UNIVERSITY OF GEORGIA
College of Agricultural & Environmental Sciences

Single-step genomic predictions for yield traits in US Holsteins with UPG and phenotype-pedigree truncation

Interbull 2021 - Virtual

Daniela Lourenco

A. Cesarani, Y. Masuda, S. Tsuruta, E. Nicolazzi, P. VanRaden, and I. Misztal

Motivation

- Missing pedigree in the US Holstein data
  - ~ 10% sires
  - ~ 20% dams

⇒ Biased EBV

- QP-transformation for $\mathbf{A}^{-1}$
- (Quaas & Pollack, 1981;Westell et al., 1988)

$$\mathbf{A}^{*}=\begin{bmatrix}\mathbf{A}^{-1} & -\mathbf{A}^{-1}\mathbf{Q}\\ -\mathbf{Q}'\mathbf{A}^{-1} & \mathbf{Q}'\mathbf{A}^{-1}\mathbf{Q}\end{bmatrix}$$

- QP-transformation for $\mathbf{H}^{-1}$ (Misztal et al., 2013)

$$\mathbf{H}^{*}=\mathbf{A}^{*}+\begin{bmatrix}0 & 0 & 0\\ 0 & \mathbf{G}^{-1}-\mathbf{A}_{\mathbf{22}}^{-\mathbf{1}} & -(\mathbf{G}^{-1}-\mathbf{A}_{22}^{-1})\mathbf{Q}_2\\ 0 & -\mathbf{Q}_2'(\mathbf{G}^{-1}-\mathbf{A}_{22}^{-1}) & \mathbf{Q}_2'(\mathbf{G}^{-1}-\mathbf{A}_{22}^{-1})\mathbf{Q}_2\end{bmatrix}$$

- Altered QP-transformation for $\mathbf{H}^{-1}$ (Tsuruta et al., 2019)

$$\mathbf{H}^{*}=\mathbf{A}^{*}+\begin{bmatrix}0 & 0 & 0\\ 0 & \mathbf{G}^{-1}-\mathbf{A}_{\mathbf{22}}^{-\mathbf{1}} & -(-\mathbf{A}_{22}^{-1})\mathbf{Q}_2\\ 0 & -\mathbf{Q}_2'(-\mathbf{A}_{22}^{-1}) & \mathbf{Q}_2'(-\mathbf{A}_{22}^{-1})\mathbf{Q}_2\end{bmatrix}$$

Motivation

- Matilainen et al. (2016): female fertility traits in Nordic Reds
- Tsuruta et al. (2019): type traits in US Holsteins

- Masuda et al. 2018 (Protein)

Data	UPG	R2	b1
Truncated 2011	Pedigree	0.52	0.78
	Ped. + Genomic	0.32	0.51
	No UPGs	0.50	0.78

UPG poorly estimated
Large number of genotyped
females with missing
pedigree and no phenotypes

- Lourenco et al. (2014): pedigree truncation helped to reduce bias

- due to missingness

Objectives

- Assess bias and reliability of GEBV for bulls and cows in ssGBLUP
  - Milk, Fat, and Protein
  - UPG for $\mathbf{A}^{-1}$ (SS_UPG)
  - UPG for $\mathbf{A}^{-1}$ and $\mathbf{A}_{22}^{-1}$ (SS_UPG2)

- Six phenotype-pedigree truncation scenarios
  - 1980, 1990, or 2000
  - Pedigree depth 2 or 3

- Feasibility of ssGBLUP for dairy evaluations in the US

Data

COUNCIL ON DAIRY CATTLE BREEDING

- US Holstein data up to December 2018

Phenotype cut-off scenario	Records		Genotypes	Animals in pedigree	
	N	Cows		Depth=3	Depth=2
Pheno1980	77.8 M	31.5 M	862 K	40.5 M	39.9 M

Analyses

- QP-transformation for $\mathbf{A}^{-1}$ in $\mathbf{H}^{-1}$

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

⇒ SS_UPG

- Altered QP-transformation for $\mathbf{H}^{-1}$ (Tsuruta et al., 2019)

$$\mathbf{H}_{UPG2}^{*} = \mathbf{A}^{*} + \begin{bmatrix} 0 & 0 & 0 \\ 0 & \mathbf{G}_{\mathrm{APY}}^{-1} - \mathbf{A}_{\mathbf{22}}^{-\mathbf{1}} & -(-\mathbf{A}_{22}^{-1})\mathbf{Q}_{2} \\ 0 & -\mathbf{Q}_{2}'(-\mathbf{A}_{22}^{-1}) & \mathbf{Q}_{2}'(-\mathbf{A}_{22}^{-1})\mathbf{Q}_{2} \end{bmatrix}$$

⇒ SS_UPG2

- BLUP90IOD2OMP1 for each phenotype-pedigree truncation scenario
  - APY with 15,000 core animals

Validation

- Complete data: 2018
- Reduced data: 2014

- 2,710 bulls
  - Reliability: $[\mathrm{CORR}(\mathrm{DYD}, (\mathrm{G})\mathrm{EBV})]^2$
  - Dispersion: $\mathrm{DYD} = b_0 + b_1(\mathrm{G})\mathrm{EBV}$

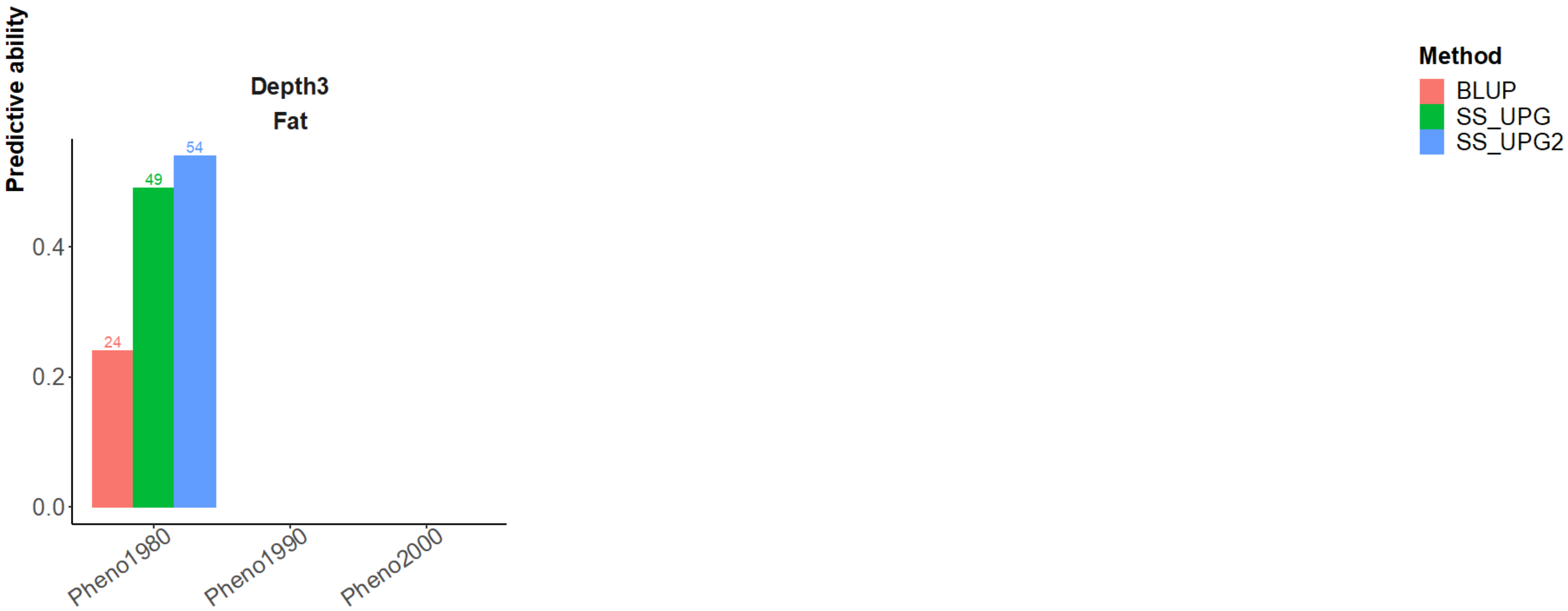
- 381,779 Cows
  - Predictive ability: CORR($y_{adj}, (\mathrm{G})\mathrm{EBV}$)
  - Dispersion: $y_{adj} = b_0 + b_1(\mathrm{G})\mathrm{EBV}$

Reliability for bulls

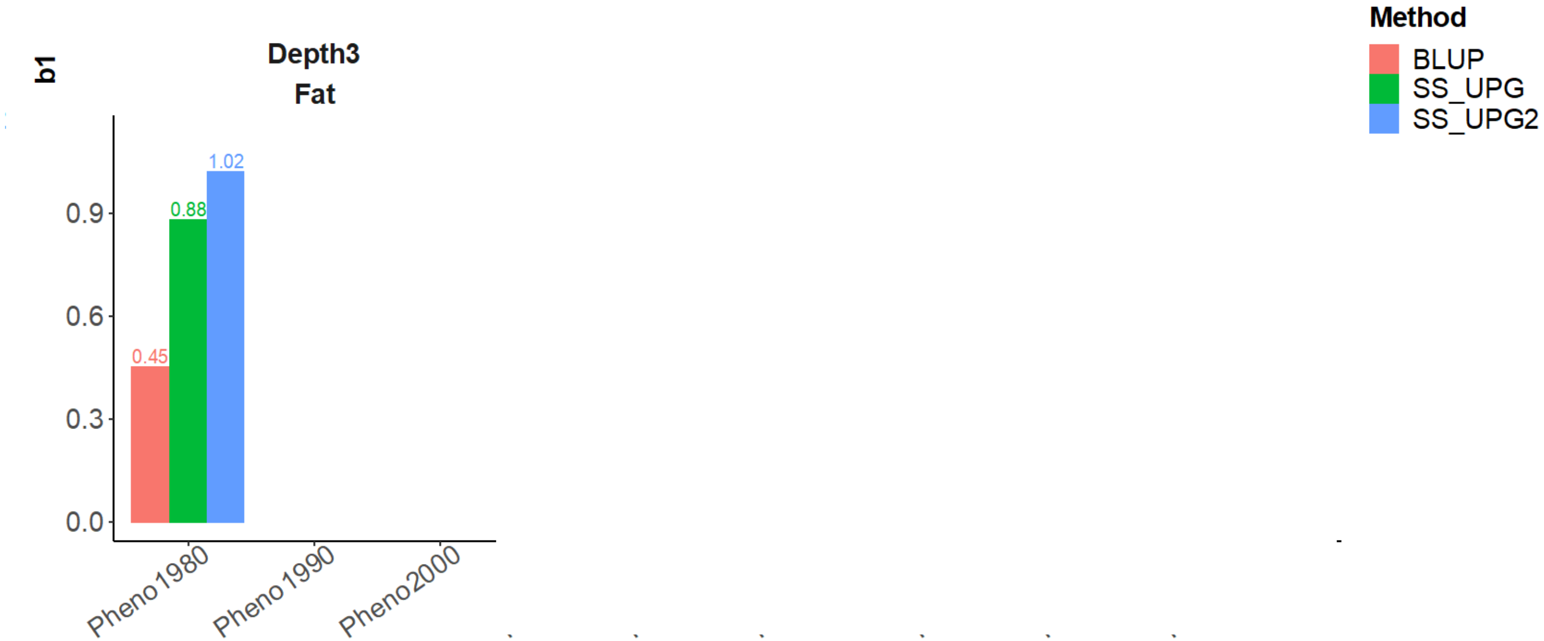
b1 for bulls

b1
Depth3
Fat
1.00
0.75
0.50
0.25
0.00
0.86
0.86
0.98
Pheno1980
Pheno1990
Pheno2000
Method
BLUP
SS_UPG
SS_UPG2

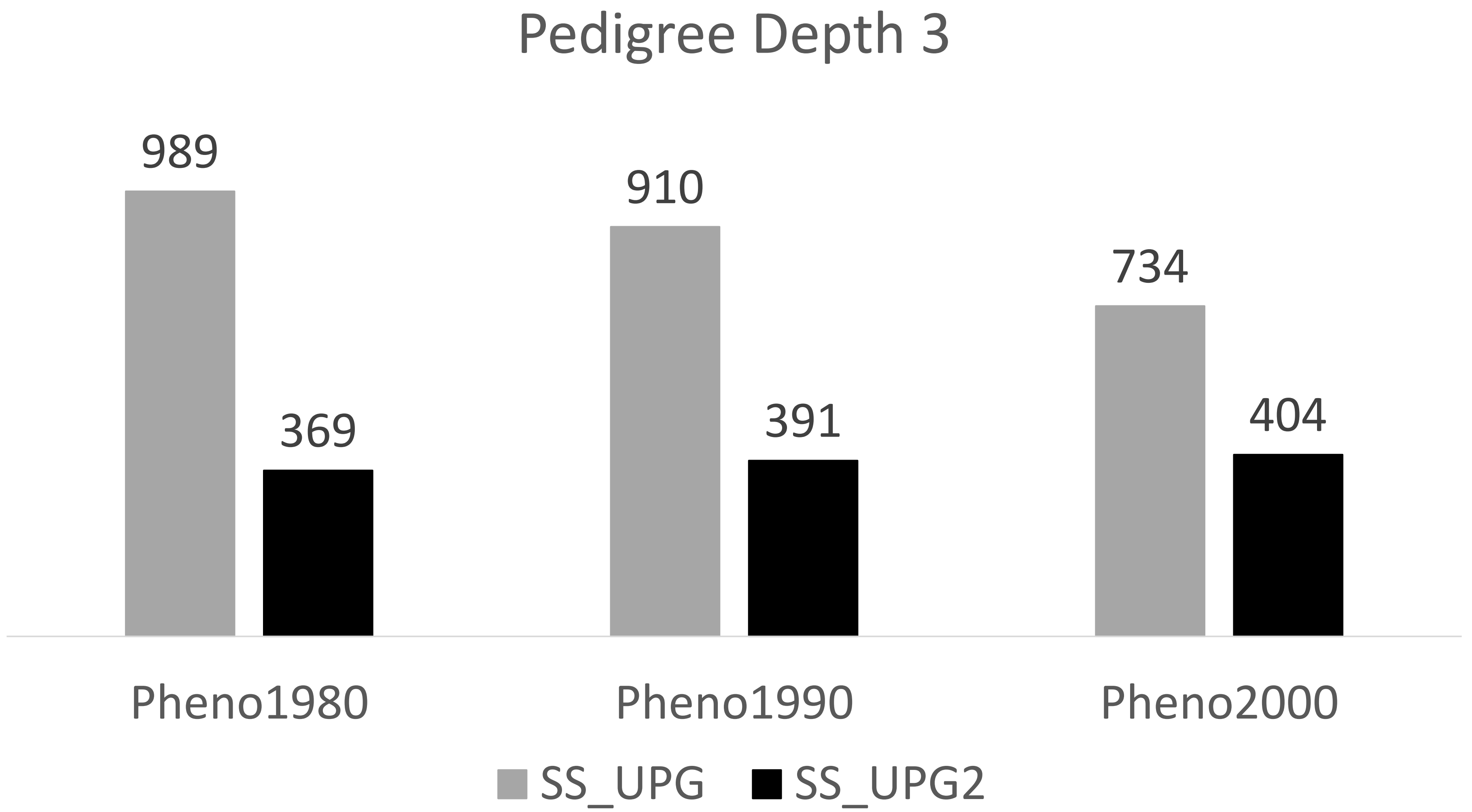
Predictive ability for cows



b1 for cows


Depth3
Fat
b1
0.0
0.3
0.6
0.9
0.45
0.88
1.02
Pheno1980
Pheno1990
Pheno2000
Method
BLUP
SS_UPG
SS_UPG2

Rounds to convergence



ssGBLUP with many more genotypes

	This study	A. Cesarani (Friday)
Genotypes	**862k**	**3.4M + data**
Validation bulls	1,529	1,529
Reliability		
Milk	0.72	0.81
Fat	0.69	0.80
Protein	0.67	0.77

Conclusions

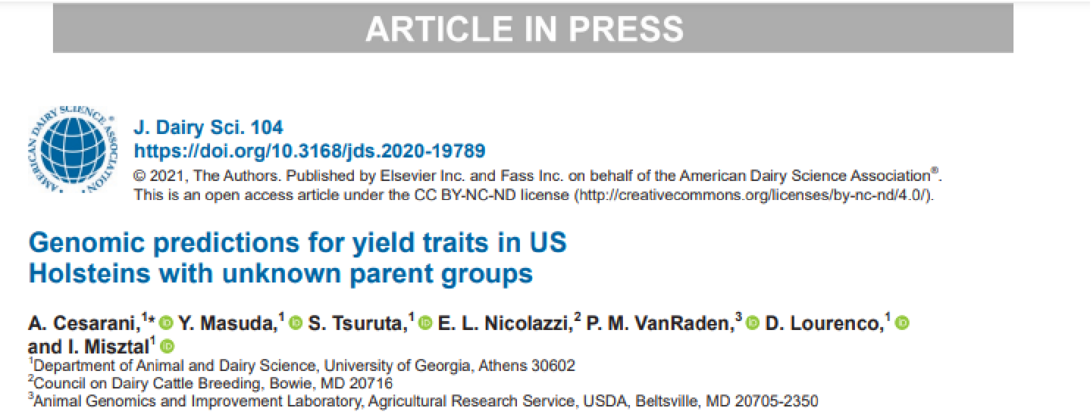
- Genomic predictions for yield traits in US Holsteins using single-step
  - UPG for $\mathbf{A}^{-1}$ and $\mathbf{A}_{22}^{-1}$
  - Reliable and unbiased
- Removing old generations of pedigree and phenotypes do not compromise predictions for young selection candidates
- Large-scale dairy genomic evaluations are feasible
  - Up to 3.4 Million genotyped animals in less than 3 days
  - Indirect predictions could further reduce computing time

Acknowledgements

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

U.S. Registered Holsteins
FOR MAXIMUM PROFIT
HOLSTEIN ASSOCIATION USA, INC.

USDA NIFA



ARTICLE IN PRESS

J. Dairy Sci. 104
https://doi.org/10.3168/jds.2020-19789

© 2021, The Authors. Published by Elsevier Inc. and Fass Inc. on behalf of the American Dairy Science Association®.
This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Genomic predictions for yield traits in US Holsteins with unknown parent groups

A. Cesarani,[1*] Y. Masuda,[1] S. Tsuruta,[1] E. L. Nicolazzi,[2] P. M. VanRaden,[3] D. Lourenco,[1] and I. Misztal[1]
[1]Department of Animal and Dairy Science, University of Georgia, Athens 30602
[2]Council on Dairy Cattle Breeding, Bowie, MD 20716
[3]Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705-2350