Changes in genetic trends for dairy cattle in the U.S. since the implementation of genomic selection

World Congress on Genetics Applied to Livestock Production
Rotterdam NL – July 6th, 2022

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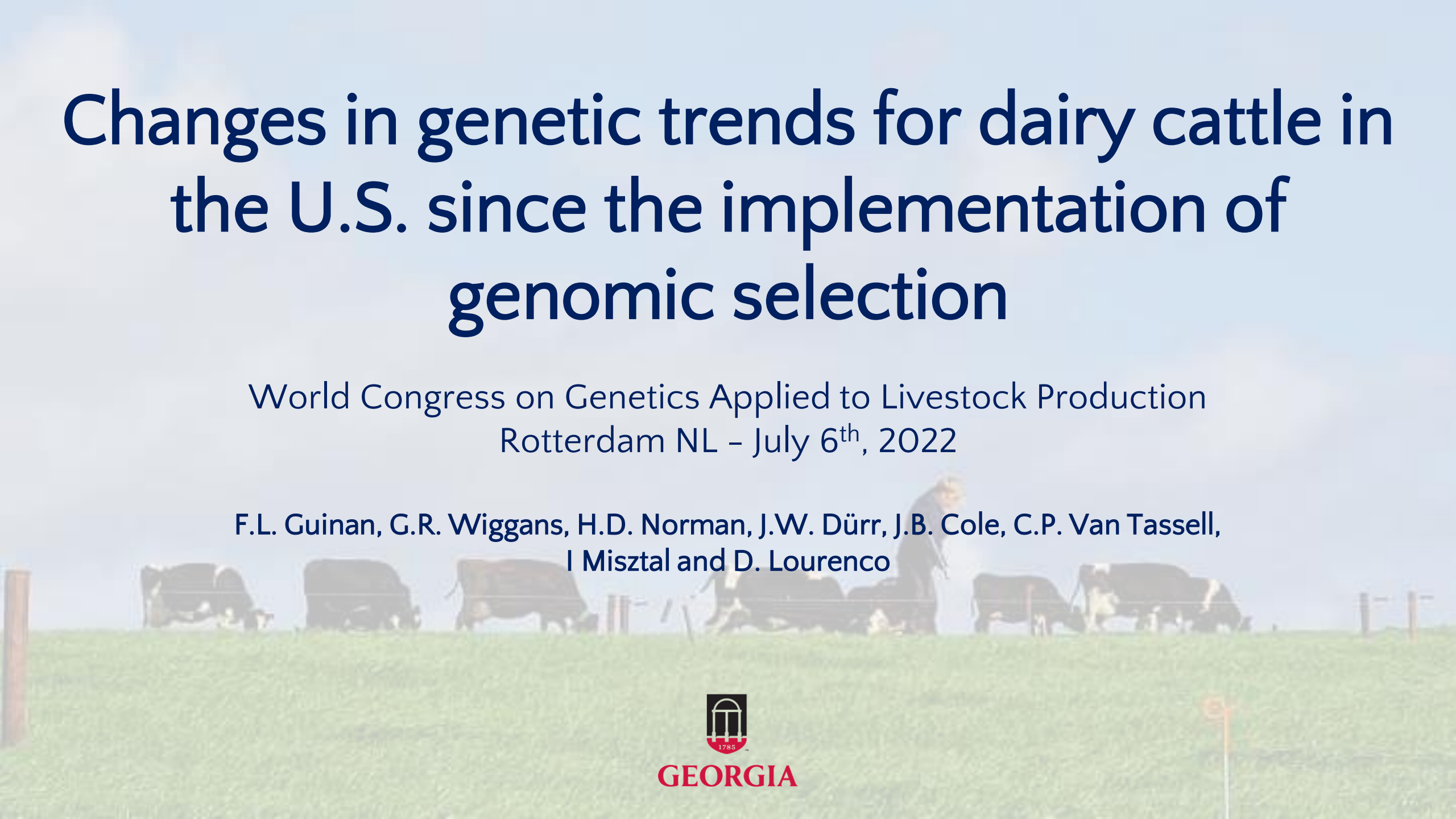

GEORGIA

U.S. Genomic Evaluations

Holstein
Jersey
Brown Swiss

2009

2013

Ayrshire

Guernsey

2016

Motivation

- Official genomic evaluations in US
  - 2009: Holstein, Jersey, Brown Swiss
  - 2013: Ayrshire
  - 2016: Guernsey

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- Increase genetic gain
  - Reliabilities
  - Generation interval

PNAS

Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection

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PNAS | Published online June 27, 2016 | E3995–E4004

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- 50 – 100% for yield traits
- 3 – 4x for low h^2 traits
  - DPR, PL, SCS

Is GS working as expected in *all* breeds?

Data

- August 2021 evaluation run
  - Milk, *fat*, protein, SCS
  - *Productive life*, daughter pregnancy rate, livability
- Based on evaluation breed code (within breed)
- Birth year since 1975
- Official genetic base year 2015
- USA, 840, and CAN only

Bulls – 154,008

USA: 89.60%

840: 2.84%

CAN: 7.56%

Cows –33,022,242

USA: 85.08%

840: 14.85%

CAN: 0.07%

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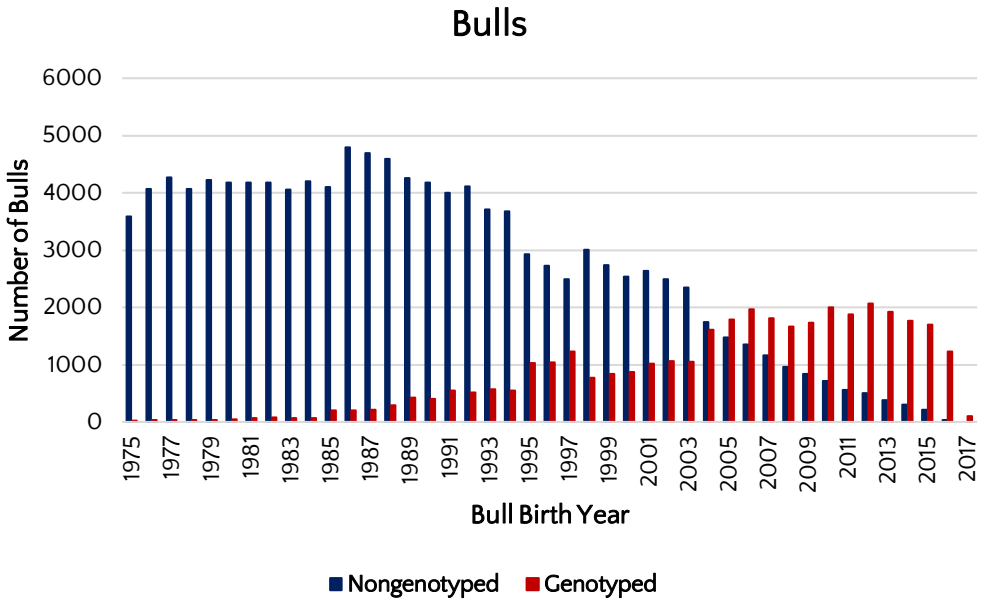
Bulls

- >= 10 daughters with milk records
- If PTA milk missing, then delete
- PBV weighted by no. of daughters per trait

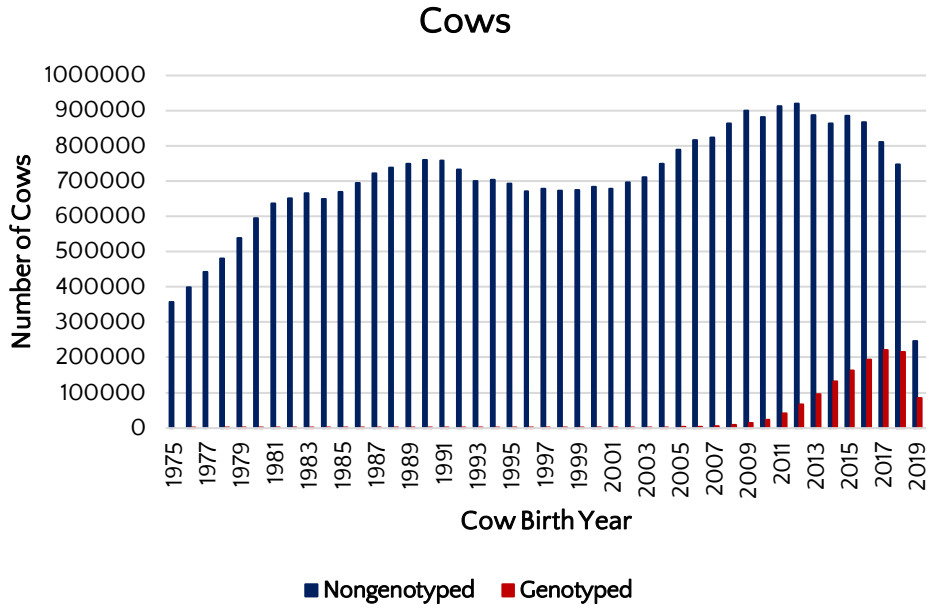
Breed Evaluation	Number	Genotyped (%)
AY	2,104	37.6
BS	2,791	41.8
GU	2,657	14.6
HO	133,995	22
JE	12,461	38.7
Total	154,008	23.8



Cows

- >= 1 calving
- If PTA milk missing, then delete
- Sire ID must be known
- Milk, fat, and protein must contribute to sire eval

Breed Evaluation	Number	Genotyped (%)
AY	138,989	0.42
BS	275,664	2.2
GU	282,295	0.77
HO	29,964,980	3.55
JE	2,360,315	8.63
Total	33,022,243	3.86



Trends

- No four-path selection model (Dechow & Rogers, 2018)
- Mean Predicted Breeding Value/Year plotted for bulls and cows separate
- Linear and nonlinear regression – to fit the small sample size
- PROC REG used to estimate breakpoints for each 5 years
- PROC NLIN to fit the piecewise model
- **Generation interval** for sire and dam of bulls and cows
- Parents and progeny same breed code
- (Animal birth – parents' birth)/365.25

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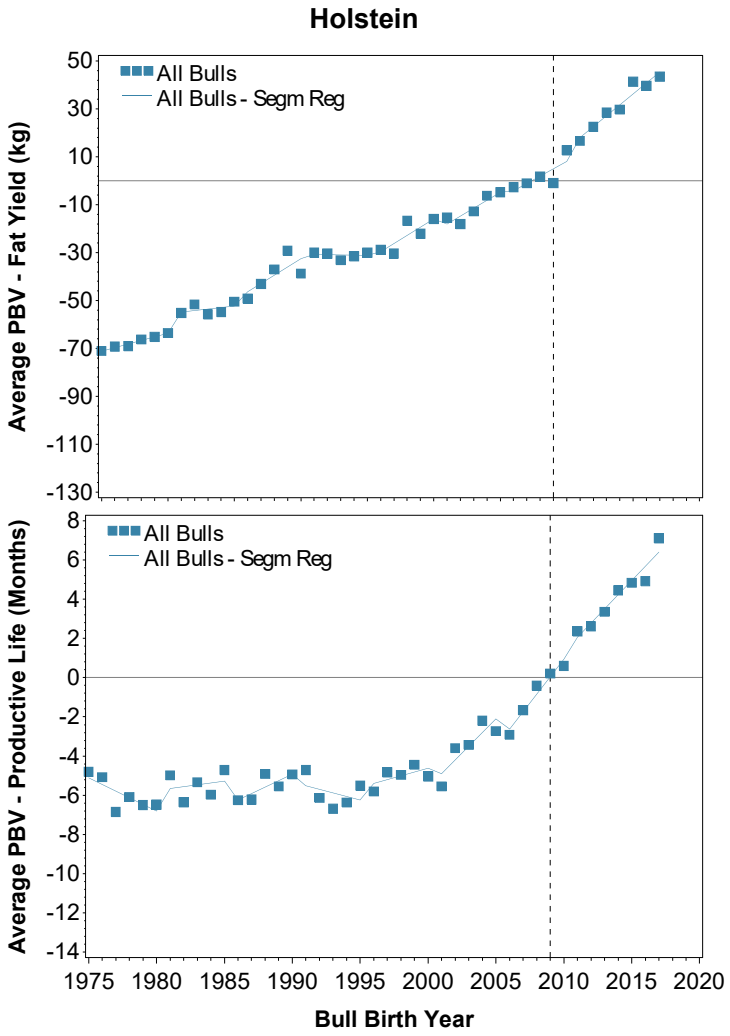
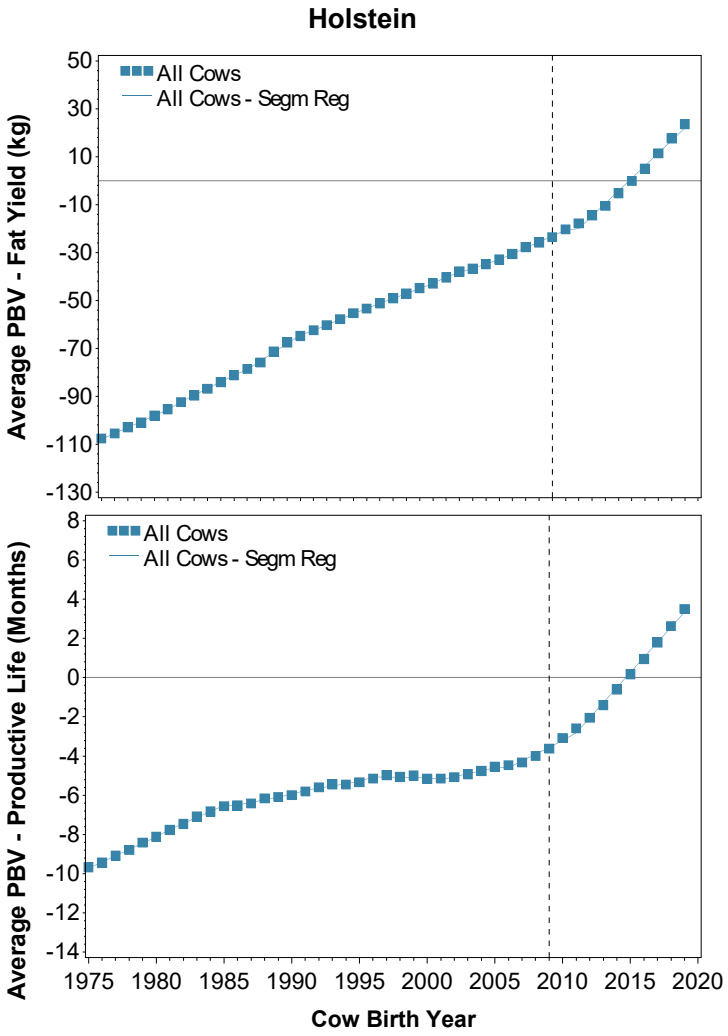
Genetic Trends – Holstein (2009)

Bulls

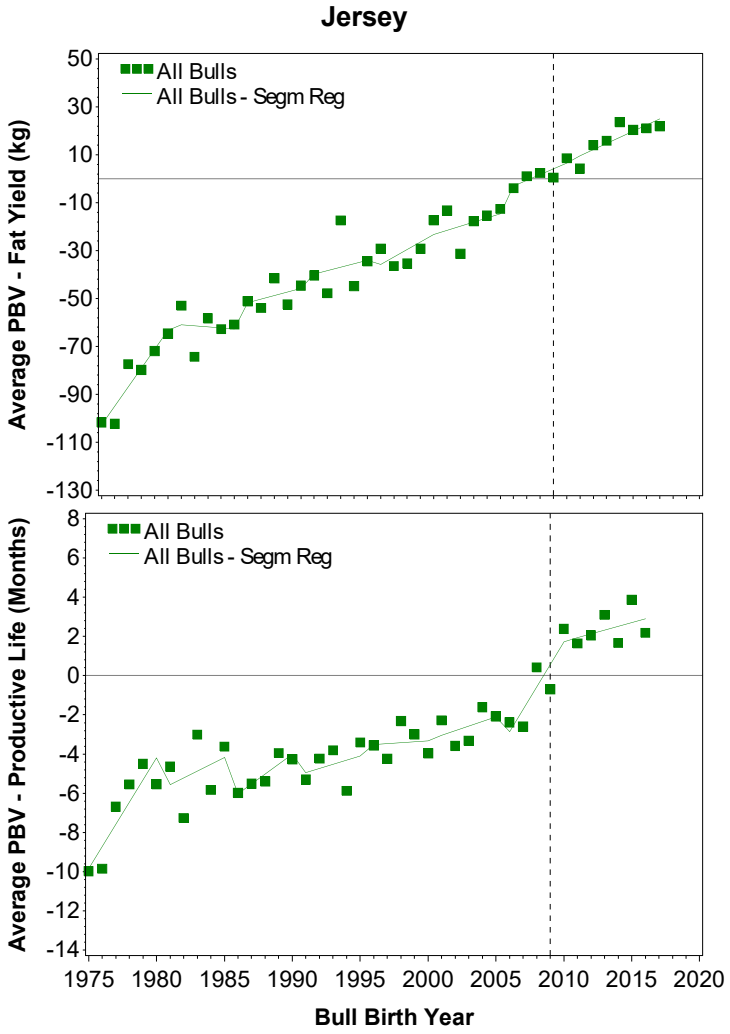


Cows

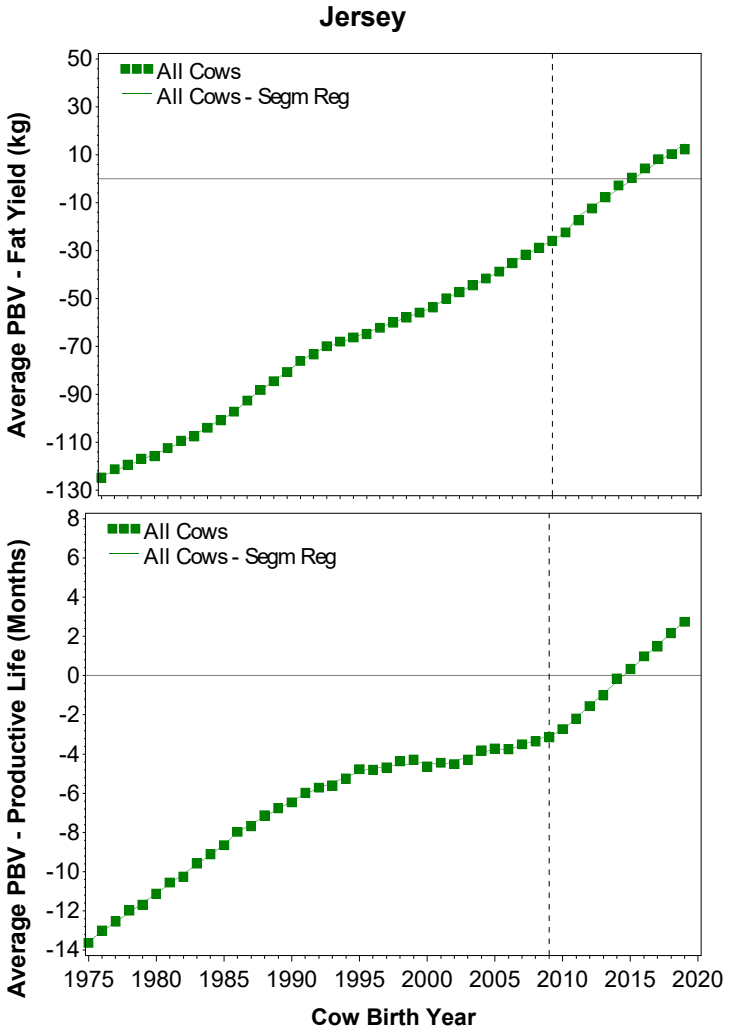


Genetic Trends – Jersey (2009)

Bulls

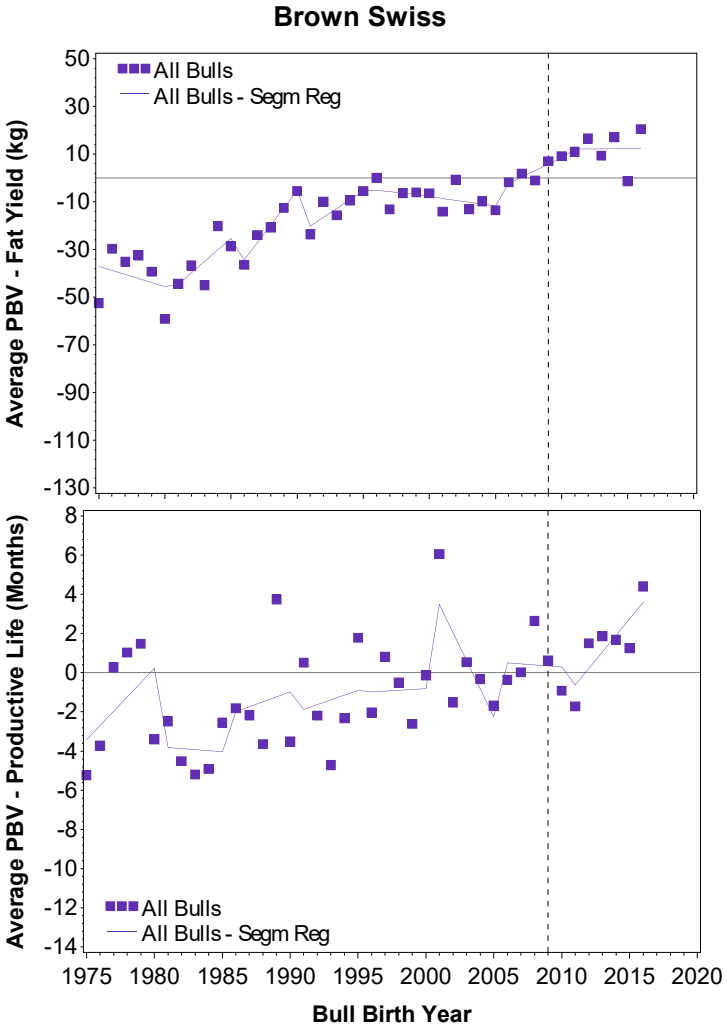


Cows

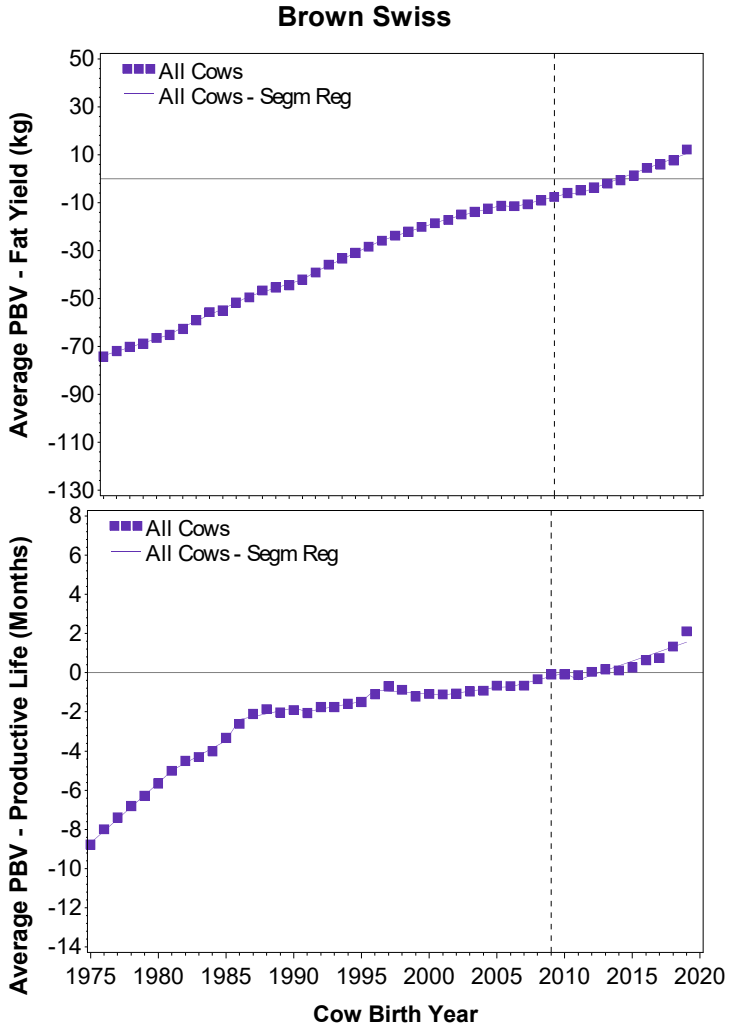


Genetic Trends – Brown Swiss (2009)

Bulls

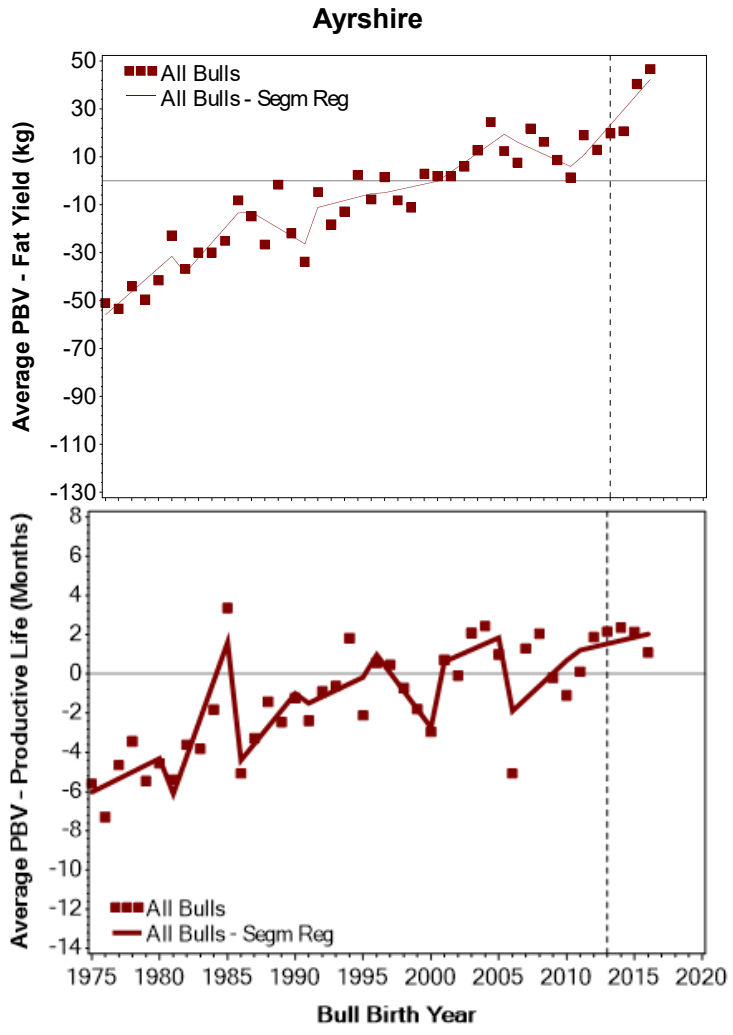


Cows

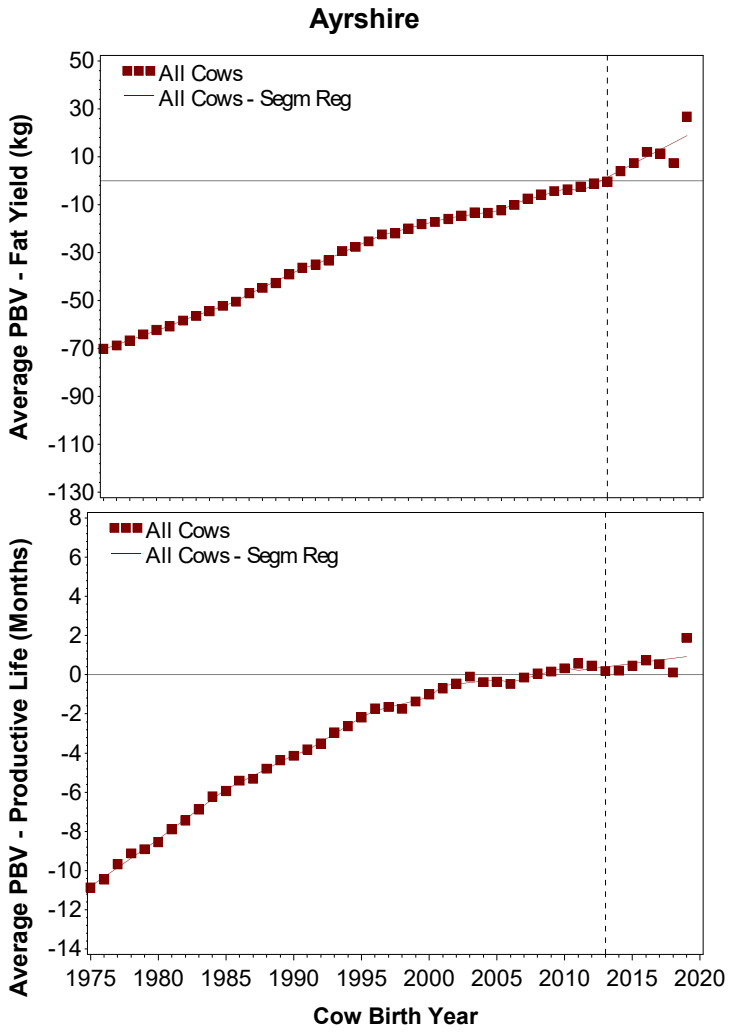


Genetic Trends – Ayrshire (2013)

Bulls

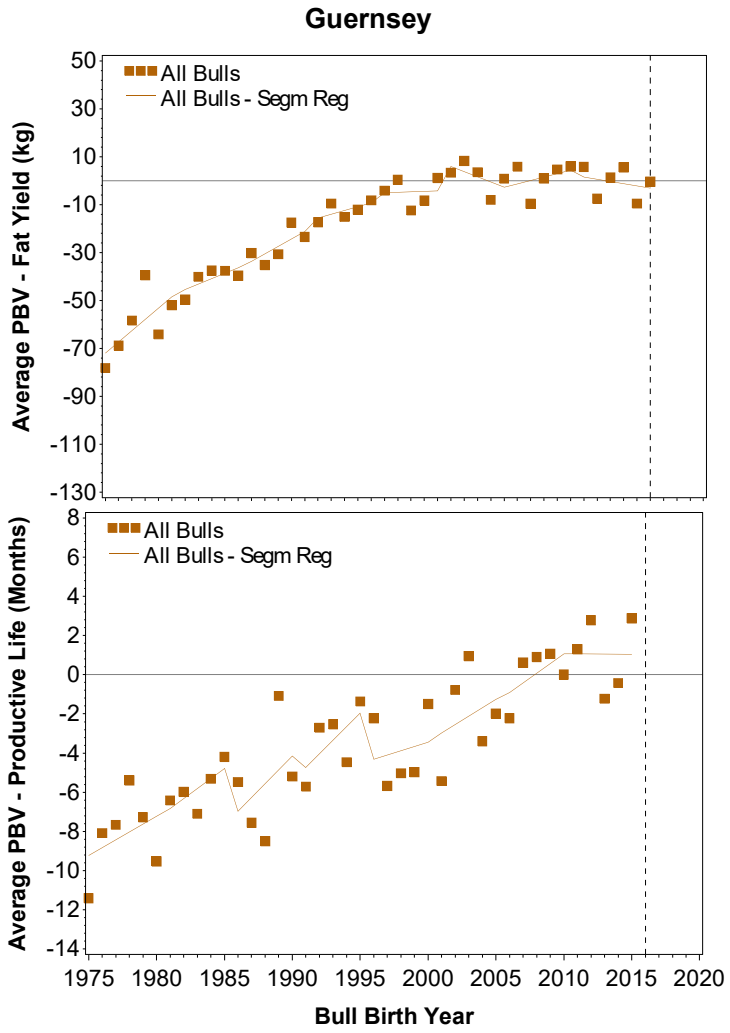


Cows

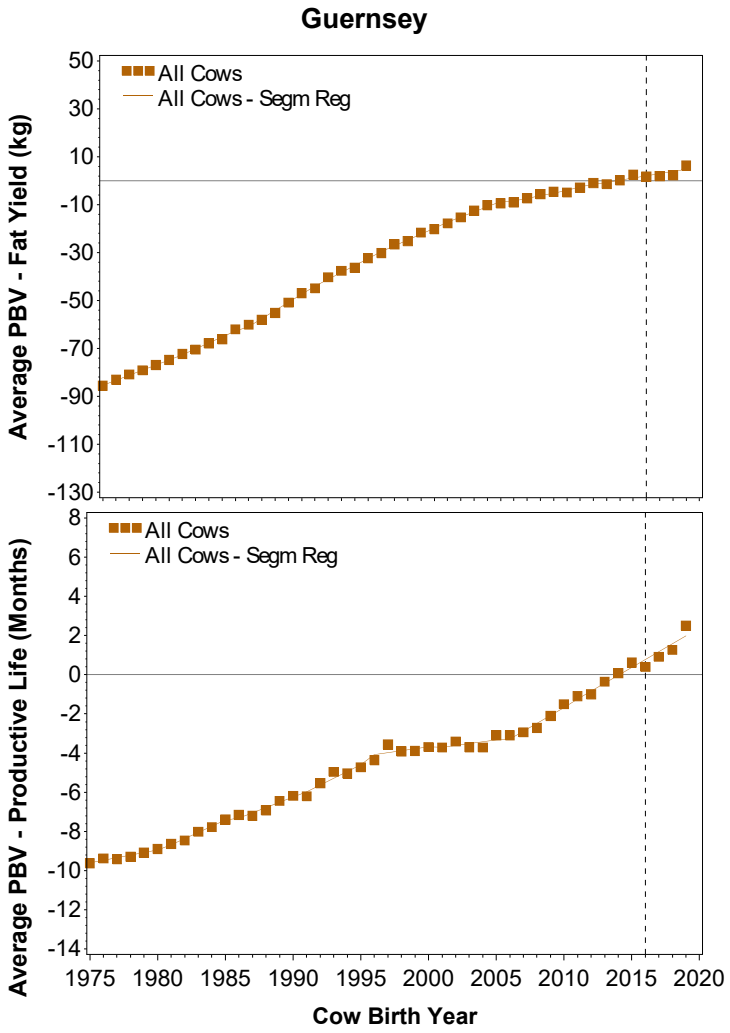


Genetic Trends –Guernsey (2016)

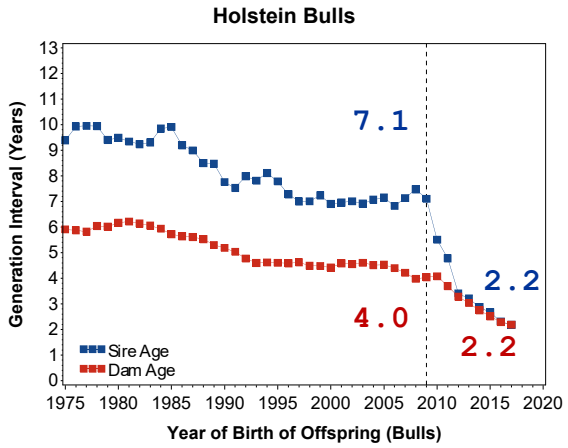
Bulls

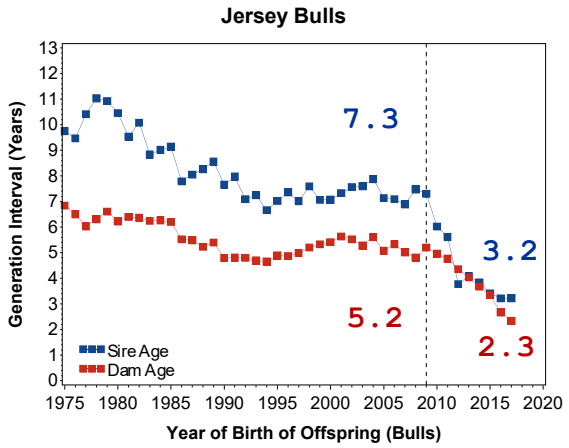


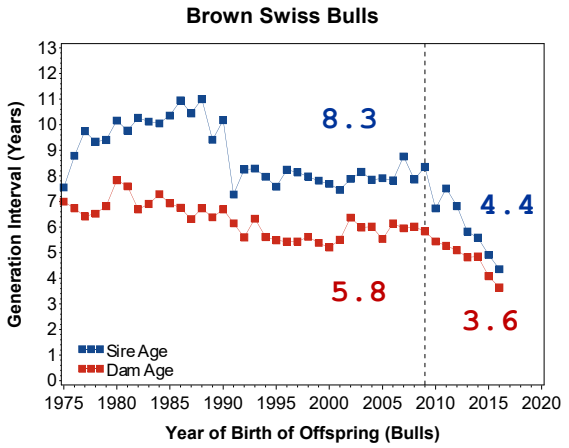
Cows

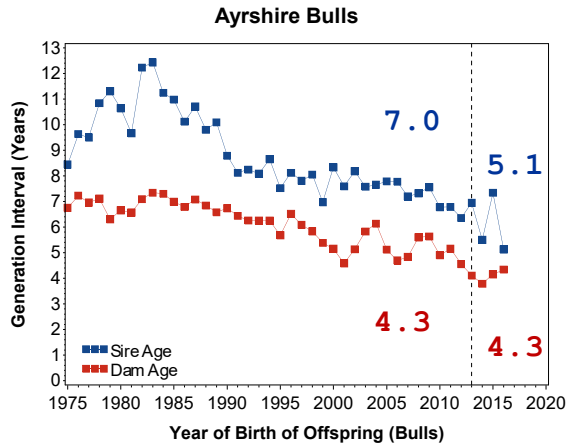


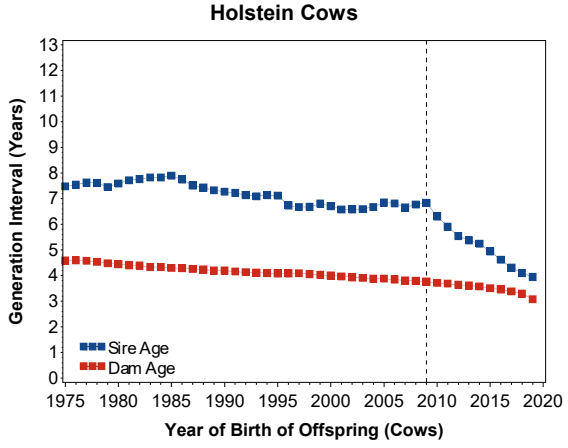
Generation Interval

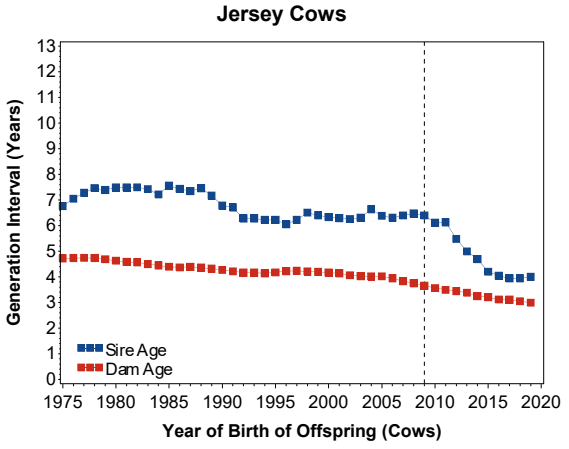


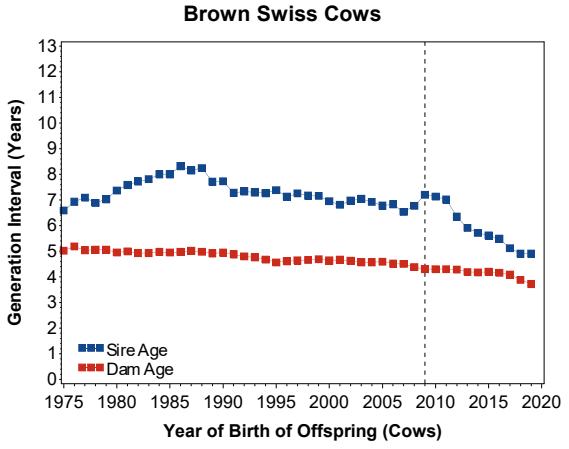


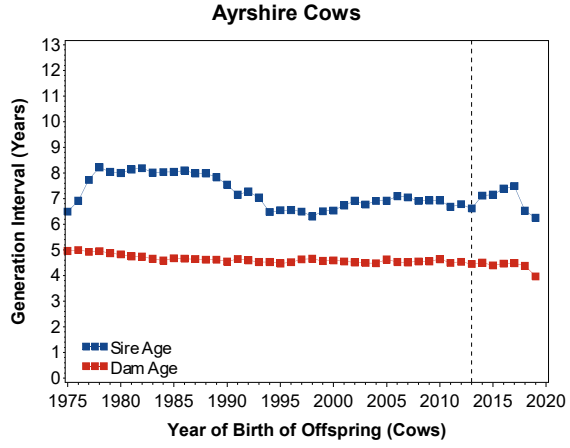












Conclusions

Benefits of genomic selection

- Holstein and Jersey (50% to 100%)
- Early adoption and amount of data
- Refined selection indexes

Less benefit for Brown Swiss, Ayrshire, Guernsey

- Amount of data
- Later adoption for Ayrshire and Guernsey
- Five more years of increased adoption of GS

Conclusions

Overall reduction in generation interval

- 2 to 3 years for breeds with higher level of adoption
- Sire and dam of bulls
- Sire of dams

Acknowledgements

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