Variance component estimation of efficiency, carcass and meat quality traits in beef cattle

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Summary

The growth efficiency of beef animals is considered an extremely relevant and important economic trait, with the main focus to date being on improving feed efficiency in younger animals through breeding. However, the impact of selection for more efficient cattle on carcass and meat quality traits is largely unknown. The objective of the present study was to estimate the genetic covariance between feed efficiency traits with both carcass and meat quality traits in Irish beef cattle. Genetic (co)variance parameters for the efficiency, carcass and meat quality traits were estimated using univariate and bi-variate animal linear mixed models on a dataset of 4,798 animals. Weak to strong heritability estimates were observed for feed efficiency, carcass and meat quality traits in the current study; this suggests the variation among animals for these traits is due, in some part, to genetic differences. Feed efficiency, carcass and meat quality traits were weak to strongly correlated with each other. Results from the present study provide new insight into the effects of selecting for efficiency and carcass traits on meat quality traits, which can be taken into consideration when outlining new breeding objectives to effectively improve beef production and meat quality in Irish herds.

Keywords: efficiency traits, carcass yield, meat quality, genetic (co)variances

Introduction

Quantifying individual animal feed intake is particularly expensive and is the primary limiting factor for genetic studies and evaluations of feed efficiency (Pech et al., 2014; Manafiazar et al., 2015). Numerous studies have published variance component estimates and genetic correlations among performance traits, but due to the lack of feed intake data, correlation estimates with feed efficiency traits is lacking, particularly with carcass and meat quality traits. Several international studies in cattle have reported weak to strong heritability estimates for efficiency traits, ranging from 0.06 to 0.62 (Berry and Crowley, 2013). Two studies have reported that cattle with better residual feed intake (RFI) have improved carcass conformation; genetic correlations between muscle score and RFI varied from -0.44 to -0.22 (Bouquet et al., 2010; Crowley et al., 2011). Genetic correlations between carcass conformation and feed conversion ratio (FCR) are generally negative (-0.12, Bouquet et al., 2010; -0.46, Crowley et al., 2011), and genetic correlations between muscle score and FCR and residual gain (RG) (Crowley et al., 2011) were similar to the genetic correlations between muscle score and RFI. The objective of the present study was to estimate the genetic co(variance) parameters among feed efficiency, carcass and meat quality traits in Irish beef

cattle.
Material and methods

Live-weight and feed intake records on 6,238 animals were obtained from the Irish national progeny test centre from 1983 to 2017, inclusive. A number of edits were applied to the data similar to those detailed in Crowley et al. (2010). Animals had to have a minimum of four feed intake records and four live-weight records. Animals entered the progeny testing centre, on average, in three separate groups annually, and for the purpose of the present study were allocated to contemporary groups based on their group of entry. The edited dataset consisted of 4,798 animals, consisting of 4,470 bulls, 4 heifers and 324 steers with 15 breeds presented.

Performance traits were estimated as detailed by Crowley et al. (2010). Average daily gain (ADG) during the test period was estimated by fitting a linear regression through all live-weight (LW) observations of each animal. Mid-test live-weight was defined as live-weight 35 days before the end of the test period, estimated from the intercept and linear regression coefficient. A linear regression was fit through all metabolic live-weight observations with mid-test metabolic live-weight then estimated from the intercept and slope of the regression line. Average feed intake (FI) per animal was calculated as the arithmetic sum of daily feed intakes per animal, which were then averaged per week, and finally averaged across the test period. Feed conversion ratio was calculated, as detailed in Crowley et al. (2010) as the average feed intake divided by ADG. Kleiber ratio (KR) was also estimated as ADG divided by the mid-test bodyweight to the power of 0.75 (Crowley et al., 2010). Residual feed intake was estimated for each animal as the residual estimates from a multiple regression model, where feed intake was regressed onto both ADG and the metabolic live-weight ($LW^{0.75}$), with contemporary group included as a class effect; fat was not included in the estimation of RFI as only 20% of the animals in the dataset had ultrasound fat records. Similarly, residual gain (RG) was estimated for each animal as the residual estimates where ADG was regressed on both feed intake and $LW^{0.75}$ in a multiple regression model that also included contemporary group. Carcass conformation, weight and fat records were available on some of the animals in the test centre, as were records on the meat quality traits flavour, juiciness and tenderness (Table 1).

Genetic (co)variance parameters for the efficiency, carcass and meat quality traits were estimated using univariate and bi-variate linear animal mixed models, with pedigree information for all animals included. The pedigree utilised for all traits included 44,588 animals, representing 12,349 sires, from 20 generations; breed groups were assigned in the pedigree. Fixed effects in the model utilised to analyse the feed efficiency traits included contemporary group, heterosis, and a two-way interaction between month of age and animal type, i.e., whether they were a bull, steer or heifer. The fixed effects unique to the carcass traits were death-date, heterosis and a two-way interaction between month of age at slaughter and animal type. The final model applied to analyse the meat quality traits included the fixed effects death-date, heterosis, test-date of the meat sample and a two-way interaction between month of age at slaughter and animal type.

Results and Discussion

Summary statistics for all traits are described in Table 1. The coefficient of genetic variation varied from 2% (flavour) to 92% (RFI). Heritability estimates were greatest for the carcass traits ranging from 0.48 (carcass conformation) to 0.80 (carcass weight), which were higher that values reported by another international study in beef cattle (0.38 to 0.60, Bouquet et al.,

2010. Feed efficiency traits were moderately heritable varying from 0.29 (RG) to 0.50 (RFI); these values were within the range reported in previous international studies in cattle (Arthur et al., 2001; Nkrumah et al., 2007; Berry and Crowley, 2012; Berry and Crowley, 2013). Heritability estimates for the juiciness (0.08) and intramuscle fat (0.45) were higher than corresponding heritability estimates reported by Mateescu et al. (2015) in beef animals (0.06 and 0.38, respectively). However, heritability estimates were within the range reported by Berry et al. (2017) for tenderness (0.08 to 0.49), juiciness (0.00 to 0.43) and flavour (0.04 – 0.36) in beef cattle. The higher heritability estimates reported in the present study could be the result of better quality data, including the removal of all pedigree errors, as all animals were genotyped and parentage errors resolved. These results suggest that the feed efficiency, carcass and meat quality traits would respond well to selection; with gains being potentially greater for traits with larger coefficients of genetic variation.

Genetic and phenotypic correlations for the feed efficiency, carcass and meat quality traits are detailed in Table 2. The negative genetic correlation between RFI with both carcass weight (-0.44) and conformation (-0.41) suggests that animals with lower RFI have improved carcass conformation; these values fall within the range reported in a review paper by Berry and Crowley (2013; -0.60 to 0.26 and -0.56 to 0.29, respectively). The moderate positive genetic correlation between RFI and carcass fat (0.51) suggests that selecting for RFI (as defined in the present study) alone will reduce carcass fat of the animal. A moderate positive genetic correlation estimated between RG and carcass fat (0.39) suggests selecting for animals with better residual gain will result in selecting for animals with greater carcass fat, which is not desirable from a producer or processor's perspective. This is in contrast with the average genetic correlation reported from other international studies in beef in a review paper by Berry and Crowley (2013; -0.06). A strong negative genetic correlation between ADG and FCR (-0.53) suggests that animals selected for improved FCR will have enhanced ADG; this result is in line with those reported by other elsewhere in cattle Berry and Crowley (2013; -0.89 to 0.75). Similarly the strong genetic correlation between ADG and RG (0.92) implies that animals with faster ADG will have greater residual gain.

A moderate negative genetic correlation between carcass fat and flavour (-0.35) suggests that selecting for lower carcass fat will negatively affect the flavour of the meat. Similarly, selecting animals for lower intramuscular fat will negatively affect the juiciness of the meat (-0.13). Juiciness and flavour were strongly genetically correlated (0.99) with each other. Selecting for larger carcass weights will have a slight negative effect on the juiciness of the meat (-0.01) and therefore, emphasis could be placed on juiciness to counteract this effect in breeding objectives. Additionally, selecting animals on RG will have a negative effect on the flavour (-0.53) of the meat. As a consequence of the strong positive genetic correlation between fat depth and muscle depth (0.72) in the current study, and the existence of negative moderate to strong genetic correlations between carcass fat traits with the meat quality traits, selecting animals for carcass fat traits without taking cognisance of these genetic correlations could result in a decrease in the flavour, juiciness and tenderness of the meat, possibly reducing its palatability.

Conclusion

Efficiency, carcass and meat quality traits were all weakly to strongly heritable (0.03; flavour to 0.80; carcass weight), and genetic correlations ranged from -0.79 (between flavour and muscle depth) to 0.99 (between flavour and juiciness). The results from the present study provide new insight into the effects of selecting for efficiency and carcass traits on meat

quality traits, which can be taken into consideration when outlining new breeding objectives to effectively improve beef production and meat quality in Irish herds.

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Table 1. List of all traits with number of records for each trait, the genetic standard deviations (σ_g), heritability estimates (h^2), standard errors (S.E) and co-efficient of genetic variation (CV_g).

Trait	No. of records	σ_g	h^2	S.E.	CV_g
Feed intake (kg/d)	4,250	0.82	0.47	0.05	0.07
ADG (kg/d)	4,250	0.15	0.31	0.05	0.08
FCR	4,250	0.64	0.33	0.05	0.09
KR	4,250	0.00	0.30	0.05	0.08
RG (kg/d)	4,250	0.13	0.29	0.05	0.78
RGR (kg/d)	4,250	0.01	0.33	0.05	0.11
RFI (kg/d)	4,250	0.58	0.50	0.05	0.92
Carcass weight (kg)	1,252	33.35	0.80	0.17	0.08
Carcass fat (scale 1 – 9)	1,252	0.71	0.55	0.15	0.12
Carcass conformation (scale 1 – 9)	1,252	0.70	0.48	0.15	0.07
Flavour (scale 1 – 9)	1,252	0.13	0.03	0.09	0.02
Juicy (scale 1 – 9)	1,252	0.23	0.08	0.10	0.04
Tender (scale 1 – 9)	1,252	0.34	0.11	0.11	0.06
Fat depth (cm)	3,164	0.45	0.31	0.14	0.23
Muscle depth (cm)	2,256	4.04	0.43	0.15	0.07
Intramuscle (cm)	1,060	4.24	0.45	0.14	0.77
Mid-test weight (kg)	4,250	41.27	0.57	0.05	0.07
Metabolic LW (kg)	4,250	6.34	0.56	0.05	0.06

Table 2. Phenotypic correlations (above diagonal: standard errors in parentheses) and genetic correlations (below diagonal; standard errors in parentheses) between the feed efficiency, carcass and meat quality traits.

	Feed intake	ADG	FCR	KR	RG	RFI	Carcass weight	Carcass fat	Carcass Conformation	Flavour	Juicy	Tender	Fat depth	Muscle depth	Intra-muscle
Feed intake (kg/d)		0.50 (0.01)	0.16 (0.01)	0.18 (0.02)	0.26 (0.02)	0.72 (0.01)	0.55 (0.03)	0.41 (0.03)	0.02 (0.04)	-0.004 (0.004)	-0.02 (0.04)	-0.08 (0.04)	0.18 (0.02)	0.11 (0.03)	0.01 (0.04)
ADG (kg/d)	0.54 (0.07)		-0.68 (0.01)	0.87 (0.004)	0.96 (0.002)	0.03 (0.02)	0.35 (0.03)	0.12 (0.04)	0.17 (0.04)	-0.05 (0.04)	-0.02 (0.04)	-0.02 (0.04)	0.003 (0.02)	0.06 (0.03)	-0.05 (0.03)
FCR	0.33 (0.09)	-0.53 (0.07)		-0.76 (0.01)	-0.79 (0.01)	0.43 (0.01)	-0.03 (0.04)	0.08 (0.04)	-0.12 (0.04)	0.05 (0.04)	0.01 (0.04)	-0.02 (0.04)	0.12 (0.02)	0.04 (0.03)	0.05 (0.04)
KR	0.11 (0.10)	0.77 (0.04)	-0.68 (0.06)		0.96 (0.001)	0.01 (0.02)	-0.02 (0.04)	-0.01 (0.04)	0.10 (0.04)	-0.06 (0.04)	-0.002 (0.04)	0.01 (0.04)	-0.06 (0.02)	-0.04 (0.03)	-0.08 (0.04)
RG (kg/d)	0.24 (0.09)	0.92 (0.01)	-0.73 (0.05)	0.94 (0.01)		-0.07 (0.02)	0.17 (0.04)	0.03 (0.04)	0.15 (0.04)	-0.05 (0.04)	-0.01 (0.04)	0.0004 (0.04)	-0.05 (0.02)	0.02 (0.03)	-0.07 (0.03)
RFI (kg/d)	0.70 (0.04)	0.09 (0.10)	0.47 (0.08)	0.15 (0.10)	0.01 (0.10)		-0.10 (0.04)	0.31 (0.04)	-0.25 (0.04)	0.03 (0.04)	-0.003 (0.04)	-0.06 (0.04)	0.16 (0.02)	-0.02 (0.03)	0.02 (0.04)
Carcass weight (kg)	0.44 (0.14)	0.49 (0.16)	-0.17 (0.20)	0.09 (0.20)	0.36 (0.18)	-0.44 (0.14)		0.16 (0.03)	0.51 (0.03)	-0.04 (0.03)	-0.05 (0.03)	-0.02 (0.03)	0.18 (0.04)	0.76 (0.02)	0.03 (0.04)
Carcass fat (scale 1 − 9)	0.63 (0.12)	0.45 (0.16)	-0.20 (0.19)	0.40 (0.19)	0.39 (0.18)	0.51 (0.13)	0.08 (0.13)		-0.12 (0.03)	0.03 (0.03)	-0.01 (0.03)	0.01 (0.03)	0.61 (0.02)	0.16 (0.05)	0.09 (0.04)
Carcass conformation (scale 1 − 9)	-0.11 (0.16)	0.18 (0.17)	-0.33 (0.18)	0.23 (0.19)	0.24 (0.18)	-0.41 (0.14)	0.53 (0.09)	-0.23 (0.12)		-0.12 (0.03)	-0.08 (0.03)	-0.03 (0.03)	-0.22 (0.04)	0.71 (0.02)	0.06 (0.04)
Flavour (scale 1 − 9)	-0.49 (0.54)	-0.57 (0.62)	0.18 (0.57)	-0.53 (0.61)	-0.53 (0.63)	-0.09 (0.48)	-0.09 (0.43)	-0.35 (0.51)	-0.38 (0.37)		0.78 (0.01)	0.72 (0.01)	0.07 (0.04)	-0.10 (0.04)	-0.04 (0.03)
Juicy (scale 1 − 9)	-0.41 (0.36)	-0.05 (0.36)	-0.24 (0.41)	0.13 (0.41)	0.07 (0.38)	-0.39 (0.36)	-0.01 (0.32)	-0.56 (0.38)	-0.10 (0.29)	0.99 (0.24)		0.76 (0.01)	0.05 (0.04)	-0.07 (0.05)	-0.06 (0.03)
Tender (scale 1 − 9)	-0.42 (0.33)	0.02 (0.37)	-0.42 (0.40)	0.10 (0.41)	0.10 (0.39)	-0.62 (0.31)	0.22 (0.33)	-0.45 (0.35)	0.13 (0.33)	0.14 (0.97)	0.50 (0.44)		0.03 (0.04)	-0.04 (0.05)	-0.04 (0.03)
Fat depth (cm)	0.27 (0.07)	0.01 (0.08)	0.23 (0.08)	-0.14 (0.09)	-0.12 (0.09)	0.20 (0.07)	0.22 (0.12)	0.82 (0.05)	-0.22 (0.11)	-0.04 (0.42)	-0.02 (0.30)	0.04 (0.31)		0.58 (0.01)	0.22 (0.04)
Muscle depth (cm)	0.17 (0.08)	0.10 (0.09)	0.09 (0.09)	-0.11 (0.09)	0.01 (0.09)	-0.07 (0.07)	0.84 (0.05)	0.32 (0.14)	0.68 (0.07)	-0.79 (0.41)	-0.35 (0.32)	-0.24 (0.33)	0.72 (0.03)		0.14 (0.04)
Intramuscle (cm)	0.17 (0.28)	-0.23 (0.32)	0.67 (0.35)	-0.52 (0.35)	-0.38 (0.34)	0.28 (0.26)	-0.05 (0.27)	0.37 (0.26)	0.57 (0.23)	-0.09 (0.75)	-0.13 (0.57)	-0.10 (0.58)	0.58 (0.21)	-0.70 (0.55)	