Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Mitochondrial genome organization of the Ochre-bellied Flycatcher, *Mionectes oleagineus*

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Abstract

We sequenced and compared the mitogenome organization of two specimens of suboscine tyrant flycatcher *Mionectes oleagineus* from western and eastern Panama, representing distinct mtDNA clades. These samples show identical gene arrangement and vary in size by less than 5 base pairs. Both depict a non-standard avian gene order with an extra non-coding region (e.g. the remnant CR_2), which differs in one base pair between them. Small size differences are also found on the control region and the 16S rRNA. Average uncorrected pairwise divergence among protein-coding genes (PCGs) was 2.8, ranging from 1.9% for COXIII and ND6 to 3.2% for ND2 and ATP6, respectively. These mitogenomes may be useful for understanding the evolutionary dynamics of gene order in bird mitochondrial genomes.

Keywords

Control region, gene order, mitogenome, suboscine, Tyrannidae

History

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Introduction

The suboscine New World flycatcher *Mionectes oleagineus* Lichtenstein (1823) is found throughout Neotropical lowland forests. Miller et al. (2008) found three fairly divergent and non-monophyletic mtDNA lineages in partial sympatry across the Isthmus of Panama, the result of periodic episodes of range expansion out of Amazonia and across the Andes during the Pliocene-Pleistocene. Here, we present mitochondrial genomes from birds sampled from Bocas del Toro and Darién Panama, representing distinct phylogeographic clades.

Genomic DNA was obtained from vouchered tissues archived in the Smithsonian Tropical Research Institute Cryological Collection: sample JK06-147 (Bocas del Toro) and sample MJM2008 (Darién). Mitogenome sequences were obtained as a by-product of ultraconserved elements target captures (UCEs, e.g. Faircloth et al., 2012; protocols at: http://ultraconserved.org/). Full details regarding DNA sequencing, assembling and genome annotation was published previously (Miller et al., 2014). A total of 22,790 reads were mapped to JK06-147 (average coverage = 195 reads) while 26,521 reads mapped to MJM2008 (average coverage = 229 reads). Genbank accessions are: KJ742590 (JK06-147) and KJ742591 (MJM2008). Uncorrected pairwise sequence divergence between samples was calculated for all genomic features based on Muscle alignments executed in Geneious 7.0.6 (Biomatters, http://www.geneious.com).

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Mitochondrial genome organization

The mitogenome of *M. oleagineus* comprises 2 rRNAs, 22 tRNAs, 13 PCGs, the control region (e.g. D-loop) and an extra non-coding region (CR_2). Both samples depict a non-standard avian mitogene order, where the D-loop is found between $tRNA^{Thr}$ and $tRNA^{Pro}$ and CR_2 is flanked by $tRNA^{Glu}$ and $tRNA^{Phe}$, first reported by Mindell et al. (1998) as the result of control region duplication and subsequent reduction having arisen independently in three bird lineages including suboscine passerines. That study suggested that mitogene order is highly constrained and that arrangements were likely to be phylogenetically informative. Subsequently, control region mitochondrial genome rearrangements have been identified within avian lineages such as the Old World warbler genus *Phylloscopus* (Bensch & Härlid, 2000) and the parrot family Psittacidae (Schirtzinger et al., 2012), suggesting evolutionary lability of such rearrangements. Curiously, despite the fact that suboscines represent over 10% of global avian biodiversity, less than five suboscine mitochondrial genomes have been published, hindering understanding of mitogenome evolution in this group.

Between the two samples, most genomic features were identical in size. However, 16S rRNA is two base pairs larger in the specimen from Bocas del Toro, and the D-loop and CR_2 differ in 1 and 2 base pairs between specimens respectively (Table 1). PCGs except ND6 were encoded on the heavy strand (H), as are 15 of the tRNAs and the 2 rRNAs. Among all mitogenome features, pairwise sequence differences varied between 0.0% (9 tRNAs) and 9.6% (CR_2); among PCGs, COXIII and ND6 had the shallowest pairwise divergence (1.9%) while ND2 and ATP6 had the largest pairwise divergence (3.2%; Table 1). We hope that these genomes aid study of the evolution of avian mitogenome organization, as well as the role of mitochondrial sequence variation in forming species limits among closely related bird taxa.

Table 1. Characteristics of two *M. oleagineus* mitogenomes.

Code	Amino Acid	Start	Stop	Size	Spacer (+) or overlap (−)	Direction	Start codon	Stop codon	Pairwise divergence
F	tRNA^{Phe}	1	70	70	0	F			0.0
	12S rRNA	71	1037	967	0	F			0.9
V	tRNA^{Val}	1038	1108	71	0	F			1.4
	16S rRNA	1109	2698 (2696)	1590 (1588)	0	F			1.9
L	tRNA^{Leu}	2699 (2697)	2772 (2770)	74	11	F			1.4
	ND1	2784 (2782)	3761 (3759)	978	8	F	ATG	AGA	3.0
I	tRNA^{Ile}	3770 (3768)	3841 (3839)	72	4	F			0.0
Q	tRNA^{Gln}	3846 (3844)	3916 (3914)	71	−1	R			0.0
M	tRNA^{Met}	3916 (3914)	3984 (3982)	69	0	F			0.0
	ND2	3985 (3983)	5025 (5023)	1041	−2	F	ATG	TAG	3.2
W	tRNA^{Trp}	5024 (5022)	5094 (5092)	71	1	F			5.6
A	tRNA^{Ala}	5096 (5094)	5164 (5162)	69	2	R			1.4
N	tRNA^{Asn}	5167 (5165)	5239 (5237)	73	2	R			2.7
C	tRNA^{Cys}	5242 (5240)	5308 (5306)	67	−11	R			0.0
Y	tRNA^{Tyr}	5298 (5296)	5378 (5376)	81	1	R			0.0
	COX I	5380 (5378)	6930 (6928)	1551	−9	F	ATG	AGG	2.6
S	tRNA$^{Ser(UCN)}$	6922 (6920)	6995 (6993)	74	2	R			1.4
D	tRNA^{Asp}	6998 (6996)	7066 (7064)	69	9	F			2.9
	COX II	7076 (7074)	7759 (7757)	684	1	F	ATG	TAA	2.5
L	tRNA^{Lys}	7761 (7759)	7830 (7828)	70	1	F			2.9
	ATP 8	7832 (7830)	7999 (7997)	168	−10	F	ATG	TAA	2.4
	ATP 6	7990 (7988)	8673 (8671)	684	6	F	ATG	TAA	3.2
	COX III	8680 (8678)	9463 (9461)	784	0	F	ATG	T−−	1.9
G	tRNA^{Gly}	9464 (9462)	9533 (9531)	70	−1	F			0.0
	ND3	9533 (9531)	9883 (9881)	351	2	F	ATT	TAA	3.1
R	tRNA^{Arg}	9886 (9884)	9954 (9952)	69	1	F			1.4
	ND4L	9956 (9954)	10,252 (10,250)	297	−7	F	ATG	TAA	3.0
	ND4	10,246 (10,244)	11,623 (11,621)	1378	0	F	ATG	T−−	2.9
H	tRNA^{His}	11,624 (11,622)	11,693 (11,691)	70	1	F			1.4
S	tRNA^{Ser}	11,695 (11,693)	11,758 (11,756)	64	0	F			0.0
L	tRNA^{Leu2}	11,759 (11,757)	11,829 (11,827)	71	0	F			0.0
	ND5	11,830 (11,828)	13,647 (13,645)	1818	11	F	GTG	AGA	3.1
	Cytb	13,659 (13,657)	14,801 (14,799)	1143	2	F	ATG	TAA	2.6
T	tRNA^{Thr}	14,804 (14,802)	14,872 (14,870)	69	0	F			2.9
	Control region	14,873 (14,871)	16,212 (16,211)	1340 (1341)					3.8
P	tRNA^{Pro}	16,213 (16,212)	16,281 (16,280)	69	12	R			1.4
	ND6	16,294 (16,293)	16,815 (16,814)	522	3	R	ATG	TAG	1.9
E	tRNA^{Glu}	16,819 (16,818)	16,888 (16,887)	70	0	R			2.9
	Non-coding region	16,889 (16,888)	17,022 (17,023)	134 (136)		F			9.6

Values are for the JK06-147 specimen collected in Panama: Bocas del Toro, while values in parentheses indicate feature differences found in specimen MJM2008 from Panama: Darién. When only one value is present, the features between the two specimens were identical.

Declaration of interest

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