

All-breed single-step GBLUP evaluations for fertility traits in U.S. dairy cattle

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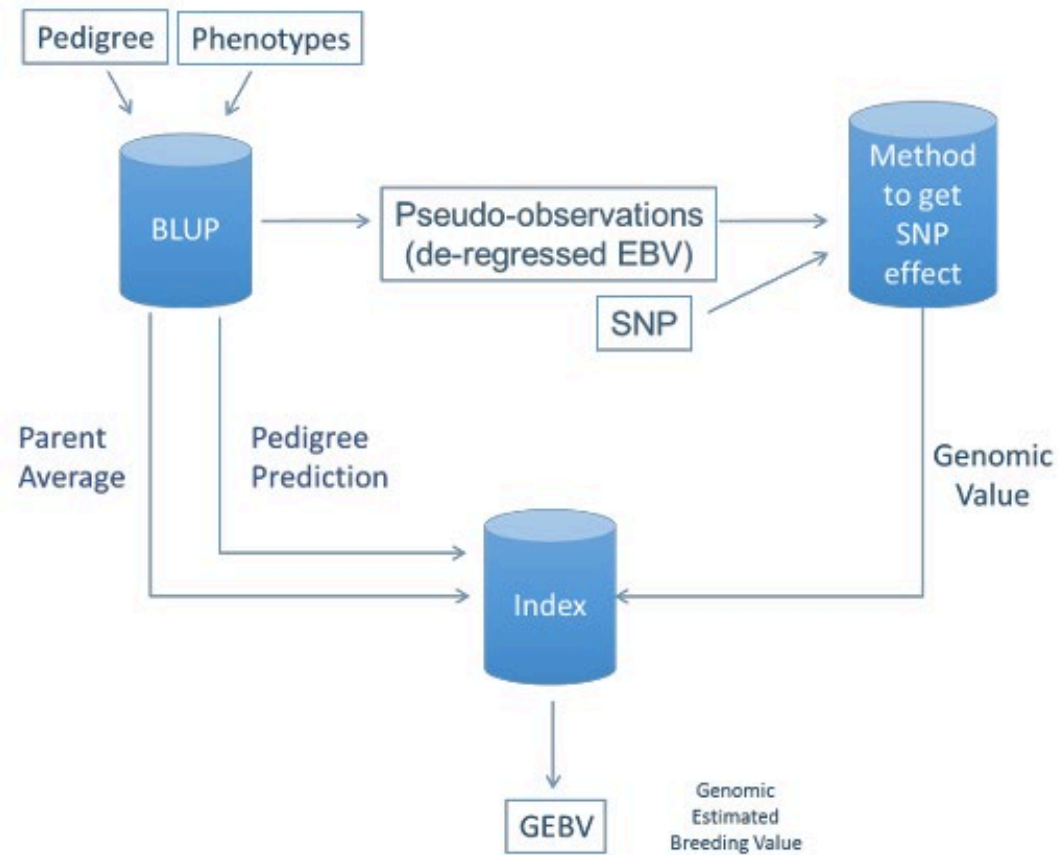
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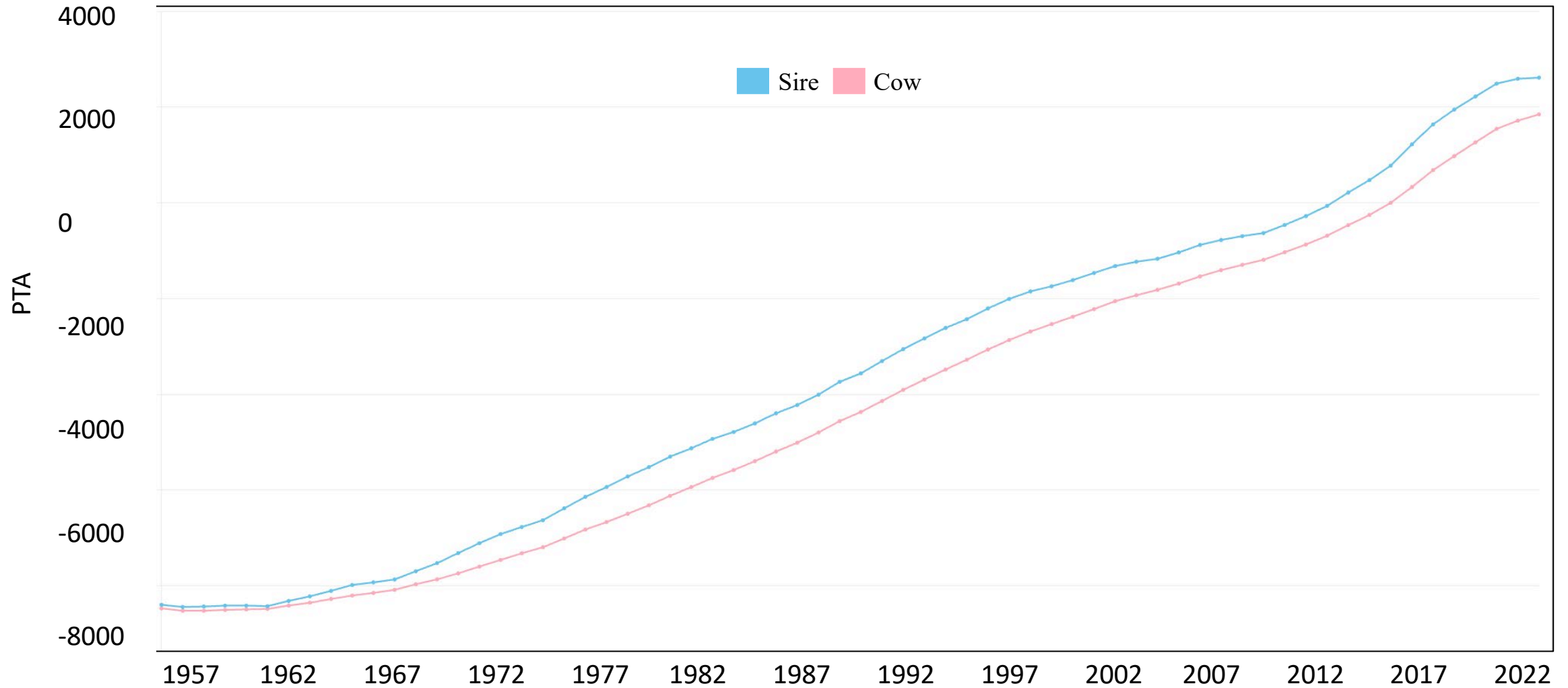


Background

- Current U.S Dairy genetic evaluation method: **Multistep process**



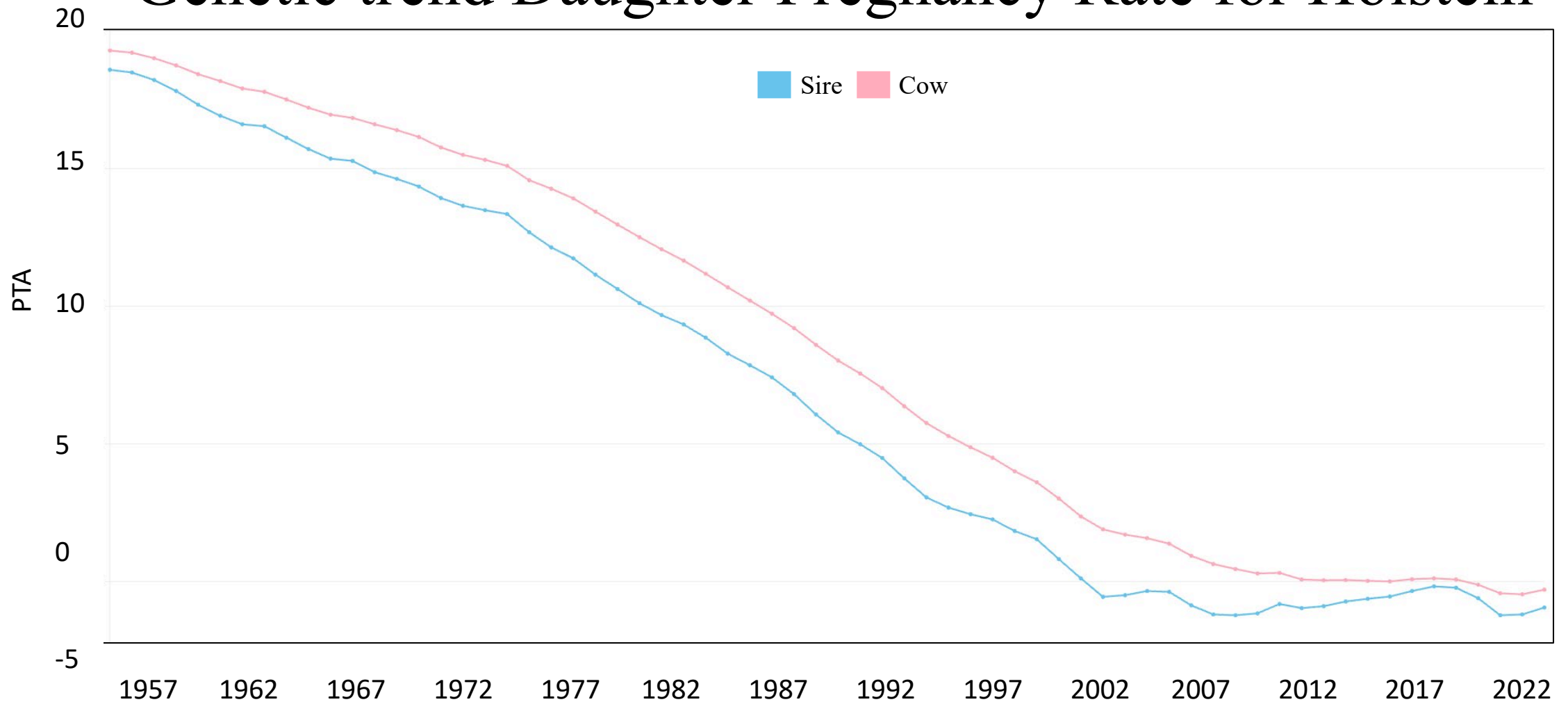
Genetic trend Milk yield for Holstein



<https://webconnect.uscdcb.com/#!/summary-stats/genetic-trend>



Genetic trend Daughter Pregnancy Rate for Holstein



<https://webconnect.uscdcb.com/#!/summary-stats/genetic-trend>



Background

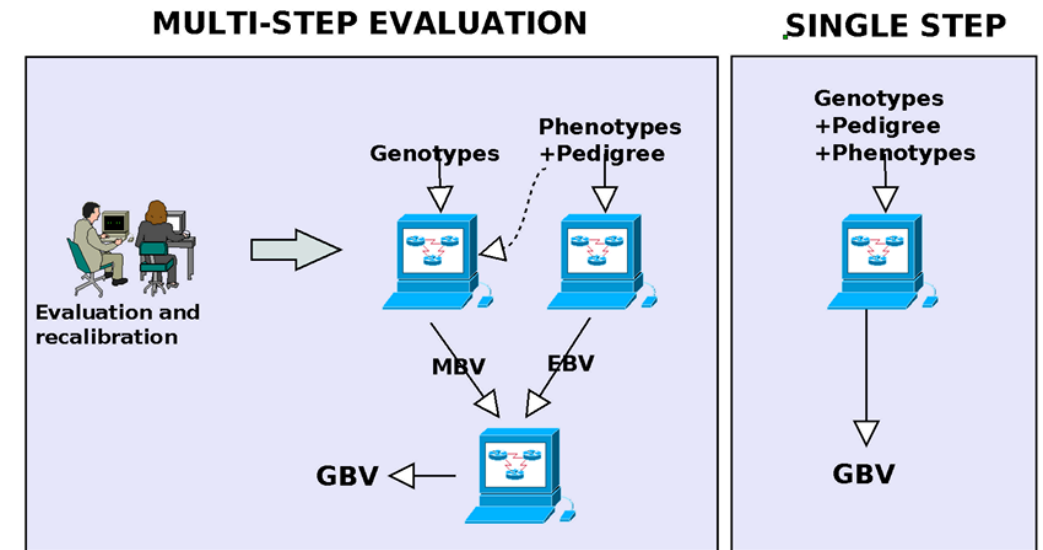
- **Single-Step GBLUP** (ssGBLUP), Aguilar et al., 2010; Chistensen and Lund, 2010; Legarra et al., 2009; Misztal et al., 2009
- Pedigree and Genomic information in the same evaluation

$$\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \mathbf{H}^{-1}\lambda \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{bmatrix}$$

Source of **Genomic** information

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

Source of **Pedigree** information



Motivation to use ssGBLUP

- One single analysis
- **Improved estimated** breeding values for non-genotyped animals
- Avoid bias in trends of breeding values due to genomic preselection

Objectives:

- Assess the accuracy and potential biases of the ssGBLUP method when applied to all-breed U.S. fertility traits
- Compare Unknown Parent Groups (UPG) and Metafounders (MF)
- Fertility traits are hard to evaluate due to low heritability, undesirable genetic correlations with milk yield, and changing management trends



Material and Methods

	Number of records
Pedigree	93.4M
Genotypes	2M
Cow Conception Rate (CCR)	35.2M
Heifer Conception Rate (HCR)	11.5M
Daughter Pregnancy Rate (DPR)	89.6M
Early First Calving (EFC)	35.4M



<https://www.hoards.com/>

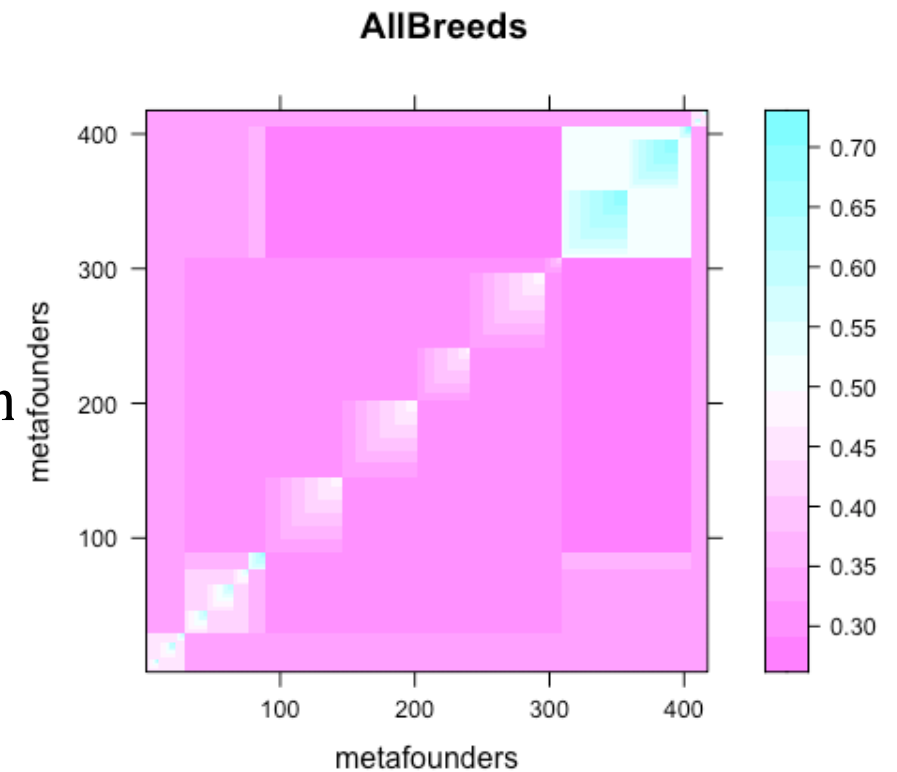
Material and Methods

- ssGBLUP approach:
 - Multibreed evaluation: Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), Holstein (HO), Jersey (JE), Milking Shorthorn and Crossbreds (XX)
 - 2M genotypes
 - Have records or have progeny with records
- Algorithm for proven and young (Misztal et al., 2014) ~ 45k
- Core sets selected within breed

Breed	# of Sires (Dams) in Core
AY	311 (1,175)
BS	611 (4,313)
GU	219 (3,258)
HO	6,890 (8,113)
JE	3,186 (11,883)
XX	141 (4,616)

Material and Methods

- 5% - 10% missing pedigree
 - Unknown Parent Groups
 - compatibility using J-factors with the same definition
 - Metafounders is a generalization of UPG where groups are related among themselves
 - compatibility between **A** and **G** using **Gamma**
- Missing parents were defined by **breed**, **year of birth**, and **pathway** = 417 groups



Material and Methods

Scenarios:

Traditional pedigree-based BLUP (PBLUP)

- UPG
- MF

ssGBLUP

- UPG5/MF5: 5% pedigree-based polygenic effect
- UPG10/MF10: 10% pedigree-based polygenic effect

Material and Methods

- Validation method
 - Linear Regression Validation (**LR**; Legarra and Reverter, 2018)
 - Two datasets
 - Whole dataset (w)
 - Partial dataset (p): Removed last 4 years of records
 - Validation candidates have $> \underline{100 \text{ daughters}}$ in the whole dataset
- Estimates:
 - Bias
 - Dispersion
 - Correlation

Results and Discussion

Dispersion in Holstein (HO) (G)EBV

Breed _{Trait}	b_1					
	² ssGBLUP				² PBLUP	
	MF10	MF5	UPG10	UPG5	MF	UPG
¹ HO _{CCR}	0.94	0.95	0.90	0.90	0.93	0.92
¹ HO _{DPR}	0.95	0.93	0.91	0.90	0.81	0.82

¹HO_{CCR}; HO_{DPR}: CCR and DPR in Holstein

²Standard errors: HO_{CCR} and HO_{DPR}: ssGBLUP = 0.03, PBLUP = 0.01

Regression (G)EBV_w on (G)EBV_p

- Inflated EBV with BLUP
 - genomic preselection
- Less inflated GEBV with ssGBLUP
- MF had even less inflated predictions
 - $b_{1_{MF10}} : 0.94 - 0.95$

Results and Discussion

Dispersion in Jersey (JE) (G)EBV

Breed _{Trait}	b₁					
	² ssGBLUP				² PBLUP	
	MF10	MF5	UPG10	UPG5	MF	UPG
¹ JE _{CCR}	0.94	0.89	0.90	0.88	0.76	0.72
¹ JE _{DPR}	0.97	0.92	0.95	0.90	0.81	0.79

¹JE_{CCR}; JE_{DPR}: CCR and DPR in Jersey

²Standard errors: JE_{CCR} and JE_{DPR}: ssGBLUP = 0.07, PBLUP = 0.02

- Inflated EBV with BLUP
 - genomic preselection
- Less inflated GEBV with ssGBLUP
- MF had even less inflated predictions
 - $b_{1_{MF10}} : 0.94 - 0.97$
- Increasing from 5% to 10% benefited JE

Results and Discussion

Breed ^{Trait}	Correlation					
	³ ssGBLUP				³ PBLUP	
	MF10	MF5	UPG10	UPG5	MF	UPG
¹ HO _{CCR}	0.87	0.87	0.86	0.85	0.54	0.53
¹ HO _{DPR}	0.90	0.90	0.88	0.89	0.49	0.50
² JE _{CCR}	0.88	0.80	0.85	0.81	0.56	0.54
² JE _{DPR}	0.86	0.85	0.86	0.86	0.65	0.63

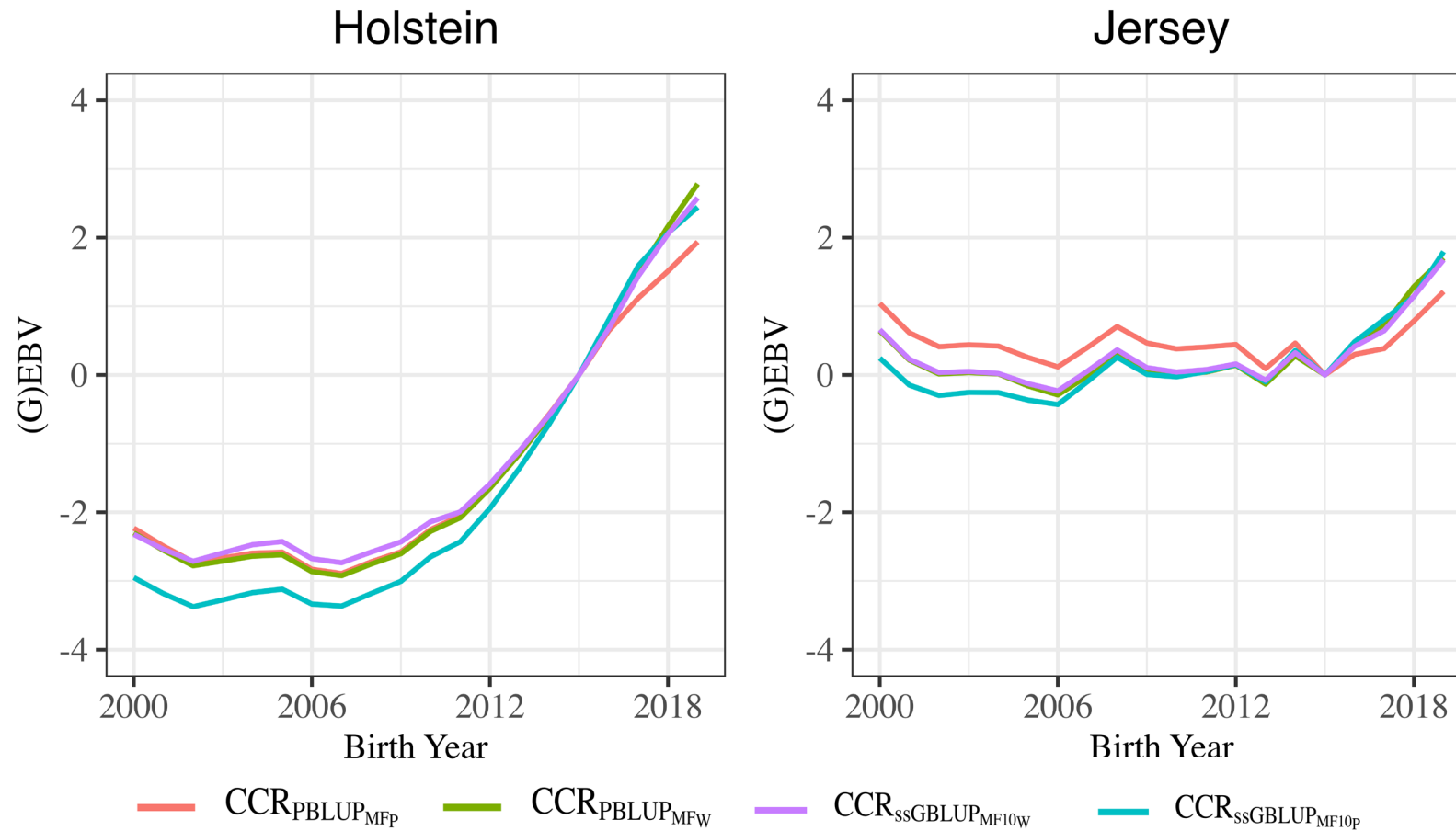
¹HO_{CCR}; HO_{DPR}: CCR and DPR in Holstein

²JE_{CCR}; JE_{DPR}: CCR and DPR in Jersey

³Standard errors: Holstein ≤ 0.02 for all traits and methods; Jersey: ≤ 0.06 for all traits and methods

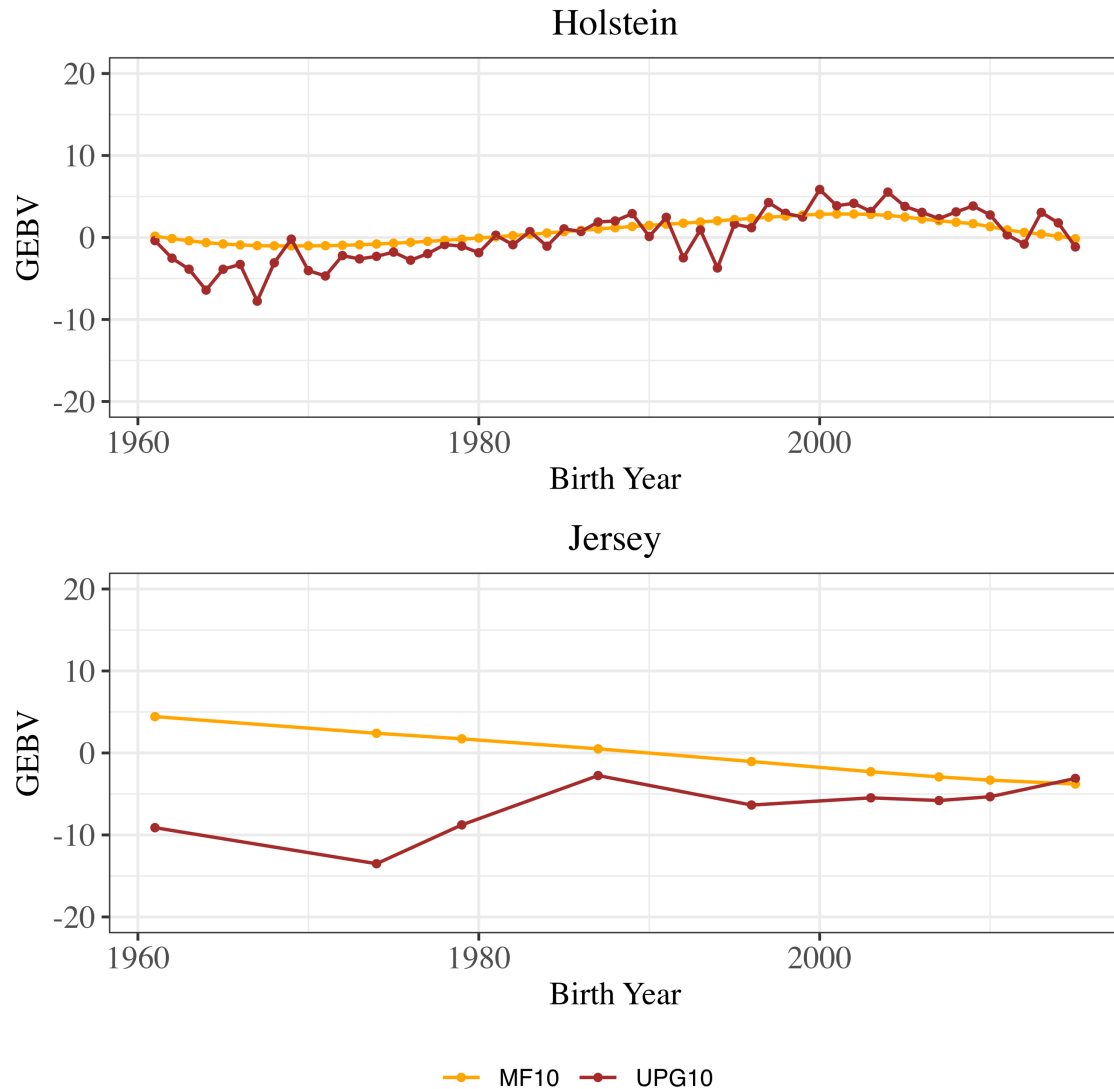
- Low correlations using pedigree-based BLUP
- Correlations using ssGBLUP_{MF10/5} $> 0.85 \rightarrow$ GEBV_{early} (partial) are good predictors of GEBV_{later} (whole)
- MF slightly better than UPG

CCR Genetic Trends in Holstein and Jersey with Metafounders



- The four trends with Metafounders exhibited a consistent direction with minor variations

CCR solution of UPG/MF including unknown sires of foreign dams

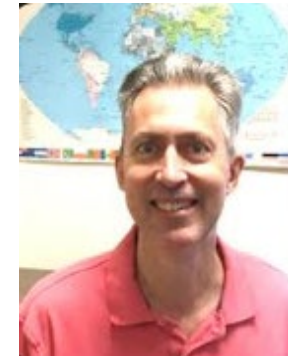


- Less heterogeneous behavior with MF
- More stable estimates using MF

Conclusion

- Single-step GBLUP is a viable alternative to the current multistep procedure
- Metafounders yielded slightly better results compared to Unknown Parent Groups with J-factors
- Single-step GBLUP correctly captures the response to selection

Acknowledgements





Thank you

Any questions?

