ESTIMATES OF GENETIC CORRELATIONS BETWEEN LIVE ULTRASOUND SCAN TRAITS AND DAYS TO CALVING IN HEREFORD CATTLE

Karin Meyer and David J. Johnston

Animal Genetics and Breeding Unit[1], University of New England, Armidale, NSW 2351

SUMMARY

Restricted maximum likelihood estimates of genetic correlations between between live ultrasound scan measurements and days to calving were obtained from bivariate analyses. Scan traits considered were fat depth at the $12/13-$th rib, P8 fat depth, percentage intramuscular fat and eye muscle area, treating records for heifers or steers and bulls as separate traits. Analyses were carried out including all days to calving records, and considering the subset of cows only which had a 'complete sequence' of records, beginning with a first mating record. Heritability estimates for days to calving were low, about 3% with a repeatability of 18%. Estimates of genetic correlations were low to moderate, and consistently negative for fat depth measurements, i.e. animals with a higher genetic potential for fat deposition tended to have better reproductive performance.

Keywords : Genetic parameters, beef cattle, scan traits, reproductive performance

INTRODUCTION

Multivariate genetic evaluation through BREEDPLAN requires estimates of covariance components among all traits considered simultaneously. Whilst there are numerous estimates of genetic parameters for growth traits, few estimates of 'cross-correlations' between groups of traits introduced more recently are available. This paper presents estimates of correlations between female reproductive performance, measured as days to calving, and traits recorded *via* live ultrasound scanning, for Hereford cattle.

MATERIAL AND METHODS

Data. Records for live ultrasound scan traits and days to calving (DC) for Australian and New Zealand Hereford and Polled Hereford cattle were extracted from the National Beef Recording Scheme data base. Scan measurements for different sexes were treated as separate traits, namely eye muscle area for heifers/steers (EMA_H) and bulls (EMA_B), fat depth at the 12th/13th rib for heifers/steers (RIB_H) and bulls (RIB_B), P8 fat depth for heifers/steers (P8_H) and bulls (P8_B), and percentage intra-muscular fat for heifers/steers (IMF_H) and bulls (IMF_B). Ages at scanning from 300 to 700 days were considered, with a single record per trait.

Basic edits for DC eliminated records from AI matings, contemporary groups (CG) with a calving rate of less than 60% and single record CG. This yielded $71,327$ DC records on $40,977$ cows. Records for cows with a successful calving were the number of days from the date the bull entered the mating paddock to the calving date. Cows not calving were assigned the highest value in their CG plus a penalty of 21 days. In BREEDPLAN analyses, cows are required to have a 'first' mating record between 271 and 1730 days of age. Extracting data for cows with such first record and subsequent records within 1.5 years of the previous record, referred to as DC* henceforth, left $13,384$ records for $7,747$ cows.

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Table 1. Characteristics of the data structure for bivariate analyses.

Scan trait	IMF_H	IMF_B	P8_H	P8_B	RIB_H	RIB_B	EMA_H	EMA_B
Analyses requiring first mating records[A]								
No. scan records	10,095	10,636	29,493	37,322	29,334	37,078	29,448	37,330
No. pairs	166	0	840	0	841	0	840	0
No. animals[B]	62,062	67,166	79,445	103,760	79,253	103,253	79,371	103,746
No. sires	2,904	3,099	3,951	4,799	3,949	4,777	3,949	4,794
Analyses using all DC records								
No. scan records	10,095	10,636	30,579	33,390	30,428	33,325	30,541	33,401
No. DC records	71,327	71,327	55,494	51,784	55,494	51,784	55,494	51,784
No. pairs	492	0	3,483	0	3,432	0	3,484	0
No. animals	106,061	110,603	105,774	113,085	105,616	113,014	105,721	113,083
No. sires	8,055	8,240	6,543	6,247	6,541	6,245	6,541	6,245

[A]No. of DC* records : $13,384$ for all analyses, [B]including parents without records

For bivariate analyses involving all DC records and scan traits other than IMF, subsets were extracted attempting to maximise the number of pairs of records on relatives while keeping analyses to a reasonable size. Hence all records for herds with at least 5 animals with pairs of records or sires of such animals were selected, as well as records in herds with at least 200 DC records. For IMF, all DC records were included. For analyses considering DC* all records were used. Scan measurements chosen were all records in herds selected on the basis of DC records or pairs, as well as herds with 100 or more records, except for IMF for which all data available was utilised. Any records in small CG were deleted, with a minimum CG size of 3 for scan traits, and 3 and 2 for DC and DC*, respectively. Characteristics of the data structure are given in Table 1.

Analyses. Estimates of covariances between DC and scan traits were obtained from bivariate restricted maximum likelihood analyses, using an average information algorithm. The model of analysis for scan traits was a simple animal model with CG, defined as herd-sex of calf-management group-date of scanning subclasses with an "age slicing" of 60 days, birth type, and the so-called "heifer factor", an age of dam class (heifer *vs.* cow), as fixed effects. Age at scanning was fitted as a linear covariable for each sex and age of dam as a linear and quadratic covariable. For DC, the model fitted CG, defined as herd-service sire-'bull in' date-lactation status $\times$ age subclasses, as the only fixed effects. There were 4 categories for the latter, namely two-year olds ('dry'), three-year olds with a previous calf ('wet'), three-year olds without a previous calf ('dry'), and others. With repeated records, random effects fitted were both animals' genetic and permanent environmental effects. Corresponding univariate analyses for DC and DC* were carried out using all records available.

Approximate sampling errors of genetic correlation estimates were derived from the inverse of the average information matrix. Results from bivariate analyses were pooled using the 'iterative summing of expanded part matrices' approach of Mäntysaari (1999), as implemented by Henshall and Meyer (2002), weighing results from different analyses according to the number of records and pairs of traits.

RESULTS AND DISCUSSION

Heritability estimates for DC and DC* from univariate analyses were low, $0.039 \pm .006$ and $0.026 \pm .016$, respectively. This was considerably lower than estimates of 0.12 for Angus (Johnston and Bunter, 1996) and 0.14 to 0.18 for Brahmans (Meyer and Johnston, 2001) reported previously, but in line with earlier estimates of 0.05 for Herefords and 0.08 for Angus (Meyer *et al.*, 1991). Corresponding estimates of the proportion of variance due to animals' permanent environmental effects were $0.137 \pm .009$ and 0.151 ± 0.021, yielding repeatabilities of $0.176 \pm .006$ and $0.177 \pm .015$. Again, the latter were somewhat smaller than respective earlier estimates of 0.163 and 0.216 for Herefords (Meyer *et al.*, 1991).

Estimates of correlations from individual, bivariate analyses are summarised in Table 2. All estimates of phenotypic correlations were close to zero, and residual correlations for traits measured on females were similar, with only one estimate for DC* larger than 0.1 (absolute value). Estimates of genetic correlations (r_G) were low to moderate for DC. Estimates for DC* suggested a stronger association, but had large sampling errors. The analysis of DC* together with IMF_B converged to an implausible estimate of -1.0 at the boundary of the parameter space. For analyses involving traits measured on distinct subset of animals, most information on the genetic correlation comes from the between sire component. Inspection of sire means for DC* and IMF_B showed a distribution inconsistent with the estimate of r_G obtained, both for raw means and means of records adjusted for fixed effects.

Estimates of r_G between fat measurements and DC were negative except for DC*and IMF_H, i.e. animals with a larger genetic potential to deposit fat had a genetic potential for better reproductive performance (shorter DC). On average, correlations were stronger, albeit with large sampling errors, for analyses requiring a first mating record for each animal, suggesting that estimates were somewhat 'diluted' when using all records, with many records on older cows. This could be indicative of a closer genetic relationship between fat deposition until 700 days of age and heifer reproductive performance, but, alternatively, could reflect the fact that older cows typically have been subject to selection for reproduction.

Combining estimates for DC* with results from 28 corresponding bivariate analyses between pairs of scan traits (unpublished), gave the pooled correlation matrix shown in Table 3. On the whole, correlations between DC* and scan traits were reduced compared to individual analyses, and closer to corresponding estimates from analyses using all DC records. Estimates of r_G of around -0.5 suggest that about 25% of the genetic variation in days to calving could be explained by rib fat depth measurements. With an estimate of r_G between IMF_H and IMF_B of 0.76, the discrepancy in estimates of r_G with DC* observed for the two sexes was unexpected. Clearly, estimates were affected by insufficient genetic links between traits in the data, and should be regarded with caution. Further analyses are required when more DC records for cows with a first mating record become available.

CONCLUSIONS

Live ultrasound scan measurements for rib fat thickness and intramuscular fat content can assist in selecting for reproductive performance, however, the low heritability of DC will limit progress. Further research is required to determine whether data quality is a contributing factor, and, if so, how it can be improved.

Table 2. Estimates of correlations with days to calving, from individual bivariate analyses

	IMF_H	IMF_B	P8_H	P8_B	RIB_H	RIB_B	EMA_H	EMA_B
Analyses requiring first mating records								
Genetic	0.162	-1.000	-0.647	-0.481	-0.846	-0.518	0.266	-0.050
s.e.[A]	0.421	0.348	0.305	0.300	0.342	0.288	0.284	0.282
Residual	-0.098	–	-0.019	–	-0.005	–	-0.110	–
Phenotypic	-0.058	-0.096	-0.080	-0.040	-0.083	-0.043	-0.061	-0.004
Analyses using all DC records								
Genetic	-0.228	-0.502	-0.328	-0.102	-0.353	-0.030	0.043	0.080
s.e.	0.168	0.169	0.103	0.117	0.109	0.120	0.118	0.122
Residual	0.025	–	-0.026	–	-0.018	–	-0.039	–
Phenotypic	-0.006	-0.051	-0.059	-0.011	-0.054	-0.003	-0.026	0.008

[A] approximate sampling error

Table 3. Pooled estimates of heritabilities (on diagonal, in bold), genetic (below diagonal) and phenotypic (above diagonal) correlations, and phenotypic variances (σ_P^2).

	IMF_H	IMF_B	P8_H	P8_B	RIB_H	RIB_B	EMA_H	EMA_B	DC*	σ_P^2
IMF_H	**0.31**	0.23	0.32	0.09	0.32	0.06	0.14	-0.01	-0.06	106.6
IMF_B	0.76	**0.25**	0.09	0.35	0.08	0.32	-0.02	0.05	-0.10	62.7
P8_H	0.42	0.34	**0.39**	0.28	0.72	0.20	0.25	0.02	-0.08	4.244
P8_B	0.32	0.40	0.75	**0.32**	0.19	0.74	-0.01	0.10	-0.04	2.763
RIB_H	0.33	0.41	0.81	0.61	**0.32**	0.21	0.24	0.03	-0.08	1.529
RIB_B	0.27	0.41	0.64	0.89	0.64	**0.27**	0.01	0.11	-0.04	0.977
EMA_H	0.03	-0.10	0.06	0.01	0.04	0.01	**0.31**	0.25	-0.06	30.36
EMA_B	-0.03	-0.07	0.08	-0.07	0.13	-0.08	0.85	**0.26**	0.00	44.99
DC*	-0.15	-0.60	-0.60	-0.51	-0.81	-0.54	0.19	0.00	**0.02**	549.9

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