Faculty of Agriculture and Nutritional Science

C | A | U

Christian-Albrechts-University of Kiel
Institute of Animal Breeding and Husbandry


Foto: Wiecha

Analysing the effective population size in the partially closed and fragmented breeding population of the Trakehner Horse breed

Rike Teegen
C. Edel
G. Thaller

Institute of Animal Breeding and Husbandry
Christian-Albrechts-University of Kiel

Introduction

- **Aim of the study**

  - to examine the population structure of the Trakehner breed in terms of:

    1. generation interval
    2. effective population size
    3. gene contributions of thoroughbreds

- **General aspects of Trakehner breeding:**
  - one of the oldest horse breeds in the world
  - partially closed population (closed studbook)
  - 10 (14) local breeding societies, centrally managed

Material and methods

- **Central pedigree (n = 36,620)**

  - birth register of all animals in the Trakehner Association to the years 1900-2005

- **Actual breeding population (n = 6,746)**

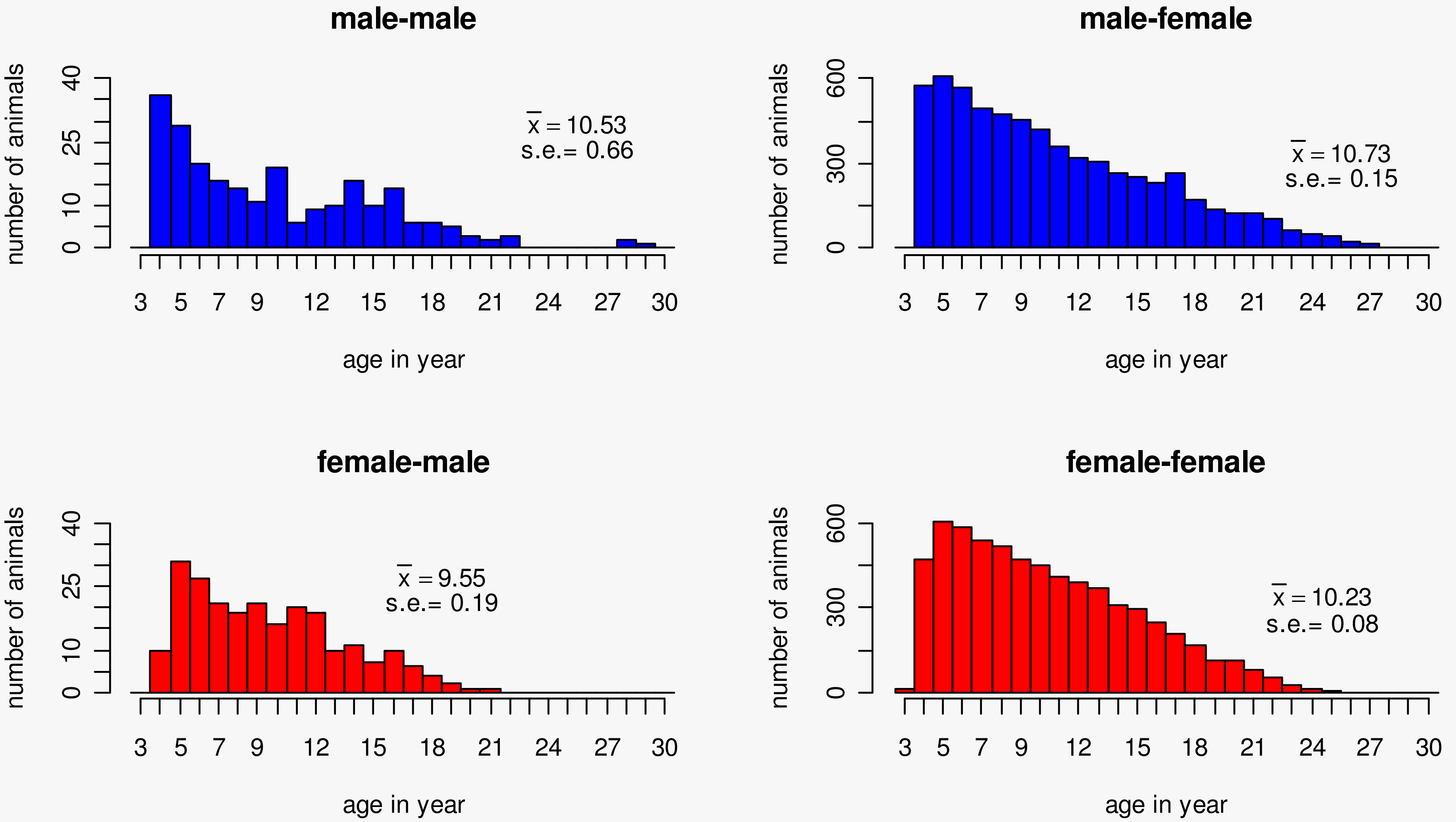
  - records of mare conformation tests 1994-2005 (n = 6,505)
  - records of sires presented to the commission for breeding approval at the central stallion certification 2001-2005 (n = 241)
  - only mares and sires with the identification label '09'

- **Pedigree of actual breeding population (n = 13,793)**

  - birth years before 1950 and/or ancestors with unknown pedigree information were treated as founder animals (non ibd, n = 198)

Generation interval

Ø *L* = 10.2 years


male-male

male-female

female-male

female-female

Effective population size

Effective population size (N_e)

estimated by the increase in average inbreeding coefficient (F_x) and average coancestry (f_{xy}) (year-wise and generation-wise) :

1

Numerator-Relationship-Matrix (NRM)

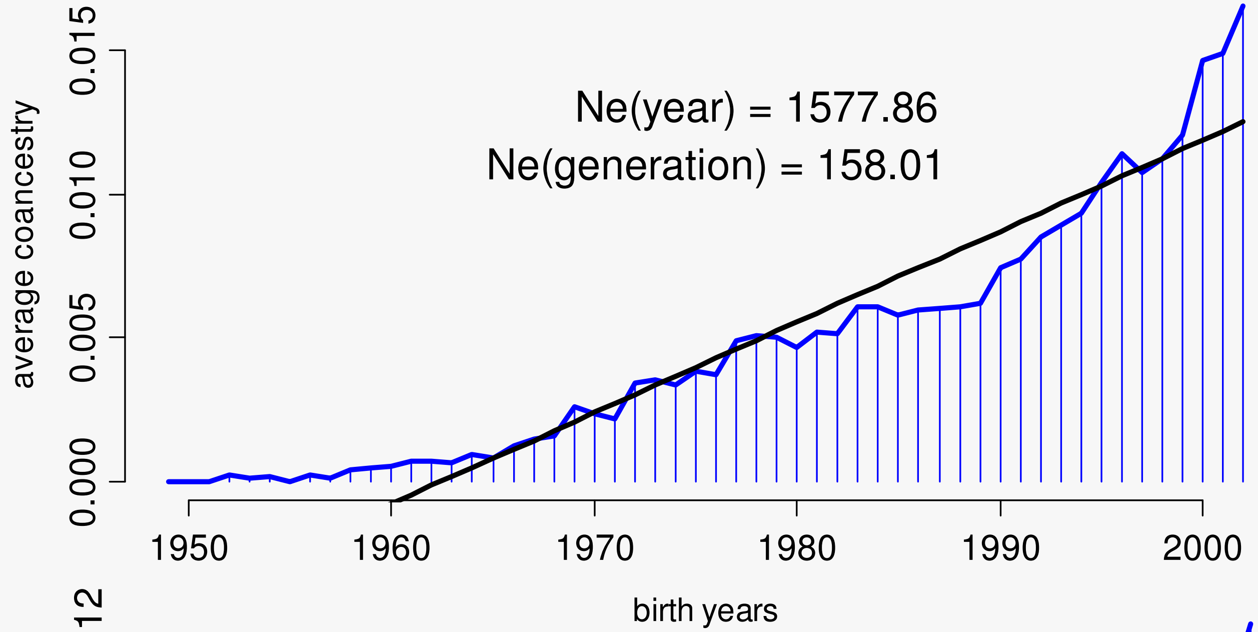
- all missing sires and dams treated as unrelated to the actual breeding population

2

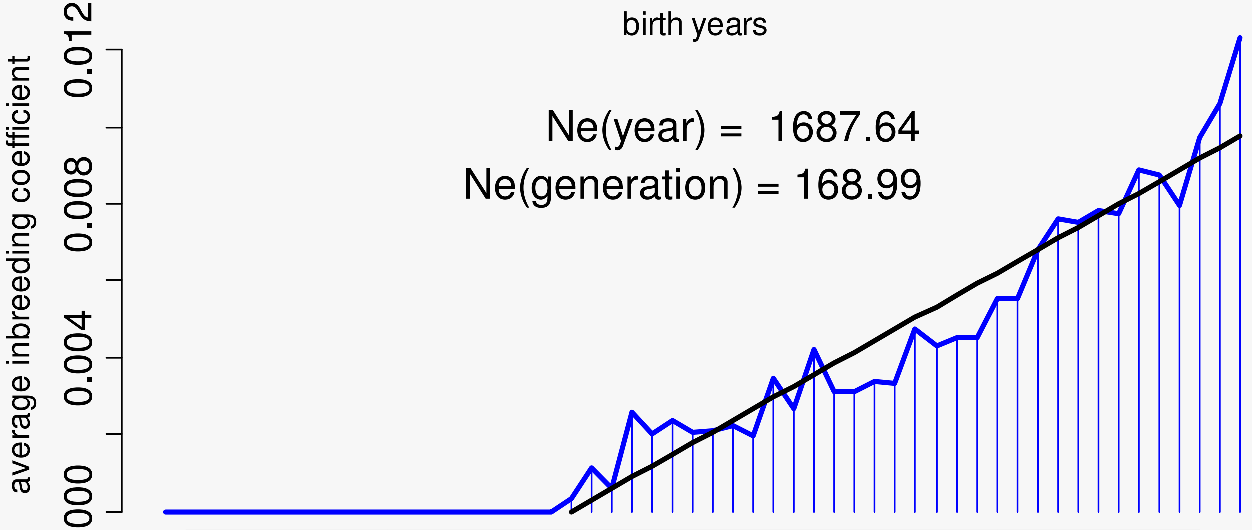
Uncertain-Parentage-Matrix (UPM)

- all potential sires or dams within 3-7 years before the birth of the animal were accounted with the same probability as sires and dams

Results: coancestry, inbreeding and N_e



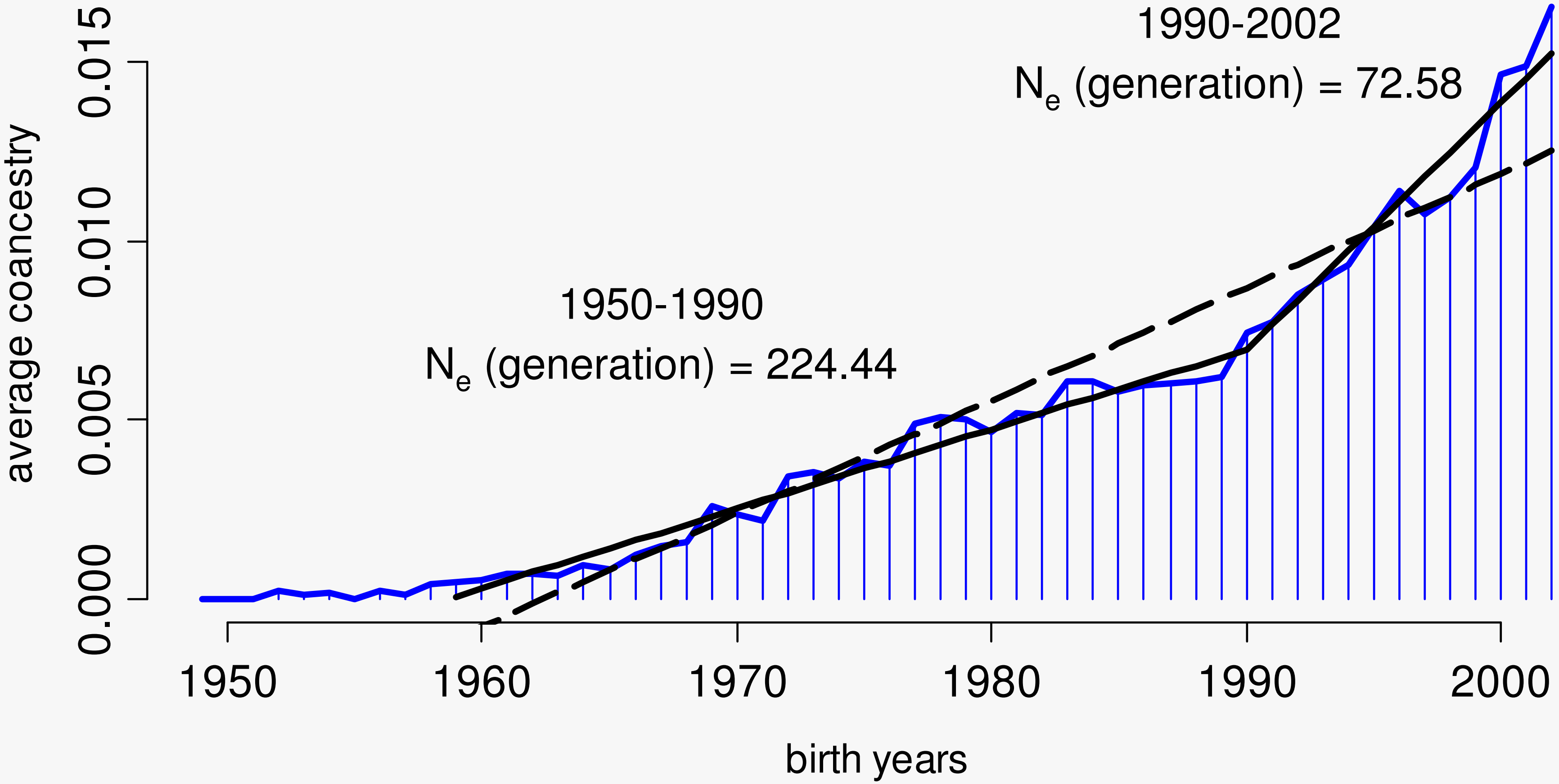
average
coancestry
(NRM-method):



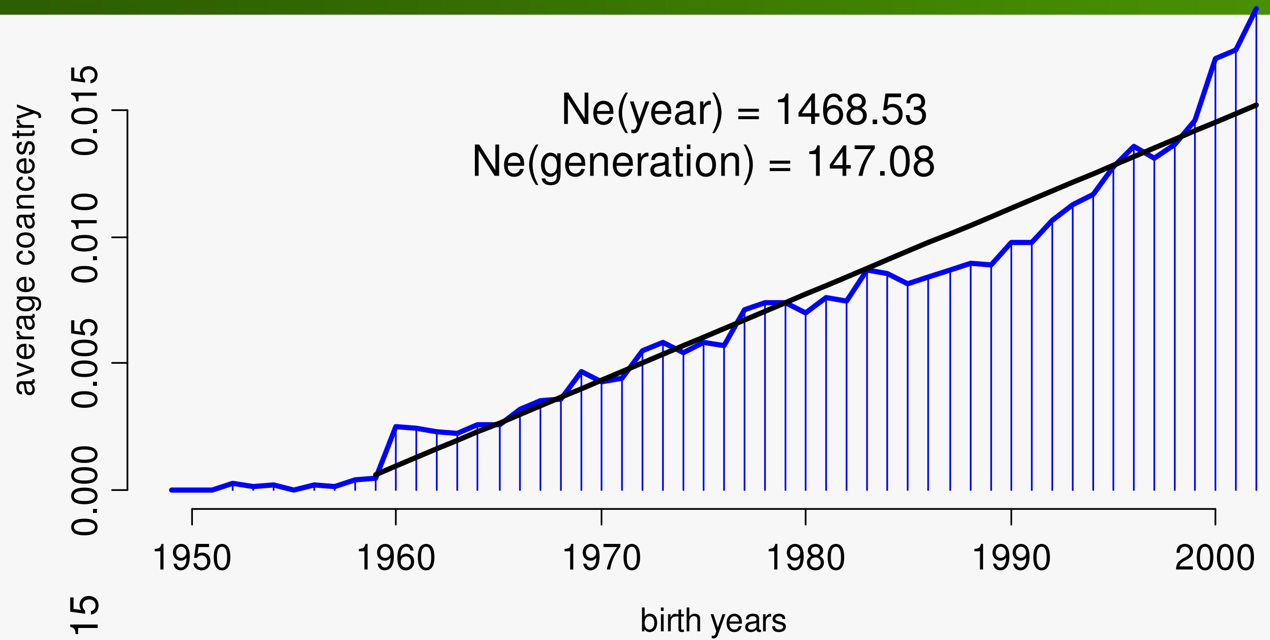
average
inbreeding
coefficient
(NRM-method):

Results: coancestry, inbreeding and N_e

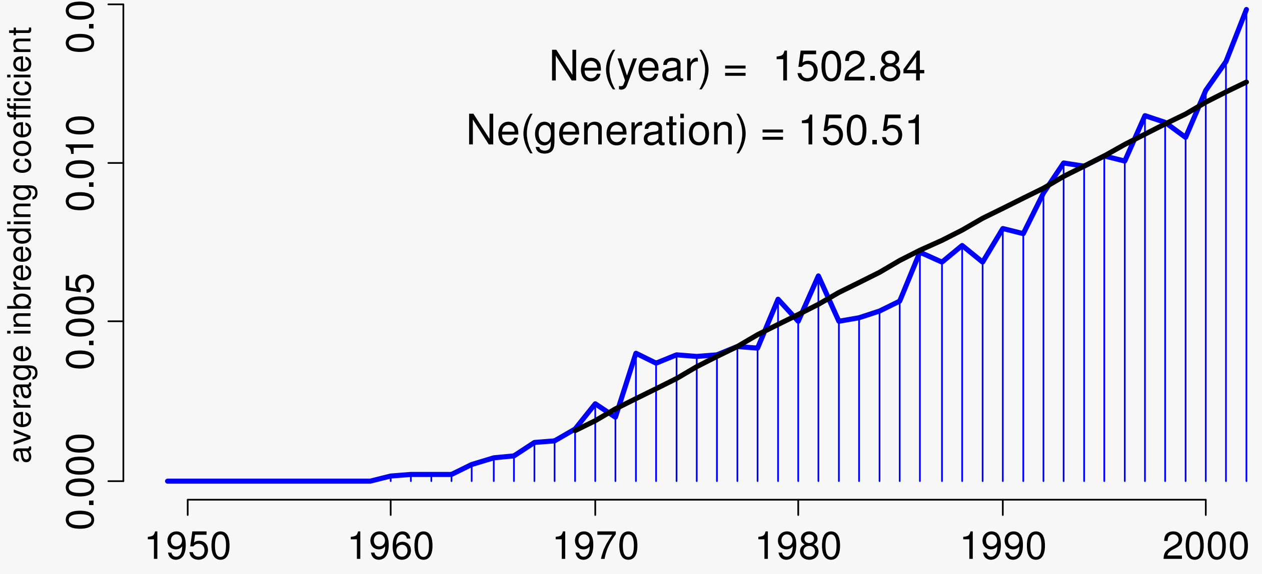
“hockey stick” regression (NRM-method):



Results: coancestry, inbreeding and N_e

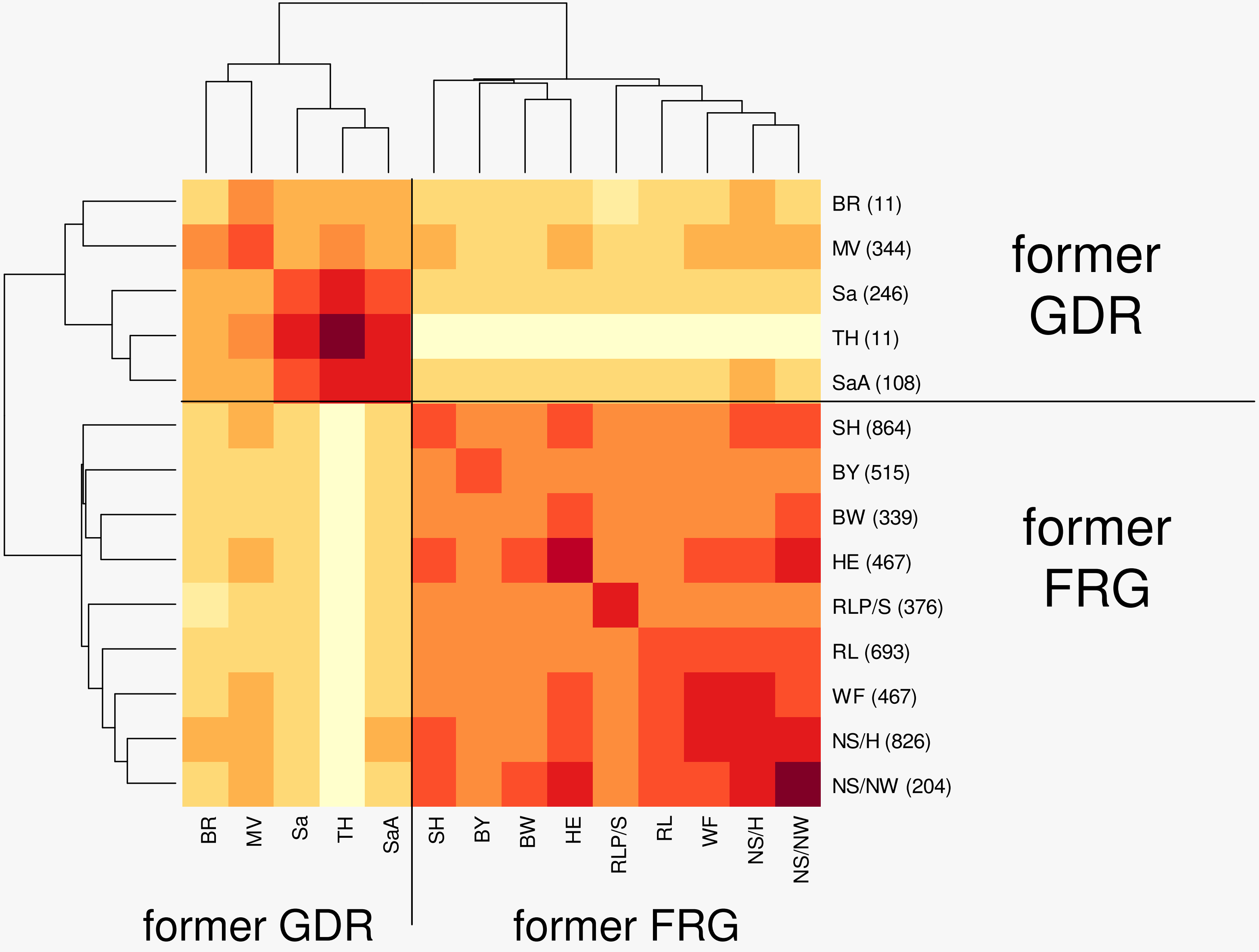


average coancestry (UPM-method):

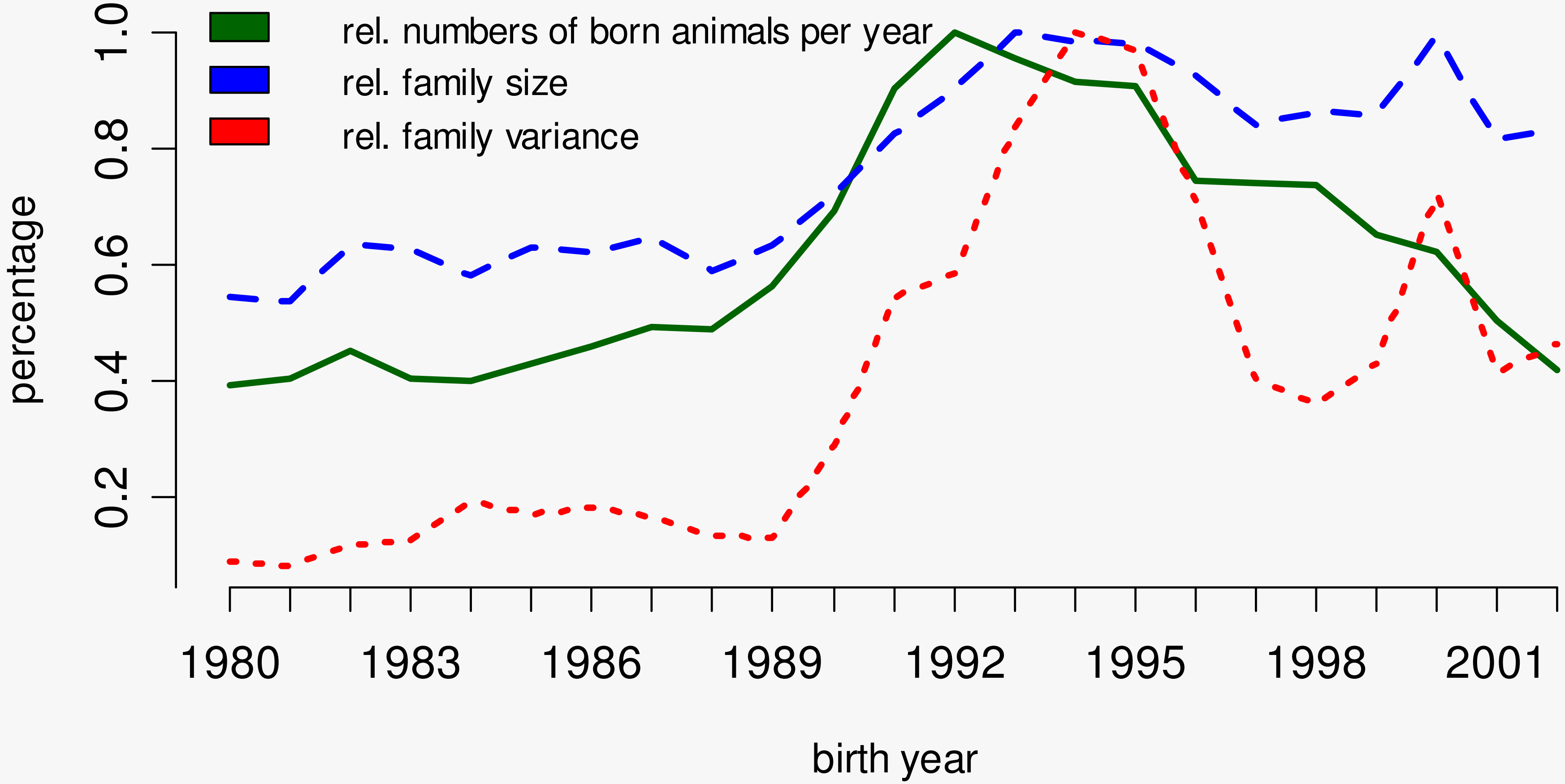


average inbreeding coefficient (UPM-method):

Coancestry in and between breeding societies



Variance of family size of sires



n = 13,973

Contribution of genes

thoroughbreds	number of animals with contribution	min	$\bar{x}$	max
English (xx)	5905	0.39%	22.3%	87.5 %
Arabian (ox)	515	0.78%	11.7%	75.0%

Summary

- Decreasing number of breeding animals
- Long generation interval in each selection path
- Estimates of N_e analysed with NRM- and UPM-method differ from calculations with census data (BMVEL, 2004)
- Estimates of N_e on a low level

Summary cont.

- Upper limit of N_e analysed with NRM- and lower limit of N_e analysed with UPM-method
- Average inbreeding coefficient is lower than average coancestry one generation before
- Genetically fragmented population
- Increasing variance of family size of sires since 1989

Conclusion

There is a need to manage
the breeding population more carefully in
order to minimise inbreeding
where possible.

Thank you for your attention!

This project is supported by the H. Wilhelm Schaumann Foundation and the Foundation Trakehner Horse.

Photo: © Beate Langels