

Accuracy of genomic breeding values from endocrine and traditional fertility traits in dairy cows

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LIVESTOCK RESEARCH
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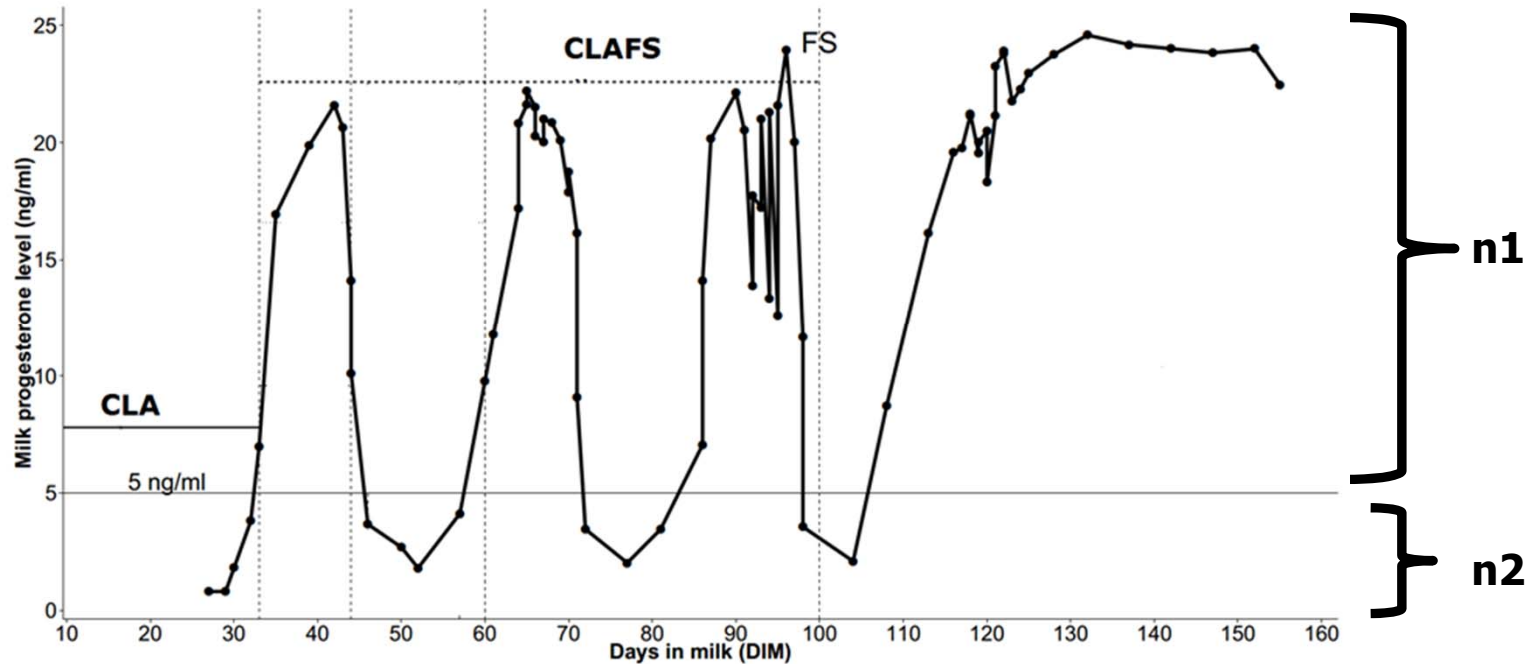


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Context

- Important for production efficiency
- Poor fertility:
 - Involuntary herd replacement
 - Increased inseminations
 - Longer calving intervals (**CI**) or **CFS**
- Traditional fertility traits for selection (e.g. CI or CFS)
 - Biased by farm management
 - Low heritability ($h^2 < 0.1$)
 - Low rate of genetic gain
 - Do not directly reflect cows own physiology

Endocrine fertility traits



$$PLA = \frac{n1}{n1 + n2}$$

- Less influenced by farm management
- Higher heritability (e.g. 16 – 28% for **CLA**)
- But expensive and labour intensive



Endocrine fertility traits

- New technologies reduce labor and cost
- Automatic sampling of milk P4 by Herd Navigator
- Applicable on a larger scale



Objective

Evaluate the added value (accuracy) of using endocrine fertility traits along with traditional traits in genomic prediction of fertility

Materials and Methods

Phenotypes

- 2,447 cows (5,339 lactations)
- 14 commercial herds
- 4 experimental herds
- Endocrine traits: CLA, PLA
- Traditional trait: CFS

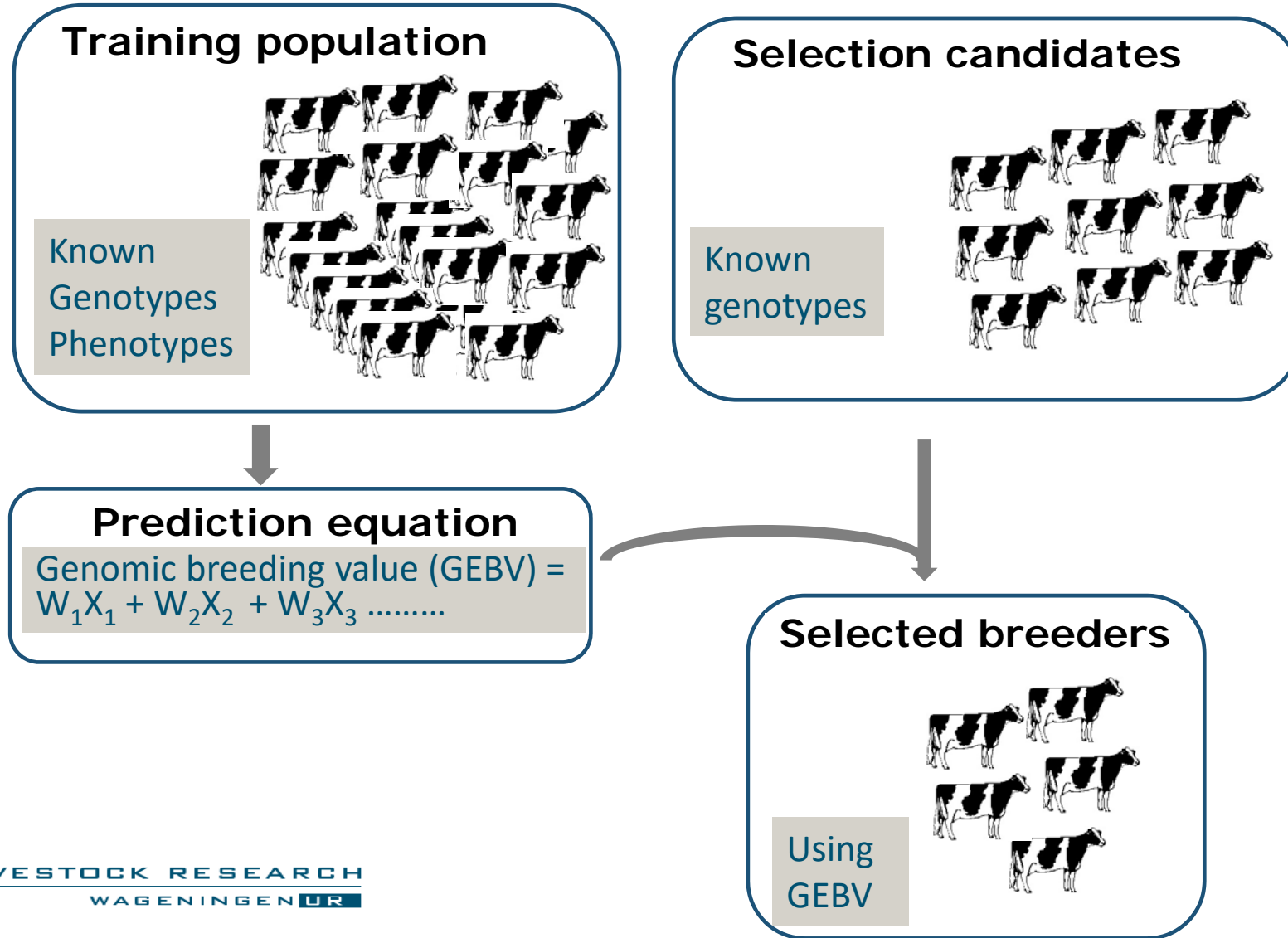
Genotypes

- 80K (commercial herds)
- 50K (experimental herds)
- Imputation to 100K
- 85k SNP after QC

GEBV from GBLUP in univariate and bivariate models
G-matrix constructed as in VanRaden, 2008

$$G = ZZ' / 2 \sum p_i (1 - p_i)$$

Genomic prediction



Scenario 1

Genotyped cows

Training set

- All cows phenotyped for CLA
- Some cows phenotyped for CFS

Validation set

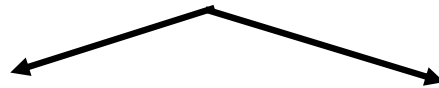
- CFS masked during training and prediction
- CLA masked during training and prediction

Scenario 1 evaluates accuracy of prediction when:

- All training animals are phenotyped for endocrine traits
- and (or not) for traditional traits

Scenario 2

Genotyped cows



Training set

Phenotypes available for both CLA and CFS

Validation set

CLA and CFS masked during training and prediction

- Scenario 2 evaluates if phenotyping all training animals for both traits improves accuracy

Cross validation

1st Fold:



$$\text{Accuracy} = \text{Corr}_{(\text{GEBV}, \text{Phen})}$$

$$\text{Realized accuracy} = \text{Accuracy}/\text{vh}^2$$

2nd



3rd



4th



5th



Genetic parameters

Trait	n	Genomic		Pedigree	
		h^2	SE	h^2	SE
CLA (d)	3,524	0.10	0.02	0.14	0.04
PLA (%)	3,597	0.12	0.03	0.15	0.04
CFS (d)	3,634	0.11	0.03	0.10	0.04

Accuracy GEBV scenario 1

Trait Training	Trait Validate	Cows Training	Cows Validate	Accuracy (SD)	Realized accuracy (SD)
Univariate model					
CLA	CLA	1,855	464	0.15 (0.05)	0.46 (0.16)
PLA	PLA	1,887	472	0.14 (0.02)	0.42 (0.07)
CFS	CFS	1,329	332	0.04 (0.07)	0.13 (0.21)
Bivariate model					
CLA and CFS	CFS	1,855	258	0.14 (0.07)	0.41 (0.21)
PLA and CFS	CFS	1,887	284	0.10 (0.03)	0.31 (0.09)

Accuracy increased in bivariate analyses where endocrine and traditional traits were used

Accuracy GEBV scenario 2

Trait Training	Trait Validate	Cows Training	Cows Validate	Accuracy (SD)	Realized accuracy (SD)
Univariate model					
CLA	CLA	1,199	300	0.13 (0.08)	0.40 (0.26)
PLA	PLA	1,202	301	0.14 (0.04)	0.42 (0.12)
CFS	CFS	1,131	283	0.04 (0.05)	0.11 (0.15)
Bivariate model					
CLA and CFS	CFS	1,128	282	0.18 (0.04)	0.55 (0.13)
PLA and CFS	CFS	1,129	282	0.07 (0.06)	0.20 (0.17)

Conclusions

- Accuracy of GEBV increased in bivariate predictions where endocrine and traditional fertility traits were used
- Better predictive ability of CFS in bivariate analysis with CLA than with PLA
- Further studies with larger training populations may show bigger improvements.

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