

Deriving genomic breeding values for feed intake and body weight in dairy goats

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Introduction

In dairy production, feed efficiency relates to amount of energy corrected milk that can be produced per unit of energy consumed. As feeding costs account for the bulk of overheads in dairy production, incorporating feed efficiency into genetic and genomic breeding programmes has enormous potential for reducing costs to producers as well as having positive implications from an environmental sustainability standpoint. Feed efficiency has long been incorporated into breeding programmes in the pig and poultry industry, and much progress has been made in the last decade in the dairy cattle sector using proxy traits. Dairy goat breeding programmes are relatively new, and to date, much of the breeding focus has been on increasing milk yield and quality. Feed efficiency and body weight in the present population have been shown to have a heritable component (average h^2 0.25; Desire et al., 2017), with sufficient genetic variation to respond to traditional selective breeding. The accuracy of breeding values calculated via pedigree based BLUP relies on accurate pedigree information, and a large number of records on an animal or its progeny. Genomic selection has been shown to be of particular value when applied to traits that are difficult or expensive to measure or are expressed later in life. It has already been successfully implemented for milk production in the UK dairy goat industry. This study sought to evaluate the accuracy of using single-step genomic BLUP to estimate genomic breeding values for feed efficiency and body weight in multiparous, mixed-breed dairy goats.

Material and methods

Animals and housing

The data consisted of 42,434 test day records for feed intake (kg) and body weight (kg) from 3,421 multiparous, mixed-breed (Saanen, Alpine, and Toggenburg) dairy goats, born between 2006 and 2016. Animals were zero-grazed year-round across 2 farm sites, and had continuous access to water and hay. Animals were fed a digestible fibre-based blended feed *ad libitum* for the first 150 days of lactation, after which feed was restricted based on MY. Feed was provided in the milking parlour and automatically dispensed, while body weights were recorded as the animals exited the milking parlour. Records were related to individuals via electronic identification devices. Animals were the progeny of 180 sires and 2,212 dams, and the pedigree contained 8,068 animals.

Genotype data

Animals were genotyped using the 50k Caprine Illumina SNP chip (Illumina Inc., San Diego, CA; Tosser-Klopp et al., 2012). SNPs were deleted if they were monomorphic, had a minor allele frequency of < 0.05 , had call rate of < 0.95 , or were not in HWE. After quality control a total of 44,907 SNPs remained.

Estimation of genomic breeding values

A single-step method was used to estimate GEBV using the software MiX99 (Lidauer et al.) fitting a random regression model. Fixed effects for feed intake and body weight included milk yield, year-season of kidding, age at kidding, herd test day, and fixed lactation curves using third order Legendre polynomials nested within lactation number. Feeding regime (*ad libitum* vs restricted feeding) was included as a fixed effect for feed intake, but not body weight, as this did not significantly contribute to the variance in this trait, as determined by Wald F statistics ($P > 0.05$). In addition, body weight was included as a fixed effect for feed intake, and vice versa. By including body weight and milk yield as fixed effects for feed intake, an approximation of feed efficiency was obtained. Additive genetic and permanent environment effects were modelled using second order Legendre polynomials across days in milk. The relationship matrix H was calculated using a blend of the genomic relationship matrix G (VanRaden, 2008) and the pedigree relationship matrix A. G was calculated as:

(1)

where S is a centered incidence matrix of SNP genotypes, n is the number of SNP markers, and p_i is allele frequency of marker i . The inverse of H is as described by (Aguilar *et al.*, 2010). To assess population stratification, the G matrix was also used to calculate principal components.

Validation of genomic breeding values

Animals with both phenotypes and genotypes with a call rate > 0.90 , and an EBV reliability ≥ 0.70 were split into training and validation sets. The training set contained 1,241 individuals born between 2006 and August 2015, with average EBV reliabilities of 0.89 and 0.83 for body weight and feed intake, respectively. The validation set contained 320 animals born between August 2015 and February 2016, with average EBV reliabilities of 0.85 and 0.84 body weight and feed intake. Reliabilities of EBVs were calculated using the approximation method of (Miszta and Wiggans, 1988). Accuracies of GEBV were calculated as a correlation between deregressed proofs (DP) and GEBVs of the validation animals. For body weight, breeding values were calculated at a fixed point of 305 days in milk, whereas for feed intake cumulative 305 day breeding values were estimated. Deregression of EBVs was performed using MiX99 (Lidauer *et al.* 2011) using a pedigree with effective daughter contributions used as a weighting factor.

Results and discussion

Descriptive statistics of the raw test day records for body weight and feed intake are presented in Table 1. As feed intake is closely associated with milk yield, descriptive statistics for milk yield are also presented in Table 1, for context.

Table 1. Characteristics of raw test day records for body weight (kg), feed intake (kg), and milk yield (kg)

Trait	<i>n</i>	Lactation	Min	Max	Mean	SD
Body weight (kg)	20,390	1	36.00	106.40	62.46	9.94
	12,729	2	35.50	121.80	78.73	10.49
	9,315	>= 3	38.00	123.50	79.23	10.57
Feed intake (kg)	20,390	1	0.28	4.51	1.83	0.55
	12,729	2	0.22	5.07	1.81	0.60
	9,315	>= 3	0.14	4.53	1.54	0.62
Milk yield (kg)	20,390	1	0.21	9.25	4.36	1.13
	12,729	2	0.20	9.49	4.70	1.35
	9,315	>= 3	0.21	10.55	4.16	1.45

Principal components (PC) 1 and 2 accounted for 40% and 13% of the variance in SNPs, respectively, however visual inspection of the plotted eigenvectors for PC 1 and 2 did not suggest stratification (Figure 1). These results suggest that despite being a composite of three breeds, the population is genetically homogenous.

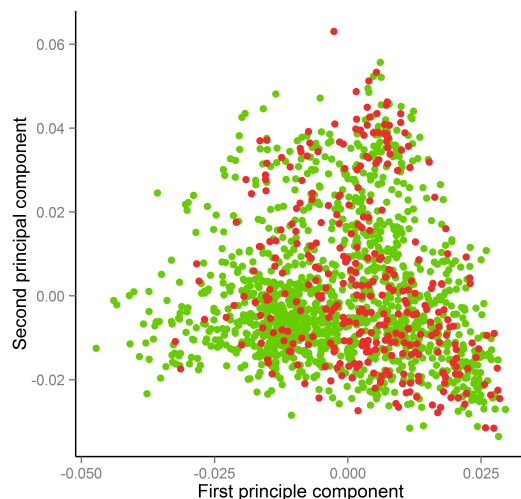


Figure 1. Principal components 1 and 2 based on genomic relationship matrix for training (green) and validation (red) animals.

The accuracies of the genomic prediction for body weight and feed intake were both 0.28 (Table 2). Regression coefficients DP and GEBVs for body weight were >1, suggesting that the models underestimated the DP, while the inverse was true for feed intake. Of living, genotyped sires, GEBVs differed by 6 kg between the top and bottom ranked animals for 305d body weight. For feed intake, cumulative 305d GEBVs differed by 142.9 kg between the highest and lowest ranked sires, suggesting daughters of top sires are genetically predisposed to consume an average of 0.47 kg per day less, compared to bottom-ranking sires. Regularly measuring feed intake and body weight on a large herd is challenging, and has only recently begun on this herd. As more phenotypes are collected on daughters of genotyped sires, we expect the accuracy of GEBVs to increase, paving the way for feed intake and body weight to be incorporated into a genomic breeding programme.

Table 2. Correlations (R) and regression coefficients (b_1) between deregressed proofs and EBVs calculated via single step HBLUP for feed intake and body weight.

Trait	b_1	R
Body weight (kg)	2.14	0.28
Feed intake (kg)	-2.29	0.28

Summary

Feed accounts for a large proportion of costs in dairy farming. Differences exist in how efficiently individual animals convert energy to milk, and genetic improvement of feed efficiency could play an important role in reducing feed costs per unit of output. Previous work has indicated a positive correlation between feed intake and body weight, therefore these traits should be incorporated into a multi trait selection index. This study aimed to investigate the accuracy of using single step genomic selection to estimate breeding values for feed efficiency and body weight in a dairy goat herd. Accuracy of genomic breeding values were low for this population (0.28 for both traits), however records have only been collected for the last year, and the validation population only contained 320 individuals. Accuracy is expected to increase as the reference population containing related animals increases.

List of References

- Aguilar, I., I. Misztal, D.L. Johnson, A. Legarra, S. Tsuruta, and T.J. Lawlor. 2010. Hot topic: a unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. *J. Dairy Sci.* 93:743–52.
- Desire, S., S. Mucha, R. Mrode, M. Coffey, J. Broadbent, and J. Conington. 2017. Genetic parameter estimations for feed intake in UK dairy goats in The 68th Annual Meeting of the European Federation of Animal Science (EAAP).
- Lidauer, M., K. Matilainen, E. Mantysaari, and I. Straden. MiX99 Manual.. MTT Jokioinen Finl. 2011 SRC.
- Misztal, I., and G.R. Wiggans. 1988. Approximation of Prediction Error Variance in Large-Scale Animal Models. *J. Dairy Sci.* 71:27–32.
- Rojo-Rubio, R., A.E. Kholif, A.Z.M. Salem, G.D. Mendoza, M.M.M.Y. Elghandour, J.F. Vazquez-Armijo, and H. Lee-Rangel. 2016. Lactation curves and body weight changes of Alpine, Saanen and Anglo-Nubian goats as well as pre-weaning growth of their kids. *J. Appl. Anim. Res.* 44:331–337.
- Tosser-Klopp, G., P. Bardou, C. Cabau, A. Eggen, T. Faraut, H. Heuven, S. Jamli, C. Klopp, C. T. Lawley, J. McEwan, P. Martin, C. Moreno, P. Mulsant, I. Nabihoudine, E. Pailhoux, I. Palhière, R. Rupp, J. Sarry, B. Sayre, A. Tircazes, J. Wang, W. Wang, T.-P. Yu, and W. Zhang. 2012. Goat genome assembly, Availability of an international 50K SNP chip and RH panel: An update of the International Goat Genome Consortium projects. Pages 1–14 in *Plant Anim. Genome Conf.*, San Diego, CA. International Plant & Animal Genome, San Diego, CA.
- VanRaden, P.M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91:4414–4423.

