WHFF 2023, Puy du fou
Session 1 The Holstein cow can do anything - the economic choice
November 21th 2023

# Loss of diversity in the Holstein breed

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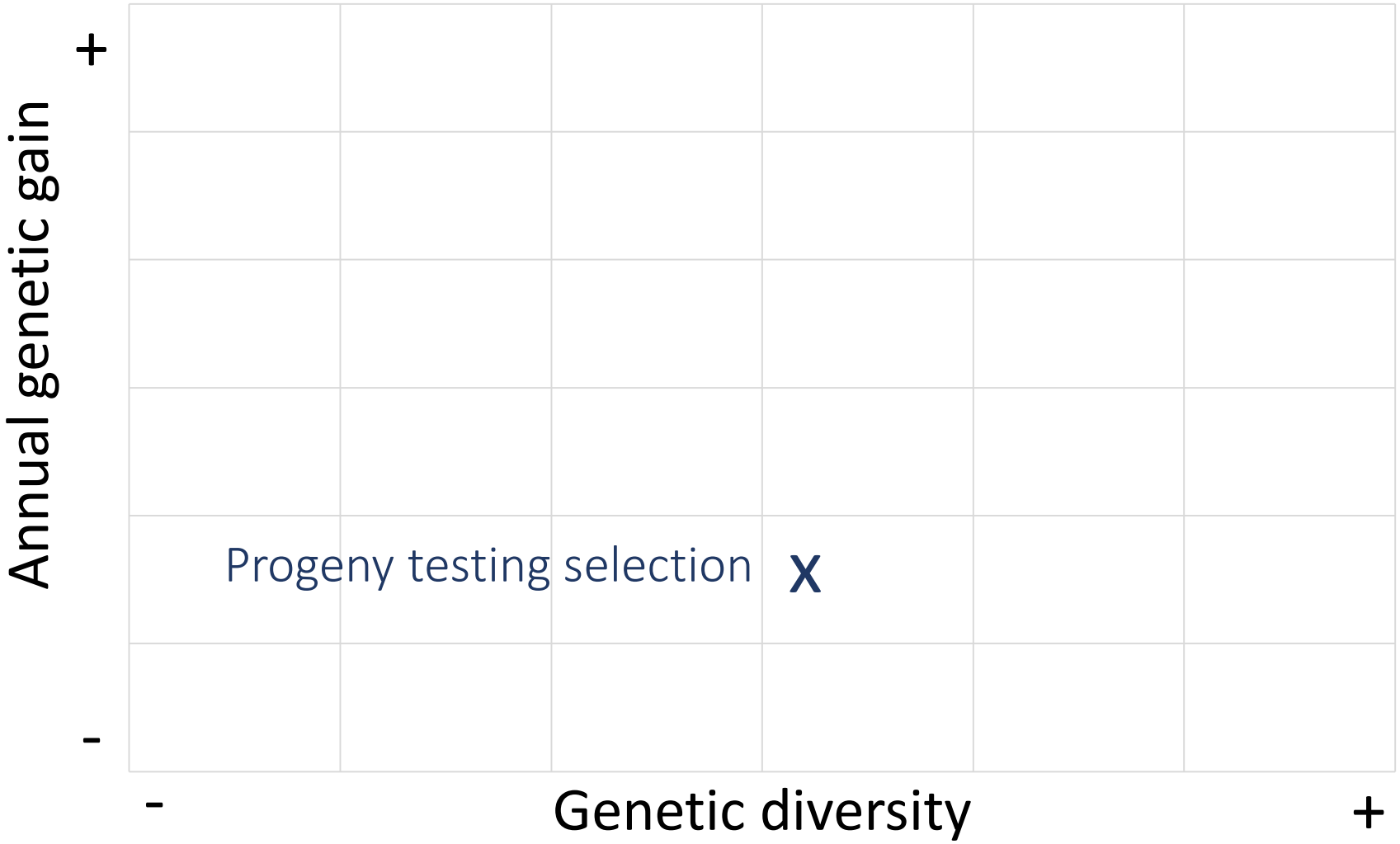
# Context: from progeny testing to genomic evaluations in France

| Before 2010: Progeny testing selection (PTS) | 2010-2012: Transition phase | Since 2012: Genomic selection |
|---|---|---|
| Progeny testing<br>Sires of bulls ≈ 6 yo<br>Dams of bulls ≈ 3 yo in farms | Intermediate situation | Genomic evaluation<br>Sires of bulls ≈ 2 yo<br>Dams of bulls ≈ 2 yo in donor stations |

Genomic selection in dairy cattle breeds ⇒ **New breeding schemes**

# Changes in dairy cattle breeding schemes



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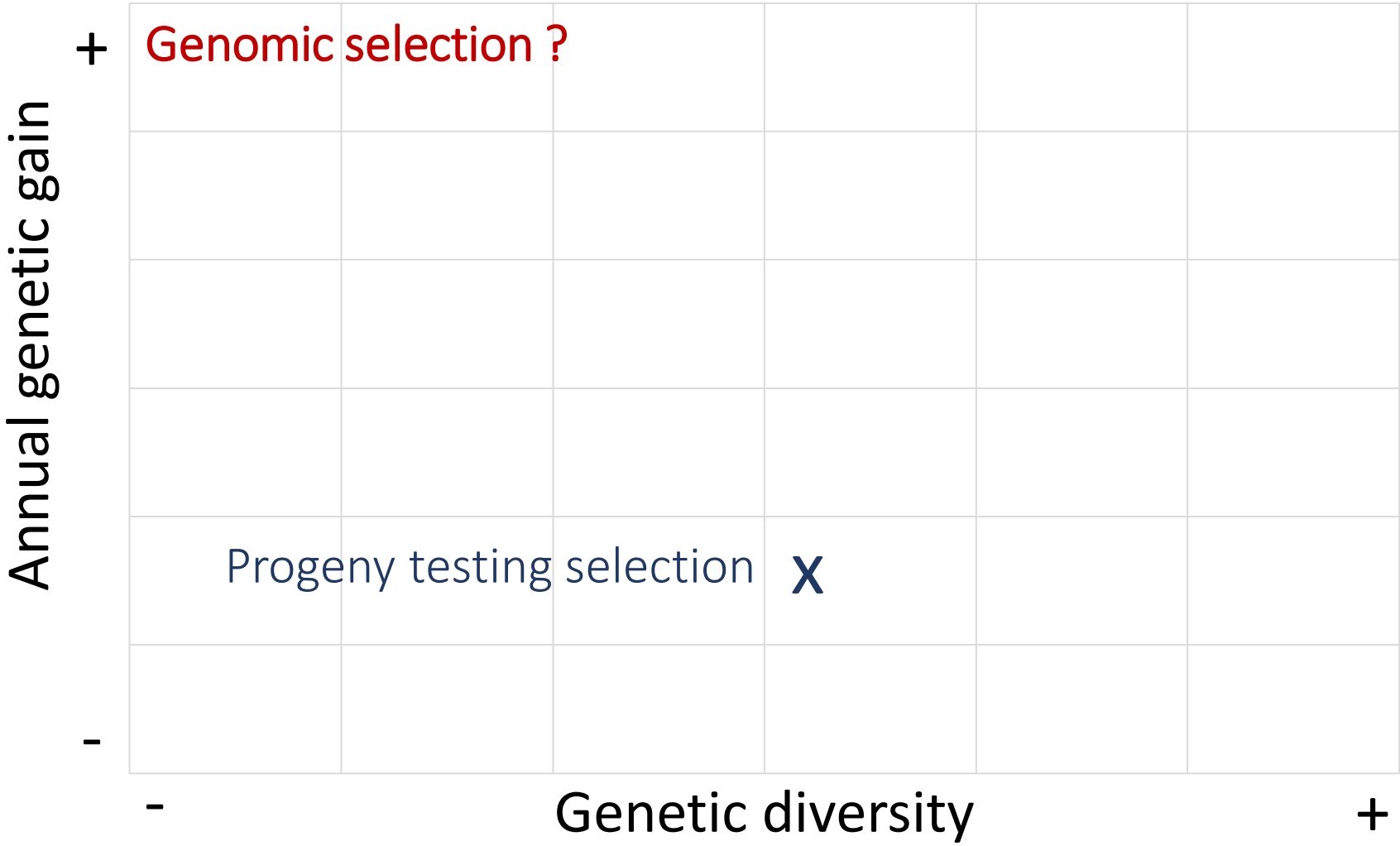

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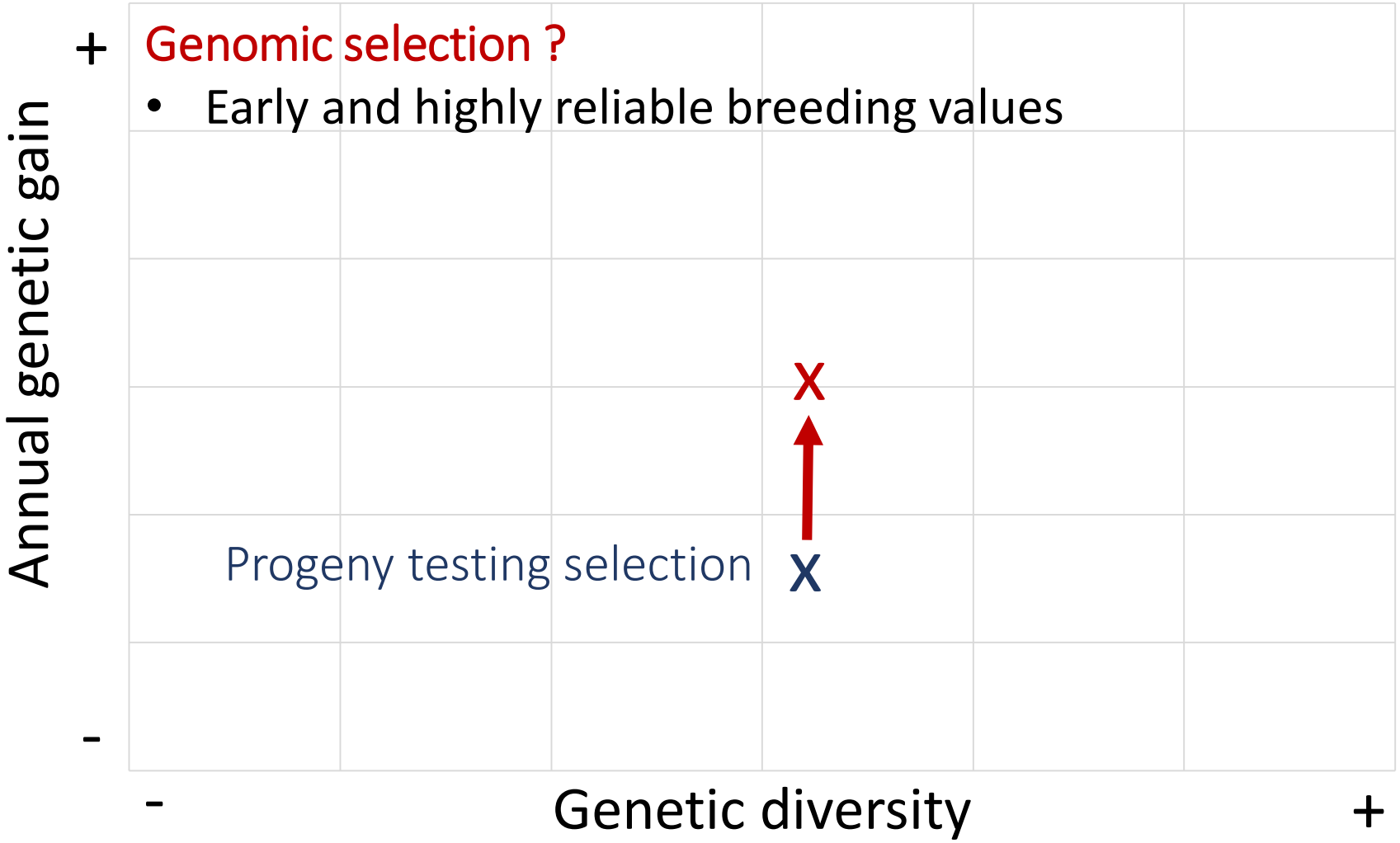

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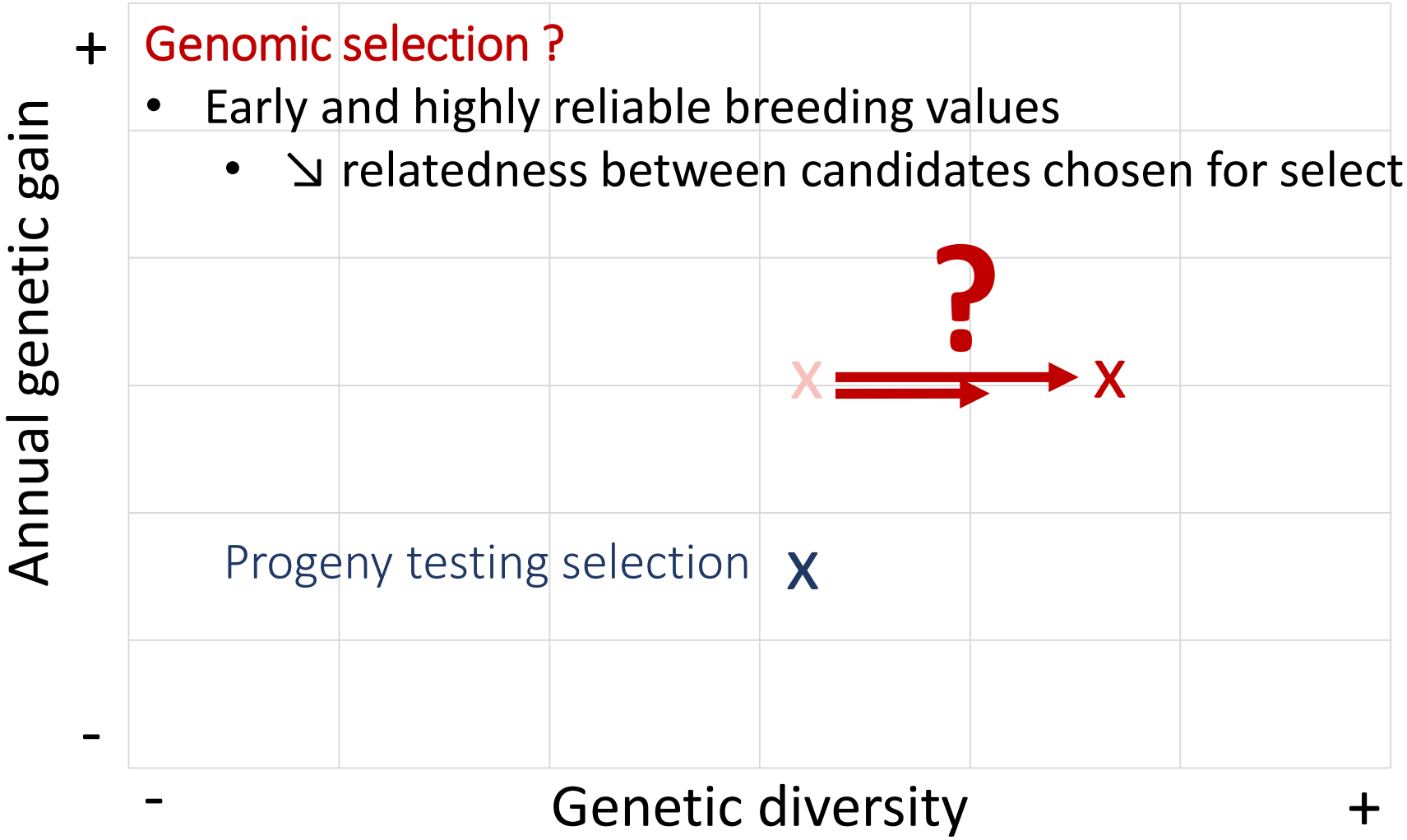

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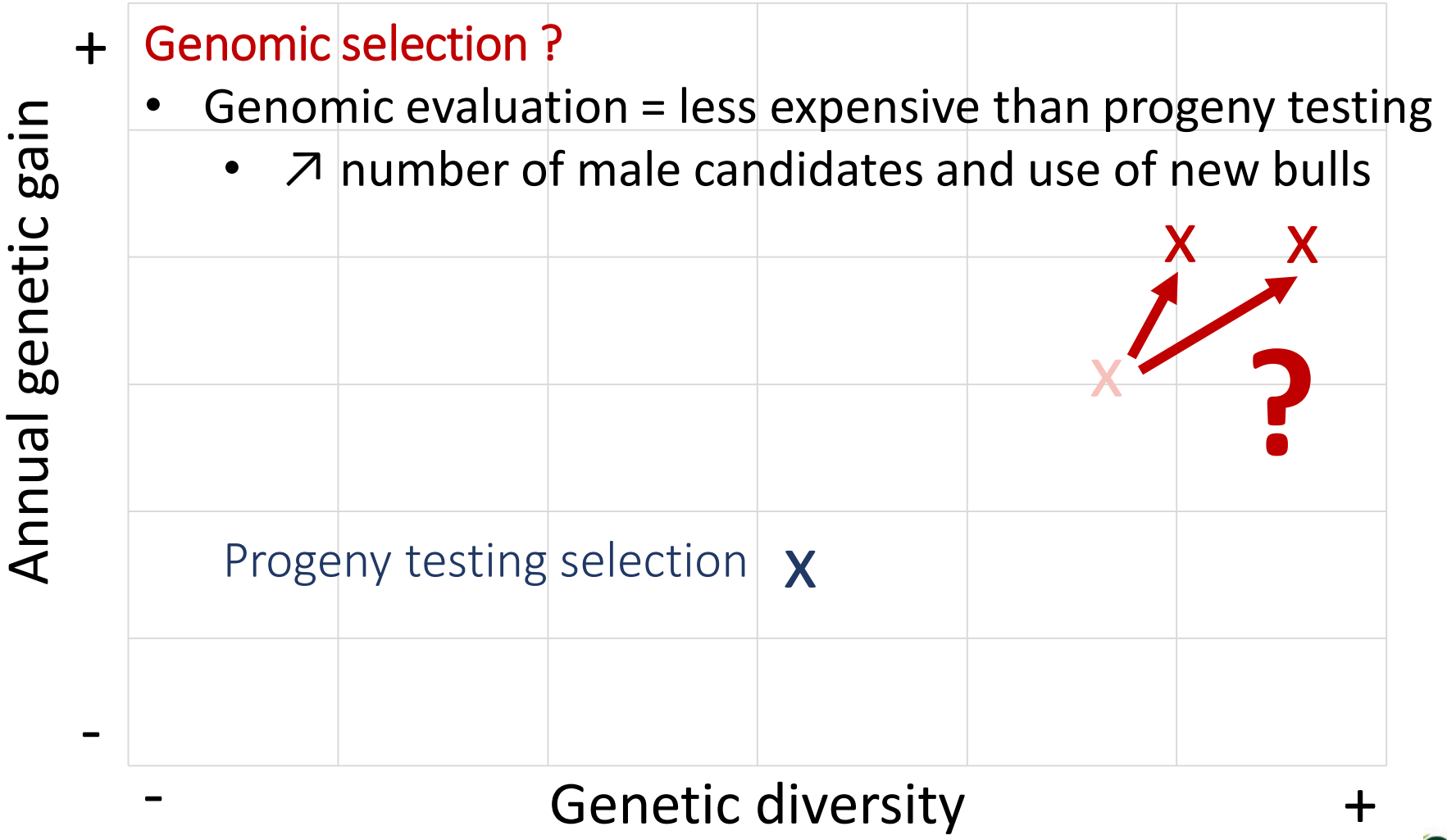

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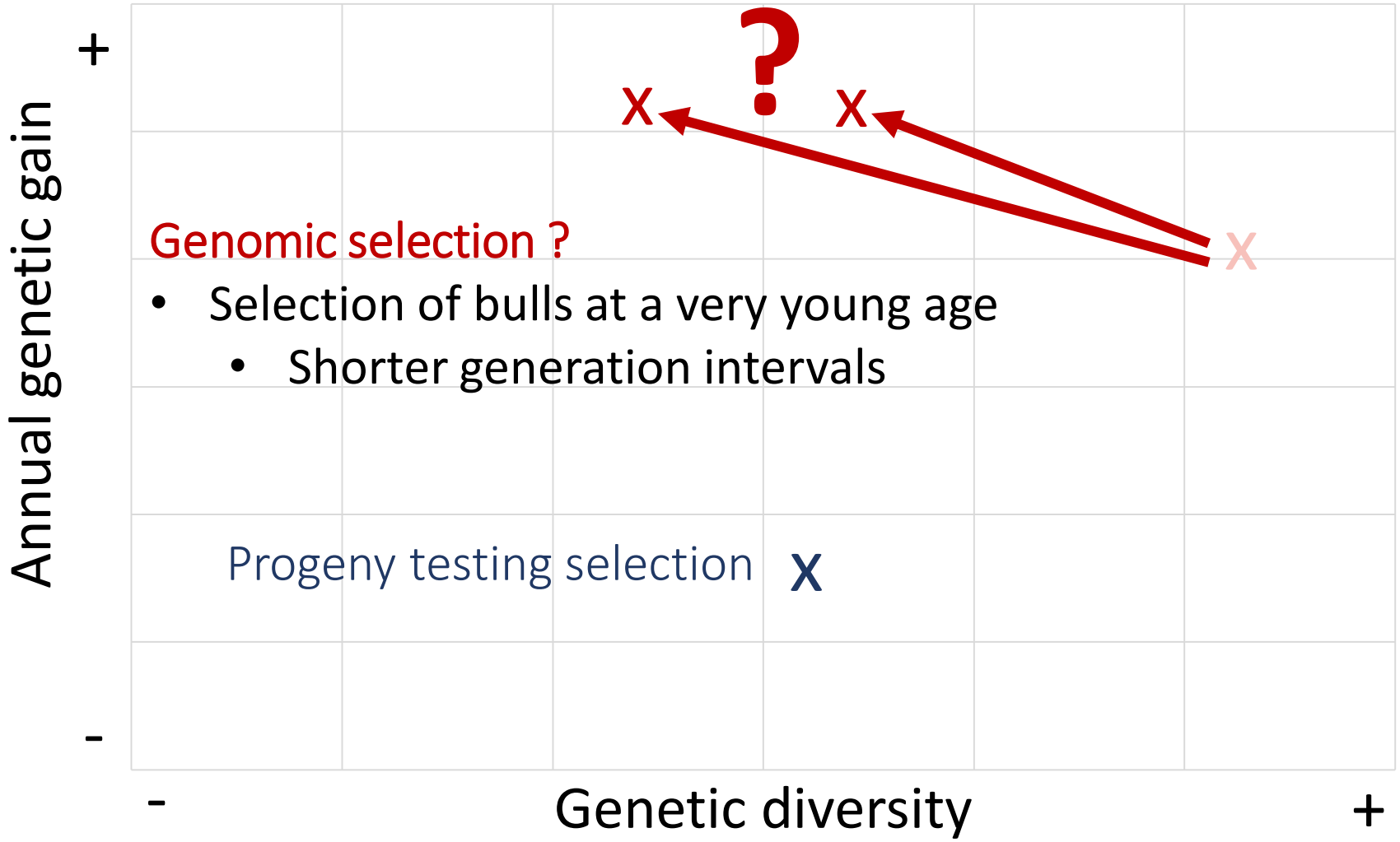

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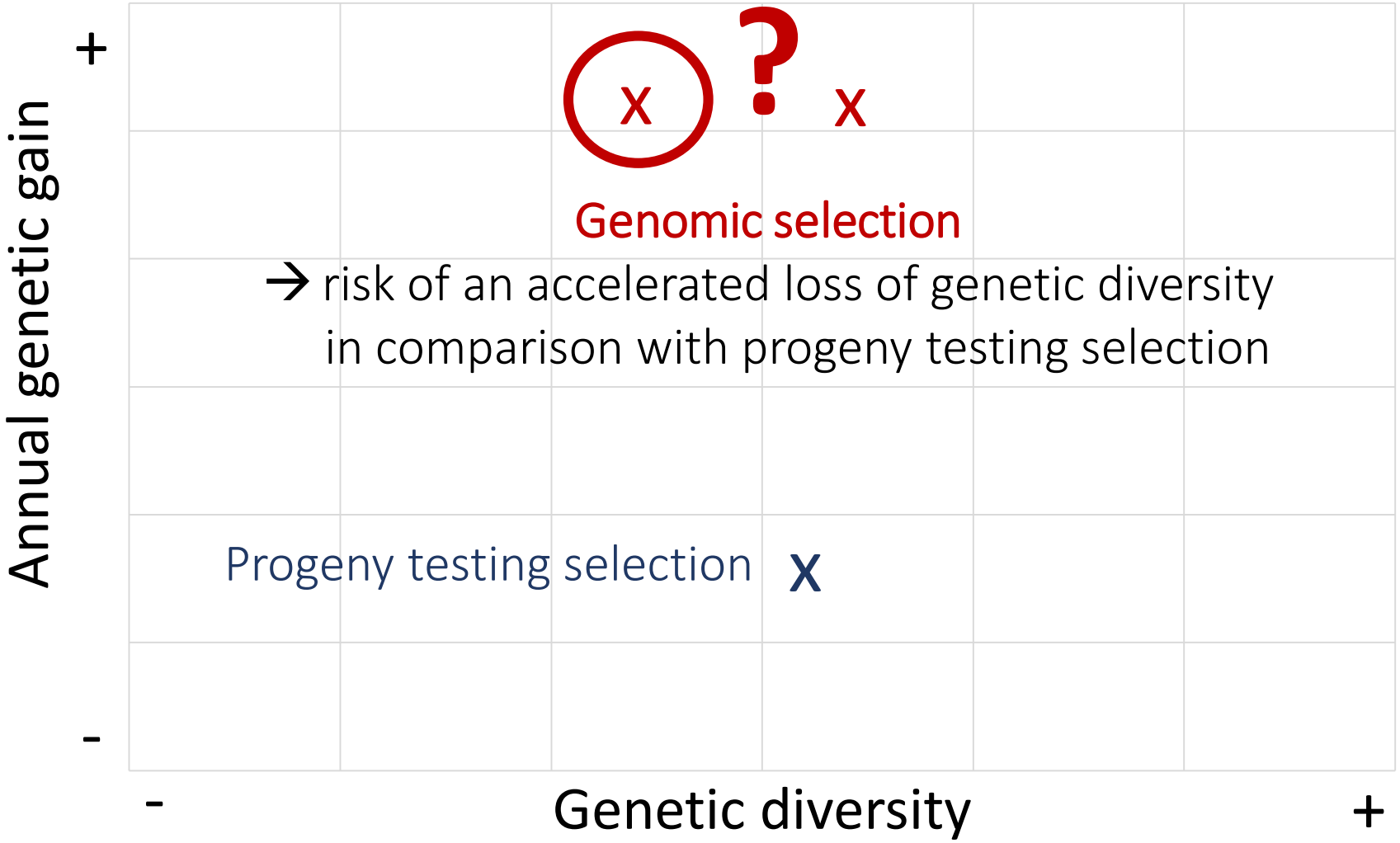

# Consequences of a loss of genetic diversity

Loss of additive genetic variance → **Loss of potential genetic gain**

Loss of overall genetic diversity → **Loss of adaptive potential**

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**→Economic impact**

**→Need to manage genetic diversity**

Doublet *et al. Genet Sel Evol* (2019) 51:52
https://doi.org/10.1186/s12711-019-0495-1

GSE Genetics Selection Evolution

RESEARCH ARTICLE Open Access

# The impact of genomic selection on genetic diversity and genetic gain in three French dairy cattle breeds

Anna-Charlotte Doublet[1,2*], Pascal Croiseau[1], Sébastien Fritz[1,2], Alexis Michenet[1,2], Chris Hozé[1,2], Coralie Danchin-Burge[3], Denis Laloë[1] and Gwendal Restoux[1]

## **Marketed sires, genotyped in France** from 3 French dairy cattle breeds

Holstein
**International** breed

Montbéliarde
**National** breed


Normande
**National** breed

## Evolution of genetic gain

## Evolution of genetic diversity

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Total Merit Index ISU

Combining production traits, functional traits and type traits

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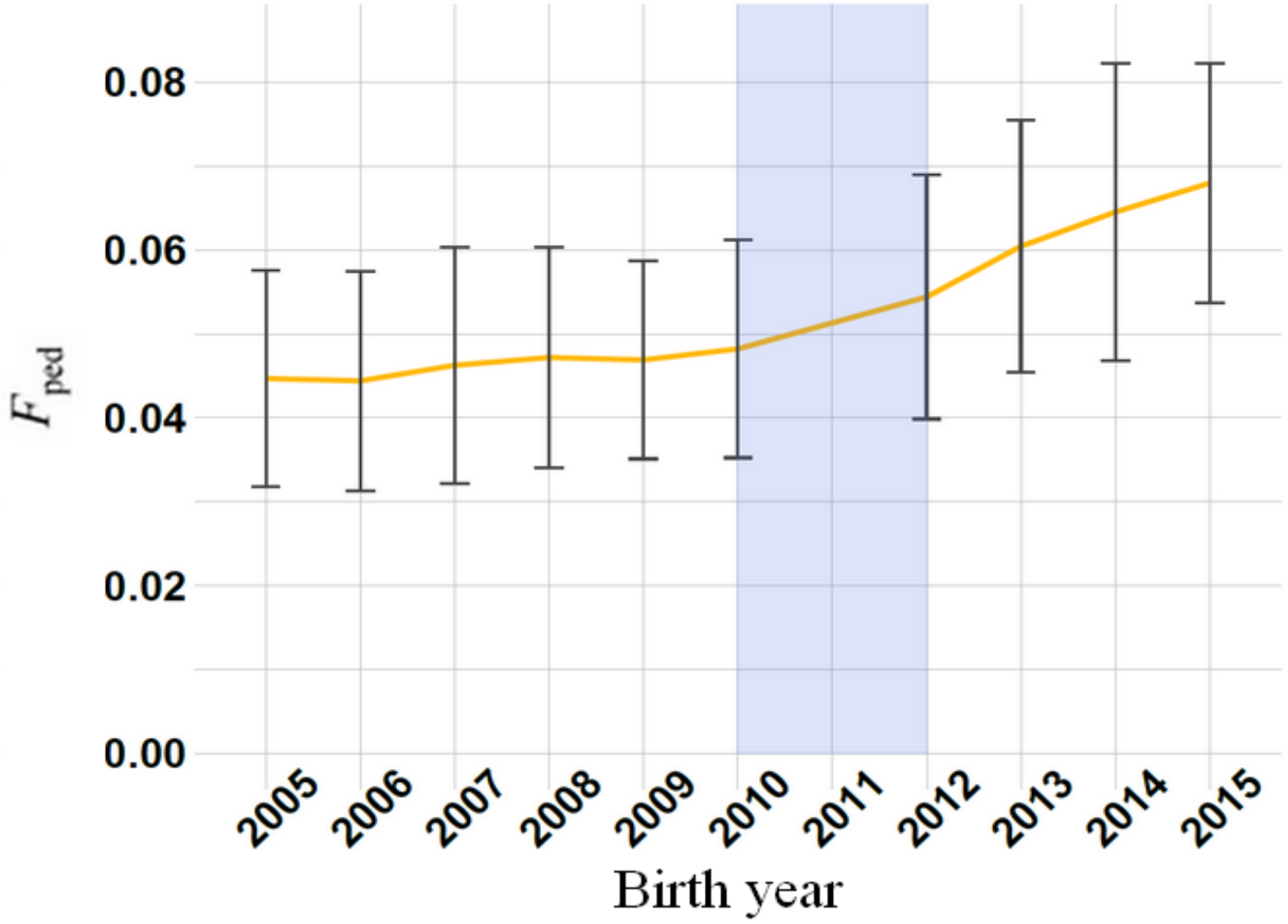
## Evolution of genetic diversity

Generation intervals
Inbreeding (pedigree and 50K genotyping data)
Kinship

# Display of results



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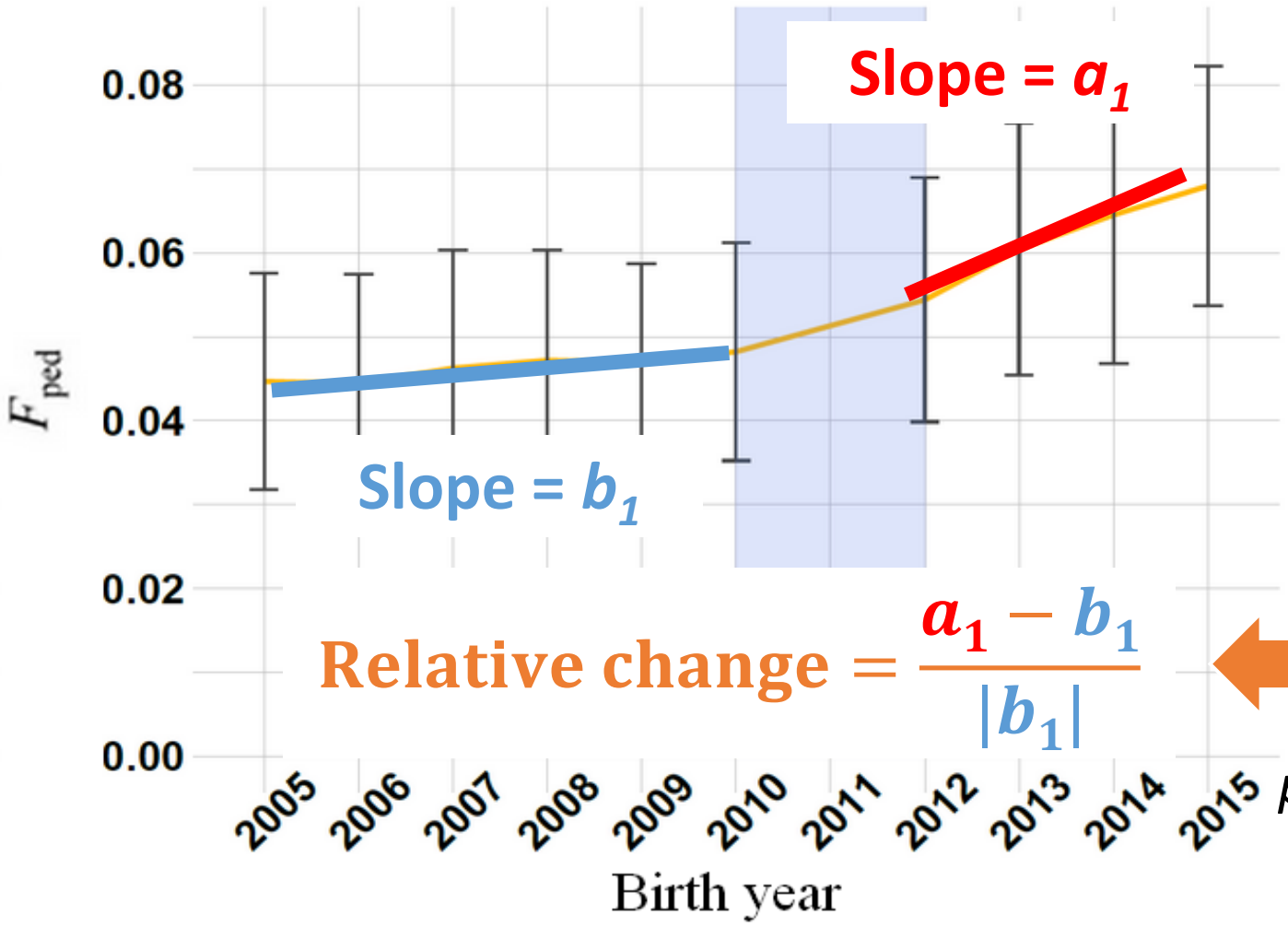



$$\text{Relative change} = \frac{a_1 - b_1}{|b_1|}$$

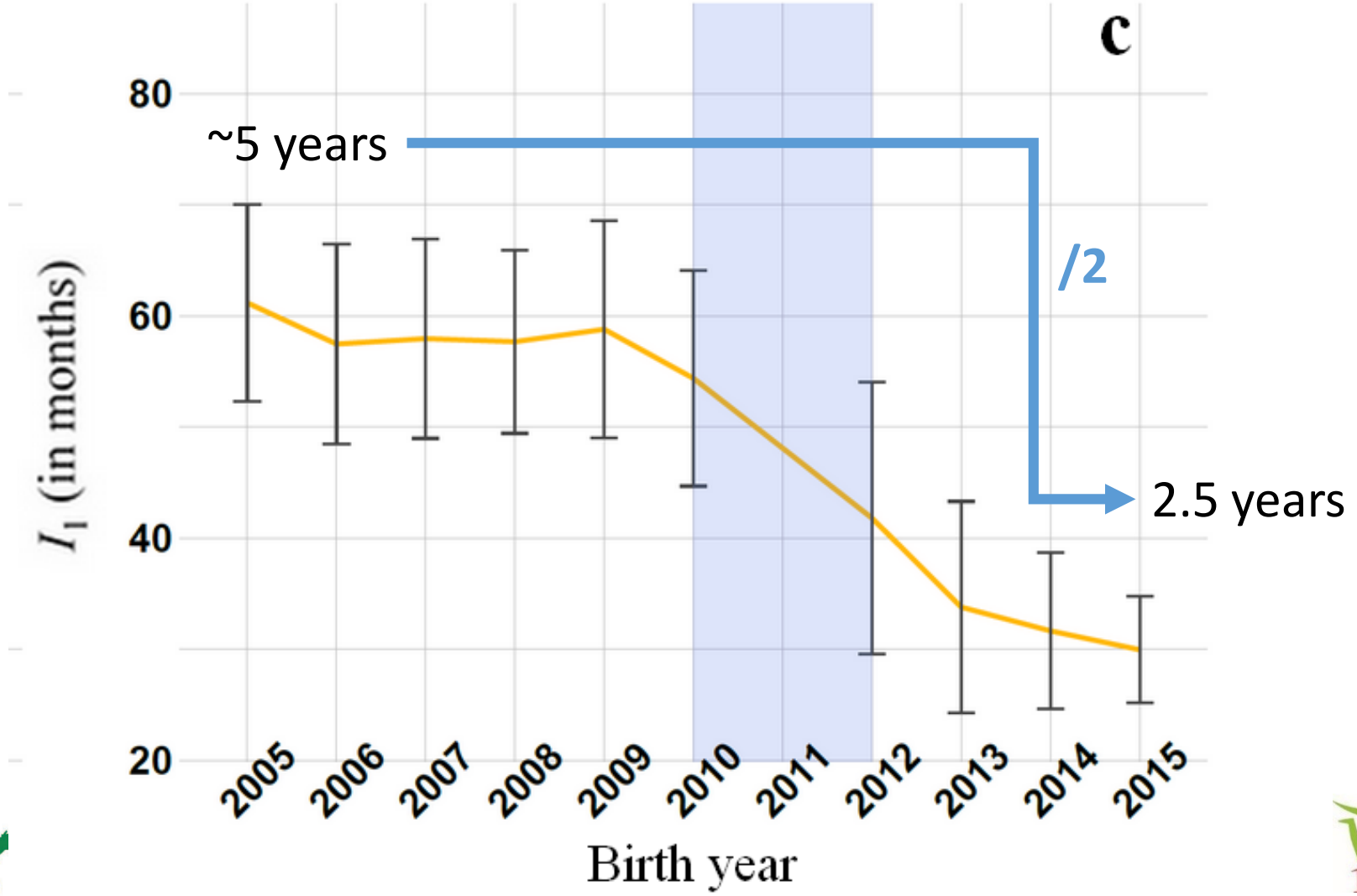
**Comparison** of the slopes of each parameter **before** and **after** the beginning of genomic selection

> 0 : acceleration
< 0 : deceleration

*p*-value: pairwise comparison of the slopes

# Generation intervals in French Holstein

average between a bull and its parents in months



# Generation intervals and genomic selection

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(Doekes *et al* 2018)

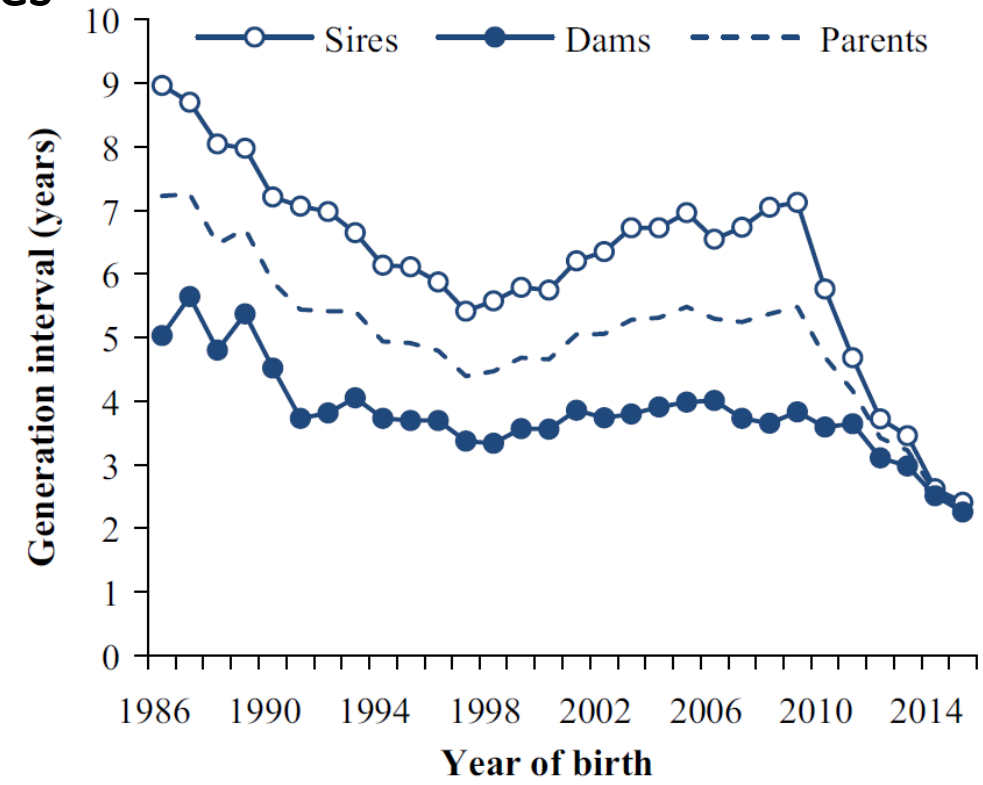


**Fig. 2** Generation interval for bull sires, bull dams and bull parents by year of birth

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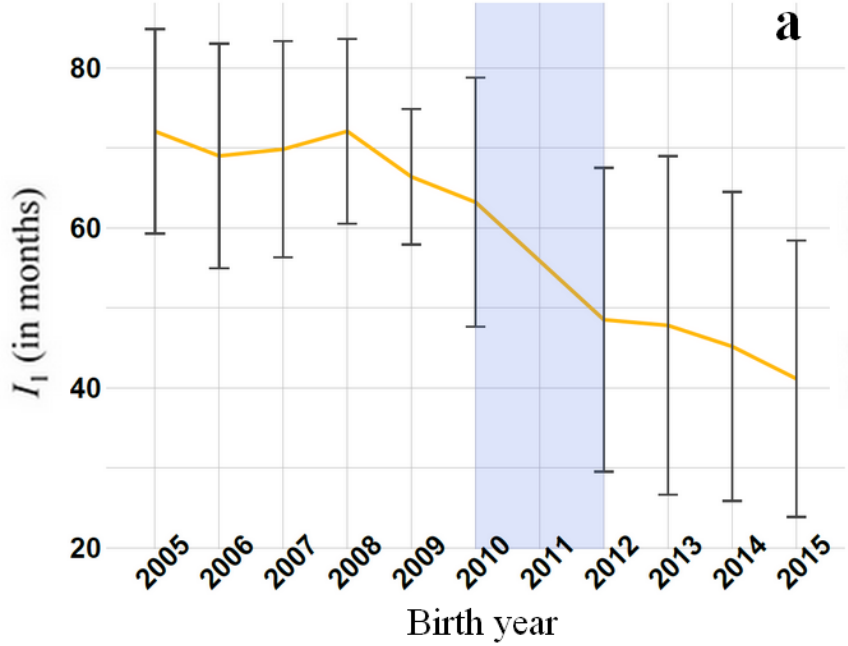
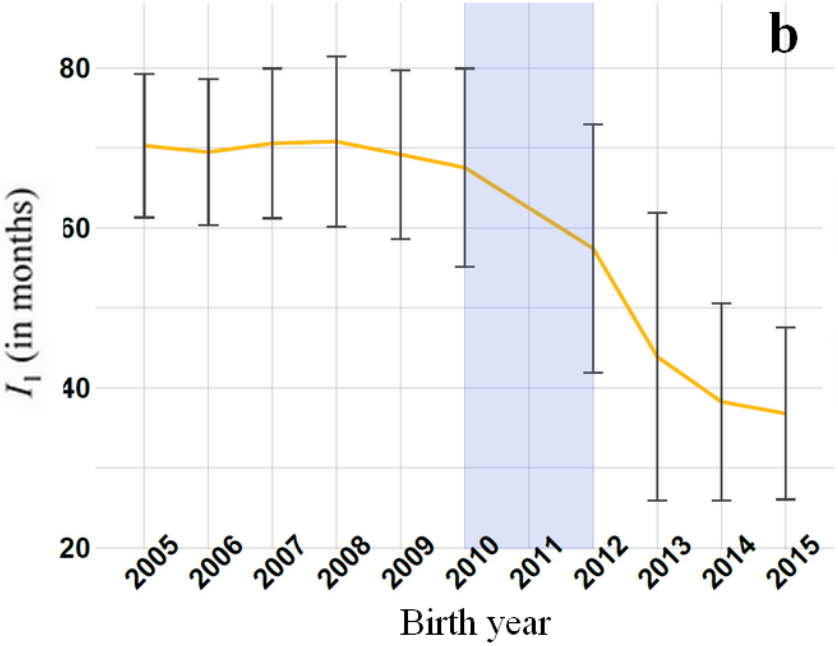



Normande

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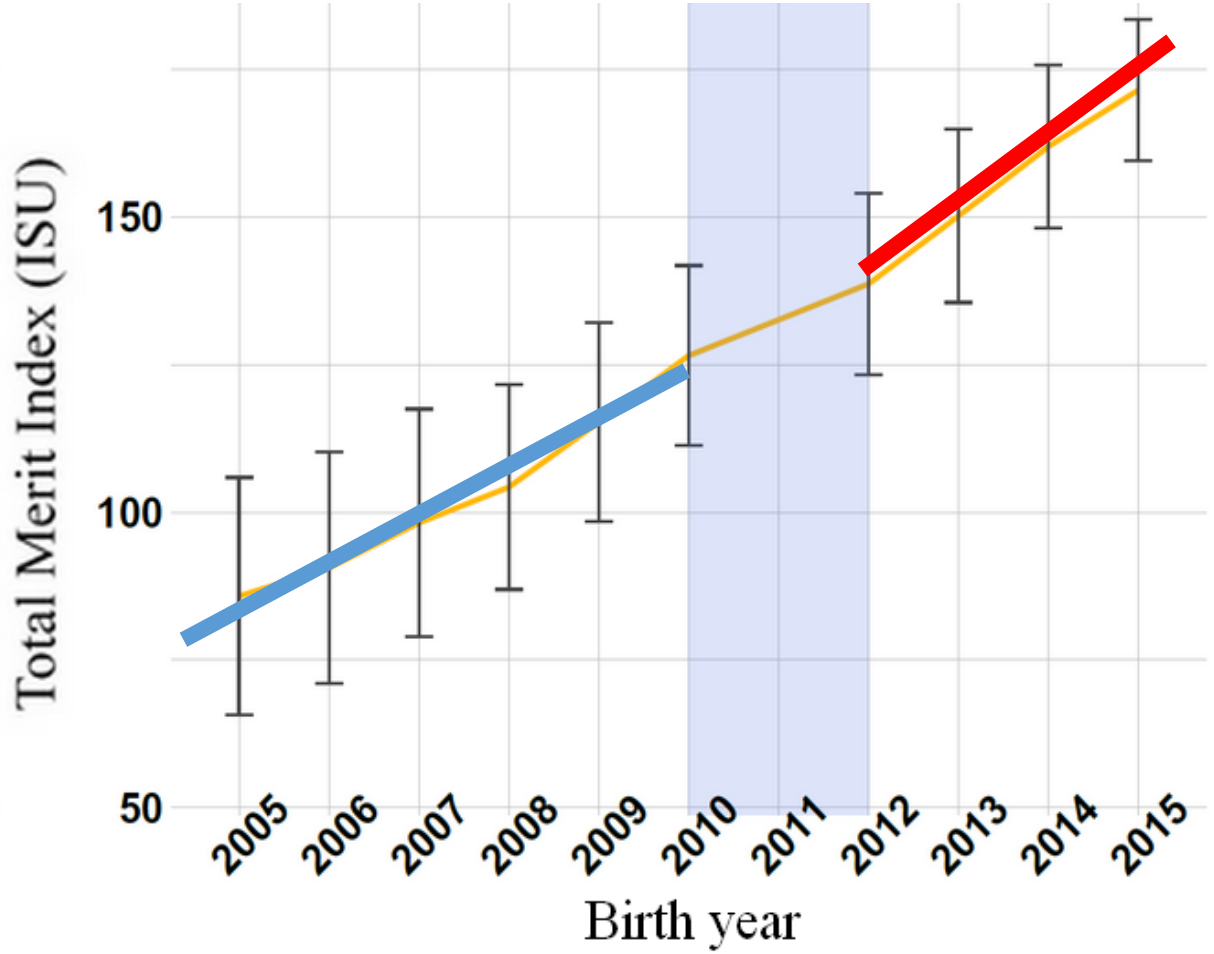
** *p*-value < 0.001
* 0.001 < *p*-value < 0.05
ns *p*-value > 0.05

# Total merit index in French Holstein




**RC = 0.33 ****

**→ Increased annual genetic gain**

**→ ΔG x 1.33**

# Genetic gain and genomic selection

- Simulations studies **predicted an increase of the annual genetic gain by up to 30 to 108%** depending on the scenarios under genomic selection (Hayes *et al* 2009, de Roos *et al* 2011, Colleau *et al* 2015)

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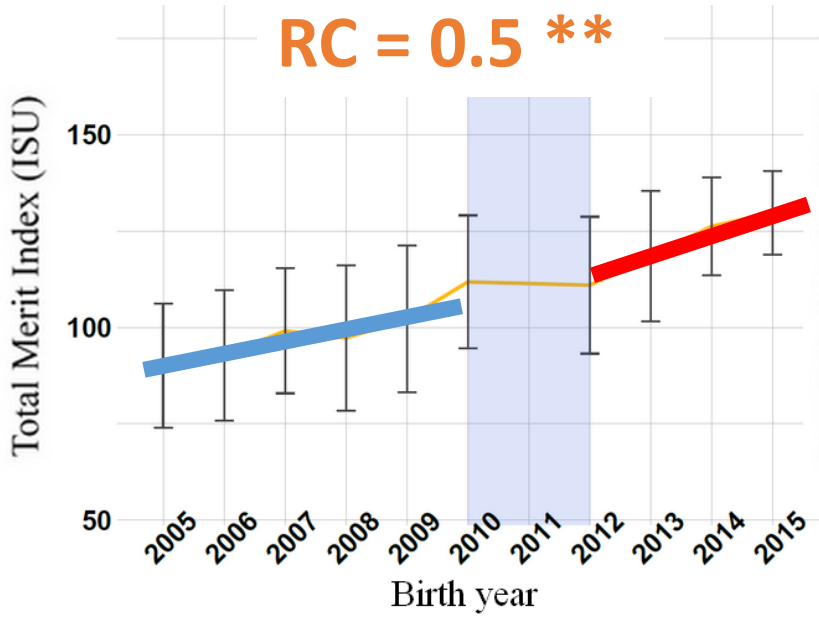
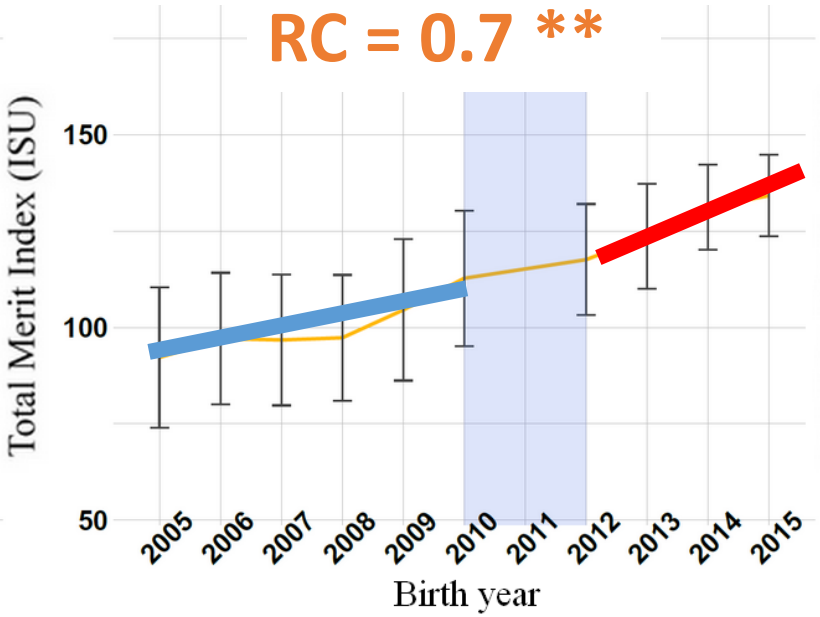



Normande



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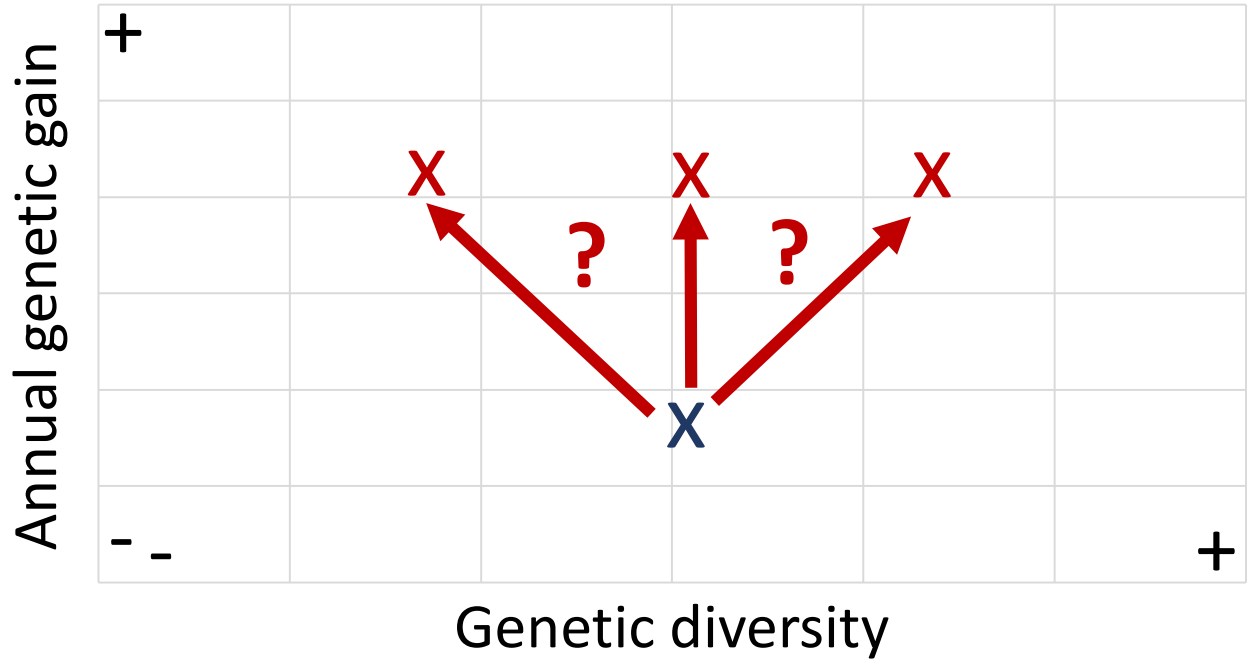
- It has been **observed in other French breeds** (Doublet *et al* 2019)
- **How does this increase in annual genetic gain translate for genetic diversity?**



# Inbreeding in French Holstein
(from pedigree data)

** *p*-value < 0.001
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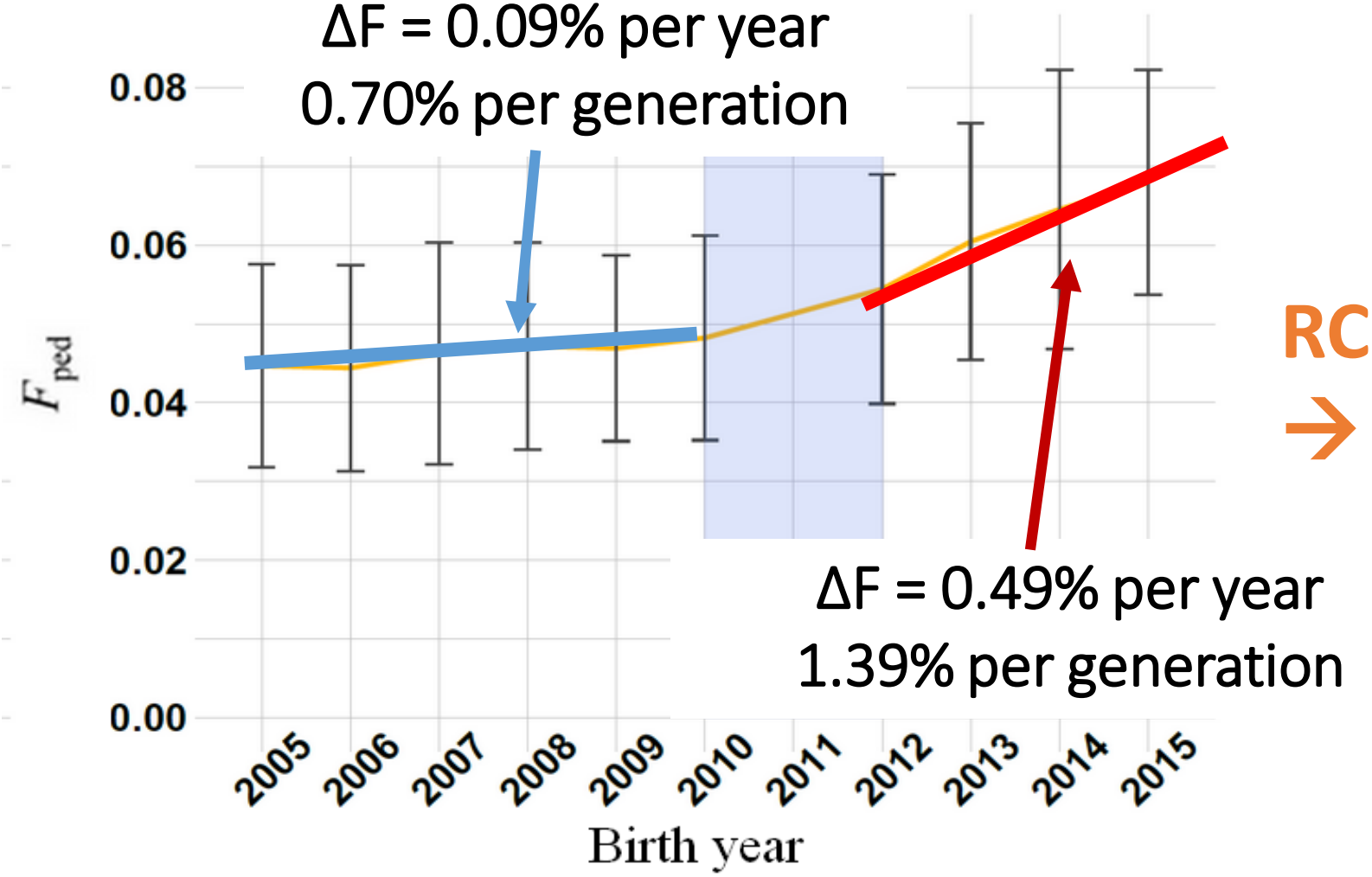
ns *p*-value > 0.05




**RC = 4.5 ****
**→ ΔF x by 5.5**

# Inbreeding in French Holstein
## (from medium density 50K genotyping data)

** *p*-value < 0.001
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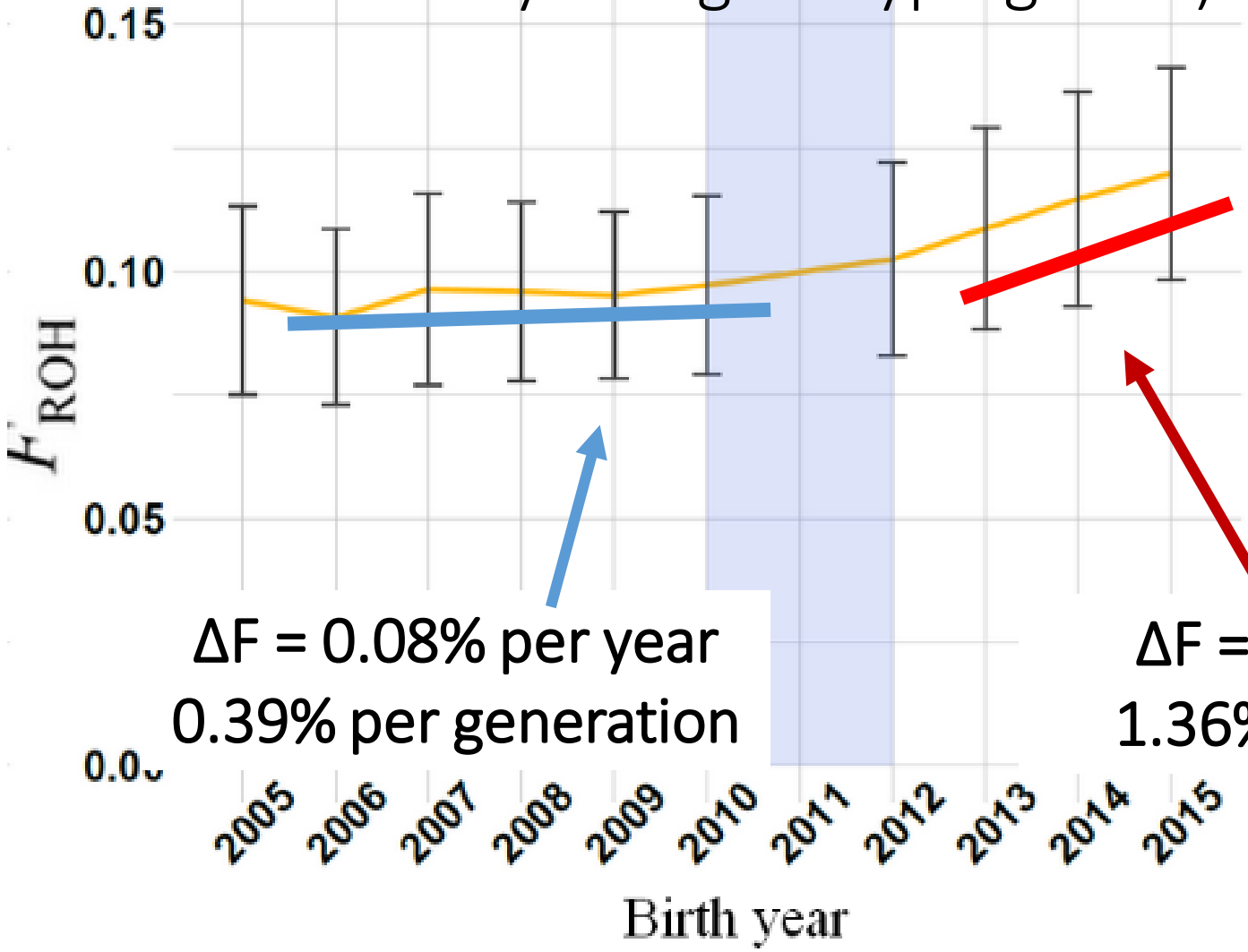
ns *p*-value > 0.05




**RC = 5.9 ****
**→ ΔF x by 6.9**

ΔF = 0.08% per year
0.39% per generation

ΔF = 0.55% per year
1.36% per generation

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# Inbreeding and genomic selection

- This increase in ΔF was also observed in Holstein **in other countries/regions**

North America (Forutan *et al* 2018)

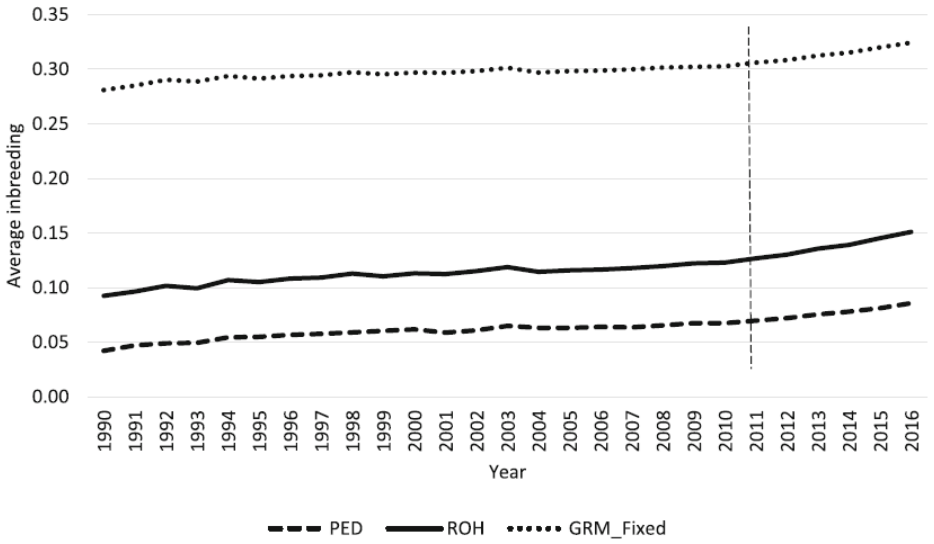
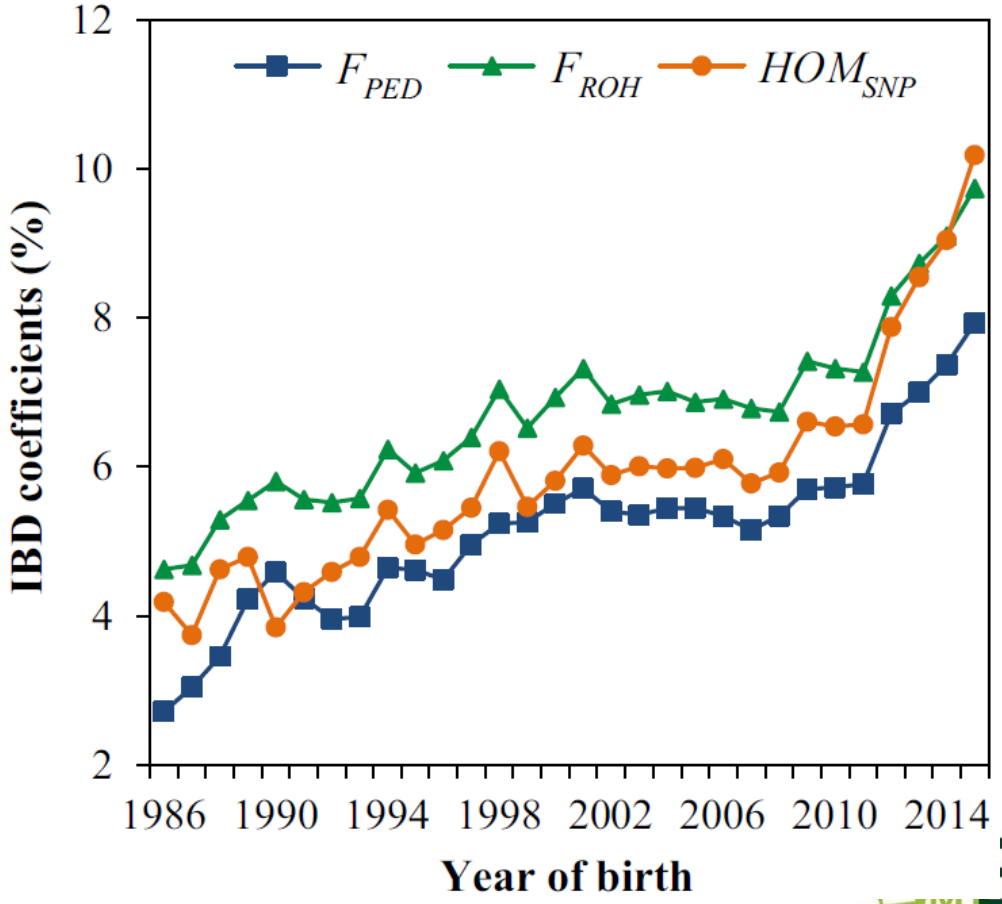



**Fig. 4** Average estimates of inbreeding per year in North American Holstein cattle. Inbreeding based on pedigree (PED), inbreeding derived from runs of homozygosity (ROH), inbreeding estimated from the genomic relationship matrix using an allele frequency of 0.5 (GRM_ Fixed). ROH was estimated using SNP1101 with minimum window size = 20SNP, genotype error = 0.001. Gray dashed line represent the start of genomic selection

The Netherlands (Doekes *et al* 2018)



# Inbreeding and genomic selection

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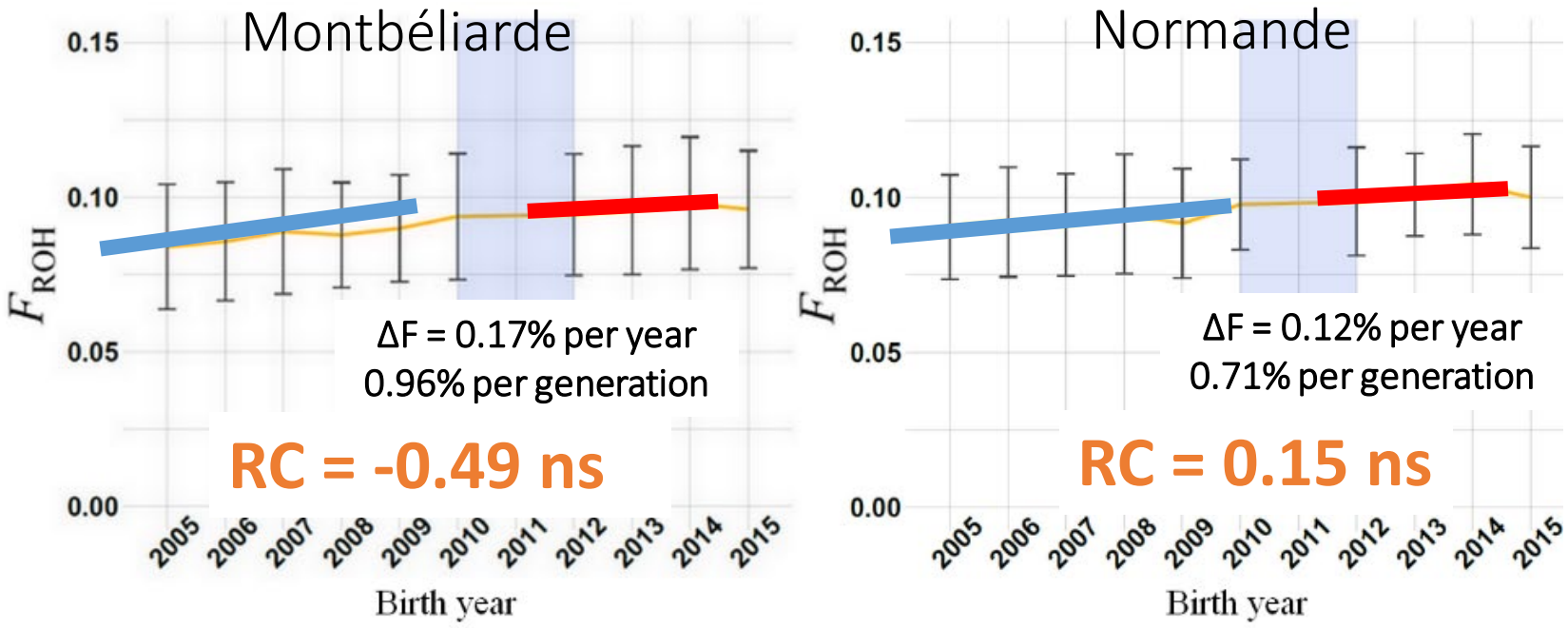
- However, in other French breeds, **annual inbreeding rates were maintained**, while annual genetic gain increased (Doublet *et al* 2019)



# Inbreeding and genomic selection

Inbreeding is increasing faster than before in Holstein

- Because of recent inbreeding? Or accumulation of old inbreeding?
  ➔ **Inbreeding for the last 5 generations**

- What kind of population structure?
  ➔ **Kinship based on pedigree data**

# Inbreeding in French Holstein 5 generations (from pedigree data)

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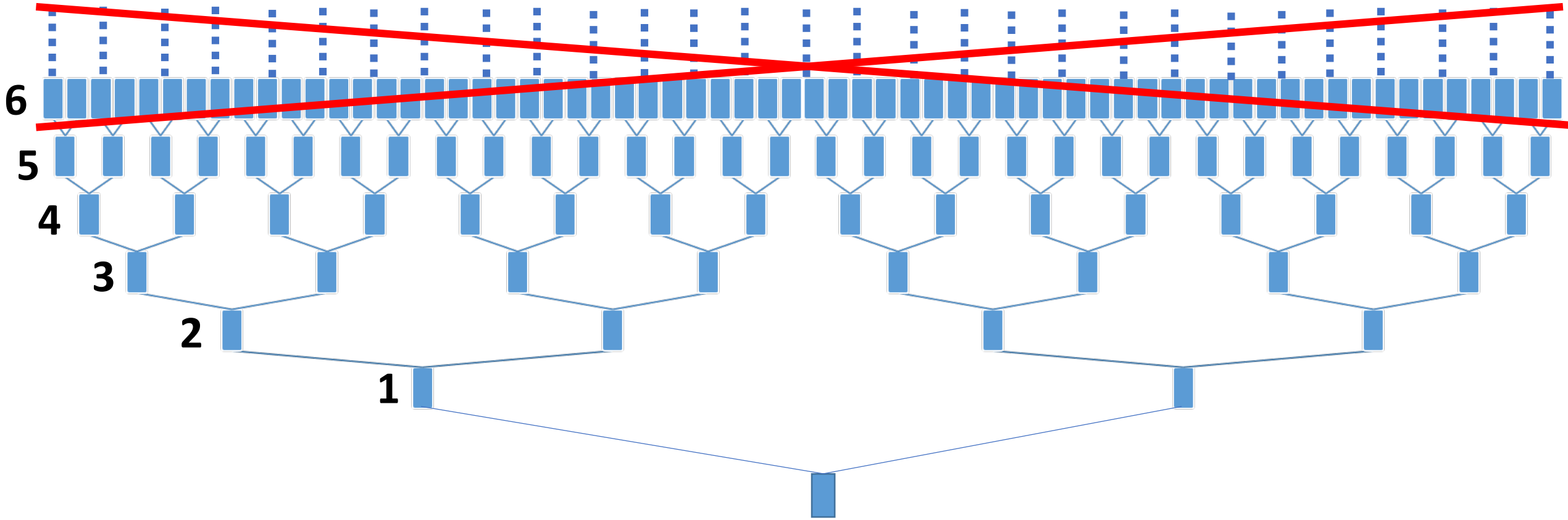

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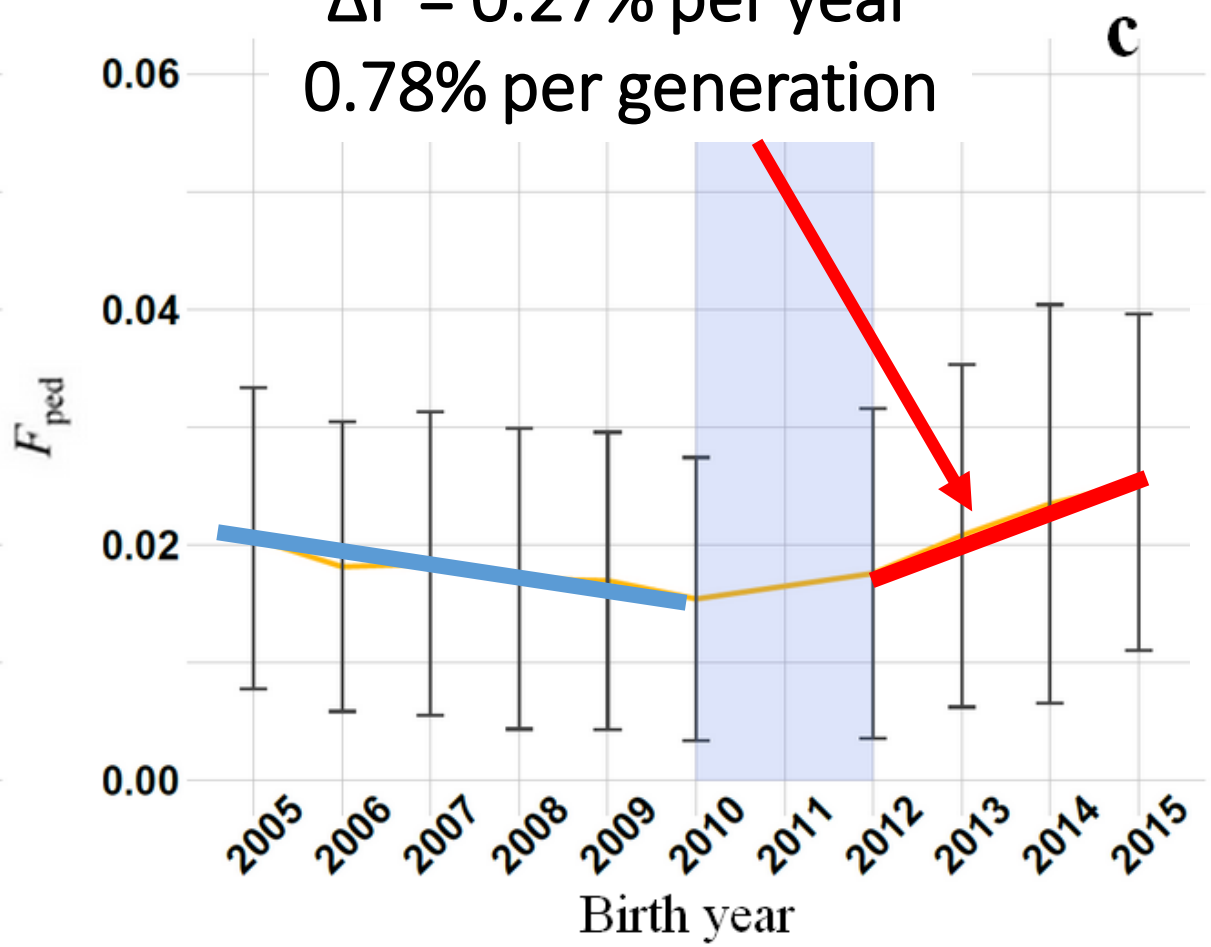
# Inbreeding in French Holstein 5 generations (from pedigree data)

ΔF = 0.27% per year
0.78% per generation




**RC = 4.3 ****

**→ Increased recent inbreeding with genomic selection**

# Kinship in French Holstein
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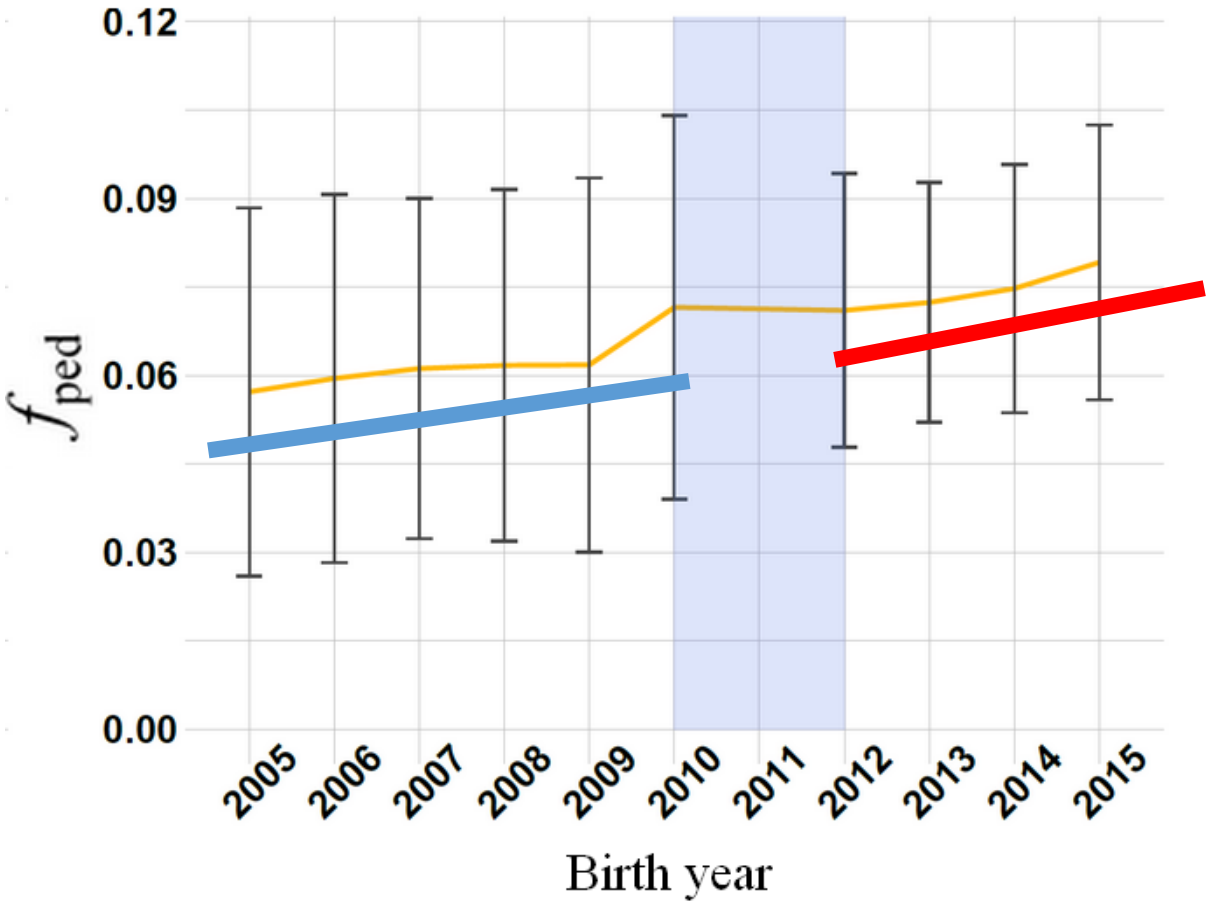


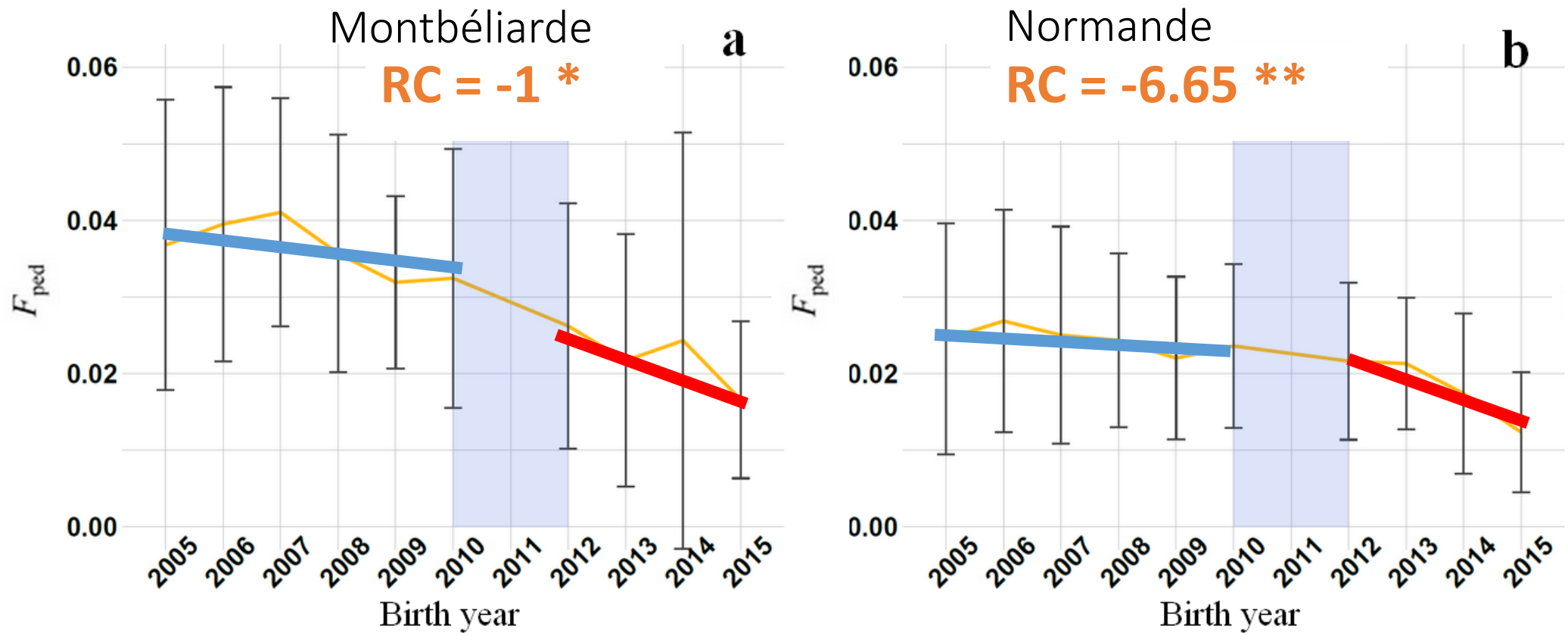

**RC = 0.09 ****

**Mean before < Mean after**

**→ Higher kinship with genomic selection**

# Recent inbreeding, kinship and genomic selection

- The increase of recent inbreeding observed in French Holstein was **not observed in two other French breeds** (Doublet *et al* 2019)



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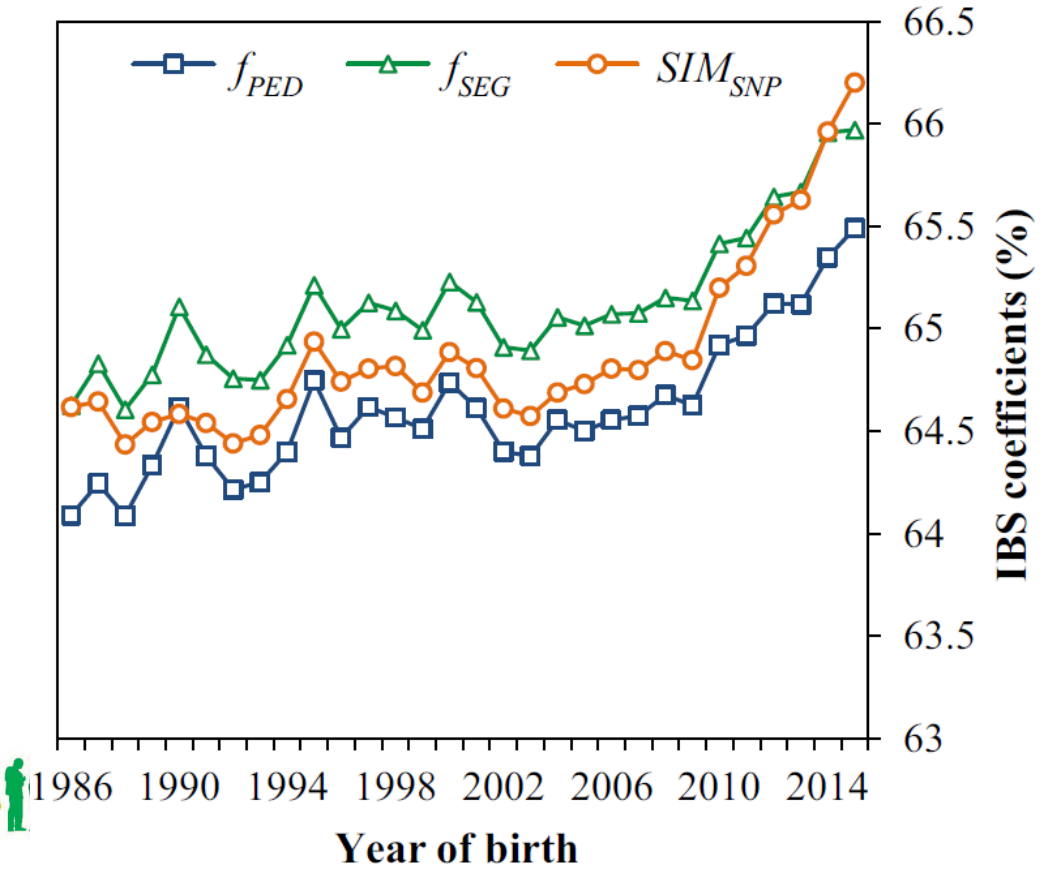

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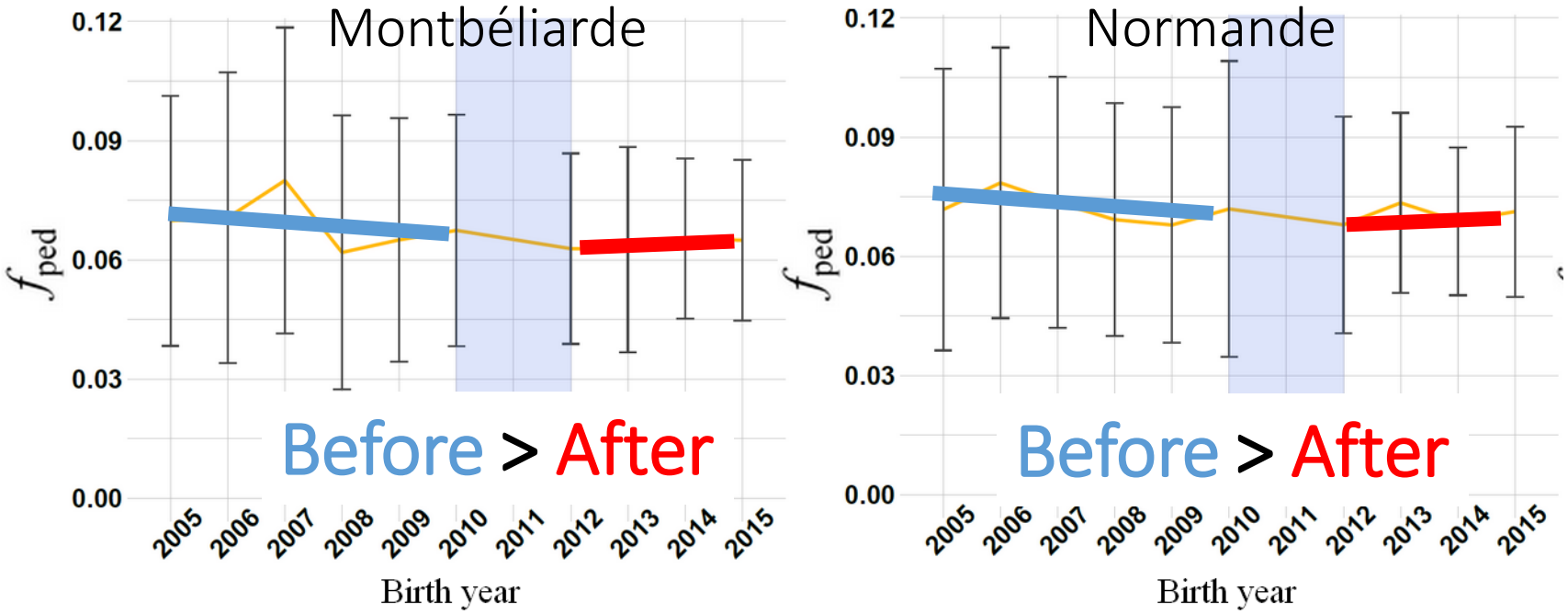

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- **Foreign bulls (mostly American): widely spread in French Holstein pedigrees** (AI performed by their descendants) → **more influence than bulls selected from French breeding programs** (Le Mézec *et al* 2018)

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→Loss of genetic diversity migth be due to the intense use of a few bulls only

→Risk of loss of genetic diversity at the global scale

# Which solutions?

Possible to reduce the impact of Holstein breeding schemes on genetic diversity without deprecating genetic gain significantly

Different types of solutions:

- **Number of bulls**, number of candidates, number of genotyped individuals
- **Choice of the bulls** (less related, /!\ grandfathers and above)
- **Management of reproductive technologies** (if ↗ intensity of MOET or OPU-FIV, need to ↗ the number of bulls)
- **Number of inseminations** per bull, **mating plans** in farms
- Using exclusively young genomic bulls (and **not confirmed bulls**)
- **Evaluation of bulls** (reference population, index including a weighting on diversity)

# Conclusion and perspectives

**Genomic selection = good tool**

- **New breeding schemes** (↘ generation intervals, ↗ candidates for selection)
- Possible to **maintain the loss of genetic diversity at the same level** while ↗ **ΔG**
- However, in Holstein: acceleration of the **loss of genetic diversity in several countries**

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- Need for an **international integrated management of genetic diversity**?
- **Consequences of new technologies** (MOET, OPU-FIV, gene editing) on breeding schemes and therefore on genetic diversity?

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**THANK YOU!**