ANIMAL MODEL ESTIMATES OF SIRE-HERD INTERACTIONS FOR PRODUCTION TRAITS FOR THE MAJOR DAIRY BREEDS IN THE UNITED KINGDOM

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SUMMARY

The variance due to sire-herd interactions for production traits was estimated in the five major dairy breeds in the United Kingdom (UK). First lactation records were analysed using an animal model, with a repeatability model used to analyse the first five lactations. Data consisted of 40066, 17674, 7245, 19994 and 16850 heifer records for the Holstein/Friesian, Jersey, Shorthorn, Ayrshire and Guernsey breeds respectively. The analysis on the first five lactations consisted of 111408 Holstein/Friesian, 20964 Shorthorn, 55044 Jersey, 58310 Ayrshire and 51008 Guernsey records. Data were obtained from the files of National Milk Records for cows born in the period 1980-1985. Heritabilities for milk, fat and protein yields in first lactation ranged from 0.26 to 0.44. The heritabilities for the five lactations were lower and ranged from 0.24 to 0.34. The estimates of the variance due to sire-herd interaction (c^2) in the first lactation varied from 0.024 to 0.063 and amounted on average to about half of the respective sire components. Log transformation of yield records resulted in a reduction of about 25% in c^2 values for the Holstein/Friesian breed but there was no change in the Jersey breed. The c^2 values from the first five lactations were lower than those of the first and ranged from 0.020 to 0.040. The c^2 estimates were considered important and should be accounted for in sire evaluations to minimise bias due to preferential treatment and to avoid over estimating the accuracy of proofs of sires with daughters in one or a limited number of herds. It was concluded that a c^2 estimate of 0.04 was appropriate for all breeds in the UK evaluation procedure.

INTRODUCTION

The performance of a group of daughters of a particular sire may differ from herd to herd due to a within herd common environmental effect. This sire by herd interaction or common environmental covariance between daughters of a sire in the same herd has been studied by several authors (Tong, Kennedy and Moxley 1977; Meyer, 1987). Reasons for the existence of a sire by herd interaction include failure to remove all herd or herd-year-season effects by applying an inappropriate model, preferential treatment of daughters of the same bull in a herd, seasonal use of sires, assortative mating and different management techniques between pedigree and non-pedigree herds. Meyer (1987) concluded that genetic evaluation procedures should account for the effect of sire-herd interaction in order to minimise bias due to preferential treatment and avoid over estimating the accuracy of sires with daughters in one or a few herds. The national evaluation procedures of the United States of America and the United Kingdom (UK) presently account for the effect of sire-herd interaction (Wiggans, Misztal and Van Vleck, 1988; Swanson and Bellamy, 1991).

Most studies that estimated the variance due to sire-herd interaction fitted sire models often ignoring the relationship among the sires and are based only on the first lactation performance of daughters of widely used bulls. This could result in bias. The estimate of variance due to sire herd interaction used for the animal model genetic evaluation for the five major dairy breeds in the UK is based on the work of Meyer (1987) using Holstein/Friesian data and a sire model. There is a need to check whether the value used is appropriate for all breeds. In addition there is a need to consider whether an animal model estimate would be different from one obtained using a sire model.

The objective of this study is to calculate animal model estimates of variance due to sire by herd interaction for the five major dairy breeds in the UK using first lactation performance and the first five lactation performance.

MATERIALS AND METHOD

Data consisted of five lactation records for milk, fat and protein yields obtained from National Milk Records for cows born between 1980 and 1985 for the Guernsey and Shorthorn breeds, 1983 and 1984 for Jerseys and Ayrshires and September 1985 and May 1985 (inclusive) for Holstein/Friesians. All cows were required to have at least a first lactation in order to be included in the analysis and sires to have at least 5 daughters. Age at first calving was restricted to a minimum of 18 months.

A Univariate Restricted Maximum Likelihood procedure was used to estimate variance components for milk, fat and protein yields using programs based on software written by Meyer (1988). The model for the analysis of first lactation production traits included the fixed effects of herd-year-season, month of calving and linear and quadratic effects of age at calving. The random effects in the model were animal and sire-herd effects. A relationship matrix for all animals was included in each analysis. The number of records included are shown in Tables 1 and 2.

The model for the first five lactations included herd-year-season, month of calving and lactation number as fixed effects, age at calving within lactation number as a linear and quadratic covariable and the random effects of animal, permanent environment and sire-herd interactions. The proportion of Holstein was fitted as a covariable in the Holstein/Friesian analysis. The analyses on five lactations were repeated with yield records transformed to a log scale for the Holstein/Friesian and Jersey breeds to examine the effect of differences in variability between herds.

RESULTS AND DISCUSSION

The estimates of heritabilities (h^2) and variance due to sire-herd interaction as a proportion of the phenotypic variance (c^2) for first lactation are presented in Table 1. Corresponding estimates together with the variance due to permanent environmental effect as a proportion of total phenotypic variance (m^2) for five lactations are given in Table 2.

Table 1.   First lactation estimates of heritability (h^2) and variation due to herd-sire interaction (c^2) for milk fat and protein yields in 5 breeds.

Breed	N	Parameters	Milk (kg)	Fat (kg)	Protein (kg)
Holstein/Friesian	40066	h^2	0.35	0.32	0.26
		c^2	0.032	0.028	0.035
Jersey	17674	h^2	0.35	0.37	0.30
		c^2	0.024	0.024	0.028
Shorthorn	7245	h^2	0.42	0.44	0.38
		c^2	0.050	0.063	0.047
Ayrshire	19994	h^2	0.29	0.33	0.27
		c^2	0.043	0.037	0.037
Guernsey	16850	h_2	0.30	0.27	0.27
		c_2	0.032	0.050	0.046

Standard errors for h^2 ranged from 0.01 to 0.03 and for c^2 from 0 to 0.001, N = number of records

Heritabilities ranged from 0.30 to 0.42 for milk yield, 0.27 to 0.44 for fat yield and 0.26 to 0.38 for protein yield. These values support the estimate of 0.35 used in the UK evaluation procedure. The estimates of heritability were in general similar across breeds except for Shorthorn which were slightly higher. This could be attributed to the small size of the data and the opening up of the Shorthorn herd book to other breeds,

therefore increased genetic variance could be due to the effects of crossbreeding. The heritability estimates for milk and fat yields for the Holstein/Friesian breed were consistent with values reported by Visscher (1991) but were lower for protein yield in this study. The Ayrshire heritability estimates were slightly lower than estimates from a more recent data set. (Mrode and Swanson, 1994)

Table 2. Estimates of heritability (h^2), variation due to permanent environmental effect (m^2) and herd-sire interaction (c^2) for production traits for 5 breeds using 5 lactations.

Breed	N	Parameters	Milk (kg)	Fat (kg)	Protein (kg)
Holstein/Friesian	111408	h^2	0.30	0.27	0.25
		m^2	0.21	0.21	0.23
		c^2	0.025	0.024	0.026
Jersey	55044	h^2	0.28	0.31	0.26
		m^2	0.17	0.12	0.18
		c^2	0.020	0.020	0.025
Shorthorn	20964	h^2	0.34	0.34	0.31
		m^2	0.19	0.15	0.20
		c^2	0.023	0.040	0.037
Ayrshire	58310	h^2	0.24	0.27	0.25
		m^2	0.26	0.21	0.24
		c^2	0.024	0.029	0.027
Guernsey	51008	h^2	0.25	0.24	0.25
		m^2	0.22	0.24	0.22
		c^2	0.032	0.033	0.040

Standard errors for h^2 ranged from 0.01 to 0.02, c^2 from 0 to 0.0001 and for m^2 about 0.01, N = number of records.

The heritability values for the five lactations were lower than the estimates from the first lactations. Estimates ranged from 0.24 to 0.34 for milk yield, 0.24 to 0.34 for fat yield and 0.25 to 0.31 for protein yield. Again these support a value of 0.30 in the UK evaluation procedure. No previous estimates of h^2 from a repeatability model on five lactations were available for comparison. However, the estimated h^2 for milk and fat yields were only slightly lower than those of Visscher (1991) for the Holstein/Friesian breed on the basis of the first two lactations from a repeatability model.

The estimates of c^2 from the first lactation performance were consistent across breeds and varied from 0.024 to 0.063. Meyer (1987) reported c^2 values of the order of 0.02 to 0.04 for Holstein/Friesians from first lactations. These c^2 values were generally similar to other estimates reported in the literature (Tong et al., 1977). The c^2 estimates from the five lactations were lower than those from the first and ranged from 0.02 to 0.04 and were again consistent across breeds.

The proportion of variation due to permanent environmental effect used in the UK evaluation procedure is 0.16 for all breeds and traits. The m^2 estimates obtained in this study ranged from 0.12 to 0.26 suggesting the current value may be slightly on the low side.

Transformation to log scale should remove the effects of differences in variability between herds on the estimates of c^2. On the log scale, heritabilities were not different from those on the observed scale. Similarly there were no differences in the estimates of c^2 from the observed or transformed data for the Jersey breed. However log transformation resulted in a reduction of about a quarter in the estimates of c^2 for the Holstein/Friesian breed. This reduction in the c^2 estimate indicates that differences in variability between herds contributed partly to the original estimates of c^2 for the Holstein/Friesian breed.

The c^2 values reflect environmental covariance between paternal half sibs in different herds and may affect the ranking of sires. The significance of the c^2 values may be evaluated by calculating the genetic correlation between performance of daughters of a sire in different herds on the basis of the c^2 estimates. Such a genetic correlation may be calculated as an intra class correlation (t) as $t = \sigma^2 s / \sigma^2 s + \sigma^2 c = h^2/(h^2 + 4c^2)$ (Meyer 1987). The c^2 values for the first lactation yields gave t values ranging from 0.57 (fat yield for Guernsey) to 0.73 (milk yield for Holstein/Friesian). Most other c^2 estimates gave t values of about 0.65. With five lactations, c^2 estimates gave t values ranging from 0.60 (protein yield for Guernsey) to 0.79 (fat yield for Jersey). Robertson (1959) considered a genetic correlation of below 0.8 between performance in different environments to be of biological importance. The t values obtained in this study were generally below 0.8 and c^2 should be accounted for in sire evaluation procedures.

The c^2 estimates from this study for the Holstein/Friesian were generally similar to the estimates of Meyer (1987) from a sire model. The value of 0.04 for c^2 presently used in the UK national evaluation for all breeds is appropriate on the basis of these results especially since later lactations receive a lower weight in the evaluation.

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