Single-step genomic evaluation of crossbreed dairy cattle in the US

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Introduction

- Genomic evaluation in US by multistep method
- Evaluation by crossbreds by SNP effects from purebreds
  - Accuracy slightly higher than parent average
- Crossbred genotypes not used for purebred evaluation
- Move to single-step models
  - Avoid preselection bias, allow more complex models, simplify pipelines

Goals

- Implement single-step evaluation for crossbreds
- Questions:
  - Are reliabilities for crossbreds higher than based on parent average?
  - Are PTA for purebreds negatively affected by crossbred data?
  - Is computing time reasonable?

Single step in dairy at UGA

- Original single-step paper (2010)
- ……many papers – inflation …….
- Holsteins – current CDCB data (2020)
  - High R^2 and low inflation
  - Data truncation before 2000 not affecting young animals
- 5 dairy breeds with 4 M genotypes (2021)
  - Similar accuracy for single- and multi-breed with choice of core animals

J. Dairy Sci. 93:743–752
doi:10.3168/jds.2009-2730

Hot topic: **A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score**[1]

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#Holstein Association USA Inc., Brattleboro, VT 05302-0808

ARTICLE IN PRESS

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

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

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J. Dairy Sci. 105
https://doi.org/10.3168/jds.2021-21505

Multibreed genomic evaluation for production traits of dairy cattle in the United States using single-step genomic best linear unbiased predictor

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[2]INRA, UMR1388 GenPhySE, Castanet-Tolosan, France, 31320
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Data

Phenotypes from 2000 recorded in Holstein, Jersey, and their crosses

Phenotypes	47,417,185
Cows with records	20,367,132
Tot. animals	27,111,201
Genotypes	1,424,863

Materials and Methods I

- Milk (MY), fat (FY), and protein (PY) 305-d yields recorded from January 2000 (Cesarani et al., 2021)

- Three-trait repeatability model $\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_a\mathbf{Q}_a\mathbf{g}_a + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_p\mathbf{p} + \mathbf{e}$

herd × sire

herd × management, age × parity,
inbreeding, heterosis

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  - $\mathbf{Z}_h\mathbf{h}$: herd × management, age × parity, inbreeding, heterosis
  - $\mathbf{Z}_a\mathbf{Q}_a\mathbf{g}_a$: herd × sire

- **Complete data**: phenotypes up to August 2021
- **Reduced data**: phenotypes up to August 2017

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  - $\mathbf{Z}_h\mathbf{h}$: herd × sire

- **Complete data**: phenotypes up to August 2021
- **Reduced data**: phenotypes up to August 2017

- UPG (8 groups per breed) in $\mathbf{A}^{-1}$ and $\mathbf{A}_{22}^{-1}$: difference by breed, YOB, and sex

Materials and Methods II

Validation cows = genotyped females with no phenotypes in the reduced dataset

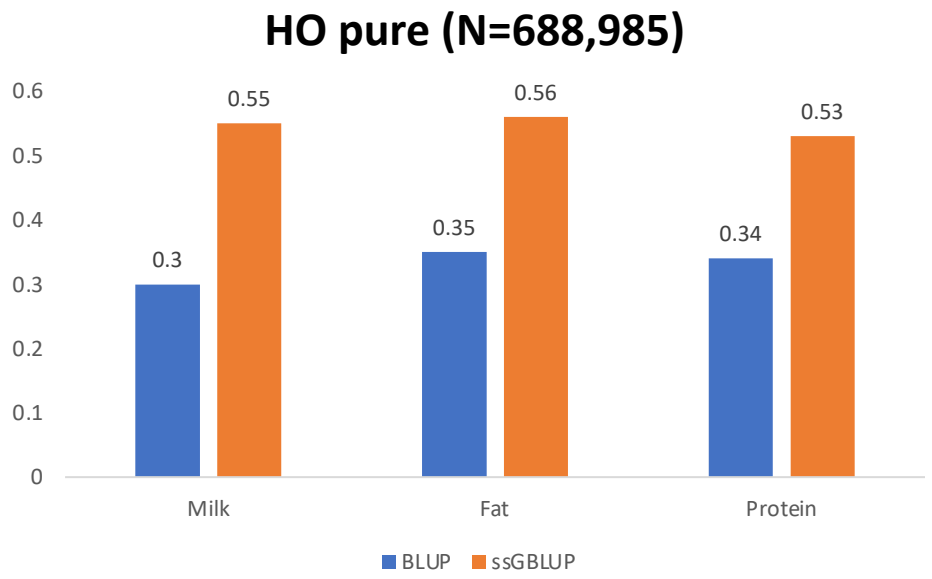
- **HO pure** = HO animals with both sire and dam HO
- **JE pure** = JE animals with both sire and dam JE
- **cross** = HO or JE animals with at least one parent of the opposite breed
- **cross F1** = cross animals with 100 heterosis

Validation method = predictivity based on adjusted phenotypes (correlation and b_1)

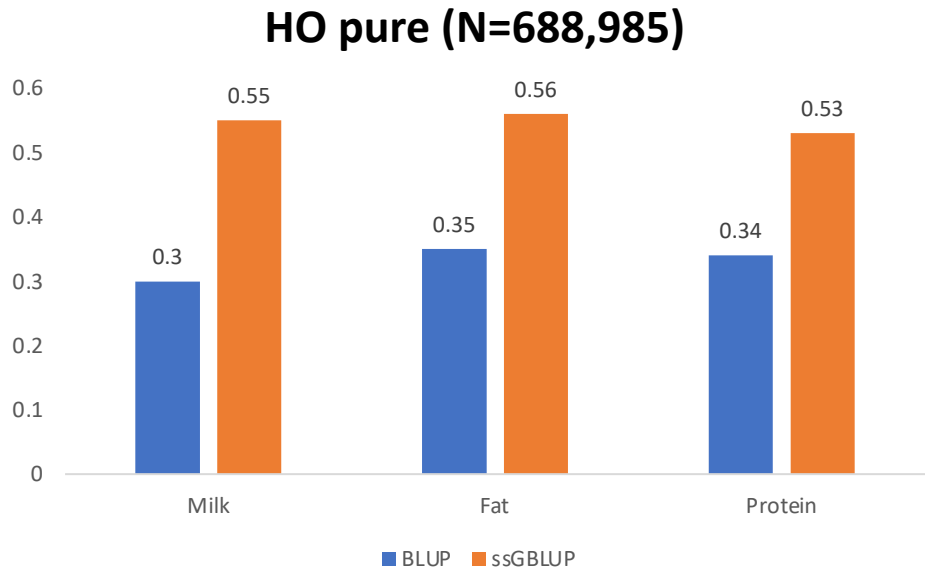
pred=corr(PTA, y-”fixed”)

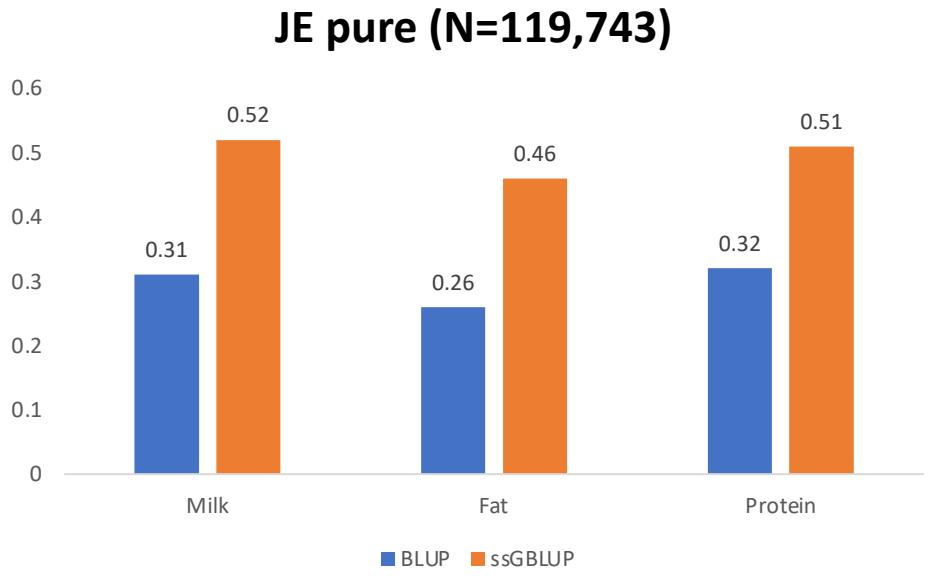
Predictive abilities for cows

Predictive abilities for cows



Predictive abilities for cows





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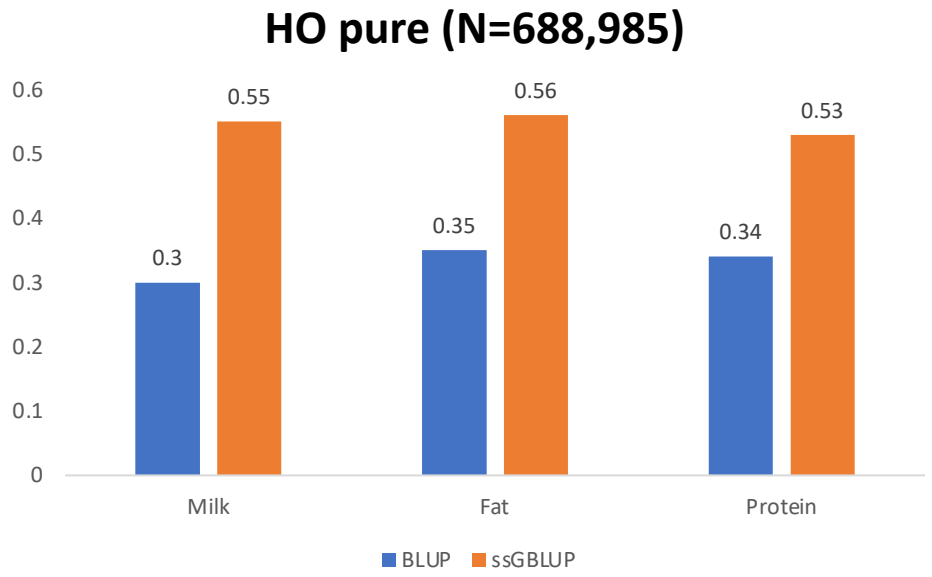
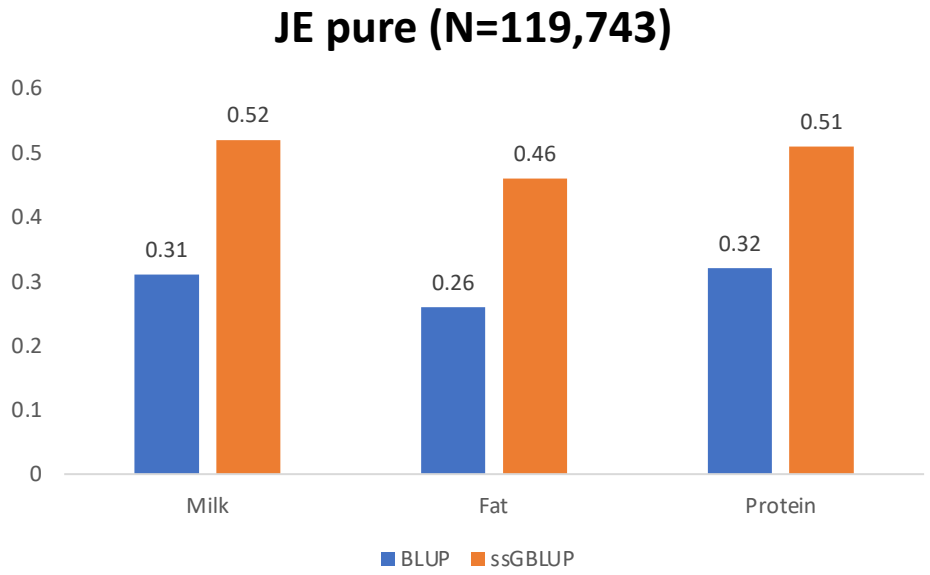
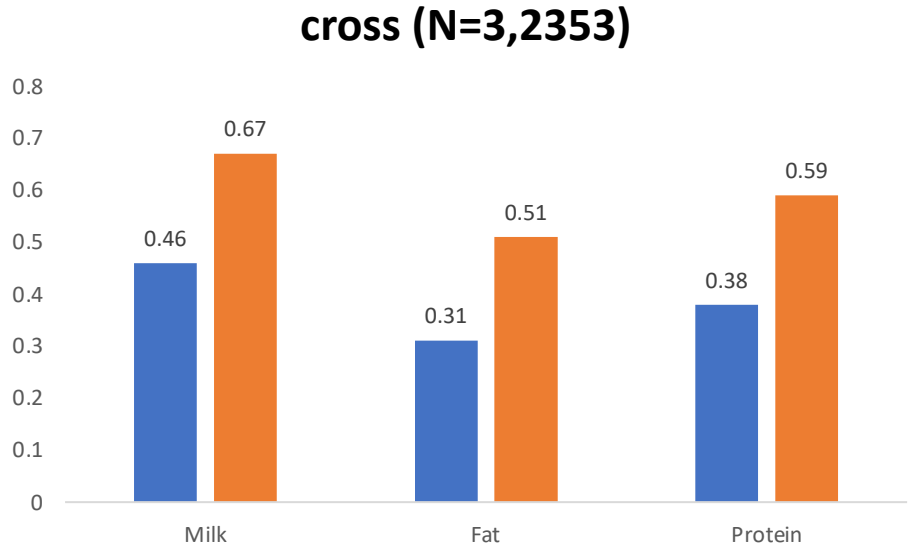
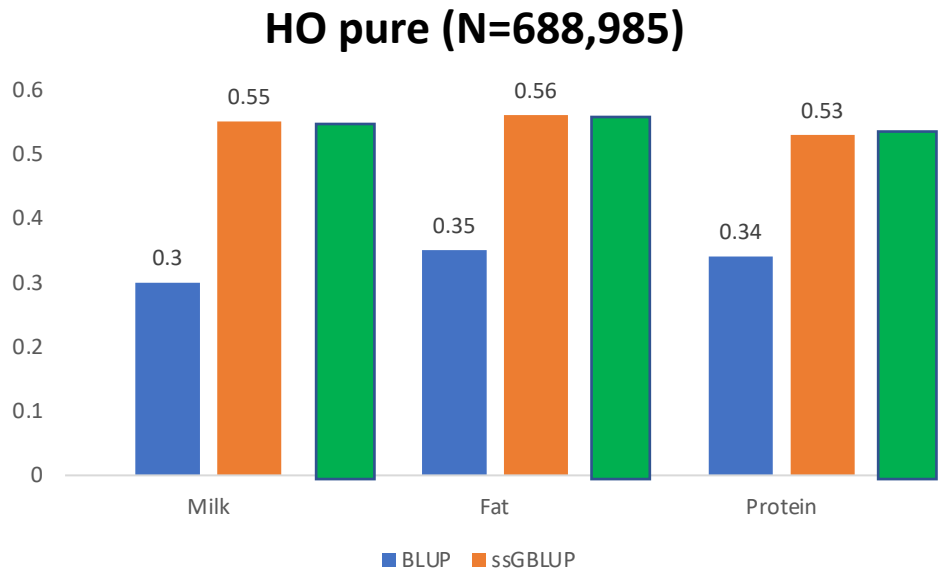
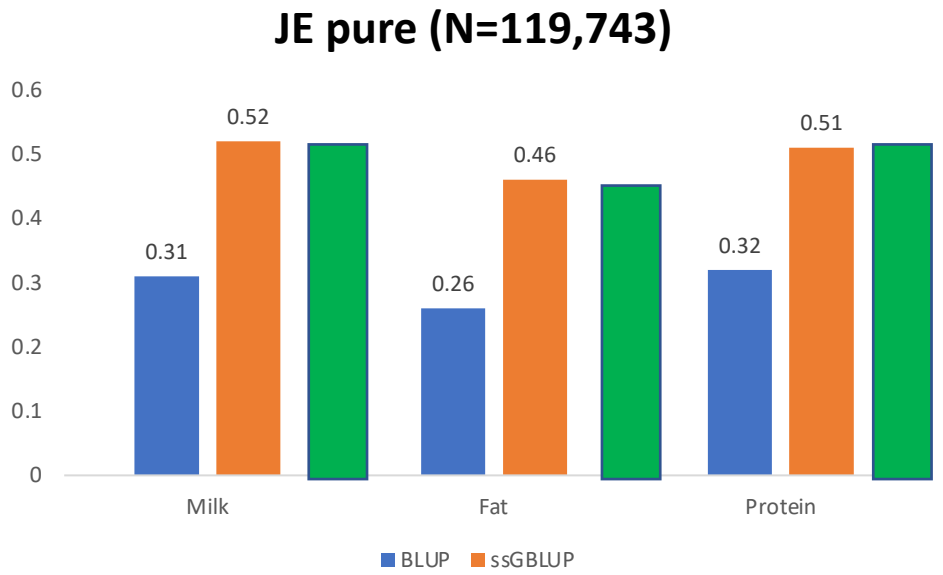


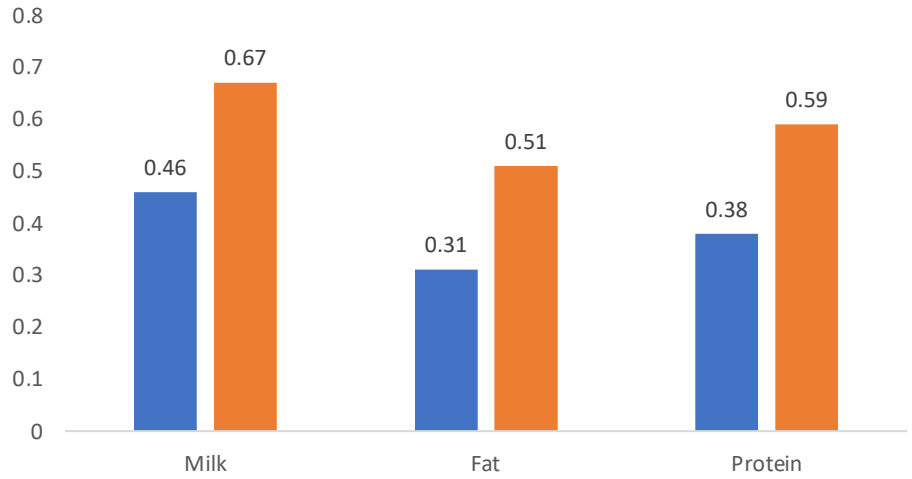




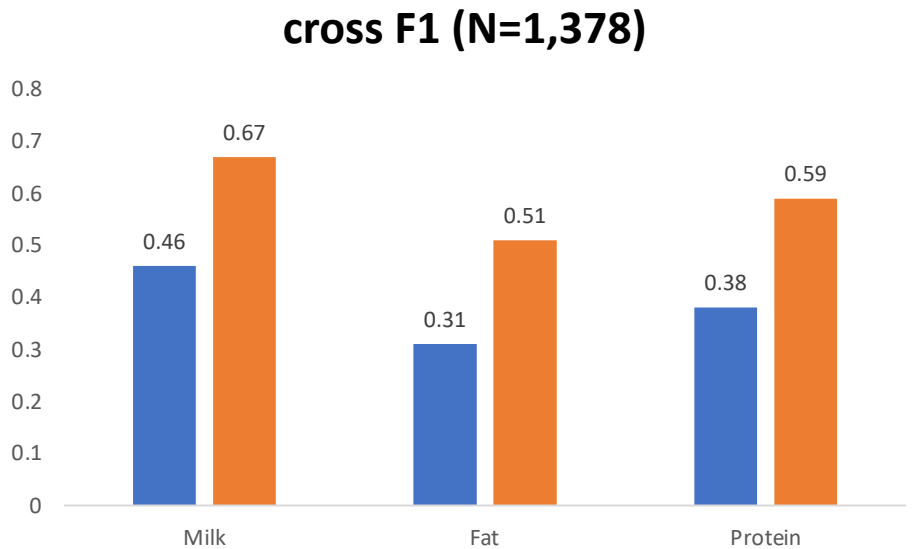
Predictive abilities for cows



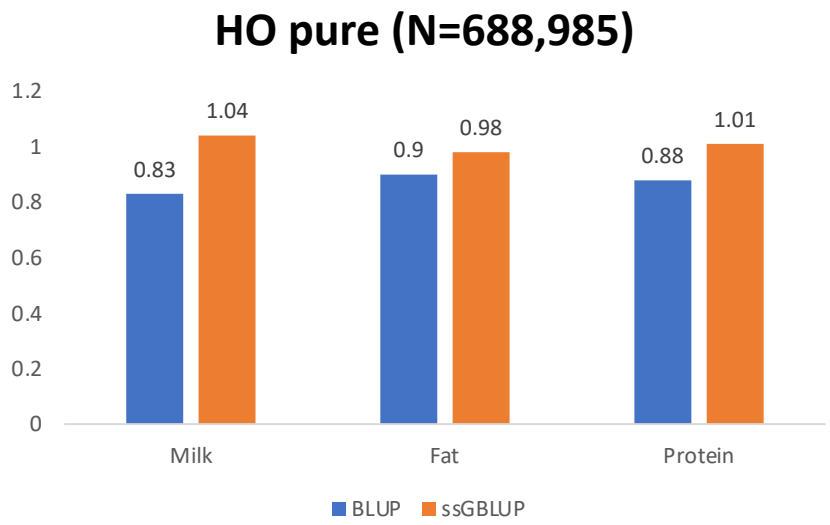




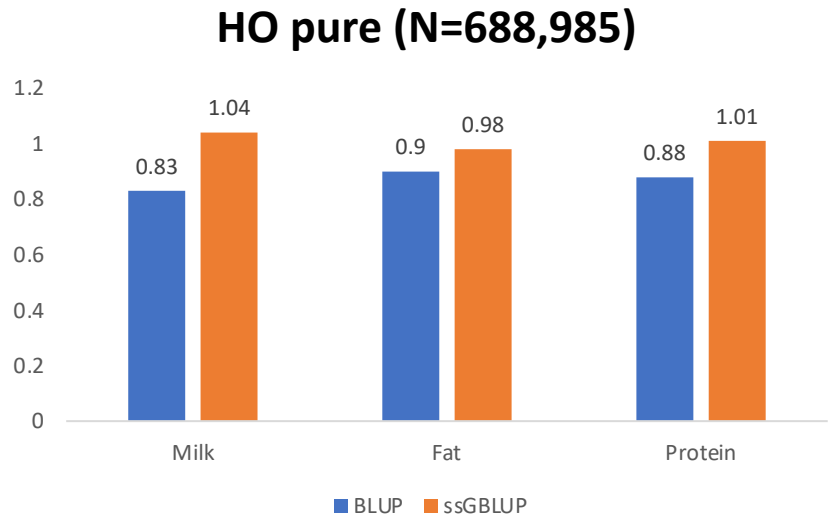
Single breed analyzes



b1 values


HO pure (N=688,985)
1.2
1
0.8
0.6
0.4
0.2
0
1.04
0.83
0.98
0.9
1.01
0.88
Milk
Fat
Protein
BLUP
ssGBLUP

b1 values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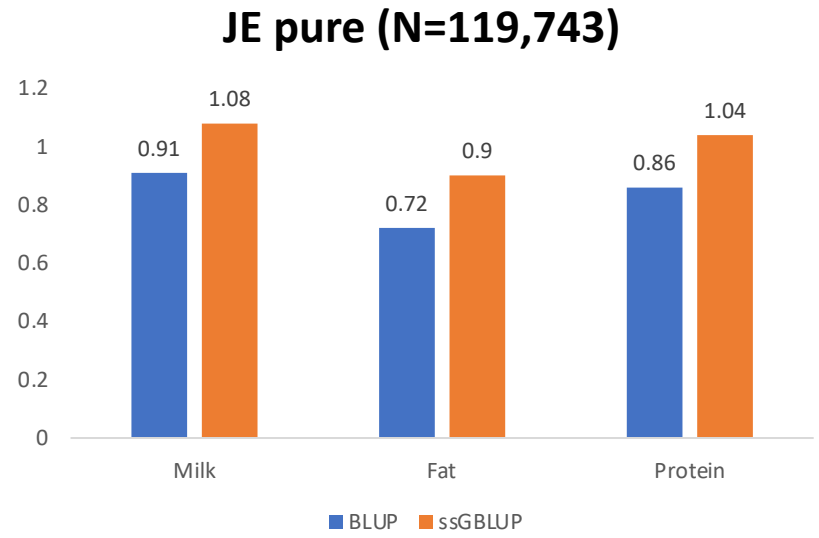
JE pure (N=119,743)
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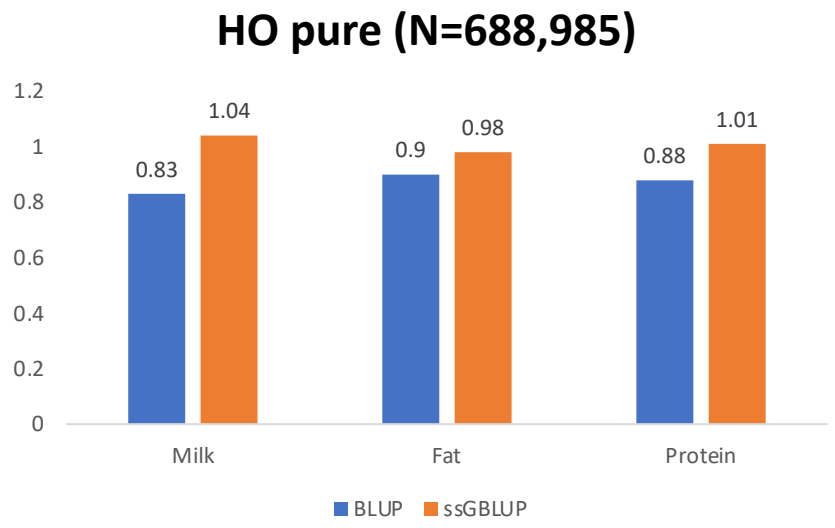
b1 values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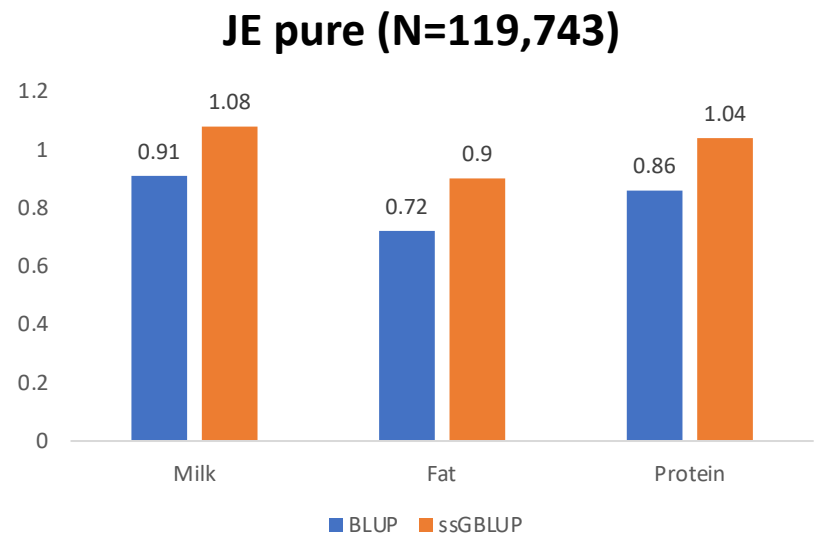
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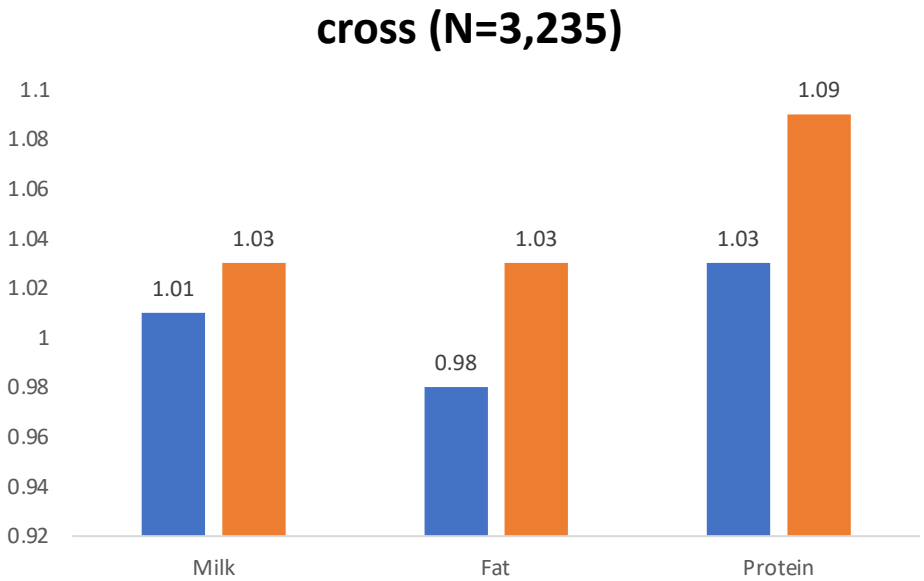
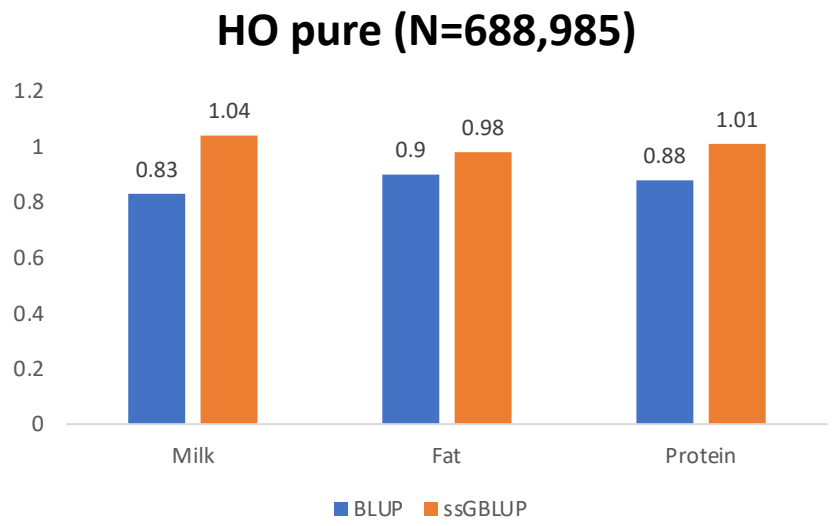

cross (N=3,235)
1.1
1.08
1.06
1.04
1.02
1
0.98
0.96
0.94
0.92
1.01
1.03
0.98
1.03
1.03
1.09
Milk
Fat
Protein

b1 values


HO pure (N=688,985)
1.2
1
0.8
0.6
0.4
0.2
0
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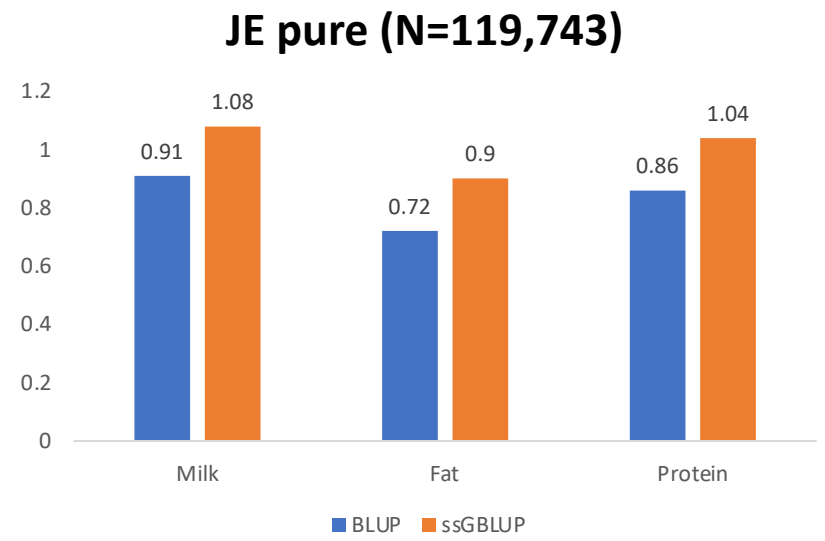
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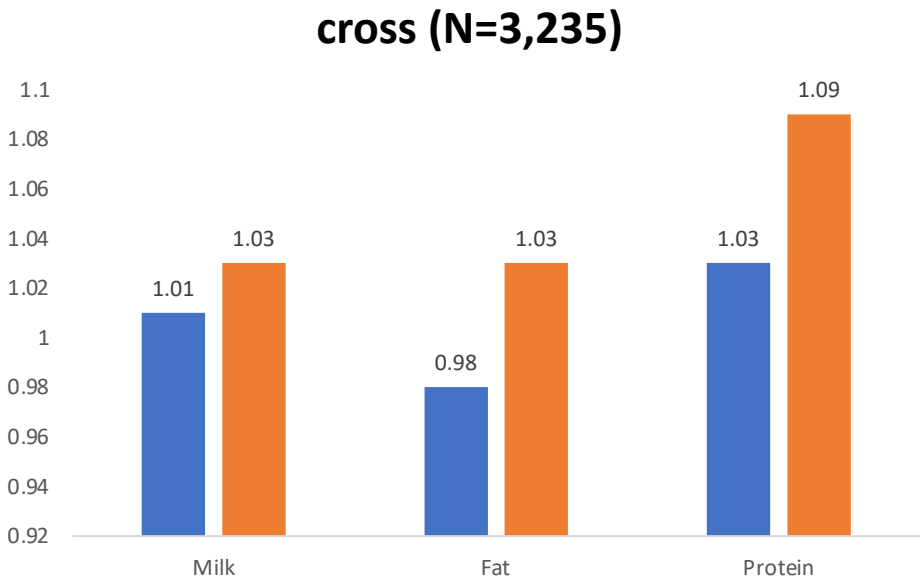
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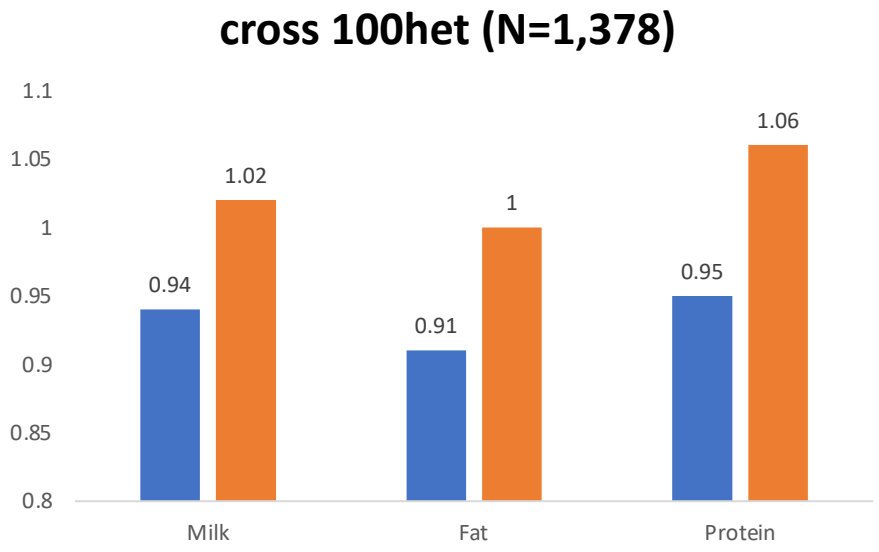

cross 100het (N=1,378)
1.1
1.05
1
0.95
0.9
0.85
0.8
0.94
1.02
0.91
1
0.95
1.06
Milk
Fat
Protein

Predictivity and accuracy

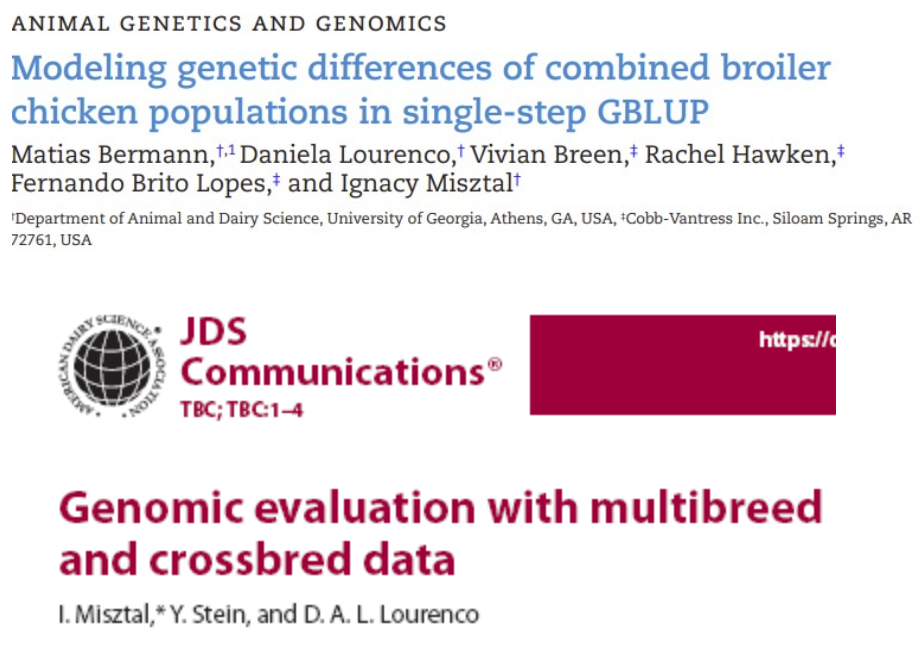
$$accuracy = \frac{pred}{h} = \frac{corr(PTA, y - \text{"fixed"})}{h}$$

For Holstein milk: pred = 0.55, acc ≈ 0.90, ➔ $h^2 \approx 0.22$

For crossbreds: pred = 0.67, assume $h^2 \approx 0.22$ ➔ acc = 1.10 ??????

Breed type(F1, F2, reciprocal…) ignored

hard to do from existing data



ANIMAL GENETICS AND GENOMICS

Modeling genetic differences of combined broiler chicken populations in single-step GBLUP

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JDS Communications®

TBC; TBC:1–4

https://

Genomic evaluation with multibreed and crossbred data

I. Misztal,* Y. Stein, and D. A. L. Lourenco

Computing time

Step	Rounds	Sec / round	Time
preGSf90			~ 10 h
BLUP	671	88.98	~ 17 h
ssGBLUP	459	134.06	~ 17 h

Conclusions

- Predictivity for crossbreds higher than expected
  - Results superior if used for management
- Purebred evaluations unaffected by crossbred data
- Computations feasible

Acknowledgements