

Approaches to improve genomic predictions in Danish Jersey

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Background

- Accuracy of genomic prediction depends on size of reference population (RP)
- In dairy cattle, RP mainly consists of progeny-tested bulls
- Small breeds have small RP
- Increase RP by sharing RP data and including cows in the reference population

Objective:

Investigate the improvement of genomic predictions
by sharing RP data
by including cows in RP
in Danish Jersey -- a numerically small breed.

Data

1,369 Danish Jersey bulls (birth year 1988 - 2010)

1,160 US Jersey bulls (2000 - 2009)

9,419 Danish Jersey cows (2010 – 2013)

Genotype data

Most bulls genotyped with 54k chip

Most cows genotyped with 7k chip

Marker data of different chips imputed to 54k chip

After editing, about 40,000 markers

Phenotype data

Deregressed proof (DRP) in Nordic scale of 8 traits available for both Danish and US Bulls.

DRP of 6 traits available for both bulls and cows

Genomic prediction

Single-trait GBLUP model

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}\mathbf{g} + \mathbf{e}$$

μ : overall mean; \mathbf{g} : additive genetic effect; \mathbf{e} : random error

It is assumed that $\mathbf{g} \sim N(\mathbf{0}, \mathbf{G}_A\sigma_g^2)$,

$$\mathbf{G}_A = 0.8\mathbf{G} + 0.2\mathbf{A}$$

The model is equivalent to a GBLUP model including a residual polygenic effect accounting for 20% genetic variance

Validation scenarios

Test	Reference
Validation on bull 338 DK bulls born 2005 onwards	DK bulls
	DK+US bulls
Validation on cow 3287 cows from 87 half-sib families	DK bulls
	DK+US bulls
	DK bulls + cows
	DK+US bulls + cows

Criteria of Validation

Reliability of GEBV for bulls in the test data measured as

$$r^2_{\text{GBV}} = \text{Cor}^2(\text{GEBV}, \text{DRP}) / r^2_{\text{DRP}}$$

Bias is measured by regression of DRP on GEBV

Validation on bull

Trait	r^2_{GEBV}		Regression	
	DK	DKUS	DK	DKUS
Milk	37.2	44.1	0.88	0.83
Fat	21.2	22.2	0.71	0.68
Protein	29.5	32.9	0.72	0.69
Fertility	28.9	27.4	1.09	1.04
Mastitis	28.3	28.9	0.73	0.72
Body conform.	29.9	34.0	0.83	0.79
Udder conform.	20.0	30.2	0.72	0.81
Longevity	15.1	14.0	0.71	0.62
Average	26.2	29.2	0.80	0.77

Validation on cow - reliability

Trait	DK	DKUS	DKCOW	DKUSCOW
Milk	44.2	53.1	65.8	68.5
Fat	24.9	31.7	36.1	38.2
Protein	28.5	35.9	40.3	42.1
Mastitis	55.5	57.0	56.3	54.9
Body conform.	42.6	49.4	40.7	43.6
Udder conform.	40.6	49.1	46.3	51.8
Average	39.4	46.0	47.6	49.9

+US → 6.6%, +cow → 8.0%, +US and cow → 10.5%

Validation on cow - regression

Trait	DK	DKUS	DKCOW	DKUSCOW
Milk	1.28	1.29	1.23	1.24
Fat	0.80	0.90	0.86	0.88
Protein	0.93	1.00	0.93	0.93
Mastitis	1.19	1.15	1.14	1.06
Body conform.	1.11	1.11	0.99	1.00
Udder conform.	1.25	1.28	1.10	1.13
Average	1.09	1.12	1.04	1.04

Compare validation on bulls and on cows

Trait	r^2_{GEBV} - Bull		r^2_{GEBV} - Cow	
	DK	DKUS	DK	DKUS
Milk	37.2	44.1	44.2	53.1
Fat	21.2	22.2	24.9	31.7
Protein	29.5	32.9	28.5	35.9
Mastitis	28.3	28.9	55.5	57.0
Body conform.	29.9	34.0	42.6	49.4
Udder conform.	20.0	30.2	40.6	49.1
Average	27.7	32.1	39.4	46.0

$$r^2_{\text{cow}} > r^2_{\text{bull}}$$

Conclusions

- Sharing reference data and including cows in reference population are efficient
- Genomic selection is promising even for numerically small population

**Thank you
for your attention**