

NEXT GENERATION FEED SAVED AUSTRALIAN BREEDING VALUES EVALUATED IN HOLSTEIN DAIRY CATTLE

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SUMMARY

The aims of this study were to: 1) update the Australian (dairy) breeding value (ABV) for lifetime residual feed intake (RFI_{life}, covering RFI at the growth and lactation stages) using 3,711 Holstein female records (584 Australian cows, 824 Australian heifers and 2,440 foreign cows) using a multivariate model and 2) re-evaluate the Feed Saved ABV in Holstein (HOL) bulls. Cow numbers have doubled compared to the original 2015 Feed Saved ABV model. Genomic heritability estimates of RFI were 0.18, 0.27, and 0.36 for Australian (AUS) and overseas (OVE) cows, and AUS heifers, respectively. The genetic correlations were 0.47 between AUS cow and heifer traits and 0.94 between AUS and OVE cow traits, but these estimates were associated with large standard errors. The standard deviation of Feed Saved (FS) ABVs in HOL bulls was 79 kg/yr. The reliability of the residual feed intake component of Feed Saved increased from 11% to 20%. The next step in calculating FS is to combine RFI ABVs with maintenance requirements estimated using bodyweight ABVs. The overall reliability of FS ABVs has increased from 33% to 43% on average. The correlations of RFI_{life} and FS ABV between the prediction equations of 2015 and 2020 in 20k Holstein bulls (born from 2010 to 2020) were 0.65 and 0.80, respectively. We conclude that expanding the reference population, especially with inclusion of the international data, has improved the reliability of feed efficiency EBVs.

INTRODUCTION

Feed costs make up a large proportion of the variable and total costs on a dairy farm and improving production efficiency remains a key breeding objective. The dairy industry has seen tremendous gains in milk yield, without a proportional increase in maintenance requirements, leading to an improvement in gross efficiency (Pryce *et al.* 2018). However, further improvements can be achieved through genomic selection for residual feed intake (RFI), defined as the difference between actual and predicted feed intake. In 2015, DataGene released the world's first Feed Saved breeding value (FS ABV) to the dairy industry, which includes the genetic component of RFI_{life} combined with the maintenance requirements calculated from liveweight EBV. The FS ABV has been incorporated in the Balanced Performance Index (BPI) to select for overall economic merit (Pryce *et al.* 2015). Selecting animals based on the best FS ABV, especially in combination with the BPI, is expected to reduce energy requirements for similar amounts of milk production.

Genomic prediction for RFI that was used to calculate FS ABV in 2015 was developed using a small reference population (n = 2,036) including 234 Australian cows. We have doubled the number of AUS cows with genotypes and phenotypes for RFI and additionally have had access to a larger dataset of non-Australian cows by participating in the Efficient Dairy Genome Project

(EDGP; an international database including research herds from Europe and North America). These 2 data sources have provided an opportunity to increase the size of reference population and hence to update the FS ABV. The aim of this study was to estimate the prediction equations of 50k SNP effects for RFIlife, to reassess the ABV and its reliability for FS, and to compare with the 2015 ABV.

MATERIALS AND METHODS

A total of 3,711 animals were used in this study including: 584 lactating Australian cows and 824 heifers and 2,440 OVE cows (USA, Canada (CAN), Netherlands (NLD), United Kingdom (UK), Denmark (DNK), and Switzerland (CHE)). The genotypes and phenotypes of the AUS and OVE cows except NLD and UK were downloaded from EDGP database, while the NLD and UK data were part of the original dataset used in the development of the 2015 FS ABV (Pryce *et al.* 2015). Additionally, the genotypes of approximately 20,000 Holstein bulls born between 2010 and 2020 were received from DataGene (Melbourne, Australia). The genotypes of cows from the EDGP database were on a variety of medium to HD SNP chips, and sporadic missing genotypes were filled using FImpute (Sargolzaei *et al.* 2014). In total, 41,276 SNP were in common between cow, heifer and bull data sets. This SNP set was chosen to conform to DataGene's national genomic evaluation for dairy cattle (i.e. the same set is used for all traits), which is based on UMD3.1 reference genome map positions. However, all the imputation of the genotypes was undertaken using ARS-UDC1.2 reference genome map positions. Before merging each country's genotypes, the allele frequency of each SNP in each country was checked to ensure that the homozygotes were likely to be in the same direction. The genomic relationship matrix (GRM) was constructed based on the 41,276 genotypes with or without the 3,413 AUS HOL bull genotypes using the method of Yang *et al.* 2010.

All 3,711 animals had milk production traits, energy corrected milk (ECM) and dry matter intake (DMI) data available on most days over a 28-day period, starting at a mean minimum of 5 days in milk (DIM). Trait deviations for RFI in AUS heifers were previously calculated as means of the difference in actual and predicted DMI that was measured over a 6-7-week period at heifers of around 6 months of age (Pryce *et al.* 2015). RFI for AUS cows was calculated based on the average DMI over the 28-day experimental period using the same model described in Pryce *et al.* (2015). The phenotypes of RFI for OVE cows were calculated as $RFI = DMI - (\text{mean} + \text{parityST} + \text{DIM} + \text{HYS} + \text{poly}(\text{age}, -2) + \text{trial} + \text{ECM} + \text{BWT} + \Delta\text{BWT})$, where DMI is the daily dry matter intake (DMI). Energy corrected milk (ECM), mean body weight (BWT), daily BWT change (ΔBWT), days in milk (DIM), and age of cows ($\text{poly}(\text{age}, -2)$) were all fitted as covariates. Daily BWT change (ΔBWT) was calculated by fitting fifth-order orthogonal polynomial regression on DIM (5 to 206 DIM) to daily BWT, and then ΔBWT was calculated as the difference in predicted BWT between consecutive days. The fixed effects in the OVE cows were parity stage (parityST), herd-year-season (HYS), and trial (diets).

A trivariate GREML analysis, where the traits were RFI in AUS cows and heifers and OVE cows, was used to calculate genetic correlations between RFI traits and GEBV. Prediction of SNP effects for RFI cow and RFI heifer was $\hat{\beta} = \mathbf{Z}'(\mathbf{Z}\mathbf{Z}')^{-1}\hat{\mathbf{g}}$, where \mathbf{Z} is the $n \times 41,276$ matrix of the genotypes of 3,711 animals in the reference set, and $\hat{\mathbf{g}}$ is the descaled DGVs for the trait RFI in Australian cows. Prediction equations of SNP effects were used to predict breeding values of 3,413 Holstein bulls that overlapped with the data used in 2015. RFI DGV for AUS cows and heifers were combined to produce a genomic breeding value of RFIlife covering the growth and lactation stages. Then FS ABV was calculated by subtracting RFIlife from the amount of the feed required to maintain 1kg of extra body weight per year (Feed_{BW} kg). The Feed_{BW} kg is a function of BWT and calculated as $\text{EV}_{\text{BWT}} * (\text{EBV}_{\text{BWT}} - 100) / (\text{feedcost} * \text{MJME})$, where EV_{BWT} (economic value of maintenance) is A\$5.14, feedcost (the cost of feed in MJ) is

AUS\$0.032/MJ, and MJME (the energy content of feed) is 11.9 MJ/kg of DMI. Details of the calculation of FS ABV and its reliability are described in Pryce *et al.* (2015).

RESULTS AND DISCUSSION

Heterozygosity predicted from GRM was compared with mean observed heterozygosity per country and heterozygosity assuming Hardy-Weinberg equilibrium. There was good concordance between these population measures, with all genotype groups displaying a similar range of heterozygosity (0.32-0.34), showing that the GRM constructed using animals from different groups is a good representation of the relationships between and within group of animals.

Phenotypic standard deviations of the RFI phenotypes were 0.42 kg/d for AUS heifers, AUS cows, and OVE cows were 1.28 kg/d and 1.82 kg/d, respectively. The single trait and multi-trait analyses provided similar genomic heritability estimates ($h^2 \pm \text{S.E.}$) for RFI (0.18 (± 0.086) for AUS cow, 0.36 (± 0.086) for AUS heifer, and 0.27 (0.034) for OVE cow). Due to the increase in size of the reference data set, the standard errors of h^2 estimates were much smaller than the comparable estimates obtained using the data available in 2015, particularly for AUS cows. The genetic correlations ($r_g \pm \text{S.E.}$) were 0.47 (± 0.274) between AUS cow and AUS heifer, 0.94 (± 0.297) between AUS cow and OVE cow, and 0.20 (± 0.175) between OVE cow and AUS heifer traits. The r_g between AUS cow and OVE cow was higher than the estimates in 2015, where it was 0.76 (± 0.60). However, the estimates are associated with quite large standard errors.

The standard deviation of FS in the 3,413 bulls was 79 kg/yr (Table 1), which was 14kg/yr higher compared with the estimates in 2015. Cows with ABVs that are one standard deviation above the mean of 0 (i.e. +79 kg/yr) could save 1.3% of annual feed costs as reported in Pryce *et al.* (2015). The correlations of RFI life and FS ABV between the prediction equations of 2015 and 2020 were 0.65 and 0.80, respectively. This is anticipated to cause some re-ranking of the bulls based on their updated BPI values with the new model.

Table 1. Mean, SD, and range of EBV and reliabilities for RFI cow, RFI heifer, RFI life, feed required for BWT (Feed_BWT_kg), and feed saved (FS) in 3,413 Holstein (HOL) bulls

	RFI cow	RFI heifer	RFI life	Feed_BW_kg	FS	BWT
	(kg*10/d)	(kg*10/d)	(kg/yr)	(kg/yr)	(kg/yr)	(kg/yr)
<i>ABV</i>						
Mean	1	0.23	23.2	8.7	-14.4	99.4
SD	2.88	0.89	65.6	46.8	79.2	3.5
Max	11.7	3.1	262.9	195.7	250.1	113.9
Min	-6.86	-2.38	-154.4	-141.7	-268.3	85.6
<i>Reliability</i>						
Mean	0.22	0.12	0.20	NA	0.47	0.71
SD	0.038	0.035	0.036	NA	0.039	0.062
Max	0.45	0.29	0.39	NA	0.69	0.99
Min	0.07	0.01	0.06	NA	0.28	0.45

NA= not estimated.

The genetic trend for RFI life, Feed_BWT_kg, and FS in 20,817 genotyped Holstein bulls that were born from 2010 onwards using the equation 2020 is shown Figure 1. From Figure 1A, since

2010 there is an increase in RFI life and a decrease for feed required for BWT, and hence a negative (unfavourable) trend for FS. The change in FS was at a much higher rate (about > 1/2 genetic SD) until the FS ABV was included as part of BPI which occurred in 2015. This change has slowed down (<1/4 SD of FS ABV) over the last 5 years, showing that adopting FS in BPI has been reasonably effective in reducing the unfavourable genetic trend in FS. The correlation between bodyweight EBV and FS EBVs was -0.5. For breeds other than Holsteins, FS is calculated using only the BWT component, as RFI is only measured in Holsteins.

The genetic variance of RFI life and BW in kg of feed DM per year was 30,318 kg²/yr and 33,325 kg²/yr, respectively, and hence the variance of FS was 63,643 kg²/yr. The mean reliabilities for RFI life and FS in the 3,413 bulls were 0.20 and 0.47, respectively (Table 1). A distribution of the reliability of FS for 20k bulls that were born from 2010 onward using the equation 2020 is presented in Figure 1B, where the mean was 0.43 (sd = 0.045), ranging from 0.15 to 0.61. This was about 10% higher than using the equation predicted based on the data set 2015 where the reference population was almost half the size.

Compared with the milk production traits, the reliability of FS is still low. Using the deterministic equation described in MacLeod *et al.* (2014), over 20,000 cows and heifers are needed to have a reliability of 0.50 for RFI life with the given effective population size (N_e) of 210 and a constant reliability of 0.12 for RFI heifer (assuming no more additional data is added at the growing stage). With the given reliability of 0.50 for RFI life, the reliability for FS would be around 0.58. Expanding the heifer population has little impact because weight on it is only 20%.

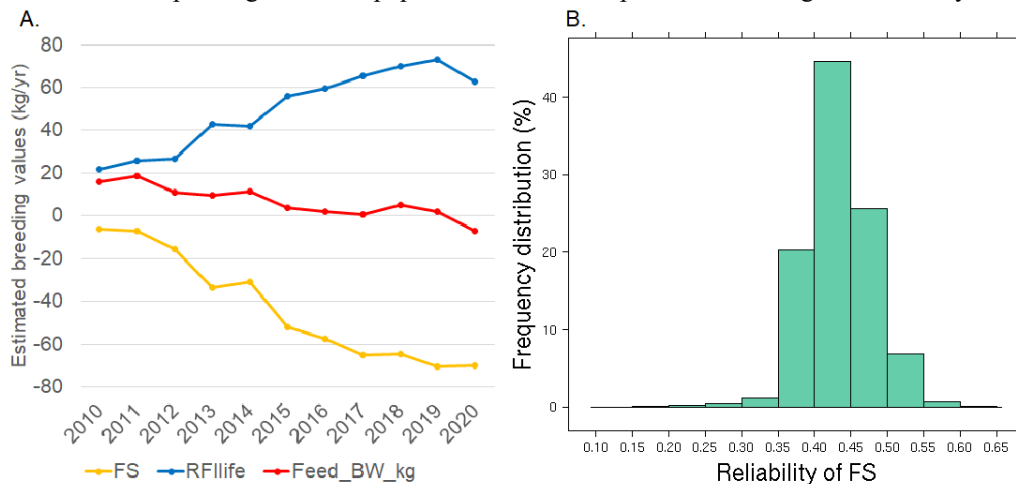


Figure 1. a) Genetic trend of EBV for RFI life, Feed_BWT_kg, and Feed Saved (FS) in 20k genotyped Holstein bulls, b) Histogram of reliability of FS EBV in 20k Holstein bulls

The reliability of RFI cow using the bivariate model with AUS cow and AUS heifer traits applied to 3,413 HOL bulls was low (0.08) compared with the reliability using the tri-variate model, showing a large benefit of using of overseas data. Continuing international collaborations for traits that are expensive to measure, such as feed intake, is immensely valuable.

The FS ABV, using the updated 2020 model, has recently been released by DataGene for farmers and breeders to use (December 2020) in addition to being included in BPI and Health Weighted Index (HWI). The economic weight of FS from the economic model (Byrne *et al.* 2016) used to derive weights for the BPI was halved based on advice from industry stakeholders to avoid a reduction in milk production gains and live weight of mature cows indirectly due to strong correlation to FS. However, the full value (\$0.385/kg) has been applied in the HWI. The

correlation between HWI and FS ABVs using bulls born from 2010 is 0.19, while between BPI and FS is 0.03, so a favourable selection response for FS is still only anticipated with selection on HWI.

CONCLUSIONS

An updated 2020 model for the FS ABV using over 3,700 Australian cows and heifers, and overseas cows implemented using a multivariate model has improved the reliability of FS by about 10% compared with the 2015 model. Feed Saved derived by combining RFI and BWT originally implemented in BPI using the 2015 model has an apparent effect on the genetic trend. The implementation of FS ABV and its inclusion in BPI and Health Weighted Index (HWI) is expected to further improve the genetic trend of FS in the Holstein bulls and cows and improve feed efficiency in dairy cattle. The current reference population based on Australian animals is still small, therefore international collaboration is still crucial to achieve higher reliabilities of feed saved ABV across dairy populations.

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