

Genomic predictability of single-step GBLUP for production traits in US Holstein

Y. Masuda¹, P. M. VanRaden², H. L. Bradford², A. Legarra³, I. Misztal¹, and
T. J. Lawlor⁴

1 University of Georgia, USA; 2 AGIL, USDA, USA;
3 INRA, France; 4 Holstein Association USA, Inc., USA

ADSA 2018, June 24-27, Knoxville, TN

Background

- Genomic prediction with single-step GBLUP (ssGBLUP)
 - Genotyped + non-genotyped animals
 - Accountability for pre-selection
 - APY: dimensionality reduction in marker genotypes
- Required: compatibility among relationship matrices

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

- Reasonable in complete pedigree
- Missing pedigree: adjustment of \mathbf{A}_{22}^{-1} by ω
- How to use unknown parent groups (UPG)?

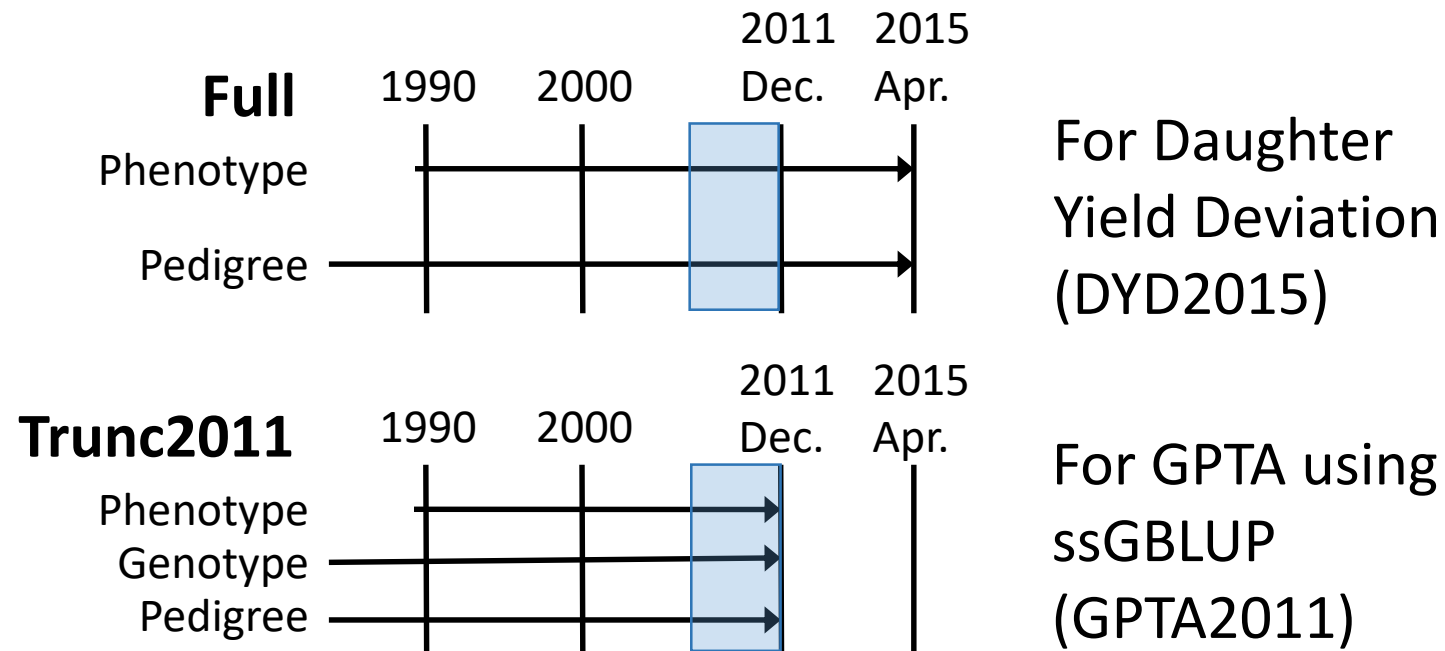
Objectives

- To validate genomic predictions for young bulls by different configurations of UPG in US Holstein
- To discuss possible modifications on \mathbf{H}^{-1} to handle UPG in ssGBLUP: a simulation study

Full data in Holstein

	Description	Number of records/animals
Phenotype	Milk, fat, and protein yield (305-d basis) for US Holstein cows recorded between Jan. 1990 and Apr. 2015	37,259,427
	Cows with phenotype(s)	15,891,366
Pedigree	Animals born in Apr. 2015 or earlier (3-gen. back from phenotyped cows) 185 UPGs	22,963,255
Genotype	Animals born in Apr. 2015 or earlier (60,671 markers)	764,029

Validation study



Validation Bulls:
Genotyped young bulls
with no tested daughters
in 2011 but with at least
50 tested daughters in
2015 (N=3,797)

$$DYD2015 = b_1 \times GPTA2011 + b_0$$

- R^2 : validation reliability
- Slope (b_1): Inflation of prediction

Different UPG in \mathbf{H}^{-1}

1. Weight (ω) on \mathbf{A}_{22}^{-1} : **0.9** or **1.0**
2. UPG: **pedigree + genomic UPG**, **pedigree UPG only**, or **no UPG**
(genomic UPG) (pedigree UPG)

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

DYD2015 vs GPTA2011 (Protein)

Data				R2	b1
Official GPTA 2011				0.51	0.81
Data	UPG	$\omega=0.9$	b1	$\omega=1.0$	b1
GPTA2011	Genomic UPG	0.39	0.74	0.32	0.51

DYD2015 vs GPTA2011 (Protein)

Data				R2	b1
Official GPTA 2011				0.51	0.81
Data	UPG	$\omega=0.9$ R2	b1	$\omega=1.0$ R2	b1
GPTA2011	Genomic UPG	0.39	0.74	0.32	0.51
	Pedigree UPG	0.50	0.96	0.52	0.78
	No UPGs			0.50	0.78

Low accuracy with exact UPG

- GPTA for young genotypes

- Pedigree UPG: $GPTA = w_1 PA + w_2 DGV - w_3 PI \approx DGV$

- Genomic UPG: $GPTA = w_1 PA + w_2 DGV - w_3 PI + w_4 UPG \approx DGV + UPG$

Larger weights with many genotypes

Too large for young animals

- Possible solutions

- Just using pedigree UPG
 - Discounting UPG effects
 - Removing double counting between DGV and UPG
 - Scaling **A** to **G** (“metafounders”)

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

Missing parents in ssGBLUP

- Genomic UPG

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

- Genomic UPG without $\mathbf{Q}'\mathbf{G}^{-1}\mathbf{Q}$

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

- Pedigree UPG

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

With A_{22}^*

- Genomic UPG

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

- Genomic UPG without $\mathbf{Q}'\mathbf{G}^{-1}\mathbf{Q}$

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

- Pedigree UPG

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

A_{22}^* : Modification with UPG

- Indirect inversion

$$A_{22}^{-1} = A^{22} - A^{21}(A^{11})^{-1}A^{12}$$

$$\text{where } A^{-1} = \begin{bmatrix} A^{11} & A^{12} \\ A^{21} & A^{22} \end{bmatrix}$$

- With UPG

$$A_{22}^* = A^{22} - [A^{21} \quad A^{23}] \begin{bmatrix} A^{11} & A^{13} \\ A^{31} & A^{33} + I \end{bmatrix} \begin{bmatrix} A^{12} \\ A^{32} \end{bmatrix}$$

$$\text{where } A^* = \begin{bmatrix} A^{11} & A^{12} & A^{13} \\ A^{21} & A^{22} & A^{23} \\ A^{31} & A^{32} & A^{33} \end{bmatrix} = \begin{bmatrix} A^{11} & A^{12} & -[A^{11} & A^{12}]Q \\ A^{21} & A^{22} & -[A^{21} & A^{22}]Q \\ -Q' \begin{bmatrix} A^{11} \\ A^{21} \end{bmatrix} & -Q' \begin{bmatrix} A^{12} \\ A^{22} \end{bmatrix} & Q'A^{-1}Q \end{bmatrix}$$

Simulation study

- Structure
 - $h^2 = 0.3$
 - Sex-limited trait (n = 90,000)
 - EBV selection
 - 10 generations (n = 164,500)
 - Ne: 200 theoretical; 25 realized
 - Mean F in last generation: 0.11
- Genotypes
 - 18,674 total
 - 5108 in gen. 10 for validation

- Assignment of UPGs
 - UPG1 for generation 0-4
 - UPG2 for generation 5-7
 - UPG3 for generation 8-10

Category	Non genotyped	Genotyped
Top bulls	0	0
Top cows	5% (dam)	0
Bottom bulls	30% (dam)	10% (dam)
Bottom cows	30% (dam)	10% (dam)

Results from simulation

	Standard A_{22}^{-1}		Modified A_{22}^*	
	R2	b1	R2	b1
Genomic UPG	0.53	0.86	0.61	1.01

* Genotyped young animals without records

Results from simulation

	Standard A_{22}^{-1}		Modified A_{22}^*	
	R2	b1	R2	b1
Genomic UPG	0.53	0.86	0.61	1.01
without $Q'G^{-1}Q$	0.62	1.05	0.63	1.04
Pedigree UPG	0.63	1.06	0.63	1.06

	R2	b1
Metafounders	0.63	1.08

* Genotyped young animals without records

Summary

- Missing pedigree may reduce the accuracy of genomic prediction in single-step GBLUP.
 - Specific data structure with many missing parents
- We have several options to discount the possible double-counting of the UPG contribution in \mathbf{H}^* .
 - Removal of \mathbf{G}^{-1} from the additional UPG contribution
 - Use of Modified \mathbf{A}_{22}^{-1}
 - Metafounders

Acknowledgement

- USDA NIFA (2015-67015-22936) and Holstein Association USA for financial support.
- Council of Dairy Cattle Breeding for phenotype, genotype, and pedigree data.
- John Cole and Melvin Tooker (USDA-AGIL) for preparing the initial data sets and a computing environment.