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Genomic Evaluation for Feed Advantage – Towards Feed Efficient Cows in UK Dairy Cattle

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Abstract

The inclusion of feed efficiency into the UK national dairy selection index contributes to reduced environmental footprint of the dairy industry and provides additional profit to dairy farmers. Feed Advantage breeding values were introduced into UK dairy cattle genomic evaluations in August 2021. Genomic breeding values (GEBV) for Feed Advantage represents the kilograms (kg) of feed saved due to better feed efficiency and lower maintenance feed costs per lactation. Feed Advantage breeding value combines GEBV of wasted feed (WF) derived as deviation of predictions for dry matter intake (DMI) from production and maintenance, and feed saved due to maintenance using predictions for maintenance and current £PLI weight for maintenance in the UK national index. To obtain GEBV for DMI, a total of 174,379 weekly average DMI records (kg/d) from around 750,000 daily DMI records were included for 4,662 lactations of 1,888 Holstein dairy cows (in Lactation 1 to 4) from the UK Langhill research herd. The 80K imputed genotypes (79,051 SNP markers) were available for 4,356 genotyped animals including 1,702 genotyped cows in the Langhill herd, 1,689 active bulls in the UK, and an extra 965 genotyped bull ancestors in the pedigree of genotyped animals. Heritability for DMI was 0.18, averaged across lactations (Lactation 1, 2, 3+). The DMI between lactations is highly genetically correlated (lactation 2 and 3+ is correlated by 0.99, lactation 1 and 2+ is correlated by 0.91). Genomic breeding values (GEBV) for DMI were then estimated using single-step GBLUP method with an animal repeatability model using DMI data across lactations. Validations were carried out to assess prediction accuracy for DMI by setting up reference and validation populations considering three scenarios (i.e., forward prediction, prediction between genetic lines, and prediction between feeding groups). In summary, the prediction accuracy for DMI in forward prediction, prediction between genetic lines, and prediction between feeding groups were 0.62, 0.34, and 0.68, respectively. The GEBV for wasted feed (WF) was derived as deviation of GEBV for DMI from GEBVs for production and maintenance. The final publication of Feed Advantage breeding value combines GEBV for WF and feed saved due to maintenance using prediction for maintenance and current £PLI weight for maintenance in the UK national index. Current findings show promising results of genomic predictions on Feed Advantage in bringing additional profit to dairy farmers without sacrificing cows' health and fertility, and in reducing environmental footprint of the dairy industry.

Key words: genomic prediction, feed efficiency, maintenance, saved feed, Holsteins

Introduction

Feed accounts for the largest part of operating cost in dairy cattle production (European Commission, 2018). The inclusion of feed efficiency (FE) into the UK national dairy selection index contributes to reduced environmental footprint of the dairy industry and provides additional profit to dairy farmers.

Genomic selection has been used as an important tool to include FE into dairy cattle breeding (Veerkamp et al., 2014; Pryce et al., 2015; Li et al., 2020). The idea of "Feed Saved" was introduced by Pryce et al. (2015) and applied to national genomic evaluations in Australia, the USA and the Netherlands. In Feed Saved, cows' metabolic efficiency and maintenance efficiency are combined. Feed Saved represents the kilograms (kg) of feed saved due to better metabolic efficiency and lower maintenance feed costs of the individual.

In the current study, we aimed to include feed efficiency into UK national dairy cattle genomic evaluation using the general idea of Feed Saved to generate a new trait of "Feed Advantage". This was included in the national dairy cattle genomic evaluation in UK from August 2021. The Feed Advantage breeding value combines GEBV for wasted feed (WF) derived as deviation of predictions for feed intake from production and maintenance, and feed saved due to maintenance using prediction for maintenance and current £PLI weight for maintenance in the UK national index. The Feed Advantage breeding value represents the kilograms (kg) of feed saved due to better feed efficiency and lower maintenance feed costs per lactation.

Materials and Methods

Data

A total of 174,379 weekly average dry matter intake (DMI; kg/d) from around 750,000 daily DMI records were available for 4,662 lactations of 1,888 Holstein dairy cows (in Lactation 1 to 4) from the SRUC Dairy Research Centre. The research centre was based at Langhill herd, Edinburgh from 1970s to September 2001, and was subsequently transferred to Crichton Royal Farm in Dumfries, Scotland. Cows raised in the centre were routinely recorded for milk production, feed intake, body weight and condition score, health status, and reproductive events per animal. As a result, a longitudinal database is in place and being continuously updated.

These cows are evenly divided into two genetic lines (selection line vs. control line). Cows in selection line are daughters of the highest genetic merit sires for milk, fat and protein yield in the UK, whereas cows in control line are daughters of sires with average genetic merit for milk fat and protein yield of the UK animals at the time of breeding. Cows in each genetic line are further split randomly into two feeding groups characterised by high-forage diet and high-concentrate diet, respectively. Feed was offered in individual feed bins (HOKO-system, Insentec B.V.). Feed offered to cows and feed refusals were measured individually to calculate the feed intake per cow. The feed dry matter (DM) content was analysed regularly and aligned with feed intake records to obtain daily DMI per cow.

The 80K imputed genotypes (79,051 SNP markers) were available for 4,356 genotyped animals including 1,702 genotyped cows in the Langhill herd (1,410 cows are genotyped and phenotyped for DMI), 1,689 active bulls in the UK, and an extra 965 genotyped bull ancestors in the pedigree of genotyped animals. The 80K SNP panel was used in national evaluation and developed based on original Illumina Bovine 50K BeadChip, 777K HD BeadChip and several other commercial genotyping chips plus extra gene tests and large-effect sequence variants. Pedigree information was extracted from the national database by tracing back as many generations as possible for the studied population.

Genomic prediction for DMI

Variance components and genetic parameters for DMI were estimated using pedigree information by an average information-restricted maximum likelihood algorithm implemented in the AIREMLF90 program (Misztal et al., 2018). The estimated variance components were applied to further genomic evaluation for DMI using single-step GBLUP (ssGBLUP) method implemented by the program BLUPF90 (Misztal et al., 2018).

An animal repeatability model was used for variance component estimation and genomic prediction for DMI. Daily dry matter intake (kg/d) averaged on a monthly basis was used as the phenotype, so that each cow has repeated measurements for DMI over lactation. Fixed effects of the model include parity-month of lactation, age of calving, year-month of recording, and feeding groups. Random effects include additive genetic effect, permanent environmental effect, and random residual.

Model-based prediction reliabilities were calculated by inverting the coefficient matrix of the mixed model equation, using

$$REL_i = 1\text{-}(PEV_{ii}/G_{ii})$$

where: G_{ii} = (1 + inbreeding coefficient) × $\boldsymbol{\sigma_a^2}$ for animal i and $\boldsymbol{\sigma_a^2}$ is the genetic variance, and PEV_{ii} is the prediction error variance for animal i.

Validation

Validations were carried out to assess the accuracy of prediction. Prediction accuracy was calculated as the correlation between corrected phenotype and GEBV in the validation population. Reference and validation populations were set up under three scenarios: Forward prediction, prediction between two genetic lines, and prediction between two feeding groups. Specifically, in forward prediction, cows born before 2015 were in the reference population, and cows born in or after 2015 were in the validation population.

Publication of Feed Advantage PTA

Wasted Feed (WF) sub-index

GEBV for daily DMI was multiplied by 305 to obtain GEBV(DMI) per lactation. GEBV of “Wasted feed (WF)” was derived from GEBV(DMI) adjusted for GEBVs for milk energy and maintenance (Meyer et al., 2017). The derivation of WF is similar to that for residual feed intake (RFI) except that WF is derived directly on the GEBV level. Based on Meyer et al. (2017), GEBV for WF was derived as:

$$\begin{aligned} GEBV(WF) = [&dGEBV(DMI) \\ &- \alpha * dGEBV(Milk\ Energy) \\ &- \beta * dGEBV(Maintenance)\ ] * \boldsymbol{\lambda} \end{aligned}$$

where GEBVs for DMI, Milk Energy, and Maintenance are de-regressed to take account of their different scales; GEBV for Milk Energy per lactation and GEBV for Maintenance were obtained from the UK national evaluation; α and β account for the relationships of DMI with Milk Energy and Maintenance, respectively; $\boldsymbol{\lambda}$ converts dGEBV(WF) back to GEBV scale using reliabilities for DMI, Milk Energy and Maintenance (Meyer et al., 2017).

Feed Advantage Breeding Values

The GEBV for Feed Advantage combines GEBV(WF) and feed saved due to lower maintenance feed costs (FS_ maintenance). The FS_ maintenance was calculated based on Equation [7] in Pryce et al. (2015) using GEBV for maintenance in the UK national evaluation and current £PLI weight for maintenance in the UK national index. The final Feed Advantage breeding values were calculated combining GEBV(WF) and FS_maintenance as shown below, to represent kilograms (kg) of feed saved due to better metabolic efficiency and lower maintenance feed costs per lactation:

$$Feed\ Advantage = FS\_maintenance - WF$$

Results & Discussion

Genetic parameters for DMI

The heritability for DMI is 0.16 (SE=0.02) for Lactation 1, and 0.19 (SE=0.02) for Lactation 2 and Lactation 3+. The DMI between lactations is highly genetically correlated (Lactation 2 and 3+ is correlated by 0.99, Lactation 1 and 2+ is correlated by 0.91). Considering the high genetic correlations for DMI across lactations, DMI data across lactations were treated as one trait in the prediction. Prediction reliabilities for individual animals were slightly higher when DMI across lactations were treated as one trait compared to multiple traits.

GEBV and Reliabilities for DMI

GEBVs for DMI were estimated for all genotyped UK Holsteins. The model-based prediction reliabilities for DMI (calculated from direct solve of mixed-model equation) were on average 36% for genotyped bulls in Langhill (i.e., sires, grandsires and so on of the phenotyped animals) and 13% for genomic young bulls in the UK.

Validation Results for DMI

The prediction accuracy and bias from validation are shown in Table 1. Prediction accuracy from forward prediction agrees with the model-based prediction reliabilities for DMI. The prediction between different feeding groups showed promising accuracies, indicating reliable predictions between animals in different diets. The prediction accuracy between two genetic lines was relatively low. The genetic relationship of reference population to the predicted population remains as the key factor for achieving a high prediction accuracy for feed efficiency.

Publication of Feed Advantage PTA

Genomic PTA for Feed Advantage were estimated and published for all genotyped UK Holsteins since August 2021. The Feed Advantage GEBV reliabilities for genomic young bulls was about 45%. The UK genomic PTA for Feed Advantage was estimated to have high correlation (0.8) with the Feed Saved GPTA in the USA.

The Feed Advantage genomic PTA has close to zero correlations with milk production traits in the UK national evaluation (Figure 1), which is as expected, since milk energy PTA has been corrected in the derivation of Feed Advantage PTA. Also as expected, the Feed Advantage PTA has negative correlation with Maintenance PTA and with PTA for DMI. The Feed Advantage PTA has positive correlations with HealthyCow index, Fertility index, and £PLI, indicating favorable correlations for simultaneously selecting for healthy, fertile, and efficient cows for UK dairy breeding. The negative correlations of the Feed Advantage PTA with type traits indicate potential influence on cows' conformation when selecting for Feed Advantage. In addition, selecting for Feed Advantage has a favorable correlation with EnviroCow index which aims to reduce methane emission in the UK dairy cattle population (Figure 1).

Conclusions

Genomic breeding values for Feed Advantage were estimated for all genotyped UK Holsteins to select for feed efficient dairy cows in the UK. Publication of Feed Advantage genomic PTAs has been available from August 2021 in the UK. Feed Advantage genomic PTA represents kilograms (kg) of feed saved due to better feed efficiency and lower maintenance feed costs per lactation. Current findings showed promising results of genomic predictions on Feed Advantage in bringing additional profit to dairy farmers without sacrificing cows' health and fertility and in reducing environmental footprint of the dairy industry.

Table 1. Validation of prediction for dry matter intake (DMI) under three scenarios: Forward prediction, prediction between two genetic lines, and prediction between two feeding groups

	Scenarios	Accuracy	Bias
1	Forward prediction*	0.62	0.94
2	Between genetic lines	0.34	1.04
3	Between feeding groups	0.68	1.09

*In forward prediction, cows born before 2015 were the reference population to predict cows born in or after 2015 as the validation population.

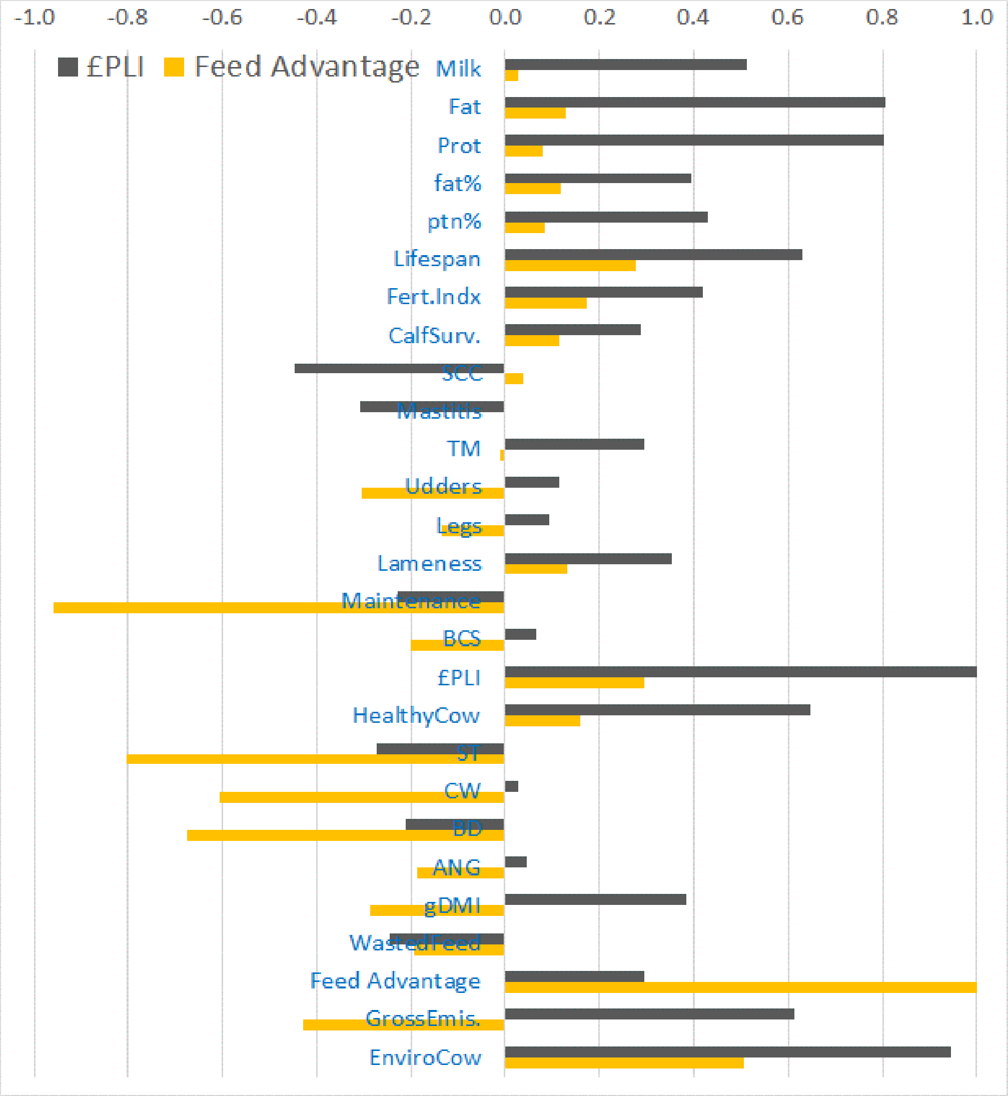

Figure 1. Correlations of Feed Advantage genomic PTA with other UK national dairy selection index traits genomic PTA (the correlations are shown as the yellow bars).

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