



Genetic analysis of anogenital distance in dairy cattle

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Dairy Cattle Fertility: Current Challenges

Complex and multifaceted trait

- Conception, pregnancy maintenance, calving, and post-calving cyclicity

Current indicators

- Calving to First Service (CTFS), Non-Return Rate at 56d (NRR)

Slow improvement

- Low heritability of traits used ($h^2 \leq 0.10$)
- Highly influenced by environment and management

Anogenital Distance (AGD)

Distance from the anus to the base of the clitoris

Phenotypic variation attributed to *in utero* exposure to **androgens**

- Reproductive programming window
- High exposure leads to elongation



Associations with Fertility

Shorter AGD is favorably associated with reproductive success in cows and heifers

Trait	Relationship with Short AGD
Age at Puberty	↓
Pregnancy per First AI (Cow)	↑
Pregnancy per First AI (Heifer)	↑
Pregnancy at 450d of age	↑

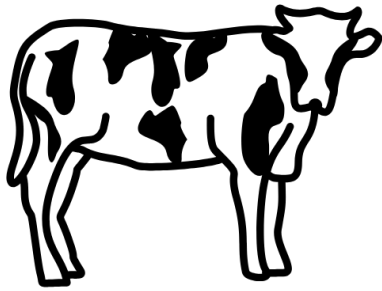
- Moderate heritability estimates
- Strong genetic correlation estimated between AGD in heifers and primiparous cows (0.89 ± 0.05)^b

Heritability	Breed	Country	Parity	Data Size
0.37 ± 0.08	Holstein-Friesian	Ireland ^a	Parities 0-3+	1,180
0.23 ± 0.03	Holstein-Friesian	New Zealand ^b	Heifers	5,010
0.29 ± 0.05	Holstein-Friesian	New Zealand ^b	First parity cows	1,956

^aGobikrushanth et al., 2019

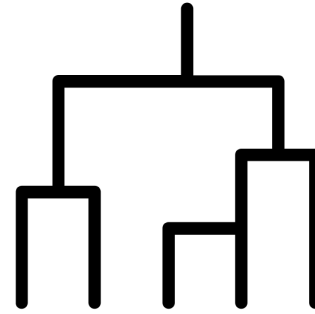
^bStephen et al., 2023

1. Estimate variance components and breeding values
2. Assess the reliability of breeding values
3. Evaluate inclusion of genomic information



PHENOTYPE

864 Heifers
4,124 Cows



PEDIGREE

26,959 Animals
(8 Generations)



GENOTYPE

1,520 Phenotyped
5,111 Unphenotyped

*No repeated records

Variance Component Estimation

$$y = Xb + Za + e$$

Fixed Effects

Animal

Residual

- Recording technician
- Age at measurement (quadratic regression)
- Days since calving (linear regression)
- Herd-year-season at birth

Variance Component Estimation

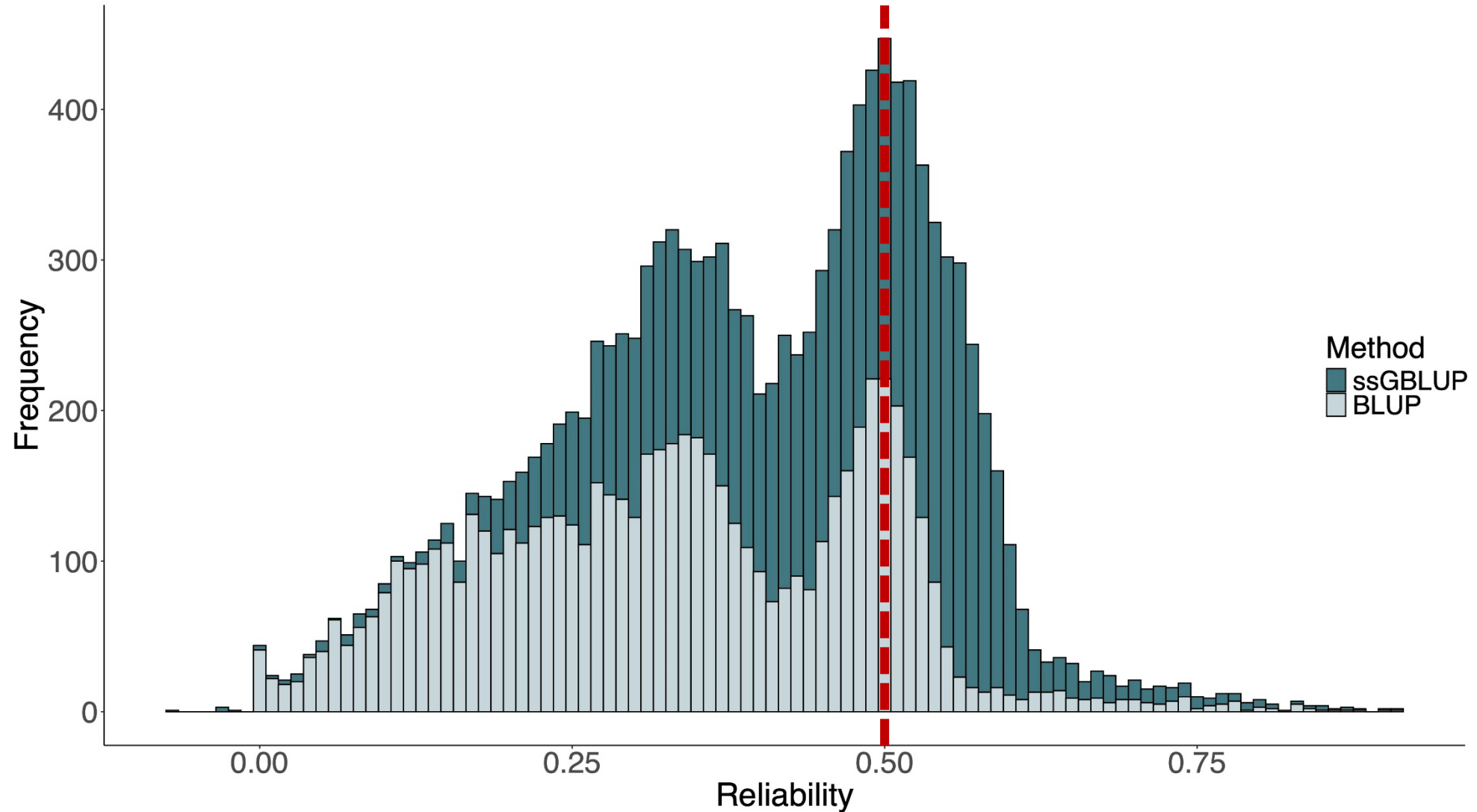
Parameter	Genetic Estimate	Genomic Estimate
Additive Genetic Variance (σ_a^2)	41.48 ± 4.85	38.94 ± 3.94
Residual Variance (σ_e^2)	65.87 ± 3.76	67.53 ± 2.94
Heritability (h^2)	0.39 ± 0.04	0.37 ± 0.03

Breeding Value Reliability

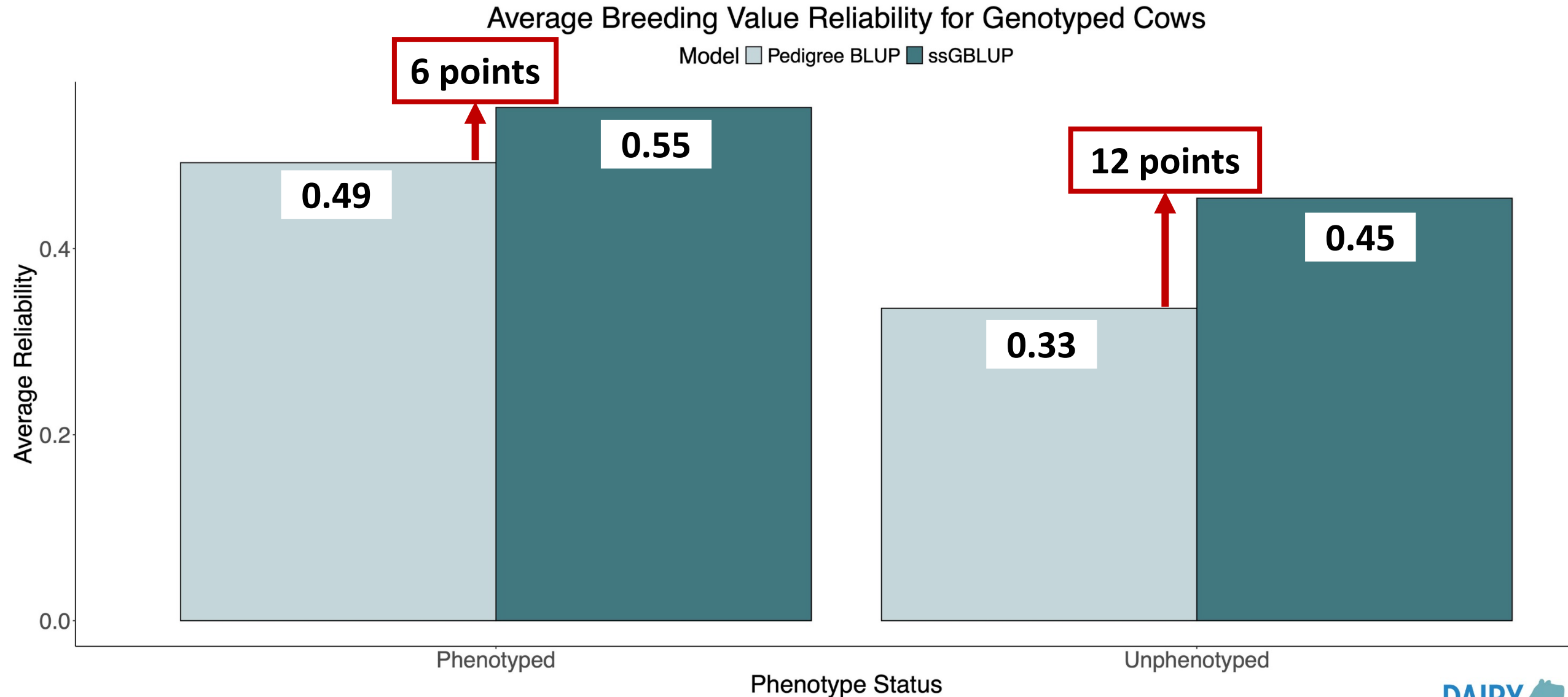
Group	Theoretical Reliability (EBVs)
Phenotyped Cows	0.50
Sires with 10+ Daughters	0.70
Sires with 30+ Daughters	0.83

Breeding Value Reliability

Distribution of Reliabilities for Genotyped Animals



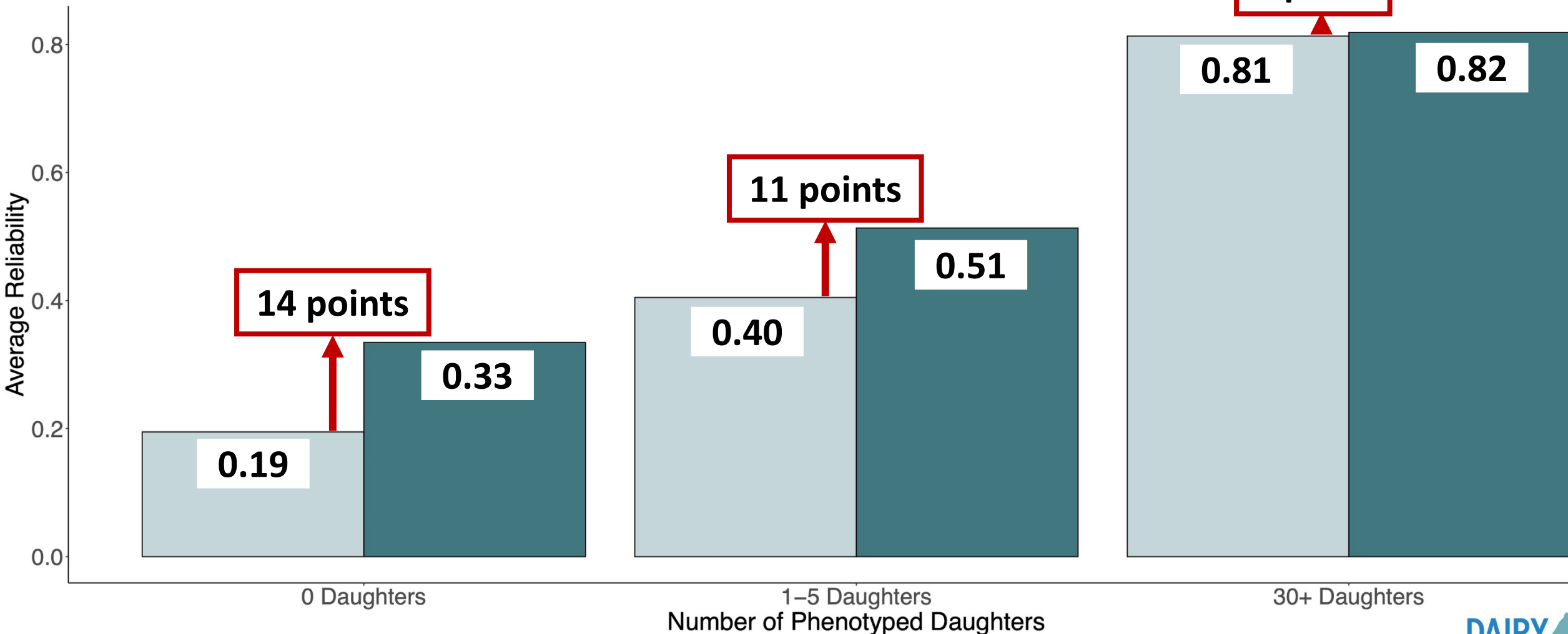
Gain in Reliability with Genomics



Gain in Reliability with Genomics

Average Breeding Value Reliability for Genotyped Sires of Phenotyped Cows

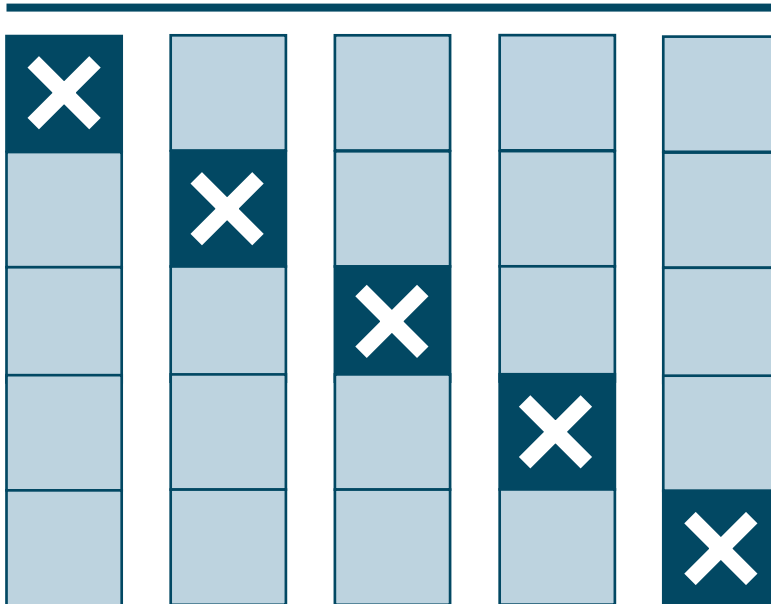
Model ■ Pedigree BLUP ■ ssGBLUP



Validation Methods

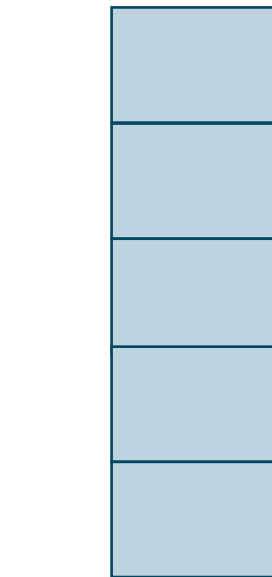
5-Fold Cross-Validation

Masked



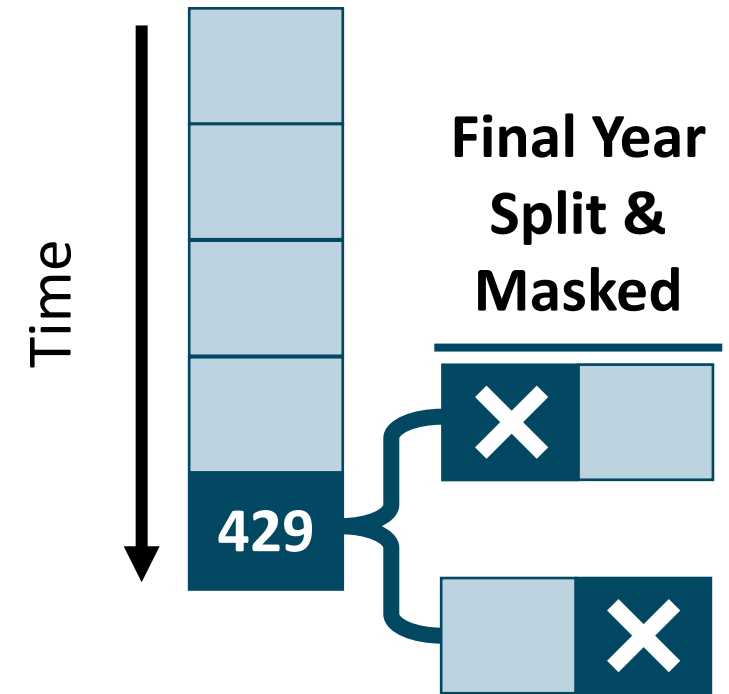
1,513 with genotypes
and phenotypes

Full Analysis



Forward Cross-Validation

Birthyear



5-Fold Cross-Validation			
	Pedigree BLUP	ssGBLUP	Gain
Theoretical Reliability	0.49 ± 0.002	0.51 ± 0.002	0.02
Observed Reliability	0.42 ± 0.005	0.56 ± 0.005	0.14

Forward Cross-Validation			
	Pedigree BLUP	ssGBLUP	Gain
Theoretical Reliability	0.50 ± 0.002	0.56 ± 0.001	0.06
Observed Reliability	0.35 ± 0.020	0.61 ± 0.030	0.26

Breeding Value Correlations

Pearson Correlation coefficients estimated between AGD breeding values and other evaluated trait breeding values

Breeding values for sires with phenotyped daughters

- Provided by Lactanet from the April 2024 evaluation run
- Production and fertility traits

Breeding Value Correlations

Favorable

Fertility Traits

Sires of Phenotyped Daughters N=912

Age at First Service

0.19 ± 0.03

First Service to Conception (heifers)

0.07 ± 0.03

First Service to Conception (cows)

-0.01 ± 0.03

56-d Non-Return Rate (heifers)

0.06 ± 0.03

56-d Non-Return Rate (cows)

0.01 ± 0.03

Calving to First Service

-0.06 ± 0.03

Breeding Value Correlations

Production Traits	Sires of Phenotyped Daughters N=912
305d Milk Yield	0.18 ± 0.03
305d Fat Yield	0.22 ± 0.03
305d Protein Yield	0.23 ± 0.03

Unfavorable

Compared to Existing Estimates

Heritability	Breed	Country	Parity	Data Size
0.37 ± 0.08	Holstein-Friesian	Ireland ^a	Parities 0-3+	1,180
0.23 ± 0.03	Holstein-Friesian	New Zealand ^b	Heifers	5,010
0.29 ± 0.05	Holstein-Friesian	New Zealand ^b	First parity cows	1,956
0.39 ± 0.04	Holstein	Canada	Parities 0-3+	4,988
$0.37 \pm 0.03^*$	Holstein	Canada	Parities 0-3+	4,988

*Estimated via ssGBLUP

^aGobikrushanth et al., 2019

^bStephen et al., 2023

Compared to Alternative Traits

Heritability	Trait	Cows	Heifers
0.06 ± 0.002	Days Open	✓	
0.01 ± 0.001	Non-Return Rate	✓	
0.01 ± 0.001	Non-Return Rate		✓
0.03 ± 0.001	First Service to Conception	✓	
0.01 ± 0.001	First Service to Conception		✓
0.06 ± 0.001	Calving to First Service	✓	
0.39 ± 0.040	Anogenital Distance	✓	✓
$0.37 \pm 0.030^*$	Anogenital Distance	✓	✓

*Estimated via ssGBLUP

- Moderate heritability
- Moderate to high reliability of breeding values
- Large relative gain with genomic information
 - Unproven sires, unphenotyped dams, unphenotyped heifers
- Favorable correlation with age at first service
 - Unfavorable correlation with production traits
- Promising trait for genetic selection
- Next steps → data collection

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Thank you!

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