

ACCOUNTING FOR HETEROGENEOUS VARIANCE COMPONENTS IN MULTIPLE BREED EVALUATIONS OF BEEF TRAITS IN BLACK AND WHITE CATTLE

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INTRODUCTION

Irish beef evaluations for beef traits comprise many breeds and their crosses and incorporates thirteen traits recorded on subsets of the data. Traits comprise of slaughterhouse data (predominantly dairy and dairy beef crosses), weight recording (beef and dairy) and conformation scoring (purebred beef), and own performance feed intake and weight (purebred beef). Estimating breeding values and genetic parameters in a multiple breed population is complicated by breed differences for trait means as well as dominance and recombination. Incorporating a heterogeneous variance correction across fixed effect classes, as often applied in the dairy situation, may not account sufficiently for heterogeneous variance components in mixed populations, as there are likely to be true differences in variance components within and between breeds and for example gender within a breed. Furthermore, heterogeneous variance components may not only differ in terms of their additive genetic or environmental variances, there may be different genetic and environmental correlations between traits within and across breeds. Several methods have been proposed to account for some of these complexities. Pool et al. (2005) assumed homogeneous (co)variances across different breeds and used fixed regressions on heterozygosity and breed fraction to account for different means. Pollock and Quaas (2005) employed a correction for heterogeneity of variance by percentage of the dominant breed. We envisage that the optimal evaluation model for the Irish mixed population would account for heterogeneous (co)variances as a function of breed and gender. The objective of this study was to test the ability of a multitrait random regression model (RR), to model genetic (co)variances for carcass weight (CW), fatness (CF) and conformation (CC) as a function of breed composition in a Holstein and Friesian crossbred population, treating these two as separate breeds.

MATERIAL AND METHODS

Data. Records for CW, CF and CC for animals of $\geq 93\%$ combined Holstein and Friesian breed composition were extracted from the Irish Cattle Breeding Federation database. Only animals with records of sire, paternal grandsire, finishing herd, abattoir of slaughter, dates of birth and slaughter, age at slaughter between 300 and 875 days and not more than two lifetime

movements between herds were retained. Animals with measurement greater than three standard deviations from the mean carcass weight daily gain were removed. Due to a small number of records for animals of $\leq 50\%$ Holstein these were removed. At this point 48,816 animals remained. Contemporary groups of finishing herd and abattoir were formed, ensuring that each contemporary group contained ≥ 4 animals while each sire had ≥ 3 offspring. Contemporary groups with records of only one sire and sires which were mated to only one breed composition percentage type were removed. The final data set contained 36,813 animals. A relationship matrix was formed for sire, grand sire and great grand sire ($n = 1469$).

Statistical models. A multivariate sire model, with CW, CF and CC as dependent variables, was fitted to estimate a 3×3 matrix representing the average genetic (co)variances. A 9×9 genetic (co)variance matrix was estimated, treating each of CW, CF and CC as different traits in each of the following classes, (1) $\geq 93.75\%$, (2) between 93.74% and 81.25% and (3) between 81.24% and 50% Holstein composition, to estimate average (co)variances for these categories. Thirdly, a multitrait random regression sire model was fitted. Random regression coefficients, on first order Legendre polynomials of Holstein composition, were fitted to account for differences along the Holstein composition trajectory, treating CW, CC and CF as dependent variables. In this model heterogeneous residual (co)variances were estimated within the three breed composition classes previously defined. No residual covariances were estimable between the breed composition classes as animals have only one record. In each model the three fixed effects were, gender, the herd-year management group of finishing and abattoir-year of slaughter contemporary group effects as well as fixed regression of Holstein composition and age modelled through fifth and second order Legendre polynomials respectively. Each model was fitted using ASReml (Gilmour et al., 2005).

RESULTS

Genetic variance. Population average variance components are given in Table 1. The RR (Figure 1) and 9×9 (results not shown) estimates of additive genetic variance (σ_a^2) for each trait were similar and the population average estimates were within their ranges. Estimates of σ_a^2 using RR (Figure 1) suggest it is heterogeneous across breed composition for CW and CF. The estimate of σ_a^2 for CW in 50% Holstein (291 kg^2) is twice as large as the estimate for pure Holstein (144 kg^2). In contrast with σ_a^2 for CW, which decreased with increasing Holstein percentage, σ_a^2 for CF increased with increasing Holstein percentage from 0.36 to 0.71 classification units². The σ_a^2 for CC did not appear to differ across breed composition (Figure 1). The trends of change in σ_a^2 with changing breed composition from both RR and 9×9 were in agreement.

Genetic correlations. The additive genetic correlations (r_a) within each trait, estimated by RR, decreased from 1.0 to 0.64 across breed composition. As an example the r_a for CC as a function of breed composition is given in Figure 2. The r_a between CC in pure Holstein and 50% Holstein is 0.64. In comparison, the 9×9 estimates of r_a within this trait across breed were all > 0.85 . The r_a between traits also changed across breed composition. For example, in contradiction with the positive population average estimate of r_a between CW and CC (0.14), the RR estimate was negative in 50% Holsteins (-0.08) and positive in purebred Holsteins

(0.28) (Figure 2). In comparison the 9 x 9 estimates were moderately positive, 0.12 and 0.30 respectively for 50% and purebred Holsteins.

Table 1. Genetic parameters estimates across the population in the for carcass traits^A.

Trait	σ^2	CW	CC	CF
CW	170.0 _{23.7}	0.18 _{0.02}	0.14 _{0.10}	0.21 _{0.09}
CC	0.19 _{0.03}	0.38 _{0.01}	0.17 _{0.02}	0.49 _{0.08}
CF	0.63 _{0.08}	0.31 _{0.01}	0.23 _{0.01}	0.26 _{0.03}

^AVariances (σ^2) in the first column, thereafter heritabilities on the diagonal, genetic (above diagonal) and phenotypic (below diagonal) correlations. Standard errors as subscripts.

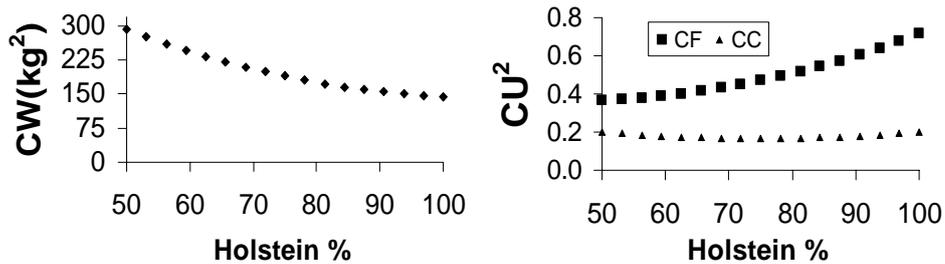


Figure 1. Estimates of additive genetic variance, using a random regression model, for carcass weight (CW) in kg², carcass conformation (CC) and carcass fatness (CF) in carcass classification units² (CU²).

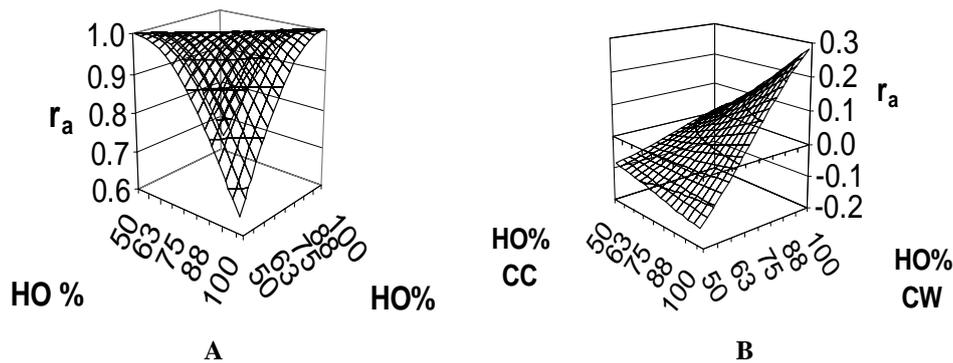


Figure 2. Estimates of additive genetic correlations (r_a), using a random regression model, (A) across breed composition for carcass conformation and (B) between carcass conformation and carcass weight.

DISCUSSION

Genetic variance. Some multibreed genetic evaluation models (e.g. Pool et al., 2005) assume homogeneity of σ_a^2 across breed. The results of this study suggest that this assumption might not be optimal due to a genotype \times genotype interaction. The RR model attempts to model any

change in σ_a^2 across breed composition. It is likely that estimates of σ_a^2 in this study include some of the non-additive variance, especially as breed composition ranges between 50% and 100% Holstein. Incorporation of the dominance relationship matrix could remove any bias due to dominance (Misztal, 1997).

Genetic correlations. The results from the RR model suggested that r_a within and between traits differ along the breed composition trajectory. As already stated the estimates of additive (co)variance components may be somewhat biased by non-additive (co)variance. Nonetheless, within trait across breed estimates of r_a less than unity suggest that the relative performance of genotypes differs depending upon the genotype to which they are mated. In Ireland, for example, selection for beef traits is carried out in purebred herds that specialise in producing terminal sires. The beef production herds keep crossbred dams to which they mate these purebred sires. Re-ranking of sires and loss of selection efficiency may occur as selection pressure is imposed on traits that have r_a with the beef production traits of less than unity. The fact that r_a between traits changes across breed composition may cause further reduction in predicted response to selection (Figure 2).

Applications. Some breed composition groups in a population may contain few records for certain traits. Estimating breeding values for these traits may be problematic due to the unreliability of estimates from random regression models in areas of a distribution with few data points (Pool and Meuwissen, 1999). We tried to accommodate this by excluding records of sires that had all offspring of the same breed composition, i.e. pure breed or F1 mostly. Especially when considering that some records have been collected in certain breed groups only, a major challenge will be how to deal with the extrapolation and maybe alternative models might be more suited. An option might be to estimate variance components as functions of clusters of similar numerically small breeds.

CONCLUSION

It is possible to model heterogeneous σ_a^2 and r_a in multiple breed populations using random regression. The results suggest that genotype \times genotype interaction for σ_a^2 and r_a exists in multiple breed populations, which may have implications for breeding programmes due to the re-ranking or re-scaling of animals and loss of selection efficiency. The effects of non-additive genetic effects and numerically small breed composition groups must be investigated before the use of a random regression model to estimate σ_a^2 and r_a in a multiple breed population is recommended.

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