

Evaluation of Genetic Diversity and Population Structure of Five Chinese Indigenous Donkey Breeds Using Microsatellite Markers

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Supplementary Online Material (SOM)

Table S1. Detailed information on genetic parameters for 15 microsatellite loci in five Chinese indigenous donkey breeds

Parameter	Breed					Parameter	Breed				
	GZ	JN	GL	DZ	HB		GZ	JN	GL	DZ	HB
<i>n</i>	35	36	27	25	30	<i>n</i>	35	36	27	25	30
AHT4						HMS2					
<i>He</i>	0.74	0.76	0.78	0.78	0.84	<i>He</i>	0.84	0.85	0.84	0.88	0.88
<i>Ho</i>	0.72	0.72	0.85	0.72	0.83	<i>Ho</i>	0.34	0.41	0.37	0.32	0.32
TNA	6.00	6.00	7.00	6.00	8.00	TNA	10.00	11.00	9.00	9.00	10.00
AR	5.71	5.63	6.83	6.00	7.71	AR	9.13	9.96	8.96	8.99	9.46
<i>P</i>	0.03	0.05	−0.10	0.08	0.01	<i>P</i>	0.59**	0.52**	0.56**	0.64**	0.63**
<i>F</i>	0.09	0	0	0	0	<i>F</i>	0.09	0.06	0	0	0.07
AHT21						HMS3					
<i>He</i>	0.74	0.73	0.79	0.73	0.81	<i>He</i>	0.63	0.61	0.57	0.68	0.72
<i>Ho</i>	0.71	0.61	0.78	0.72	0.70	<i>Ho</i>	0.62	0.64	0.63	0.72	0.63
TNA	8.00	8.00	7.00	7.00	7.00	TNA	5.00	5.00	4.00	5.00	6.00
AR	7.32	7.57	6.96	6.84	6.98	AR	4.65	4.83	3.85	4.84	5.53
<i>P</i>	0.04	0.17*	0.01	0.02	0.13	<i>P</i>	0.02	−0.04	−0.10	−0.07	0.12
<i>F</i>	0.03	0	0	0	0	<i>F</i>	0.09	0	0	0	0
UM011						HTG6					
<i>He</i>	0.80	0.87	0.64	0.87	0.74	<i>He</i>	0.72	0.70	0.67	0.71	0.72
<i>Ho</i>	0.78	0.74	0.56	0.76	0.86	<i>Ho</i>	0.80	0.78	0.67	0.92	0.83
TNA	8.00	11.00	7.00	9.00	8.00	TNA	4.00	4.00	4.00	4.00	4.00
AR	7.87	10.30	6.83	8.84	7.34	AR	4.00	4.00	3.85	4.00	4.00
<i>P</i>	0.03	0.15*	0.14	0.13	−0.17	<i>P</i>	−0.12	−0.11	0.00	−0.30	−0.16
<i>F</i>	0.08	0.03	0	0	0.03	<i>F</i>	0	0	0	0	0

Table S1 to be continued

Parameter	Breed					Parameter	Breed				
	GZ	JN	GL	DZ	HB		GZ	JN	GL	DZ	HB
<i>n</i>	35	36	27	25	30	<i>n</i>	35	36	27	25	30
HTG7						COR095					
<i>He</i>	0.75	0.85	0.67	0.75	0.83	<i>He</i>	0.35	0.59	0.51	0.61	0.43
<i>Ho</i>	0.66	0.83	0.48	0.64	0.70	<i>Ho</i>	0.31	0.39	0.30	0.24	0.40
TNA	9.00	9.00	9.00	6.00	9.00	TNA	3.00	6.00	5.00	9.00	5.00
AR	8.35	8.62	8.53	5.92	8.97	AR	3.00	5.28	4.85	8.75	4.66
<i>P</i>	0.13	0.03	0.28**	0.14	0.16*	<i>P</i>	0.09	0.34**	0.42**	0.60**	0.08
F	0	0	0	0	0	F	0	0	0	0	0
HTG10						UCDEQ425					
<i>He</i>	0.67	0.69	0.71	0.70	0.70	<i>He</i>	0.53	0.72	0.79	0.67	0.76
<i>Ho</i>	0.60	0.61	0.70	0.91	0.69	<i>Ho</i>	0.14	0.19	0.15	0.40	0.33
TNA	8.00	8.00	6.00	6.00	7.00	TNA	5.00	5.00	5.00	5.00	4.00
AR	7.25	7.33	5.96	6.00	6.71	AR	4.85	4.87	5.00	5.00	4.00
<i>P</i>	0.11	0.11	0.01	−0.31 [#]	0.02	<i>P</i>	0.73**	0.73**	0.81**	0.40**	0.56**
F	0.09	0	0	0.08	0.03	F	0	0	0	0	0
COR070						UCDEQ437					
<i>He</i>	0.66	0.64	0.64	0.52	0.71	<i>He</i>	0.75	0.53	0.52	0.44	0.70
<i>Ho</i>	0.63	0.58	0.70	0.32	0.80	<i>Ho</i>	0.60	0.28	0.56	0.24	0.60
TNA	4.00	4.00	5.00	3.00	5.00	TNA	4.00	6.00	4.00	3.00	7.00
AR	3.96	3.64	4.70	3.00	4.99	AR	4.00	5.93	4.00	2.92	6.43
<i>P</i>	0.05	0.10	−0.10	0.39*	−0.13	<i>P</i>	0.20*	0.47	−0.07	0.46**	0.14
F	0	0	0	0	0	F	0	0	0	0	0
COR071						UCDEQ505					
<i>He</i>	0.43	0.68	0.74	0.46	0.54	<i>He</i>	0.80	0.54	0.76	0.78	0.68
<i>Ho</i>	0.17	0.56	0.59	0.48	0.40	<i>Ho</i>	0.83	0.53	0.59	0.75	0.57
TNA	3.00	7.00	5.00	4.00	5.00	TNA	7.00	5.00	6.00	6.00	7.00
AR	3.00	6.45	5.00	3.92	4.48	AR	6.62	4.35	5.96	5.96	6.53
<i>P</i>	0.60**	0.18	0.20	−0.05	0.26	<i>P</i>	−0.04	0.02	0.22*	0.04	0.16
F	0	0	0	0	0	F	0	0.06	0	0.04	0
COR082											
<i>He</i>	0.82	0.83	0.69	0.83	0.83						
<i>Ho</i>	0.37	0.22	0.26	0.40	0.43						
TNA	7.00	7.00	7.00	7.00	7.00						
AR	6.95	6.63	6.83	7.00	7.00						
<i>P</i>	0.54**	0.73**	0.62**	0.52**	0.48**						
F	0	0	0	0	0						

n = sample size; GZ = Guanzhong donkey; JN = Jinnan donkey; GL = Guangling donkey; DZ = Dezhou donkey; HB = Huabei donkey; *He* = expected heterozygosity; *Ho* = observed heterozygosity; TNA = total number of alleles; AR = allelic richness; *P* = *P*-value in detection of Hardy–Weinberg equilibrium and significant levels of deficit or excess in heterozygotes (deficit: **P* < 0.05; ***P* < 0.01; excess: [#]*P* < 0.05; ^{##}*P* < 0.01); F = frequency of null-alleles per locus