



Supplementary Material

Complete Mitochondrial Genome of Blue-Throated Bee-eater *Merops viridis* (Coraciiformes: Meropidae) with its Taxonomic Consideration

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Supplementary Table S1.- The fourteen primer combinations used for amplifying the complete mitogenome of *M. viridis*.

Primer name	Primer sequence (5'→ 3')	Positions on the H-strand	Size of PCR product (bp)
F1	GAATCCCTGAATGAGACGG	17751-17769	1441
R1	AACGGGCCGTCTAATCTCG	878-896	
F2	CACTAACAAGACAGGTCAAGG	755-775	1682
R2	GGATTGCGCTGTTATCCCTGG	2416-2436	
F3	GTTGGGGCGACCTTGAG	2290-2307	1644
R3	GGAAGTATGGAGAGGTTTG	3915-3933	
F4	CTCAAACCCCGGAAATGTGCC	3792-3812	1692
R4	GATGTCTTTGTGGTTGGTTGAG	5462-5483	
F5	GATGAGCTTGCAACTCAACATG	5326-5347	1679
R5	GTGAGGGTTCGACTCCTTCC	6985-7004	
F6	CATCTGAGAAGCCTTGCATCC	6851-6872	1568
R6	CCTAAGGACATGGATGGTTGG	8398-8418	
F7	CCCTAATCCTAACATCCCTG	8247-8266	1710
R7	CAACTGTCTTAGTGTTAGAC	9937-9956	
F8	CTCCCATGAGCCACCCAAC	9800-9818	2131
R8	GGATGGTTGTAAGGGTGAGC	11911-11930	
F9	CTGAGTCTAGAACCTCAGC	11780-11798	727
R9	GGGTTGTGGGTTGAGAGGAG	12487-12506	
F10	GCAGAAGCCAACACAGCTG	12365-12383	811
R10	GGCTTGTTTGGACGAGCAG	13157-13175	
F11	CCTAGCAGGATTCTACTCC	13030-13048	1054
R11	GCTATGAGAGTGAGGAGGAG	14064-14083	
F12	GACTAATCCGAAACCTCCATGC	13939-13960	1066
R12	CATAGGCTGCGTGCAAGAAG	14984-15004	
F13	CTTCCCCATCATCAGTACCC	14804-14823	1742
R13	GGTCTTAGGTTATGGAGTG	16527-16545	
F14	TAGAGCACAGCAACCCAC	16396-16414	1542
R14	GGTGAAAAGTGCCTAGTGTTG	17917-17937	

Supplementary Table S2.- Characteristics of mitochondrial genome for *M. viridis*.

Gene	Position		Size (bp)	Strand	Codon	
	From	To			Start	Stop
tRNA-Phe (F)	1	68	68	H		
12S rRNA	69	1038	970	H		
tRNA-Val (V)	1039	1110	72	H		
16S rRNA	1111	2724	1614	H		
tRNA-Leu (UUR)	2725	2808	84	H		
<i>Nd1</i>	2810	3784	975	H	ATG	TAA
tRNA-Ile (I)	3802	3874	73	H		
tRNA-Gln (Q)	3879	3949	71	L		
tRNA-Met (M)	3949	4017	69	H		
<i>Nd2</i>	4018	5059	1042	H	ATG	TAG
tRNA-Trp (W)	5057	5128	72	H		
tRNA-Ala (A)	5130	5198	69	L		
tRNA-Asn (N)	5221	5295	75	L		
tRNA-Cys (C)	5299	5364	66	L		
tRNA-Tyr (Y)	5364	5433	70	L		
<i>Cox1</i>	5435	6985	1551	H	ATG	AGG
tRNA-Ser (UCN)	6977	7050	74	L		
tRNA-Asp (D)	7055	7123	69	H		
<i>Cox2</i>	7125	7808	684	H	ATG	TAA
tRNA-Lys (K)	7810	7880	71	H		
<i>Atp8</i>	7880	8047	168	H	ATG	TAA
<i>Atp6</i>	8083	8721	639	H	ATG	TAA
<i>Cox3</i>	8721	9504	784	H	ATG	T
tRNA-Gly (G)	9505	9573	69	H		
<i>Nd3</i>	9574	9924	351	H	ATC	TAA
tRNA-Arg (R)	9927	9997	71	H		
<i>Nd4l</i>	9999	10295	297	H	ATG	TAA
<i>Nd4</i>	10289	11666	1378	H	ATG	T
tRNA-His (H)	11667	11736	70	H		
tRNA-Ser (AGY)	11737	11804	68	H		
tRNA-Leu (CUN)	11804	11874	71	H		
<i>Nd5</i>	11875	13689	1815	H	ATG	AGA
<i>Cytb</i>	13706	14848	1143	H	ATG	TAA
tRNA-Thr (T)	14851	14919	69	H		
CR	14920	16208	1289	H		
tRNA-Pro (P)	16209	16279	71	L		
<i>Nd6</i>	16283	16801	519	L	ATG	TAG
tRNA-Glu (E)	16805	16872	68	L		
CCR	16806	18295	1490	H		

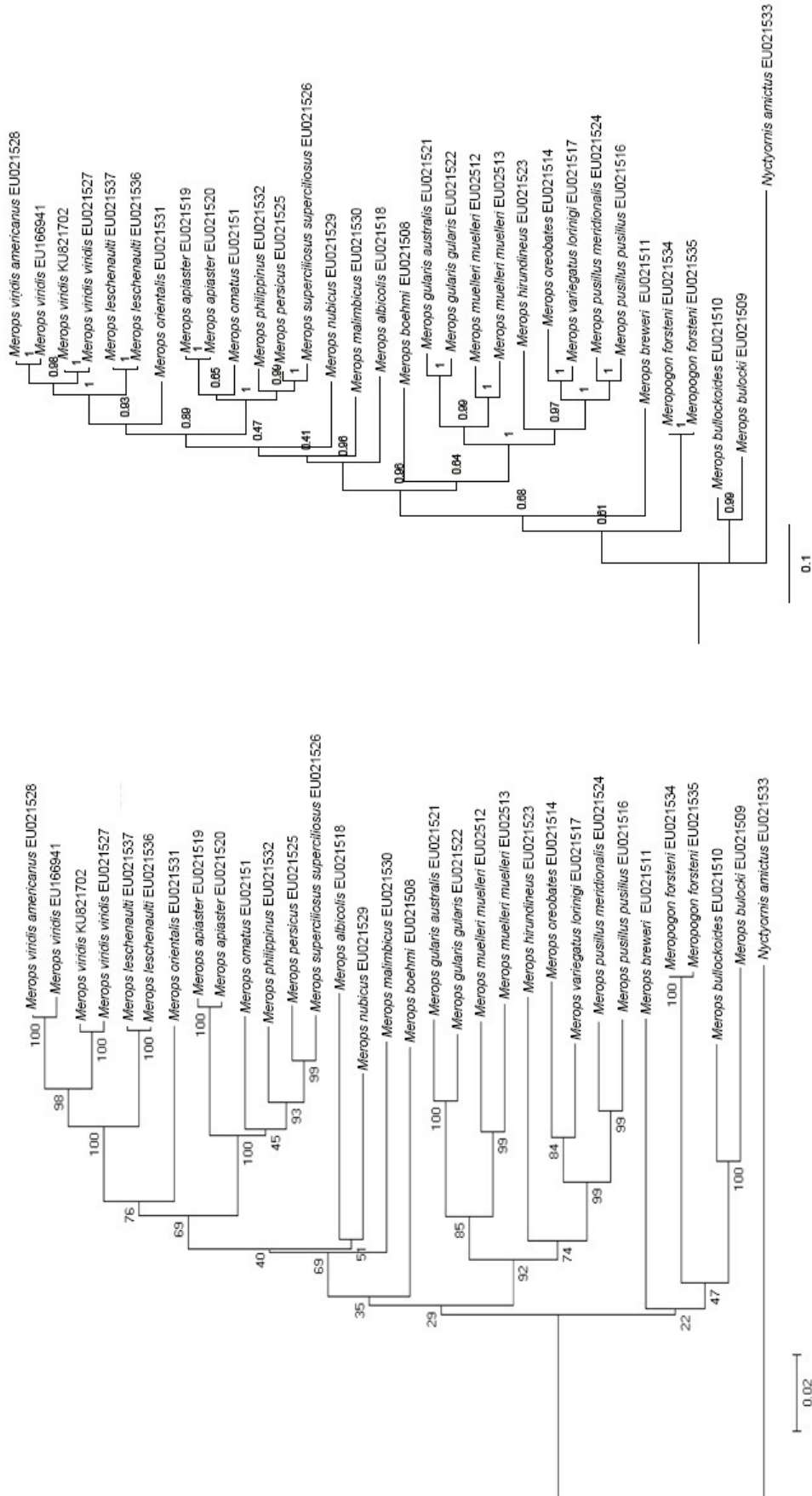


Fig. S1. Neighbor-joining and Bayesian inference trees constructed from ND2 sequences. Numbers represent supporting values.

ATCATGACCTTCCCCCCCCCACCCTCCAGGCTCTTATAGTCACTGGTAATCTATGTACTTCTGTGCATTAACCTATATTCCTCCATTAACTATGCACCTAACTAGGACATTATACCTTAATGTACGA
TCCACATTACATGTAATGTTTTAACTACATATCAATTATTATACTCGGGCATAATAATATCCTATACATTCATACCCCATGGATTATATGTAATGGCCCCATCTACACATTCACCTACCTTTACCCAAAC
CAITTAATATCATAGCTTATACATACAGTCTTTACTACACGAAAGTGCTTACCCTACTAACTATGCACCGTCACAGGTATATAGTTCGGTCTTCTCTCTATGCTCGCGTACCCCTAGCCGCGTA
CCAGGTGGATTATTAGTCTGATACATCAGGTGAAATCAGCAACGCACCGCATATAATGTCTTAGTTACTAGCTTCAGGCCATATCTTCCCCCTAAACCCCTAGCACAACTTGCTCTTTTGGG
CCTCTGGTCTCTGTGACAGGCCATAAAGTGGTCACTCCCTTGCAGATTGCCCTTTCATGAGACATTTGGTTGGGTTCTTGGTATTACATCTCACCCGTGATCGCGGCATTCCTGTGTTTGGCGCC
TTTGGTATCTTTTTTTTTGGGGCGTCTTCAGTAAACCTTCTAGTGCACCGGGTAATAACAATCTAAGACCTGTACATACATGGTATACGACCAAGTGTGCGCCCTCAGGTGCTGATGGCGTCA
TGGCTTAAGGATAAAGTATAGTCTCATCCTGACACTGATGCACCTTGGGTGGCATTGGTTATGGGTATCCCCCTAGCAGGTATATATGCTGCTATTAGTGAATGCTGTGAGGACATAGTTTTTA
CCTTCAACACTTCTACTGATTTTCTCAACAAATCTAGTAAGATTCCAGCTAAAACTAACAACATTCATTCGTTTCAATTCGTTCATTCATTCCTGTC

Fig. S2. The CAACAA repeated motifs in the control region. “...” represent the N-terminal sequence of control regions have been omitted. The CAACAA repeated motifs have been underlined and italicized.