

Contribution of herd characteristics to best linear unbiased estimates of slaughter traits in beef cattle



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ABSTRACT

Genetic evaluations separate phenotypes into their contributing additive genetic effects and non-(additive) genetic effects, with the former termed best linear unbiased predictions, and the latter termed best linear unbiased estimates (**BLUEs**). For the purpose of the present study, genetic evaluations, along with phenotypic data from 4 137 376 animals, were used to generate herd, year of slaughter and sex contemporary group BLUEs for various slaughter-related traits. These slaughter traits included carcass weight (**CW**), carcass conformation (**CC**) and carcass fat (**CF**). For the 4 665 herds that were consistently slaughtering ≥ 10 animals/year between the years 2014 and 2018, inclusive, all relevant contemporary group BLUEs were collapsed into a single herd-year value; results herein relate to these herds. The within-year herd-year BLUE correlations between CW and CC, between CW and CF, and between CC and CF were 0.51, 0.10 and -0.04 , respectively. The repeatability across years of the herd-year BLUEs for CW, CC and CF was 0.66, 0.59 and 0.50, respectively. Furthermore, when the herds were stratified, within year, on the percentile rank of their herd-year BLUEs, herds had the greatest probability of remaining in the same BLUE stratum from one year to the next. In addition, results from the present study determined that various herd characteristics are associated with differences in the herd BLUEs. Results from the present study could be used to advise beef producers on the most promising strategy to improve the carcass merit of their animals.

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Implications

For the present study, solutions representing the environmental contribution, independent of the genetic contribution, to differences in carcass metrics of beef cattle were generated from genetic evaluations. Knowledge of the relationship among these solutions for the different carcass traits, and of how they differed by the characteristics of the herd from which they are derived can help better understand the environmental effects that underpin herd performance for carcass merit. Findings from the study could also be incorporated into a decision support tool to advise producers on the most promising strategy to improve carcass performance.

Introduction

Improved carcass metrics in beef cattle, such as the achievement of imposed carcass specifications, would be of significant

economic and environmental benefit to the beef sector (Nguyen et al., 2010; Capper, 2011; Kenny et al., 2020a). Previous studies have documented the presence of genetic variability in carcass weight (**CW**), carcass conformation (**CC**) and carcass fat (**CF**), as well as in the achievement of desired carcass metrics, namely a CW of 270–380 kg, as well as a CC score ≥ 5 and a CF score of 6–11 on 15 point scales (Kenny et al., 2020a). There is potential, therefore, to deploy animal breeding strategies to make cumulative and permanent genetic improvement in carcass-related traits. Nonetheless, the performance of farmed livestock is an expression of the animal's genotype, the environment(s) which that animal was exposed to, and the interaction between the two (Visscher et al., 2008). Therefore, the co-evolution of both management practices and genetic merit could facilitate performance gains beyond the consideration of breeding strategies alone (Dunne et al., 2019).

Genetic evaluations separate phenotypes into contributing additive genetic effects, termed best linear unbiased predictions, as well as contributing non-additive and environmental effects, termed best linear unbiased estimates (**BLUEs**). The generated additive genetic merit estimates, and the downstream ranking of

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potential parents based on their estimated genetic merit, have been extensively and successfully deployed to facilitate genetic improvement (Berry et al., 2014, 2016). Conversely, the applications of BLUEs generated from genetic evaluations, which typically include estimates for systematic groups of animals based on shared environments (i.e., herd-year contemporary groups), have been explored in only a handful of previous cattle studies (Bastin et al., 2009; Englishby et al., 2017; Dunne et al., 2018). For example, using data from up to 1 582 beef herds, Englishby et al. (2017) generated herd-year solutions for carcass traits and used the solutions to quantify the association between herd-specific environmental measures and phenotypic variability in carcass traits; Englishby et al. (2017) reported that 11–72% of the phenotypic variation in CW, CC and CF can be explained by herd-year variance. Furthermore, Dunne et al. (2018) generated herd-level BLUEs for milk, fertility and survival traits in Irish dairy herds and continued by describing the characteristics of those dairy herds that underline their respective BLUE.

While Dunne et al. (2018) previously outlined the contribution of herd characteristics to BLUEs for traits of importance to dairy production systems, no studies have, to date, attempted to generate similar metrics for beef production systems and associative traits of importance. The objective of the present study was therefore two-fold: (1) quantify the relationship among the generated herd-year(-sex) BLUEs for the different traits, specifically, CW, CC and CF, and (2) determine how the herd-year(-sex) BLUEs differ by various herd characteristics. Results from the present study should provide a deeper understanding of the environmental (i.e., management) effects underpinning slaughter-related traits. These findings could also be incorporated into the management decisions of beef finishers, perhaps through decision support tools, to favourably alter the carcass metrics of cattle within the feedlot by focusing on herd attributes that would deliver the greatest gains.

Material and methods

Data

Carcass information was available on 17 522 824 cattle, of which the majority were some crossbred combination of the following breeds: Angus, Aubrac, Belgian Blue, Blonde d'Aquitaine, Charolais, Hereford, Holstein-Friesian, Jersey, Limousin, Saler, Shorthorn and Simmental. For the purpose of the present study, only data from young bulls, heifers and steers slaughtered between the years 2003 and 2018, inclusive, were retained. In addition, all young bulls, heifers, and steers had to be slaughtered between the ages of 13 and 36 months with CWs of 100–800 kg. The birth herd of each young bull, heifer and steer was classified as either a beef herd (i.e., a herd where the average dam breed composition consisted of ≤65% dairy breeds) or a dairy herd (i.e., a herd where the average dam breed composition consisted of >75% dairy breeds; Ring et al., 2018). Any animal born in a herd that remained unclassified as a beef or dairy herd was not considered further. Furthermore, any cattle born from dams with a parity number >10 or from embryo transfer were removed from the study. Animals with >3 inter-locations movements during their lifetime, or that had moved herds within 100 days of slaughter, were also discarded. Additionally, the sire and dam had to be known for all animals. Carcass information was subsequently available for 5 456 820 cattle.

A general heterosis coefficient and recombination loss coefficient were calculated for all animals in the dataset using formulae outlined previously by VanRaden and Sanders (2003):

$$\text{heterosis} = 1 - \sum_{i=1}^n \text{sire}_i \times \text{dam}_i,$$

$$\text{recombination loss} = 1 - \sum_{i=1}^n \frac{\text{sire}_i^2 + \text{dam}_i^2}{2},$$

where sire_i and dam_i are the proportion of breed i in the breed composition of the sire and dam, respectively. Heterosis coefficients were subsequently classified as 0%, >0% and ≤10%, >10% and ≤20%, >20% and ≤30% ... >90% and <100%, and 100%. The recombination loss coefficients were categorised as 0%, >0% and ≤10%, >10% and ≤20%, >20% and ≤30%, >30% and ≤40%, >40% and ≤50%, and > 50%.

Contemporary groups of finishing herd, year of slaughter and sex were formed using an algorithm routinely used in the Irish genetic evaluations (Pabiou et al., 2012; Mc Hugh et al., 2014). The algorithm formed groups of cattle of the same sex that were finished in the same herd provided the start and end date of slaughter within the group were ≤60 days apart. Following the formation of the contemporary groups, only groups with at least five records were retained. Following all edits, carcass data from 4 137 376 cattle remained, comprising data from 864 840 bulls, 1 294 088 heifers and 1 978 448 steers slaughtered from 40 485 distinct herds.

Trait definition

Data on three carcass metrics, namely CW, CC and CF, were available for all animals in the dataset. CW is measured, on average, within one hour after slaughter following the removal of the head, hide, legs, thoracic organs, abdominal organs and internal fat (Englishby et al., 2017). CC reflects the shape and development of the carcass, with a particular emphasis on the round, back and shoulders, whereas CF is a measure of the level of fat covering the carcass, as well as within the thoracic cavity (Englishby et al., 2017). Both CC and CF are measured by video-image analysis (Pabiou et al., 2012) in accordance with the EUROP grading system. CC scores are represented by the letters E (best), U, R, O and P (worst), with CF scored from 1 (thin) to 5 (fat). All CC and CF scores are divided into three subdivisions (i.e., –, = and +).

Genetic evaluations

The BLUEs used in the present study were calculated from univariate genetic evaluations conducted for CW, CC and CF using the Mix99 software suite (Lidauer et al., 2017). The variance components used were those estimated by Kenny et al. (2020b) for CW, CC and CF using a subset of the data used in the present study. The models fitted for the variance component estimation, as well as for the downstream genetic evaluation, were those outlined by Kenny et al. (2020b):

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{e}$$

where \mathbf{y} is a vector of phenotypes for a particular carcass trait (i.e., CW, CC or CF); $\boldsymbol{\beta}$ is a vector of fixed effects, which included contemporary group of herd, year of slaughter and sex, birth herd type (i.e., beef or dairy), dam parity, heterosis and recombination loss classes, and whether the animal was born as a singleton or twin; \mathbf{a} is a vector of direct additive genetic effects; \mathbf{e} is a vector of random residuals; \mathbf{X} is an incidence matrix for the fixed effects and \mathbf{Z} is an incidence matrix for the random effects. The distribution of the random additive effect was assumed as $\mathbf{a} \sim N(\mathbf{Q}\mathbf{g}, \mathbf{A}\sigma_a^2)$, where \mathbf{Q} is a matrix relating \mathbf{a} with genetic groups, \mathbf{g} is a vector of genetic group means, and \mathbf{A} and σ_a^2 are, respectively, a numerator relationship matrix and the genetic variance. The numerator relationship matrix was constructed by tracing the pedigree of all animals back to the founder animals, which were allocated to genetic groups based on

breed. The distribution of the random residual term was assumed as $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$, where \mathbf{I} and σ_e^2 are, respectively, the identity matrix and the residual variance.

Herd-year best linear unbiased estimates

Contemporary group BLUEs for each trait were estimated for all 358 226 herd-year-sex contemporary groups in the genetic evaluations. In a single year, multiple contemporary groups of animals were generally slaughtered from the same herd; therefore, to generate herd-year BLUEs for each trait, all contemporary group BLUEs for that trait associated with a single herd and a given year were averaged, with the average weighted by the number of cattle within each of the contributing contemporary groups. Additionally, as the majority of herds slaughtered more than one animal sex each year, weighted average herd-year-sex BLUEs were also calculated for each herd. Only herds that consistently slaughtered ≥ 10 cattle each year between the years 2014 and 2018, inclusive, were retained for the purpose of analysis. Herd-year BLUE data were available across all five years for 4 665 finishing herds, which represented a total of 1 268 771 cattle. Each herd-year was stratified, for each carcass trait of interest separately, into one of five groups based on the percentile rank of their corresponding BLUE value (e.g., herds with the lowest 20% of herd BLUEs for a given trait were grouped into a single stratum). The standard deviation of the herd-year BLUEs and herd-year-sex BLUEs for each trait is in [Supplementary Table S1](#).

Herd-year characteristics

Prior to defining the herd-year characteristics, production systems were defined based on those described in detail by [Teagasc \(2015\)](#), in conjunction with the observed frequency distribution of age at slaughter for each sex in the 4 665 finishing herds of interest. Eight production systems were defined, which comprised two bull production systems, three heifer production systems and three steer production systems. The bull production systems defined in the present study were bulls slaughtered ≤ 16 months of age or bulls slaughter between 17 and 22 months of age. The production systems for heifers and steers were defined using the same age at slaughter thresholds, namely 18–20 months of age, 21–24 months of age or 25–30 months of age.

The herd-year characteristics defined for each herd-year included: (1) number of cattle slaughtered in a given year, (2) proportion of bulls, heifers and steers contributing to that year's slaughter, (3) proportion of dairy-origin cattle slaughtered, (4) the average proportion of the slaughtered animals' life spent in the herd, (5) number of production systems operated on the farm (a system was only considered to be operated on a farm if at least 15% of the cattle slaughtered in a given year aligned with a given system), (6) mean breed composition of the cattle slaughtered within that herd-year, and (7) geographical location. Additionally, herd characteristics were also defined on a herd-year-sex basis which included: (1) number of bulls, heifers or steers slaughtered per year, (2) proportion of dairy-origin bulls, heifers or steers slaughtered, (3) mean proportion of the relevant animals' life spent in the herd, (5) mean breed composition of cattle of the relevant sex slaughtered within a herd-year, and (6) geographical location. With the exception of breed composition and geographical location, all herds were separately stratified into five groups for each of the herd characteristics based on percentile rank. The thresholds associated with the various herd characteristic groups are in [Supplementary Table S2](#).

Statistical analyses

Partial Pearson correlation coefficients between the herd-year(-sex) BLUEs for the various traits of interest were estimated using PROC CORR in SAS 9.4 (SAS Institute Inc., Cary, NC); all correlations were adjusted for year of slaughter. The probability of herds remaining in the same BLUE stratum or of moving to a different BLUE stratum from one year to next was estimated using transition matrices. Each transition matrix was firstly generated between adjacent years for the various BLUE strata, and was then averaged across all years. Additionally, the repeatability of the continuous herd-year(-sex) BLUEs, and the association between the continuous herd-year(-sex) BLUEs for CW, CC and CF and the herd characteristics of interest, were quantified using linear mixed multiple regression models in SAS 9.4 (SAS Institute Inc., Cary, NC). The linear regression model fitted for herd-year BLUEs was as follows:

$$HY_{jklmnopqrst} = \text{Slaughter}_j + \text{Dairy}_k + \text{On farm}_l + \text{Location}_m + \text{Year}_n + \sum_{o=1}^{12} \text{Breed}_o + \text{Bull}_p + \text{Heifer}_q + \text{Steer}_r + \text{Systems}_s + \text{Herd}_t + e_{jklmnopqrst}$$

where $HY_{jklmnopqrst}$ is the continuous herd-year BLUE for CW, CC or CF from herd t and the year n ; Slaughter_j is the fixed effect of stratum j for the number of cattle annually slaughtered ($j = 1-5$); Dairy_k is the fixed effect of stratum k for the proportion of dairy-origin cattle slaughtered annually ($k = 1-5$); Onfarm_l is the fixed effect of stratum l for the average proportion of the slaughtered animals' life spent on the farm ($l = 1-5$); Location_m is the fixed effect of the geographical location of the herd ($m =$ one of the 26 counties in the Republic of Ireland); year_n is the fixed effect of year of slaughter n ($n = 2014, 2015, 2016, 2017$ or 2018); $\sum_{o=1}^{12} \text{Breed}_o$ is the average breed proportion of the slaughtered animals fitted as individual linear covariate terms for the various breeds (i.e., Angus, Aubrac, Belgian Blue, Blonde d'Aquitaine, Charolais, Hereford, Holstein-Friesian, Jersey, Limousin, Saler, Shorthorn and Simmental); Bull_p is the fixed effect of stratum p for the proportion of bulls slaughtered annually ($p = 1-5$); Heifer_q is the fixed effect of stratum q for the proportion of heifers slaughtered annually ($q = 1-5$); Steer_r is the fixed effect of stratum r for the proportion of steers slaughtered annually ($r = 1-5$); System_s is the fixed effect of the number predefined production system operated ($s = 1-5$); Herd_t is a repeated herd effect, and $e_{jklmnopqrst}$ is a random residual term. Based on the Akaike's information criterion ([Bozdogan, 2000](#)), the most appropriate covariance structure for the different models was determined and fitted for each linear mixed multiple regression model separately.

The linear regression model fitted for the herd-year-sex BLUEs was as follows:

$$HYS_{jklmnop} = \text{Slaughter}_j + \text{Dairy}_k + \text{Onfarm}_l + \text{Location}_m + \text{Year}_n \sum_{o=1}^{12} \text{Breed}_o + \text{Herd}_p + e_{jklmnop}$$

where $HYS_{jklmnop}$ is the continuous herd-year-sex BLUE for CW, CC or CF from herd t and the year n for bulls, heifers or steers; Herd_p is a repeated herd effect, and $e_{jklmnop}$ is a random residual effect. The fixed effects fitted in the models were the same as those outlined above for the linear regression models which included the continuous herd-year BLUEs as the dependent variable, only the fixed effects here were defined, where relevant (i.e., Slaughter_j , Dairy_k , Onfarm_l and $\sum_{o=1}^{12} \text{Breed}_o$) on a herd-year-sex basis corresponding to the sex in question, as opposed to on a herd-year basis. Furthermore, the most appropriate covariance structure for the different models was again determined and fitted for each linear mixed multiple regression model separately based on the Akaike's information criterion ([Bozdogan, 2000](#)).

Results

Correlations

The partial correlations between the herd-year BLUEs and the herd-year-sex BLUEs for the various slaughter traits are in Table 1. The correlation between the herd-year BLUEs for CW and CC, between the herd-year BLUEs for CW and CF, and between the herd-year BLUEs for CC and CF was 0.51, 0.10 and -0.04 , respectively (Table 1). Furthermore, the herd-year-sex BLUE correlations between CW and CC, between CW and CF, and between CC and CF were, respectively, 0.71, 0.49 and 0.44 in bulls, 0.69, 0.47 and 0.33 in heifers, and 0.64, 0.50 and 0.23 in steers (Table 1).

Repeatability estimates and transition matrices

The repeatability of the herd-year BLUEs for CW, CC and CF was 0.66, 0.59 and 0.50, respectively (Table 2). The repeatability of the herd-year-sex BLUEs for the various slaughter traits ranged from 0.45 to 0.62 in bulls, from 0.42 to 0.61 in heifers, and from 0.51 to 0.67 in steers (Table 2). The transition matrices depicting the probability of a herd changing BLUE stratum from one year to the next are in Table 3. Regardless of the trait in question, herds had the greatest probability of remaining in the same BLUE stratum from one year to the next. Additionally, the probability of a herd transitioning to a different BLUE stratum in the subsequent year reduced as the distance, in terms of the number of strata, between the strata compared increased. For example, from one year to the next, finishing herds in the highest BLUE stratum for CW had a 72.4% probability of remaining in that stratum the following year but a probability of 20.4%, 4.9%, 1.8% and 0.5% of transitioning down one, two, three or four strata, respectively (Table 3).

Contribution of herd characteristics to best linear unbiased estimates for carcass weight, conformation and fat

Regardless of the trait, differences in the herd-year BLUEs were associated ($P < 0.05$) with the proportion of each sex slaughtered from that herd, as well as whether they were of a dairy- or beef-herd origin. The mean proportion of the slaughtered animals' life spent in the herd, the breed composition of the herd, the geographical location of the herd as well as the year of slaughter were also associated ($P \leq 0.05$) with the herd BLUEs for all traits. Furthermore, the herd-year BLUEs for CW and CF were also associated with the number of production systems operated in the herd, although no such association was detected for the herd-year BLUE for CC. However, the herd-year BLUE for CC was associated with

Table 1
Partial correlation coefficients between the herd-year best linear unbiased estimates (BLUEs), as well as between the herd-year-sex BLUEs of bulls, heifers and steers for carcass weight (CW), carcass conformation (CC) and carcass fat (CF).

BLUE/Trait	CW	CC
Herd-year BLUE		
CC	0.51	
CF	0.10	-0.04
Herd-year-sex BLUE		
Bull		
CC	0.71	
CF	0.49	0.44
Heifer		
CC	0.69	
CF	0.47	0.33
Steer		
CC	0.64	
CF	0.50	0.23

the number of animals slaughtered in that herd for a given year ($P \leq 0.05$), but no such association was evident for the BLUEs for either CW or CF.

For the various geographical locations (i.e., the 26 counties of the Republic of Ireland), the standard deviation of the corresponding regression coefficients was 3.87 kg, 0.14 CC scores and 0.12 CF scores for the herd-year BLUE for CW, CC and CF, respectively. A greater proportion of animals slaughtered from a herd that were bulls was associated with a more positive BLUE for both CW and CC but a more negative BLUE for CF (Fig. 1). A greater proportion of heifers slaughtered from a herd was associated with a more positive BLUE for CF but a more negative BLUE for both CW and CC. A greater proportion of slaughtered animals that were steers was associated with a more positive BLUE for both CW and CF but a more negative BLUE for CC. Furthermore, increasing the proportion of dairy-origin animals slaughtered from a herd was associated with a more positive BLUE for CF, but was associated with no consistent trends in the BLUEs for CW and CC. No consistent trends in the herd-year BLUEs for CW, CC and CF was evident as the proportion of the slaughtered animals' life spent in a herd changed (Fig. 1). While there was no association between the number of animals slaughtered per year and the BLUE for either CW or CF, a greater number of animals slaughtered were associated with a more positive BLUE for CC. In addition, a greater number of production systems operated on farm were associated with a more negative herd-year BLUE for CW and CF (Fig. 1), although there was no association with the herd-year BLUE for CC.

The regression coefficients from the regression of the herd-year-sex BLUEs of bulls, heifers and steers on the various herd characteristics are in Figs. 2–4, respectively. From hereon, only results for the herd-year-sex BLUEs associated ($P \leq 0.05$) with each of the herd characteristics are presented. Regardless of the trait in question, herd-year-sex BLUEs were associated with both the geographical location of the herd and the year of slaughter. Furthermore, a greater number of animals of a given sex slaughtered from a herd were generally associated with a more positive herd-year-sex BLUE for CC in bulls, heifer and steers, and a more positive herd-year-sex BLUE for CF in heifers. The proportion of dairy-origin animals slaughtered was also associated with all of the herd-year-sex BLUEs for CC, as well as all of the herd-year-sex BLUEs for CW. Additionally, an increase in the mean proportion of the relevant animals' life spent in the herd was associated with, on average, a more negative herd-year-sex BLUEs for CW in bulls, heifers and steers, and a more negative herd-year-sex BLUE for CF in bulls.

Discussion

The potential applications of herd-level BLUEs have been discussed in only a limited number of previous cattle studies, with Bastin et al. (2009) and Dunne et al. (2018, 2019) describing such for dairy production systems, and Englishby et al. (2017) describing such for beef production systems. Given that the performance of livestock is a manifestation of their genotype and environment (Visscher et al., 2008), the herd BLUEs, in conjunction with the corresponding estimated breeding values (EBVs) of animals within the herd, could potentially be used to independently partition the performance of animals into their contributing factors. In turn, the ability to separate the phenotypic performance of a herd into its genetic and environmental influences can not only provide a vehicle to identify the influences that underpin poor performance within a herd, but also may well facilitate more informed, bespoke breeding and management advice.

In terms of generating these BLUE solutions, both fixed (i.e., BLUEs) and random (i.e., EBVs) effect solutions are simultaneously generated in routine genetic evaluations, with each term estimated

Table 2

Repeatability estimates of the herd-year and herd-year-sex best linear unbiased estimates (BLUEs) for carcass weight (CW), carcass conformation (CC) and carcass fat (CF) in cattle.

Trait	Repeatability estimates ¹			
	Herd-year BLUE	Herd-year-sex BLUE		
		Bull	Heifer	Steer
CW	0.66	0.62	0.61	0.67
CC	0.59	0.49	0.52	0.60
CF	0.50	0.45	0.42	0.51

¹ All SE were ≤ 0.008 .

Table 3

Transition matrices for the herd-year best linear unbiased estimate strata for carcass weight (CW), carcass conformation (CC) and carcass fat (CF) in cattle.

Trait/Initial stratum	Transition stratum				
	1	2	3	4	5
CW					
1 (lightest)	65.02	24.14	7.56	2.42	0.87
2	22.64	40.46	26.09	8.44	2.39
3	6.41	23.64	38.30	25.53	6.14
4	2.12	7.26	23.31	45.30	22.02
5 (heaviest)	0.45	1.81	4.94	20.38	72.43
CC					
1 (worst)	67.05	23.51	7.29	2.07	0.08
2	29.81	40.21	22.45	6.47	1.08
3	10.39	26.60	37.69	21.76	3.58
4	2.28	9.65	26.22	44.63	17.23
5 (best)	0.48	1.55	5.02	22.40	70.54
CF					
1 (leanest)	61.73	21.82	10.55	3.91	2.00
2	25.47	33.65	22.59	13.25	5.04
3	10.60	23.73	29.95	23.68	12.04
4	5.07	13.39	24.36	31.54	25.65
5 (fattest)	2.31	5.73	12.17	27.12	52.68

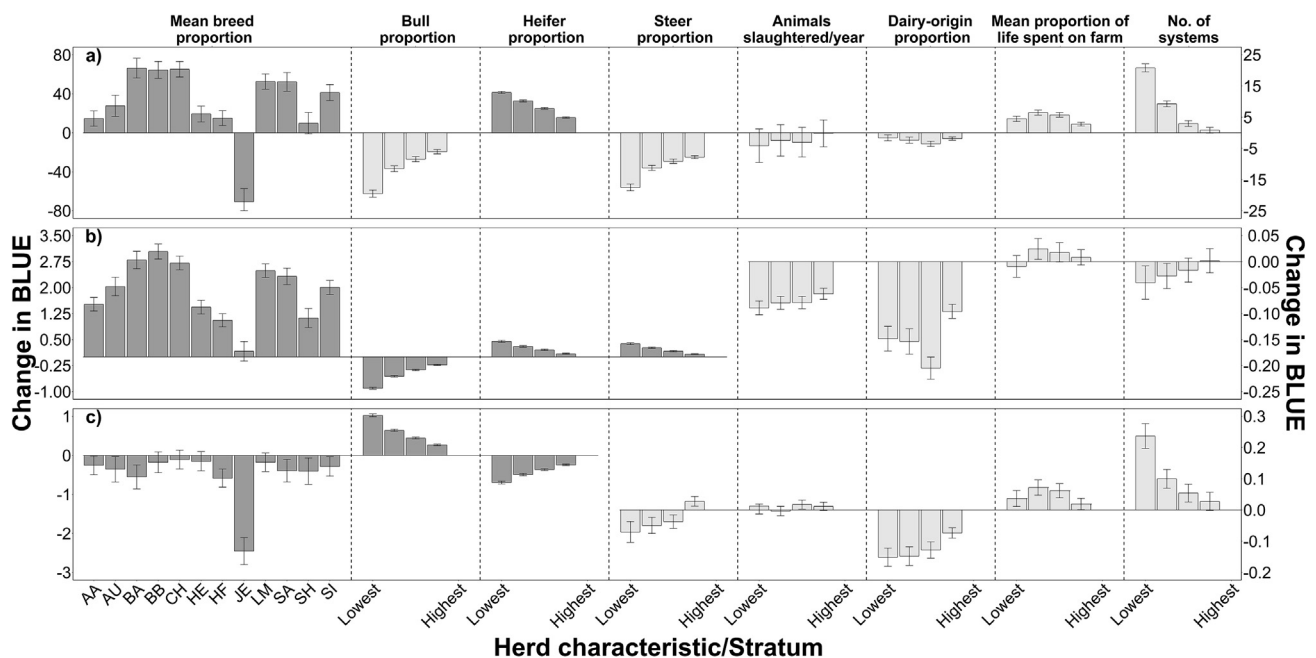


Fig. 1. Regression coefficients (SE as error bars) from the regression of the herd-year best linear unbiased estimates (BLUEs) for carcass weight (kg; a), carcass conformation (scored 1–15; b) and carcass fat (scored 1–15; c) in cattle on the herd characteristics of average proportion of Angus (AA), Aubrac (AU), Blonde d’Aquitaine (BA), Belgian Blue (BB), Charolais (CH), Hereford (HE), Holstein-Friesian (HF), Jersey (JE), Limousin (LM), Saler (SA), Shorthorn (SH) and Simmental (SI), proportion of slaughtered animals that were bulls, heifers or steers, or that were born in dairy herds, number of animals slaughtered per year, average proportion of life spent on farm, and the number of production systems operated within the herd. Dark grey columns are plotted on the primary axis, and light grey columns are plotted on the secondary axis.

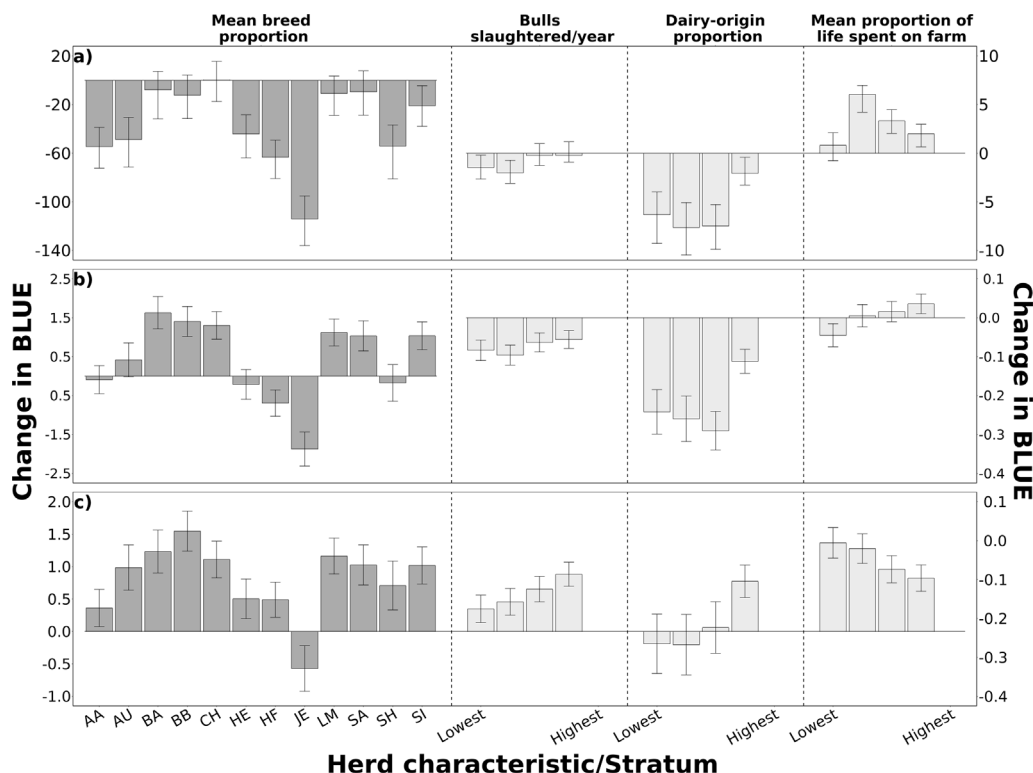


Fig. 2. Regression coefficients (SE as error bars) from the regression of the herd-year-sex best linear unbiased estimates (BLUES) for carcass weight (kg; a), carcass conformation (scored 1–15; b) and carcass fat (scored 1–15; c) in bulls on the herd characteristics of average proportion of Angus (AA), Aubrac (AU), Blonde d'Aquitaine (BA), Belgian Blue (BB), Charolais (CH), Hereford (HE), Holstein-Friesian (HF), Jersey (JE), Limousin (LM), Saler (SA), Shorthorn (SH) and Simmental (SI), number of bulls slaughtered per year, proportion of slaughtered bulls that were born in dairy herds, and average proportion of life spent on farm. Dark grey columns are plotted on the primary axis, and light grey columns are plotted on the secondary axis.

independent of all other terms in the model (Mrode and Thompson, 2014). Unlike EBVs though, which are generated for all animals, even those that have no phenotype (i.e., estimated using the numerator relationship matrix), herd BLUEs are only available for herds that have phenotypic records included in the evaluation (Mrode and Thompson, 2014). Therefore, given that carcass traits are recorded postslaughter, in reality, herd BLUEs for carcass traits cannot be estimated for live animals in a feedlot. Given that the herd BLUEs for carcass traits have a high repeatability, and the tendency observed in the present study of herds to remain in the same BLUE stratum over time, the expected BLUE for a given herd in the upcoming year could, in fact, be based on its most recent BLUE. For herds that do change BLUE category over time, these changes might be explained by changes in the herd's characteristics. In the case that a producer does make a change to their production system in a given year (e.g., to castrate all male calves rather than finishing them as bulls), the regression coefficients from the present study could be added to the expected BLUE (i.e., the previous year's BLUE) to derive a more representative BLUE for the present year. In addition, the movement in herd BLUE stratum may also be affected by the precision associated with the BLUEs themselves. When only herds that annually slaughtered ≥ 50 animals were considered in the transition matrices, the percentage of herds that remained in the lowest and highest CW BLUE stratum from one year to the next was 67.5% and 83.0%, respectively; this is compared to 65.0% and 72.4%, respectively, when all herds slaughtering ≥ 10 animals per year were considered. Movement in the herd BLUE categories over time that cannot be explained by information in the national database (e.g., herd breed composition), or by the precision associated with the BLUEs, may warrant deeper

discussion with the producer, particularly if their BLUE is deteriorating. For example, such deteriorations could be indicative of an increasing pathogen load in the herd over time, or a mineral deficiency in the blood of the animals. Hence, unexplained movements in a herd's BLUE over time can act as an alert system for underlining issues within a herd.

While the herd characteristics that underpin herd-level solutions representing the environmental contribution to the carcass metrics of beef cattle have not been reported previously, studies examining the animal-level factors associated with performance do exist (Connolly et al., 2016; Hickey et al., 2007). For example, the mean carcass merit of bulls, heifers and steers reported by Connolly et al. (2016) are in agreement with the herd-level regression coefficients estimated in the present study. Furthermore, the differences in carcass merit between various breeds reported in previous studies (Albertí et al. 2008; Hickey et al., 2007) are consistent with the herd-level regression coefficients reported in the present study for the various breeds. For instance, similar to the herd-level results of the present study, Hickey et al. (2007) reported that, in comparison to progeny of Holstein-Friesian dams that were sired by a variety of breeds, the progeny of Belgian Blue and Charolais sires, on average, produced the heaviest carcasses. In addition, differences in carcass metrics have previously been associated with different breed crosses (Wetlesen et al., 2020). Therefore, differences in the carcass trait herd BLUEs could also be explained by the breed crosses present in a herd. Moreover, observed differences in herd BLUEs by geographical location can be attributed to regional differences in soil type and climate (Gardiner and Ryan, 1969; McGrath et al., 2005), both of which underline the potential for grass growth on farms (Ryan, 1974; Brereton, 1995). In addition,

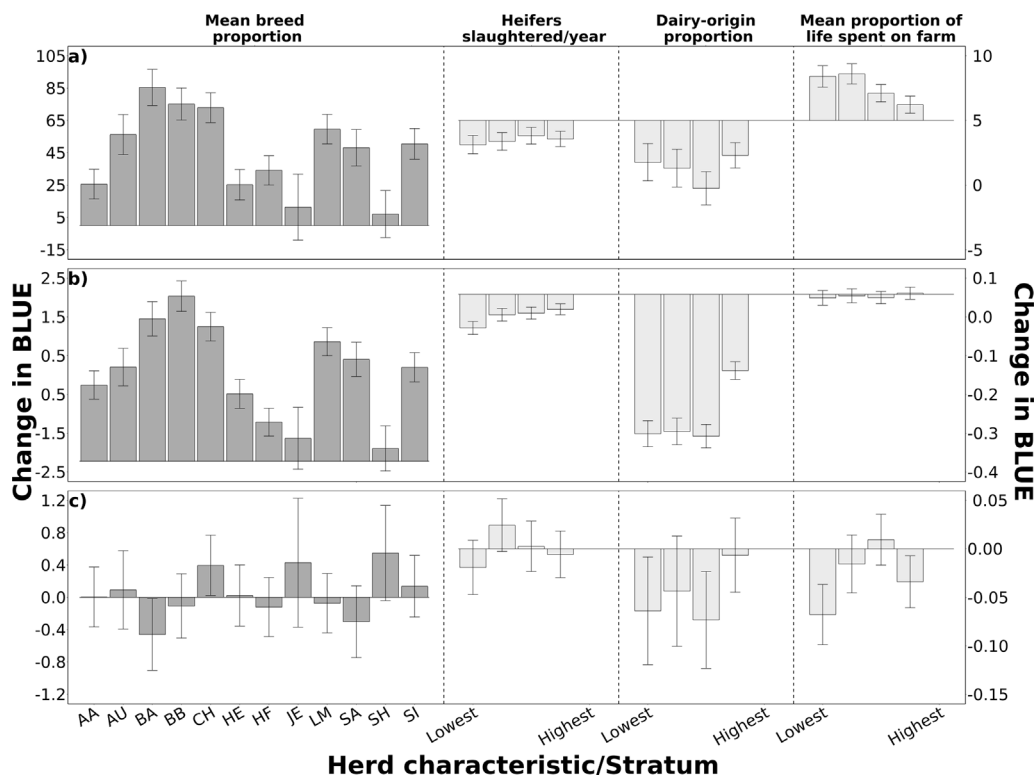


Fig. 3. Regression coefficients (SE as error bars) from the regression of the herd-year-sex best linear unbiased estimates (BLUEs) for carcass weight (kg; a), carcass conformation (scored 1–15; b) and carcass fat (scored 1–15; c) in heifers on the herd characteristics of average breed proportion of Angus (AA), Aubrac (AU), Blonde d’Aquitaine (BA), Belgian Blue (BB), Charolais (CH), Hereford (HE), Holstein-Friesian (HF), Jersey (JE), Limousin (LM), Saler (SA), Shorthorn (SH) and Simmental (SI), number of heifers slaughtered per year, proportion of heifers that were born in dairy herds, and average proportion of life spent on farm. Dark grey columns are plotted on the primary axis, and light grey columns are plotted on the secondary axis.

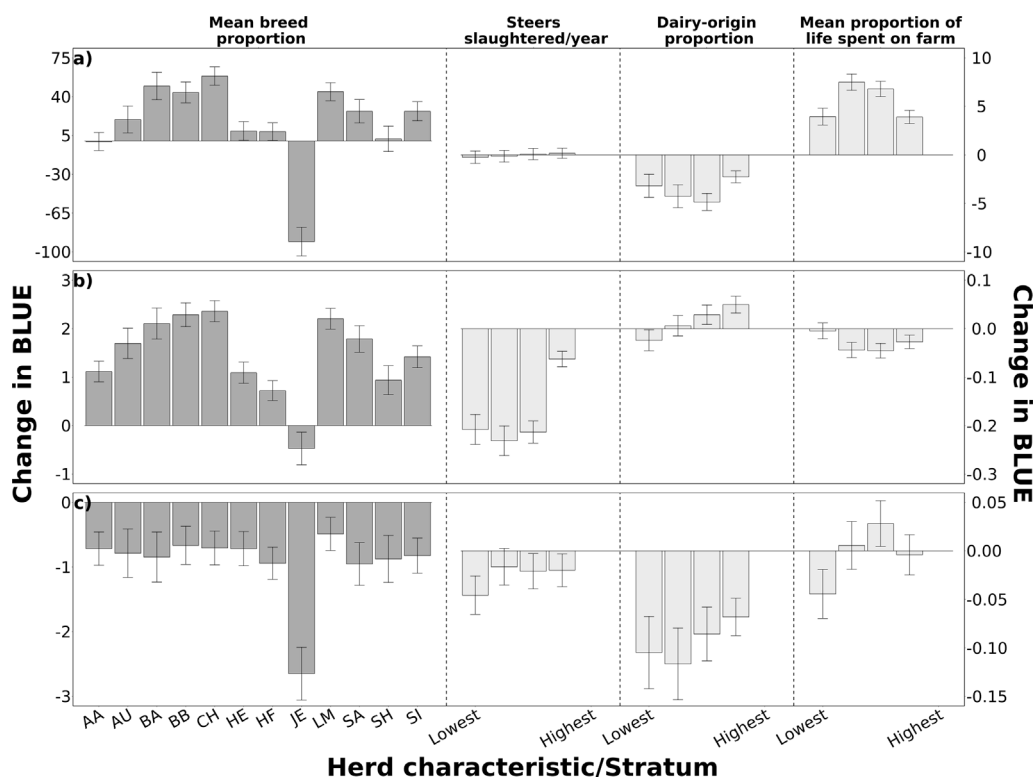


Fig. 4. Regression coefficients (SE as error bars) from the regression of the herd-year-sex best linear unbiased estimates (BLUEs) for carcass weight (kg; a), carcass conformation (scored 1–15; b) and carcass fat (scored 1–15; c) in steers on the herd characteristics, of average breed proportion of Angus (AA), Aubrac (AU), Blonde d’Aquitaine (BA), Belgian Blue (BB), Charolais (CH), Hereford (HE), Holstein-Friesian (HF), Jersey (JE), Limousin (LM), Saler (SA), Shorthorn (SH) and Simmental (SI), number of steers slaughtered per year, and proportion of slaughtered steers that were born in dairy herds, and average proportion of life spent on farm. Dark grey columns are plotted on the primary axis, and light grey columns are plotted on the secondary axis.

results from the present study signify that, relative to smaller herds, larger herds produce carcasses with better conformation. Such differences could be reflective of diluted fixed costs, due to economics of scale, in larger herds, which could mean that such herds can justify the purchase of superior quality animals (i.e., better conformed animals) for finishing.

The majority of Irish beef cattle fail to achieve one or more of the desired carcass specifications imposed on CW, CC and CF by Irish meat processors through price penalties (Kenny et al., 2020a). The justification for the stipulation of these specifications are based on the cost of processing individual carcasses, as well as the ability of carcass cuts to adhere to the desires of consumers. One of the primary applications of the herd-level BLUEs could be to aid in correcting this misalignment through the use of decision support tools that provides both management (i.e., herd BLUE) and genetic (i.e., EBVs) solutions. Dunne et al. (2018) previously described how a decision support tool for dairy producers, which uses both EBVs and herd-level BLUEs, could differentiate between the contributing factors to observed performance, and, in doing so, could aid in targeting which factors should be focused on to improve herd performance. A similar tool which uses the herd BLUEs for CW, CC and CF, in tandem with herd-average EBVs, might help beef producers in predicting the eventual carcass metrics of their cattle, as well as in understanding the underlining influence (i.e., genetic or management) of these carcass metrics. This knowledge could then facilitate the targeting of specific strategies (i.e., breeding strategies and/or the management strategies) to improve the carcass metrics of all animals finished in that herd. For instance, should a herd produce carcasses that consistently fail to achieve a minimum desired carcass threshold, and that herd has a low average EBV for the trait in question, then sires of superior genetic merit for that trait could be used to improve the carcass metrics (Kenny et al., 2020b). In the case of a herd that consistently produces carcasses that do not meet the minimum desired carcass thresholds and has a low corresponding herd BLUE, various management strategies could be employed to correct the performance issue(s). These strategies might include increasing the level of concentrates fed during the finishing period or increasing the duration of the finishing period (Sami et al., 2004). On the other hand, given that CW and CF have intermediate optimums, herds that produce over-heavy or over-fat carcasses and that have a high corresponding herd BLUE could reflect an opportunity to make cost savings within the herd, such as the provision of a lower concentrate feeding level (Sami et al., 2004).

Results of the present study, once integrated within a decision support tool, could also provide producers with the knowledge of how their (future) herd BLUE may change in response to purposed changes in their management system. For instance, if a producer was planning to expand their herd (i.e., increase the number of animals slaughtered in a year), the corresponding regression coefficients could be used to predict the herd's BLUE when herd size is stabilised, and to determine the effect of the purposed expansion on carcass performance. Additionally, while some of the herd-level factors, such as geographical location, cannot be changed by producers, herd-level factors that are under the control of the producer could be changed in an attempt to favourably alter the carcass metrics of their cattle. For example, if a herd consistently produces bull carcasses that fail to achieve the minimum desired CF threshold, male calves could be castrated to increase the fat cover of carcasses produced in the herd (Nogalski et al., 2018).

Supplementary material

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.animal.2021.100321>.

Ethics approval

The data used in the present study were obtained from a pre-existing database managed by the Irish Cattle Breeding Federation (ICBF; Bandon, Co. Cork, Ireland). Therefore, ethics approval was not required in advance of conducting the study.

Data and model availability statement

None of the data were deposited in an official repository but are available upon request.

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Donagh P. Berry: Conceptualisation, Methodology, Writing – Review & Editing, Supervision, Funding acquisition.

Declaration of interest

The authors do not have any conflicts of interest to declare

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