Supplementary material

Supplementary Table S1. List of ten species-specific microsatellite markers primer sequences developed for this study and primers used for mitochondrial sequencing for Southern Ground-Hornbill DNA analyses.

Supplementary Table S2. Details of the selected model for each gene fragment with the lowest BIC scores (Bayesian Information Criterion) in MEGAX. AICc value (Akaike Information Criterion, corrected), Maximum Likelihood value (lnL), the number of parameters (including branch lengths) Gamma distribution (+G), evolutionarily invariable (+I) and nucleotide frequencies (Freq) are also presented.

Supplementary Table S3. Outgroup CYTB DNA sequences included in the molecular dating analysis and their NCBI accession numbers.

Supplementary Fig. 1. A) Plots of assignment probabilities from STRUCTURE (correlated allele frequencies) for K=2 to K=6 indicating the posterior probability of assigning each individual to each of the inferred clusters. Each individual is represented by a vertical bar and the colours refer to the different clusters. B) Output from STRUCTURE HARVESTER showing Probability (-LnPr) of K=1 to 6 averaged over 20 runs. C) Delta K values for real population structures of K=1 to 6 average cluster membership (over 20 runs).

Supplementary Fig. 2. A) Plots of assignment probabilities from STRUCTURE (independent allele frequencies) for K=2 to K=6 indicating the posterior probability of assigning each individual to each of the inferred clusters. Each individual is represented by a vertical bar and the colours refer to the different clusters. B) Output from STRUCTURE HARVESTER showing Probability (-LnPr) of K=1 to 6 averaged over 20 runs. C) Delta K values for real population structures of K=1 to 6 average cluster membership (over 20 runs).

Supplementary Fig. 3. Principal component analysis (PCA) of Southern Ground-Hornbills. BOT = Botswana, KEN = Kenya, MOZ = Mozambique, NAM = Namibia, SAE = South Africa Eastern Cape, SAG = South Africa Kruger National Park, SAK = South Africa KwaZulu-Natal, SAL = South Africa Limpopo, TAN = Tanzania, ZAM = Zambia, ZIM = Zimbabwe, DRC = Democratic Republic of Congo.

Supplementary Fig. 4. Correlogram illustrating the autocorrelation coefficient (r) for the Southern Ground-Hornbill populations. This is a measure of the genetic distance between individuals as the geographic distance between them increases. The 95% confidence intervals around r are indicated by the error bars at each distance class. These were determined using 1000 bootstrap iterations. The dotted lines represent the upper and lower 95% confidence intervals for the hypothesis of randomly distributed genotypes in space.

Supplementary Fig. 5. Mantel test showing lack of correlation between geographic and genetic distance for A) female and B) male birds.

Supplementary Fig. 6. Maximum likelihood tree of mitochondrial DNA sequences conducted in MEGAX for (A) 12S, (B) COI, (C) CYTB, (D) ND2. Numbers indicate bootstrap values.