

Preliminary genetic analysis of beef carcass data

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Introduction Selective breeding of farm livestock is one of the most cost-effective ways of improving the performance and efficiency of livestock enterprises. Genetic improvement of British beef cattle over a ten year period was recently estimated to be worth approximately £23, and the benefits continue to rise (Amer *et al.*, 2007). While these returns are impressive, they could be improved by increasing the rate of improvement in the purebred population, for example by increasing the relevance of estimated breeding values (EBVs) to beef production by using final carcass weight and grading information. This study will examine the feasibility carcass weights and classifications from UK commercial abattoirs for the genetic evaluation of cattle for carcass weight, carcass fatness class, and carcass conformation class.

Materials and methods This study used data from Dovecote Park, which supplies beef to Waitrose supermarket chain. Extensive data is recorded on the animals after slaughter. Carcasses were classified at the abattoir using the EU beef classification scheme for conformation (EUROP) and fat class (1-5). The carcass traits analysed in this study included carcass weight (CWT, kg), adjusted carcass conformation score (CCON), and adjusted carcass fat score (CFAT), the latter two adjusted to a 15 point scale. The identity of the animal was linked to a sire via British Cattle Movement Survey data and data were edited to only include records with a valid sire identity. A final edit required each sire to have a minimum of 2 offspring with valid data and last herd (i.e., finishing herd) was required to have a minimum of 2 observations. This resulted in a final dataset of 14923 records pertaining to 1449 sires. Variance components were estimated in a multiple trait model for CWT, CCON and CFAT by REML based on a sire model using ASReML (Gilmour *et al.*, 2006). Relevant significant model effects were fitted, with non significant components dropped. For all 3 traits breed of dam, age at slaughter (linear and quadratic terms), sex of animal and interaction of last herd with year were fitted in the model with sire identity fitted as a random effect. Additional effects fitted included season and year of birth for in the models for CCON and CFAT.

Results Figure 1 shows the distribution of phenotypic records for CFAT and CCON, with a skewed and narrow distribution in both traits. Animals were, on average, 24.8 months of age at slaughter with an average CWT of 305.6 kg (164.4 – 446.5 kg). Table 1 gives the genetic parameters for the three carcass traits, CWT, CCON and CFAT. Carcass classifications (CCON and CFAT) have a moderate heritability, with a moderate correlation between the two traits. Carcass weight resulted in a high heritability (0.85), which is generally higher than in other reported studies (Ríos Utera and Van Vleck, 2004). However, it

should be noted that this analysis does not fit the genetic relationships between sires in estimating the genetic components. Also, heterosis is likely to have an effect on the carcass traits of crossbred animals, which is not considered in this study. The results indicate that there is considerable genetic variation among sires for the studied traits. For example, the carcass of offspring of the genetically top 5 sires for carcass weight is expected to be, on average, 72.9 kg heavier than the carcass of offspring of the worst 5 sires for this trait; this is equivalent to 24% of the mean carcass weight.

Conclusions The results of this study provide a strong indication of the existence of genetic variation in carcass traits of UK beef animals and therefore improving beef carcass quality traits through genetic selection is possible. The development of routine EBVs for carcass traits will be enhanced with increased capture of accurate abattoir carcass data and more detailed analysis of the genetic parameters.

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References

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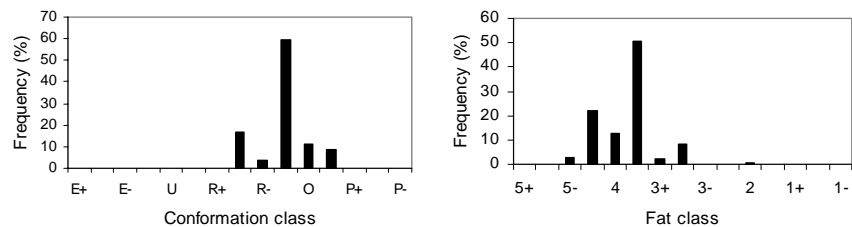


Figure 1 Distribution of carcass conformation score and carcass fat score in the data (E+ is best conformation and P- is worst; 1- is leanest and 5+ is fattest)

Table 1 Genetic parameters for carcass traits, CCON, CFAT and CWT. Heritabilities on the diagonal, genetic correlations above diagonal and residual correlations below diagonal (standard errors in brackets).

	CCON	CFAT	CWT
CCON (1-15 scale)	0.39 (0.035)	0.40 (0.071)	-0.02 (0.059)
CFAT (1-15 scale)	0.18 (0.009)	0.23 (0.029)	0.14 (0.066)
CWT (kg)	0.27 (0.008)	0.21 (0.009)	0.89 (0.049)