

MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of *Salminus brasiliensis*
(Characiformes, Characidae)**Pedro Ferreira Pinto Brandão-Dias¹, Anderson Oliveira do Carmo¹, Ana Paula Vimieiro Martins¹,
Ricardo José Gonzaga Pimenta¹, Carlos Bernardo Mascarenhas Alves², and Evanguedes Kalapothakis¹¹Departamento de Biologia Geral, Instituto de Ciências Biológicas – Universidade Federal de Minas Gerais, Avenida Presidente Antônio Carlos, Pampulha, Belo Horizonte – MG, Brasil and ²Nuvelhas-Projeto Manuelzão, Universidade Federal de Minas Gerais, Avenida Presidente Antônio Carlos, Belo Horizonte – MG, Brasil**Abstract**

We report the complete mitochondrial genome of the fish *Salminus brasiliensis*, popularly known as dourado. It is a circular, 17,721 bp long DNA molecule, containing 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes and a non-coding Control Region of 2128 bp, a relatively large molecule when compared to other closely related fishes. All protein-coding genes are on the heavy strand, except for *Nd6*, and all have ATG as the start codon, except for *Cox1* gene which has a GTG start codon. Seven protein-coding genes have incomplete stop codons (*Nd2*, *Cox2*, *Atp6*, *Nd4*, and *Cytb* have T–, and *Cox3* and *Nd3* have TA–). TAG is the stop codon for *Nd6* and AGG is the stop codon for *Cox1*.

KeywordsDourado, fish, mtDNA, mitochondrion,
next-generation sequencing**History**Received 6 August 2014
Accepted 23 August 2014
Published online 10 September 2014

Salminus brasiliensis (Cuvier, 1816), popularly known as dourado, is one of the largest fishes in the order Characiformes, with adults weighing more than 20 kg. It lives mainly in the Paraná-Paraguay and Uruguay rivers basins in Brazil, Argentina, Uruguay, and Paraguay, but it also occurs in other places, such as Lagoa dos Patos, Brazil (Rueda et al., 2011). *Salminus brasiliensis* is an important predatory piscivore that migrates upstream in the rainy season to reproduce (Esteves & Lôbo, 2001; Filho & Schubart, 1955; Lima & Britski, 2007). During migration, some populations are affected by dam constructions (Agostinho et al., 2003). Dourado is also prized by both commercial and amateur fisherman due to its flesh flavor and its resistance when caught (Lima & Britski, 2007).

A *S. brasiliensis* was caught in the Grande River (20°01'53.8' S, 48°13'27.5' W) and DNA was extracted from its muscular tissue according to Sambrook & Russell (2001). A genomic library was built using Nextera Kit (Illumina, San Diego, CA) according to the manufacturer's protocol, and the library was then sequenced using MiSeq sequencer (Illumina, San Diego, CA) with a 500 cycles paired-end strategy. We performed a *de novo*

assembly using MIRA assembly 4.0 (Chevreux et al., 1999), and a unique 17,721 bp contig with 148× coverage was extracted (GenBank accession number KM245047; Table 1). It had overlapping edges, and the highest BLAST (Basic Local Alignment Search Tool) hits for this contig in Nucleotide Database of NCBI were to other complete Characiformes mtDNAs, confirming it as a mitochondrial genome sequence. We used Mitoannotator feature from Mitofish (Iwasaki et al., 2013) to annotate it. The molecule contains 13 protein-coding genes (PCGs), 2 rRNA genes, 22 tRNA genes, and a major non-coding Control Region. All PCGs, except for *Nd6*, are coded on the heavy strand. The gene order and coding strand were consistent with the order Characiformes. AT proportion was 55.7%.

All of the PCGs had ATG as the start codon, except for *Cox1*, which had an unusual GTG start codon. Of the 13 PCG's, only five had a complete TAA stop codon. TAG was the stop codon in *Nd6*, AGG was the stop codon in *Cox1*, and seven genes had incomplete stop codons (*Nd2*, *Cox2*, *Atp6*, *Nd4* and *Cytb* have T–, and *Cox3* and *Nd3* have TA–). Of the 22 tRNAs, eight were coded on the light strand and 14 were coded on the heavy strand. A tRNA inference analysis using MITOS (Bernt et al., 2013) revealed that 21 out of 22 tRNAs fold into the typical cloverleaf structure. The exception, tRNA^{Ser}(GCT), may lack the D-arm. The Control Region was between tRNA^{Pro} and tRNA^{Phe}, and was 2128 bp long. Of the 18 complete Control Regions published for the order, the average length was 1020 bp. The longest currently known is from *Lebiasina astrigata* (Nakatani et al., 2011) with 1222 bp long. The enlarged D-loop in *S. brasiliensis* was due to an insertion of 1019 bp, which has no significant BLAST hits in the nr database of NCBI.

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Table 1. Characteristics of the *S. brasiliensis* mitochondrial genome.

Gene	Position		Size (bp)	Codon			Strand
	From (bp)	To (bp)		Amino acid	Start codon	Stop codon	
tRNA ^{Phe} (GAA)	1	68	68				H
12S rRNA	69	1015	947				H
tRNA ^{Val} (TAC)	1016	1087	72				H
16S rRNA	1088	2762	1675				H
tRNA ^{Leu2} (TAA)	2763	2836	74				H
<i>Nd1</i>	2838	3812	975	324	ATG	TAA	H
tRNA ^{Ile} (GAT)	3820	3891	72				H
tRNA ^{Gln} (TTG)	3890	3960	71				L
tRNA ^{Met} (CAT)	3960	4028	69				H
<i>Nd2</i>	4029	5073	1045	348	ATG	T--	H
tRNA ^{Trp} (TCA)	5074	5143	70				H
tRNA ^{Ala} (TCG)	5145	5213	69				L
tRNA ^{Asn} (GTT)	5215	5287	73				L
tRNA ^{Cys} (GCA)	5315	5380	66				L
tRNA ^{Tyr} (GTA)	5381	5450	70				L
<i>CoxI</i>	5452	7008	1557	518	GTG	AGG	H
tRNA ^{Ser2} (TGA)	7000	7070	71				L
tRNA ^{Asp} (GTC)	7071	7143	73				H
<i>CoxII</i>	7156	7846	691	230	ATG	T--	H
tRNA ^{Lys} (TTT)	7847	7922	76				H
<i>Atp8</i>	7924	8088	165	54	ATG	TAA	H
<i>Atp6</i>	8079	8761	683	227	ATG	T--	H
<i>CoxIII</i>	8762	9545	784	261	ATG	TA-	H
tRNA ^{Gly} (TCC)	9546	9615	70				H
<i>Nd3</i>	9616	9961	346	115	ATG	TA-	H
tRNA ^{Arg} (TCG)	9962	10,030	69				H
<i>Nd4L</i>	10,031	10,327	297	98	ATG	TAA	H
<i>Nd4</i>	10,321	11,701	1381	460	ATG	T--	H
tRNA ^{His} (GTG)	11,702	11,770	69				H
tRNA ^{Ser1} (GTC)	11,771	11,837	67				H
tRNA ^{Leu1} (TAG)	11,839	11,910	72				H
<i>Nd5</i>	11,911	13,773	1863	620	ATG	TAA	H
<i>Nd6</i>	13,726	14,235	510	169	ATG	TAG	L
tRNA ^{Glu} (TTC)	14,236	14,304	69				L
<i>Cytb</i>	14,313	15,453	1141	380	ATG	T--	H
tRNA ^{Thr} (TGT)	15,454	15,525	72				H
tRNA ^{Pro} (TGG)	15,524	15,592	69				L
D-loop	15,593	17,721	2128				N/A

Declaration of interest

The authors declare that there are no conflicts of interest. This study has received funding from agreement number 4020000572 - GT455 CEMIG, Peixe Vivo, CEMIG. Contract number 4570011274/510.

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