Estimation of genomic breeding values for three milk traits in the Frizarta dairy sheep

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Abstract

In the present study, first, we estimated 'classical' (EBVs) and genomic breeding values (GEBVs) for three milk traits (MY: milk yield, FC: fat content and PC: protein content) in a sample of Frizarta dairy ewes. Next, we performed GEBVs - EBVs comparison and finally attempted to predict phenotypic values of the three traits based on genomic data (plus fixed effects). A total number of 468 Frizarta dairy ewes genotyped with the 50K SNP array with pedigree and phenotypic data on the three traits were used. 'Classical' EBVs were estimated using the BLUP method while estimation of GEBVs was based on the GBLUP method and 46,232 SNPs passing typical marker quality criteria. Phenotypic values prediction performance was assessed via k-fold cross-validation. Pearson correlations between EBVs and GEBVs were as high as 0.51, 0.53 and 0.61, for MY, FC and PC, respectively. Respective correlations between GEBVs and phenotypic values were 0.69 (MY), 0.58 (FC) and 0.70 (PC). Pearson correlations between predicted and observed phenotypic values were 0.68, 0.39 and 0.41 for MY, FC and PC, respectively. Current findings imply efficiency of genomic selection but they warrant to be verified in a larger sample before a clear conclusion could be drawn.

Introduction

Traditional genetic evaluation relies on the ***additive relationship matrix (A)*** derived from pedigree data. With advancement in high-throughput genotyping technologies, the ***A*** matrix can be replaced by the ***genomic relationship matrix (GRM).*** In theory, the use of animals' realized genomic relationships can produce more accurate genetic predictions than its pedigree-based counterpart because ***GRM*** can more precisely capture ***Mendelian sampling*** among related animals. The present report examined the validity of such an hypothesis in a sample of Frizarta dairy ewes. To this end, first we estimated BVs for three milk traits using pedigree and dense genomic data. Next, we compared estimates of animals' genetic merit of the two methods and finally investigated whether genomic data can be used to predict animals' performance.

Material & Methods

Genotypic data*:* 468 Frizarta dairy ewes genotyped with the OvineSNP50 BeadChip. 46,232 SNPs remained after marker quality criteria: (call rate>0.95, minor allele frequency≥0.05, Fisher test for Hardy-Weinberg Equilibrium $p<10^{-4}$).

Phenotypic data:

Descriptive statistics of the three milk traits are shown on Table 1.

Estimation of BVs

Classical: BLUP method (ASREML software). Fixed effects: herd, production year, lambing month, litter size, days in milk (covariate). Random: animal.

Genomic: GBLUP method (SNP & Variation Suite program). Fixed effects: as in BLUP plus SNP effects.

Phenotypic values prediction performance was assessed via 5-fold cross-validation.

Trait	mean	SD	min	max
Milk yield (kg)	221.1	88.22	23.6	596.0
Fat content (%)	5.98	1.30	2.3	12.6
Protein content (%)	5.47	0.64	3.2	7.8

Table 1. Descriptive statistics of three milk traits in Frizarta dairy sheep (n=468)

Results

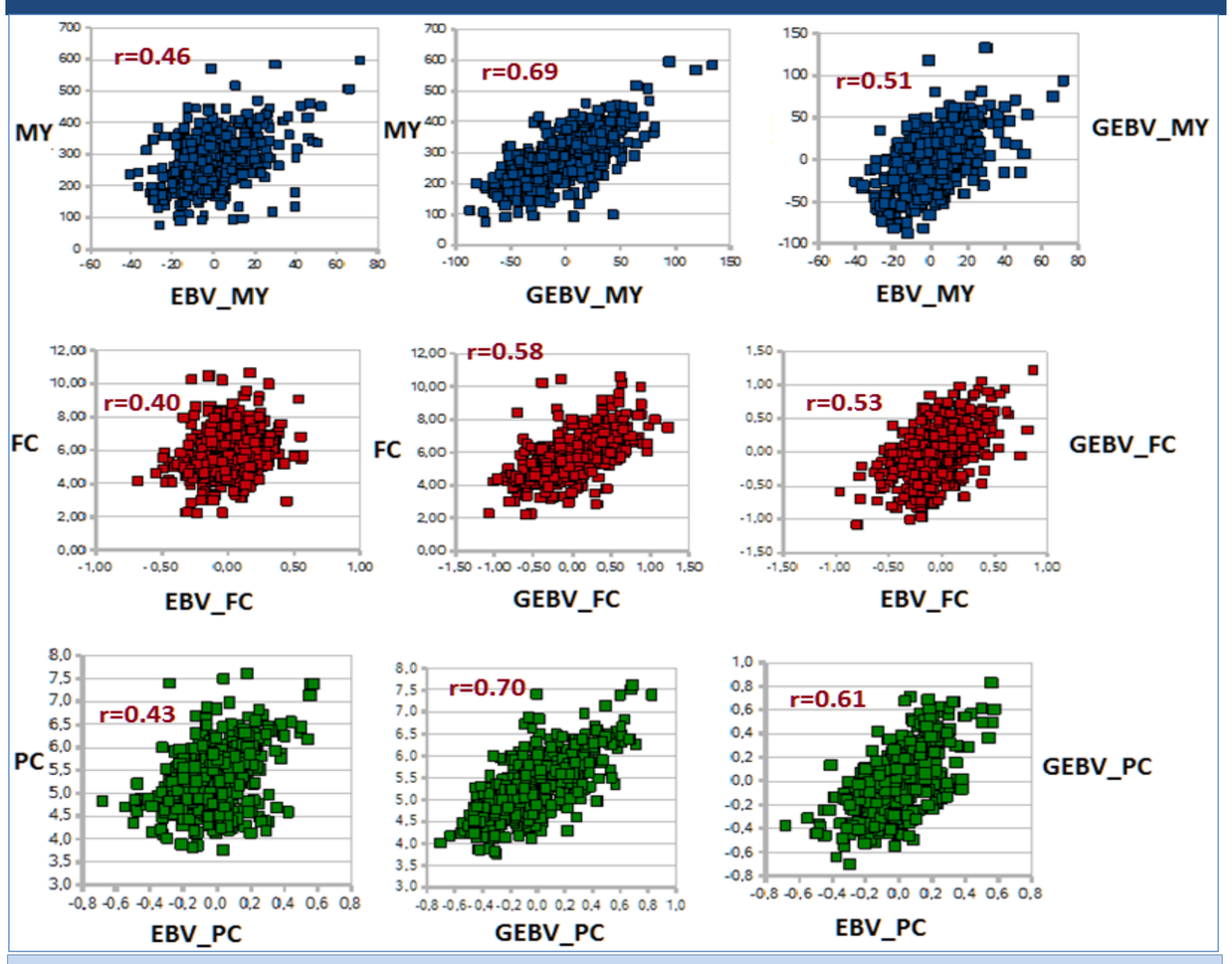

Figure 1. Plots of Estimated Breeding Values (EBV) against Genomic Estimated Breeding Values (GEBV) and phenotypic values for three milk traits (MY: Milk Yield, FC: Fat Content, PC: Protein Content). Pearson correlations (r) are also shown

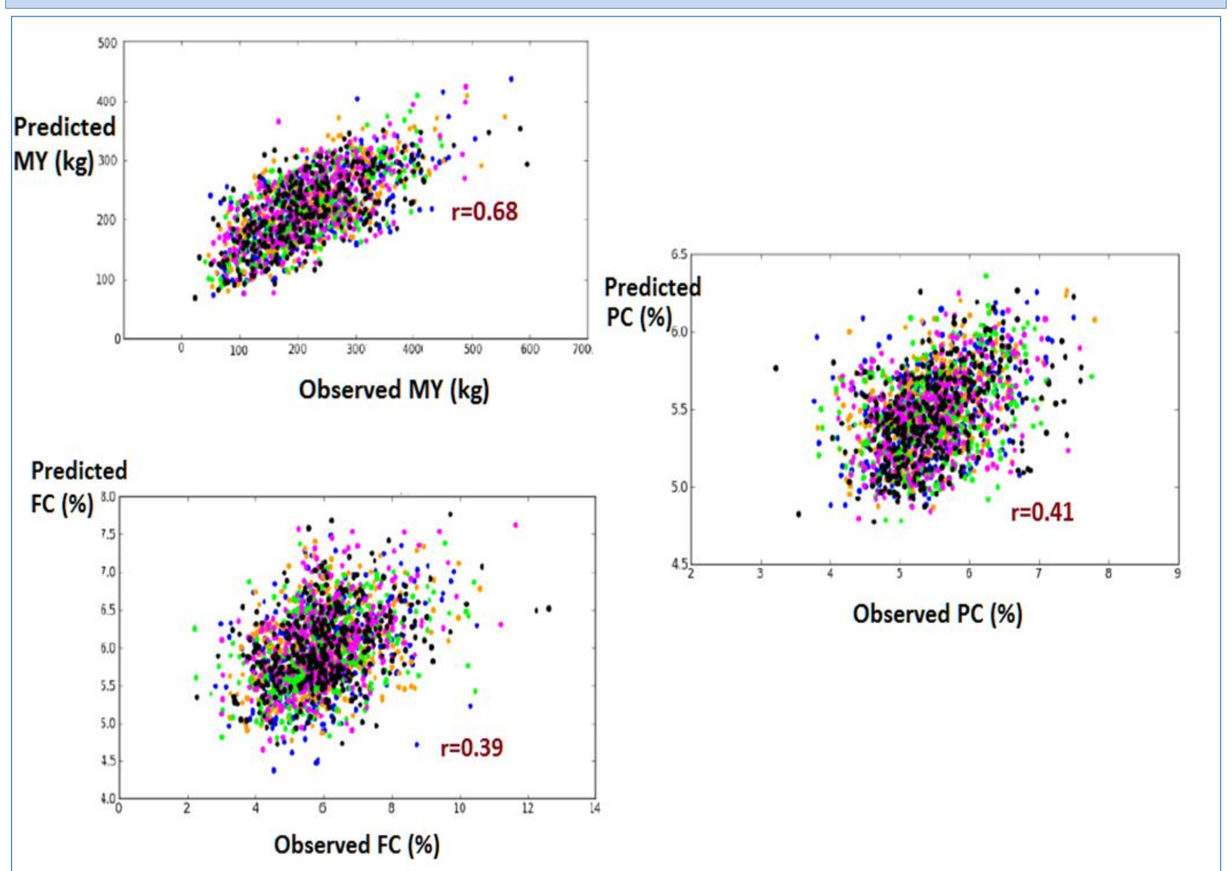

Figure 2. Plots of predicted against observed phenotypic values for MY (Milk Yield), FC (Fat Content) and PC (Protein Content). Different colors denote the 5 random subsamples used for prediction of trait phenotypic values. Averaged Pearson correlations (r) over the 5 random subsamples are also shown

Conclusions

- Correlations between GEBVs and phenotypic values were 45% to 60% higher than the EBVs-phenotypic values correlations
- The use of genomic data was associated with relatively high prediction ability for MY, but lower for FC or PC

Funding

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