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Service & Daten aus einer Quelle

Runs of homozygosity and genomic inbreeding in the German riding horse population

Project motivation / Introduction

- routine genome-wide SNP genotyping of all registered foals in most German Warmblood studbooks
  - ➢ related to introduction of SNP-based imputation of STRs used for parentage testing
- broad availability of genome-wide SNP genotypes implying suitability for analyses of pedigree structure and inbreeding
  - ➢ high coverage of cohorts of riding horses from 2021 onwards
- monitoring of genetic diversity as integral part of responsible breeding programs
  - ➢ reliable assessment of diversity measures by genomic tools

objective: using genome-wide SNP genotypic data to derive key genomic parameters and assess
- **genomic inbreeding**
- **development of genetic diversity**

Conclusion

moderate mean genomic inbreeding (F_{ROH} of 6.8%) in the German riding horse population

low frequencies of long ROH
➢ **smaller role of recent inbreeding** than historical inbreeding

results of pedigree structure analyses as basis of new tools for **support of mating planning** and **improved breed management**

Results

Table 1: Mean F_{ROH} with standard deviation (std.), minimum and maximum for N = 63,196 German Warmblood horses born 2021-2023, determined with different lengths of DNA stretches considered as ROH.

window size [kb]	mean	std.	minimum	maximum
500	0.0783	0.0229	0.0005	0.5424
1,000	0.0777	0.0228	0.0005	0.5256
1,500	0.0745	0.0225	0.0000	0.4478
2,000	0.0679	0.0219	0.0000	0.3555
3,000	0.0511	0.0203	0.0000	0.3140
4,000	0.0388	0.0185	0.0000	0.2899
5,000	0.0298	0.0169	0.0000	0.2722
6,000	0.0229	0.0153	0.0000	0.2628
10,000	0.0090	0.0101	0.0000	0.2306

ROH = Runs of homozygosity, F_{ROH} = genomic inbreeding coefficient based on ROH (McQuillan[b])

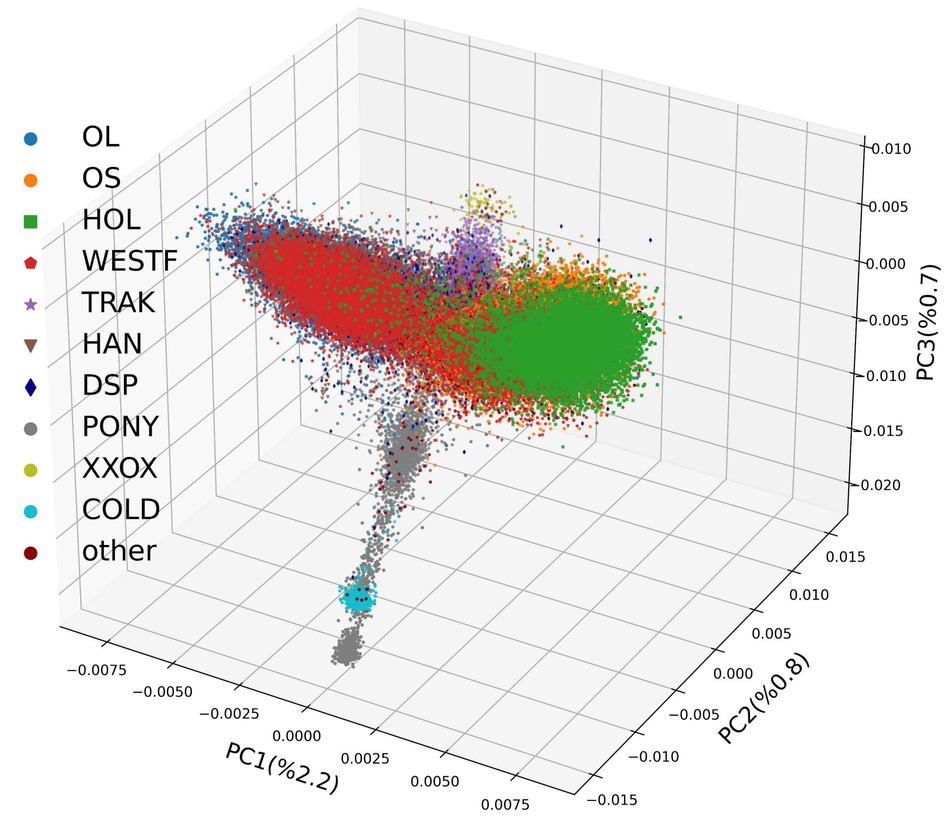

Figure 1: Principal component plot from all horses in the central genome database (N=78,779); PC1 (PC2, PC3) = Vector to the 1st (2nd, 3rd) principal component

Breeds and breed groups of equids as indicated in figure 1:

OL	= Oldenburg	Pony	= different pony breed
OS	= Oldenburg Internat. (jumping)	XXOX	= Thoroughbred and Arabians
HOL	= Holstein	COLD	= different heavy horse breeds (draught horses, Coldblood)
WESTF	= Westphalian	other	= Warmblood horses with foreign ID and horses of unknown breed
TRAK	= Trakehner		
HAN	= Hanoverian		
DSP	= German Sport Horse		

Material and methods

70K+ SNP genotypes of **N = 63,196 German Warmblood horses** were used to determine **runs of homozygosity (ROH)** with **PLINK** software[a] and the following functions / settings:
-- homozyg
-- homozyg-window-kb (different windows see Table 1)
-- homozyg-snp 25 (minimum number of SNPs in one ROH)
-- homozyg-window-het 0 (no heterozygotes allowed in ROH)
N = 57,286 quality controlled autosomal SNPs entered the analyses

calculation of **genomic inbreeding** for each individual and each scenario (different window sizes) according to McQuillan[b]:

$$F_{ROH} = \frac{total\ length\ of\ all\ ROH}{autosomal\ genome\ length\ covered\ by\ SNPs}$$

afterwards: **mean F_{ROH}** over all horses for each scenario (Table 1)

Literature / Acknowledgements

[a] Purcell, S., et al. (2007): PLINK: a toolset for whole-genome association and population-based linkage analysis. Am. J. Hum. Genet. 81, 559-575.
[b] McQuillan, R., et al. (2008): Runs of homozygosity in European populations. Am. J. Hum. Genet. 83, 359-372.

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IAFH
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