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

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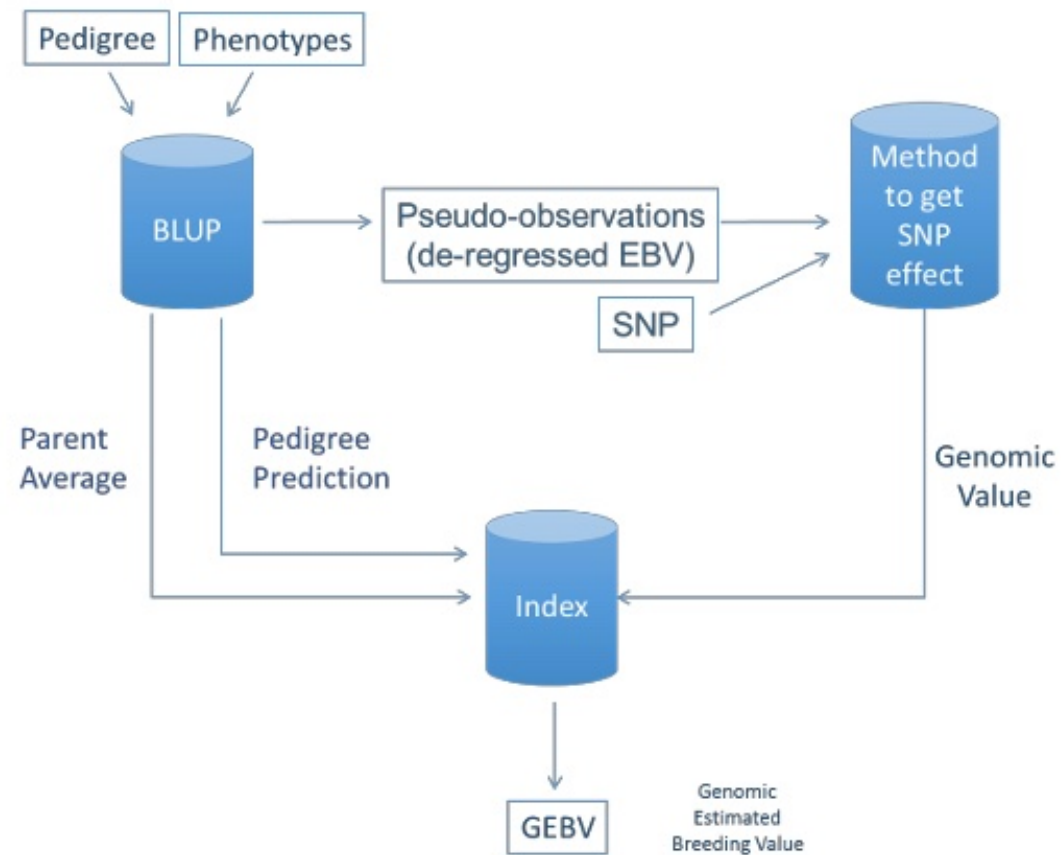[4] GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326 Castanet Tolosan, France

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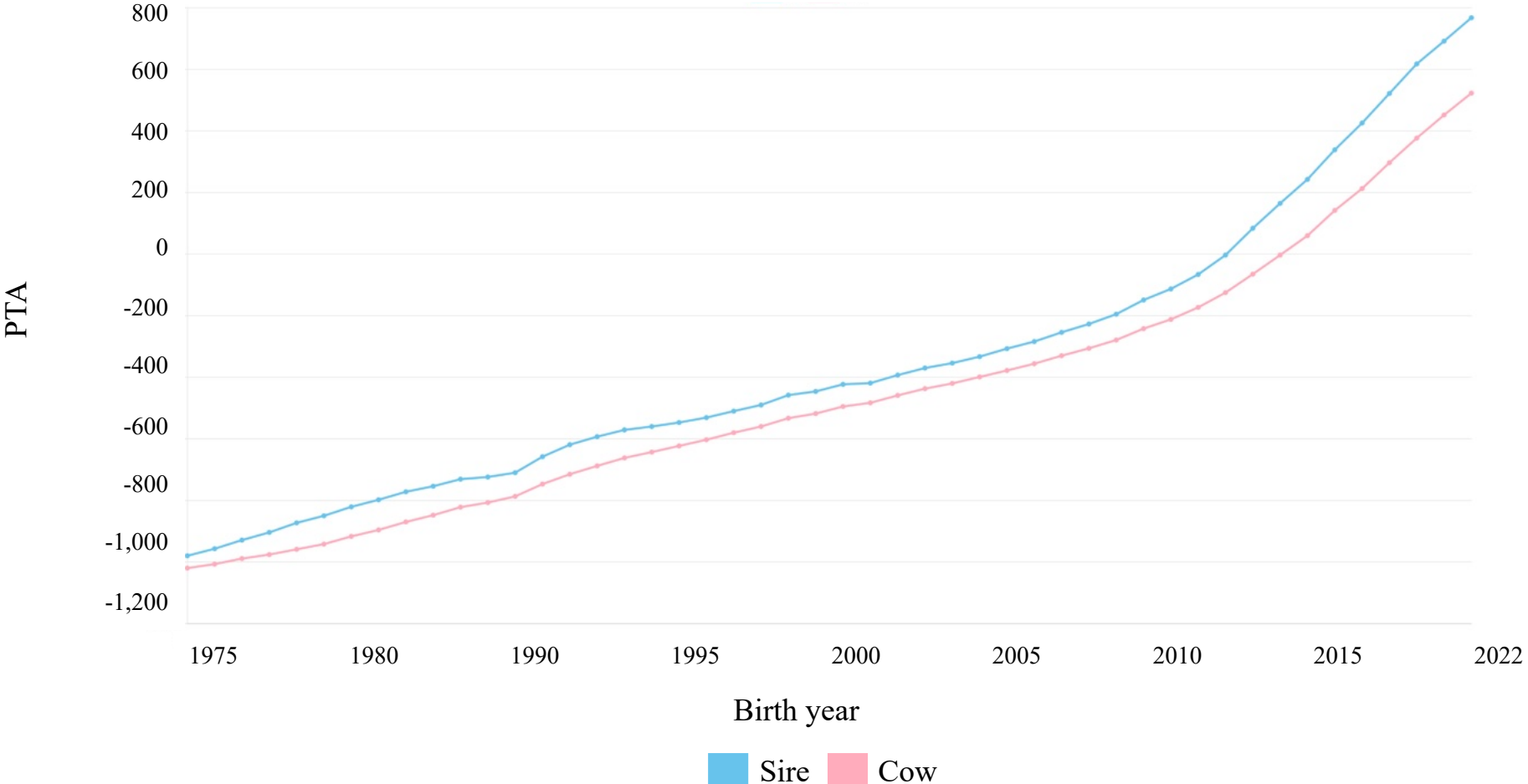COUNCIL ON DAIRY CATTLE BREEDING

Background

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

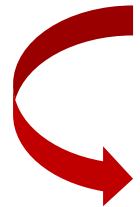# Genetic trend of Net Merit for Holstein

Background

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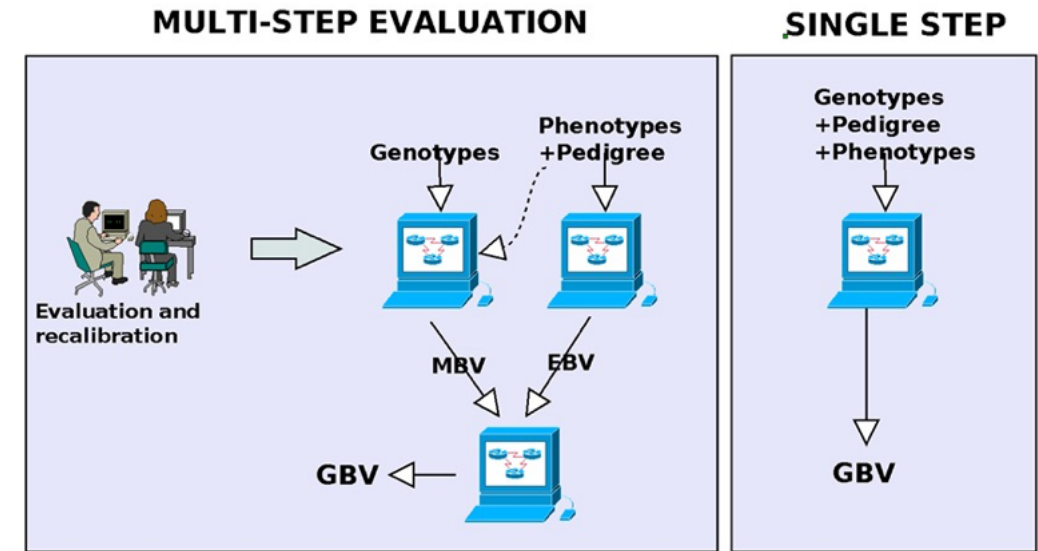- Pedigree and Genomic information in the same evaluation

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

Source of **Genomic** information

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

Source of **Pedigree** information

www.blnzgenetics.com/

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)

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/

- Fertility traits are hard to evaluate due to low heritability, genetic correlations with milk yield, and changing management trends

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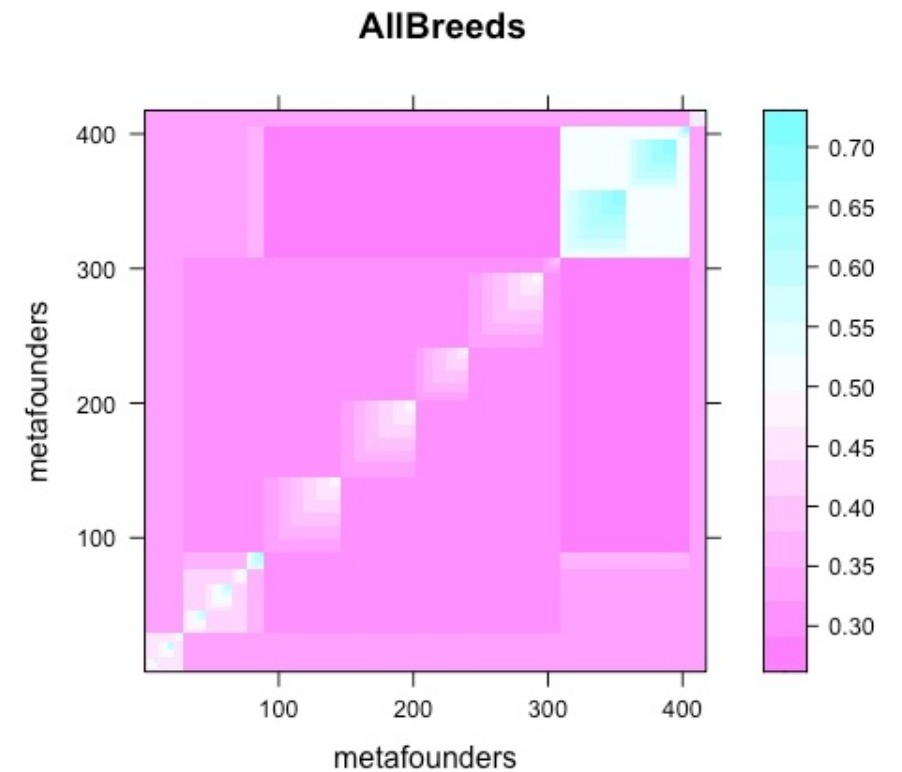
Material and Methods

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

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

- Unknown Parent Groups models missing pedigree

- Metafounders is a generalization of UPG where groups are related among themselves

- 5% - 10% missing pedigree

AllBreeds

- 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
- UPG
- MF5: 5% pedigree-based polygenic effect
- MF10: 10% pedigree-based polygenic effect
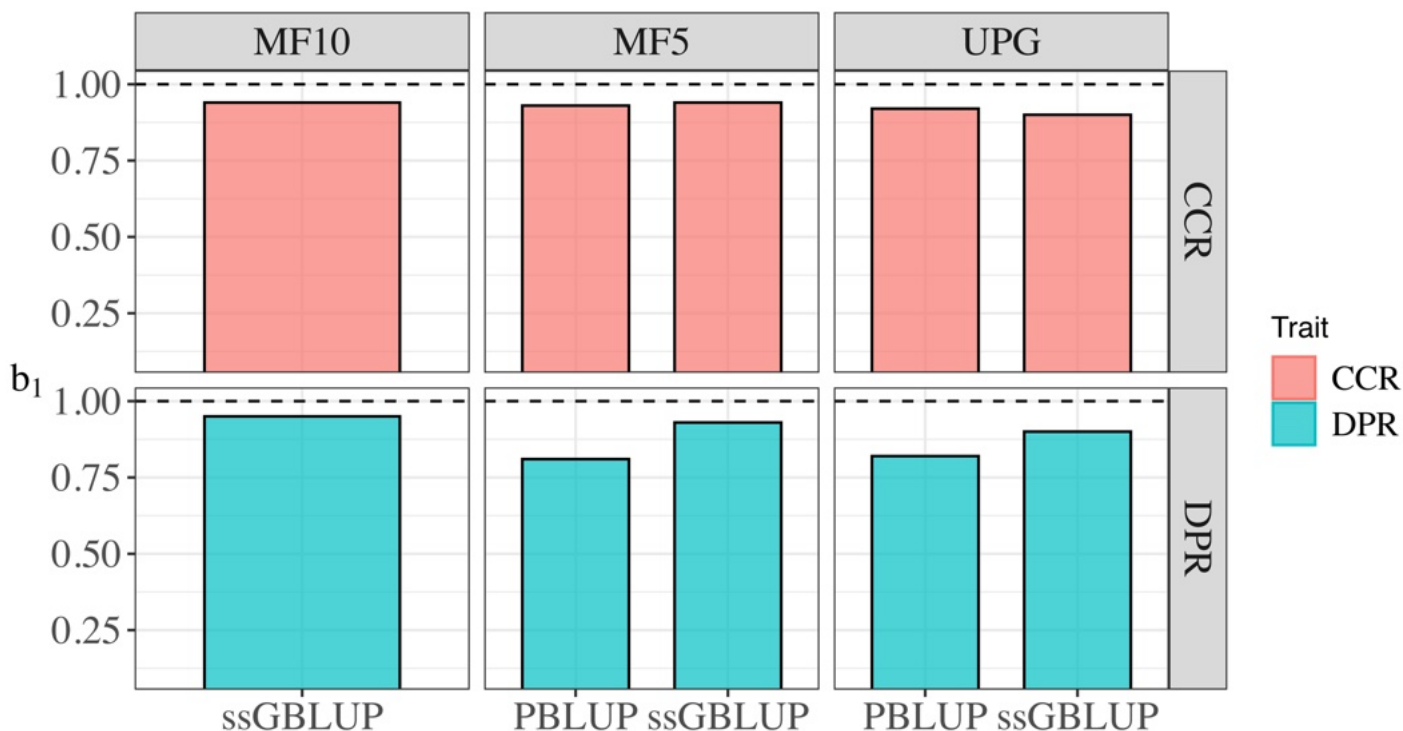
Material and Methods

- 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 > 100 daughters in the whole dataset

  - Estimates:
    - Bias
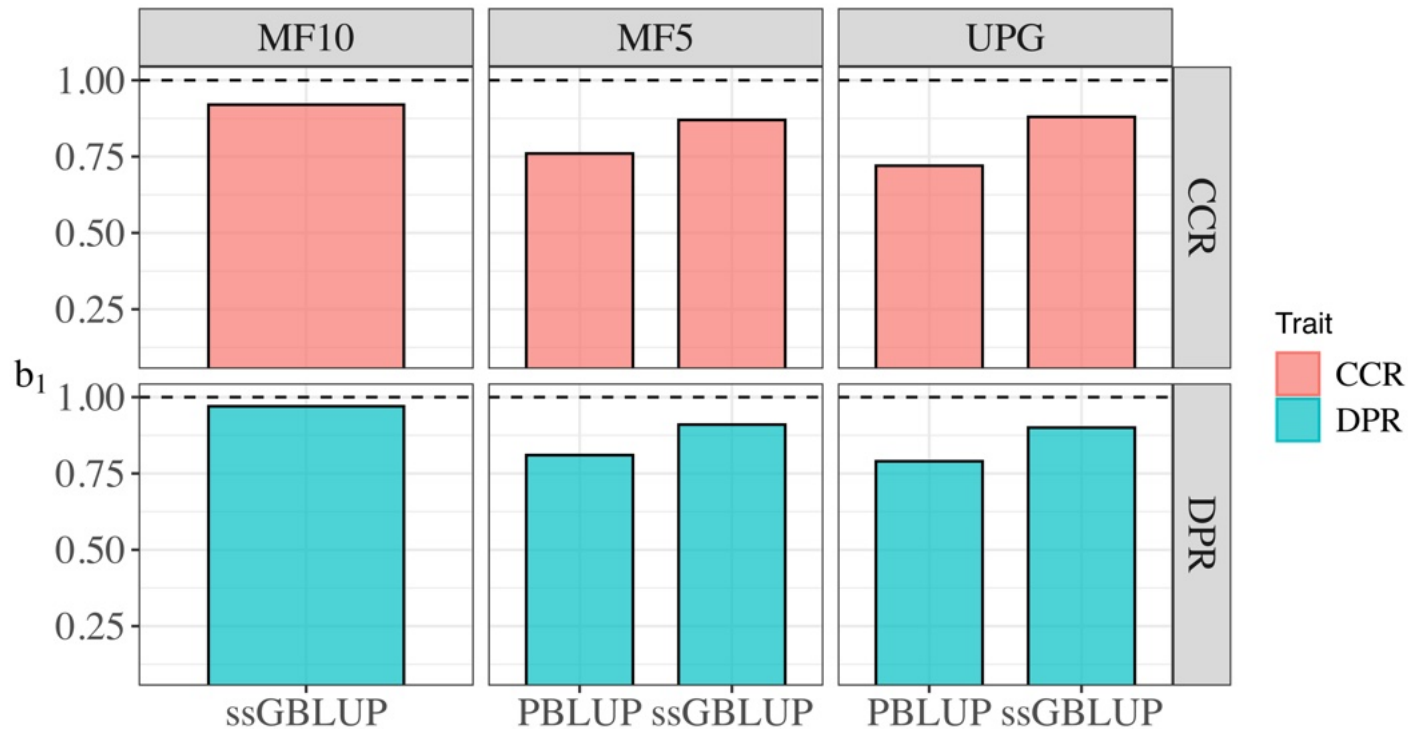   - Dispersion
    - Correlation

Results and Discussion

Dispersion in Holstein (HO) (G)EBV

- 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
  - $b_{1_{MF}} : 0.93 - 0.95$

Results and Discussion

Dispersion in Jersey (JE) (G)EBV

- Inflated EBV with BLUP
  - genomic preselection

- Less inflated GEBV with ssGBLUP

- **MF** had even less inflated predictions
 - $b_{1_{MF}} : 0.90 - 0.97$

Results and Discussion

| Breed$_{Trait}$ | Correlation of (G)EBV$_w$ and (G)EBV$_p$ | | | | |
| | ssGBLUP | | | PBLUP | |
	MF10	MF5	UPG	MF	UPG
[1]HO$_{CCR}$	0.87	0.87	0.85	0.54	0.53
[1]HO$_{DPR}$	0.90	0.90	0.89	0.49	0.50
[2]JE$_{CCR}$	0.88	0.80	0.81	0.56	0.54
[2]JE$_{DPR}$	0.86	0.85	0.86	0.65	0.63

[1]HO$_{CCR}$; HO$_{DPR}$: CCR and DPR in Holstein
[2]JE$_{CCR}$; JE$_{DPR}$: CCR and DPR in Jersey

- Low correlations using pedigree-based BLUP

- Correlations using ssGBLUP$_{MF10/5}$ > 0.85 → GEBV$_{early}$ (partial) are good predictors of GEBV$_{later}$ (whole)

- MF provided more stable GEBV

DPR and CCR Genetic Trends in Holstein and Jersey with Metafounders
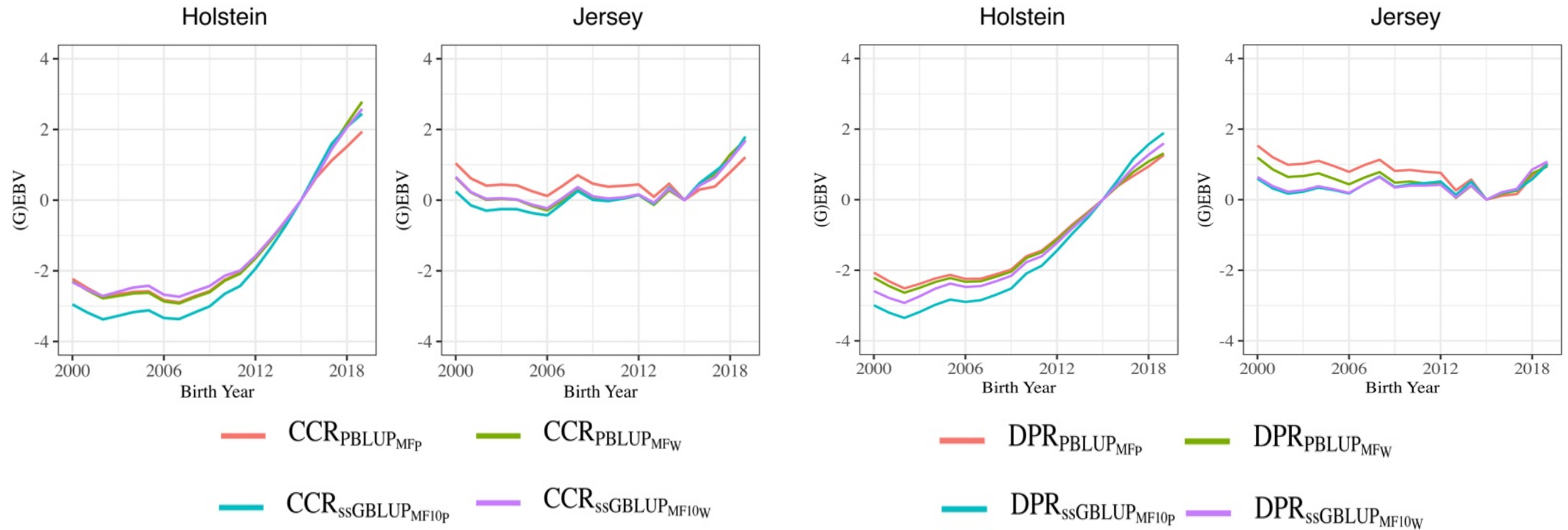
- The four trends with Metafounders exhibited a consistent direction with minor variations

CCR solution of UPG/MF including unknown sires of foreign dams
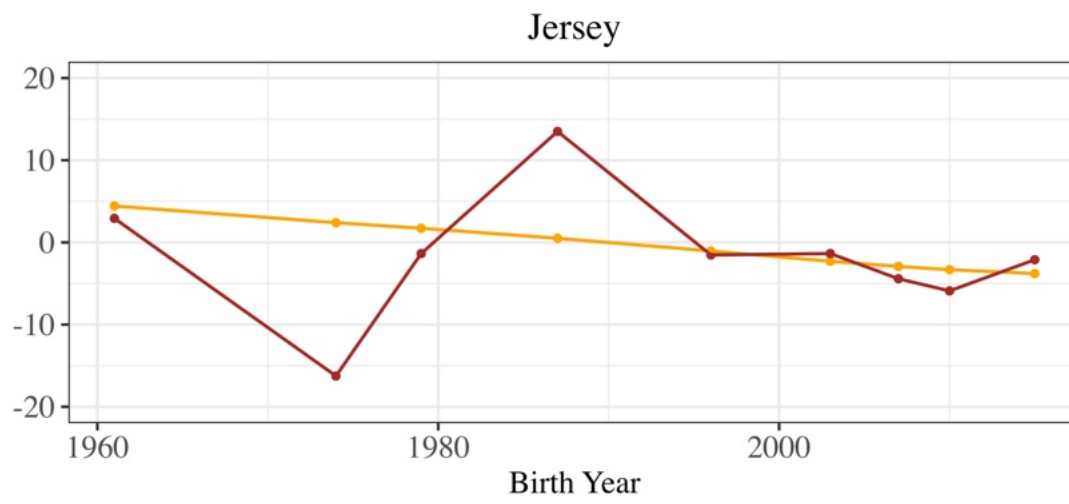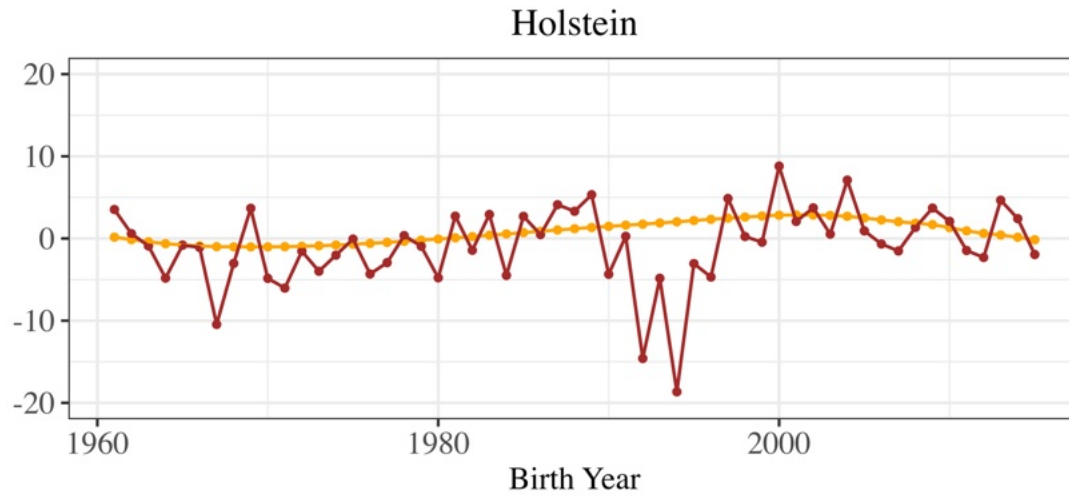
- Less heterogeneous behavior with MF

  - More stable estimates using MF

Conclusion

- Single-step GBLUP is a viable alternative to the current multistep procedure

- Metafounders yielded better results compared to Unknown Parent Groups

- Single-step GBLUP correctly captures the response to selection

Acknowledgements

Thank you

Any questions?