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Investigations on genetic variability in Holstein Horse breed using pedigree data

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Introduction

- Holstein Horses are expressive sport horses with preferential aptitude for show jumping, originated in Schleswig-Holstein, Germany
- Breeding organisation founded in 1935
- Formation of the breed influenced by Yorkshire Coach and Thoroughbred horses
- Due to agricultural mechanisation, breeding goal shifted from medium weight draft horse to large framed riding horse
- Refinement driven by Anglo Normans and Thoroughbreds
- Studbook for mares strictly closed, use of foreign stallions is minimized

Aims of the Study

- Point out updated levels of inbreeding (incl. “age” of inbreeding) and effective population size
- Determine proportion of foreign blood in population
- Specify genetic contributions of outstanding ancestors to current structure of breeding stock

Material and Methods

Pedigree data :

- Breeding stock: 7,693 mares, 225 licensed stallions (2012)
- Total pedigree: 131,272 animals (until 2010)
- After revision: 129,923 animals analysed
- First recorded ancestor born in 1869
- Reference population: horses born 1990 until 2010 (n = 78,677)
- Essential metrics of population structure calculated for reference population
  - software: PEDIG (Boichard, 2002)

Material and Methods

Inbreeding:

- Calculated by methods of Meuwissen and Lou (1992) and van Raden (1992).
- Method of Kalinowski et al. (2000) used to determine “age of inbreeding”:

  ’ Classical inbreeding (Wright, 1922) divided into two parts:
  ancestral inbreeding (homozygous alleles, met in the past)
  new inbreeding (alleles which are homozygous first time)

Effective population size (N_e) :

- Computed with classical approach (Sölkner et al. 1998):

$$N_e = 1/(2” F)$$

Results

Population structure:

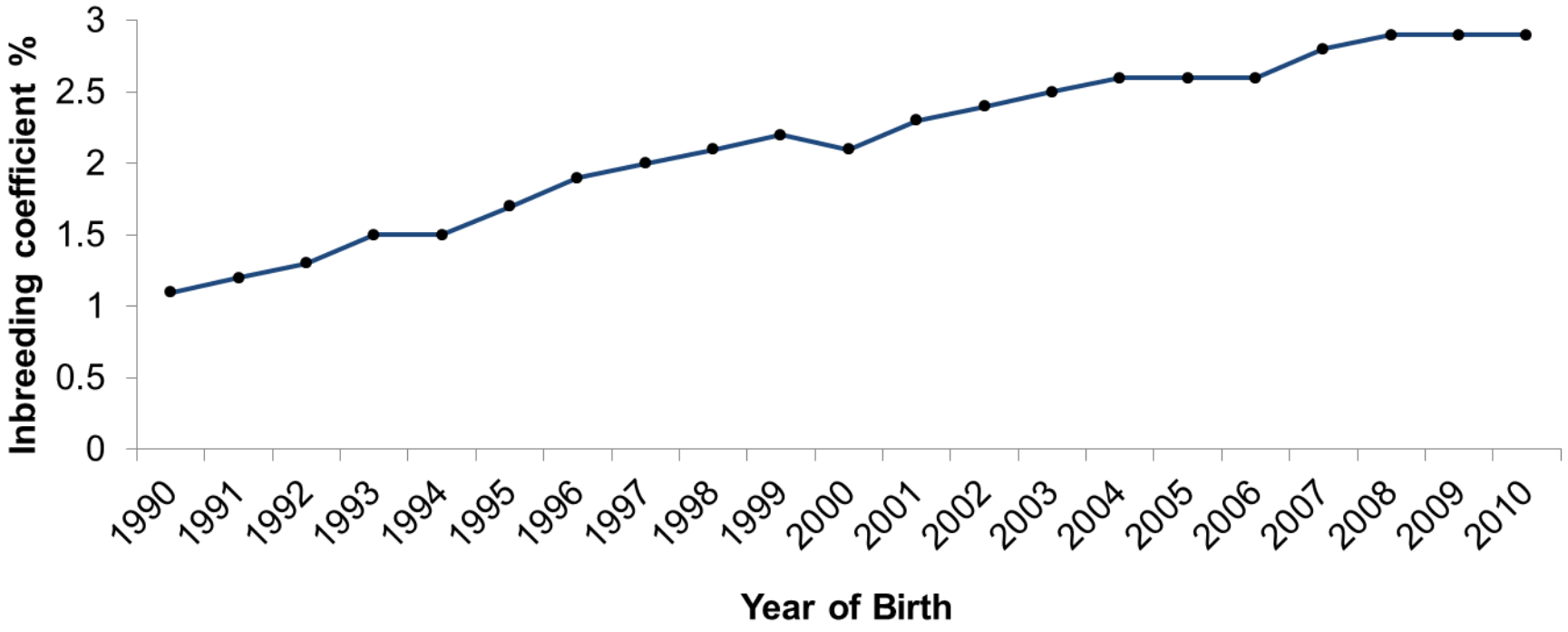
Metrics of pedigree analysis for reference population

Parameter	Unit	Value
Pedigree Completeness	%	88
average Generation equivalent	generations	5.62
Generation Interval	years	10.3
F reference population (all horses)	%	2.27
F_{anc} (Kalinowski, 2000)	%	0.08
F_{new} (Kalinowski, 2000)	%	1.38
Effective population size	n	55.3
Founders	n	3,194
Effective founders	n	50.2
Ancestors to explain 50% of gene pool	n	11

Results

Inbreeding:

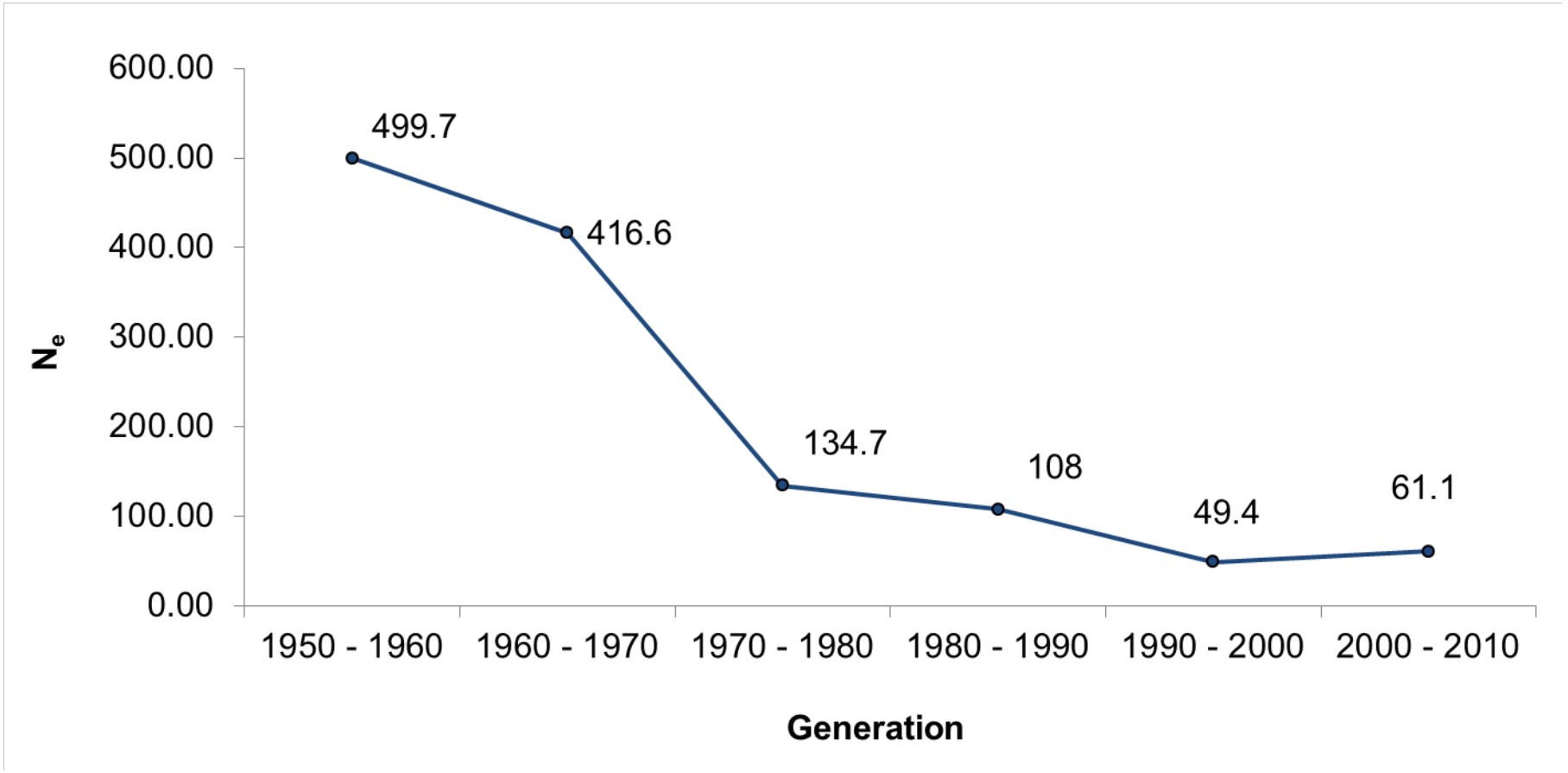
Average inbreeding per time (inbred and non-inbred horses)



Results

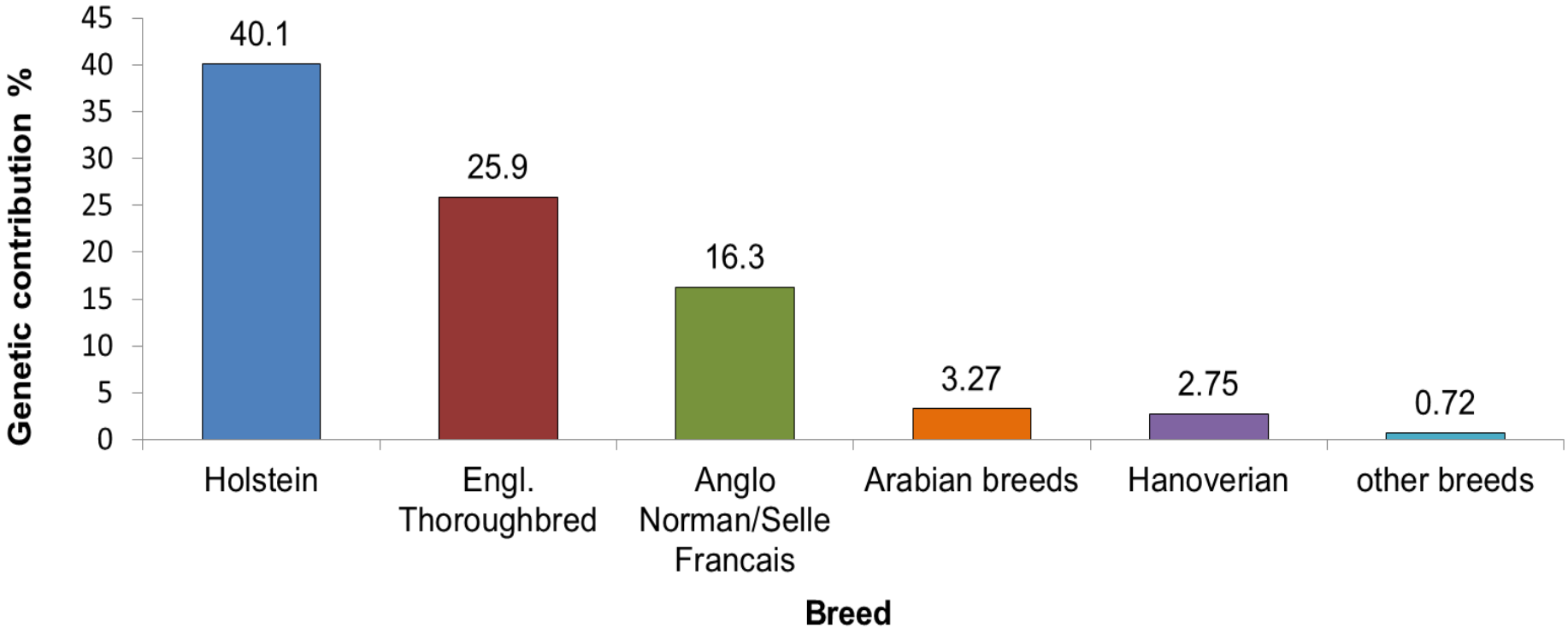
Effective population size:

Development of effective population size (N_e) per generation



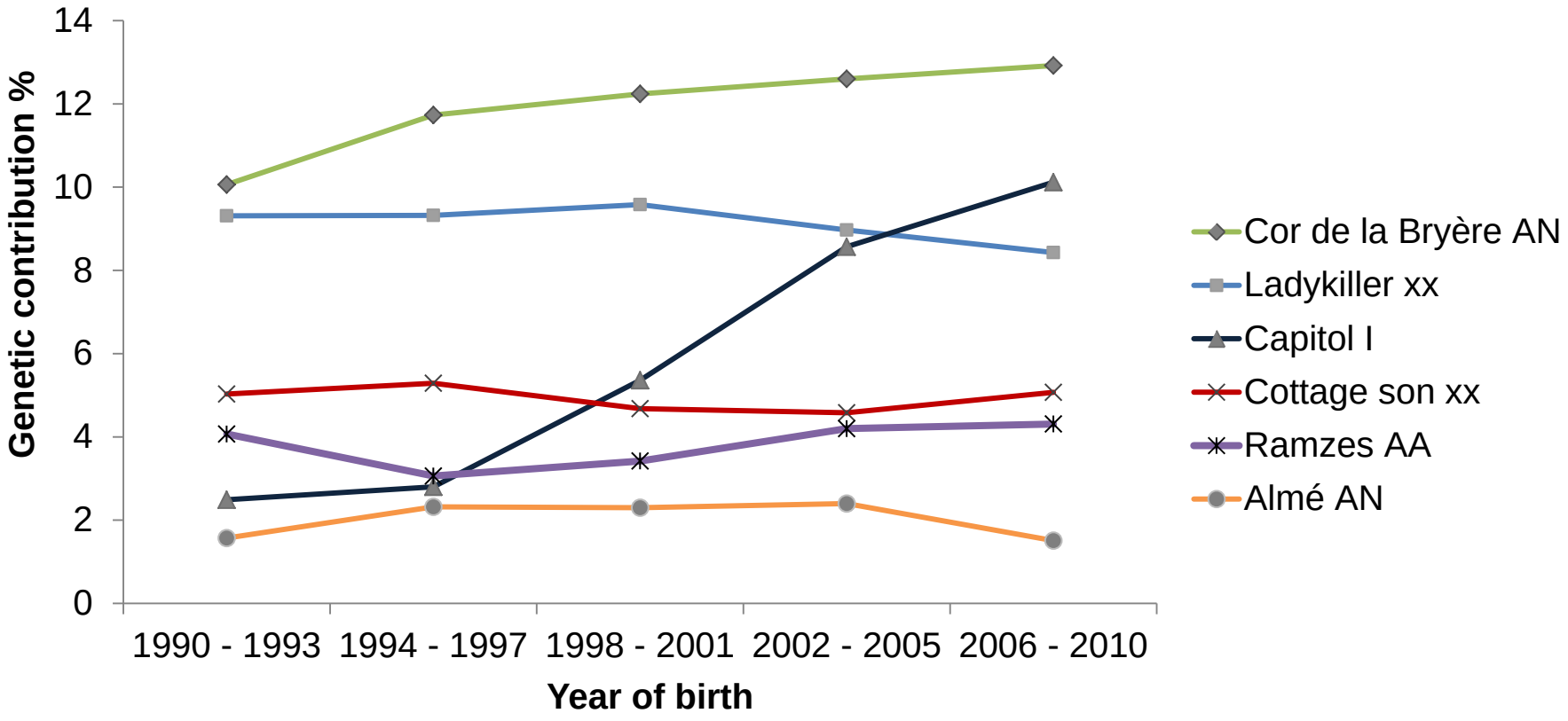
Results

Genetic contributions of foreign breeds (%):



Results

Most formative male ancestors:



Discussion

Inbreeding:

- Reason for increase in average inbreeding could be concentration on few stallions out of certain sire lines enforced by artificial insemination
- With closed Studbooks, access of different breeds into breeding program is limited

Effective population size:

- With 55 animals, effective population size was determined on low level
- FAO (1981) constitutes critical value of 50 animals to achieve a minimum amount of genetic variability

Conclusion

- Results illustrate loss of genetic diversity related to unequal contributions caused by intensive use of particular sires
- Inbreeding mostly occurred in newer generations
- Low N_e endangers preservation of genetic variability
- In recent past: stagnation in rate of inbreeding and slight increase in number of effective animals
- Rising trend in N_e might caused by changes in breeding policies ’ more open access for foreign stallions

Thank you for your attention !!

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