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Transition of the UK dairy national evaluation to across-breed and single-step genomic evaluation: somatic cell counts as a case trait

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Introduction

Current UK genomic evolutions follow a two-step approach; initially, a genetic evaluation based solely on pedigree information, followed by a SNBBLUP analysis for genotyped animals using de-regressed proofs from Interbull.

Nowadays, with recent advances in computational feasibility and growing interest in across-breed genomic evaluations for dairy herds, there is a compelling need to adopt a single-step genomic evaluation approach within the UK dairy industry.

Objective

This study aims to evaluate the impact of using genomic information with single-step genomic approach (SSGBLUP)

Compare the prediction ability of SSGBLUP and pedigree-based genetic evaluation (PEDBLUP) employing cross-validation techniques (Linear Regression method).

Data

- Somatic cell count (SCC)
- 19,056,954 SCC lactation records from 7,527,712 cows
- 11,271,959 animals in the pedigree
- Genotypic data were available for 891,480 animals, imputed at 79,051 SNPs using findhap.f90 V3
- Foreign information was incorporated for 182,844 bulls.

De-regressed proofs adjustments

$$\lambda = (1-h^2)/h^2$$

$$\mathrm{ERC_i} = \lambda \frac{\mathrm{REL_i}}{1-\mathrm{REL_i}}$$

$$\mathrm{dERC_i} = \mathrm{ERC_i} \text{- } \mathrm{ERC_{PA}}$$

$$\mathrm{DRP_i} = \mathrm{PA_i} + \frac{(\mathrm{EBV_i} - \mathrm{PA_i})}{\left(\frac{\mathrm{dERC_i}}{\mathrm{dERC_i} + \lambda}\right)}$$

$$\mathrm{dERC_i}^* = \mathrm{dERC_{INT_i}} \text{ -} \mathrm{dERC_{NAT_i}}$$

$$\mathrm{DRP_i}^* = \frac{(\mathrm{dERC_{INT_i}} \cdot \mathrm{DRP_{INT_i}}) - (\mathrm{dERC_{NAT_i}} \cdot \mathrm{DRP_{NAT_i}})}{\mathrm{dERC_i}^*}$$

DRP* as pseudo-records and dERC* as weights
Bonifazi et al. (2023)

Cross-validation: Linear Regression

- ❑ Comparison of Ped-BLUP and SSGBLUP with LR method:
  - ➢ Level bias
  - ➢ Dispersion bias
  - ➢ Prediction ability

Legarra & Reverter (2018)

- ❑ Validation group comprises bulls born after 2016 and cows after 2018.

- ❑ Analyses were performed using the MiX99 V23.1026 software, applying an ssSNPBLUP model with 10% polygenic effects.

Results: bulls

Number of animals	Breed	Level Bias Genomic	Level Bias Ped	Dispersion Bias Genomic	Dispersion Bias Ped
28	Guernsey	0.048	-0.049	0.975	1.113
6,087	Holstein	-0.069	-0.025	0.989	1.012
453	Jersey	-0.001	-0.056	1.038	1.020
245	Ayrshire	-0.045	-0.019	0.972	0.963

Results: cows

Number of animals	Breed	Level Bias Genomic	Level Bias Ped	Dispersion Bias Genomic	Dispersion Bias Ped
855	Guernsey	-0.016	-0.040	0.994	0.978
95,965	Holstein	-0.012	-0.005	1.021	1.049
3,512	Jersey	-0.006	-0.068	1.042	0.986
382	Ayrshire	-0.017	-0.053	1.018	1.170

Results: bulls

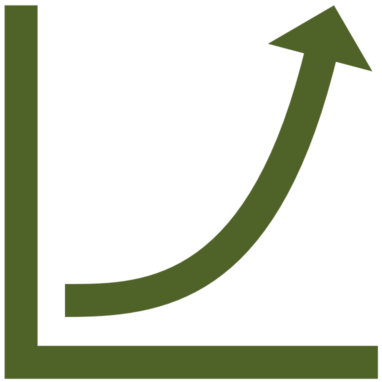
Number of animals	Breed	Accuracy Genomic	Accuracy Ped	Increase % ACC	Correl Full Ped # Partial Genomic
28	Guernsey	0.495	0.383	29.243	0.500
6,087	Holstein	0.786	0.690	13.913	0.901
453	Jersey	0.614	0.567	8.289	0.865
245	Ayrshire	0.510	0.444	14.865	0.788

Results: cows

Number of animals	Breed	Accuracy Genomic	Accuracy Ped	Increase % ACC	Correl Full Ped # Partial Genomic
855	Guernsey	0.445	0.270	65.129	0.400
95,965	Holstein	0.648	0.320	102.202	0.596
3,512	Jersey	0.501	0.350	43.114	0.598
382	Ayrshire	0.421	0.270	56.100	0.419

Take home message

Single Step Genomic Evaluation is a promising approach to integrate genomic information to improve the accuracy of genetic predictions in both purebred and crossbred animals, accelerates genetic progress, and improves selection efficiency.



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