

Estimation of inbreeding and effective population size in Simmental cattle using genomic information



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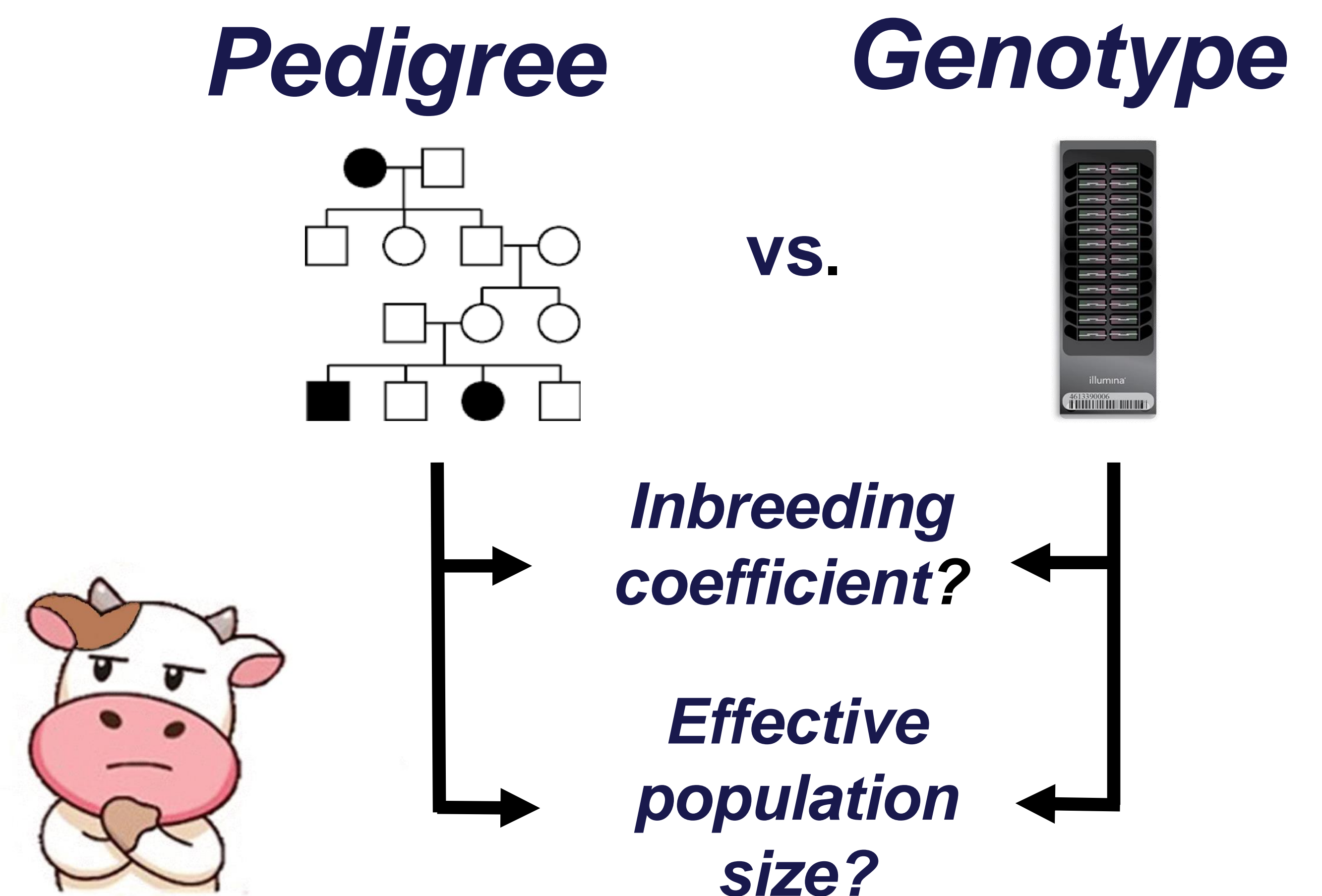
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Introduction

- Dual purpose Simmental breed represents 62.8% of Croatian cattle population under recording scheme
- Calculations based on pedigree data are often unreliable and imprecise
- The objective of this study was to estimate levels of inbreeding (F) and effective population size (N_e) based on pedigree and genotype data



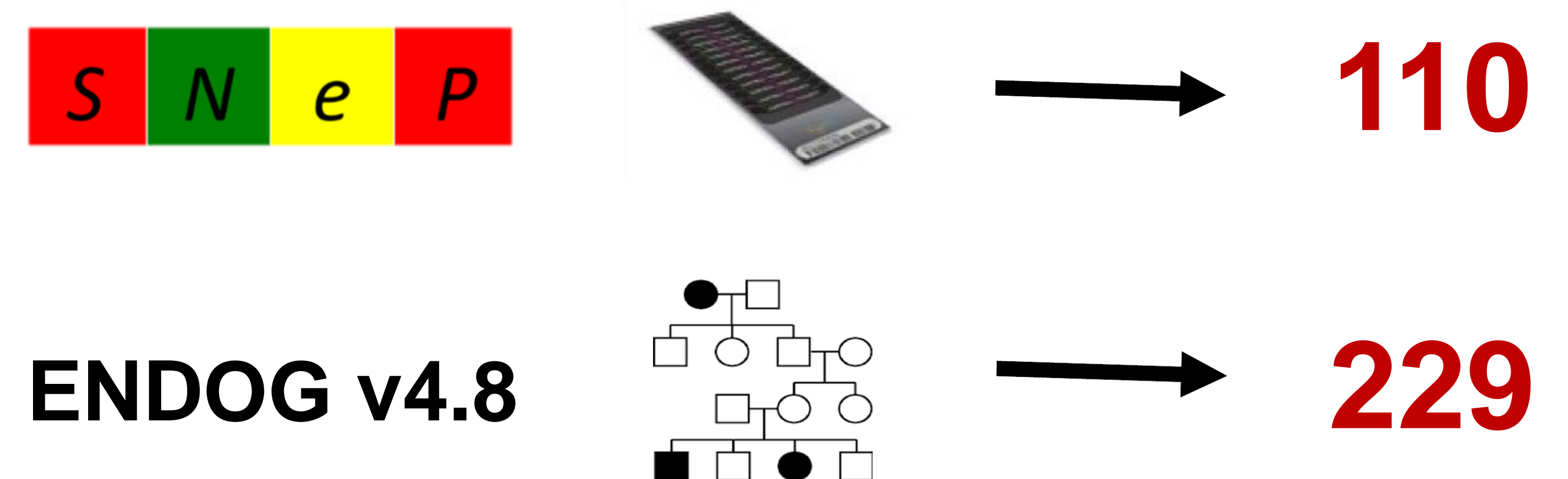
Results

Inbreeding coefficient

Inbreeding coefficient	Mean±std	Min	Max
F_{PED}	0.004±0.018	0	0.312
F_{ROH1}	0.026±0.005	0.015	0.045
F_{ROH2}	0.01 ±0.003	0.004	0.019
F_{ROH4}	0.002 ±0.001	0	0.006

F_{PED} =Inbreeding coeff. estimated from pedigree data; F_{ROH1} =Inbreeding coeff. estimated using ROH >1 Mb; F_{ROH2} =Inbreeding coeff. estimated using ROH >2 Mb; F_{ROH4} =Inbreeding coeff. estimated using ROH > 4 Mb

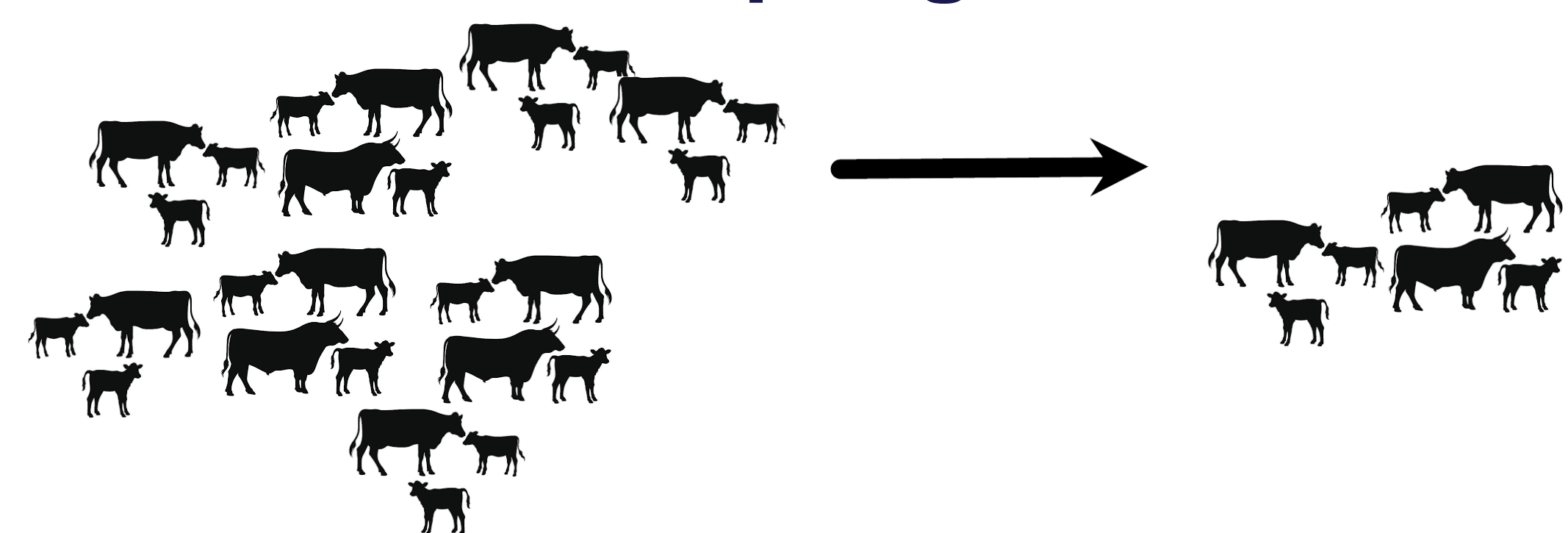
Effective population size



Conclusion

- Genomic information is key for understanding genetic diversity
- It will help to identify genomic regions which have been preferentially selected

Estimated linear decrease:
30 animals per generation



Material and methods

- 109 genotyped animals with Illumina BovineSNP50 chip
- 3 406 pedigree records from Central database of the Croatian Agricultural Agency
- SAS, Plink v1.9, ENDOG v4.8, SNeP
- Runs of homozygosity (ROH)