Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the versicoloured emerald hummingbird *Amazilia versicolor*, a polymorphic species

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Abstract

The genome of the versicoloured emerald hummingbird (*Amazilia versicolor*) was partially sequenced in one—sixth of an Illumina HiSeq lane. The mitochondrial genome was assembled using MIRA and MITObim software, yielding a circular molecule of 16,861 bp in length and deposited in GenBank under the accession number KF624601. The mitogenome contained 13 protein—coding genes, 22 transfer tRNAs, 2 ribosomal RNAs and 1 non—coding control region. The molecule was assembled using 21,927 sequencing reads of 100 bp each, resulting in ~130 × coverage of uniformly distributed reads along the genome. This is the forth mitochondrial genome described for this highly diverse family of birds and may benefit further phylogenetic, phylogeographic, population genetic and species delimitation studies of hummingbirds.

Keywords

Atlantic Forest, hummingbird, mitochondrial genome, next-generation-sequencing

History

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The Trochilidae is the second most diverse family of birds and contains about 331 species described (Dickinson, 2003). Hummingbirds are restricted to the New World and occupy diverse environments reaching longitudes from sea level up to 5000 m from Alaska to Patagonia (Ruschi, 1982). *Amazilia versicolor* is a member of the ''Emeralds'' clade (McGuire et al., 2009), being a sedentary species with a wide distribution from below the Amazonian River to the East, South and Southwest Brazil, reaching also the frontiers with Argentina and Uruguay. This species is reported to present torpor states, a mechanism related to the energetic metabolism relevant to cope with periods of food deprivation and to save energy mainly during the night (Bech et al., 1997).

A specimen of *A. versicolor* was collected in Santa Teresa (Espírito Santo, Brazil) and deposited in the National Museum of Rio de Janeiro under the label MN45689. Genomic DNA was extracted from pectoral muscle tissue using the salt extraction method. The partial genome sequencing of *A. versicolor* produced 2.3 Gb of DNA sequences using an Illumina HiSeq (San Diego, CA). The entire set of reads was input into a *de novo* assembly using MIRA software (Chevreux et al., 1999). Since MIRA was unable to assemble the whole mitochondrial genome into a single scaffold, we used the program MITObim (Hahn et al., 2013) to enlarge the assembled sequence.

The complete circularized genome was found to be 16,861 bp in length and was deposited in GenBank under the accession number KF624601. The mitochondrial genome organization followed the typical pattern observed in vertebrates and birds, presenting 13 protein coding genes, 22 transfer RNAs, 2 ribosomal RNAs and a control region (d-loop; Table 1). Genome coverage was observed using Tablet software (Milne et al., 2013) resulting in ~130 × uniformly distributed reads along the genome. Automatic annotation was performed using MITOS Web Server (Bernt et al., 2013) and mitoMaker software (http://sourceforge.net/projects/mitomaker/), followed by careful manual curation using Artemis (Carver et al., 2012). Transfer RNA predictions were confirmed using tRNAscan-SE (Lowe & Eddy, 1997). Genome structure, gene order and orientation were similar to the mitochondrion of other hummingbirds from the genera *Archilochus* (Morgan-Richards et al., 2008) and *Chrysolampis* (Souto et al., 2014).

The complete mitogenome of *A. versicolor* may benefit further phylogenetic, phylogeographic and species delimitation studies, which are essential for ongoing conservation efforts and will also foster our understanding of hummingbird evolution and energetic metabolism.

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Table 1. Mitochondrial genome characteristics of *A. versicolor*.

	Position		Size		Codon			
Gene	From	To	Nucleotide	Amino acid	Start	Stop	Intergenic nucleotide	Strand
tRNA(Phe)	1	71	71				–1	H
12S rRNA	71	1041	971				–1	H
tRNA(Val)	1041	1111	71				0	H
16S rRNA	1112	2708	1597				–1	H
tRNA(Leu)	2708	2787	80				0	H
ND1	2788	3765	975	325	AUG	UGG	–2	H
tRNA(Ile)	3764	3836	73				11	H
tRNA(Gln)	3848	3918	71				–1	L
tRNA(Met)	3918	3986	69		AUG	UAA	0	H
ND2	3987	5026	1038	346			0	H
tRNA(Trp)	5027	5099	73				1	H
tRNA(Ala)	5101	5169	69				2	L
tRNA(Asn)	5172	5244	73				3	L
tRNA(Cys)	5248	5314	67				–1	L
tRNA(Tyr)	5314	5385	72				1	L
COX1	5387	6937	1542	514	GUG	CAA	–9	H
tRNA(Ser)	6929	7002	74				2	L
tRNA(Asp)	7005	7073	69				3	H
COX2	7077	7760	681	227	AUG	UAA	1	H
tRNA(Lys)	7762	7831	70				1	H
ATP8	7833	8000	165	55	AUG	UAA	–10	H
ATP6	7991	8674	681	227	AUG	UAA	–1	H
COX3	8674	9457	783	261	AUG	UGC	–2	H
tRNA(Gly)	9458	9526	69				6	H
ND3	9533	9878	342	114	AUA	UAA	2	H
tRNA(Arg)	9881	9950	70				1	H
ND4-L	9952	10,248	294	98	AUG	UAA	–7	H
ND4	10,242	11,612	1368	456	AUG	AGA	21	H
tRNA(His)	11,634	11,702	69				0	H
tRNA(Ser)	11,703	11,769	67				1	H
tRNA(Leu)	11,771	11,842	72				3	H
ND5	11,846	13,660	1812	604	AUA	UAA	8	H
CYTB	13,669	14,811	1140	380	AUG	UAA	4	H
tRNA(Thr)	14,816	14,894	79				1	H
tRNA(Pro)	14,896	14,965	70				17	L
ND6	14,983	15,504	519	173	AUG	UAA	0	L
tRNA(Glu)	15,505	15,575	71				0	L
Control region	15,576	16,861	1286					H

Declaration of interest

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