Supplementary Information

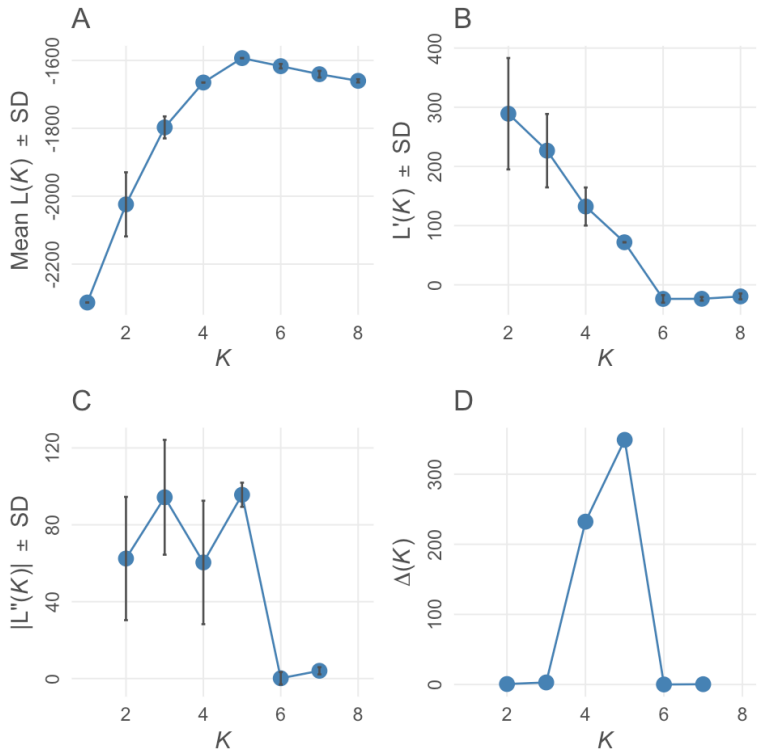
for **"**Genetic diversity and population structure of the spot-nosed monkey (*Cercopithecus petaurista*) of the Bijagós Archipelago, Guinea-Bissau, West Africa"

Details on genotype calling

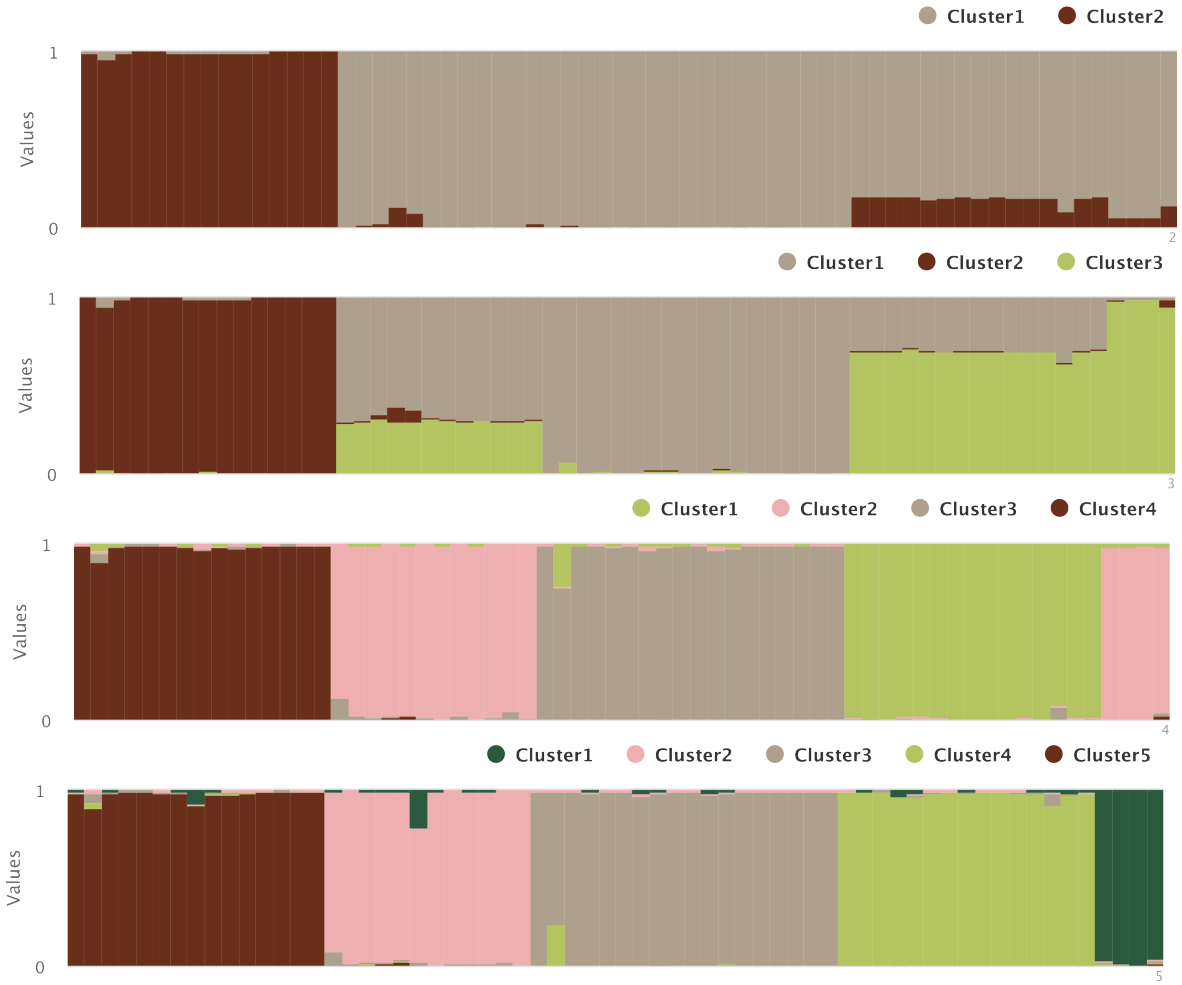
Initially, a maximum likelihood approach implemented in Pedant v1.0[1] was used to estimate a preliminary ADO and FA rates per locus using a subset of samples. Considering that the model is based on the assumption of a population in Hardy-Weinberg Equilibrium (HWE) and that population substructure between islands is plausible, only samples from a single island (Uno Island, N = 18) were used to estimate the error rates. We estimated that for the faecal samples, the consensus genotype obtained from four independent PCR repeats across loci would produce 95% confidence genotypes. Genotypes at any loci were considered as heterozygous after each allele was scored in at least two independent PCR repeats. In the particular case where three homozygotic amplifications and a fourth heterozygotic amplification were observed, a fifth PCR repeat was conducted. Considering the higher quality of the DNA obtainable from tissue and blood samples, the samples were only amplified twice for each multiplex and for the D7s503 locus. The final genotypes were reviewed by a second independent scorer (MJFS) to reduce the subjectivity associated with allele calling.

1. Johnson, P. C. D. & Haydon, D. T. Software for quantifying and simulating microsatellite genotyping error. *Bioinform. Biol. Insights* **1**, 71–75 (2007).

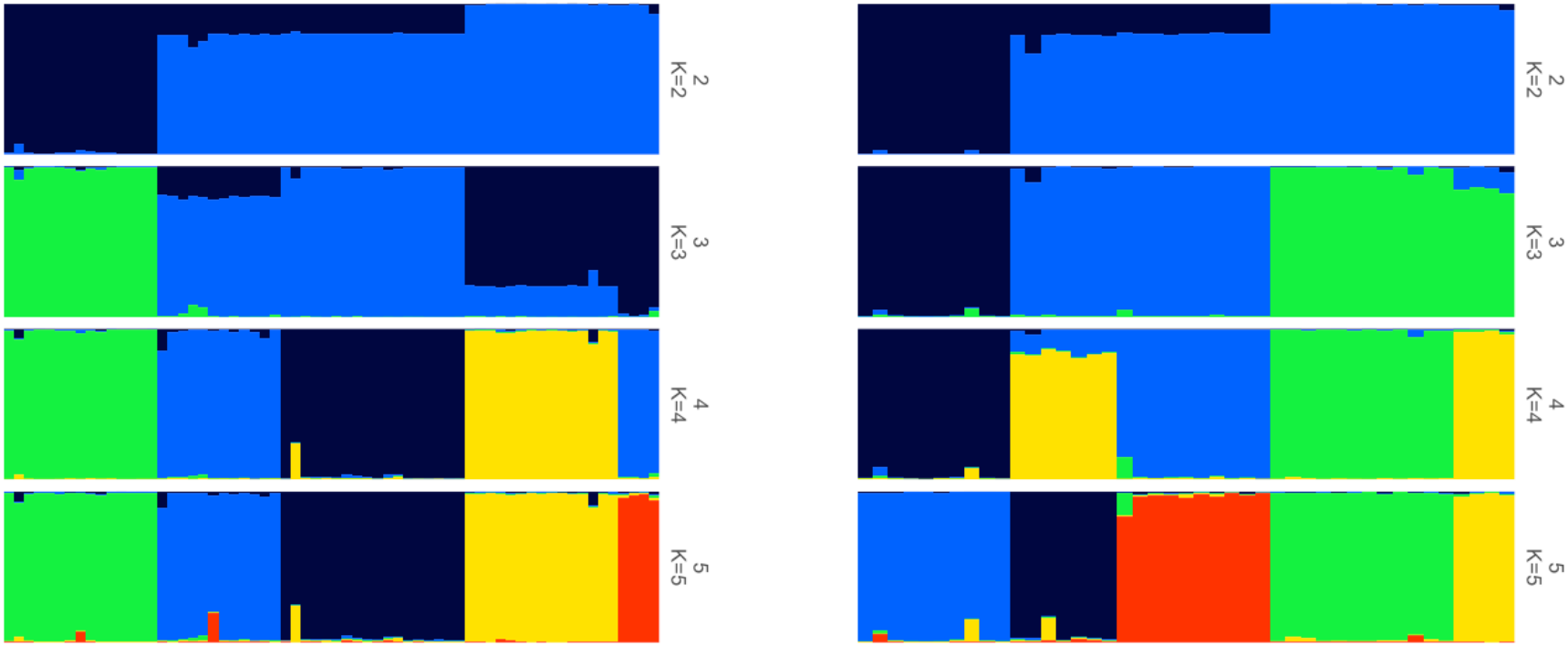
Supplementary figures



Supplementary Fig. 1 Diagnostic plots for STRUCTURE best number of genetic clusters (*K*). Based on mean L(*K*) and *ΔK*, the most likely number of *K* is *K* = 5. There is some support for *K* = 4.



Supplementary Fig. 2 STRUCTURE results for increasing numbers of *K*. Bars depict the average individual cluster assignment probabilities across 10 independent runs.



a b

Supplementary Fig. 3 STRUCTURE results to test for the effect of unbalanced sampling (A) and the inclusion of related individuals (B). Bars depict the average individual cluster assignment probabilities across 10 independent runs. Results suggest STRUCTURE runs were shown to be insensitive to these potential sources of bias.

Supplementary Table 1 Details of the three Multiplex Polymerase Chain Reactions employed.

Multiplex	ATemp (ºC)	AT (s)	ET (s)	Locus	Forward Primer Reverse Primer (5' – 3')	Repeat Motif	Concentration (µM)
D7s503	57	50	40	D7s503	ATGACTTGGAGTAATGGG AACCTTTAATCAGGATACAGAC	CA	0.30
M1	57	40	60	D2s1326	AGACAGTCAAGAATAACTGCCC CTGTGGCTCAAAAGCTGAAT	TCTA	0.50
				D14s306	AAAGCTACATCCAAATTAGGTAGG TGACAAAGAAACTAAAATGTCCC	GATA	0.13
				D1s548	GAACTCATTGGCAAAAGGAA GCCTCTTTGTTGCAGTGATT	TCTA	0.20
M2	57	50	40	D5s1457	TAGGTTCTGGGCATGTCTGT TGCTTGGCACACTTCAGG	GATA	0.10
				D7s2204	TCATGACAAAACAGAAATTAAGTG AGTAAATGGAATTGCTTGTTACC	GATA	0.40
				D3s1768	GGTTGCTGCCAAAGATTAGA CACTGTGATTTGCTGTTGGA	GATA	0.075
M3	59	90	90	D2s442	AAGGGAAGGAGCATAGCAAC GATTTGGTAGATAGACAGATGTGA	TCTA	0.10
				D11s2002	CATGGCCCTTCTTTTCATAG AATGAGGTCTTACTTTGTTGCC	GATA	0.12
				D12s372	TGGACCACAGGGTATCATCT TCCAATGGAAAGAAATGGAG	GATA	0.05
				FESFPS	GGAAGATGGAGTGGCTGTTA CTCCAGCCTGGCGAAAGAAT	ATTT	0.08

ATemp – annealing temperature; AT – annealing time; ET – extension time

Supplementary Table 2 Optimisation of EEMS deme size

Number of demes	r^2 between demes	r^2within demes
200	0.80	0.58
400	0.79	0.72
800	0.41	0.28

r^2 – coefficient of determination

Supplementary Table 3. Mitochondrial and nuclear genetic diversity of primates in Guinea-Bissau.

Species	Hd	π	H_E	Reference
Spot-nosed monkey (*Cercopithecus petaurista*)				This study
Guinea-baboon (*Papio papio*)	0.68-0.91	1.04-2.10x10^{-2}	0.55-0.64	[1,2]
Black-and-white colobus (*Colobus polykomos*)	0.16	0.04x10^{-2}	0.42	[3]
Western red colobus (*Piliocolobus badius temminckii*)	0.83	3.80 x10^{-2}	0.51	[3]
Western chimpanzee (*Pan troglodytes verus*)	0.90-0.95	3.40-3.70 x10^{-2}	0.63-0.75	[2,4]

Hd – Haplotype diversity; π – nucleotide diversity; H_E – expected heterozygosity.

1. Ferreira da Silva, M. J. *et al.* Assessing the impact of hunting pressure on population structure of Guinea baboons (Papio papio) in Guinea-Bissau. *Conservation Genetics* **15**, 1339–1355 (2014).
2. Gerini, F. Structure and connectivity of sympatric primate species across a human-dominated landscape: population genetics of Western Chimpanzee (Pan troglodytes verus) and Guinea Baboon (Papio papio) in Guinea Bissau, West Africa. (University of Pisa, MSc, 2018).
3. Minhós, T. *et al.* Genetic evidence for spatio-temporal changes in the dispersal patterns of two sympatric African colobine monkeys. *Am. J. Phys. Anthropol.* **150**, 464–474 (2013).
4. Borges, F. A country-level genetic survey of the IUCN critically endangered western chimpanzee (Pan troglodytes verus) in Guinea-Bissau. (University of Porto, MSc, 2017).