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Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland¹

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ABSTRACT: The first objective of this study was to test the ability of systems of weighing and classifying bovine carcasses used in commercial abattoirs in Ireland to provide information that can be used for the purposes of genetic evaluation of carcass weight, carcass fatness class, and carcass conformation class. Secondly, the study aimed to test whether genetic and phenotypic variances differed by breed of sire. Variance components for carcass traits were estimated for crosses between dairy cows and 8 breeds of sire commonly found in the Irish cattle population. These 8 breeds were Aberdeen Angus, Belgian Blue, Charolais, Friesian, Hereford, Holstein, Limousin, and Simmental. A multivariate animal model was used to estimate genetic parameters within the Holstein sire breed group. Univariate analyses were used to estimate variance components for the remaining 7 sire breed groups. Multivariate sire models were used to formally test differences in genetic variances in sire breed groups. Field data on 64,443 animals, which were slaughtered in commercial abattoirs between the ages of 300 and 875 d, were analyzed in 8 analyses. Carcass fat class

and carcass conformation class were measured using the European Union beef carcass classification system (EUROP) scale. For all 3 traits, the sire breed group with the greatest genetic variance had a value of more than 8 times the sire breed group with least genetic variance. Heritabilities ranged from zero to moderate for carcass fatness class (0.00 to 0.40), from low to moderate for carcass conformation class (0.04 to 0.36), and from low to high for carcass weight (0.06 to 0.65). Carcass weight was the most heritable (0.26) of the 3 traits. Carcass conformation class and carcass fatness class were equally heritable (0.17). Genetic and phenotypic correlations were all positive in the Holstein sire breed group. The genetic correlations varied from 0.11 for the relationship between carcass weight and carcass fatness class to 0.44 for the relationship between carcass conformation class and carcass fatness class. Carcass weight and classification data collected in Irish abattoirs are useful for the purposes of genetic evaluation for beef traits of Irish cattle. There were significantly different variance components across the sire breed groups.

Key words: commercial field data, crossbred beef cattle, EUROP carcass trait, genetic parameter

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INTRODUCTION

Initial genetic evaluations for carcass traits were recently introduced for Irish cattle using field data from commercial abattoirs (Olori et al., 2005). More accurate

knowledge of genetic parameters should improve genetic evaluation procedures and facilitate a breeding program that maximizes response to selection. Reviews of the literature (Koots et al., 1994b; Rios Utrera and Van Vleck, 2004) show that large differences in estimates of heritability for beef traits can depend upon the breed present in the analyzed data. Hirooka et al. (1996), Van der Werf et al. (1998), and Engelland et al. (1999) show large differences in the estimates of genetic (co)variances for carcass traits between different breeds.

In Ireland, most male progeny of dairy cows are raised for beef production (Keane and Allen, 2002; Keane, 2003). Gene flow occurs within the Irish cattle

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population from the dairy herd to the beef herd (Berry et al., 2006). Most animals slaughtered are the offspring of dams with Holstein and Friesian genes and sires that are a dairy breed such as Holstein or Friesian, an early maturing beef breed such as Aberdeen Angus or Hereford, or a late maturing beef breed such as a Belgian Blue, Charolais, Limousin, or Simmental. Therefore genetic improvement of beef traits is relevant to beef and dairy animals, and a breeding value estimation procedure may need to account for different variance components across breeds.

This study aimed firstly to quantify the ability of systems of weighing and classifying carcasses used in commercial abattoirs in Ireland to provide useful information for the genetic evaluation of Irish cattle for carcass weight, carcass fatness class, and carcass conformation class. Secondly, the study aimed to test whether genetic and phenotypic variances differed depending upon the breed of sire.

MATERIALS AND METHODS

Animal Care and Use Committee approval was not obtained for this study because the data were obtained from an existing database (Irish Cattle Breeding Federation Database, Bandon, Co. Cork, Ireland).

Data

Data from the Irish Cattle Breeding Federation database contained carcass records on 1,032,902 animals, across several different breeds and crossbreeds. The national pedigree file for cattle contained 8,881,713 animals. The data and pedigree were dominated by animals with varying degrees of Holstein breeding.

Extraction

A data set containing animals with records for carcass weight, carcass fatness class, and carcass conformation class, which were gathered in 9 commercial abattoirs, was extracted from the database. Animals without information on each of these traits and without information on birth date, slaughter date, sire, dam, sex, herd of birth, herd of finishing period, abattoir of slaughter, and those with greater than 2 lifetime movements between herds were removed from the extracted data set, as were animals that were slaughtered before 300 d of age or after 875 d of age.

The sire of each animal was required to have at least 87.5% of its breed composition known. The breed composition of the dam of each animal was required to be at least 75% combined Holstein or Friesian. To meet this 75% known criteria, the breed composition of each dam was taken as the value recorded through the pedigree or directly by the farmer or else expected to be Holstein or Friesian. This expectation was based on the breed composition of the known dams in the herd of birth of the animal. If these were at least 90% of one of Holstein

or Friesian genotypes, the unknown breed composition of a dam was taken to be the same as its herd mates. In the final data set, 21.4% of the dams had some part of their breed composition predicted in this manner.

To remove records with unrealistic values because of errors such as incorrectly recorded birth and death dates, an average carcass weight daily gain was calculated for each animal by dividing its carcass weight by its age at slaughter. Animals with records of average daily carcass weight gain of greater than 3 SD from the mean of the sire breed group nested within sex were removed from the data set. The resulting data set contained 120,799 animals that were slaughtered between the ages of 300 and 875 d over a 5-yr period between January 2001 and December 2005. Most of the animals that were deleted had incomplete pedigree or missing breed composition information.

From this data set, 8 subsets were extracted based on the breed composition of an animal's sire being $\geq 87.5\%$ of one of the following: Aberdeen Angus, Belgian Blue, Charolais, Friesian, Hereford, Holstein, Limousin, or Simmental.

Carcass Data

Under the EU beef carcass classification (**EUROP**) scheme, each carcass is assessed and classified at the weighing point on the slaughter line (Anon, 2004). The classification of the carcasses described in this data set was done either subjectively by technicians trained by the Department of Agriculture or, since December 2004, by automatic visual-image carcass assessment equipment. Carcass weight is typically measured within 2 h of slaughter and is the weight of the animal after the removal of its head, hide, feet/legs, thoracic organs, internal fats, and abdominal organs and is expressed as cold carcass weight, which is 0.98 times the HCW (Anon, 2004).

The carcass conformation classes describe the development of carcass profiles, in particular the essential components of the round, back, and shoulder (Anon, 2004). Under the EUROP system, 5 conformation classes are defined, represented by the letters E, U, R, O, and P. The letters represent an incremental scale ranging from P, which denotes the worst conformation, to E, representing the best conformation. European Union regulations allow for 3 subdivisions of each conformation and fat class. In Ireland, conformation class P is subdivided into P+, P, and P-, describing declining conformation (Anon, 2004).

The carcass fat classes describe the amount of fat on the outside of the carcass and in the thoracic cavity. Five classes are defined, represented by the numbers 1, 2, 3, 4, and 5. This incremental scale ranges from 1, which denotes the least fat, to 5, denoting most fat. In Ireland, fat class 4 is subdivided into low fat (4L) and high fat (4H; Anon, 2004).

Some carcasses were classified by the 5- and 7-point scales described, whereas others were classified on a

Table 1. Numerical values on a 15-point scale in classification units (cu) given to carcass conformation class and carcass fatness class scores using a 15-, 7-, or 5-point scale

Conformation class scale			Fat class scale		
15-point scale ¹	5-point scale	Numerical value, cu	15-point scale ²	7-point scale	Numerical value, cu
E+		15	5+		15
E=	E	14	5=	5	14
E-		13	5-		13
U+		12	4+	4H	12
U=	U	11	4=		11
U-		10	4-	4L	10
R+		9	3+		9
R=	R	8	3=	3	8
R-		7	3-		7
O+		6	2+		6
O=	O	5	2=	2	5
O-		4	2-		4
P+	P+	3	1+		3
P=	P	2	1=	1	2
P-	P-	1	1-		1

¹E+ is best conformation, and P- is worst.

²1 is leanest, and 5+ is fattest.

15-point scale. A number of alternative methods of transforming the data were tested to make these scales equivalent. These included transforming the 15-point scores back to 5- and 7-point scales. Different transformations were found to have no important effect on the estimates of genetic parameters. To be consistent with the methods employed in national genetic evaluations of cattle for beef traits in Ireland, scores on the EUROP scales were transformed to numerical classification units (**cu**) on 15-point scales (Table 1).

Heterosis and Recombination

Coefficients of general heterosis were calculated as functions of the degree of heterozygosity of animals using the following formula from Van der Werf and de Boer (1989):

$$\text{Heterozygosity} = Pd(1 - Ps) + Ps(1 - Pd),$$

where Ps and Pd are the proportions of genes of the primary breed in the sire and dam, respectively. The breed that is most prevalent across each sire and dam pairing is regarded as the primary breed for that parental pair.

Coefficients of general recombination loss effects were calculated by the formula:

$$\text{Recombination} = Ps(1 - Ps) + Pd(1 - Pd)$$

and is derived from the heterozygosity of the parental gametes, representing a within-gamete epistatic loss effect (Van der Werf and de Boer, 1989).

Contemporary Groups

Contemporary groups were formed iteratively, within each of the subsets, on the basis of (a) finishing herd, year, and season; and (b) factory year and season, using algorithms outlined by Schmitz et al. (1991) and Crump et al. (1997). This method optimizes the composition of contemporary groups based on slaughter dates and intervals between consecutive slaughter dates in a herd or abattoir (Calus and Veerkamp, 2003). For each of the sire breed groups, restrictions were placed at each of the iterations to ensure that the maximum span of a contemporary group was 365 d, that each sire breed group contained a minimum number of 4 animals in a group, and that each sire had at least 3 offspring across all contemporary groups. Because a greater volume of data was available in the Holstein sire breed group, which facilitated more stringent editing, these restrictions were 365, 6, and 6, respectively.

A finishing herd was denoted as the herd where the animal was resident for at least 2 months immediately before its slaughter. A total of 64,443 animals remained across all subsets of the data. Tables 2 and 3 summarize the numbers and structure of records in each sire breed group in the final data sets that underwent analysis.

(Co)variance Component Estimation

A 3 × 3 multivariate analysis of carcass conformation class, carcass fatness class, and carcass weight in the Holstein sire breed group was carried out, applying the following model in ASReml (Gilmour et al., 2004):

$$Y_{ijklmopz} = \mu + \sum_{i=1}^3 b_i \text{Age}_i + s_g + s_g \times \sum_{i=1}^3 b_i \text{Age}_i \\ + b_j \text{HoDam} + b_k \text{FrDam} + \text{FinHys}_l + \text{FactY}_{s_m} \\ + b_o \text{Het} + b_p \text{Rec} + \text{animal}_z + e_{ijklmopz},$$

where $Y_{ijklmopz}$ = the observed carcass weight, carcass conformation class and carcass fatness class on animal z of sex g , age at slaughter i , of breed composition of dam j , in finishing herd year season l , factory year season m , heterosis coefficient o , and recombination coefficient p ; μ = the overall mean; s_g = the fixed effect of sex (g = male or female); $b_i \text{Age}_i$ = the fixed regression of age i of animal z at slaughter; $b_j \text{HoDam}$ = the fixed regression of Holstein % of dam j in animal z ; $b_k \text{FrDam}$ = the fixed regression of Friesian % of dam k in animal z ; FinHys_l = the fixed effect of finishing herd year season l ; FactY_{s_m} = the fixed effect of factory year season m ; $b_o \text{Het}$ = the fixed regression of the heterosis o coefficient in animal z ; $b_p \text{Rec}$ = the fixed regression of the recombination p coefficient in animal z ; animal_z = the random animal effect; and $e_{ijklmopz}$ = the residual error term.

The distributions of the random effects were assumed to be multivariate normal with means of zero and $\text{var}(e) = \mathbf{R}_0 \otimes \mathbf{I}$ in the case of environmental variance

Table 2. Number of animals with records, number of animals in pedigree, arithmetic mean (\bar{x}), and SD (σ) for each of the sire breed groups for each carcass trait

Breed group	No. of records	No. of pedigrees	CW, ¹ \bar{x}	CW, σ	CC, ¹ \bar{x}	CC, σ	CF, ¹ \bar{x}	CF, σ
Aberdeen Angus	10,739	44,353	290.8	46.3	5.84	1.40	9.46	1.80
Belgian Blue	5,965	22,833	318.0	54.9	7.62	1.47	8.00	1.79
Charolais	1,059	6,481	322.7	48.1	7.16	1.43	8.69	1.74
Friesian	6,354	25,143	308.4	41.9	5.11	1.09	8.63	1.81
Hereford	4,881	22,375	293.1	46.1	5.70	1.34	9.79	1.80
Holstein	29,318	98,471	309.2	45.1	4.38	1.16	7.76	2.04
Limousin	4,135	19,105	306.4	48.5	6.88	1.51	8.74	1.73
Simmental	1,992	9,821	306.4	48.9	6.23	1.53	8.67	1.74

¹CW = Carcass weight, kg; CC = carcass conformation class, transformed numerical scale; CF = carcass fatness class, transformed numerical scale.

and $\mathbf{G}_0 \otimes \mathbf{A}$ in the case of the additive genetic variance, where \mathbf{I} is an identity matrix, \mathbf{A} is the numerator relationship matrix using 3 generations of pedigree, \otimes is the Kronecker product, and \mathbf{R}_0 and \mathbf{G}_0 are covariance matrices between residuals and additive genetic components for the 3 traits, respectively. For each model, the \mathbf{A} matrix was generated without genetic groups because regressions were used to account for mean differences in breeds.

There were insufficient data to estimate the genetic correlations among the 3 traits for each of the 7 remaining sire breed groups. Therefore genetic and phenotypic variances were estimated for each trait in these sire breed groups using 21 separate analyses, each fitting univariate versions of the multivariate model already described. A number of other interaction terms were tested for inclusion in the fixed effects part of the model; however, none proved to be significant.

Heritability was estimated as the proportion of the total variance attributable to the additive genetic variance: $h^2 = \sigma_a^2/\sigma_p^2$, where σ_a^2 is the additive genetic variance, σ_e^2 is the environmental variance, and σ_p^2 is the phenotypic variance, which is $\sigma_a^2 + \sigma_e^2$. The SE of heritability was calculated in ASReml, which uses the following formula:

$$\text{Var}(\sigma_a^2/\sigma_p^2) = \{\sigma_a^2/\sigma_p^2\}^2 \times \{[\text{Var}(\sigma_a^2)/\sigma_p^4] + [\text{Var}(\sigma_p^2)/\sigma_a^4] + [2\text{Cov}(\sigma_a^2, \sigma_p^2)/\sigma_a^2\sigma_p^2]\}.$$

Genetic correlations between traits i and j were derived from the (co)variance components as: $r_g = \sigma_{ai,aj}/(\sigma_{ai}^2 + \sigma_{aj}^2)$. The SE of each genetic correlation was calculated in ASReml, which uses the following formula:

$$\begin{aligned} \text{Var}(r_g) = & r_g^2 \{[\text{Var}(\sigma_{ai}^2)/(4\sigma_{ai}^2)^2] + [\text{Var}(\sigma_{aj}^2)/(4\sigma_{aj}^2)^2] \\ & + [\text{Var}(\sigma_{ai,aj})/(\sigma_{ai,aj}^2)] + [2\text{Cov}(\sigma_{ai}^2)\sigma_{aj}^2/4\sigma_{ai}^2\sigma_{aj}^2] \\ & - [2\text{Cov}(\sigma_{ai}^2)\sigma_{ai,aj}/2\sigma_{ai}^2\sigma_{ai,aj}] - [2\text{Cov}(\sigma_{aj}^2)\sigma_{ai,aj}/2\sigma_{aj}^2\sigma_{ai,aj}]\}. \end{aligned}$$

Significance Testing

To formally test for significant differences, the data for all sire breed groups were analyzed together by fitting three 8×8 multitrait sire models for each of carcass weight, carcass conformation class, and carcass fatness class. Sire model 1 estimated separate genetic and phenotypic variance in each of the 8 sire breed groups. Sire model 2 constrained estimates of the genetic and

Table 3. Number of sires, number of contemporary groups of finishing (CG), number of abattoirs (Abat), and percentage of records (rec) in contemporary groups¹

Breed group	No. of sires	No. of CG	No. of Abat	% of rec in CG > 60 d	% of rec in CG > 10 rec	% of rec with sire > 10 rec
Aberdeen Angus	503	1,395	9	38	40	85
Belgian Blue	64	949	9	58	21	97
Charolais	88	143	7	63	39	73
Friesian	167	872	7	64	35	92
Hereford	351	581	5	59	48	74
Holstein	599	1,900	8	43	93	95
Limousin	247	523	8	61	42	78
Simmental	138	224	3	62	54	78

¹Finishing spanning more than 60 d, percentage of records in contemporary groups of finishing containing more than 10 records, and percentage of records that had sires with more than 10 records.

phenotypic variances to estimates that were equal within 3 clusters of sire breed groups, namely Continental sires, British sires, and Dairy sires. Continental sires contained the Charolais, Belgian Blue, Limousin, and Simmental sire breed groups; British sires contained the Hereford and Aberdeen Angus sire breed groups, whereas Dairy sires contained the Holstein and Friesian sire breed groups. Sire model 3 constrained the estimates of genetic and phenotypic variance to estimates that were equal across all sire breed groups.

In each of the multivariate sire models, the genetic and phenotypic covariances were fixed to zero because the different sire breed groups were genetically unlinked and assumed to be independently managed. One issue not addressed in this study was contemporary groups in a multibreed scenario. If animals from different sire breed groups were in the same contemporary group, an environmental covariance would exist between them. However, in this study it was assumed that this was not the case, and different contemporary groups were defined for different sire breed groups.

To test the significance of differences in genetic variances across the sire breed groups, the sire models were compared using log likelihood ratio tests, Akaike information criterion (AIC; Akaike, 1973), and Bayesian information criterion (BIC; Schwarz, 1978) to see if models that account for heterogeneity of variance across sire breed groups were more optimal than those that did not. Sire models 3 and 2 were regarded as submodels of sire model 1, and sire model 3 was regarded as a submodel of sire model 2. The AIC and BIC were also chosen because likelihood ratio tests tend to favor models with many parameters (Jensen, 2001), whereas these criteria penalize models with many parameters.

The likelihood ratio test for 2 models, i and j , in which i is nested within j , is given by

$$\text{LRT} = -2[\log(L_i) - \log(L_j)] \sim \chi_{t_j - t_i}^2,$$

where L_i and L_j are the restricted log likelihoods of the models to be compared, and t_i and t_j are the corresponding number of parameters in those models. Related are the AIC and BIC, which are defined as

$$\text{AIC} = -2\log(L_i) + 2t_i, \text{ and}$$

$$\text{BIC} = -2\log(L_i) + t_i \log v,$$

where t_i is the number of variance parameters in model i and $v = n - p$ is the number of residual degrees of freedom. The AIC and BIC were calculated for each model and the model with the lowest value was assumed to be the most optimal.

RESULTS

Arithmetic Means

Arithmetic means and SD for each trait, in each subset of the data, are presented in Table 2. The Charolais

sire breed group had the highest mean for carcass weight, whereas Belgian Blue had the highest mean for carcass conformation class with the Aberdeen Angus sire breed group being the lowest mean for carcass weight. The Hereford sire breed group was fattest. The Holstein sire breed group was the leanest and had the lowest mean for carcass conformation class. The similar values for mean carcass fatness class in the Holstein and Belgian Blue sired group may be due to animals being sold for slaughter once they attain a certain degree of fatness.

Genetic and Phenotypic Variation and Heritability of Carcass Traits

Heritability estimates and the genetic and phenotypic variances are given for each trait within each sire breed group in Tables 4. The data, which were collected in 9 commercial abattoirs in Ireland, provided information, which allowed estimation of genetic and phenotypic variances for each of carcass weight, carcass conformation score, and carcass fatness score (Table 4). The estimates of variances and heritabilities obtained with the multivariate sire models (results not shown) were generally similar but slightly higher than the estimates from the animal models. The higher estimates may be due to poor ancestral relationship information for dams; 18.8% of dams had an unknown sire. The estimate of heritability for carcass weight in the Charolais sired breed group was greater than 1 for the sire model.

For each of the 3 traits, the sire breed group with the highest estimate of genetic variance had a value that was more than 8 times the value of the estimate for the sire breed group with the lowest genetic variance (Table 4). For carcass weight the Friesian sire breed group displayed a relatively low estimate of genetic variance (44.0 kg²), and the Simmental (416.8 kg²) and Charolais (633.1 kg²) sire breed groups displayed relatively higher genetic variance. The Simmental and Charolais sire breed groups had high SE for their estimates, which were possibly due to the low numbers of records in each class and consequential inability to accurately partition the variance into genetic and environmental components. The remaining sire breed groups had intermediate estimates of genetic variance for carcass weight, which were similar to each other. For carcass conformation class the Friesian also displayed a relatively low estimate of genetic variance (0.04 cu²). The remaining sire breed groups were similarly intermediate, with the exception of the Belgian Blue and Limousin, which had higher genetic variances, 0.60 and 0.73 cu², respectively. The Hereford and Limousin sire breed groups displayed no genetic variance for carcass fatness classification. The Simmental had the highest estimate of genetic variance for carcass fatness classification (0.87 cu²); however, this estimate had a high SE. The 5 remaining sire breed

Table 4. Genetic and phenotypic variances, and heritability for each carcass trait in each of the sire breed groups

Breed group	CW ¹			CC ¹			CF ¹		
	σ_a^2	σ_p^2	h^2	σ_a^2	σ_p^2	h^2	σ_a^2	σ_p^2	h^2
Aberdeen Angus	116.1 (35.5) ²	694.6 (14.0)	0.17 (0.05)	0.19 (0.07)	1.61 (0.03)	0.12 (0.04)	0.49 (0.12)	2.10 (0.05)	0.23 (0.06)
Belgian Blue	122.9 (43.7)	718.7 (18.3)	0.17 (0.06)	0.60 (0.15)	1.8 (0.06)	0.33 (0.08)	0.31 (0.10)	2.06 (0.05)	0.15 (0.05)
Charolais	633.1 (252.4)	978.7 (81.2)	0.65 (0.21)	0.16 (0.33)	1.64 (0.11)	0.09 (0.20)	0.46 (0.41)	1.88 (0.14)	0.24 (0.20)
Friesian	44.0 (21.8)	718.1 (14.8)	0.06 (0.03)	0.04 (0.03)	0.97 (0.02)	0.04 (0.03)	0.26 (0.10)	1.95 (0.05)	0.13 (0.05)
Hereford	115.5 (52.9)	641.8 (19.8)	0.18 (0.08)	0.19 (0.11)	1.52 (0.05)	0.13 (0.07)	0.00 (0.00)	2.07 (0.05)	0.00 (0.00)
Holstein	147.4 (19.6)	847.7 (9.0)	0.18 (0.02)	0.22 (0.03)	1.11 (0.01)	0.20 (0.02)	0.47 (0.06)	2.25 (0.03)	0.21 (0.02)
Limousin	151.1 (67.8)	767.6 (25.1)	0.20 (0.08)	0.73 (0.23)	2.03 (0.08)	0.36 (0.10)	0.00 (0.00)	1.82 (0.04)	0.00 (0.00)
Simmental	416.8 (162.0)	769.5 (51.5)	0.54 (0.18)	0.18 (0.28)	1.81 (0.10)	0.10 (0.15)	0.87 (0.42)	2.19 (0.14)	0.40 (0.17)

¹CW = Carcass weight, kg²; CC = carcass conformation class, transformed numerical scale; CF = carcass fatness class, transformed numerical scale; σ_a^2 = genetic variance; σ_p^2 = phenotypic variance; and h^2 = heritability.

²Numbers in parentheses represent SE.

groups ranged from 0.26 cu^2 for the Friesian to 0.49 cu^2 for the Aberdeen Angus.

Heritabilities ranged from zero to moderate for carcass fatness class (0.00 to 0.40), from low to moderate for carcass conformation class (0.04 to 0.36), and from low to high for carcass weight (0.06 to 0.65). There were large differences within traits across the different sire breed groups. On average across all groups, carcass conformation class and carcass fatness class were least heritable (0.17), whereas carcass weight was most heritable (0.26). The Simmental sire breed group displayed the highest average heritability across all 3 traits (0.35), whereas the Friesian and Hereford sire breed groups displayed the lowest average heritability (0.08). For carcass weight and carcass conformation class the Friesian sire breed group had the lowest heritability with estimates of 0.06 and 0.04, respectively. The heritabilities of carcass fatness class in the Hereford and Limousin sire breed groups were zero. For each of the 3 traits a different sire breed group displayed the highest heritability. The Charolais sire breed group had the highest heritability for carcass weight (0.65), whereas the Limousin sire breed group had the highest heritability for carcass conformation class (0.36). The Simmental sire breed group displayed the highest heritability for carcass fatness class (0.40).

Testing Differences in Variances

Large differences existed in the estimates of genetic variance and heritability across the different sire breed groups. The SE of the estimates suggested that some of these differences were significant. There appeared to be no relationship between the arithmetic means for the different sire breed groups and their respective genetic and phenotypic variances. Results for the log likelihood ratio tests, the AIC and BIC are in Table 5. These indicate that, for each carcass trait, sire model 1, the model which estimated separate variances in each of the 8 sire breed groups was an improvement over sire model 2 and 3, which estimated separate variances for 3 clusters of sire breed groups and a single pair of genetic and phenotypic variances across all 8

sire breed groups, respectively. Sire model 2 was also significantly better than sire model 3.

Relationship Between Traits

The genetic and phenotypic correlations among all 3 traits for the Holstein sire breed group are given in Table 6. They were all positive among each of the 3 carcass traits. The genetic correlations ranged from 0.11 for the relationship between carcass weight and carcass fatness class to 0.44 for the relationship between carcass conformation class and carcass fatness class. The phenotypic correlations ranged from 0.22 to 0.36 for the relationship between carcass conformation class and carcass fatness class and the relationship between carcass weight and carcass conformation, respectively.

DISCUSSION

This study illustrates that carcass weight and classification data, which are collected in commercial abattoirs in Ireland, provide information to facilitate the estimation of genetic and phenotypic variance for carcass weight, carcass conformation class, and carcass fatness class. The estimates of heritability are similar in magnitude to estimates of EUROP carcass traits found in other studies (e.g., Van der Werf et al., 1998; Parkkonen et al., 2000). These estimates were possible despite the extensive editing of the data that was required, that the data were collected primarily for reasons other than for the estimation of genetic parameters and breeding values, and that there was no proper experimental design for such estimation (i.e., sires were not evenly distributed across contemporary groups). Such results suggest that commercial carcass classification data can provide low cost information for the purposes of genetic evaluation of cattle in Ireland for beef traits.

Heritability of Carcass Traits

The results of our study indicate that the genetic variances and consequently heritability for EUROP

Table 5. Estimates of likelihood ratios (LRT), Akaike information criterion (AIC), and Bayesian information criterion (BIC) comparing sire models 1, 2, and 3, across each of the carcass traits

Trait ¹	LRT			AIC			BIC		
	1 vs. 2	1 vs. 3	2 vs. 3	1	2	3	1	2	3
CW	81.12	283.06	201.94	450,416	450,478	450,672	450,461	450,494	450,677
CC	51.8	1,517.5	1,465.7	86,653	86,685	88,143	86,697	86,701	88,148
CF	61.48	96.62	35.14	114,023	114,064	114,091	114,067	114,081	114,097

¹CW = Carcass weight; CC = carcass conformation class; and CF = carcass fatness class.

carcass traits are different in different breeds of cattle in Ireland. Such a finding is in agreement with the extensive reviews of genetic parameters for carcass traits in beef cattle carried out by Koots et al. (1994a) and Rios Utrera and Van Vleck (2004). Part of the differences may be due to difference in connectedness in the different sire breed groups. Nonetheless, failure to take account of such heterogeneity may lead to inaccurate and biased predictions of breeding values (Visscher and Hill, 1992). This suggests that the multiple breed genetic evaluation models currently used for the genetic evaluation of cattle in Ireland (Pool et al., 2005), which assume homogeneity of genetic and phenotypic variances, could be enhanced by accounting for heterogeneity of genetic and phenotypic variance across different breed composition groups.

With respect to the Friesian sire breed group, the estimates of heritability for carcass weight and carcass conformation class were considerably lower than the previous estimates for these traits, of 0.32 and 0.24, respectively, using Irish Friesian sire breed data (More O'Ferrall et al., 1989). Higher estimates of heritability have to be expected from the results of More O'Ferrall et al. (1989) because these workers analyzed progeny test data. Progeny test data are collected with a greater degree of accuracy than the commercial data used in our study. Such data would consequently allow better correction for environmental effects, thus reducing the residual variance, as well as supplying more accurate pedigree information, which would increase the estimates of genetic variance.

The estimates of heritability for the Hereford, Charolais, and Simmental sire breed groups in our study were different to those estimated for purebred Charolais, Hereford, and Simmental cattle reported by Eriksson et al. (2003), with no particular trend in the differences

being observed. The zero estimates of heritability for carcass fatness class in the Hereford and Limousin sire breed groups were due to estimates of genetic variances that were fixed to extremely low positive values during the estimation process, suggesting that the real estimated values may be negative. Negative estimates of genetic variance are expected to be obtained by chance, especially in small population sizes (Koots et al., 1994a) due to sampling variances (Lynch and Walsh, 1998) or because the underlying assumptions are incorrect (Gill and Jensen, 1968).

Several studies in different species (Van der Werf and de Boer, 1989; Bishop and Russell, 1997) have shown that the estimates of heritability increase in magnitude as the level of crossbreeding in a group increases. Whereas sire breed groups were used to define each data subset in our study, an animal model was used in the analysis for the presented estimates of variance components. Therefore, in each analysis the pedigree includes animals of at least 2 breeds, Holstein and Friesian in the case of both the Holstein and Friesian sired groups, and a third breed in the case of the other sire breed groups. Because the data set is dominated by Holstein genes, the Holstein-sired breed group can be considered almost entirely purebred. Higher average heritabilities for a number of traits, compared with the Holstein sire breed group, were observed in the Simmental, Charolais, and Belgian Blue sire breed groups. An obvious reason is that some of the between breed genetic variance may be included in the estimates of genetic variance (Bishop and Russell, 1996). Wei et al. (1991) state that dominance variance, as well as differences in gene frequencies in parental breeds, inflates estimates of genetic variance in crossbred populations. Some heterosis effects may be included in the estimate of genetic variance for the crossbreds.

Relationship Between Carcass Traits

The positive genetic and phenotypic relationships between the 3 carcass traits are consistent with what has been reported in the literature for similar traits in similar breeds. Positive correlations between carcass fatness class and each of carcass weight and carcass conformation classes were found by Parkkonen et al. (2000) in 7 out of 8 cases in Finnish dairy cattle, with the single negative value found not being significantly

Table 6. Genetic (r_a) and phenotypic (r_p) correlations between each carcass trait in the Holstein sire breed group

Trait ¹	r_a	r_p
CW – CC	0.11 (0.09)	0.36 (0.01)
CW – CF	0.26 (0.08)	0.22 (0.01)
CC – CF	0.44 (0.07)	0.31 (0.01)

¹CW = Carcass weight; CC = carcass conformation class; and CF = carcass fatness class.

different from zero. More O'Ferrall et al. (1989), using Irish Friesian data, and Van der Werf et al. (1998) and Liinamo et al. (1999) also found positive genetic associations between carcass fatness class and both carcass conformation class and carcass weight in pure and crossbred dairy breeds. However, the genetic correlation between carcass conformation class and carcass weight, although still positive, was lower (0.11) than found in other studies carried out on dual purpose and dairy breeds of cattle, which ranged from 0.25 to 0.66 (Hirooka et al., 1996; Van der Werf et al., 1998; Liinamo et al., 1999; Parkkonen et al., 2000). Direct selection to increase carcass conformation or carcass weight in Holsteins, without imposing direct selection pressure to reduce or maintain carcass fatness class, would result in higher fat levels for carcasses at higher weights. Slaughtering such animals earlier in life, at lower weights, when they are less mature may be required if direct selection pressure on carcass fatness class is not included in a selection index for carcass traits.

IMPLICATIONS

Bovine carcass data as currently collected in Irish abattoirs are suitable for the purposes of genetic evaluation. The systems of grading and weighing carcasses in abattoirs are able to provide information that allows the genetic and phenotypic variance in carcass weight, carcass conformation class, and carcass fatness class to be estimated. Heritabilities and their constituent variance components displayed differences in different sire breed groups. Selection for increased quantities of lean meat in the Holstein sire breed group requires the disentangling of the antagonistic relationship between carcass fatness class and carcass conformation and carcass weight.

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