Genetics of Wholesale Carcass Cuts in Beef Cattle Predicted from Digital Images of Carcasses at Slaughter

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Introduction

Most breeding objectives attempt to identify the most profitable animals by appropriately weighting well defined and accurately measured breeding values into an overall objective. Inclusion of all pertinent traits in the breeding objective is fundamental to its uptake and success in increasing genetic gain for profitability. The main source of revenue for beef farmers, either directly or indirectly, is carcass value. Despite its importance, phenotypes included in European breeding objectives are limited to carcass weight, carcass conformation score and carcass fat score, as implemented by the European Council regulations 1208/81 and 2930/81 (United Kingdom: Amer et al., 1997 ; Italy: Albera et al., 2004 ;Czech Republic: Wolfova et al., 2005). In Ireland, mechanical grading of cattle carcasses for conformation and fat using the VBS2000 technology (EplusV GmbH, Germany) was introduced in 2003. and digital images are currently used to generate EUROP carcass classification of conformation and fat scores (Anon et al., 2004). Since July 2005, the Irish Cattle Breeding Federation has stored digital images taken by the grading machines. Pabiou et al. (2010) showed that predictions of wholesale carcass cuts using parameters derived from these digital images explained more of the variability in carcass distribution of wholesale cuts that the current EUROP classification grading system. Additionally, Pabiou et al. (2009) documented significant genetic variation in actual primal carcass cut weights using a small dataset of carcass dissections; however, the standard errors of those estimates were large, attributable mainly to the relatively small dataset. The objective, therefore, of this study was to quantify the genetic variation in predicted carcass cuts using national data.

Material and methods

Carcass images and predicted wholesale cuts. A total of 521,605 carcass images from steers and heifers slaughtered in 15 different abattoirs between November 2006 and May 2009 were available for inclusion in the analysis. A daily calibration of the grading machine is necessary in the factory to account for variation in light, camera angle, and distance from the camera to the measuring board using two sets of template boards (vertical grid and vertical bars).

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Equations developed by Pabiou et al. (2010) to predict wholesale carcass cuts from the digital images were used in the present study to predict wholesale carcass cuts for all carcasses. Prediction equations were specific to steer versus heifer carcass images. The wholesale cuts created were described previously (Pabiou et al., 2009) and were based on retail value of individual cuts. The wholesale cuts were: Lower Value Cut group (LVC) including fore- and hind shins, flank, ribs, brisket, neck, and lean trimmings; Medium Value Cut group (MVC) comprising of the shoulder and the chuck cuts; High Value Cut group (HVC) including the sirloin and the round cut weights; Very High Value Cut group (VHVC) comprising of the weights of the rib roast, strip-loin, and fillet cuts. Carcass weight, EUROP carcass conformation, and EUROP carcass fat grade were also recorded on each carcass; the EUROP classification grades were transformed to a 15-point scale as outlined by Hickey et al. (2007). Images associated with incorrect calibrations files were discarded (n = 27,814). Animals slaughtered younger than 10 months or older than 60 months (n = 1,223) as well as animals with no known sire (n = 369,782) were also discarded. Wholesale cuts greater than three standard deviation from their respective mean, within steers and heifers separately were discarded (n = 2,571). In Ireland farmers tend to manage heifers and steers separately and therefore herd-specific contemporary groups were defined within males and females separately. The contemporary groups were generated, within sex, using the iterative algorithm of Crump et al. (1997) parameterised by the minimum (30 days) and maximum (60 days) span of a group for date of slaughter, and the minimum number of records (n = 5) per group. The edited dataset consisted of 58,645 animals: 41,604 (71%) steers, and 17,041 (29%) heifers. Steers and heifers were from 5,570 and 2,499 different contemporary groups, respectively.

Statistical analyses. (Co)variance components for predicted wholesale cuts were estimated separately for steers and heifers and subsequently as a combined dataset. Model building for fixed effects used PROC GLM (SAS, 2007) for both the steers and the heifers and variance components were estimated using an animal model in ASREML (Gilmour et al., 2007). Covariances between predicted cuts were estimated using a sire model in ASREML accounting for the relationships among sires.

Fixed effects considered for inclusion in the model were dam age when the animal was born (<3 years, 3 to 5 years, 6 to 8 years, and >8 years), whether the animal was a singleton or multiple, contemporary group, abattoir effect defined as slaughter date within abattoir, and slaughter date. Covariates tested for inclusion in the model were heterosis, recombination, age at slaughter centered within sex, carcass weight.. The effect of the sex of the animal was confounded with the contemporary groups. Relationships among animals were accounted for using a relationship matrix where unknown ancestors were included as phantom groups of the breeds Charolais, Friesian, Holstein, Limousin, Angus, Simmental, Belgian Blue, oth-er beef breeds, and unknown breed in both the steers and heifer pedigree files.

Results and discussion

Heritability estimates for carcass weight were 0.49 (steers) and 0.58 (heifers) (Table 1). Heritability estimates for the EUROP classification score for conformation and fat in the steers and heifers ranged from 0.29 (fat score in steers) to 0.48 (conformation score in steers). Heritability for the wholesale cut weights were similar across both the steers and the heifers, and ranged from 0.14 (MVC steers) to 0.47 (HVC heifers). The coefficient of genetic variation for the wholesale cuts varied from 1.5% (HVC in steers) to 5.7% (VHVC in steers).

Table 1. Mean (standard deviation in parenthesis), heritability (h^2; standard error in parenthesis) for carcass traits and wholesale cut weights of steers and heifers.

	Steers		Heifers	
Trait	Mean (s.d)	h^2 (s.e.)	Mean (s.d)	h^2 (s.e)
Carcass weight (kg)	344 (47.8)	0.49 (0.029)	292 (43.9)	0.58 (0.050)
Conformation (1 [poor] to 15 [good])	5 (1.8)	0.48 (0.029)	7 (2.0)	0.30 (0.039)
Fat (1 [lean] to 15 [fat])	7 (1.5)	0.29 (0.024)	7 (2.0)	0.44 (0.046)
Total meat (kg)	231 (34)	0.13 (0.017)	176 (30.3)	0.73 (0.051)
Total fat (kg)[1]	44 (15.5)	0.43 (0.027)		
Total bone (kg) [1]	76 (9.2)	0.46 (0.028)		
Lower Value Cuts (kg)	88 (18.7)	0.34 (0.027)	92 (14.6)	0.30 (0.042)
Medium Value Cuts (kg)	49 (8)	0.14 (0.019)	20 (3.5)	0.18 (0.040)
High Value Cuts (kg)	60 (9.3)	0.26 (0.024)	46 (8.3)	0.47 (0.047)
Very High Value Cuts (kg)	26 (3.8)	0.33 (0.026)	21 (3.5)	0.32 (0.043)

[1] Data were not available for the development of prediction equations in heifers (Pabiou et al., 2010).

The sum of the average predicted wholesale cuts was 222 kg or 96% of the predicted total meat weight for the steers, and 178 kg (101% of the predicted total meat weight) for the heifers. Despite the higher accuracy of prediction for total meat weight in steers (accuracy=0.97) compared to in heifers (accuracy=0.84) (Pabiou et al., 2010), the heritability for total meat weight was lower in steers, albeit the standard error of the heritability in the heifers was more than double that of the steers.

Because carcass weight was included as a covariate in the model for estimating genetic parameters, the genetic correlations between the wholesale cuts and carcass weight were not very strong and ranged from 0.20 to 0.45 in the steers, and from 0.02 to 0.17 in the heifers (Table 2) ; these correlations exceeded 0.94 across both genders when carcass weight was excluded from the models. The strong correlations between carcass conformation and both HVC (>0.69) and VHVC (>0.75) is expected since one of the aims of the EUROP carcass grading for conformation is to estimate the volume of the hindquarter. However, the correlations were not unity suggesting that genetic variation in HVC and VHVC exist over and above that accounted for by genetic merit for carcass conformation. Carcass fat was negatively correlated with the wholesale cut weights in both genders, but was strongly positively correlated with total fat weight (r=0.92; SE=0,03); this clearly shows that genetic merit for the current score (subcutaneous) carass fat grade predicts accurately genetic merit for total carcass fat. The genetic correlation between the wholesale cut weights were all moderate to strongly positive.

Table 2. Genetic correlations (standard error in parenthesis) between carcass weight, EUROP scores for conformation and fat, and wholesale cuts weights for the steers (above diagonal) and heifers (below diagonal).

	Carcass weight	Carcass conf.	Carcass fat	Lower value cuts	Medium value cuts	High value cuts	Very high value cuts
Carcass weight		0.44 (0.04)	-0.26 (0.06)	0.43 (0.05)	0.24 (0.06)	0.20 (0.06)	0.45 (0.07)
Carcass conformation	0.22 (0.09)		-0.36 (0.04)	0.67 (0.04)	0.62 (0.04)	0.69 (0.04)	0.75 (0.03)
Carcass fat	-0.19 (0.09)	-0.31 (0.10)		-0.70 (0.04)	-0.54 (0.06)	-0.59 (0.05)	-0.69 (0.04)
Lower Value Cuts	0.26 (0.09)	0.57 (0.09)	-0.89 (0.05)		0.47 (0.08)	0.74 (0.05)	0.69 (0.07)
Medium Value Cuts	0.02 (0.10)	0.91 (0.07)	-0.43 (0.10)	0.56 (0.11)		0.79 (0.04)	0.84 (0.04)
High Value Cuts	0.17 (0.08)	0.91 (0.07)	-0.73 (0.06)	0.87 (0.05)	0.84 (0.06)		0.87 (0.03)
Very High Value Cuts	0.17 (0.08)	0.95 (0.04)	-0.50 (0.08)	0.74 (0.06)	0.94 (0.05)	0.69 (0.06)	

Conclusion

Clear evidence of the existence of genetic variation in wholesale cut weights predicted by using the digital images taken after slaughter is presented. Genetic correlations between all wholesale carcass cuts was moderate to positive but genetic correlations between HVC and VHVC and carcass conformation were less than unity.

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