Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the ruby-topaz hummingbird *Chrysolampis mosquitus* through Illumina sequencing

Helena Magarinos Souto[1], Piero Angeli Ruschi[2,3], Carolina Furtado[4], W. Bryan Jennings[2], and Francisco Prosdocimi[1]

[1]Genomics and Biodiversity Laboratory, Instituto de Bioquímica Médica Leopoldo de Meis, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil, [2]Molecular Laboratory of Biodiversity Research, Departamento de Vertebrados, Museu Nacional, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil, [3]Museu de Biologia Prof. Mello Leitão/MBML, Santa Teresa, Espírito Santo, Brazil, and [4]Division of Genetics, National Cancer Institute, Rio de Janeiro, Brazil

Abstract

The complete mitochondrial genome of the Ruby-Topaz Hummingbird, *Chrysolampis mosquitus*, was determined using 1/11 of an Illumina Hi-seq lane ran with a Nextera kit. We assembled the mitogenome in a two-step approach using both (i) *de novo* (SOAPdenovo-Trans) and (ii) reference-based (MITObim) genome assembly software. A circular molecule containing 17,767 bp was assembled. As expected for most vertebrates, the *C. mosquitus* mitogenome contained 13 protein-coding genes, 22 transfer RNA, 2 ribosomal RNA genes, and 1 non-coding control region. We assembled the whole mitogenome using 0.45% of the total amount of reads and produced a high-coverage mitochondrial genome (>1000×). We deposited the assembled mitogenome into GenBank (accession number KJ619585).

Keywords

Genome assembly, hummingbird, mitogenome

History

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Introduction

Next-Generation Sequencing (NGS) is considered a revolutionary approach to sequence genomes because of the large amount of data generated per run as well as the reduced complexity, costs, and time required to assemble genomes using NGS data (Mardis, 2008). We present for the first time the complete mitochondrial genome of the Ruby-Topaz Hummingbird (*Chrysolampis mosquitus*; Linnaeus, 1758). This species, which is monotypic, sexually dimorphic and migratory, is distributed throughout Colombia, the Guyanas, Trinidad and Tobago, Aruba, Curacau, Bonaire, Venezuela, Bolivia, and Brazil (Ruschi, 1986). The Ruby-Topaz Hummingbird is a member of the Mangoes (Polytmini) clade, which is the basal clade of the subfamily Trochilinae (McGuire et al., 2009). Although there are at least 300 known species of Hummingbirds, the present work represents only the second complete hummingbird mitogenome to be made available in GenBank.

Materials and methods

Sample collection, DNA extraction and next-generation sequencing

An individual of *C. mosquitus* was collected in state of Roraima, Brazil. Genomic DNA was purified using the salt extraction method and sequenced using Nextera kits as 1/11 of a lane in an Illumina HiSeq (San Diego, CA).

Read assembly and annotation of mitochondrial genomes

SOAPdenovo-Trans (Xie et al., 2013) ran with the entire set of pair-end reads for *de novo* assembly using a k-mer size of 61. The result was used as input to run MITObim (Hahn et al., 2013), which performs reference assemblies using MIRA iterations (Chevreux et al., 1999). Tablet (Milne et al., 2013) software was used to check the read coverage along the assembled mitogenome.

Automatic annotation was performed using the MITOS WebServer (Bernt et al., 2013) followed by manual curation using Artemis software (Carver et al., 2012). The software tRNAscan-SE (Lowe & Eddy, 1997) was used to confirm tRNA annotations and BLAST (Altschul et al., 1997) searches against amino acids were done to check for precise genes boundaries.

Results and discussion

We obtained 7.14 gigabases (Gb) of partial genome sequencing for *C. mosquitus* in two paired-end files, totaling 71,436,256 sequences. After the first assembly using SOAPdenovo-Trans, a partial mitogenome was used as input for reference assembly using MITObim.

The complete mitogenome sequence of *C. mosquitus* is 16,767 bp in length and was deposited in GenBank with the accession number KJ619585. It consists of circular DNA organized as 13 protein coding genes, 22 transfer RNAs, 2 ribosomal RNAs, and a control region (d-loop) (Table 1). All genes were encoded at heavy strand (h-strand) with the exception of ND6 and 8 tRNAs. The assembly step involved 323,424 (0.45%) mitochondrial reads providing coverage of 1928×. Circularization was confirmed by the overlap of the start and end sequence regions after MITObim assembly.

The genome organization observed was common to Paleognathae and Neognathae birds (Pereira, 2000). Overall base composition of the H-strand was A: 30.64%; T: 23.68%;

Correspondence: Francisco Prosdocimi PhD, Genomics and Biodiversity Laboratory, Universidade Federal do Rio de Janeiro, Medical Biochemistry Institute, Rua Carlos Chagas 373, Rio de Janeiro, Brazil. E-mail: prosdocimi@bioqmed.ufrj.br

Table 1. Mitochondrial genome characteristics of *C. mosquitus*.

	Position		Size		Códon			
Gene	From	To	Nucleotide	Amino acid	Start	Stop	Intergenic nucleotide	Strand
tRNA(Phe)	1	71	71				−1	H
12S rRNA	71	1045	975				−1	H
tRNA(Val)	1045	1117	73				−1	H
16S rRNA	1117	2708	1592				−1	H
tRNA(Leu)	2708	2781	74				8	H
ND1	2790	3764	975	325	AUG	AGG	14	H
tRNA(Ile)	3779	3851	73				6	H
tRNA(Gln)	3858	3928	71				−1	L
tRNA(Met)	3928	3997	70				0	H
ND2	3998	5035	1038	346	GUG	UAG	1	H
tRNA(Trp)	5037	5108	72				1	H
tRNA(Ala)	5110	5178	69				3	L
tRNA(Asn)	5182	5254	73				3	L
tRNA(Cys)	5258	5324	67				−1	L
tRNA(Tyr)	5324	5395	71				1	L
COX1	5397	6937	1541	513	GUG	TA	1	H
tRNA(Ser)	6939	7012	74				2	L
tRNA(Asp)	7015	7083	69				2	H
COX2	7086	7766	681	227	AUG	UAA	4	H
tRNA(Lys)	7771	7839	69				2	H
ATP8	7842	8006	165	55	AUG	UAA	−7	H
ATP6	8000	8680	681	227	AUG	UAA	2	H
COX3	8683	9465	783	261	AUG	UGC	1	H
tRNA(Gly)	9467	9535	69				6	H
ND3	9542	9884	343	116	AUA	UAA	5	H
tRNA(Arg)	9890	9959	70				1	H
ND4-L	9961	10,254	294	98	AUG	UAA	−4	H
ND4	10,251	11,618	1368	456	AUG	AGA	14	H
tRNA(His)	11,633	11,701	69				0	H
tRNA(Ser)	11,702	11,768	67				−1	H
tRNA(Leu)	11,768	11,839	72				3	H
ND5	11,843	13,651	1809	603	AUA	UAA	16	H
CYTB	13,668	14,807	1140	380	AUG	UAA	7	H
tRNA(Thr)	14,815	14,896	82				3	H
tRNA(Pro)	14,900	14,969	70				24	L
ND6	14,994	15,512	519	173	AUG	UAA	1	L
tRNA(Glu)	15,514	15,584	71				0	L
Control region	15,585	16,767	1183					H

C: 31.67%; G: 13.99%. The A + T content was in accordance with other bird mitogenomes (Kan et al., 2010; Liu et al., 2013).

Our study represents only the second complete mitogenome sequence available in GenBank for the hyper-diverse hummingbird clade. Besides documenting the molecular nature of avian biodiversity, we expect that our results will contribute to an improved taxonomy and systematics of hummingbirds.

Declaration of interest

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References

Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. (1997). Gapped BLAST and PSI-BLAST: A new generation of protein database search programs. Nucl Acids Res 25: 3389–402.

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, et al. (2013). MITOS: Improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol 69:313–19.

Carver T, Harris SR, Berriman M, Parkhill J, McQuillan JA. (2012). Artemis: An integrated platform for visualization and analysis of high-throughput sequence-based experimental data. Bioinformatics 28: 464–9.

Chevreux B, Wetter T, Suhai S. (1999). Genome sequence assembly using trace signals and additional sequence information. Computer Sci Biol: Proc German Bioinformatics Conference 99:45–56.

Hahn C, Bachmann L, Chevreux B. (2013). Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads – A baiting and iterative mapping approach. Nucleic Acids Res 41:e129.

Kan XZ, Li XF, Zhang LQ, Chen L, Qian CJ, Zhang XW, Wang L. (2010). Characterization of the complete mitochondrial genome of the Rock pigeon, *Columba livia* (Columbiformes: Columbidae). Genet Mol Res 9:1234–49.

Liu G, Zhou L, Zhang L, Luo Z, Xu W. (2013). The complete mitochondrial genome of bean goose (*Anser fabilis*) and implications for Anseriformes Taxonomy. PLoS One 8:e63334.

Lowe TM, Eddy SR. (1997). tRNAscan-SE: A program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 25:0955–64.

Mardis E. (2008). The impact of next-generation sequencing technology on genetics. Trends Genet 24:133–41.

McGuire JA, Witt CC, Remsen JV, Dudley R, Altshuler DL. (2009). A higher-level taxonomy for hummingbirds. J Ornithol 150:155–65.

Milne I, Stephen G, Bayer M, Cock PJA, Pritchard L, Cardle L, Shaw PD, Marshall D. (2013). Using Tablet for visual exploration of second-generation sequencing data. Brief Bioinform 14:193–202.

Pereira SL. (2000). Mitochondrial genome organization and vertebrate phylogenetics. Genet Mol Biol 4:745–52.

Ruschi A. (1986). Aves do Brasil. Vol. 5. Beija-flores. Rio de Janeiro: Expressão e Cultura.

Xie Y, Wu G, Tang J, Luo R, Patterson J, Liu S, Huang W, et al. (2013). SOAPdenovo-Trans: De novo transcriptome assembly with short RNA-Seq reads. Bioinformatics. [Epub ahead of print]. doi: 10.1093/bioinformatics/btu077.