

Molecular Analysis Using Mitochondrial DNA and Microsatellites to Infer the Formation Process of Japanese Native Horse Populations

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Figure 2 and Table 1 of “Molecular analysis using mitochondrial DNA and microsatellites to infer the formation process of Japanese native horse populations” (H. Kakoi, T. Tozaki, and H. Gawahara, *Biochemical Genetics* 45, Nos. 3/4, April 2007), appearing on pages 383–385, contain errors in the arrangement of data. Commonly, the haplotypes H-32 and -33 are identical to H-27; H-34 is identical to H-28; H-35, -36, and -37 are identical to H-29. The corrected figure and table appear here. The haplotypes H-32–37 are eliminated from them. Consequently, 42 haplotypes with 44 variable sites were observed in all populations. The haplotype sequences have been deposited in DDBJ/EMBL/GenBank database (accession nos. AB329587–628).

We apologize for any confusion these errors may have caused.

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Table 1 Distribution of haplotypes among samples from 11 horse populations

Haplotype	Cluster ^a	Number of samples									
		Japanese native horse population ^b						Mongolian and European horse population ^b			
		HK	KS	NM	TS	MS	TK	YN	MG	TH	BR
H-1	A							1	2		
H-2	A				12	1		1			
H-3	A	1									
H-4	A								2	1	
H-5	A			12							
H-6	A							1			
H-7	A								3	4	
H-8	A								1		
H-9	A								5		
H-10	A	26			2	3		10			12
H-11	A									2	
H-12	A						19	9			
H-13	B								3		
H-14	B		2								
H-15	B								1		
H-16	B								24		
H-17	C										2
H-18	C							3	1	4	
H-19	C								4		
H-20	C							1			
H-21	C								1		
H-22	C							1	18		
H-23	C			2							
H-24	C								1		
H-25	D								3		
H-26	D								14		
H-27	D							1	3	4	
H-28	D				2			1			
H-29	D							3	23	3	2
H-30	D								11		
H-31	D									2	
H-38	D							1			
H-39	E										1
H-40	E	1									
H-41	E								6		
H-42	F							1			
H-43	F							2			
H-44	F					22					

Table 1 continued

Haplotype	Cluster ^a	Number of samples										
		Japanese native horse population ^b						Mongolian and European horse population ^b				
		HK	KS	NM	TS	MS	TK	YN	MG	TH	BR	PR
H-45	F							2				
H-46	F		7									
H-47	F		3					1				
H-48	F							1				
Diversity measures ^c												
<i>N</i>		28	12	14	16	26	19	19	21	126	20	17
<i>h</i>		0.14	0.62	0.26	0.43	0.28	0.00	0.53	0.96	0.89	0.88	0.50
π		0.004	0.009	0.007	0.010	0.006	0.000	0.001	0.021	0.020	0.020	0.014

^a Letters indicate the phylogenetic clusters shown in Fig. 3

^b Hokkaido (HK), Kiso (KS), Noma (NM), Taishu (TS), Misaki (MS), Tokara (TK), Yonaguni (YN), Mongolian (MG), Thoroughbred (TH), Breton (BR), Percheron (PR)

^c *N*, Total number of samples in a population. *h*, Haplotype diversity π , Nucleotide diversity