

Genetic trends, generation interval, and inbreeding changes since the implementation of genomic selection in US dairy cattle

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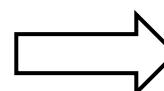


Motivation



Guinan et al.
(2022)

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



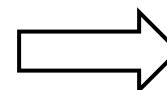
- Increase genetic gain
- Reliabilities
- Generation interval

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

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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?

Objectives

Holstein



Jersey



Genetic trends

Generation interval

Brown
Swiss



Inbreeding changes

Guernsey



Ayrshire



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 – 154,602

USA: 89.34%

840: 3.09%

CAN: 7.57%

Cows – 27,802,645

USA: 80.93%

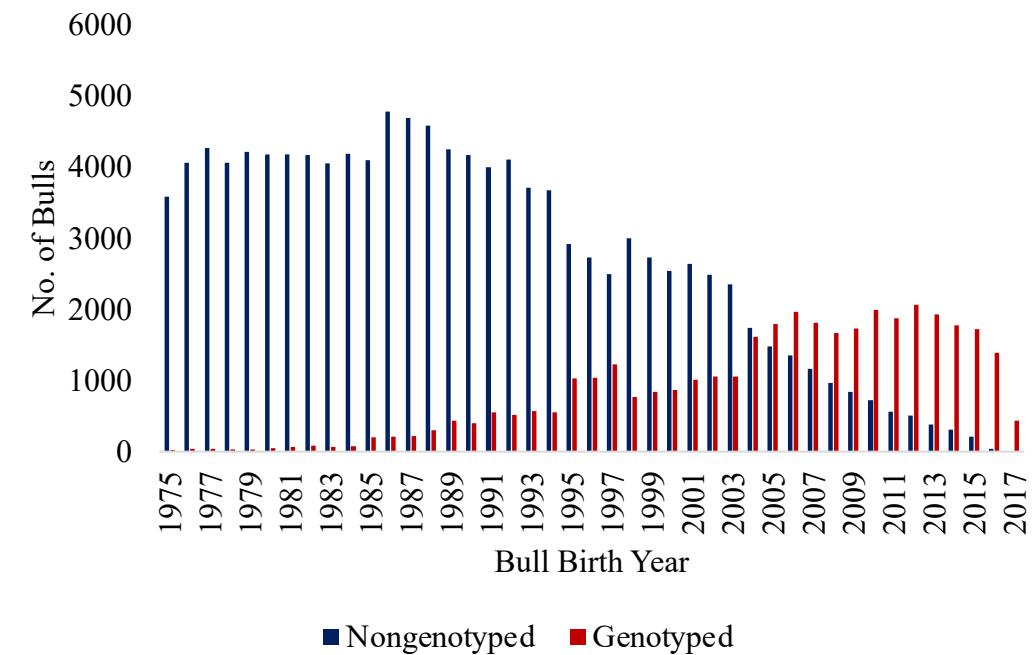
840: 18.98%

CAN: 0.08%

Bulls

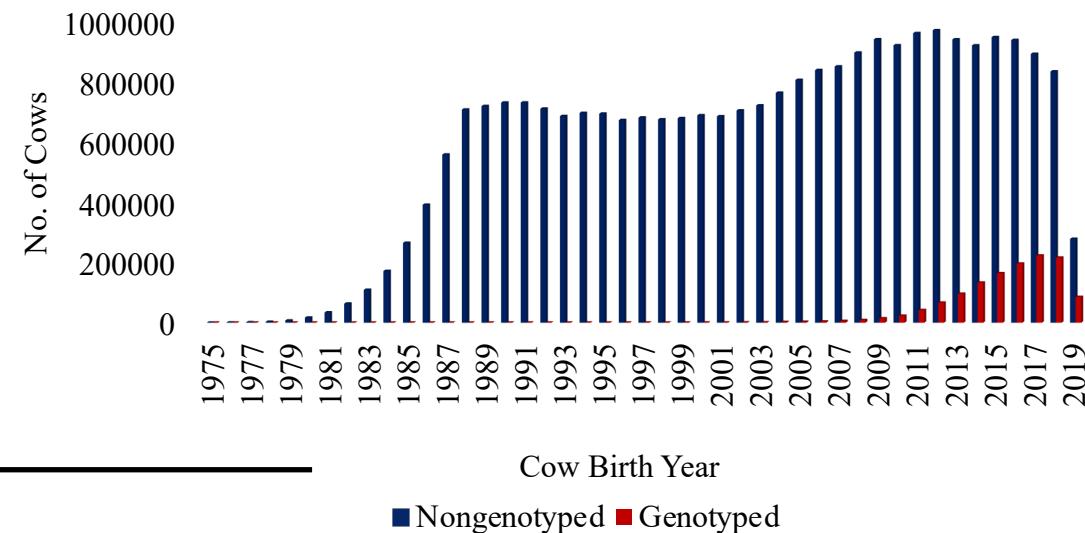
- ≥ 10 daughters with lactation records
- If PTA milk missing, then delete
- PBV weighted by no. of daughters per trait

Genomics indicator	Breed Evaluation						Total (No.)
	AY	BS	GU	HO	JE	Total	
Nongenotyped (%)	62.32	57.97	85.31	77.75	60.82	75.94	117,403
Genotyped (%)	37.68	42.03	14.69	22.25	39.18	24.06	37,199
Total (No.)	2,107	2,803	2,662	134,461	12,569	-	154,602



Cows

- ≥ 1 calving (lactation record)
- If PTA milk missing then delete
- Sire ID must be known
- Milk, fat, and protein must contribute to sire eval.



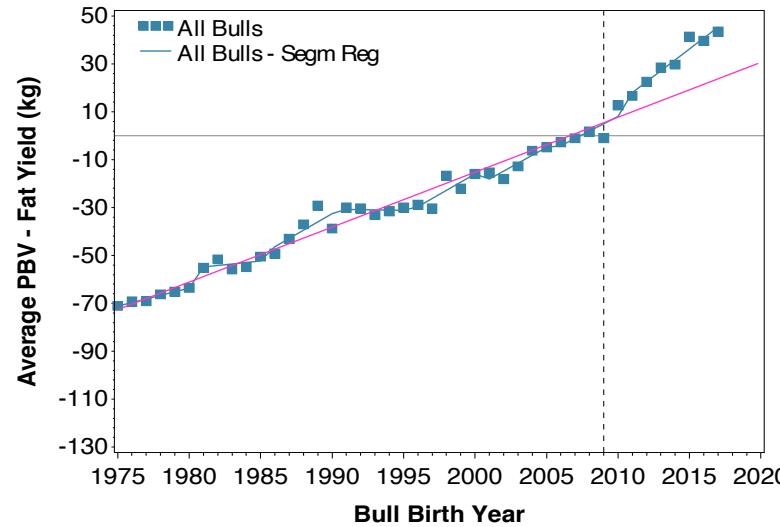
Genomics indicator	Breed Evaluation					Total	Total (No.)
	AY	BS	GU	HO	JE		
Nongenotyped (%)	99.48	97.48	98.46	95.72	91.27	95.38	26,518,215
Genotyped (%)	0.52	2.52	1.54	4.28	8.73	4.62	1,284,430
Total (No.)	137,962	243,936	142,992	24,877,547	2,400,208		27,802,645

Trends

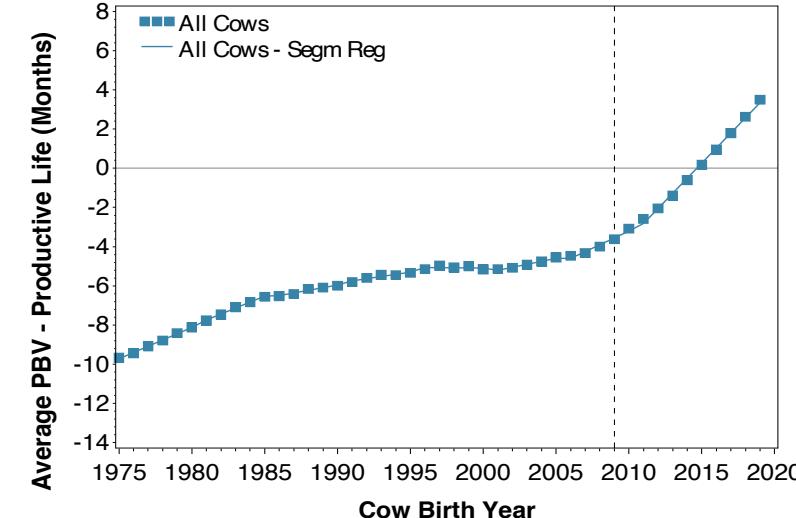
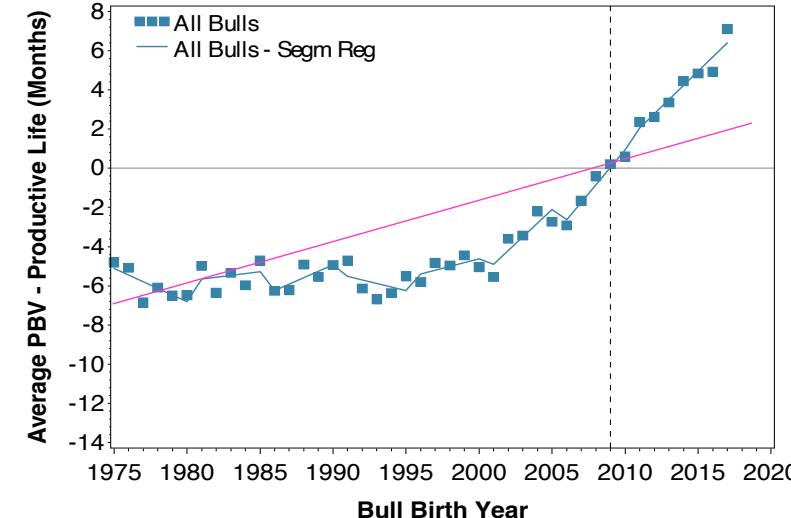
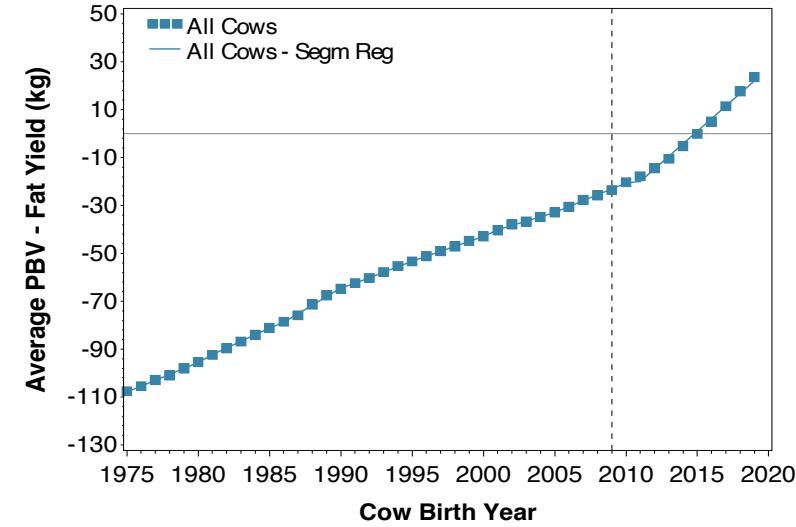
- No four path selection model (Dechow & Rogers, 2018)
- Mean Predicted Breeding Value/Year plotted for bulls and cows separate
- Linear and nonlinear regression – to fit the small sample size
- PROC REG used to estimate breakpoints for each 5 years
- PROC NLIN to fit the piecewise model
- Generation interval for sires and dams of bulls and cows
- Parents and progeny same breed code
- $(\text{Animal birth} - \text{parents birth})/365.25$
- Inbreeding levels only for genotyped animals
- Linear and nonlinear regression

Genetic trends – Holstein (2009)

Bulls

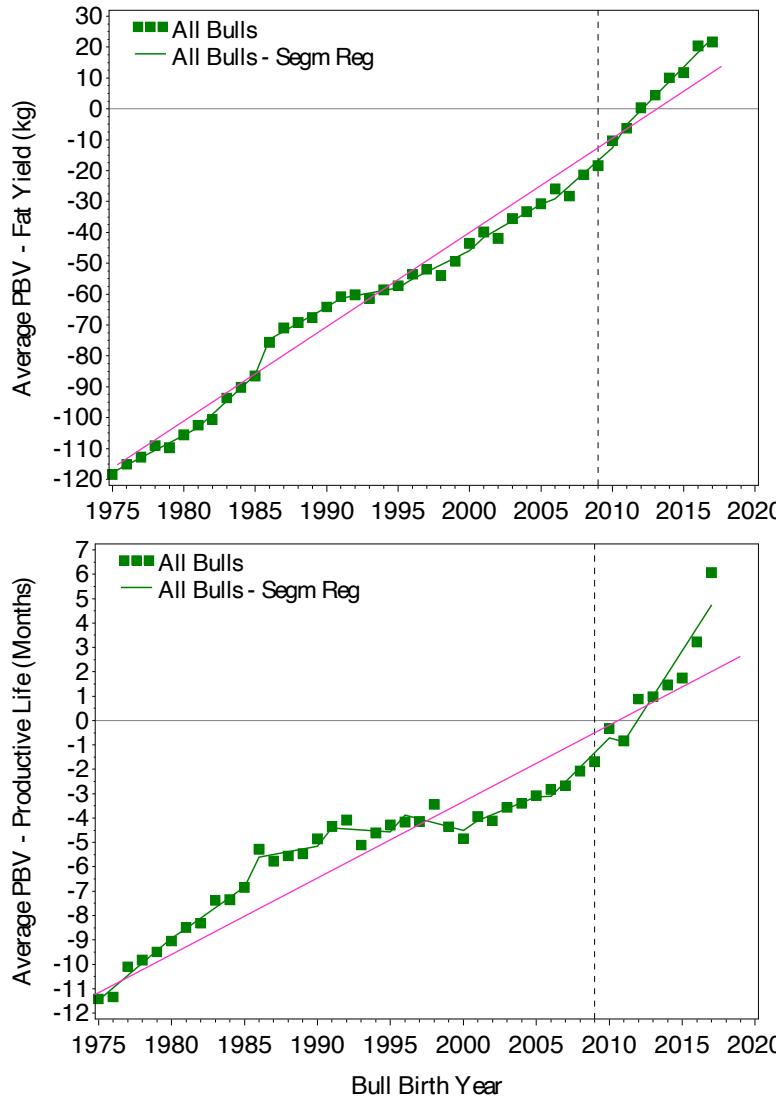


Cows

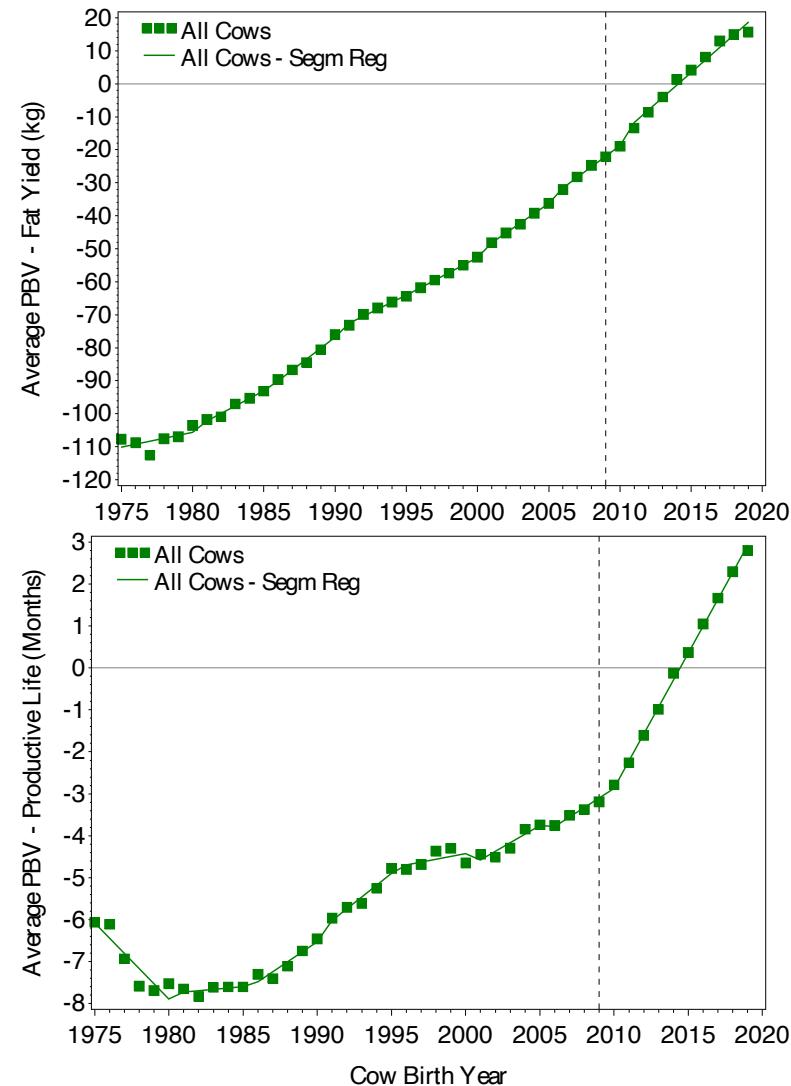


Genetic trends – Jersey (2009)

Bulls

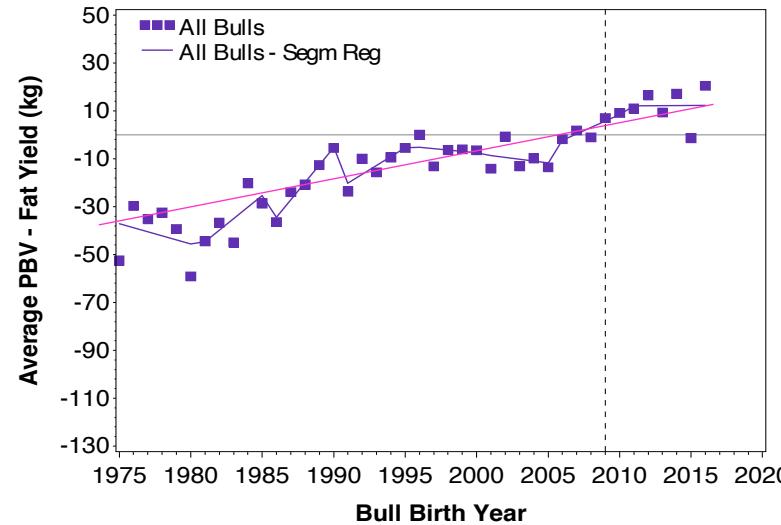


Cows

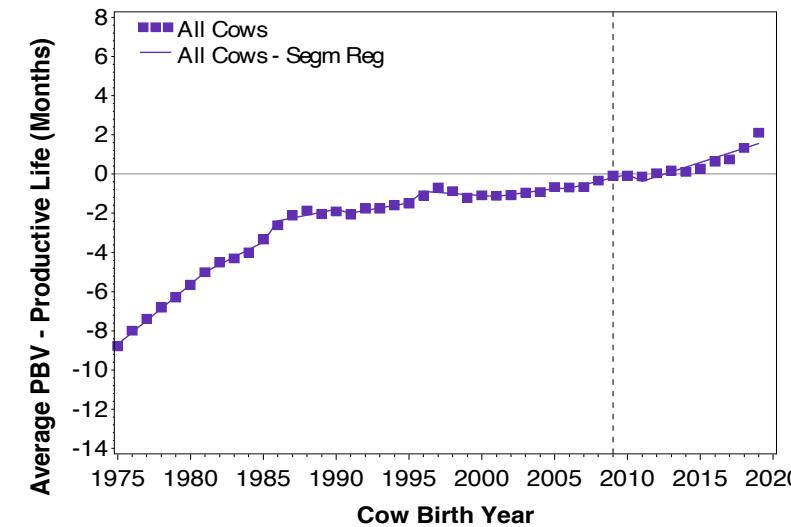
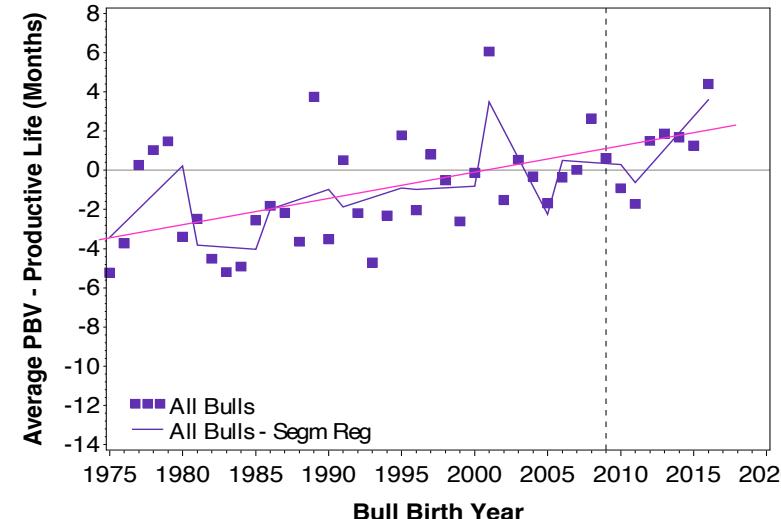
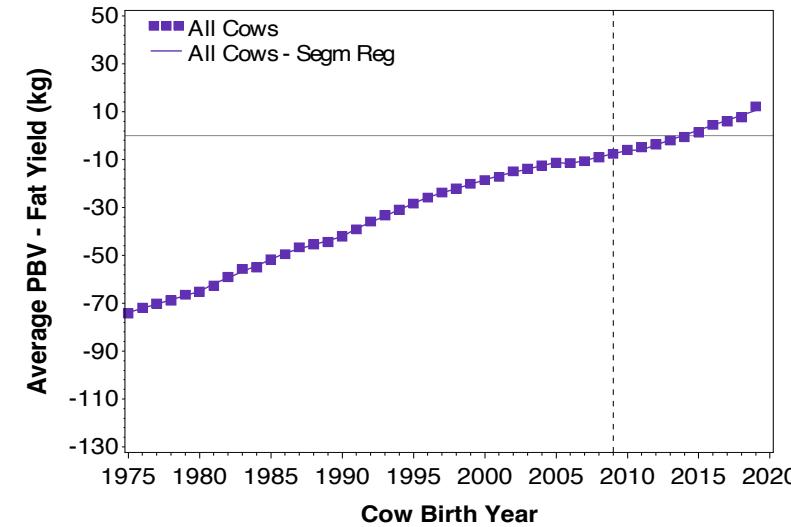


Genetic trends – Brown Swiss (2009)

Bulls

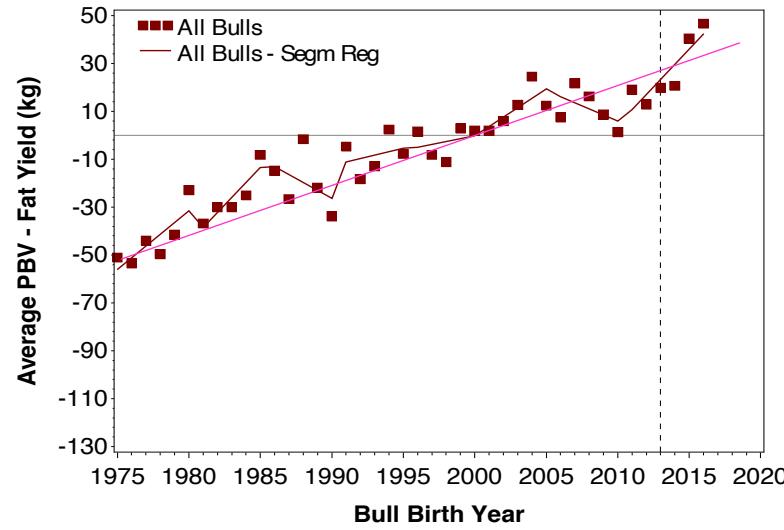


Cows

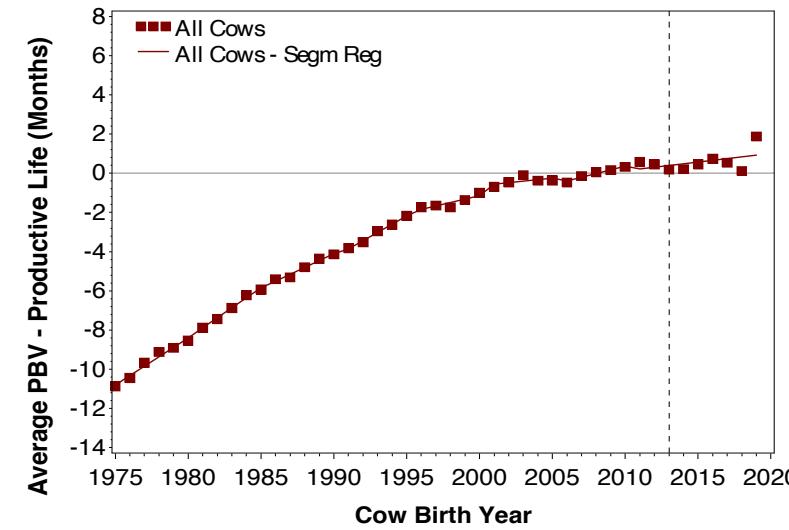
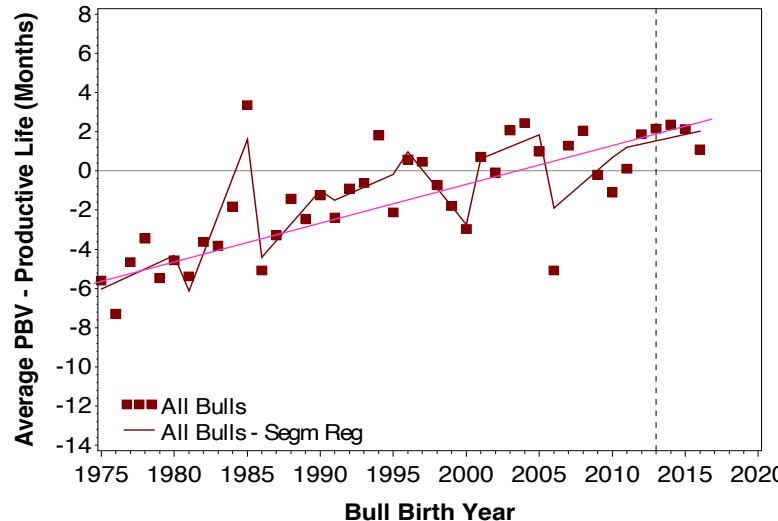
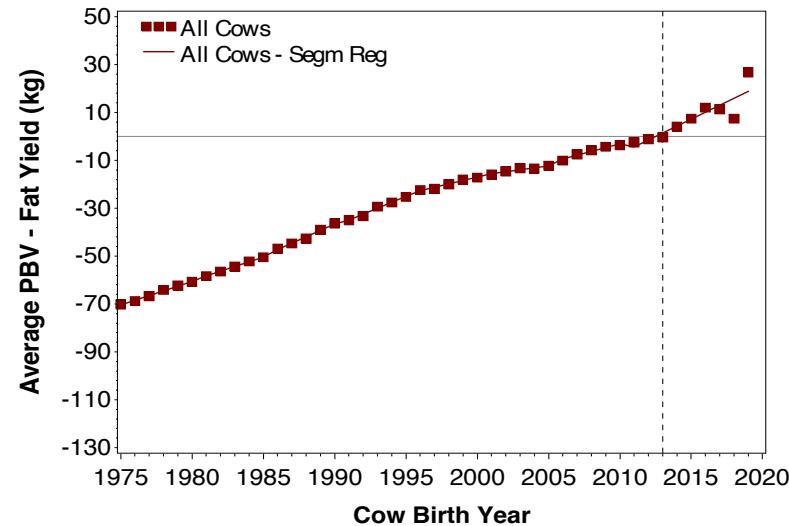


Genetic trends – Ayrshire (2013)

Bulls

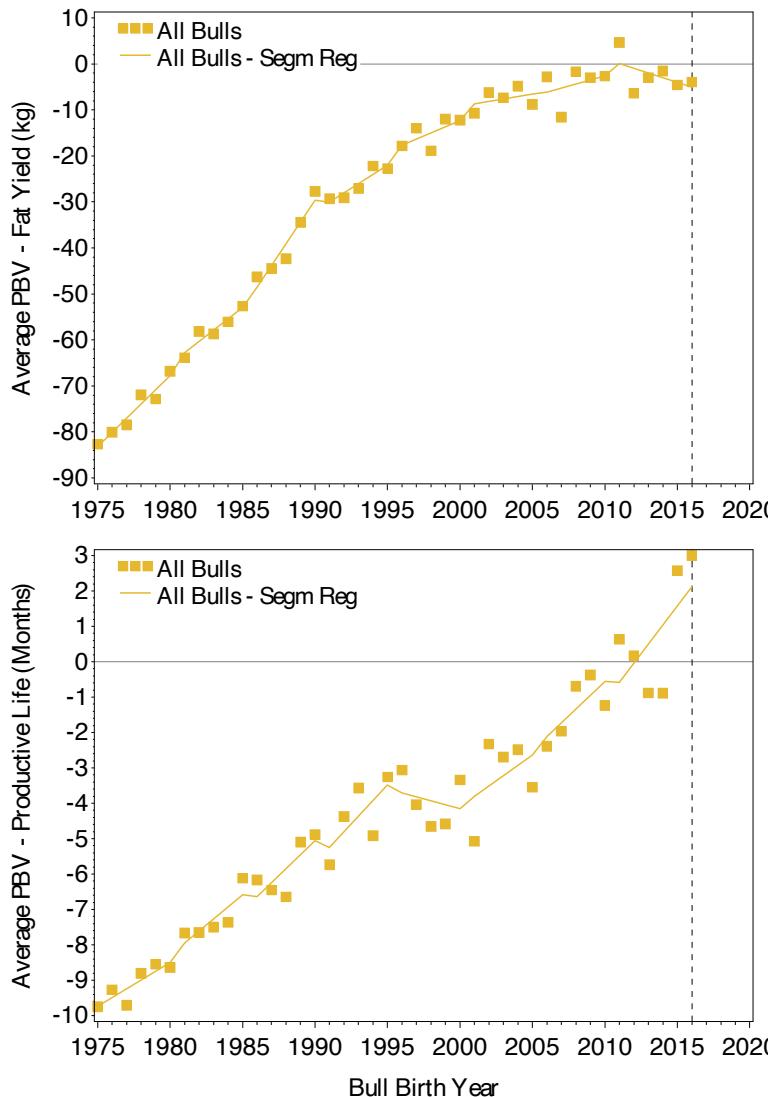


Cows

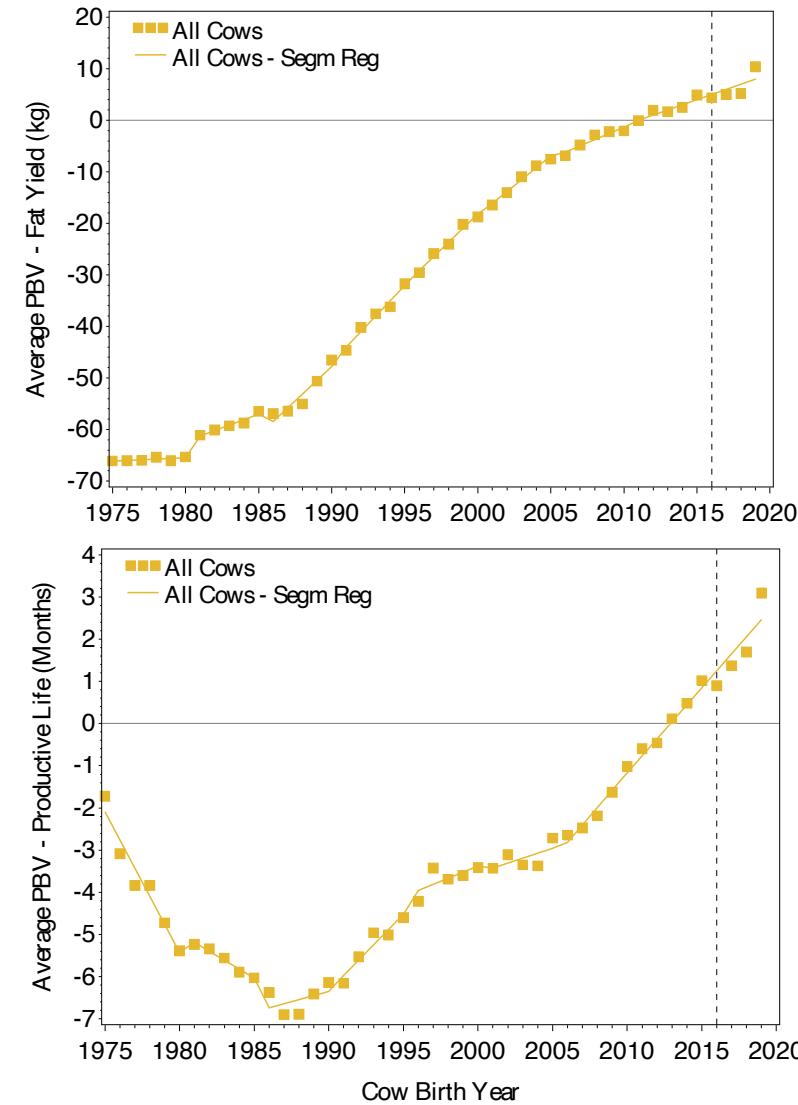


Genetic trends – Guernsey (2016)

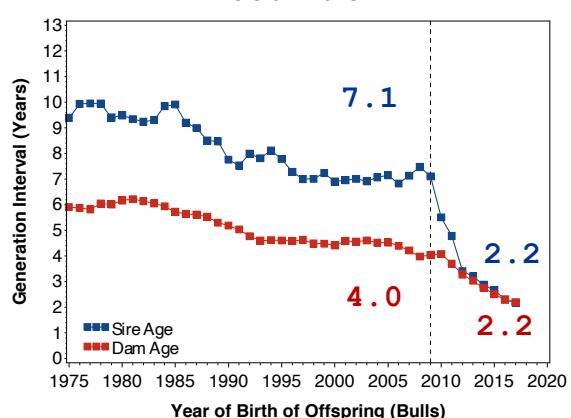
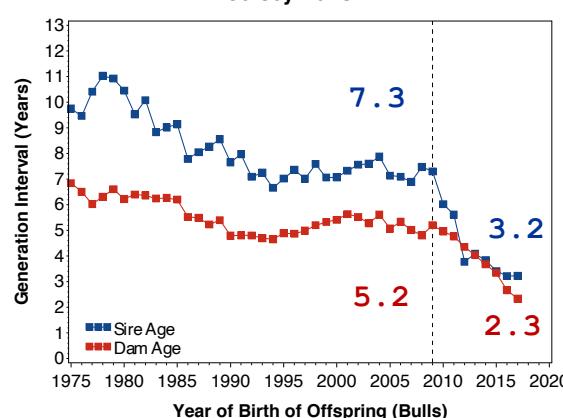
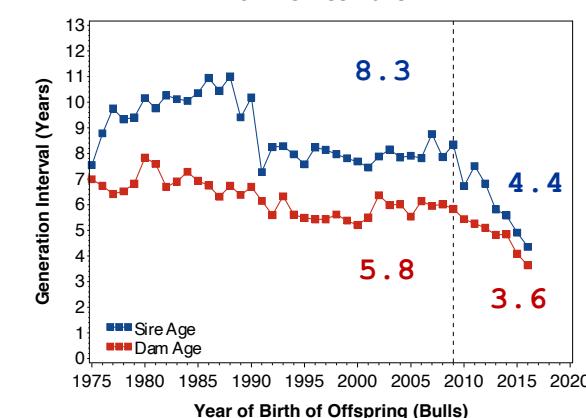
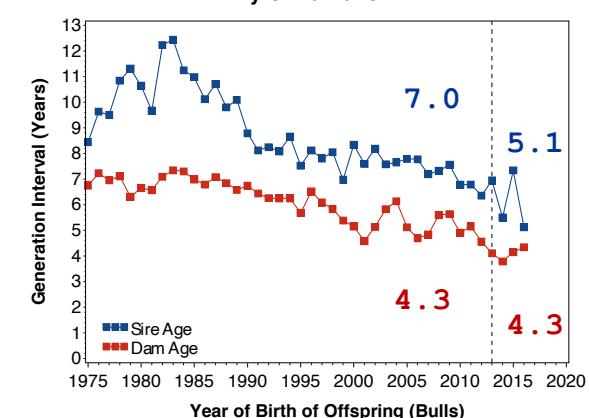
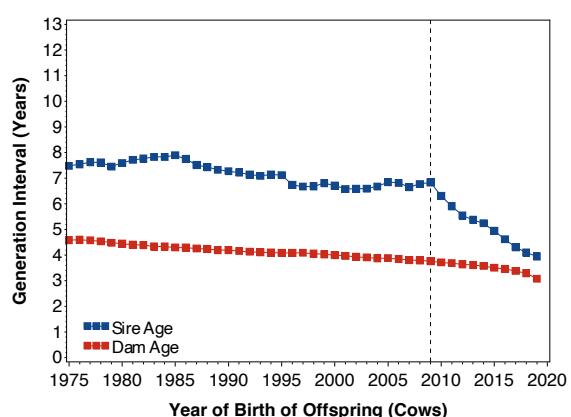
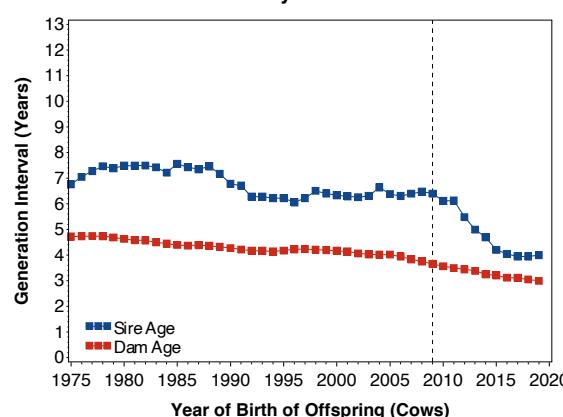
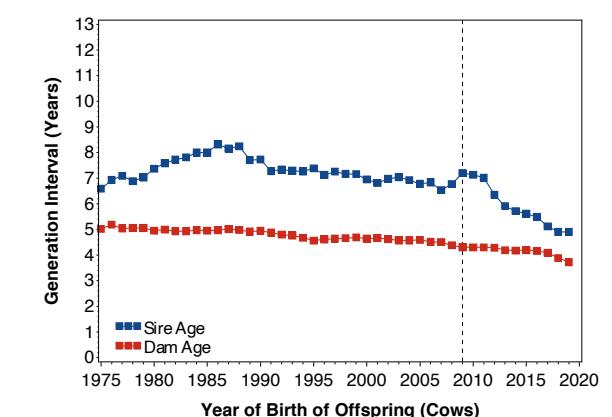
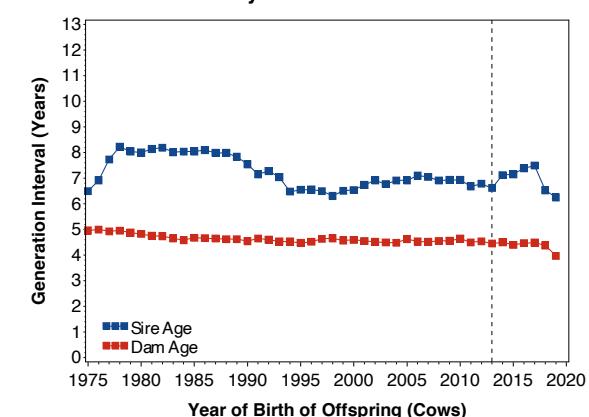
Bulls



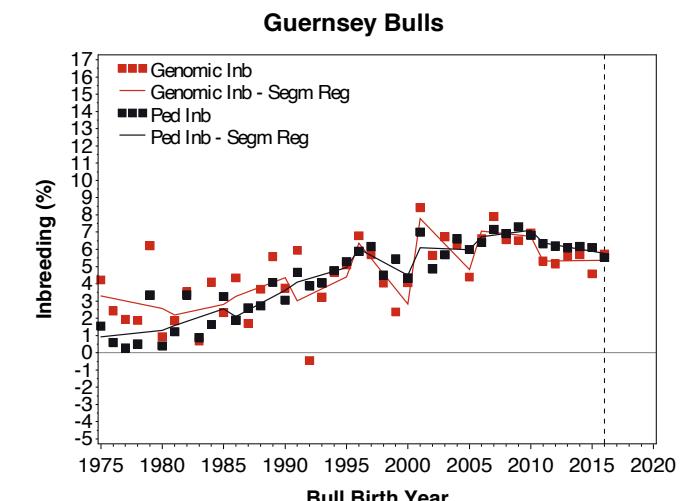
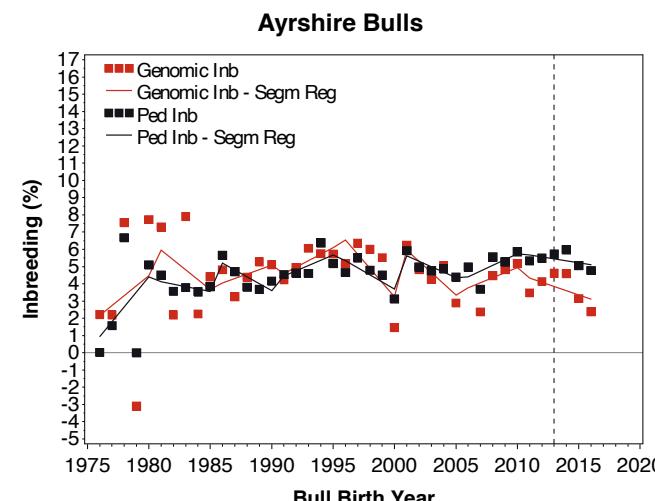
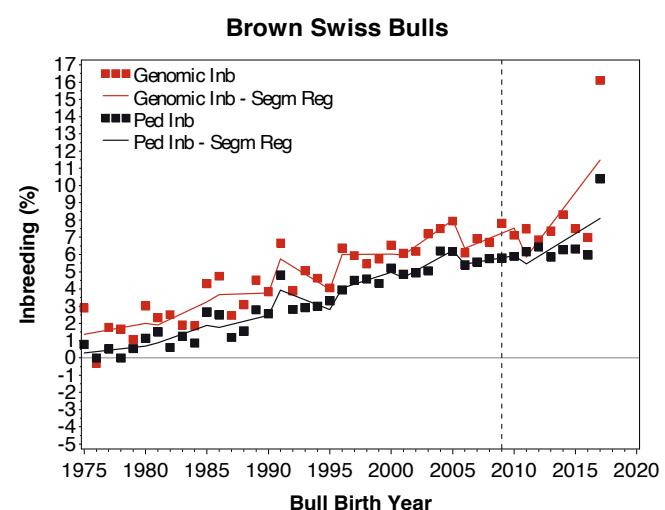
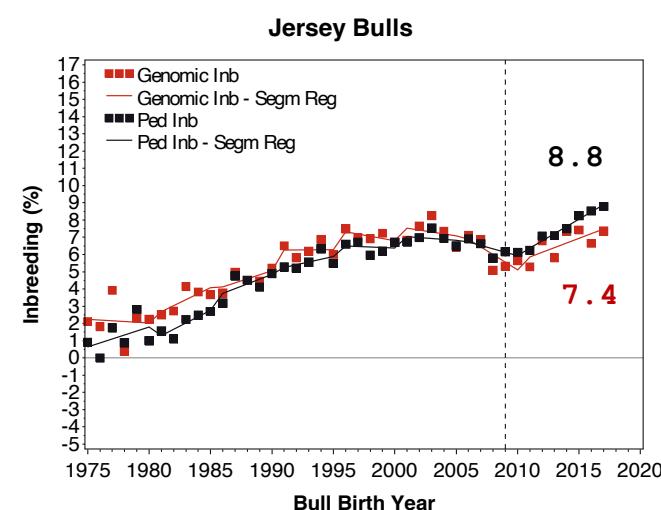
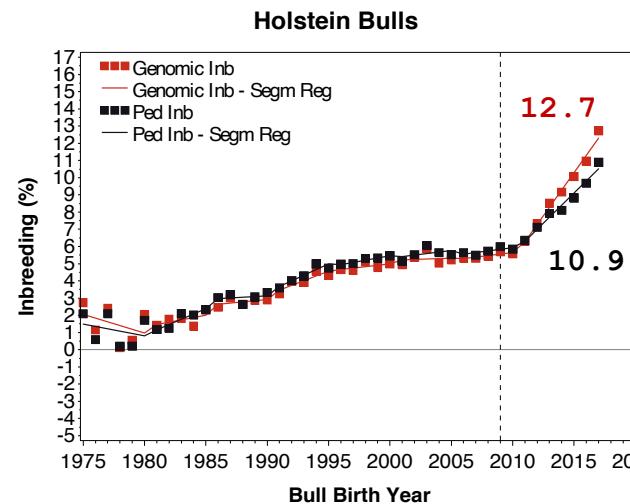
Cows



Generation interval

Holstein Bulls

Jersey Bulls

Brown Swiss Bulls

Ayrshire Bulls

Holstein Cows

Jersey Cows

Brown Swiss Cows

Ayrshire Cows


Inbreeding – bulls



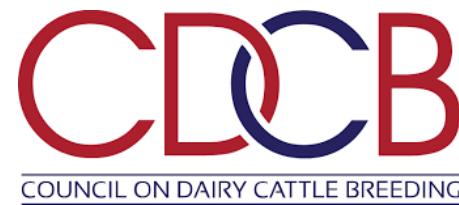
Conclusions I

- 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 II

- Overall reduction in generation interval
 - 2 to 3 years for breeds with higher level of adoption
 - Sires and dams of bulls
 - Sires of dams
- Inbreeding levels are increasing
 - More focus on how GPTA are used
- Trends may differ
 - Data editing + selection of animals
 - Methods

Acknowledgments



Dairy producers who supplied data through their participation in the Dairy Herd Improvement program and Dairy Records Processing Centers that edited and relayed information on to the Council of Dairy Cattle Breeding