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Comparison of genetic diversity between Holstein and Simmental breeds reared in Croatia

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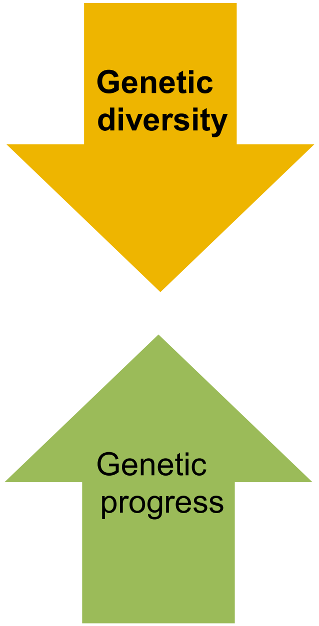
Challenges in breeding

- Dairy cattle breeding programs



- Genetic diversity - variety of alleles and genotypes present in population

Description of genetic variability

- Demographic description
  - Generation interval, family size, no. of males and females
- Pedigree quality
  - No. of fully traced generations, maximum no. of complete generations, no. of equivalent complete generations, pedigree completeness
- Probability of identity by descent of genes
  - Inbreeding coefficient, effective population size
- Probability of gene origin
  - Effective number of founders, ancestors, and founder genomes

Objective

- Pedigree analysis
  - – Holstein (HOL) and Simmental (SIM) breeds

- Estimates of genetic diversity
  - – Generation interval
  - – Genetic variability parameters
    - Coefficient of inbreeding (F) and effective population size (N_e)

Material and method

- Pedigree
  - All known ancestors for 200,760 (HOL) and 231,329 (SIM) phenotyped cows

    ➡ 307,486 (HOL) and 330,556 (SIM) animals
  - **Reference population** – animals born between years 2013 and 2018

- OptiSel package

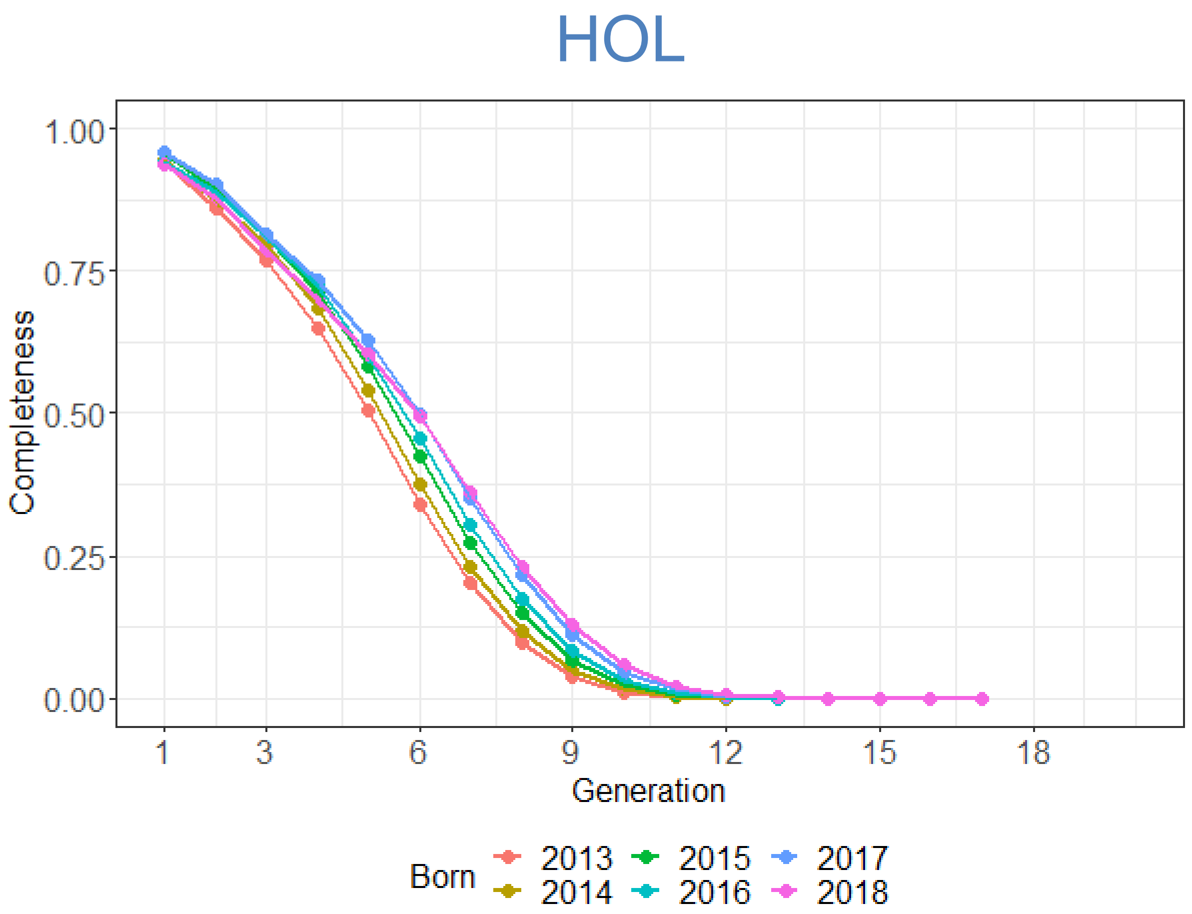
Generation interval (GI) for the four pathways parent-offspring

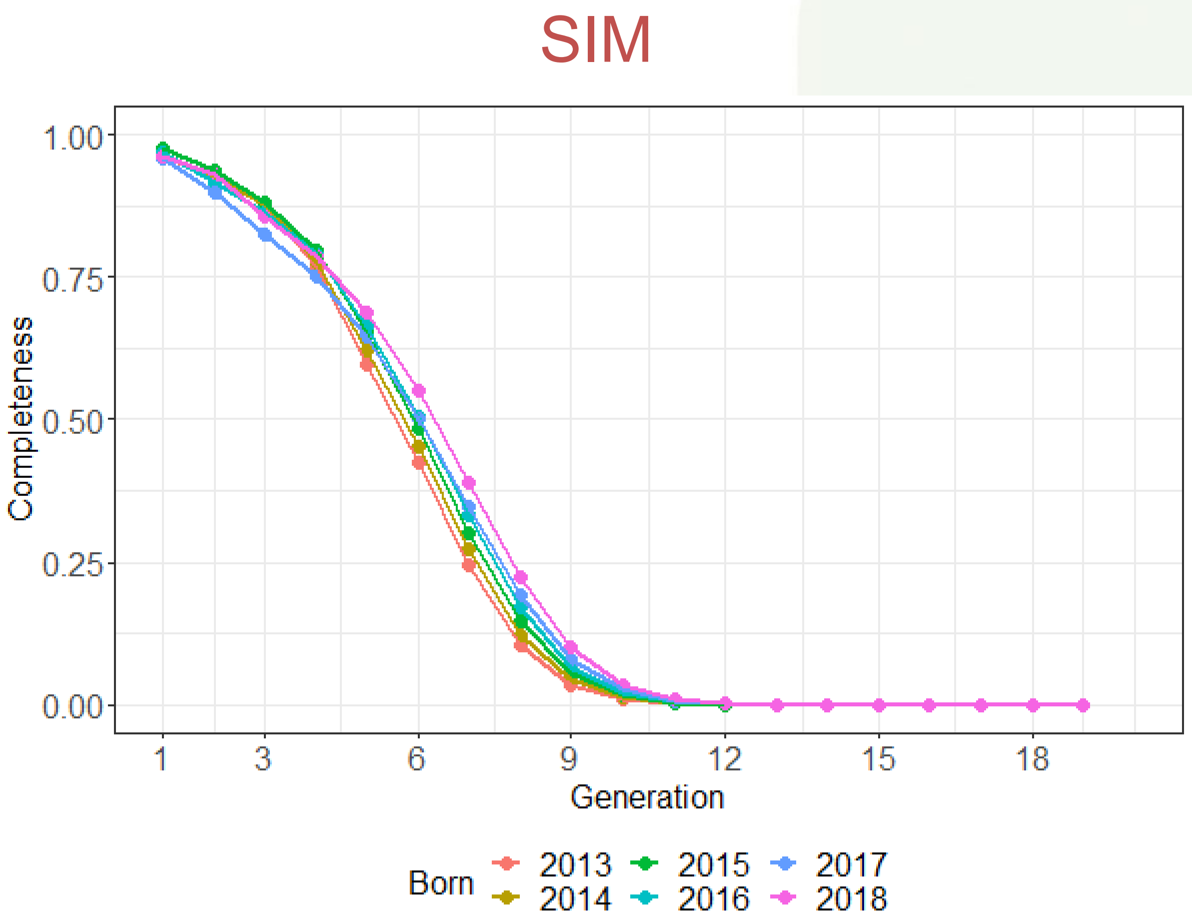
Pathway	Breed	
	HOL	SIM
Sire-son	6.4	7.3
Sire-daughter	5.6	6.2
Dam-son	5.4	5.9
Dam-daughter	5.5	5.8
Average GI	**5.7**	**6.3**

Pedigree quality

Item	Breed	
	HOL	SIM
No. of fully traced generations	1.22	1.47
No. of maximum complete generations	8.22	8.11
No. of equivalent complete generations	**2.99**	**3.35**
Index of pedigree completeness	0.51	0.58

Pedigree completeness by breed – Reference population

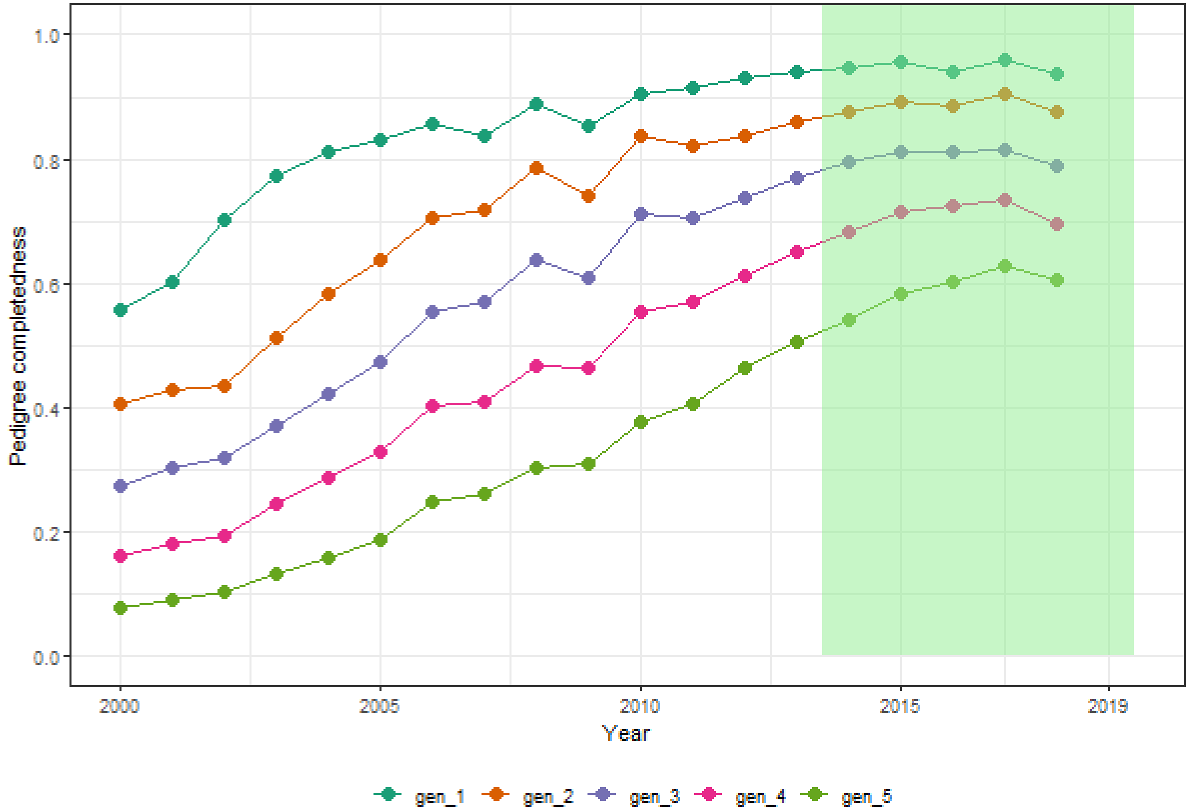




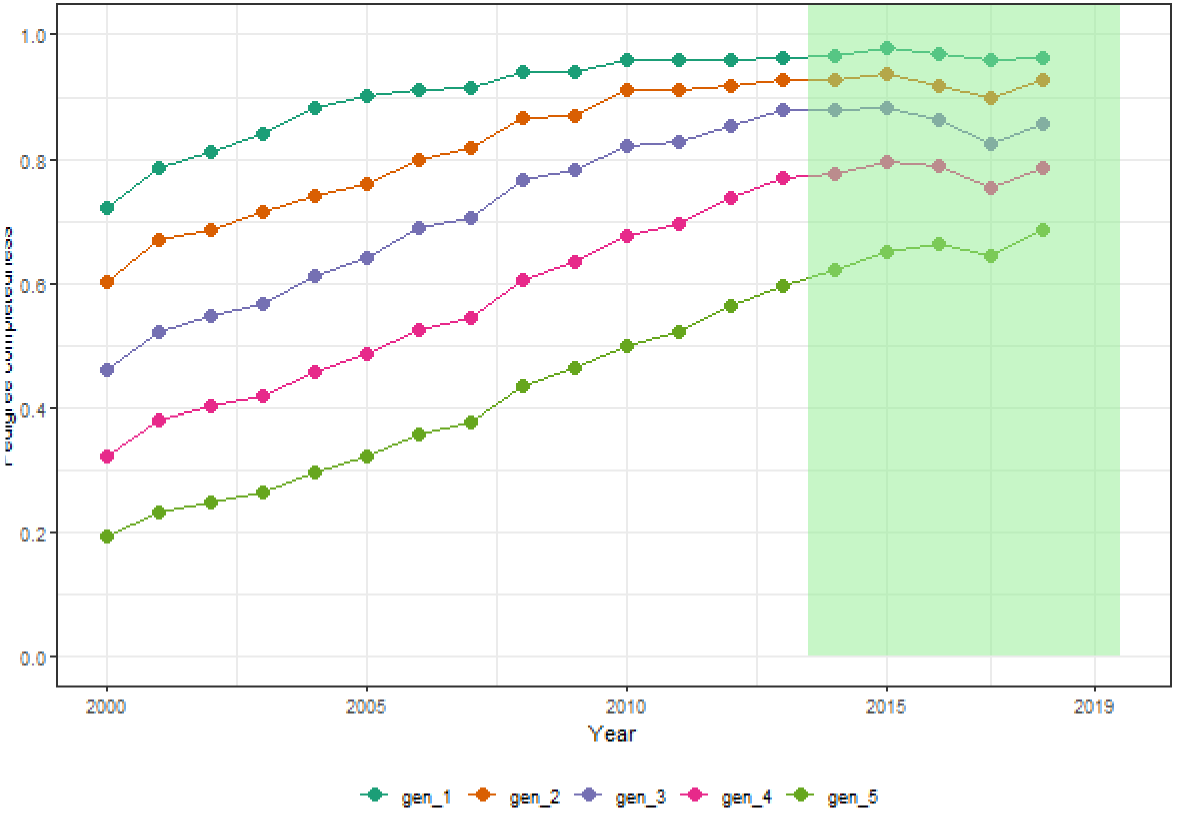
Pedigree completeness index by generation and birth year

equiGen>3

HOL

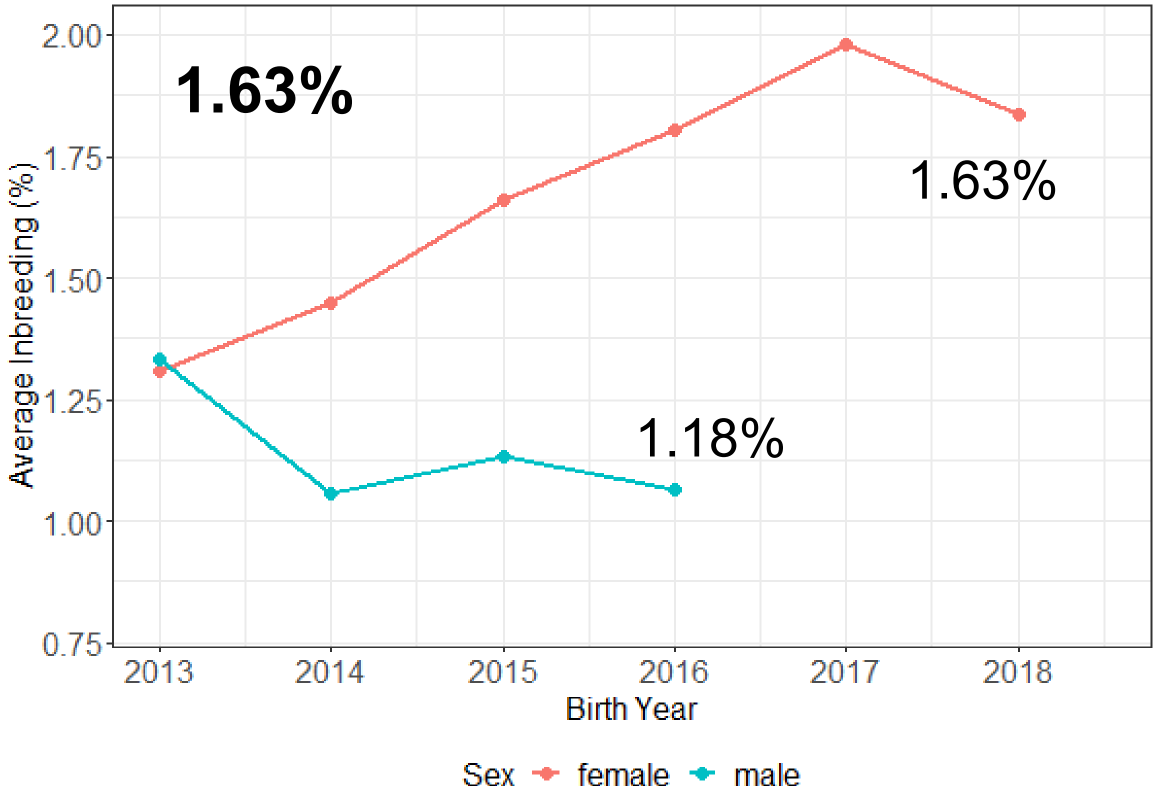


SIM

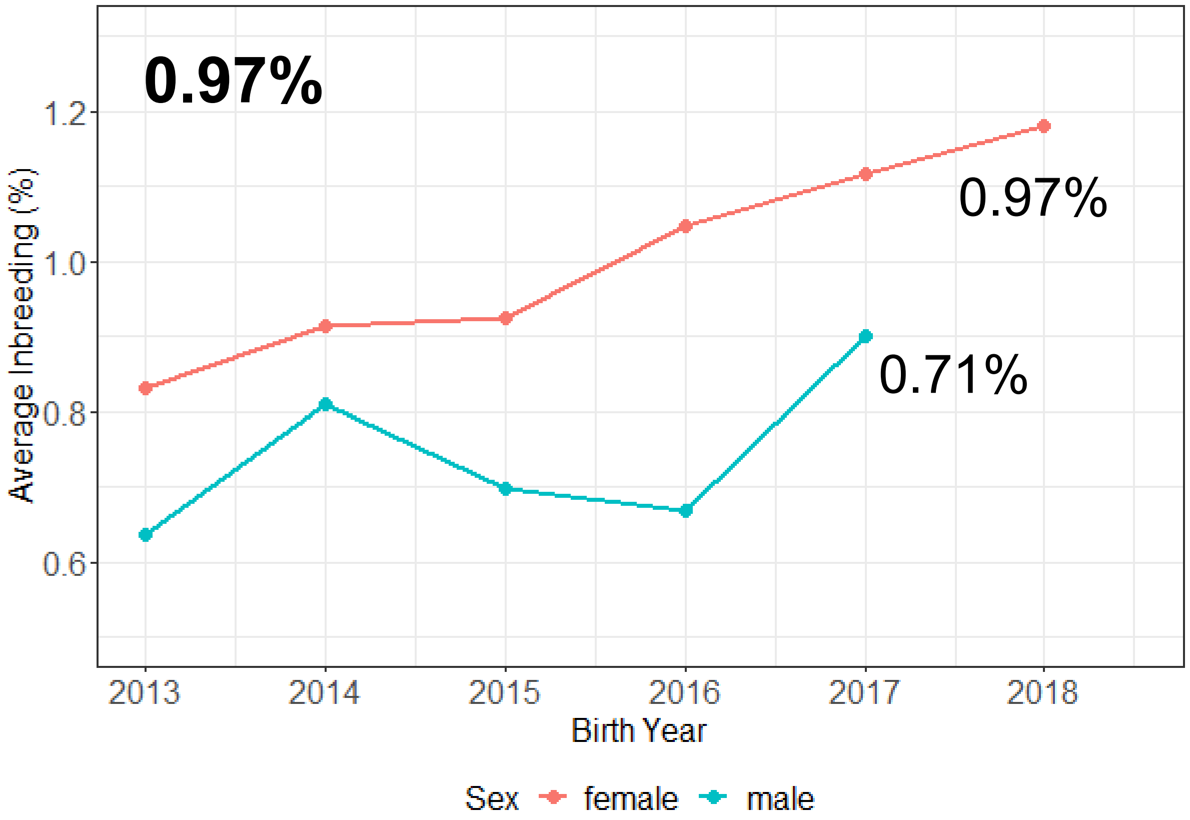


Inbreeding

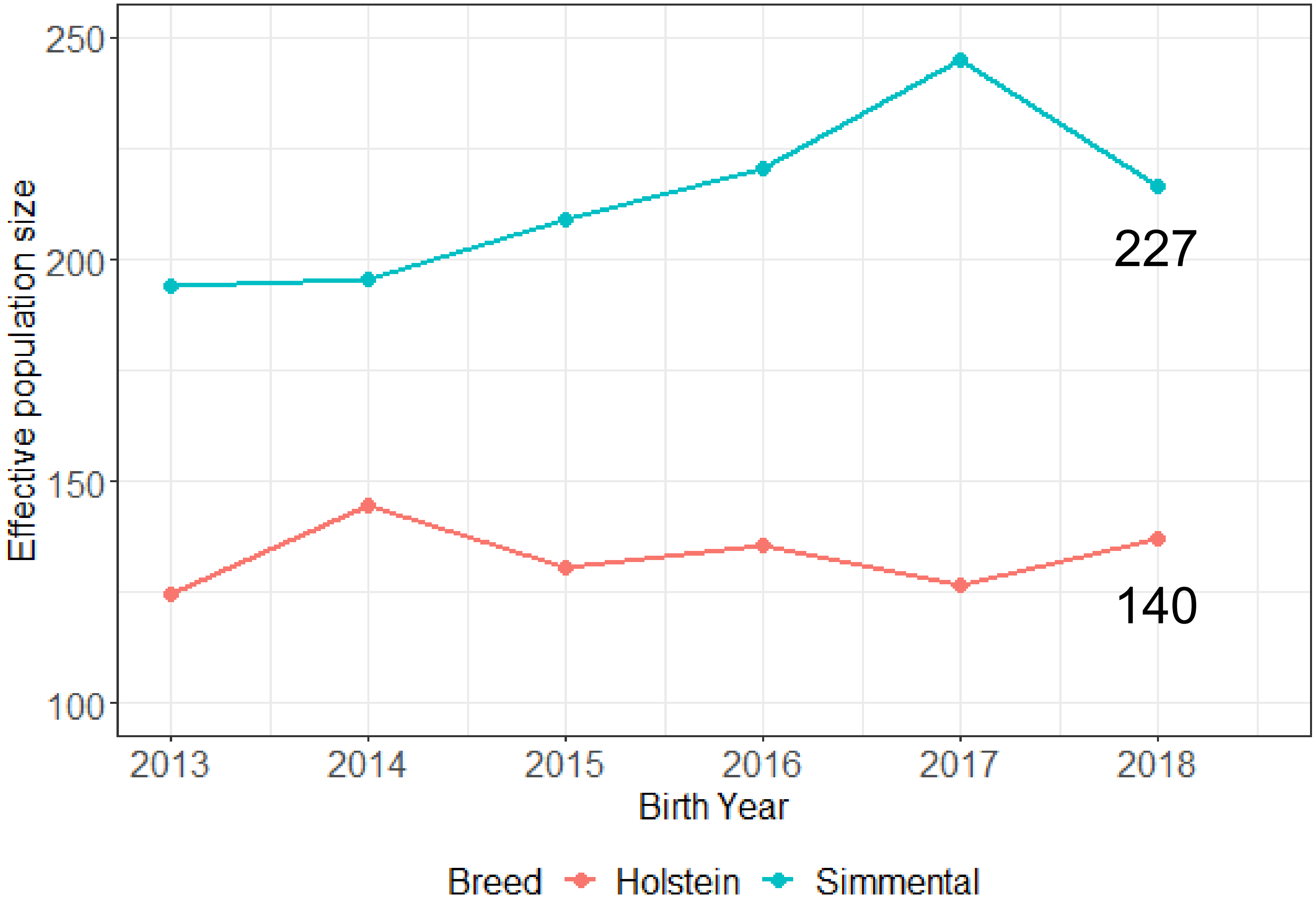
HOL



SIM



Effective population size



Conclusion

- Low average inbreeding coefficient in both breeds
- Satisfied pedigree depth

- Greater genetic variability of SIM compared to HOL breed
- Accordance with the expectations based on the known history of intensive selection work in HOL

Thank you for attention