

Supplementary Material for the article

Evolutionary history of the Galápagos Rail revealed by ancient mitogenomes and modern samples

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Table of Contents

Figure S1: Graphic representation of the <i>L. spilonota</i> mitochondrial genome assembly	p 2
Table S1: Primer information for Sanger sequencing	p 3
Table S2: Illumina sequencing and mapping characteristics for five museum samples	p 3
Table S3: Mitogenome sequence variation among five Galápagos Rail samples.....	p 4
Table S4: Sequence information <i>cytb</i> , ND2, and RAG-1	pp 5–6

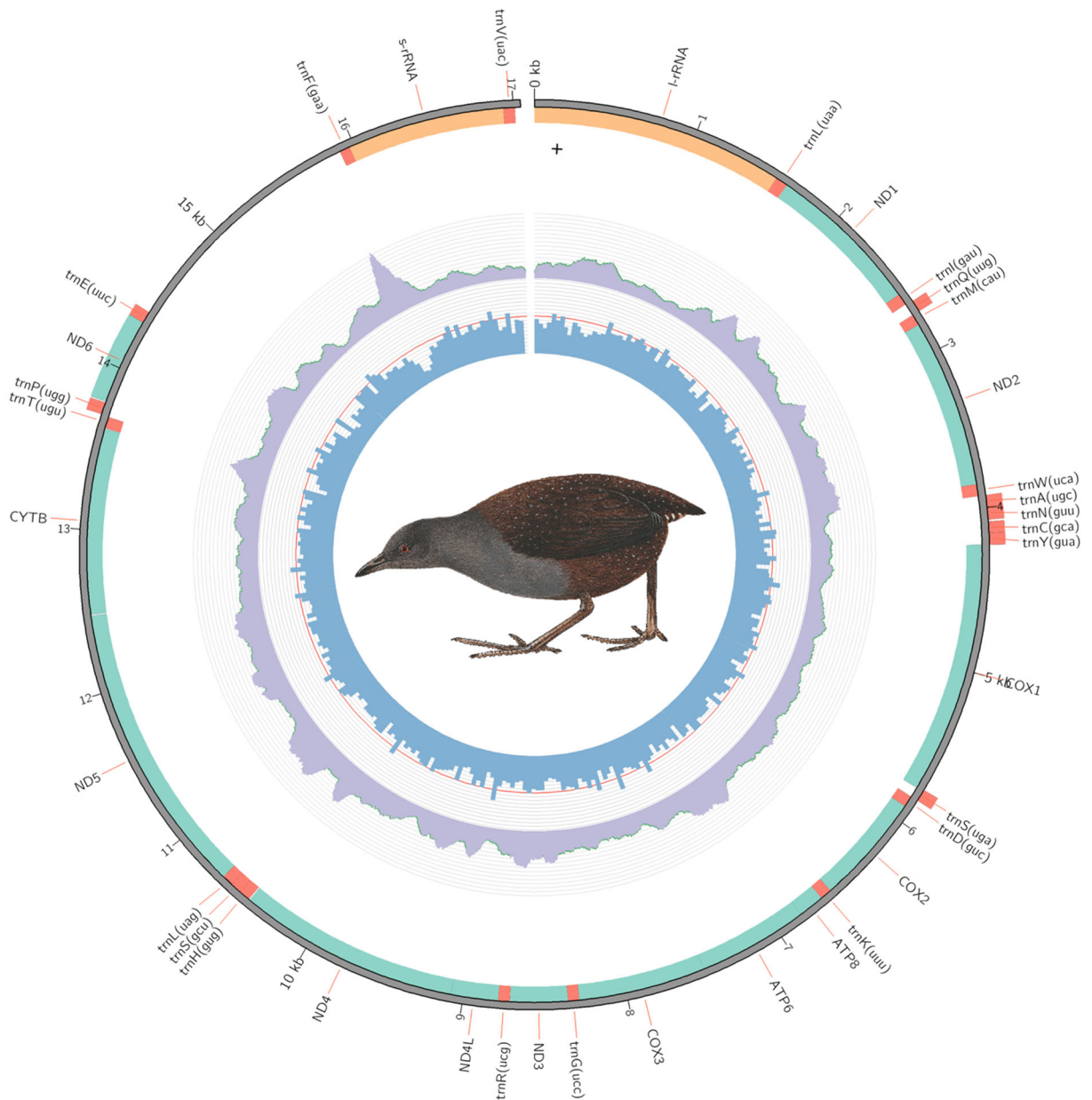


Figure S1. Graphic representation of the *Laterallus spilnota* reference mitochondrial genome assembly produced by MitoZ. The outer panel represents annotations of protein coding genes (teal), ribosomal RNAs (peach), and transfer RNAs (red); drawn on the inside for features on the +strand and on the outside for features on the -strand. The non-annotated region around 15 kbp is the control region (D-loop). Read coverage is drawn in grey in the middle panel, and GC content is represented by bluish bars in the inner panel. Illustration reproduced with permission from Lynx Edicions ©.

Table S1. Primer information

Primer	Sequence (5'-3')	Reference
Cytb		
L14990	CCATCCAACATCTCAGCATGATGAAA	(Bonaccorso et al., 2010)
H16065	GGAGTCTTCAGTCTCTGGTTTACAAGAC	(Bonaccorso et al., 2010)
ND2		
L5143	GAACCTACACARAAGRGATCAAAAC	(Bonaccorso et al., 2010)
H6313	ACTCTTRTTTAAGGCTTTGAAGGC	(Bonaccorso et al., 2010)
RAG-1		
R52	CAAGCAGATGAAYTGGAGGC	(Johansson et. al., 2001)
R53	TCCATGTCTTTAAGGCACA	(Johansson et. al., 2001)

Table S2. Sequencing characteristics of the five samples (first part of name), specified for read 1 (R1 in the last part of the sample name) and read 2 (R2). The Q20 and Q40 columns refer to proportion of bases of said quality or higher, with Q20 corresponding to a 99% and Q40 to a 99.99% base call accuracy. Number of reads mapped refers to the mapping onto the GR9 MitoZ reference *de novo* assembly.

Sample name	Number of reads	Duplicates	GC content	Mean length	Failed	≥Q20 (%)	≥Q40 (%)	N reads mapped
GR2_S8_R1	49,940,830	15.40%	43%	62 bp	27%	94.8	79.7	16,488
GR2_S8_R2		14.90%	43%	62 bp	36%			
GR5_S9_R1	45,265,162	15.60%	44%	58 bp	27%	94.4	79.4	22,466
GR5_S9_R2		14.80%	44%	59 bp	36%			
GR7_S10_R1	45,841,624	14.80%	43%	63 bp	27%	95.0	80.1	14,796
GR7_S10_R2		14.10%	43%	64 bp	36%			
GR8_S11_R1	44,396,890	14.60%	43%	71 bp	18%	96.2	81.7	57,476
GR8_S11_R2		14.20%	43%	72 bp	18%			
GR9_S12_R1	46,749,420	19.90%	41%	76 bp	27%	94.1	80.3	59,396
GR9_S12_R2		19.60%	41%	76 bp	27%			

Table S3. Mitogenome sequence variation among five samples of the Galápagos Rail *Laterallus spilonota*. Position is indicated relative to the first base pair of the ND1 gene in the reference assembly of sample GR9 (GenBank accession no. MW067132). The last columns indicates in which sample a private allele occurs, length of insertions (+) or deletions (-), and/or the grouping of samples for phylogenetically informative variants.

Variation type	Position	Unit	Codon position	Amino acid change	Informative	Sample / grouping
SNP	285	ND1	3	synonymous	private	GR7
SNP	2,126	ND2	1	non-synonymous	private	GR9
SNP	3,716	COI	3	synonymous	private	GR5
SNP	5,726	ATP6	1	non-synonymous	private	GR8
SNP	6,039	COIII	3	synonymous	phylogenetically informative	(GR7,GR9) (GR2,GR5,GR8)
SNP	6,384	COIII	3	synonymous	private	GR5
SNP	7,716	ND4	3	synonymous	private	GR7
SNP	7,833	ND4	3	synonymous	private	GR2
SNP	7,980	ND4	3	synonymous	private	GR7
SNP	8,622	ND4	3	synonymous	private	GR5
SNP	9,146	ND5	3	synonymous	private	GR7
SNP	9,344	ND5	3	synonymous	private	GR7
SNP	9,971	ND5	3	synonymous	private	GR8
SNP	11,808	CYTB	1	non-synonymous	private	GR8
Indel	12,765	control region			private	GR9 -1bp
SNP	12,901	control region			private	GR2
SNP	12,909	control region			private	GR2
SNP	13,189	control region			private	GR8
SNP	13,369	control region			private	GR7
SNP	13,660	control region			private	GR9
SNP	13,776	control region			private	GR5
Indel	13,839	control region			private	GR7 +1bp
SNP	13,997	control region			private	GR9
SNP	14,022	control region			private	GR9
Indel	14,244	control region			phylogenetically informative	(GR5+GR9) (GR2+GR8) +1bp GR7 +2bp
Indel	15,401	16S rRNA			?	Ambiguous mononucleotide length variation

Table S4. Sequence information for mitochondrial markers *cytb* (A), ND2 (B) and nuclear RAG-1 (C). Haplotype name, frequency, polymorphic sites at given nucleotide position, sample ID, island, GenBank accession number and Sequence ID as submitted to GenBank.

A) Cytochrome *b*

Haplotype	Freq	Nucleotide position		Individuals	Island	GenBank accession number	Sequence ID
		450	535				
LS02	43	C	G	LS02 LS03 LS04 LS08 LS09 LS12 LS13 LS14 LS17 LS18 LS19 LS20 LS21 LS22 LS23 LS24 LS25 LS27 LS28 LS29 LS30 LS31_XX LS32 LS33 LS34 LS35 LS36 LS37 LS38 LS39 LS40 LS42 LS43 LS45 LS46 LS47 LS51 LS52 LS54 LS57 LS58 LS60 LSNN	Sta. Cruz Isabela Pinta Santiago	MW074873	LS02_Cytb
LS06	7	T	.	LS06 LS11 LS16 LS49 LS50 LS53 LS55	Sta. Cruz Santiago	MW074874	LS06_Cytb
LS07	9	.	A	LS07 LS10 LS15 LS26 LS41 LS44 LS48 LS56 LS59	Sta. Cruz Isabela Santiago	MW074875	LS07_Cytb

B) ND2

Haplotype	Freq	Nucleotide position				Individuals	Island	GenBank accession number	Sequence ID
		297	439	930	961				
LS05	32	A	C	T	G	LS05 LS09 LS12 LS13 LS14 LS17S LS18S LS19S LS20S LS25S LS26S LS27S LS28S LS29S LS31_XX LS34 LS38 LS40 LS42 LS44 LS45 LS46 LS47 LS54 LS56 LS57 LS32- LS35 LS37 LS52 LS59 LSNNNS	Sta. Cruz Isabela Pinta Santiago	MW074876	LS05_ND2
LS03	4	.	.	.	A	LS03 LS04 LS08 LS60	Sta. Cruz Santiago	MW074877	LS03_ND2
LS06	7	.	T	.	.	LS06 LS11 LS16 LS50 LS53 LS55 LS49	Sta. Cruz Santiago	MW074878	LS06_ND2
LS07	3	.	.	G	.	LS07 LS10 LS15	Sta. Cruz	MW074879	LS07_ND2
LS21	5	G	.	.	.	LS21S LS22S LS23S LS24S LS30S	Isabela	MW074880	LS21_ND2

C) RAG-1

Haplotype	Freq	Nucleotide position	Individuals	Island	GenBank accession number	Sequence
		535				
LS02	57	C	LS02 LS03 LS04 LS05 LS06 LS07 LS08 LS09 LS10 LS11 LS12 LS13 LS14 LS15 LS16 LS17 LS18 LS19 LS20 LS21 LS22 LS23 LS24 LS25 LS26 LS27 LS28 LS29 LS31 LS32 LS33 LS34 LS35 LSNN LS36 LS37 LS38 LS39 LS41 LS42 LS43 LS44 LS45 LS46 LS47 LS48 LS49 LS50 LS51 LS52 LS53 LS54 LS55 LS56 LS57 LS59 LS60	Sta. Cruz Isabela Pinta Santiago	MW074881	LS02_RA G1
LS58	1	G	LS58	Santiago	MW074882	LS58_RA G1



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