

SUPPLEMENTARY MATERIAL

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Assessment of genetic and morphological differentiation among populations of the Diederik Cuckoo *Chrysococcyx caprius*

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Supplementary Table S1: Pairwise genetic distances between members of the genera *Chrysococcyx*, *Coccyzus* and *Cuculus* estimated from the mitochondrial ribosomal RNA subunit 12S

	1	2	3	4	5	6
[1] <i>Chrysococcyx caprius</i> (Clade 1)						
[2] <i>Chrysococcyx caprius</i> (Clade 2)	0.004					
[3] <i>Chrysococcyx caprius</i>	N/A	N/A				
[4] <i>Chrysococcyx klaas</i>	0.026	0.027	0.029			
[5] <i>Coccyzus erythrophthalmus</i>	0.037	0.036	0.041	0.054		
[6] <i>Cuculus canorus canorus</i>	0.041	0.041	0.046	0.056	0.008	
[7] <i>Cuculus solitarius</i>	0.039	0.042	0.044	0.056	0.011	0.003

Supplementary Table S2: Pairwise genetic distances between members of the genera *Chrysococcyx* and *Cuculus* estimated from the mitochondrial ribosomal RNA subunit 16S

	1	2	3	4	5	6	7	8
[1] <i>Chrysococcyx caprius</i> (Clade 1)								
[2] <i>Chrysococcyx caprius</i> (Clade 2)	0.010							
[3] <i>Chrysococcyx caprius</i>	N/A	N/A						
[4] <i>Chrysococcyx klaas</i>	0.069	0.068	0.069					
[5] <i>Cuculus solitarius</i>	0.139	0.145	0.140	0.121				
[6] <i>Cuculus gularis</i>	0.143	0.141	0.143	0.118	0.018			
[7] <i>Cuculus poliocephalus</i>	0.144	0.142	0.144	0.126	0.036	0.030		
[8] <i>Cuculus canorus</i>	0.143	0.141	0.142	0.117	0.021	0.009	0.027	
[9] <i>Cuculus micropterus</i>	0.143	0.141	0.143	0.118	0.020	0.015	0.027	0.006

Supplementary Table S3: Pairwise genetic distances between members of the genera *Chrysococcyx* and *Cuculus* estimated from the nuclear intron 5 of the β -fibrinogen gene (FIB5)

	1	2	3	4	5	6
[1] <i>Chrysococcyx caprius</i> (Clade 1)						
[2] <i>Chrysococcyx caprius</i> (Clade 2)	0.000					
[3] <i>Chrysococcyx caprius</i>	N/A	N/A				
[4] <i>Chrysococcyx klaas</i>	0.012	0.012	0.012			
[5] <i>Cuculus solitarius</i>	0.049	0.049	0.049	0.052		
[6] <i>Cuculus gularis</i>	0.055	0.055	0.055	0.058	0.012	
[7] <i>Cuculus canorus</i>	0.053	0.053	0.053	0.056	0.016	0.021

Supplementary Table S4: Pairwise genetic distances between members of the genera *Chrysococcyx* and *Cuculus* estimated from the nuclear recombination activating gene 1 (RAG1)

	1	2	3	4	5
[1] <i>Chrysococcyx caprius</i> (Clade 1)					
[2] <i>Chrysococcyx caprius</i> (Clade 2)	0.000				
[3] <i>Chrysococcyx caprius</i>	N/A	N/A			
[4] <i>Chrysococcyx klaas</i>	0.018	0.018	0.018		
[5] <i>Cuculus solitarius</i>	0.029	0.029	0.029	0.018	
[6] <i>Cuculus canorus</i>	0.032	0.032	0.032	0.040	0.004

Supplementary Figure S1: (a) Maximum-likelihood tree of the Diederik Cuckoo *Chrysococcyx caprius* dataset based on the mitochondrial ribosomal RNA subunit 16S under the Kimura 2-parameter (K2) + gamma (G) model; numbers below branches indicate bootstrap values. (b) Maximum-likelihood tree indicating distribution of haplotypes and (c) median-joining network

Supplementary Figure S2: (a) Maximum-likelihood phylogenetic tree of the Diederik Cuckoo *Chrysococcyx caprius* dataset based on the mitochondrial ribosomal RNA subunit 12S under the Kimura 2-parameter (K2) model; numbers below branches indicate bootstrap values. (b) Maximum-likelihood tree indicating distribution of haplotypes and (c) median-joining network

Supplementary Figure S3: Mismatch distribution for the Diederik Cuckoo *Chrysococcyx caprius* dataset showing observed and expected pairwise difference frequencies for concatenated datasets of (a) mitochondrial and (b) nuclear markers

Supplementary Figure S4: (a) Maximum-likelihood tree of the Diederik Cuckoo *Chrysococcyx caprius* dataset based on the nuclear intron 5 of the β -fibrinogen gene (FIB5), and the respective (b) median-joining network

Supplementary Figure S5: (a) Maximum likelihood tree of the Diederik Cuckoo *Chrysococcyx caprius* dataset based on the nuclear recombination activating gene 1 (RAG1) and the respective (b) median-joining network

Supplementary Figure S6: Principal component analysis (PCA) scatter plots based on the morphological measurements of Diederik Cuckoos *Chrysococcyx caprius* across Africa, in relation to sex, locality, and phylogenetic lineage (Clade 1 or Clade 2)