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SELECTION OPPORTUNITIES FROM USING ABATTOIR CARCASS DATA

E. Wall, M. Coffey and T. Pritchard

SRUC, Edinburgh, EH25 9RG, Scotland

SUMMARY

Genetic improvement of UK beef carcass traits currently uses predictor traits (weights and ultrasound measurements) taken on live performance recorded pedigree selection candidates. These phenotypes are very low in numbers and have only a moderate-high correlation with the goal traits in crossbred slaughter populations. However, carcass phenotypes taken from abattoir records are available in large quantities and are a key target goal trait for many terminal pedigree beef breeders. The extra information from abattoir data will improve the accuracy of future genetic evaluations on carcass traits. This study uses carcass information from UK abattoirs and information from the national cattle tracing system to create files for the genetic evaluation of carcass traits. A combination of sources merged together might contain sufficient information which could then be used to produce Estimated Breeding Values (EBVs) for carcass traits. The major breeds present in the carcass population (with over 100,000 animals, including crosses) were Limousin, Aberdeen Angus, Holstein Friesian, Charolais, Hereford, Simmental, and Belgian Blue, and these accounted for 92% of the animals (2.4 million records in the merged dataset, 2001-2012). Genetic analyses were performed on a subset of the data for animals with a Charolais sire (17,125 records after editing). Heritability estimates for carcass weight, conformation and fat class were 0.31, 0.24, and 0.14 respectively. The results of this feasibility study indicate that genetic analysis for carcass traits is realistic, particularly for breeds which make up a major part of the carcass population and have sufficient information on the sire. This, in turn, suggests that improving carcass traits through genetic selection is entirely possible, thereby warranting more detailed investigation of their genetic background, particularly their relationship with other traits of importance and within, between and across breeds.

INTRODUCTION

Currently, genetic improvement of beef carcass traits in the UK makes use of predictor traits, weight and ultrasound measurements, taken on live animals (Amer *et al*. 1998). One of the UK beef breeding goals, “Beef Value” (a function of weight and carcass merit, in terminal sire and dual purpose breeds), has been shown to be effective in bringing about genetic change. For example in the period 1999-2003, there were substantial annual increases in Beef Value £0.69/yr (Amer *et al*. 2007). These are mainly recorded on pedigree animals in low numbers and this is where the majority of the genetic change is expressed. However, carcass phenotypes taken from abattoir records are mostly measured outside the pedigree sector and are available in large quantities. The extra information from abattoir data may improve the accuracy of future genetic evaluations on carcass traits. However, abattoir data alone would not be informative enough for genetic evaluations i.e. without pedigree and management information. A combination of sources merged together might contain sufficient information which could then be used to produce Estimated Breeding Values (EBVs) for carcass traits. These sources include abattoirs, Beef and Sheep Company (BASCO), breed societies, milk recording organisations and British Cattle Movement Service (BCMS). The overall aim of the study ‘Carcass Trait Evaluations,’ was to produce a consolidated dataset of carcass traits and pedigree for beef and dairy cattle by combining all sources of information. Data description was undertaken in this study to reveal the suitability of its use for genetic evaluations in the future.

MATERIALS AND METHOD

Phenotypic data. The sources of data that were combined for these analyses are described in Figure 1. The carcass data was obtained from three UK based meat processing/slaughter companies from 2001-2012 [NOTE: not all companies had data for all years]. These carcass records were joined to the BCMS database based on UK eartag. Initially, 3 million individual carcass abattoir records (from 3 abattoirs) and approximately 48 million BCMS animal records were made available for this project. Using intelligent string matching, 82% of the individual carcass records could be matched to BCMS animal records, using UK eartag identity, resulting in a dataset of ~ 2.4 million abattoir records for further investigation. In addition to the carcass measures, the abattoir data provided information on date of birth, kill date, breed and sex. However, in some cases these were incomplete, thus data merging with BCMS data was used to fill in some of the gaps. The three additional traits available from abattoir records were carcass weight, conformation and fat class .

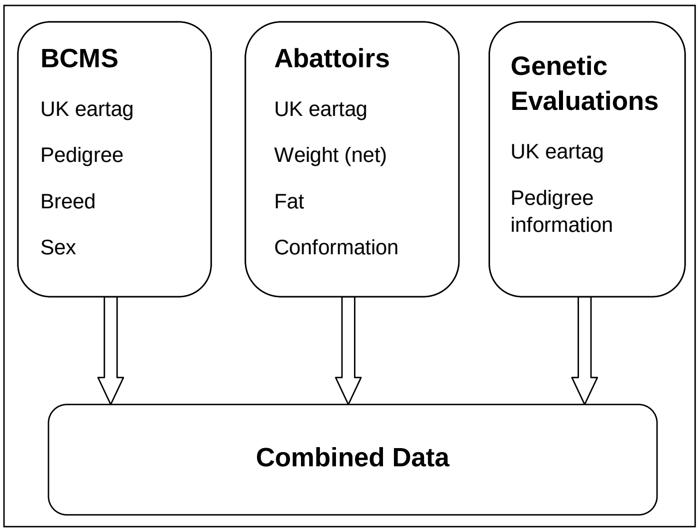

Figure 1. Compiling data from the available information sources

Pedigree data. A pedigree file was created based upon BCMS records and by matching to other national data sources to provide as much pedigree information as possible. This resulted in a pedigree file containing over 50 million animals going back a maximum of 13 generations. The pedigree data contained over 2.3 million additional records obtained from milk recording organisations (MROs) and BASCO.

Editing the data for genetic analysis. A subset of the abattoir/BCMS matched data was extracted for all slaughter animals with Charolais as a sire breed (the third most numerous sire breed). Various edits were then carried out to create a file for genetic parameter estimation, resulting in a considerable reduction in the size of the dataset (as expected), with 28% of the animals remaining. The pedigree was extracted for 6 generations and consisted of 43,069 animals.

Data analysis. The complete combined dataset were described and results are presented below. Genetic analyses were conducted for the traits: carcass weight, conformation, carcass fat grades using ASReml (Gilmour *et al.* 2009). In each case the model accounted for the fixed effects of sex, dam breed, birth herd, birth-year-season, location of death, finishing herd-year-season; linear and quadratic covariates of age at slaughter; and, the random effect of the animal. A year consisted of two seasons for the definition year-season due to relatively small contemporary group size.

RESULTS AND DISCUSSION

Description of BCMS and abattoir data. In BCMS data the five breeds (including crosses) with most animals registered each year were Holstein Friesian, Limousin, Charolais, Simmental and Aberdeen Angus. The major breeds present in the slaughter population were Limousin, Aberdeen Angus, Holstein Friesian, Charolais, Hereford, Simmental, and Belgian Blue, and these accounted for 92% of the animals present in the matched abattoir/BCMS dataset. Records on dam breed emphasise that dairy cows are a major component of beef production with Holstein-Friesian being the most common dam breed, accounting for 46% of the slaughter population. The majority of offspring from dairy cows were crossbreds and these were most commonly sired by Aberdeen Angus or Hereford bulls. Similar results of breed distribution in the UK are shown by Todd *et al*., (2011)

Although sire identity it is not compulsory to record it was known for approximately 23% of animal records in BCMS, with the level of recording generally higher in more recent years (e.g., 11% in 2001 and 23% in 2011). When the BCMS records were merged with other pedigree sources (e.g., MRO data, breed society data) 25% of slaughter animals had a sire record.

Table 1. Overall distribution of carcasses for fat and conformation class in animals slaughtered from 3 to 36 months of age

Fat class	%	Conf. class	%
1	0.6	E	0.6
2	6.8	U	14.8
3	28.5	R	41.8
4L	50.9	O	41.4
4H	11.8	P	1.4
5L	1.3		
5H	0.1		

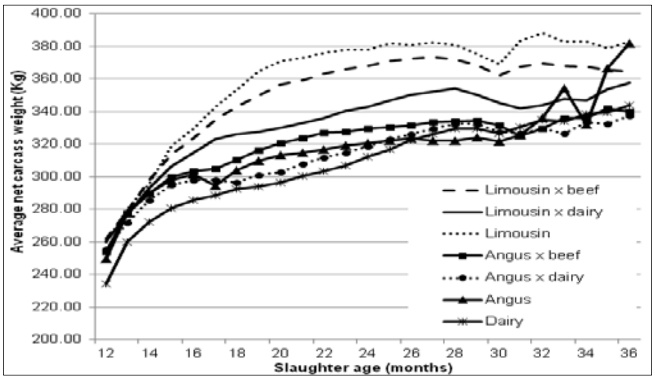

Figure 2 Average carcass weight of male animals grouped by slaughter age for different breed types of cattle

Just over 1.9 million animals were slaughtered between 3 and 36 months of age. The average carcass weight of males and females was 335 kg and 298 kg respectively. Average conformation and fat were equivalent to –R and +3/-4, respectively (Table 1). Overall, the mean number of days to slaughter and average carcass daily weight gain were 743 days and 0.45 kg, respectively. Carcass traits differ between breed types as illustrated in Figure 2.

Table 2. Genetic parameter estimates of carcass traits in Charolais using an animal model

	Animal variance	Residual variance	Phenotypic variance (s.e.)	Heritability (s.e.)
Carcass wt.	196.80	447.07	643.9 (9.89)	0.31 (0.04)
Conformation	2.29	7.20	9.48 (0.14)	0.24 (0.04)
Fat	1.72	10.48	12.21 (0.17)	0.14 (0.03)

Genetic Parameters. Heritability estimates (and standard errors) for carcass weight, conformation, and fat class were 0.31 (0.04), 0.24 (0.04), and 0.14 (0.03) respectively, using an animal model (Table 2). Genetic correlations between carcass weight and conformation, carcass weight and fat, and conformation and fat were 0.38 (0.09), -0.54 (0.12), and -0.67 (0.11). These estimates are in line with other studies (e.g., Gregory *et al.*1995, Hickey *et al*. 2007).

CONCLUSIONS

There is a wealth of data recorded in the UK, some of it being compulsory, which could have uses other than its original purpose (for instance BCMS), and when combined with other data sources, provide added value. The creation of a pedigree file has allowed us to link dairy and beef genetics as well as opening up the opportunity to perform genetic analysis for traits in the commercial populations with multiple breeds and crosses represented. As well as carcass traits, the merging of pedigree information also provides opportunities for other traits that are affecting both dairy and beef populations.

The results indicate that genetic analysis for carcass traits is realistic, particularly for breeds which make up a major part of the cattle population and where sire identity is recorded. The use of carcass trait evaluations should reduce the current knowledge gap between the pedigree breeders and the commercial beef producer. Providing clearer signals to pedigree breeders on where improvements need to be made should lead to benefits being filtered down into commercial beef production with cattle that perform more efficiently and hit market specifications. To move the cattle industry forward, the various parts of the food chain need to work together and share information, which in part this study has demonstrated.

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