

Genetic diversity in and relationships between Dutch horse populations

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Aim

Investigate the genetic make-up of nine horse populations in the Netherlands

- increase our understanding of their evolutionary history
- provide valuable information on how to best conserve or improve these populations

Conclusions

- Genetic diversity and most quantified relationships were in agreement with their history and classifications
- Runs of homozygosity (ROHs) aid in understanding breeding history
- Future research to identify populations with unique genes and significant contribution to genetic diversity



Gelder horse – one of the investigated Dutch warmblood horse populations

Materials and methods

- 50k genotype data from nine populations with about 20 horses per population (n = 184)
- Parameters estimated using PLINK software v1.9 (Purcell, 2007)

Results

- Distinct clusters except for four Dutch warmblood populations
- Largest differentiation from other populations for Shetland ponies and Friesian horses

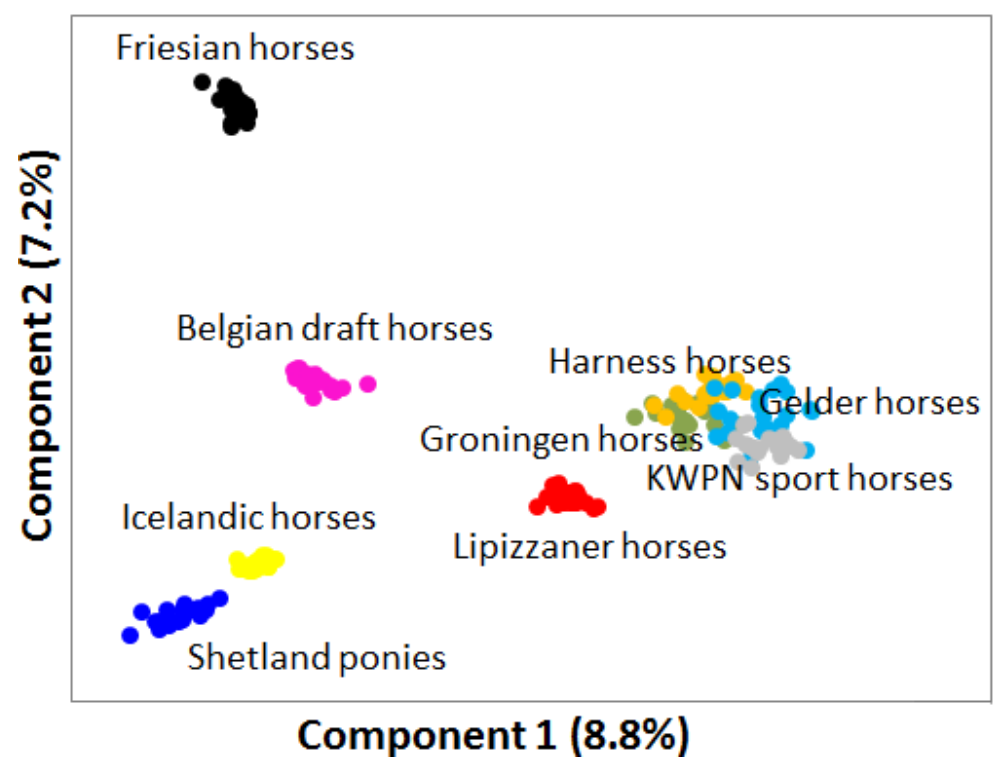


Figure 1 – Relationships within and between populations

- Limited inbreeding in open populations e.g. Gelder horses
- Many long ROHs within a population represents inbreeding of recent origin in e.g. Shetland ponies
- Short ROHs and limited inbreeding in Icelandic horses, an ancient population with past inbreeding

Table 1 – Mean ROH characteristics per population (SE in superscript)

population	inbreeding	number	length, Mb
Belgian draft horse	10.1 ^{3.1}	36.3 ^{6.8}	6.2 ^{5.5}
Friesian horse	22.3 ^{4.5}	74.3 ^{9.5}	6.7 ^{5.4}
Gelder horse	5.9 ^{2.8}	22.2 ^{7.0}	6.0 ^{5.1}
Groningen horse	6.2 ^{2.3}	25.5 ^{7.7}	5.5 ^{4.0}
Harness horse	9.7 ^{4.1}	28.0 ^{8.9}	7.8 ^{6.8}
Icelandic horse	4.1 ^{2.7}	15.1 ^{6.7}	6.1 ^{6.0}
KWP sport horse	5.3 ^{2.4}	22.2 ^{6.7}	5.4 ^{4.2}
Lipizzaner horse	9.0 ^{2.5}	31.7 ^{5.6}	6.4 ^{4.9}
Shetland pony	14.4 ^{6.6}	45.3 ^{8.9}	7.2 ^{7.7}
across populations	9.7 ^{6.4}	33.5 ^{18.1}	6.5 ^{5.8}

ROHs were segments of at least 50 consecutive homozygous SNPs; inbreeding being the proportion of the genome that was homozygous based on ROHs

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