Handling of inbreeding & semen sire breed in the Nordic Holstein fertility evaluations as part of EuroGenomics

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Holstein fertility evaluations

- NAV fertility models were updated in 2016 to meet requirements of genomic prediction and EuroGenomics consortium
- Multi-trait multi-lactation animal model (Muuttoranta et al., 2015;Tyrisevä et al., 2017)
- Traits in focus of current presentation:
- Interval as days from first to last service (IFL)
    - 9,032,686 females with records
- Conception rate as success, failure or probability (CR)
    - 9,075,954 females with 42,502,561 repeated records

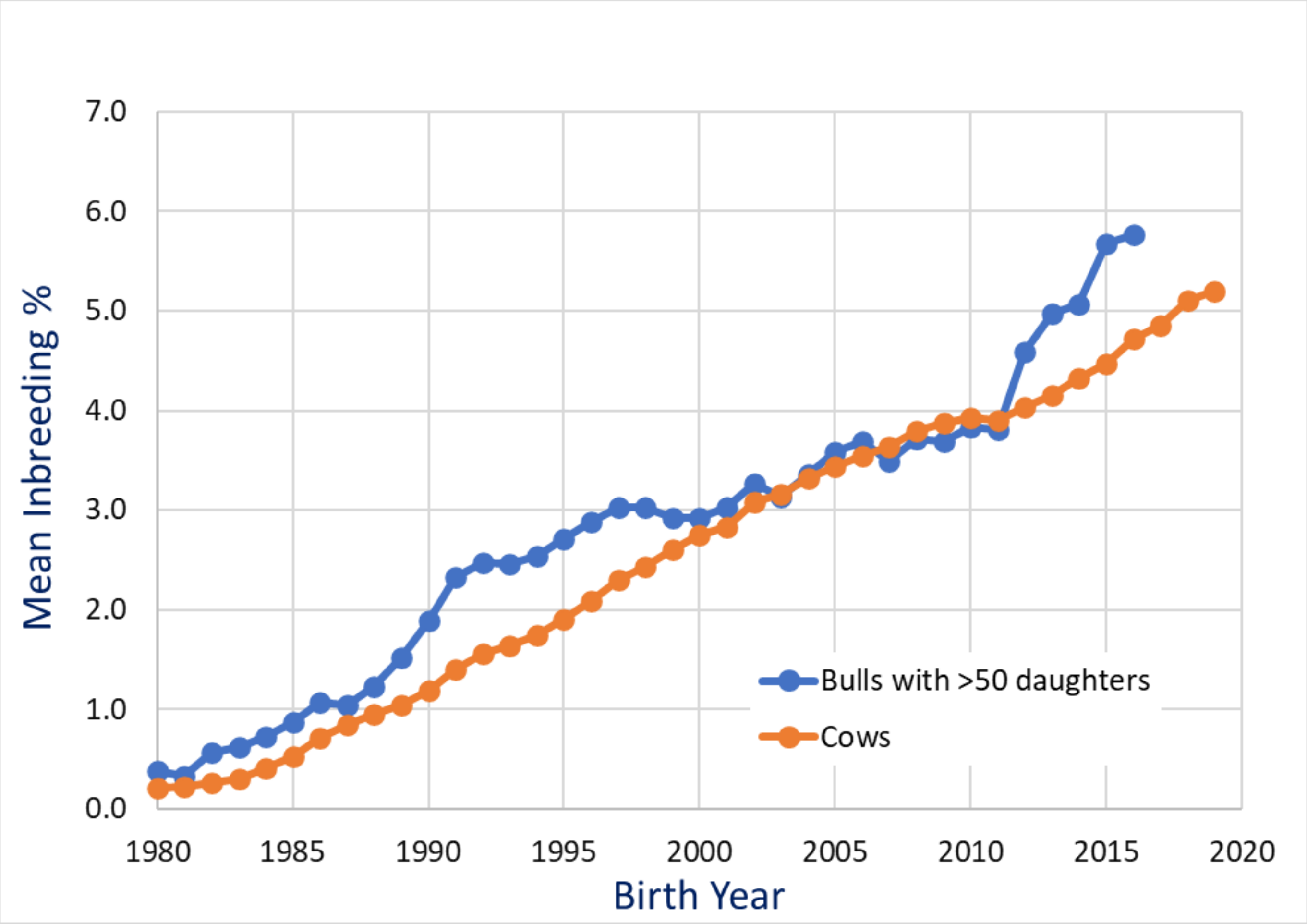
Handling of pedigree-based inbreeding in EuroGenomics fertility evaluations.

EG Harmonisation is the way to get more valuable information from foreign bulls.

- **Correction for inbreeding (INBR) in A^{-1}**
- **Linear regression on INBR**
- **Service sire breed as part of the conception rate (CR) genetic evaluation model**

Inbreeding level in HOL fertility pedigree

Mean inbreeding (%) by birth year in cows and AI-bulls

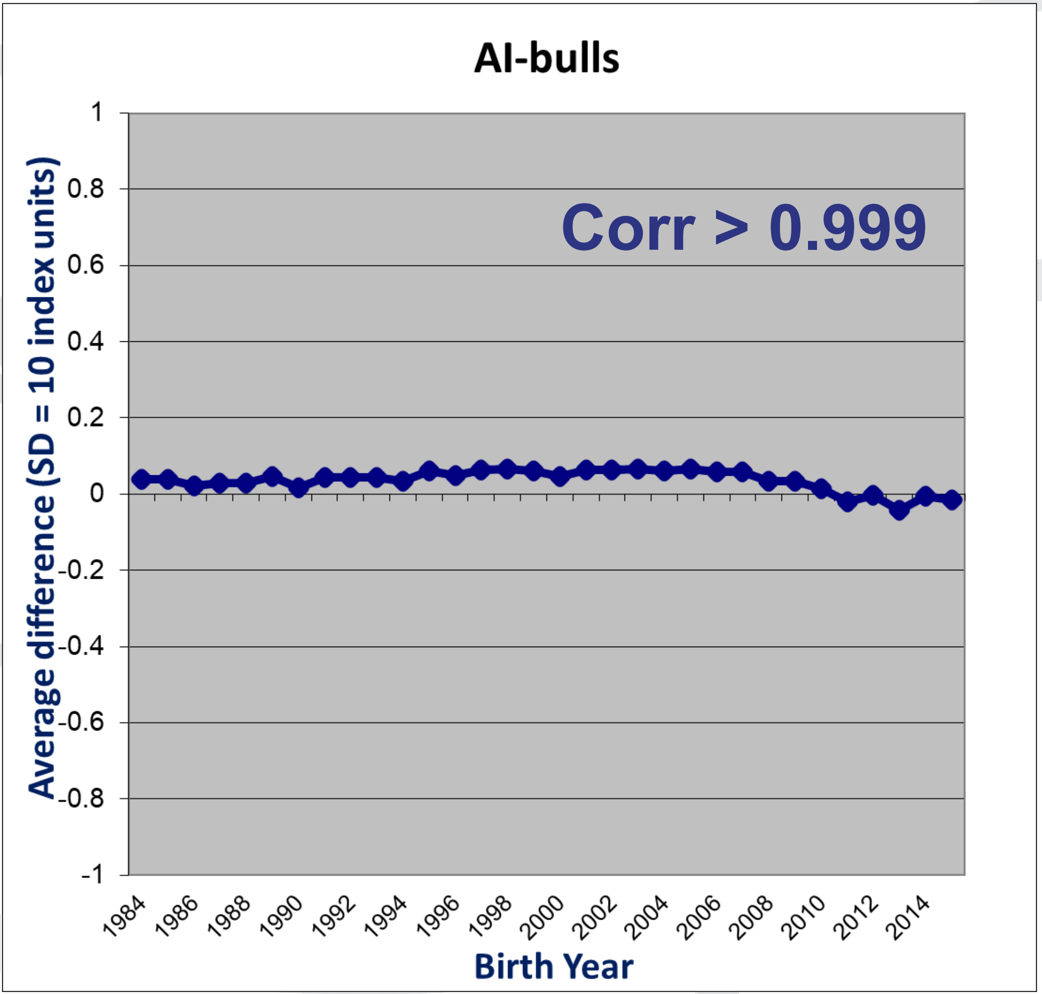


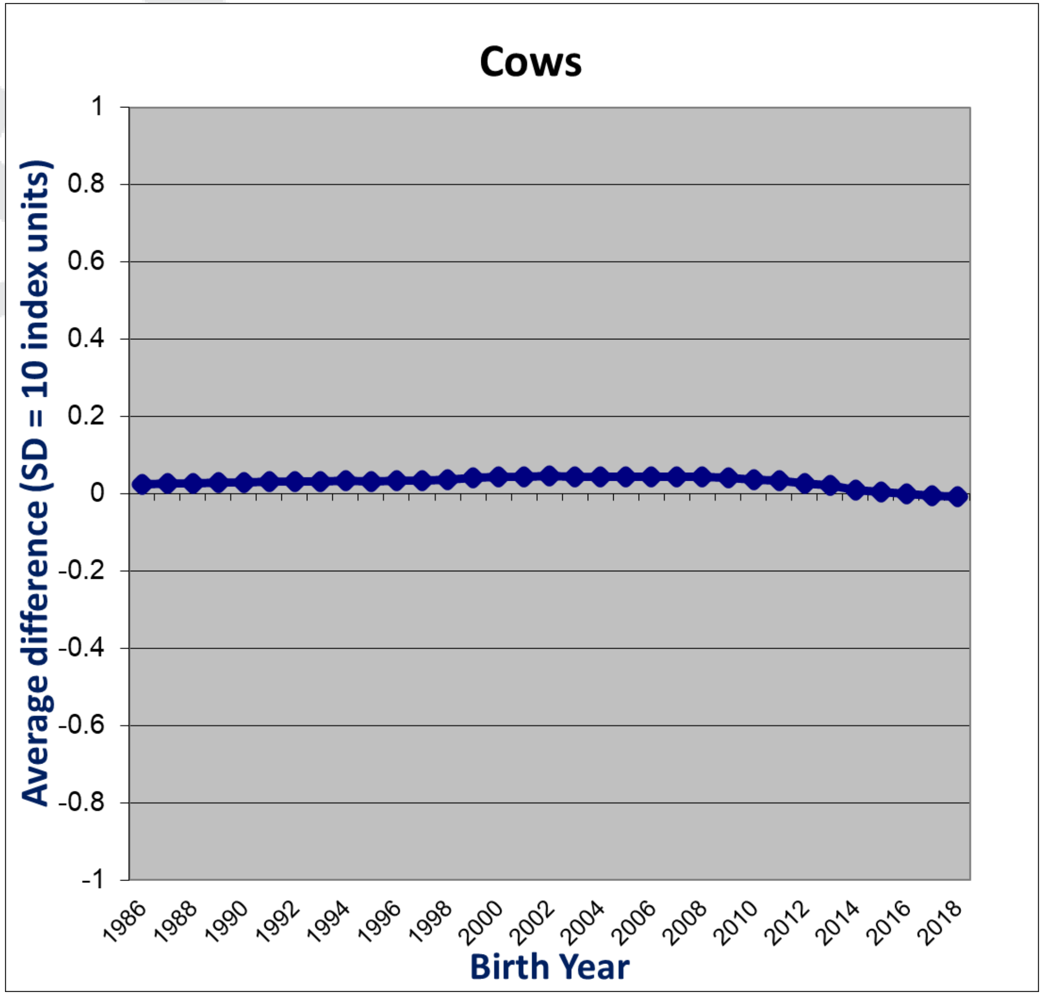
Correction for inbreeding in A^{-1}

- Individual INBR coefficients precomputed for 11,584,136 individuals by Meuwissen & Luo (1992) algorithm in Relax2 (Strandén & Vuori, 2006)
- INBR accounted in A^{-1} by MiX99 (Strandén & Lidauer, 1999)
- Inclusion was done for all fertility traits
- Results will be presented in IFL index

Average change in IFL index

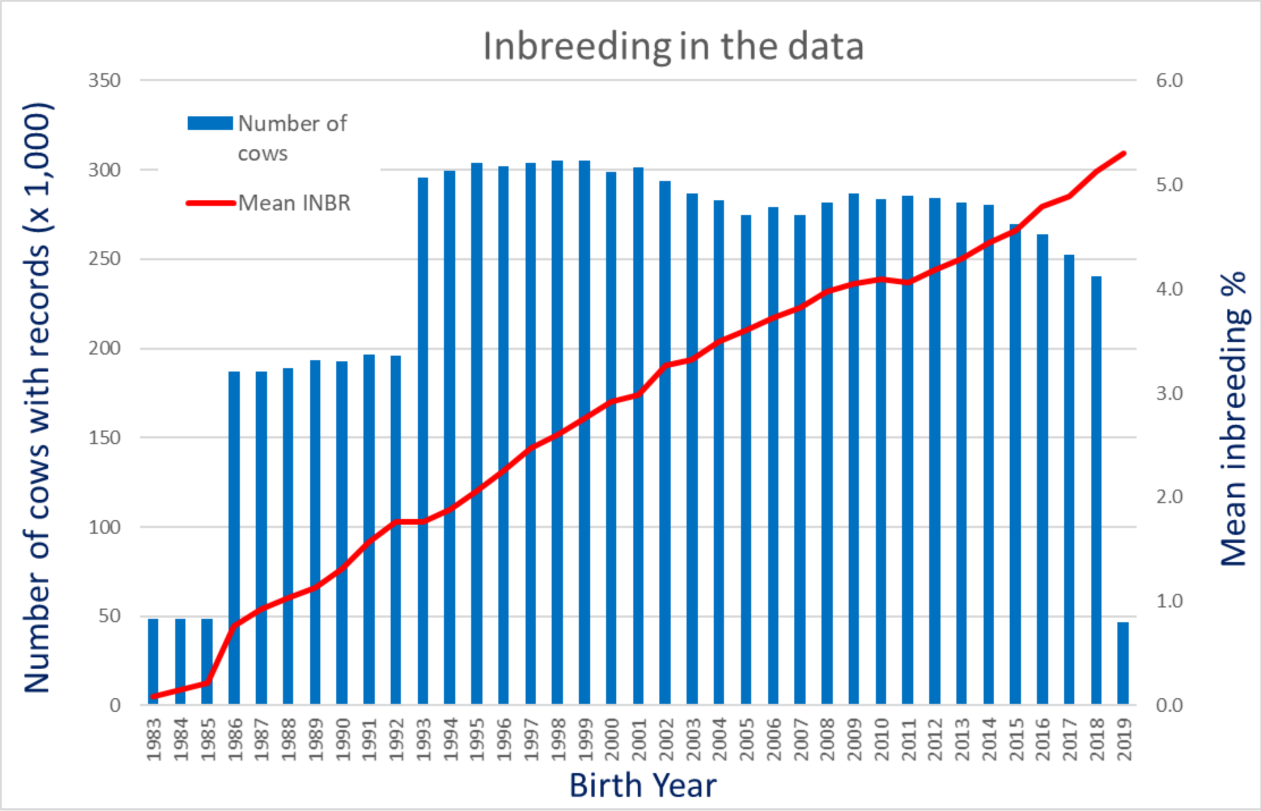
Change = INBR in A - Current model





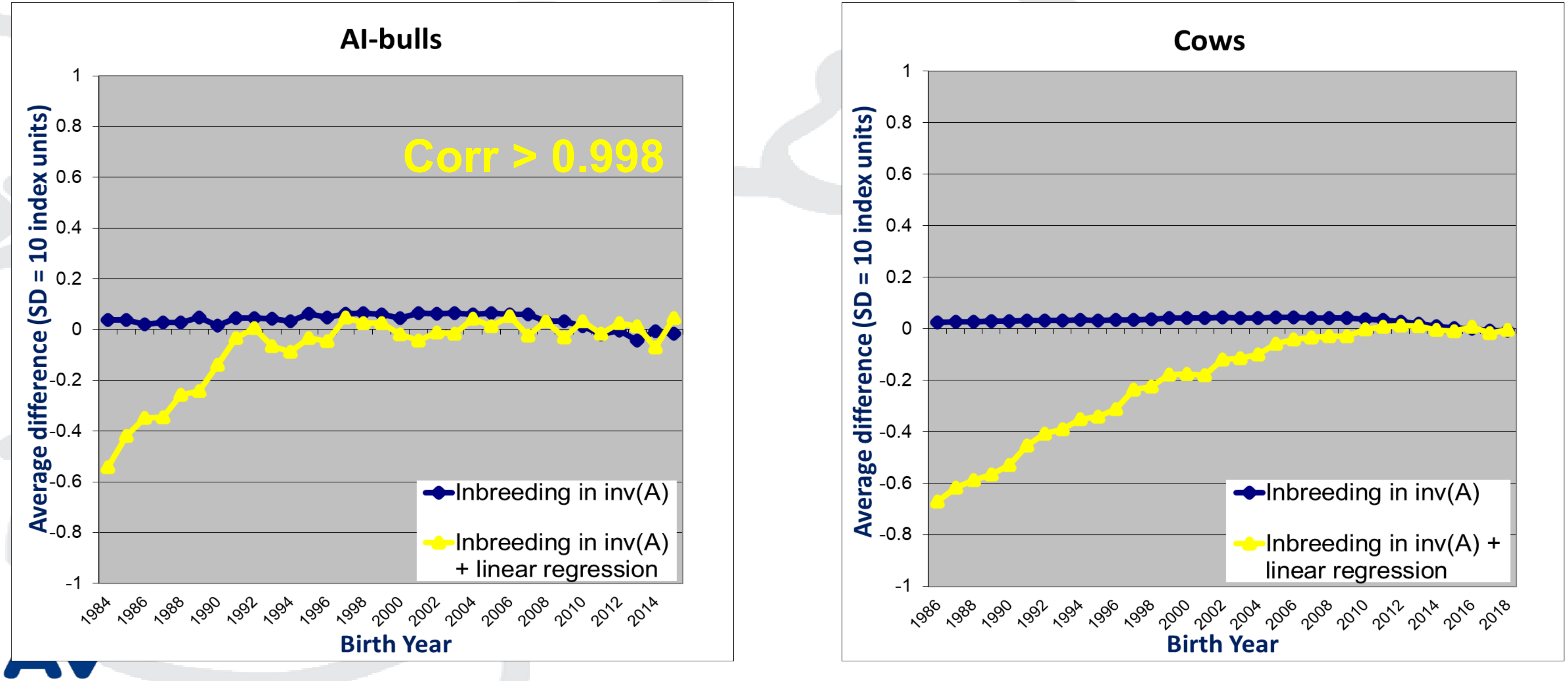
Linear regression on INBR
(inbreeding depression)

- **INBR was accounted for in the relationship matrix and by inclusion of a linear regression on INBR in the model**



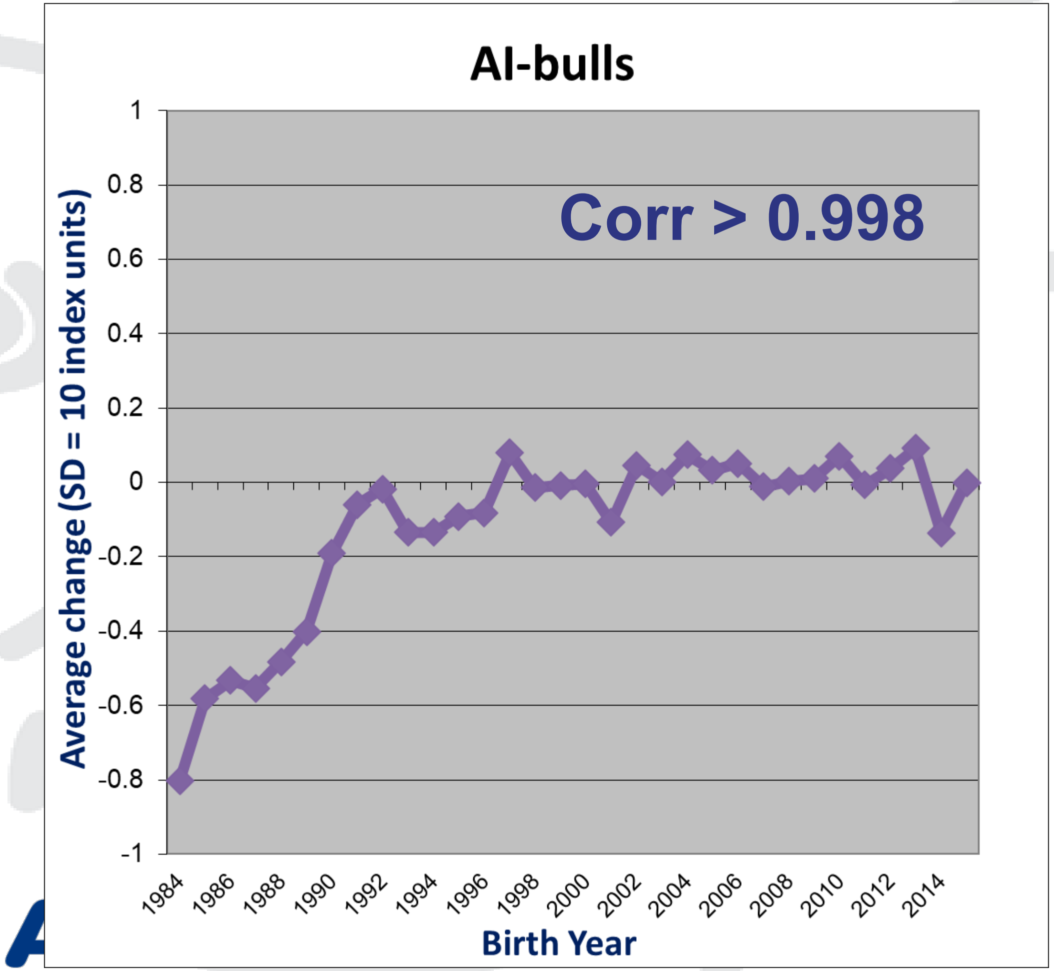
Average change in IFL index

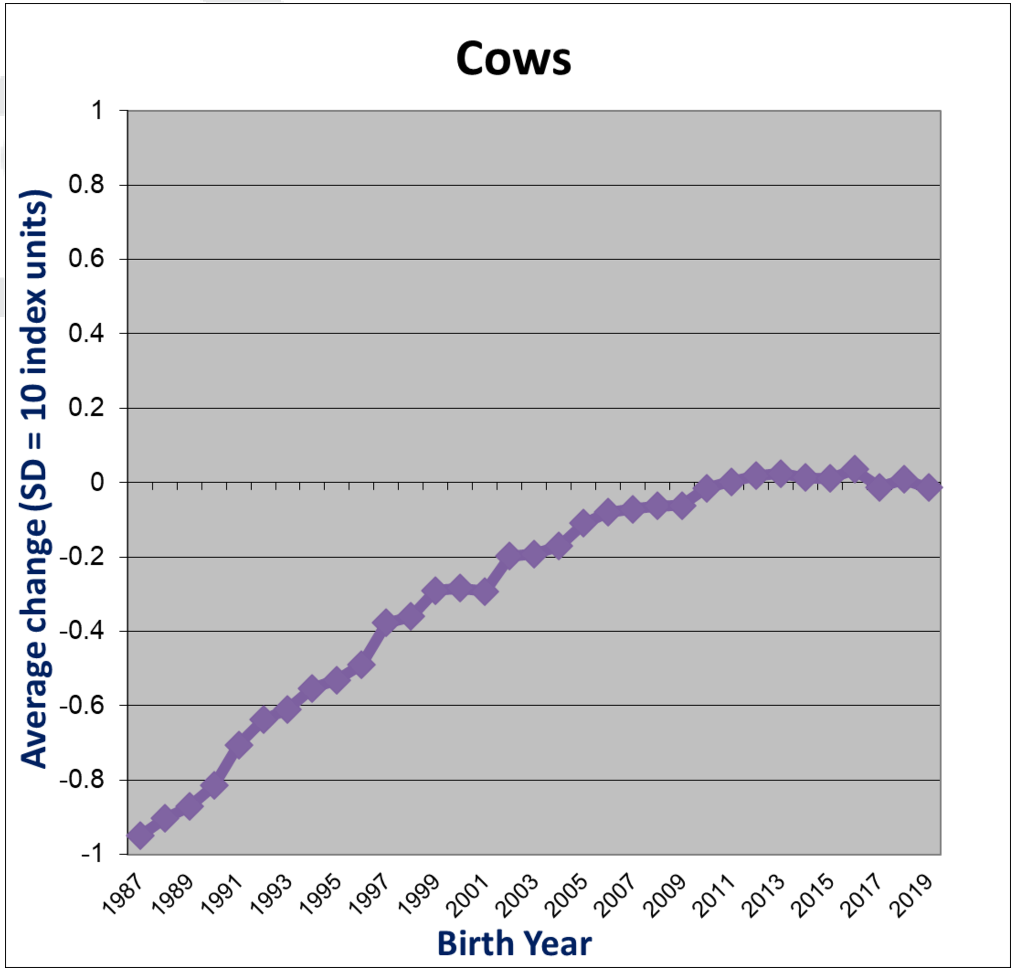
Change = INBR in A + linear regression model - Current model



Average change in CR index

Change = INBR in A + linear regression model - Current model





Regression coefficients solutions

1% of inbreeding cause corresponding:

decrease in probability of successful conception (for CR)

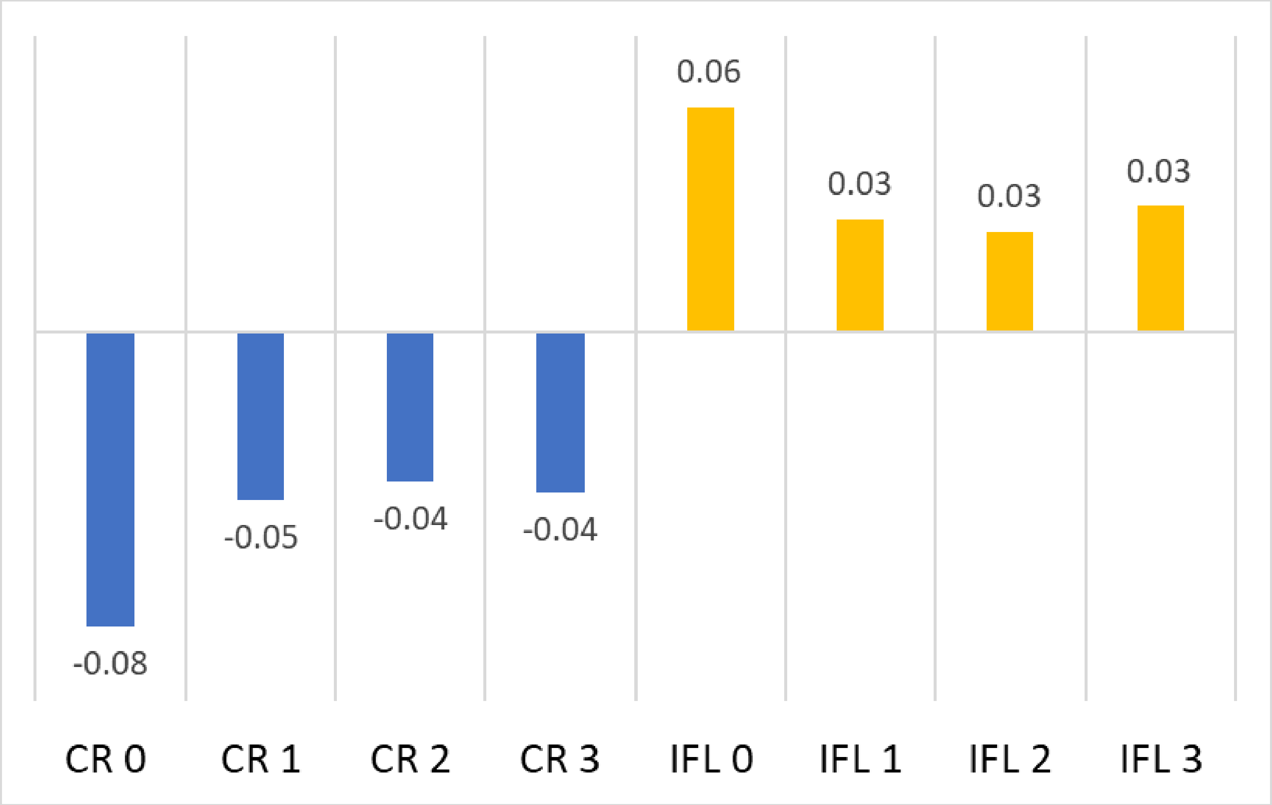
increase in days from first to last service (for IFL)

IFL SD Units**

$$\frac{\text{IFL INBR reg. coef.}}{\text{IFL SD}}$$

CR SD Units*

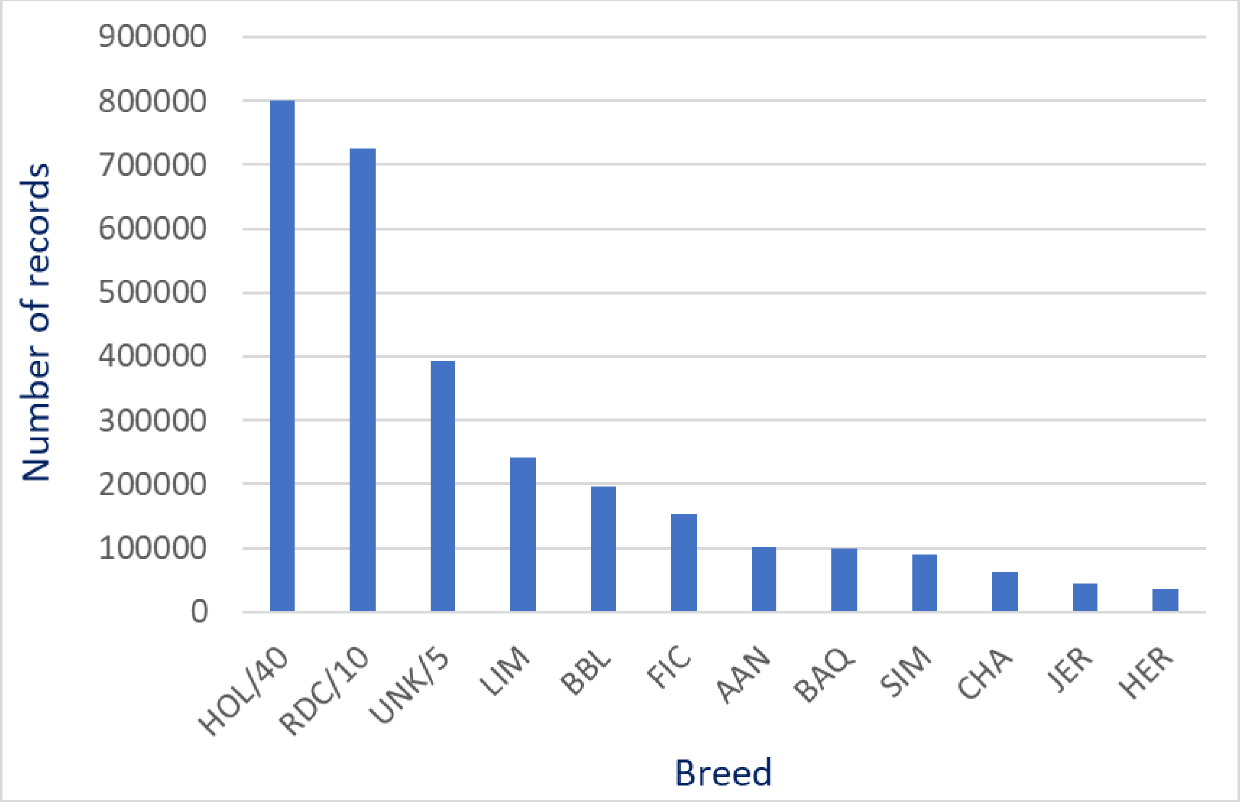
$$\frac{\text{CR INBR reg. coef.}}{\text{CR SD}}$$



0 = heifers; 1-3 = cows

Breed of service sire in the conception rate genetic evaluation model

- 1,961,392 out of 46,234,248 records had no information about service sire (UNK)
- Service sire breed was included into CR model as fixed effect
- Most frequent breeds of service sire in the HOL CR records:

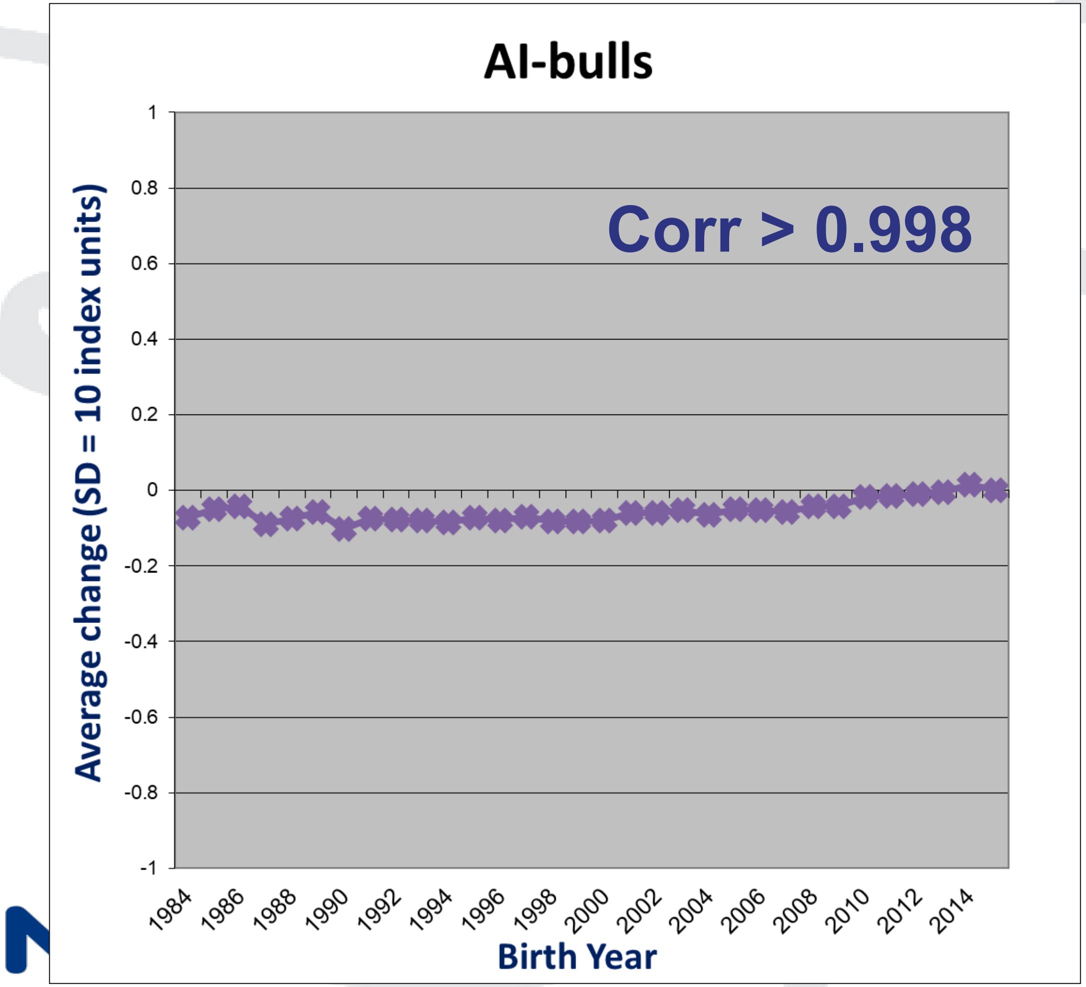


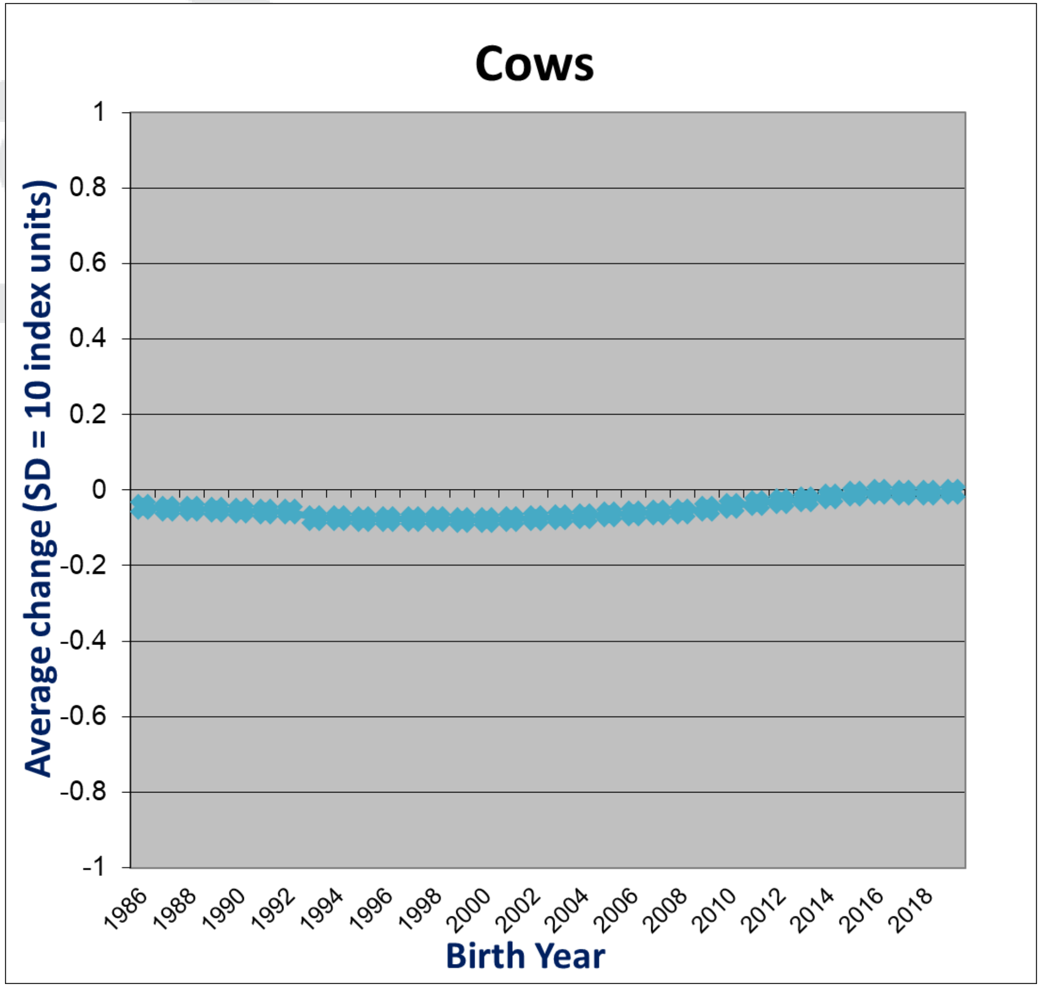
Breed of service sire effect

- Effect was grouped by 10-year intervals
- Service sire breed were derived from cow breed for records with UNK group.
  - 83% of UNK converted to HOL, 16% to RDC
- Modified CR model included: INBR accounted in the A^{-1}, linear regression on INBR, and fixed effect service sire breed

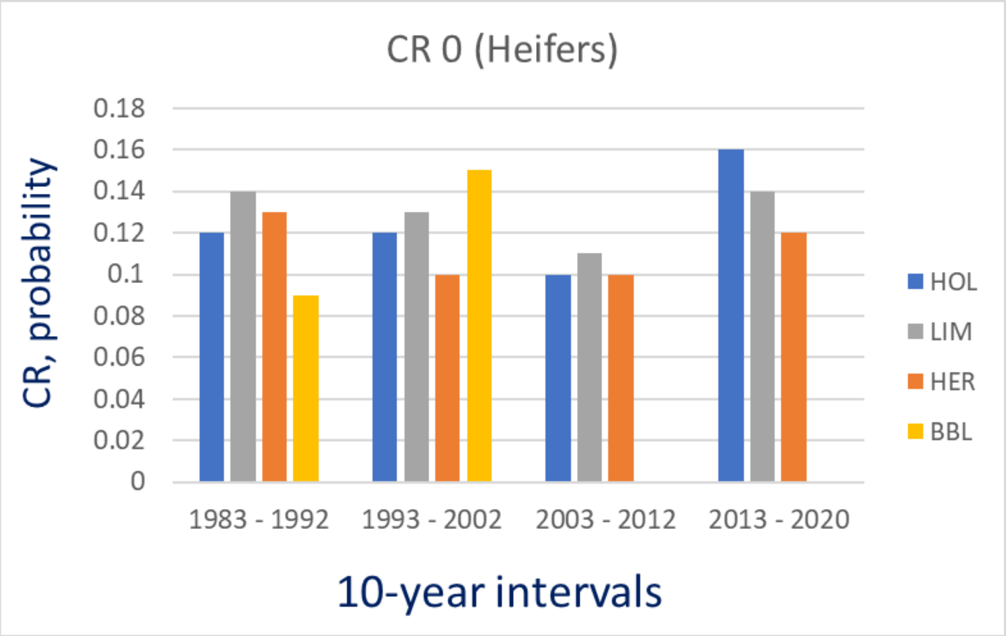
Average change in CR index

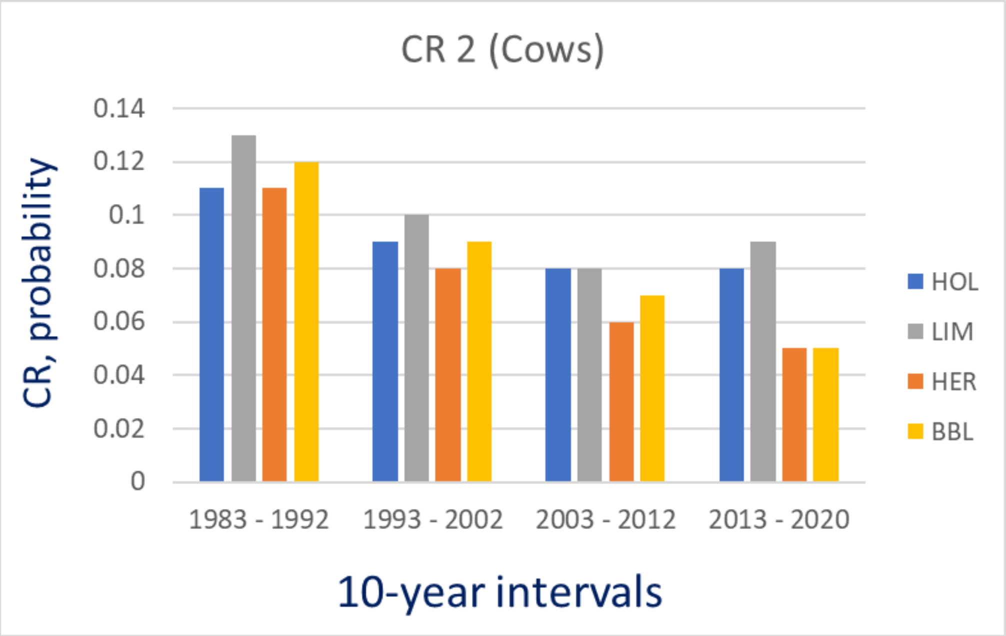
Change = CR INBR + insemination sire breed - CR INBR model





Solutions for service sire effects in CR





Take home message

- Effect of inclusion of inbreeding in A-matrix, inbreeding depression and service sire on EBV of sires was small
- Effect of service sire breed important as beef breeds today are used widely in dairy herds
- Results are important for consideration in EuroGenomic harmonisation and moving towards single-step genomic predictions

Thank you!