International Genetic Evaluations for Feed Intake in Dairy Cattle

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Abstract

Feed represents a large proportion of the variable costs in dairy production systems. The omission of feed intake measures explicitly from national dairy cow breeding objectives is predominantly due to a lack of information on which to make selection decisions. Individual cow feed intake data are available in different countries, mostly from research or nucleus herds. None of these datasets are sufficiently large enough on their own to generate accurate genetic evaluations. Here we collate data from ten populations in nine countries. A total of 224,174 test-day records from parity one to five animals, as well as 1,784 records from growing heifers were available. Random regression models fitted to lactating cow test-day records were used to predict feed intake at 70 days post calving. Heritability estimates of predicted cow feed intake 70-days post-calving was 0.34 across the entire dataset and varied, within population, from 0.08 to 0.52. Repeatability of feed intake across lactations was 0.66. Heritability of feed intake in growing heifers was 0.20 to 0.34. The genetic correlation between feed intake in lactating cows and heifers was 0.67. A combined pedigree and genomic relationship matrix was used to improve linkages between populations for the estimation of genetic correlations between countries categorized as North America, Grazing, Other low input, and High input EU. Genetic correlation estimates between populations varied from 0.14 to 0.84 but was stronger (0.76 to 0.84) between the populations representative of high input production systems.

1. Introduction

Despite the known large contribution of feed costs to the variable costs of production in dairy cattle production systems, feed intake is currently not explicitly included in the breeding goal of any dairy cattle population. The omission of feed intake from national breeding goals is principally due to an absence of routine recording of feed intake information on which to estimate breeding values of individual animals. Feed intake data in dairy cattle are almost exclusively recorded in research herds or nucleus breeding herds. The objective of this study was to collate feed intake phenotypic data from nine different countries across a range of production systems and evaluate both the possibility and plausibility of combining these data for use in an international genetic evaluation for feed intake.

2. Materials and Methods

Data on individual daily feed intake of Holstein-Friesian cows and heifers were available from nine countries (Ireland, UK, Canada, US, Netherlands, Germany, Denmark, Australia, New Zealand), with data from Iowa State University and Wisconsin University contributing to the US data. Only cow data from parity one to five were retained for inclusion in the analysis. A total of 224,174 test-day records from 10,641 parities from 6,953 cows were available. An additional 1,784 feed intake records (averaged over a 56-70 day test period) from 1,784 growing heifers in Australia and New Zealand were also available; lactating cow records on 101 of the Australian heifers was also available.

Data were from a range of experimental treatments across all populations; some experimental treatments were imposed at different stages of lactation. Furthermore, some populations only had observations for DMI at particular stages of lactation. Therefore, to facilitate the derivation of a common DMI trait across all animals as well as account for temporal experimental treatment effects, a random regression model was fit to all individual daily DMI observations.

The random regression model fitted was:

$$DMI = parity \cdot \sum_{n=1}^{5} DIM^n + HYS + CG +$$

$$animal \cdot parity \cdot \sum_{n=1}^{2} DIM^n + Herd \cdot \sum_{n=1}^{2} DIM^n$$

where DMI is dry matter intake, $parity \cdot \sum_{n=1}^{5} DIM^n$ is a fixed effect for a fifth order Legendre polynomial on days in milk for each parity separately, HYS is the fixed effect of herd-year-month of calving, CG is contemporary group (i.e., experimental treatment) which for some population varied across lactation, $animal \cdot parity \cdot \sum_{n=1}^{2} DIM^n$ is a random second order Legendre polynomial on DIM for the animal effect, $Herd \cdot \sum_{n=1}^{2} DIM^n$ is a random second order Legendre polynomial on days since calving for the herd effect. Lactations were divided into 4 stages ≤30 DIM, 31 to 100 DIM, 101 to 200 DIM and >200 DIM. A separate residual variance was fit for each class of herd-parity-stage of lactation.

Predicted DMI was obtained for each animal-parity for every DIM for which there was at least one actual phenotype in the dataset. Average contemporary group effect for each animal-lactation was absorbed into the herd-year-season of calving effect for the purposes of subsequent analysis. Predicted DMI at 70 days post-calving was used as the dependent variable for further genetic analysis and only lactations with at least one actual DMI observation were retained.

Genetic analysis

Phenotypic and genetic variance components for predicted DMI at 70 days post-calving from the random regression model were estimated using an animal repeatability linear mixed model; fixed effects included in this model were parity and herd-year-season of calving. The genetic correlation between heifer actual DMI and cow predicted DMI was also estimated.

To facilitate the estimation of the genetic correlation between DMI of lactating cows in different countries a combined pedigree and genomic relationship matrix was constructed. Genotype information was available on 5429 animals that also had phenotypic information. Furthermore, lactating cow records within countries were grouped as "Grazing" (Ireland + Australia), "Other low input" (UK low-input production system), "North America" (Iowa, Wisconsin + Canada), and "High input EU" (UK high-input production system, The Netherlands, Germany + Denmark) and genetic correlations for DMI between these country groups were estimated; no residual or permanent environmental covariances between populations were assumed. Pedigree information was traced back to the founder population; the pedigree file consisted of 271,545 records.

3. Results

Mean lactation profiles for first lactation DMI for each population are in Figure 1. The shape of the DMI lactation profile was relatively consistent across populations despite the random regression model applied facilitating the modelling of differently shaped lactation profiles for different populations. Data from the UK was separated into two groups to reflect the high and low feeding system in that country (Pryce *et al.,* 1998). The stage of lactation when DMI was measured in the Australian lactating cow population varied from 62 and 217 DIM so therefore no information was available in early lactation;

hence extrapolation to early lactation in this population of limited size should be undertaken with caution. Dry matter intake was, on average, greatest in both US populations (i.e., Iowa and Wisconsin) and was lowest for Ireland, Australia and the low-input feed system in the UK.

Mean DMI at 70 DIM for the different populations is in Table 1. The heritability of DMI in lactating cows (Table 1) in the entire dataset was 0.34 (0.03) and is consistent with most recent international estimates for feed intake in dairy cows in both confinement (0.10 to 0.60; Veerkamp and Brotherstone, 1997; Søndergaard et al., 2002; Vallimont et al., 2011; Hüttmann et al., 2009; Spurlock et al., 2012) and grazing (Berry et al., 2007) production systems.

Within population heritability estimates for DMI (Table 1) varied from 0.08 (Germany) to 0.52 (Denmark); heritability could not be estimated in the 103 Australian lactating dairy cows. The relatively low heritability estimate of DMI in the German population is consistent with that documented using a similar German dataset (Buttchereit et al., 2011), and lower than found in more recent data. Heritability of DMI in the nulliparous heifers was 0.20 and 0.34 for New Zealand and Australia, respectively (Table 1).

The genetic standard deviation for DMI in lactating animals varied from 0.64 kg DM/day (Germany) to 1.48 kg DM/day (Iowa and Denmark). This suggests a coefficient of genetic variation of between 2.4% to 6.7%. Taking note of the differences in heritability estimates between populations, the phenotypic standard deviation for DMI in the lactating animals was very similar, varying from 1.83 kg DM (Wisconsin) to 2.32 kg DM (Canada); the exception was lactating cows in Ireland (1.38 kg DM/day). Ireland operates a dairy production system relying predominantly on grazed grass and grazed grass constituted the vast majority if not all of the diet of the Irish cows included in the analysis. The coefficient of genetic variation for DMI in the nulliparous heifers was 8.7 to 9.3%.

Across lactation repeatability estimates for DMI in the lactating animals (Table 1) was 0.66 in the entire population and varied from 0.46 (Canada) to 0.84 (Germany); no repeated records existed for the Iowa, Wisconsin, or Australian lactating cow datasets or for either heifer dataset. Repeatability estimates for DMI for populations not included in the present study have been documented to be approximately 0.51 (Søndergaard et al., 2002).

The genetic correlations between DMI in different groups of countries are in Table 2. The standard errors of all correlations were relatively large, contributed to by the relatively poor genetic linkages among some countries. Positive genetic correlations (0.14 to 0.84) existed between all populations. As expected, the genetic correlations with the production systems representing grazing (i.e., Irish + Australian lactating cows) were weakest (0.14 to 0.57). The genetic correlations among the other production systems were strong (0.76 to 0.84). The existence of weak genetic correlations with the grazing production systems, albeit associated with large standard errors) indicate the presence of genotype-by-environment interactions. Characteristics influencing cow DMI in confinement and grazing production systems is likely to differ. For example, (rumen) capacity is likely to have a greater influence on DMI in grazing production systems because of the high filling capacity associated with grass (Gill et al., 1988).

The genetic correlation between heifer DMI and DMI of lactating cows 70 days post-calving was 0.67 (0.24). This is consistent with the genetic correlation of 0.74 reported by Nieuwhof et al. (1992) between growing nulliparous heifers (n=417) and first lactation cows (n=360) in early to mid lactation. However, the diets (and other management factors) that both the heifers and cows were exposed to in the present meta-analysis study differ; only 101 Australian animals had DMI observations both as heifers and cows and no New Zealand cows were included in the analysis. Nonetheless, the moderate to strong genetic correlation between heifer DMI and

cow DMI suggests that the former is a useful predictor of genetic merit for DMI in lactating cows. Measurement of DMI in heifers may be more feasible since the management regime in heifers can be disturbed for a short period to measure DMI without any considerable consequences on performance.

4. Conclusions

It is possible to combine international data on DMI from research farms and nucleus herds to generate estimated breeding values. Cognisance however must be taken of genotype-by-environment interactions especially for grazing production systems.

5. Acknowledgements

8. References

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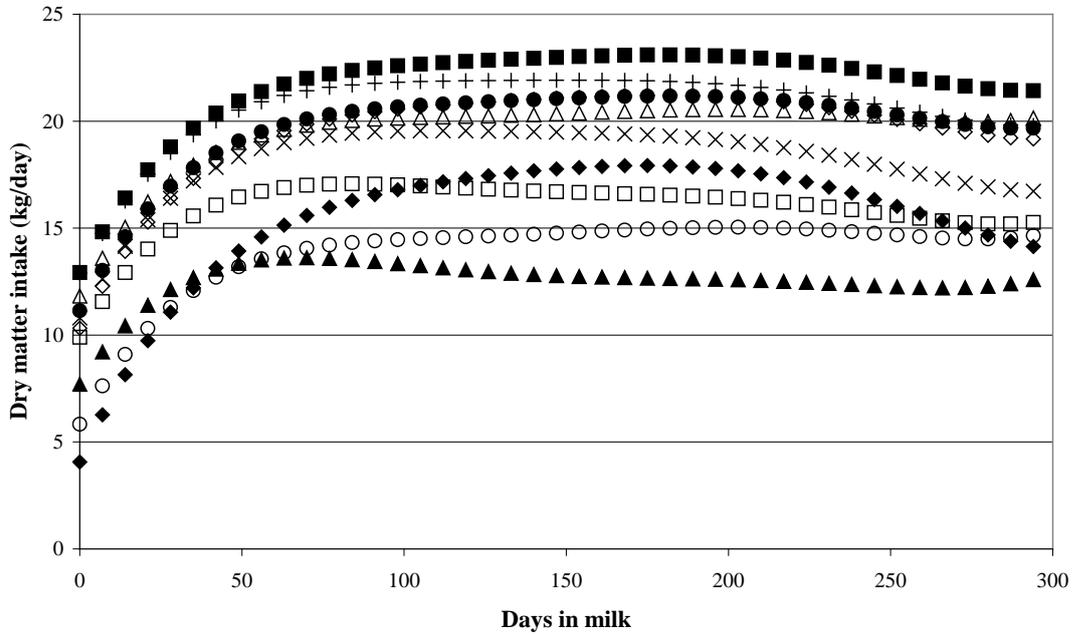
Figure 1. Predicted daily dry matter intake across lactation for first parity cows from UK low input feed system (▲), Ireland (○), Australia (♦), UK high input feed system (□), the Netherlands (X), Denmark (Δ), Canada (●), Germany (◊), Iowa (+) and Wisconsin (■).

Table 1. Number of lactations as well as the mean, genetic standard deviation (SDg), heritability and repeatability of dry matter intake in all countries (i.e., All countries) or each individual country.

Country	Lactations	Mean	SDg	h^2	Repeatability
Cows					
All countries	10068	19.7	1.13	0.34 (0.03)	0.66 (0.01)
Canada	411	22.2	1.01	0.19 (0.14)	0.46 (0.06)
Denmark	668	22.1	1.48	0.52 (0.12)	0.62 (0.04)
Germany	1141	20.2	0.64	0.08 (0.06)	0.84 (0.05)
Iowa	398	23.5	1.48	0.41 (0.14)	
Ireland	1677	16.7	0.88	0.41 (0.10)	0.64 (0.02)
Netherlands	2956	21.4	1.15	0.39 (0.05)	0.54 (0.03)
UK	2207	17.4	1.07	0.31 (0.06)	0.72 (0.02)
Wisconsin	447	24.9	0.90	0.24 (0.16)	
Australia	103	15.6			
Heifers					
Australia	843	8.3	0.77	0.20 (0.11)	
New Zealand	941	7.6	0.66	0.34 (0.12)	

Table 2. Genetic correlations (below diagonal; standard er0072ors in parenthesis) between dry matter intake measured in groups of countries[1] as well as the number of sires common (above diagonal; sires plus maternal grandsires in common in parenthesis) between the groups of countries.

Region	EU-high input	EU-low input	Grazing	North-America
EU-high input		125 (144)	23 (28)	39 (72)
EU-low input	0.84 (0.14)		4 (4)	4 (10)
Grazing	0.33 (0.20)	0.57 (0.43)		6 (8)
North-America	0.76 (0.21)	0.79 (0.38)	0.14 (0.43)	

[1]EU-high input = Netherlands+Germany+Denmark+high input feeding treatment in the UK; EU-low input= low input feeding treatment in the UK; Grazing = Ireland + Australia; North-America = Iowa + Wisconsin + Canada