Impact of genomic selection on genetic diversity in 5 European local cattle breeds

EAAP 2023

Renzo Bonifazi, Gwendal Restoux, Pascal Croiseau, Theo Meuwissen, Stephanie Minery, Jack Windig

WAGENINGEN UNIVERSITY & RESEARCH

INRAE

NMBU

INSTITUT DE L'ELEVAGE idele

Rumigen

TOWARDS IMPROVEMENT OF RUMINANT BREEDING THROUGH GENOMIC AND EPIGENOMIC APPROACHES

Acknowledgments

- Breeding companies for providing pedigree and SNP data
- Gerben de Jong (CRV)
- Mathijs van Pelt (CRV)

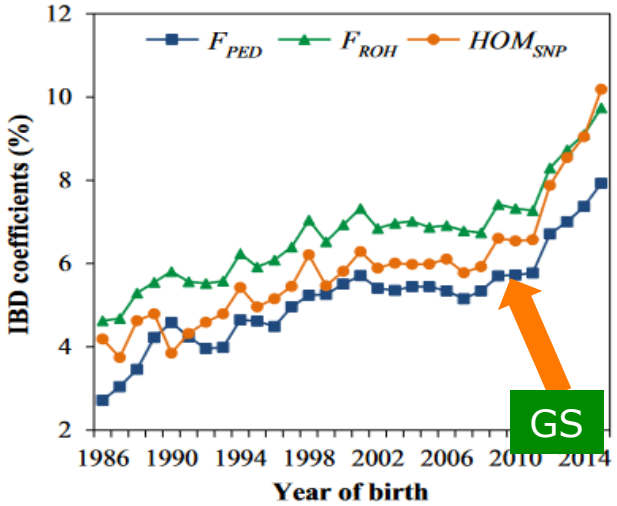
- This project has received funding from the European Union's Horizon 2020 Programme for Research & Innovation under grant agreement n°101000226.
- This project is part of EuroFAANG (https://eurofaang.eu).

Genetic diversity in local cattle populations

- Strong selection can lead to high inbreeding rates
  - associated los of genetic diversity
  - + inbreeding depression
  - + risk expression genetic defect
- Especially in small populations
- Genomic selection (GS) now applied in local breeds
- Main question
  - Did inbreeding rates change after the introduction of GS in 5 local breeds?

Changes in inbreeding rate after introduction GS

- Genomic selection (GS): starting ~2008 (VanRaden, 2008)
- Larger genetic gains, shorter generation intervals
- Expectation ΔF to go down



Up
- Holstein
  - the Netherlands (Doekes et al. 2018)
  - USA (Forutan et al. 2018; Makanjuola et al. 2020)
  - Poland (Topolski and Jagusiak 2020)
  - France (Doublet et al. 2019)
  - Australia (Scott et al. 2021)
  - Italy (Ablondi 2022)
- Jersey (Makanjuola et al. 2020)
- Finnish Ayrshire (Sarviaho et al. 2023)

Not up
- Normande
- Mont Beliarde
  - Doublet et al. 2019
- Aberdeen Angus
  - Lozada-Soto et al. 2021

5 cattle populations

MRY (NL)

Abondance (F)

Tarentaise (F)

Norwegian Red (N)

Vosgienne (F)

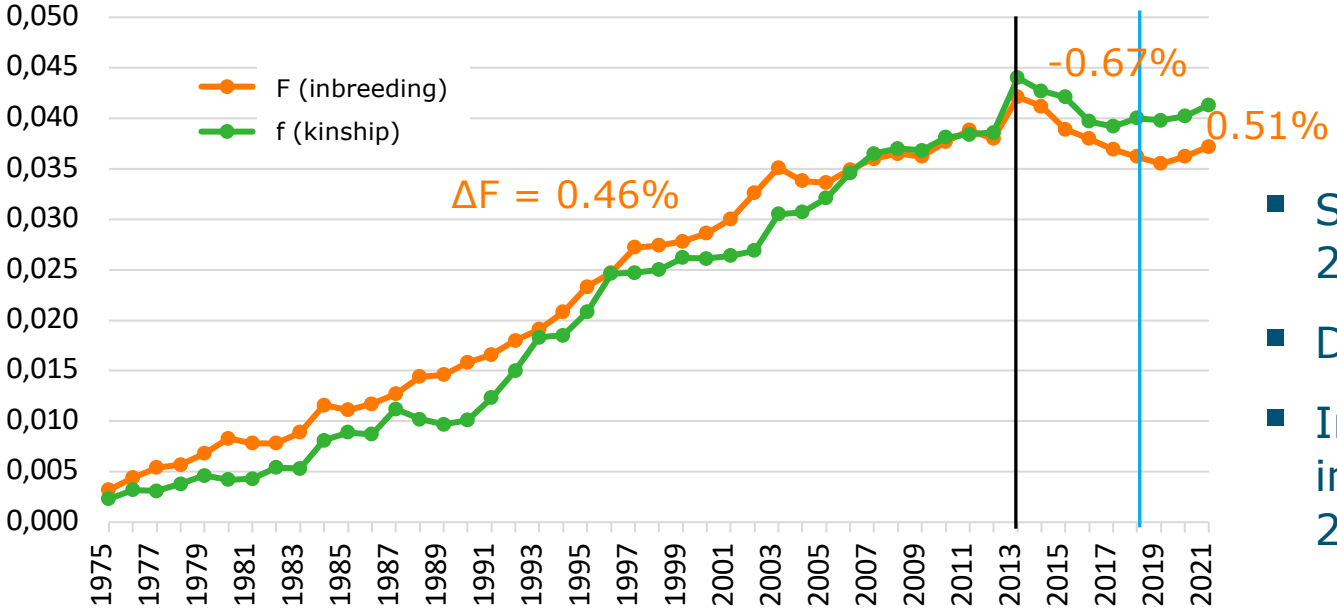
WAGENINGEN
UNIVERSITY & RESEARCH

Some data

Breed	Calf/year	Pedigree	Genotypes	Years analysed	Introduction GS
MRIJ	5,053	205,934	4,645	1975-2021	2018
Norwegian Red	35,701	721,805	193,489	2000-2020	2016
Abondance	25,020	807,387	16,427	2000-2020	2014
Tarentaise	9,514	259,150	8,882	2000-2020	2014
Vosgienne	3,738	99,833	4,466	2000-2020	2014

MRY inbreeding and kinship levels

- All animals in pedigree

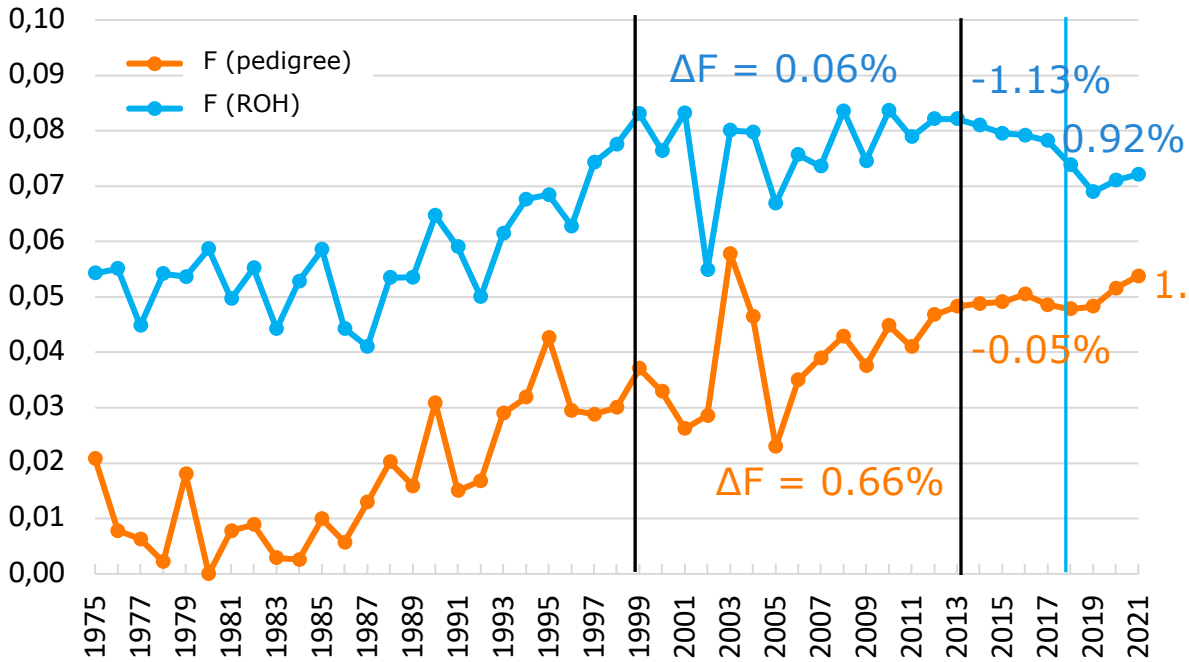


- Steady increase up to 2013
- Decrease 2013 – 2018
- Increase since introduction GS in 2019

WAGENINGEN
UNIVERSITY & RESEARCH

MRY inbreeding and kinship levels

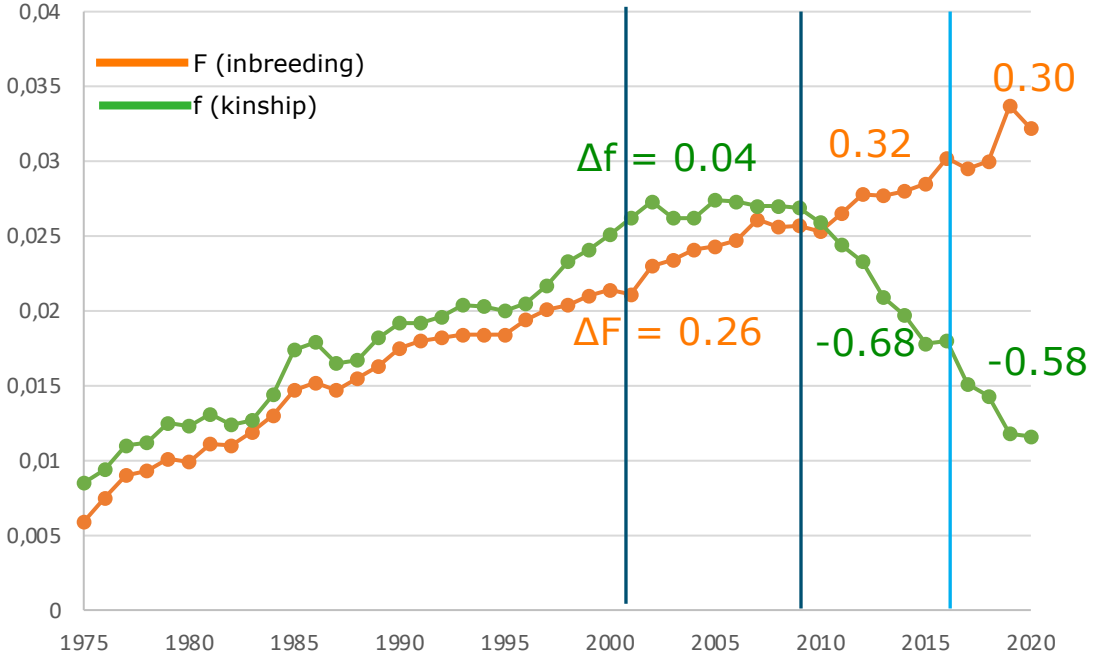
- Genotyped animals only



- Steady but irregular increase up to 2013
- Decrease F(ROH) but not F(ped) 2013 – 2018
- Increase since introduction GS in 2019

Norwegian Red inbreeding and kinship levels

- All animals in pedigree

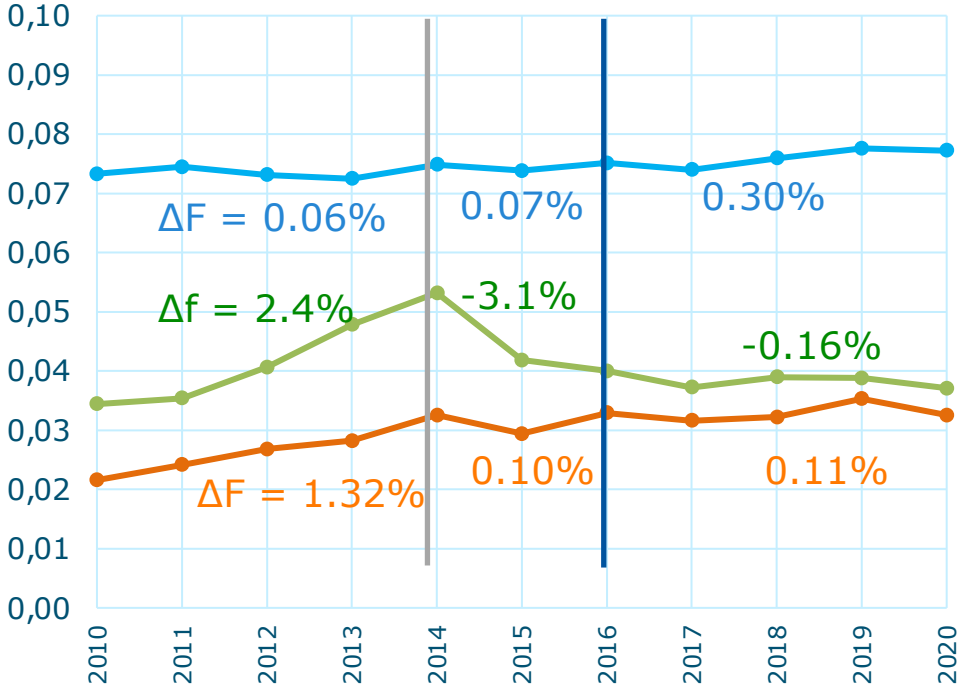


- Steady increase of inbreeding
- Kinship decreases since 2009
- Inbreeding continues to increase since introduction GS in 2016
- Kinship continues to decrease

WAGENINGEN
UNIVERSITY & RESEARCH

Norwegian Red inbreeding and kinship levels

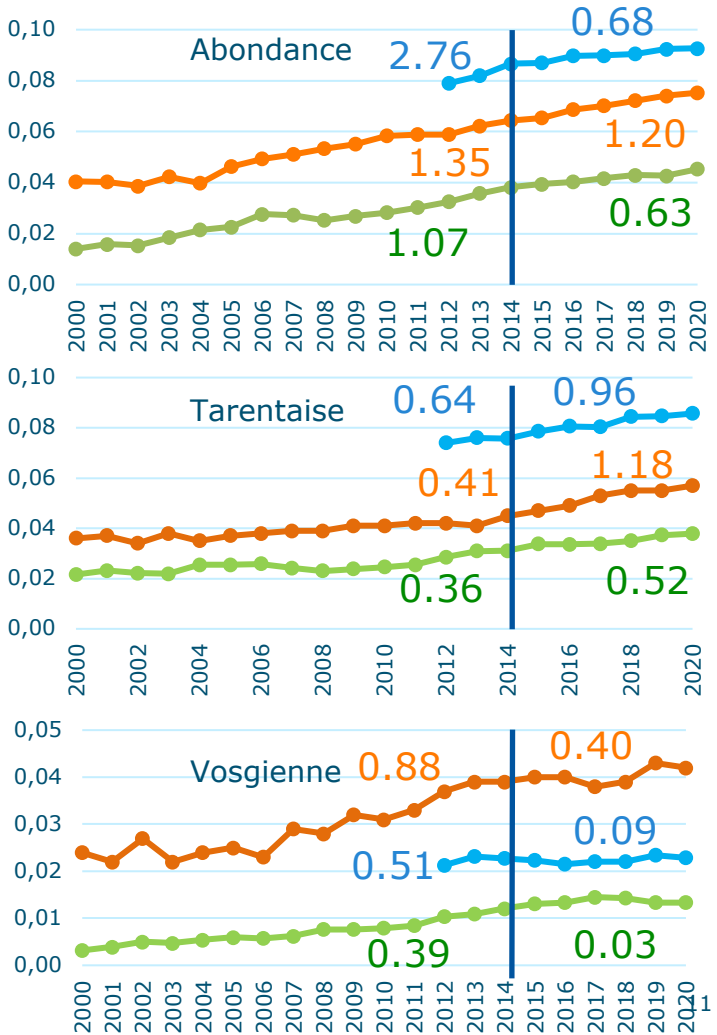
- Genotyped animals only



- F(ROH) stable, slight increase since introduction GS
- Kinship decrease after 2014, stable after 2016
- F(ped) increase but less after 2014

French breeds

- Steady increase in all levels
- After introduction GS (2014)
    - Abondance
        - Less steep
        - Especially F(ROH)
    - Tarentaise
        - Steeper
        - especially F(Ped)
    - Vosgienne
        - Clearly less steep
        - Especially F(ROH)

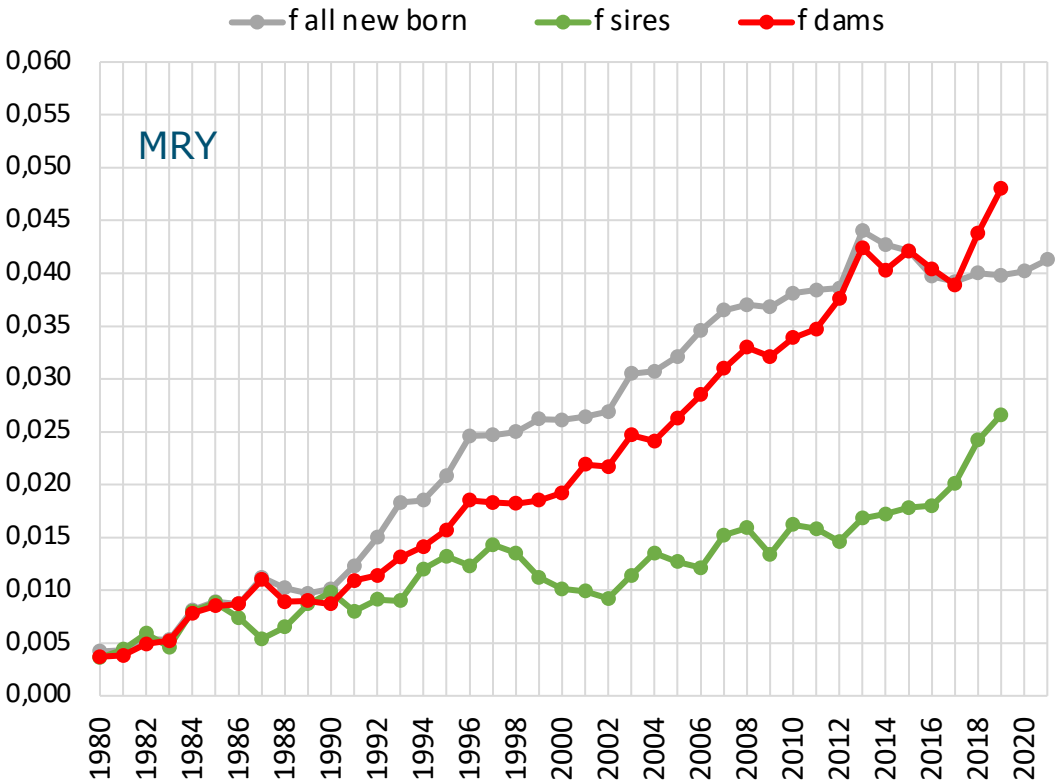


Change in inbreeding and kinship rates

Breed	F_{ped}	F_{ROH}	f
MRIJ all	~~Stable/Up~~	-	~~Stable/Up~~
MRIJ genotyped	UP	UP	~~Stable/Up~~
NR all	Stable	-	~~Down/up~~
NR genotyped	~~Down/Stable~~	UP	~~Down/up~~
Abondance	Down	Down	Down
Tarentaise	Up	Up	Up
Vosgienne	Down	Down	Down

- Mixed pattern: rates can go
  - up
  - or down
  - or remain stable
- after introduction of GS

Genetic management can reduce kinship



- MRIJ and Norwegian Red both use optimal contributions to select sires
- After introduction of OC a clear reduction in kinship

WAGENINGEN
UNIVERSITY & RESEARCH

Summary

- Inbreeding rates (ΔF_{gen}):
  - Increased (MRIJ, Tarentaise)
  - More or less stable (Norwegian Red)
  - Decreased (Abondance, Vosgienne)
- Genomic Selection:
  - shorter generation intervals
  - screening more individuals
  - preselection of less sires

Main take-home message

- **genetic management** of local breeds more important than implementation of genomic selection per se