

Genetic Diversity and Admixture in Three Native Draught Horse Breeds Assessed Using Microsatellite Markers

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Supplementary Online Material (SOM)

Table S1. Summary of parameters describing the state of diversity of each population at each locus. Number of successfully genotyped individuals (N), number of alleles (N_A), effective allele number (N_e), observed heterozygosity (H_O), gene diversity (H_e), Wright's F_{IS} index and Hardy–Weinberg equilibrium statistics (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$)

Populations		Microsatellite marker												
		AHT4	AHT5	ASB2	HMS1	HMS2	HMS3	HMS6	HMS7	HTG10	HTG4	HTG6	HTG7	VHL20
SN	N	348	348	345	348	347	323	349	342	337	348	349	345	349
	N_A	8	7	10	7	8	8	6	6	10	6	6	4	9
	H_O	0.78	0.79	0.78	0.61	0.73	0.69	0.67	0.73	0.64	0.66	0.43	0.70	0.79
	H_e	0.79	0.76	0.74	0.62	0.69	0.63	0.64	0.79	0.65	0.65	0.42	0.67	0.79
	F_{IS}	0.02	-0.04	-0.04	0.02	-0.06	-0.09	-0.04	0.08	0.02	-0.02	-0.01	-0.04	-0.01
	HWE								***					
N	N	396	391	395	392	391	381	396	390	383	396	395	395	396
	N_A	9	8	7	6	7	8	6	6	10	6	5	6	10
	H_O	0.83	0.78	0.80	0.65	0.71	0.75	0.72	0.73	0.68	0.63	0.58	0.66	0.80
	H_e	0.81	0.89	0.79	0.66	0.72	0.71	0.70	0.76	0.67	0.67	0.56	0.67	0.79
	F_{IS}	-0.03	0.02	-0.01	0.00	0.02	-0.07	-0.02	0.03	-0.02	0.06	-0.04	0.01	-0.01
	HWE		*					*	*					
CMB	N	553	547	550	552	551	526	551	546	543	551	551	540	552
	N_A	9	8	10	7	10	7	6	6	10	6	6	4	10
	H_O	0.82	0.77	0.62	0.41	0.66	0.72	0.73	0.67	0.78	0.74	0.38	0.74	0.80
	H_e	0.82	0.76	0.63	0.40	0.66	0.70	0.70	0.74	0.80	0.73	0.39	0.70	0.79
	F_{IS}	0.00	-0.02	0.02	-0.03	-0.01	-0.02	-0.06	0.10	0.03	-0.01	0.02	-0.04	-0.01
	HWE				*		*		*	*			*	

SN = Silesian Noriker, N = Noriker, CMB = Czech-Belgian horse breed

Table S2. Statistics from Bayesian clustering implemented in the STRUCTURE programme (Pritchard et al. 2000) through all samples computed from 10 iterations

K	mean lnP(K)	SD lnP(K)	ΔK
1	−50 172.37	0.0483	NA
2	−48 154.82	2.4367	651.87
3	−47 725.66	3.8272	58.52
4	−47 520.48	22.3498	11.96
5	−47 047.81	5.4858	63.43
6	−46 923.14	8.6239	NA

mean lnP(K) and SD lnP(K) are means and standard deviations of the log-likelihood function for a different hypothetical number of genetic groups (K), ΔK is statistics computed by the Evanno et al. (2005) method, NA is not available data