

Genomic prediction for new traits combining cow and bull reference populations

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Objective

Combine cow and bull reference population information in a Bayesian genomic prediction model, to increase accuracy of genomic breeding values.

Table 1. Accuracy of genomic prediction for fat and protein yield, for various reference populations. Accuracy = r (genomic breeding values ; cow phenotypes) / $\sqrt{h^2}$.

Reference population	Trait			
	Fat		Protein	
	Accuracy	SE	Accuracy	SE
Cows	0.328	0.068	0.189	0.050
Bulls	0.238	0.053	0.146	0.050
Bulls & cows	0.347	0.063	0.206	0.055

Table 2. Numbers of regions (< 3Mb in size) in which effects with Bayes Factors > 10.1 were identified for fat and protein, using either the cow, bull or combined data (diagonals), and the number of regions that were identified by two analyses (off-diagonals).

Trait	Data used	Cows	Bulls	Cows & Bulls
Fat	Cows	3		
	Bulls	1	5	
	Cows & Bulls	1	4	15
Protein	Cows	2		
	Bulls	0	2	
	Cows & Bulls	2	1	12

Table 3. Estimated heritabilities of fat and protein yield measured on cows and based on bull DYD's, and estimated genetic correlations (and SEs) between cows and bulls for fat and protein. Estimates were obtained with two bivariate pedigree based models.

		Fat	Protein
Heritabilities	Cows	0.618 (0.055)	0.630 (0.055)
	Bulls	0.920 (0.040)	0.959 (0.017)
Genetic correlations		0.540 (0.126)	0.562 (0.127)

Background

Genomic selection enables selection for difficult to measure traits, like feed efficiency and methane emission in dairy cattle, for which only a few thousand phenotypic records may be collected.

Model

- Bayesian stochastic search variable selection (Bayes-SSVS)
- Univariate: 1 cow *or* 1 bull trait
- Bivariate: 1 cow *and* 1 bull trait
- One QTL-indicator sampled for both traits per locus
- Zero residual correlation between (cow & bull) traits

Conclusions

The bivariate Bayes-SSVS model:

- Showed a marginal increase in accuracy for the cow traits (0.02; Table 1); a higher increase is expected when adding more bulls
- Revealed several QTL peaks not found in the separate analyses (Table 2; see **examples** in Figures 1 & 2)

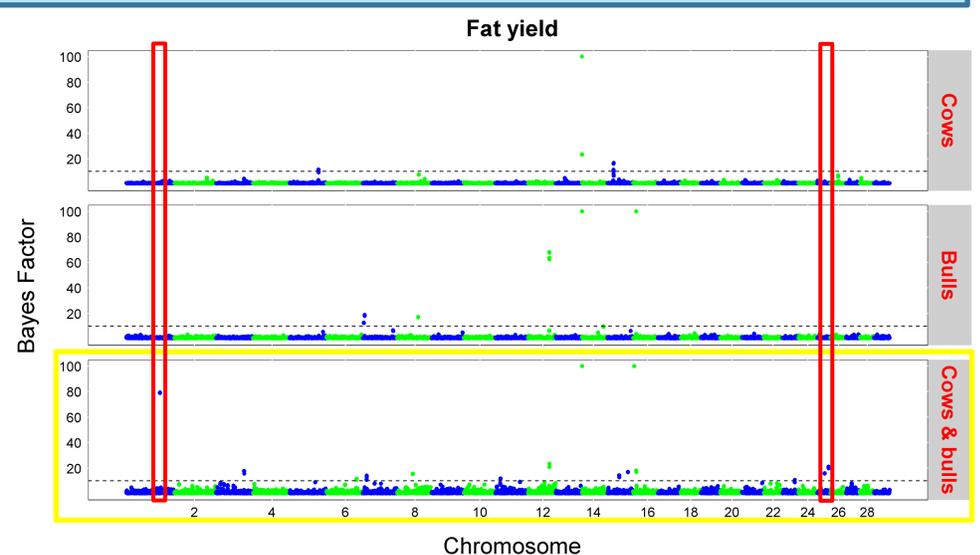


Figure 1. Bayes Factors (BF) across the genome for fat yield, using cow, bull, or cow & bull data (BF > 100 are set to 100).

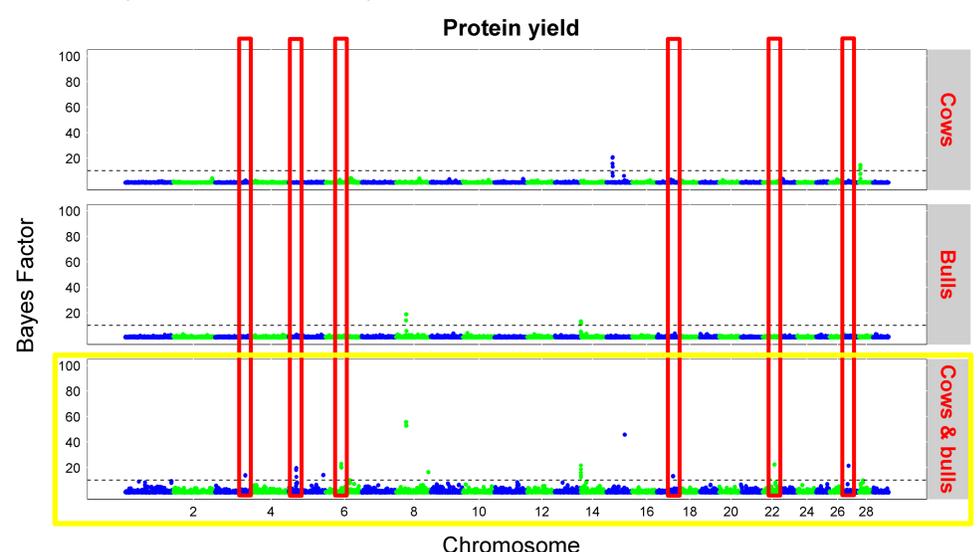


Figure 2. Bayes Factors across the genome for protein yield, using cow, bull, or cow & bull data.

Data

- 1,609 cows with phenotypes for fat and protein yield
- 296 bulls had highly accurate daughter yield deviations (DYD) for fat and protein yield from the Irish national evaluations
- Genotypes for 36,346 SNPs were available for all animals

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