FEED SAVED BREEDING VALUES FOR AUSTRALIAN DAIRY CATTLE

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SUMMARY

A new breeding value is described that includes the amount of feed saved per year through assumed improvements in lifetime metabolic efficiency and reduced maintenance requirements. The breeding value includes a genomic breeding value for residual feed intake, which is available for Holsteins only, combined with either genomic or pedigree estimated breeding values for maintenance requirements predicted using type traits. The standard deviation of estimated breeding values for feed saved was 65.6 kg/year. The mean reliability of feed saved was 0.37 and the standard deviation was 0.06, with the range from 0.24 to 0.74. The breeding value, which will be known as “feed saved”, has been available for dairy farmers and breeding companies to use in their selection decisions since April 2015.

INTRODUCTION

While it is widely recognised that selecting for feed efficiency in dairy cattle is highly desirable, as feed costs comprise a large proportion of variable costs, there has been little success in developing breeding values to select directly for this trait in dairy cattle breeding (Berry and Crowley, 2013).

Genomic selection is well suited to traits that are measured in small, well recorded populations. Residual feed intake (RFI) is one such trait that fits this description when measured on genotyped individuals. The reference population can be used to develop genomic prediction equations that can then be applied to genotyped animals without phenotypes.

Here, a breeding value called feed saved is proposed. Feed saved is made up of genomic breeding values for RFI of cows and calves combined with maintenance requirements predicted from type breeding values, so that feed requirements are quantified in a single breeding value. For example, where 2 individuals have similar breeding values for milk production traits, it becomes obvious that the animal requiring less feed (for maintenance predicted from BW and RFI combined) will be more efficient and save more feed, all other things being equal.

The aim of this paper is to describe how breeding values could be calculated and implemented for this new trait.

MATERIALS AND METHODS

The process to estimate genomic breeding values (GEBVs) for feed saved includes: 1) calculating phenotypes for RFI of animals included in the reference population; 2) calculating direct genomic values (DGVs) for RFI in the growth and lactation stages of life, and 3) calculation of feed saved GEBVs by combining body weight (BW) EBVs with RFI DGVs.

The reference population used for genomic prediction of RFI was similar to the population used by de Haas *et al.* (2012) and Pryce *et al.* (2014), except additional Australian lactating cows were included and RFI was the phenotype instead of dry matter intake (DMI).

The residual feed intake of 843 growing calves (RFIcalf) was calculated from means of DMI measured over a 6 to 7 week period in growing Holstein calves of around 6 months of age, regressed on average BW and growth over the experimental period (Williams *et al.* 2011).

Phenotypes for RFI in Australian lactating cows (RFIcow) were calculated from means of DMI measured over a 30 day period in multiparous lactating cows regressed on average BW and energy corrected milk.

The UK and Dutch data reported by de Haas *et al.* (2012) were used to calculate RFI in overseas cows (RFIov), and included DMI phenotypes pre-corrected for fixed effects and regressed on energy corrected milk calculated from GEBVs for milk production traits and BW. These GEBVs were calculated using Australian Dairy Herd Improvement Scheme's (ADHIS) official genomic prediction equations, as phenotypes for these overseas animals were not available.

There were 28,621 SNPs in common between Australian and overseas datasets and the SNPs were very similar to those used in the study of de Haas *et al.* (2012). Briefly, the Australian calves were genotyped using the Illumina High Density Bovine SNP chip (Illumina, San Diego, CA; www.illumina.com/agriculture), after quality control procedures described by Pryce *et al.* (2014), 624,930 SNP remained. The Australian, UK and Dutch cows were genotyped using the Bovine SNP50 Beadchip (Illumina Inc., San Diego, CA) and were edited as described by de Haas *et al.* (2012).

A multi-trait analysis (RFIcalf, RFIcow, RFIov) was used to generate GEBVs for RFI in Australian calves and cows, and in overseas cows. This model allowed for the correlations between traits to be estimated.

The model used was:

$$\mathrm{y_T = X_T b_T + Z_T g_T + e_T}$$

Where $\mathbf{y_T}$ is the 3xn matrix of observations on all traits, $\mathbf{X_T}$ is the incidence matrix for fixed effects, $\mathbf{b_T}$ is the matrix of solution of fixed effects (in this case the mean for each trait and country of origin), $\mathbf{Z_T}$ is an incidence matrix mapping records to animals, $\mathbf{g_T}$ is the corresponding genomic breeding values for animals with genotypes for all traits, and $\mathbf{e_T}$ is a 3xn matrix of residual terms. Variance components were estimated with ASREML (Gilmour, 2006).

Regression equations that allow both RFIcalf and RFIcow to be computed from SNP markers were calculated by back solving the mixed model equations. The estimation of SNP coefficients was calculated as $\beta = H'(HH')^{-1}\hat{g}$, where H is the n x 28,621 matrix of the genotypes of n animals in the reference set, with genotypes coded as 0, 1, 2 for aa, Aa and AA respectively, and $\hat{g}$ is the DGV for RFIcalf or RFIcow.

RFIcalf and RFIcow DGVs were combined to calculate lifetime RFI (RFIlife). RFIlife was expressed in kg of feed per year and it was assumed that the rearing period is 2 years and cows have 4 lactations on average. This was done by multiplying the DGV for RFIcow by days in lactation (days), which was assumed to be 305d and deliberately excluded the dry period when feed costs and daily feed intake were lower (than during lactation). Similarly, RFIcalf was multiplied by days of life before lactation commenced, which was assumed to be 700d (i.e. ignoring the period from birth to weaning, which is approximately 30d, when the diet is predominantly milk). Finally, there is a division by 6 (2 years as a calf + 4 years as a lactating cow).

The feed saved breeding value is defined as the annual feed required for maintenance combined with residual feed intake. Maintenance requirements (in MJME) are generally considered to be a function of BW (e.g. Visscher *et al.* 1994). In Australia, BW breeding values are calculated from type traits (see Haile-Mariam *et al.* (2014) for more details). The marginal change in feed required to maintain a given EBV of BW was calculated. Finally, the direction of the EBV was reversed, so that high values meant that more feed was saved.

The reliabilities of BW EBVs are already calculated routinely as part of the genetic evaluation service of the ADHIS. A method to estimate the reliabilities for RFIcalf and RFIcalf for genotyped animals without phenotypes was also required. This was achieved by inverting the coefficient matrix that incorporates animals with and without records in the system of equations.

RESULTS AND DISCUSSION

The rationale for combining RFI and feed required for maintenance predicted from BW is that annual feed requirements are accounted for in the same breeding value. Selecting for this trait in tandem with other traits of economic importance via a selection index, leads to selection for improved feed efficiency. The advantage of feed saved is that animals with the same RFI can be distinguished on the basis of their maintenance requirements. Then, everything else being equal, larger animals will be penalised for greater maintenance costs. An important distinction and the reason why feed saved (integrating RFI and maintenance costs associated with higher BW) is a more desirable trait for implementation than RFI, is because RFI is corrected for BW.

Table 1. Phenotypic SD, heritability (diagonal) and genetic correlation estimates for RFI measured in Australian cows (RFIcow), Australian calves (RFIcalf) and UK and Dutch cows (RFIov) (above the diagonal). Standard errors are presented in parentheses.

	Phenotypic SD	RFIcow	RFIcalf	RFIov
RFIcow	1.26	0.20 (0.20)	0.67 (0.45)	0.76 (0.60)
RFIcalf	0.42		0.35 (0.08)	0.30 (0.22)
RFIov	0.97			0.35 (0.06)

The heritability of RFI in Australian cows, estimated using genomic relationships between animals, was 0.20 and for growing calves and a combined dataset of Dutch and UK cows, respectively, was 0.35 (Table 1), both of which are in the range of previous studies (e.g. Berry and Crowley, 2013). The standard errors of the estimates were large in general, as expected given the limited data, especially for Australian lactating cows. As more Australian lactating cow data accumulates, the standard errors are expected to reduce, which would lead to less reliance on data from other countries.

In addition to a small number of Australian cow records for RFI, the other limitation in how RFI has been evaluated in this study, was a failure to account for differences in body composition or changes in body composition. Although body condition score (BCS) is the accepted measure of fat reserves in dairy cattle, it is generally scored on a relatively limited scale which makes evaluating changes in BCS difficult for a dataset of only several hundred cows over a relatively short time period. Advancements in accurately quantifying body reserves in dairy cattle will benefit genetic prediction of RFI. For the time being, including feed saved as part of a multi-trait selection index for profit, that also includes fertility as well as traits like survival and mastitis resistance, should help to guard against undesirable correlated responses, for example in fertility.

The DGVs for RFIcalf and RFIcow had standard deviations of 0.09 kg/d and 0.21 kg/d respectively. The standard deviations of estimated breeding values for RFIlife and feed saved were 50.5 and 65.6 kg/year. The mean reliability of feed saved was 0.37 and standard deviation was 0.06, with the range from 0.24 to 0.74.

The genetic trend for feed saved is shown in Figure 1 and includes a subset of the genotyped bulls that were born from 1990 onwards. It can be seen that from around 2000 there has been an increase in breeding values for maintenance requirements and RFI, consequently the genetic trend for feed saved is unfavourable.

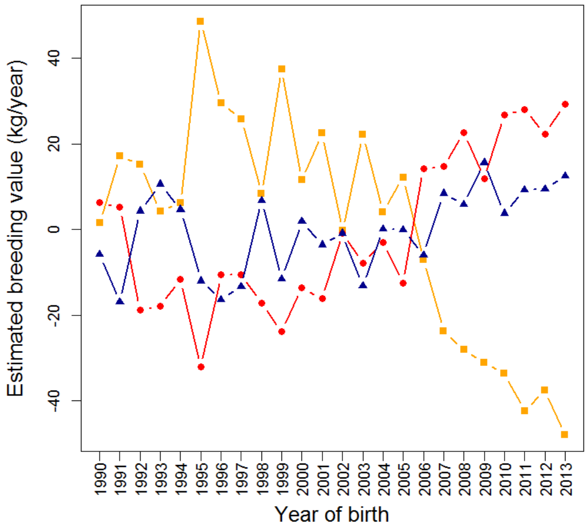

Figure 1. Genetic trend of estimated breeding values for bulls born in or after 1990 for RFIlife (▲), annual feed required for maintenance (●) and Feed Saved (■).

To conclude, selection for feed efficiency in dairy cattle historically has relied on approximations of maintenance requirements. However, this is unlikely to capture all the variation in feed efficiency. Through genomic selection, there are now opportunities to extend this to include measures of efficiency derived from actual feed intake data, such as RFI. This study described how a feed efficiency breeding value can be derived by combining RFI with maintenance requirements. Although the mean reliability of this new trait was comparatively low when compared to other traits, this is expected to improve as the reference population is expanded.

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