

Breeding Value for Dry Matter Intake for Dutch Bulls based on DGV for DMI and BV for Predictors

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ABSTRACT: Dry matter intake (DMI) was available for (part of) 3,179 lactations in the Netherlands. Using a fixed regression test-day model, genetic variances were estimated for yield and DMI in parity 1, 2 and 3+, and stature, body depth and chest width in parity 1. The combined pedigree and genomic relationship matrix was used to predict genomic breeding values (DGV) for DMI and used to back solve the solutions to obtain SNP effects. Using genetic correlations with predictor traits, combined breeding values (GEBV) for DMI were produced. The s.d. of the combined GEBV was 1.2 kg/d and the median for the reliability was 0.56. For DGV s.d. was 0.45 and median reliability was 0.18. Genetic trend showed an increase of 1.1 kg DMI/d per decade for the combined GEBV, versus 0.12 for the DGV. Future developments include the expansion of the reference population in collaboration with other partners worldwide.

Keywords:

Dairy cattle

Feed intake

Genomic selection

Introduction

There is no doubt that feed intake or feed efficiency should be included in the breeding goal (de Haas et al. (2012); Veerkamp et al. (2012)). However, recording feed intake on individual daughters of test bulls has been too expensive, and hampered inclusion of feed intake or feed efficiency in a national selection index for dairy cattle.

Genomic selection enables selection for traits that are recorded on a genotyped reference population, independent of whether these are daughters of test bulls or not. Therefore, genomic selection provides an interesting opportunity to include feed intake or feed efficiency in the national breeding programs, at least if sufficiently large reference populations can be built. Several international projects are running combining thousands of lactations with feed intake recorded at research herds, aiming to deliver genomic prediction equations that are accurate enough for selection. These genomic predictions for feed intake are essential to identify the net feed efficiency (i.e. feed intake not attributed to milk production or maintenance), but the accuracy of these breeding values is likely to be still low for the near future. Therefore the genomic predictions will be aided by including daughter information for predictor traits that are well known to be important components of feed use: milk production and body size.

The objective here is to develop a national breeding value for dry matter intake (DMI), combining

genomic prediction for feed intake from Dutch research herds with national breeding values for yield and type traits.

Materials and Methods

Phenotypic data. Originally, a total of 307,007 daily records from 2,977 Holstein-Friesian cows that calved between 1990 and 2011 were available, for cows that had DMI, LW or milk, fat and protein yield recorded. These cows participated in experiments conducted on several farms in Netherlands. Description of the methodology of most of the experiments is summarized in previous studies (Veerkamp et al. (2000); Beerda et al. (2007); Zom et al. (2012)). All records from animals with <75% Holstein Friesian genes, or without information on pedigree, parity number, calving date or date of measurement were removed, and only measures that were taken in the first 324 DIM were retained. Daily DMI records were converted to the average weekly DMI in order to homogenize the data across experiments. Linear type classification score of these animals, and additional lactations with production records were added from the national database. The latter was undertaken to more appropriately correct for selection on yield. Data editing resulted in a final dataset with 147,771 weekly records from 2,538 animals with 8,417 lactations with yield, of which 3,179 lactations had at least one weekly record for DMI and 3,393 for LW. Stature and body depth were available for 2,272 animals in their first parity, and chest width for 1,390 animals.

Variance components estimation. A fixed regression test-day model accounting for the mean lactation curves but assuming one genetic animal effect in each parity, was used to estimate the variance and covariance components with ASReml (Gilmour et al. (2009)) using the full pedigree (35,005 animals). DMI, milk, fat and protein yield were treated as a different trait in parity 1, 2 and 3+, and fixed effects fitted within each parity were experimental treatment, year-month of measurement and year season of calving (four classes: Jan-Mar, Apr-Jun, Jul-Sep, Oct-Dec). Age of cow at calving, proportion of major breed and DIM were modeled as regressions. For the three type traits, herd by inspection date, and classification standard (red or black and white) were also fitted. The residual, additive genetic and permanent environmental covariance matrices were 15x15 (3 parities for milk, fat, protein and DMI each plus stature, body depth and chest width). Since type traits were only scored once in first parity, normally no permanent environmental variance would be fitted. However, such model ignores the

environmental covariance between type and DMI recorded at other days during the same lactation, resulting in overestimated genetic correlations. Therefore, the residual variance for the type traits was artificially divided between a residual and permanent term, to enable the full environmental covariance to be estimated.

Genomic prediction. Genotypes were available for 1,013 cows (with DMI records) and 5,967 sires with 41,235 SNP (with no phenotypes). The inverse of the combined pedigree and genomic relationship matrix (H^{-1}) was constructed, assuming a weight on the G versus the A matrix of 0.95, and genomic breeding values (DGV) were estimated using the model described above but using the DMI data only. MIXBLUP, (<http://www.mixblup.eu/>) was used for this analysis. Variance components were from the pedigree analysis. To be able to predict DGV for animals with known genotypes, SNP prediction equations (a_j) were obtained from the vector \mathbf{u} with DGV for each animal (Stranden and Garrick (2009)): $\mathbf{G}=\mathbf{ZDZ}'/k$; $\mathbf{a}=\mathbf{DZ}'(\mathbf{ZDZ}')^{-1}\mathbf{u}$. Where \mathbf{Z} is the centered design matrix, \mathbf{G} is the genomic relationship matrix, $k = 2 \sum_{i=1}^n p_i(1 - p_i)$, p_i is the allele frequency for locus i , and \mathbf{D} is an identity matrix following the assumptions in \mathbf{G} , and \mathbf{a} is the derived vector with effects for each SNP.

Blending predictor traits. For 5,864 HF bulls born after 1980, final breeding values (GEBV) for DMI were calculated by first combining the DGV in each parity with available national proofs (BV) for milk, fat and protein yield and stature, chest width and body depth in the different parities, then the three DMI traits were combined weighing the relative importance of parity 1, 2 and 3 as 0.41, 0.33 and 0.26 to get overall DMI. Selection index weights were based on the reliability of the different DGV and the BV for each bull. To approximate reliability (r_i^2) of the DGV for each animal (i), the model was rerun in ASREML, and using the standard errors of the DGV (SEP) and σ_A^2 the reliability was calculated as:

$$r_i^2 = 1 - \frac{SEP_i^2}{\sigma_A^2}$$

Results and Discussion

Recording of DMI was sparse across DIM and lactations (Figure 1), so therefore a fixed regression test day model was used to obtain variance components. The h^2 ranged from 0.18 to 0.24 for DMI (Table 1) when the model with all traits was used. In a model without accounting for selection on yield and type the heritability were lower (0.16 to 0.18). Both h^2 are lower than found with a RR model accounting more properly for changes of (co-)variances during lactation (Manzanilla Pech et al. (2014)). Also, as expected, h^2 estimates for weekly records are lower than usually found when DMI records are averaged over a longer period (Veerkamp (1998); Berry and Crowley (2013)). Genetic correlation between DMI in

parity 1 and in 3+ was 0.73. Genetic correlations with type traits were moderately small, ranging from 0.21 to 0.33. For the yield traits, correlations in the same lactation had a small range: 0.55 to 0.64. Based on the genetic correlations, the type traits can predict DMI with maximum reliability of 0.17, when bulls have a large number of daughters. In that situation the yield traits predict DMI with reliability 0.64. Together type and yield explained 0.96 of the variation in DMI, however this value is probably overestimated because the genetic correlations are estimated with large errors.

Genomic breeding values for the 5,864 HF bulls ranged from -1.9 to +1.6 with a s.d. of 0.45 kg/d (Figure 2). For a few bulls the reliability was above 0.80. These bulls were famous Dutch bulls used at the research farms as well, and having several daughters with feed intake records (Figure 3). The median for the reliability of the DGV was 0.18, reflecting the relatively small reference population. When combined with the BV of the predictor traits, the range of the GEBV increased considerable (Figure 2), and the s.d. became 1.2 kg/d. Also, the median for the reliability was 0.56, bringing most bulls above the national publication criteria of 0.35. A few of the older bulls had no national BV for type or for the milk yield traits, and their reliability averaged around 0.45.

The genetic trend for DGV was virtually zero with an increase of 0.12 kg DMI/d per decade, whereas the GEBV with predictors had a trend of 1.2 kg DMI/d per decade. This difference in trend appeared somewhat surprising, and there might be several reasons. The most likely reason is the lower reliability of the DGV, they are more regressed to the mean, resulting in a smaller slope. However, also, little feed intake records in the last few years, and a different response on true feed intake compared to predicted intake might be the reasons. Overall, higher reliability of the genomic prediction of DMI should be aimed for to identify the variance in feed intake that is not accounted for by type and yield (i.e. residual feed intake).

Conclusions

This is the first time that breeding values for feed intake are available for common bulls in The Netherlands, and considerable variation exists. It is useful to combine research herd data for genomic prediction. More precise modelling of variation in DMI and averaging across a longer period will increase the heritability. A relatively large part of the variation in DMI comes from variation in yield and body size, but the genomic predictions for feed intake are essential to improve net feed efficiency. Therefore, expansion of the reference population through international collaboration should be an important step forward.

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Tables and Figures

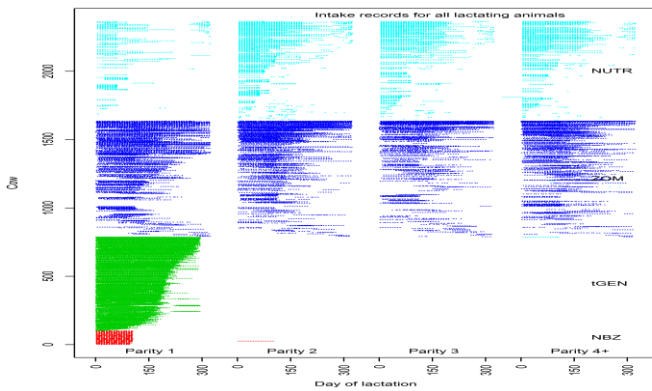


Figure 1. DMI records available during parity 1, 2, 3 and 4+ for 2,538 cows in four data sources. Each dot represents a record for a cow in a particular week of lactation.

Table 1. Heritability for DMI in parity 1, 2 and 3+, and genetic correlations with three type traits and the average of the correlations with milk, fat and protein yield in parity 1, 2 and 3+

	h^2	DMI2	DMI3	Stature	Chest	Body	Yield
DMI1	0.24	0.83	0.73	0.34	0.23	0.26	0.63
DMI2	0.24		0.82	0.34	0.22	0.21	0.59
DMI3	0.18			0.34	0.27	0.21	0.57

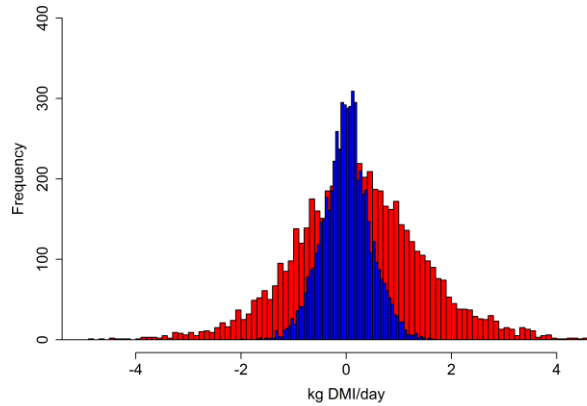


Figure 2. Distribution of breeding values for DMI in Dutch bulls, i) genomic breeding values (DGV in blue) and ii) genomic breeding values blended with national BV for type and yield (GEBV in red).

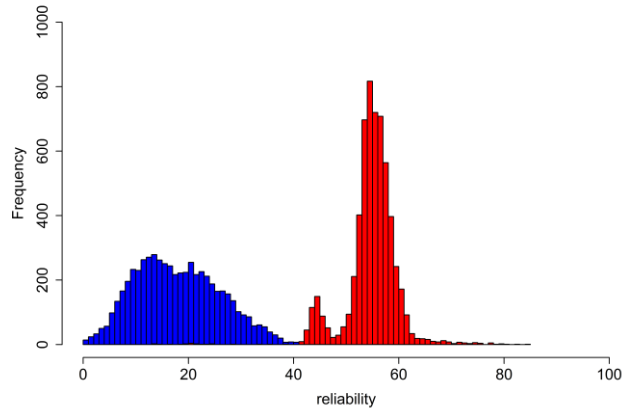


Figure 3. Distribution of reliability of breeding values for DMI (%) for i) genomic breeding values (DGV in blue) and ii) genomic breeding values blended with national BV for type and yield (GEBV in red).

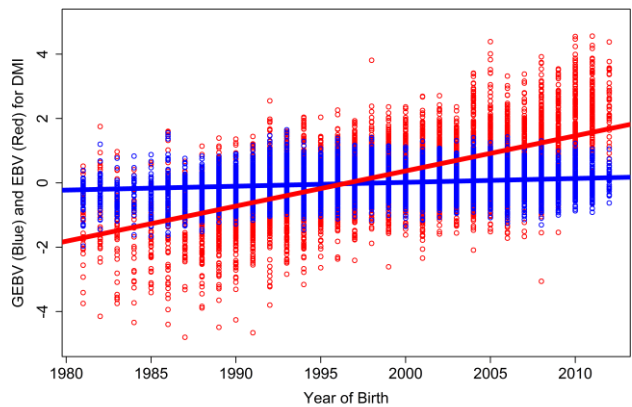


Figure 4. Genetic trend for i) genomic breeding values (DGV in blue) and ii) genomic breeding values blended with national BV for type and yield (GEBV in red).