Genomic selection and inbreeding trends in Dutch-Flemish Holstein Friesian cattle

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WAGENINGEN
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Introduction

- Holstein-Friesian (HF) breed
  - Dominates production worldwide
  - Intense selection and AI
  - N_e of 50-150

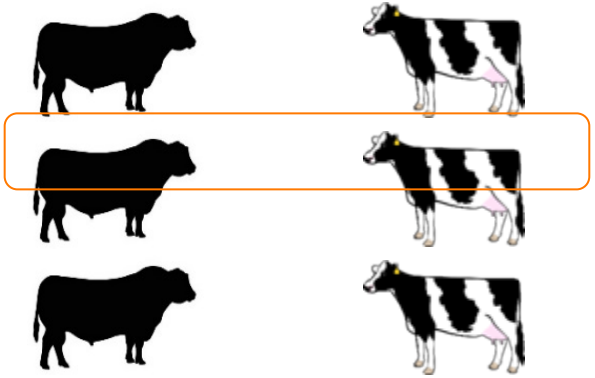
- Since 2009, genomic selection (GS):
  - GEBVs; exploit MS
  - Accelerated progress
  - **Effect on inbreeding?**

Study objective

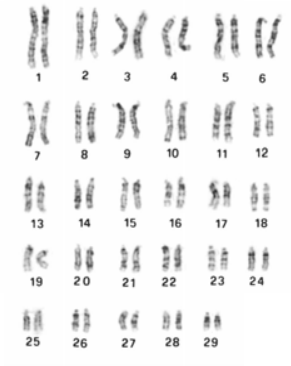
Assess how GS has affected inbreeding trends

in Dutch-Flemish HF cattle

In AI-bulls & In cow pop.

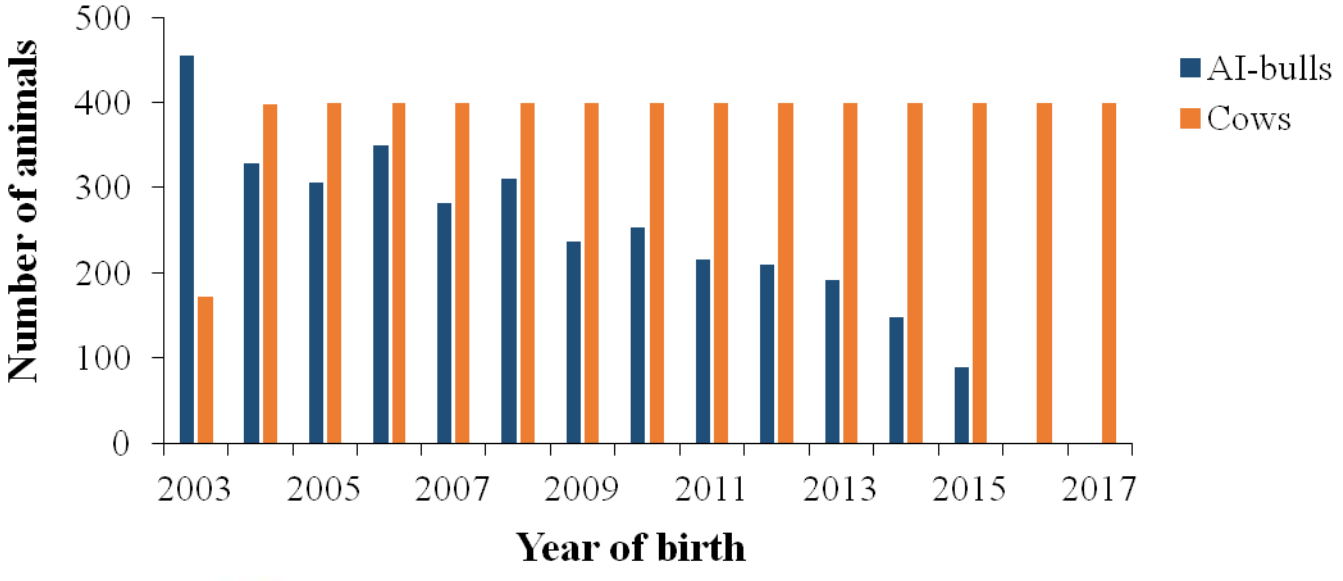


Genome-wide & Region-specific



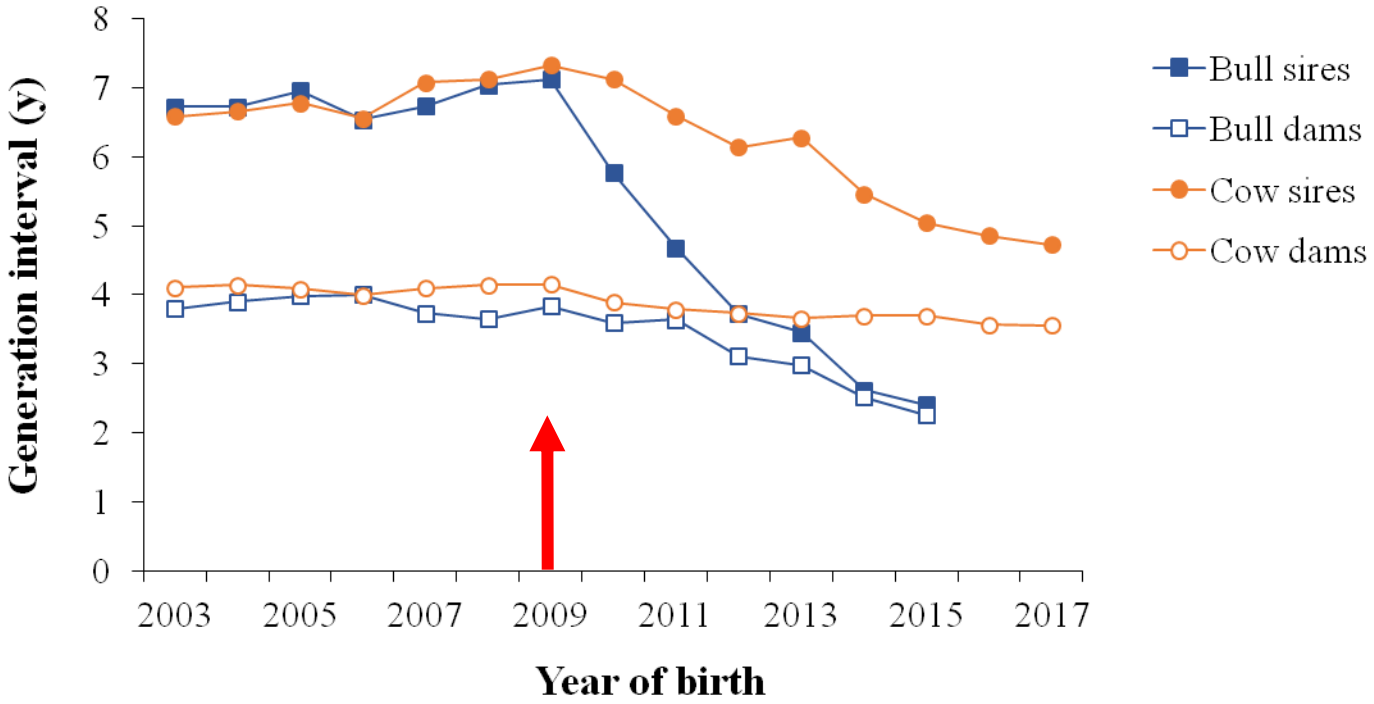
Material & methods: data

- Pedigree & phased genotypes (~75 k):
  - 3,373 AI-bulls
  - 5,770 cows



Material & methods: generation interval

- Sharp decrease for AI-bull sires with GS



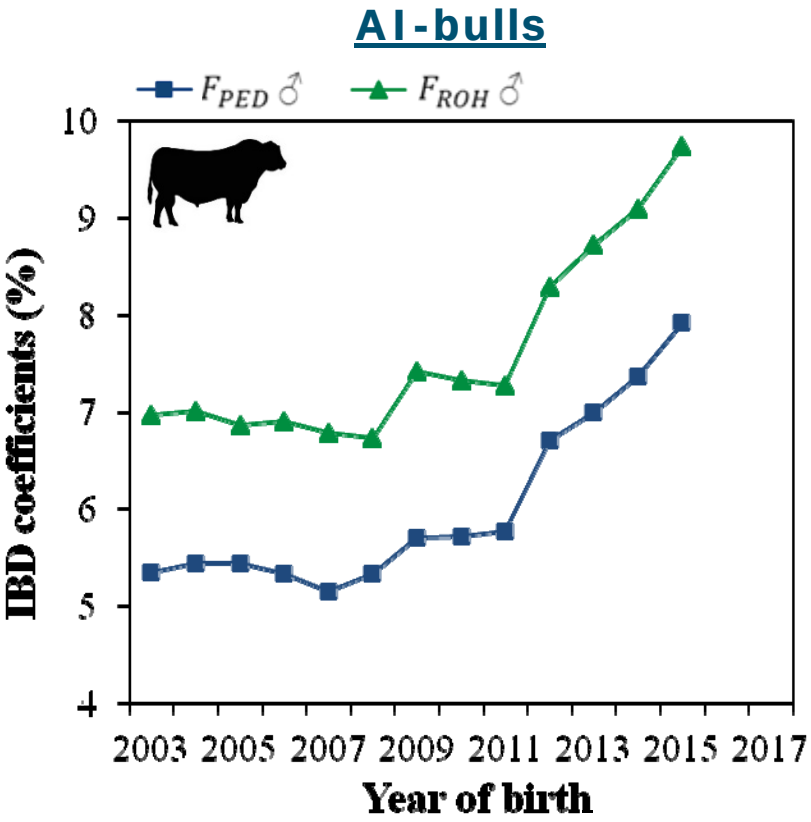
Material & methods: inbreeding measures

- Genome-wide:
  1. Pedigree-based F_{PED} = expected IBD
  2. Marker-based HOM_{SNP} = IBS
  3. Segment-based F_{ROH} = realised IBD
     - ≥3.75 Mb

  } ***Rate per generation*** (ΔF)

- Region-specific:
  - Positional F_{ROH} for cohorts of 3y

Results: genome-wide trends



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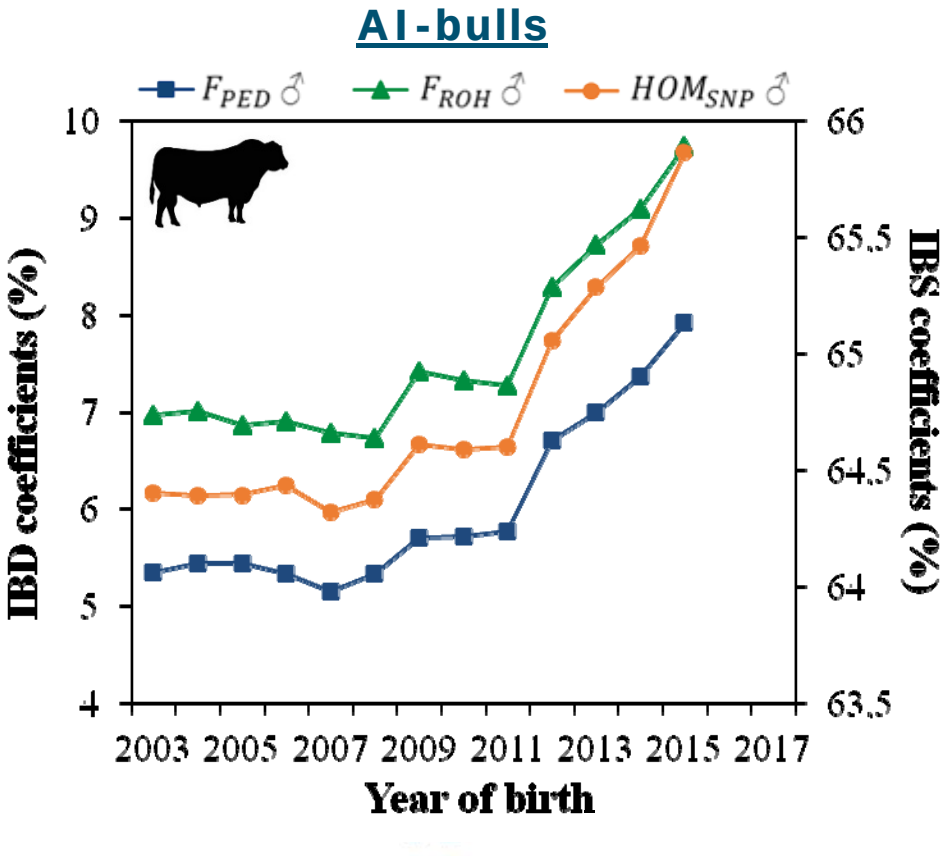

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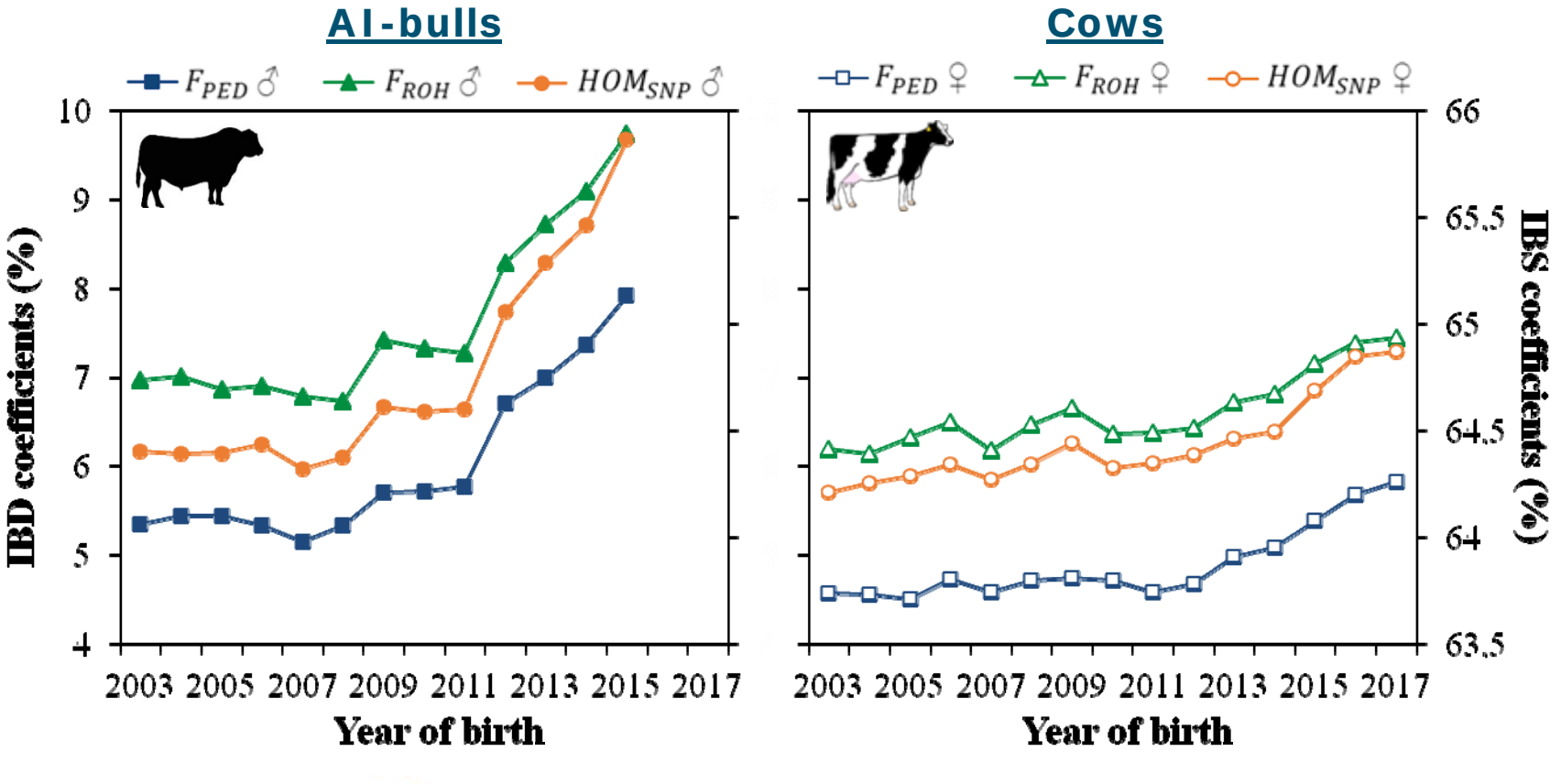
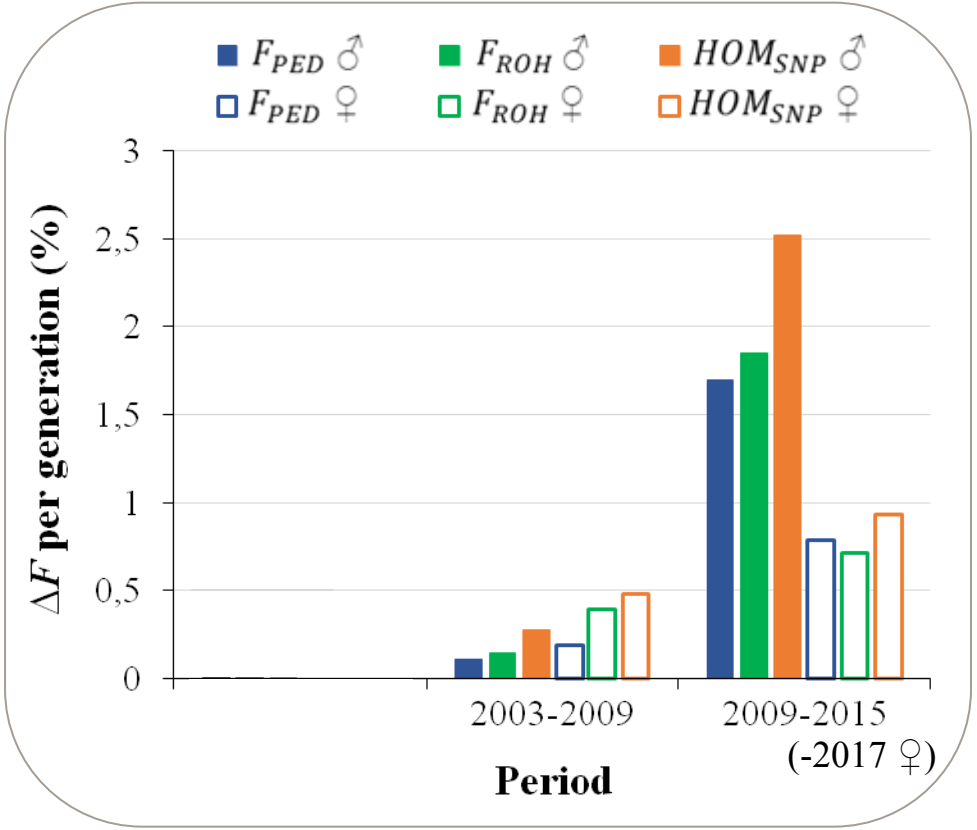
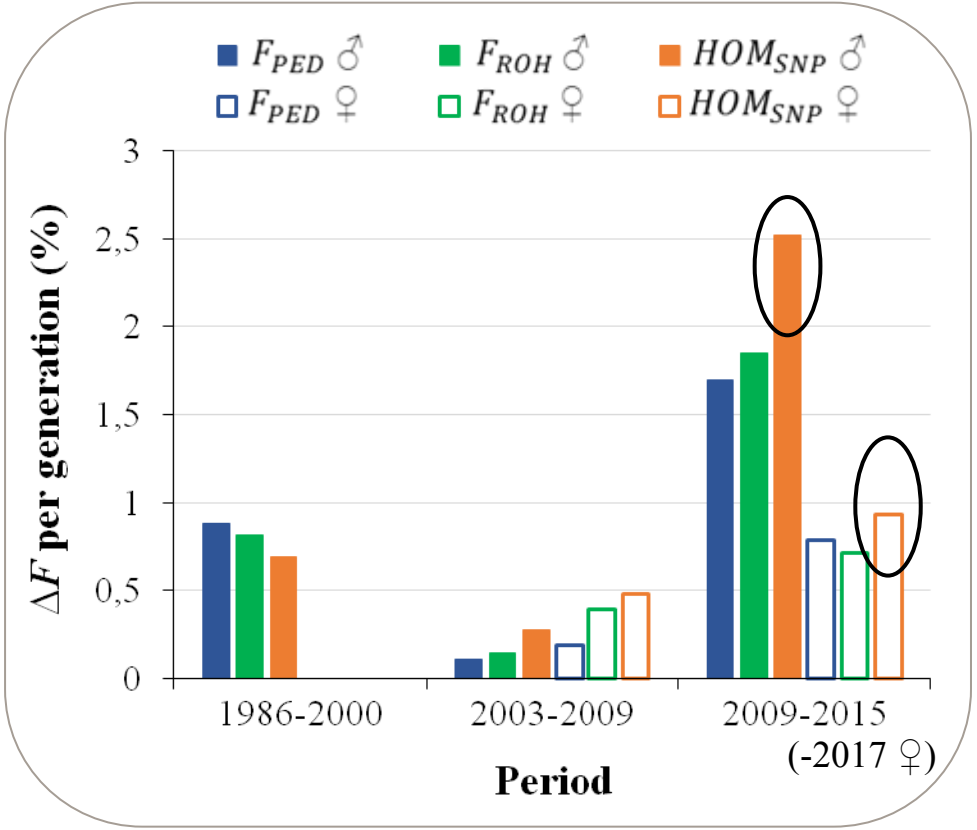


Results: rate of inbreeding (ΔF)



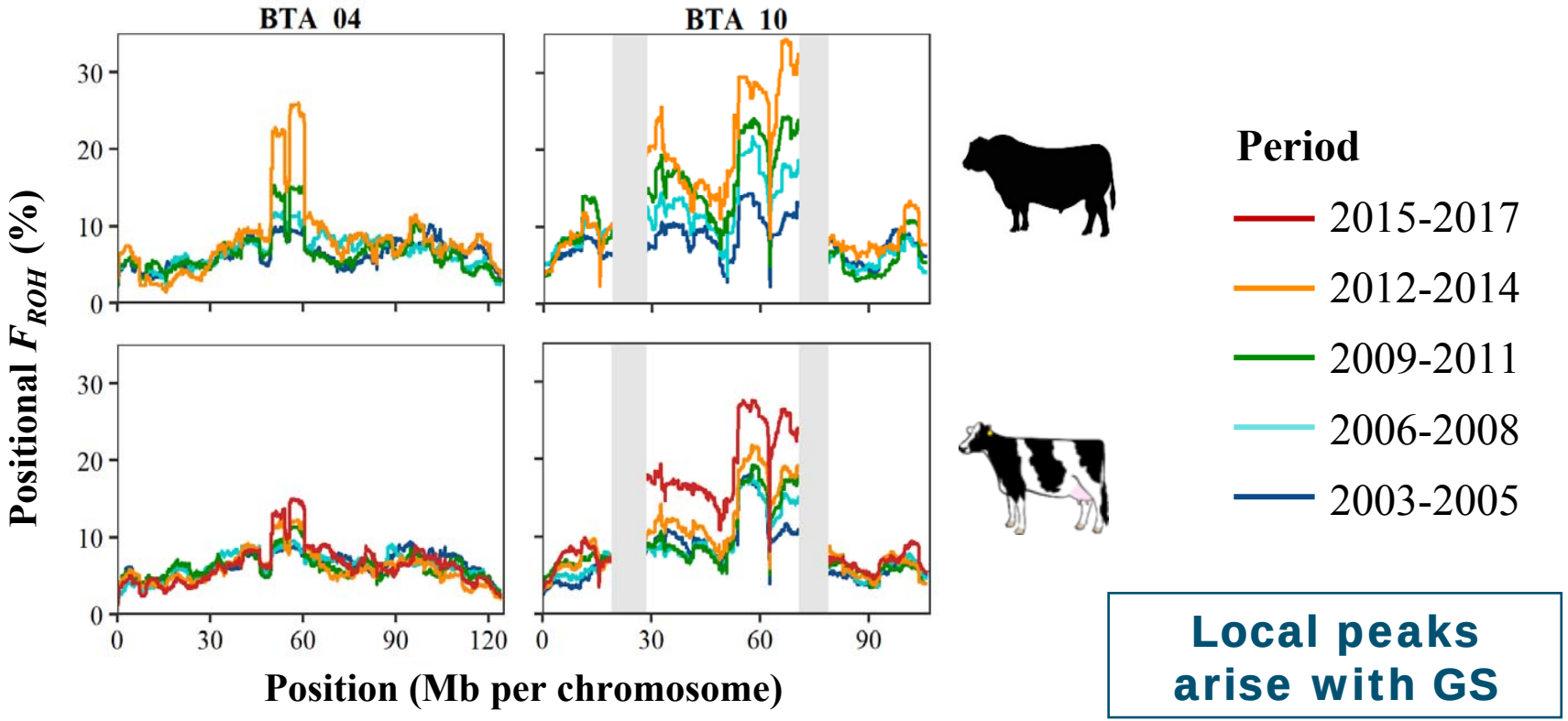
- Since 2009:
  - N_e = 20-30 for AI-bulls
  - N_e = 54-70 for cows

Results: rate of inbreeding (ΔF)



- Since 2009:
  - N_e = 20-30 for AI-bulls
  - N_e = 54-70 for cows
  - $\Delta IBS > \Delta IBD$

Results: region-specific F_{ROH}



Local peaks arise with GS

Conclusions

- Genome-wide: GS accompanied by high ΔF
  - Per year & generation
  - Especially in AI-bulls
  - $\Delta IBS > \Delta IBD$

- Region-specific: heterogeneity in F and ΔF
  - Local peaks with GS

Thank you for your attention

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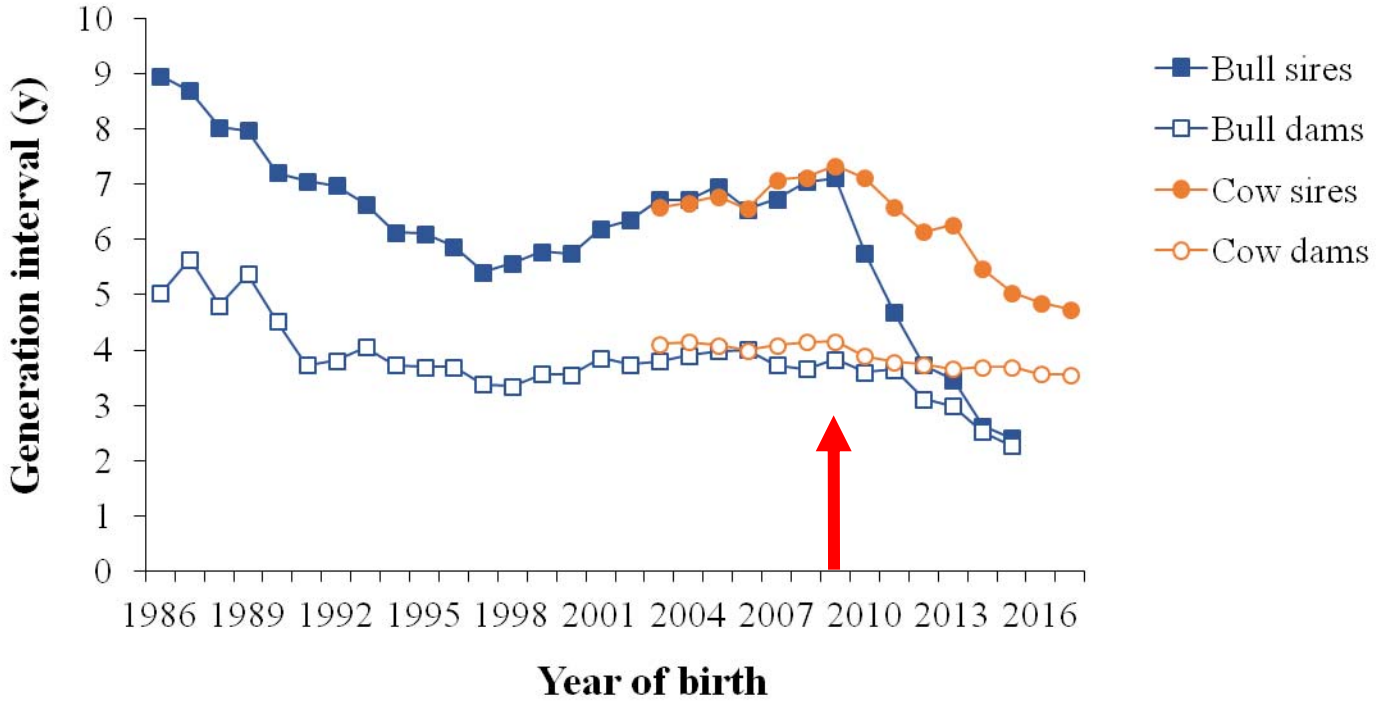
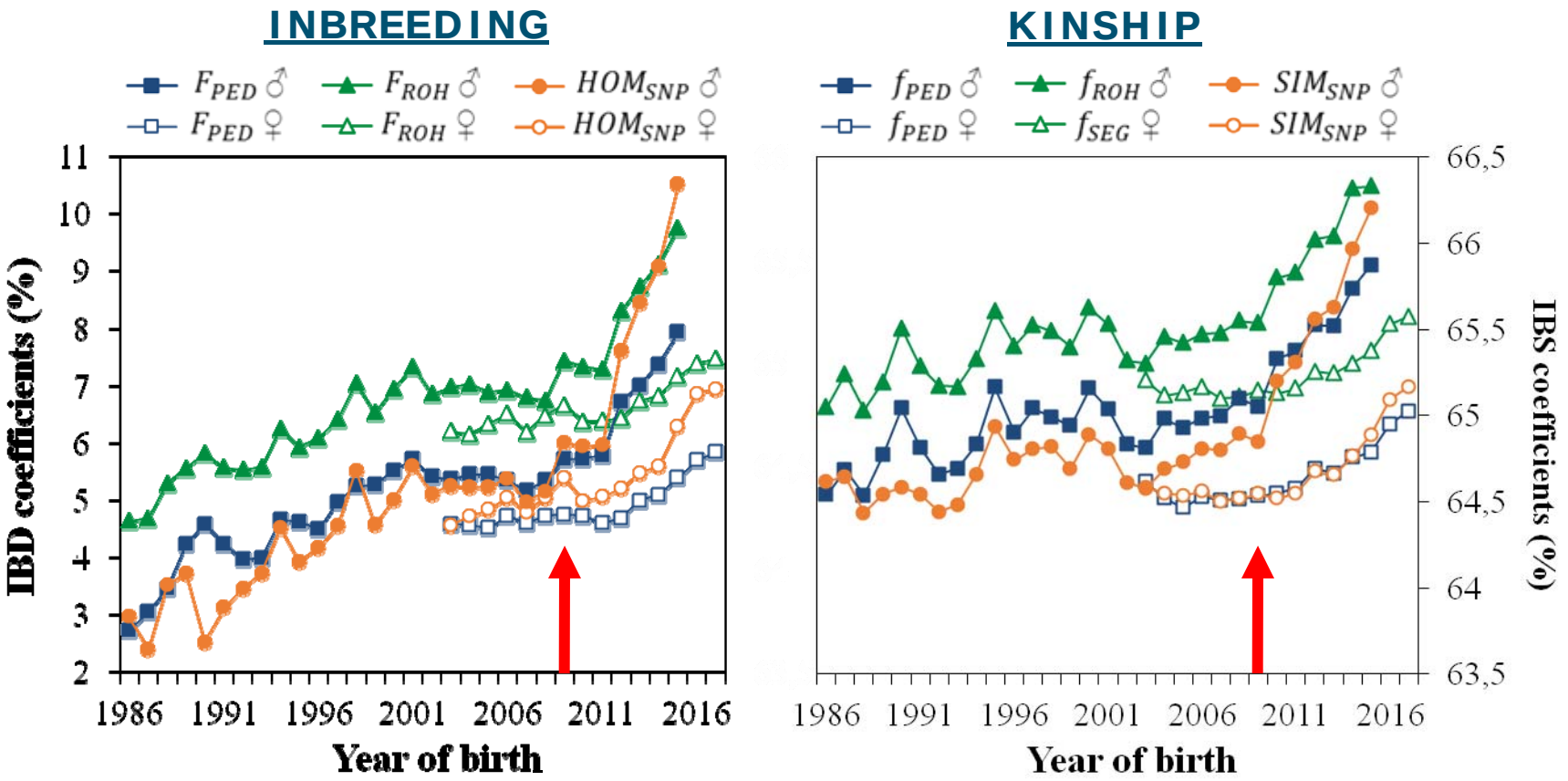
Material & methods: generation interval

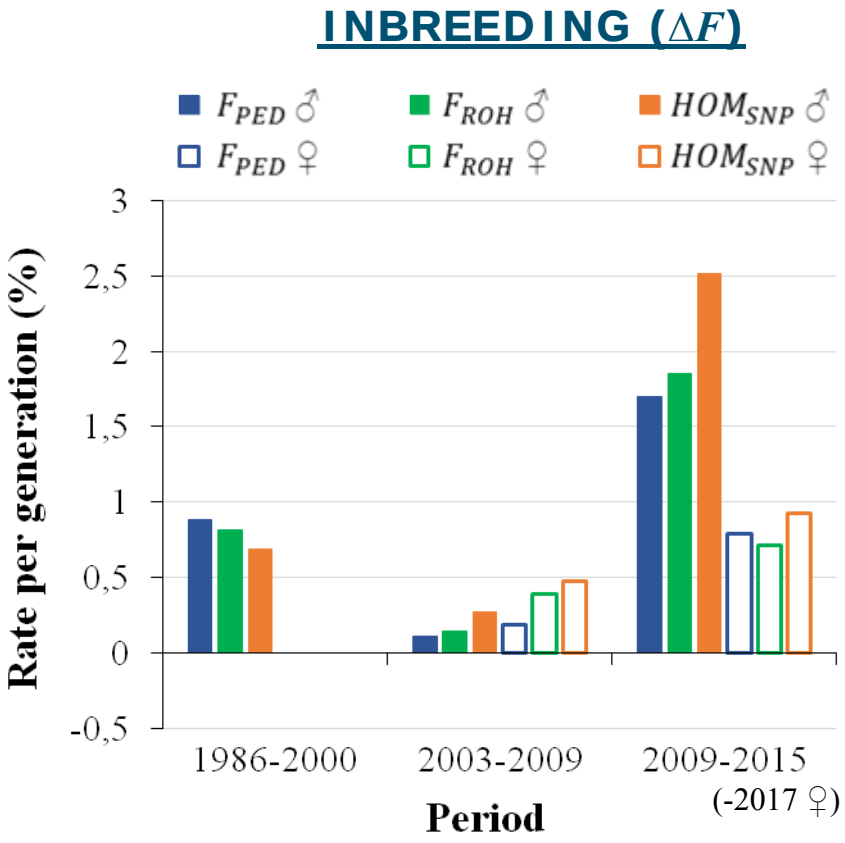
- Sharp decrease for AI-bull sires with GS

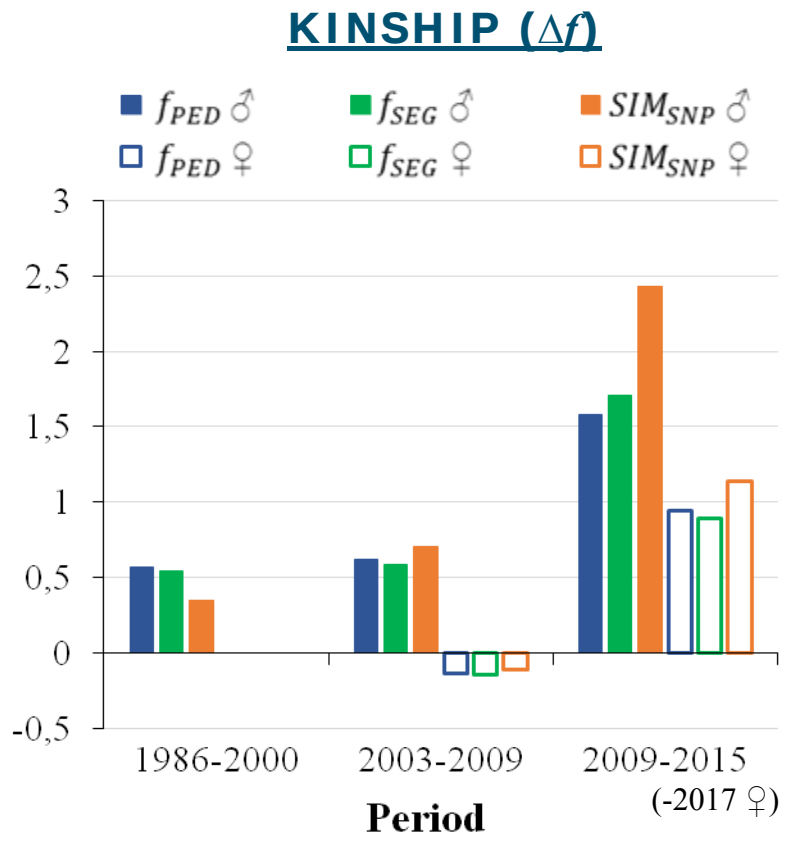


Results: genome-wide trends

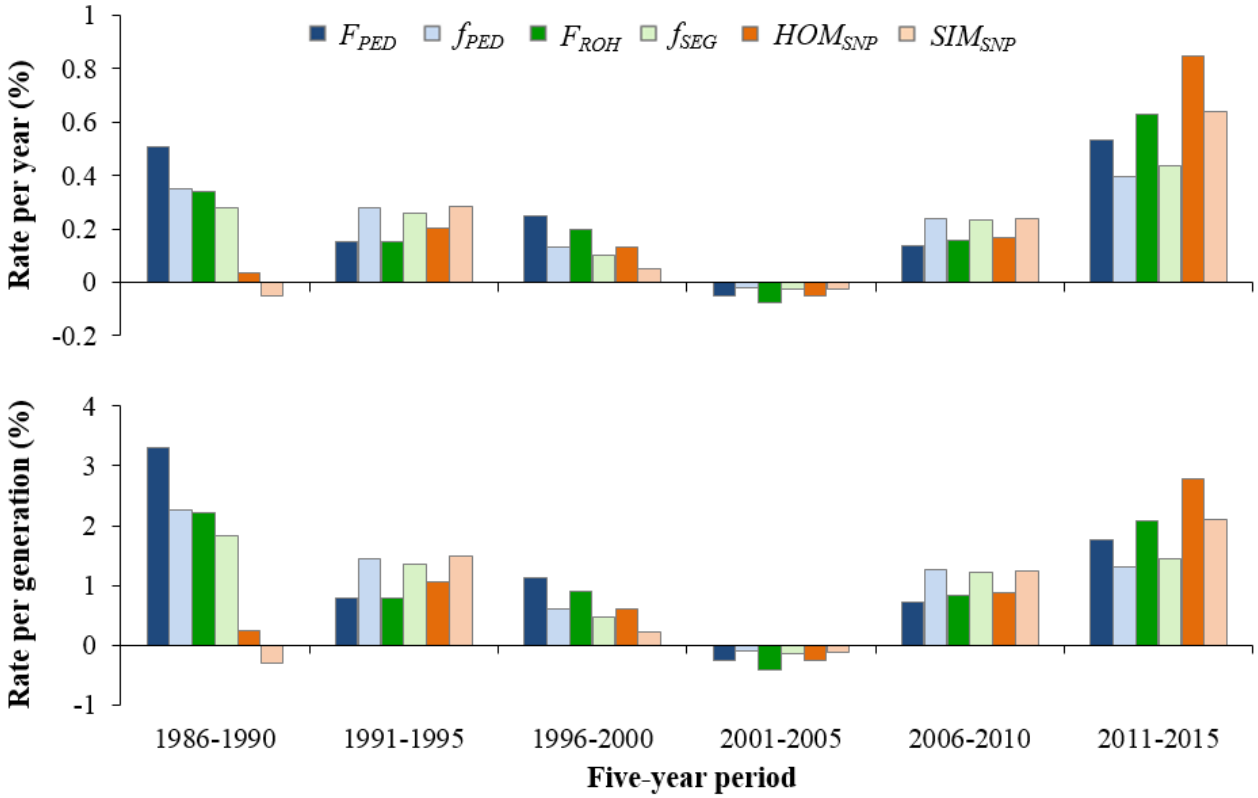
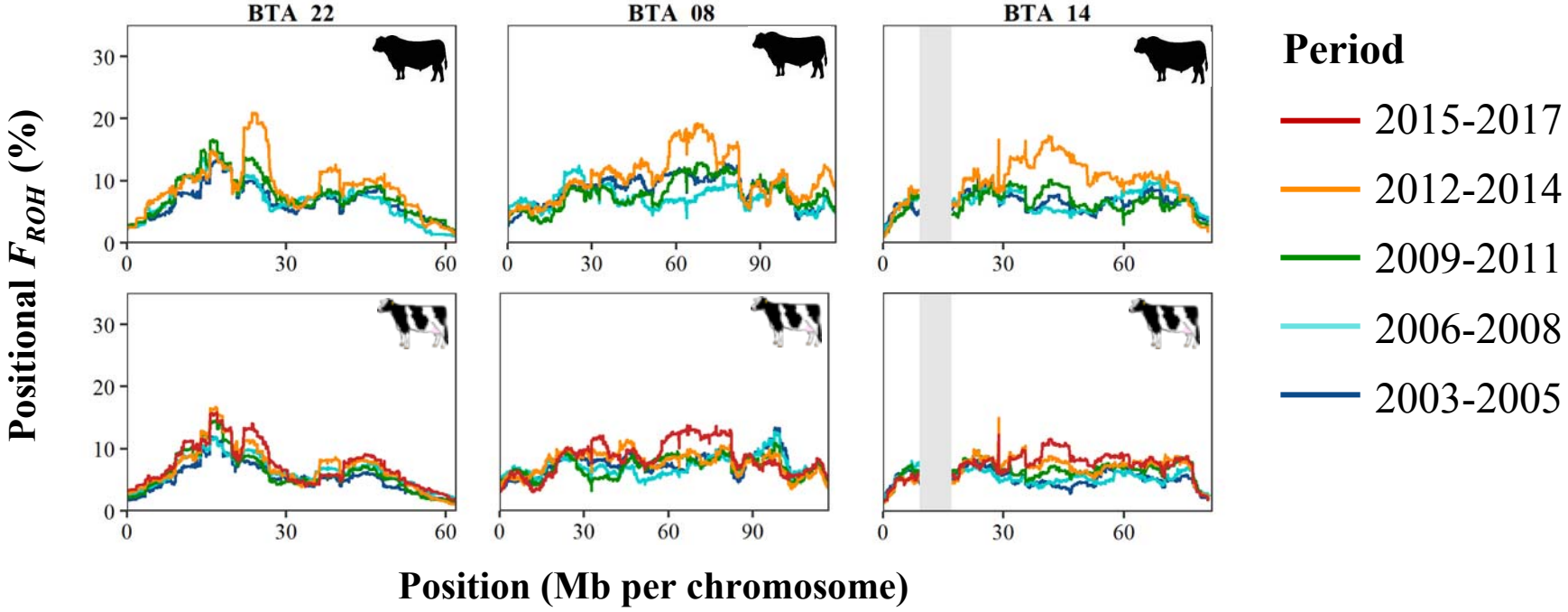


Results: rate of change





Rates of change per 5y AI-bulls



Results: region-specific F_{ROH}