC runs was analyzed (Huelsenbeck and Ronquist 2001; Darling et al. 2012). Runs were evaluated using Tracer software (tree.bio.ed.ac.uk).

The *M. surinamensis* mitochondrial genome comprises 17,375 bp. It consists of 13 protein-coding genes, 2 rRNA (12S and 16S), and 22 tRNA genes, and two control regions typical of snake mitochondrial genomes. This genome has a composition of 27.5% A, 33.1% T, 27.5% G, and 12.0% C. A phylogenetic analysis was performed based on available sequences in GenBank, using the *Alligator mississippiensis* mitochondrial genome as an outgroup (Figure 1). Three clades (*Bungarus*, *Micrurus* and *Naja*) represented terrestrial elapids and *Laticauda* exemplified aquatic elapids. Among terrestrial elapids *Bungarus* is a sister group of *Micrurus* with *Naja* as an outgroup, all with highly supported nodes, and patterns identical to those reported previously (Kim et al. 2018; Yi et al. 2019). The complete mitochondrial genome sequence of *Micrurus surinamensis* has been deposited in GenBank (accession number: MN587874).

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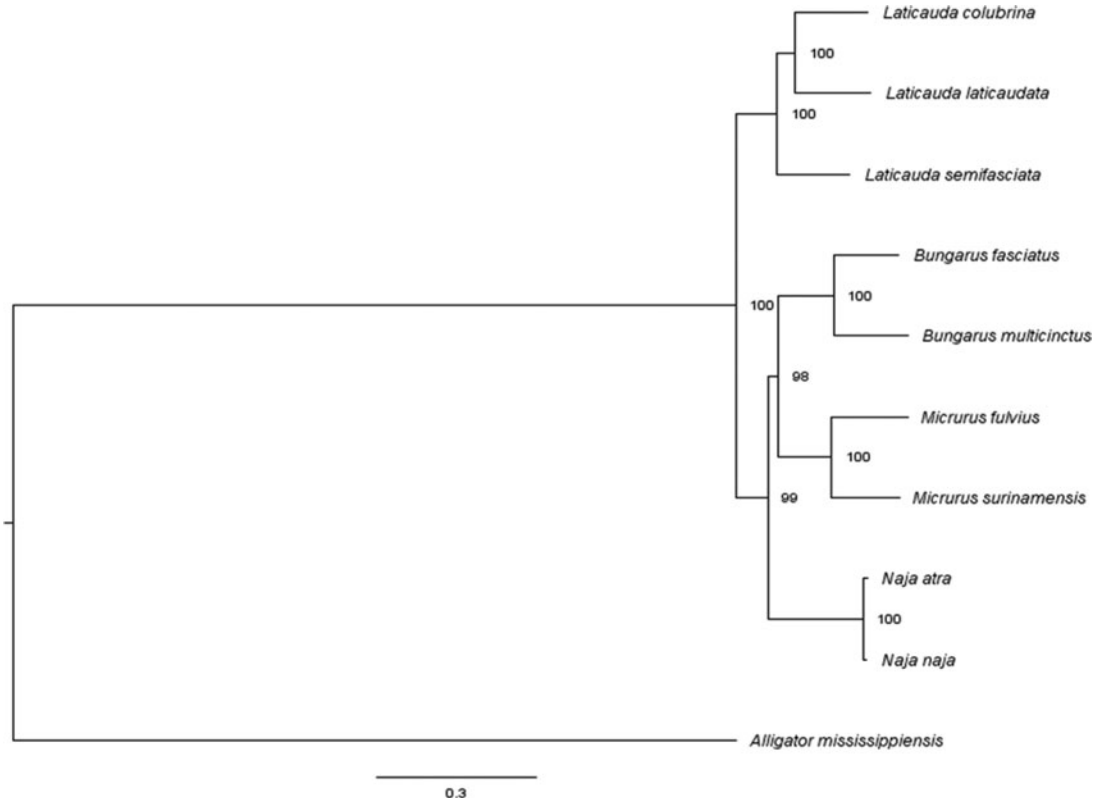

Figure 1. Bayesian phylogenetic tree constructed using 13 protein-coding genes from complete mitochondrial genomes. *Alligator mississippiensis* was used as outgroup. Genbank accession numbers: *Laticauda colubrina* (KY496324.1), *Laticauda laticaudata* (KY496323.1), *Laticauda semifasciata* (KY496325.1), *Bungarus fasciatus* (EU579523.1), *Bungarus multicinctus* (EU579522.1), *Micrurus fulvius* (GU045453.1), *Micrurus surinamensis* (this work), *Naja atra* (EU913475.1), *Naja naja* (DQ343648.1), and *Alligator mississippiensis* (AKHW00000000.3).

Based upon mitochondrial genomes, *Micrurus surinamensis* is clustered with *Micrurus fulvius*, as predicted they represent two different but related clades among New World coralsnakes (Roze 1996; Silva Jr and Sites 2001; Silva Jr et al. 2016).

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Disclosure statement

No potential conflict of interest was reported by the authors.

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