

Conservation of genetic diversity in German draught horse breeds using DNA markers (session G3.14)

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Introduction

German draught horse breeds suffered severe decreases in population size in the 1960s and 1970s. Currently, seven draught horse breeds are distinguished in Germany (Table 1). The smallest German draught horse population, the Schleswig Draught Horse, is mainly bred in Schleswig Holstein and Lower Saxony. The Mecklenburg, Saxon Thuringa and Altmärkisch Coldblood are East German subpopulations of the Rhenish German Draught Horse. South German Coldblood and the Black Forest Horse are mainly bred in Bavaria and Baden-Wuerttemberg, respectively. The objectives of this study were to show the levels of genetic variability among the German draught horse breeds and to estimate genetic distances between them.

Table 1. Population size (N), effective population size (N_e), and inbreeding coefficients (F) for the German draught horse breeds

Population	N	N_e	F (%)
South German Coldblood	2110	413	2.79
Rhenish German Draught Horse	850	300	1.53
Black Forest Horse	799	184	5.75
Saxon Thuringa Coldblood	358	113	2.13
Schleswig Draught Horse	231	89	4.68
Mecklenburg Coldblood	131	34	2.61
Altmärkisch Coldblood	125	60	-



Materials and methods

We collected representative samples from six German draught horse breeds and from a total of six riding, wild and primitive horse populations (Table 2). One highly polymorphic microsatellite marker per autosome was chosen. The 31 loci were: AHT34, ASB17, COR007, COR017, COR018, COR022, COR024, COR045, COR056, COR058, COR069, COR070, COR071, COR082, HMS03, HMS07, HTG03, HTG06, LEX07, LEX33, LEX34, LEX63, LEX68, LEX73, SGCV16, SGCV28, TKY19, UCDEQ425, UM011, VHL20, and VHL209.

Amplification was carried out in 11 independent PCR reactions. Gelelectrophoresis was performed on a LI-COR 4200S-2 automated sequencer. The programmes GENEPOP, FSTAT and PHYLIP were employed for the statistical analysis.

Results

Multilocus G_{ST} values in the heavy horse populations indicated that 11.6 % of the total genetic variation was explained by breed differences and 88.4 % by differences among individuals. The mean number of alleles per draught horse breed varied between 5.20 and 6.33. Observed heterozygosity ranged from 0.64 to 0.71. With exception of the Mecklenburg

and Saxon Thuringa Coldblood, all pairwise differentiation tests showed significant differences ($P < 0.01$). Inbreeding coefficients were negatively correlated with observed heterozygosity ($P < 0.05$).

Table 2. Sample size (N), observed (H_O), and expected heterozygosity (H_E) and total number of private alleles (PA) averaged over the microsatellite loci analysed

Population	N	H_O	H_E	PA
South German Coldblood	45	0.707	0.705	2
Rhenish German Draught Horse	45	0.700	0.678	-
Black Forest Horse	45	0.696	0.660	1
Saxon Thuringa Coldblood	23	0.685	0.654	2
Schleswig Draught Horse	45	0.696	0.685	1
Mecklenburg Coldblood	22	0.635	0.644	-

The phylogenetic tree constructed from the Cavalli-Sforza distance (D_C) by the neighbour-joining method showed the clear demarcation from other horse breeds investigated here (Fig. 1). Schleswig Draught Horse was the most divergent breed among the German heavy horse breeds and the smallest genetic distances were found between Saxon Thuringa, Mecklenburg Coldblood and Rhenish German Draught Horse.

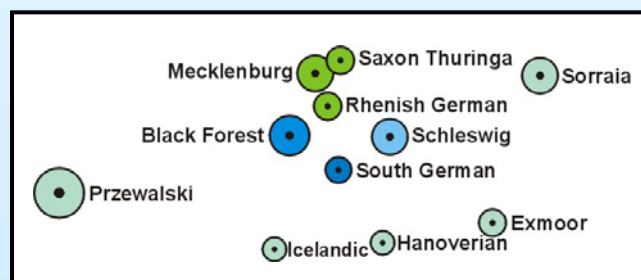


Figure 1. Phylogenetic relationships among German Draught Horse breeds and Hanoverian Warmblood, Arabian, Icelandic Horse, Exmoor Pony, Sorraia Horse and Przewalski's Horse

Conclusions

The reproductive isolation of East German coldblood breeds led to significant genetic and genotypic differentiations between the Rhenish German Draught Horse and its East German subpopulations. Crossbreeding of these breeds would offer a good opportunity to increase genetic variability and stabilize their population size as these breeds have the same genealogical origin.

All other German Draught Horse breeds can be genetically distinguished and should be maintained as independent populations.