

Supporting Information
Genetic origin of donkeys in Brazil

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Online Resource 1 Donkeys in Brazil. a. Brazilian donkey. b. Nordestino donkey. c. Pêga donkey



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Population	N	GenBank accession number
Brazilian donkey	10	Present study (OM416453 - OM416462)
Nordestino donkey	10	Present study (OM416433 - OM416442); MG656392-MG656403
Pêga donkey	10	Present study (OM416443 - OM416452)
China	126	AF532118-AF532126; DQ368497- DQ368596
Egypt	30	MG656081-MG656110
Ethiopia	196	MG656111-MG656306
Peru	85	MG656307-MG656391
Italy	28	KX622700-KX622727
Iran	8	MK619364-MK619371
Kenya	7	YPO88, YPO92, YPO111, YPO116, YPO118, YPO120, YPO122
Kyrgyzstan	5	MK619382; MK619410-MK619411; MK896303; MK896307
Tadzhikistan	13	MK619373-MK619375; MK619383- MK619391; MK896298
Nigeria	9	MK619357-MK619363; MK896292- MK896293
<i>Equus africanus africanus</i>	2	HM622632, HM622636
<i>Equus africanus somaliensis</i>	6	HM622661, HM622663, HM622669, AY569545-AY569547
<i>Equus asinus</i>	1	X97337
<i>Equus caballus</i>	1	NC_001640.1
Total	559	

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28 **Online Resource 3** Structure and polymorphic sites of mitochondrial DNA (D-loop) haplotypes in Brazilian donkeys

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		Nucleotide position																						
		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1				
		5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5				
		4	4	5	5	5	5	6	6	6	6	6	7	8	8	8	8	8	8	8				
		8	9	0	6	8	9	9	2	4	5	6	9	7	0	0	2	2	2	6	Brazil			
Haplotype		4	0	3	9	0	8	9	1	4	2	2	8	0	1	6	0	1	2	8	Brazilian	Nordestino	Pêga	
X97337		G	C	T	A	A	C	A	A	G	C	A	C	T	C	C	C	G	G	C	N			
H1		.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	T	7		2	5	
H2		A	T	C	G	G	T	G	G	A	T	G	T	C	T	T	T	A	A	.	3		3	
H3		A	T	C	G	G	T	G	.	A	T	G	T	C	.	T	T	A	A	.	5		5	
H4		.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	.	13	10		3	
H5		A	T	C	G	G	T	G	.	A	T	G	T	C	T	T	T	A	A	.	2		2	

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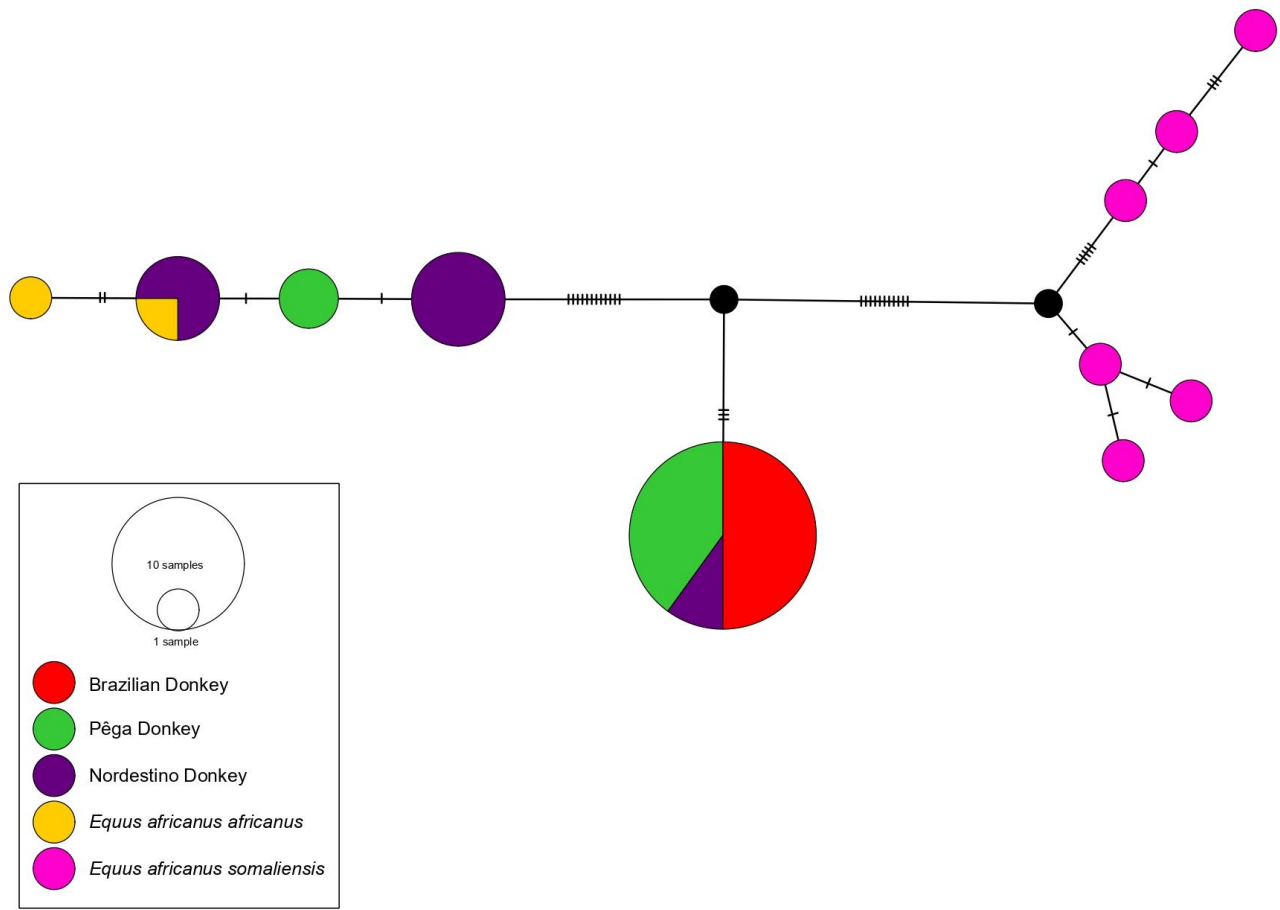
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Online Resource 4 Haplotype network of the 38 sequences of the Brazilian donkey (N=10), Pêga donkey (N=10), Nordestino donkey (N=10), Somali wild ass (N=6), and Nubian wild ass (N=2), obtained based on 437 bp of the mitochondrial DNA D-loop. Each circle corresponds to one haplotype and the size is proportional to its frequency. The dashes indicate mutational steps between haplotypes. The colors represent the breeds as shown in the legend



61 **Online Resource 5** Donkey breeds, sample size (N), number of haplotypes per group (H), haplotype frequency, haplotype diversity ($H_d \pm SD$), and nucleotide diversity ($\pi \pm$
62 SD)

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Breed	N	Clade I		Clade II		$H_d \pm SD$	$\pi \pm SD$
		H	Frequency	H	Frequency		
Brazilian Donkey	10	0	0.0	1	1.0 (10)	0.00 ± 0.00	0.00 ± 0.00
Nordestino Donkey	10	2	0.80 (8)	1	0.20 (2)	0.689 ± 0.104	0.01264 ± 0.00478
Pêga Donkey	10	1	0.20 (2)	2	0.80 (8)	0.689 ± 0.010	0.01192 ± 0.00487

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66 **Online Resource 6** Hierarchical analysis (AMOVA) between the three donkey breeds

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Source of variation	d.f.	Percentage of variation
Between populations	2	47.01*
Within populations	27	52.99
$F_{ST}=0.47009$		

68 * Between-population variation; F_{ST} : significant ($P<0.05$).

69 d.f. = degrees of freedom.

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Online Resource 7 Topology recovered by Bayesian inferences based on 202 mitochondrial DNA sequences (399 bp) of donkeys, together with eight sequences of African wild asses (*Equus africanus africanus*: HM622632, HM622636; *Equus africanus somaliensis*: HM622661, HM622663, HM622669, AY569545–AY569547). One *Equus caballus* sequence (NC_001640) was used as outlier group. Posterior probabilities higher than 50% are shown



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