



## Prediction of genetic merit for live weight and body condition score in dairy cows using routinely available linear type and carcass data

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### ABSTRACT

Accurate estimates of genetic merit for both live weight and body condition score (BCS) could be useful additions to both national- and herd-breeding programs. Although recording live weight and BCS is not technologically arduous, data available for use in routine genetic evaluations are generally lacking. The objective of the present study was to explore the usefulness of routinely recorded data, namely linear type traits (which also included BCS but only assessed visually) and carcass traits in the pursuit of genetic evaluations for both live weight and BCS in dairy cows. The data consisted of on-farm records of live weight and BCS (assessed using both visual and tactile cues) from 33,242 dairy cows in 201 commercial Irish herds. These data were complemented with information on 6 body-related linear type traits (i.e., stature, angularity, chest width, body depth, BCS, and rump width) and 3 cull cow carcass measures (i.e., carcass weight, conformation, and fat cover) on a selection of these animals plus close relatives. (Co)variance components were estimated using animal linear mixed models. The genetic correlation between the type traits stature, angularity, body depth, chest width, rump width, and visually-assessed BCS with live weight was 0.68,  $-0.28$ , 0.43, 0.64, 0.61, and 0.44, respectively. The genetic correlation between angularity and BCS measured on farm (based on both visual and tactile appraisal) was  $-0.79$ ; the genetic and phenotypic correlation between BCS assessed visually as part of the linear assessment with BCS assessed by producers using both tactile and visual cues was 0.90 and 0.27, respectively. The genetic (phenotypic) correlation between cull cow carcass weight and live weight was 0.81 (0.21), and the genetic (phenotypic) correlation between cull cow carcass fat cover and BCS assessed on live cows was 0.44 (0.12). Estimated breeding values (EBV) for live weight and

BCS in a validation population of cows were generated using a multitrait evaluation with observations for just the type traits, just the carcass traits, and both the type traits and carcass traits; the EBV were compared with the respective live weight and BCS phenotypic observations. The regression of phenotypic live weight on its EBV from the multitrait evaluations was 1.00 (i.e., the expectation) when the EBV was generated using just linear type trait data, but less than 1 (0.83) when using just carcass data. However, the regression changed across parities and stages of lactation. The partial correlation (after adjusting for contemporary group, parity by stage of lactation, heterosis, and recombination loss) between phenotypic live weight and EBV for live weight estimated using the 3 different scenarios (i.e., type only, carcass only, type plus carcass) ranged from 0.38 to 0.43. Although the prediction of phenotypic BCS from its respective EBV was relatively good when using just the linear type trait data (regression coefficient of 0.83 with a partial correlation of 0.22), the predictive ability of BCS EBV based on just carcass data was poor and should not be used. Overall, linear type trait data are a useful source of information to predict live weight and BCS with minimal additional predictive value from also including carcass data. Nonetheless, in the absence of linear type trait data, information on carcass traits can be useful in predicting genetic merit for mature cow live weight. Prediction of cow BCS from cow carcass data is not recommended.

**Key words:** weight, condition, fat, carcass, type

### INTRODUCTION

Dairy cow breeding goals continue to evolve through the consideration of new constituent traits (Miglior et al., 2005; Cole and VanRaden, 2018) as well as revisions of the relative emphasis placed on each trait (Roche et al., 2017). Efficiency and resilience of productivity is emerging as a feature of particular interest among breeders and producers alike. Although genetic evaluations for all of the individual energy sources and sinks across the lifetime of an animal are required to fully

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capture lifetime efficiency, such a scenario is currently not realistic. The main energy sources for dairy cows are feed intake and body tissue mobilization; others include the digestive and absorptive capacity of the gastrointestinal tract and how those nutrients are utilized, to name but a few. Although activities are underway to derive both national (Pryce et al., 2015; Li et al., 2020) and international genetic evaluations for feed intake (Berry et al., 2014; de Haas et al., 2015), many populations use live weight as a proxy for maintenance within their dairy cow breeding goals (Berry et al., 2007b; Harris, 2005). Even if EBV for feed intake were available, there may still be a desire to derive estimates of genetic merit for live weight (Pryce et al., 2015) and BCS (Byrne et al., 2013). Body condition score is a good predictor of health (Pryce et al., 1998; Dechow et al., 2004), fertility (Berry et al., 2003), and resilience (Roche et al., 2017), justifying the interest in this as a trait for genetic evaluations; moreover, BCS in itself also commands an explicit economic value in some dairy cow production systems (Byrne et al., 2013).

Weighing scales are a simple and easy-to-use approach to generate individual cow live weight records. Irrespective of whether it is due to a lack of a weighing scale on farm, the fact that producers tend not to submit these weights for use in a genetic evaluation, or indeed are not aware that their live weight records could contribute to genetic evaluations, few live weight records are actually available for use in genetic evaluations. Similarly, body condition scoring is a quick, easy-to-learn, noninvasive technique to assess body energy reserves; yet, BCS data recorded by producers are lacking for inclusion in genetic evaluations. Although technologies and approaches to generating cow live weight and BCS records are constantly being developed (Bewley et al., 2008; Hansen et al., 2018), these are likely to still suffer from the same issues that currently exist. Hence, strategies which exploit “freenotypes” (i.e., data that are readily and freely available) for the generation of EBV for cow live weight (or indeed feed intake) and BCS warrant investigation.

Several previous studies have evaluated the contribution of routinely recorded linear type traits in predicting dairy cow live weight and BCS both phenotypically (Banos and Coffey, 2012; Berry and Kelleher, 2021) and genetically (Vallimont et al., 2010; Banos and Coffey, 2012). Becoming more available, however, is information on the carcass characteristics of slaughtered animals. Even though the focus in meat processing plants is generally on the carcass metrics of prime cattle, the system of generating and storing these metrics is generally also used in culled cows, especially if the slaughter plant processes both cull and prime cattle. Estimates

of genetic correlations between cull cow carcass credentials with both cow live weight and BCS, especially in dairy cows, is sparse in the scientific literature (Coyne et al., 2019); moreover, the value added of exploiting information on cull cow carcasses over and above that from linear type trait information (and vice versa) when predicting genetic merit for dairy cow live weight and BCS has, as yet, never been quantified.

Therefore, the objective of the present study was to use a large cross-sectional database of dairy cow records to estimate the genetic correlations between both live weight and BCS with both linear type traits and carcass traits. The marginal information content in explaining the genetic variability in both live weight and BCS by exploiting carcass trait data over and above that captured by the linear type traits was also quantified, as was the opposite. Also of interest were the associations between estimated genetic merit for live weight and BCS, derived using alternative genetic evaluation approaches with phenotypic live weight and BCS. Results from the present study will contribute to a greater appreciation of the usefulness of these readily available data sources as part of a multitrait genetic evaluation to predict genetic merit for live weight and BCS in dairy cows.

## MATERIALS AND METHODS

The data used in the present study all originated from the Irish Cattle Breeding Federation (<http://www.icbf.com>) database. A total of 156,408 live weight and BCS observations were available from 56,871 lactations on 38,842 Irish dairy cows recorded between the years 2000 and 2020. Live weight was recorded using calibrated weighing scales, and BCS was assessed using a combination of tactile and visual cues on a scale of 1 (emaciated) to 5 (obese; Edmonson et al., 1989). Both traits were recorded either by producers themselves or by 2 hired technicians. The data collection procedures and quality controls applied are described in detail by Berry and Kelleher (2021). Only data from parities 1 to 15 were retained. Parity was subsequently collapsed into 1, 2, 3, 4, and 5+. The lactation was stratified into 7 stages of 0 to 49, 50 to 99, . . . , 250 to 299, and 300 to 365. For animals to be considered further, they had to have been weighed and body condition scored in the herd where they last calved, and must also have resided in that herd for at least 100 d before weighing or body condition scoring. All considered records had information for both live weight and BCS.

Data were also available on stature, angularity, body depth, chest width, rump width, and BCS, all scored as part of the national linear classification system of dairy

cows. Linear type traits are subjective biometric scores that describe the biological extremes of animals for a set of different (morphological) characteristics (<https://www.icar.org/Guidelines/05-Conformation-Recording.pdf>); all linear scoring was undertaken by trained classifiers. Stature reflects the height of an animal from the top of the spine, in between the hips, to the ground, and angularity is a measure of the angle and openness of the ribs combined with flatness of bone. Body depth is the depth of the rear rib, chest width is the width of the chest between the top of the front legs, and rump width reflects the distance between the most posterior point of the pin bones. Finally, BCS as scored during linear assessment is the covering of fat over the tail head and rump. All scores were recorded on a 1-to-9 scale (Berry et al., 2004) by professional classifiers in the first 330 d of first lactation. Body condition score as part of the linear assessments was assessed visually, and to distinguish it from BCS recorded by farmers and technicians using also tactile appraisal, BCS scored as part of the linear assessment will hereon in be referred to as visual BCS (**VBCS**). Differences between classifiers in their range of scoring were accounted for by adjusting each of the 6 type traits by the ratio of the standard deviation of each classifier to the mean of the standard deviation calculated for each classifier for that trait in that year as outlined by Brotherstone (1994) and described for linear type trait data in Irish dairy cows by Berry et al. (2004).

Carcass weight, conformation, and fat score are measured on animals of all ages at slaughter. Carcass weight, which was known for all animals, is measured, on average, 1 h postslaughter, following the removal of the head, hide, legs, thoracic and abdominal organs, and internal fat. Carcass conformation (**CC**) and carcass fat (**CF**) are both recorded using the 15-point EUROP classification systems (Englishby et al., 2016) determined from video image analysis (Pabiou et al., 2011). Carcass conformation score reflects the shape and development of the carcass, particularly on the round, back, and shoulders. Carcass fat score represents the level of fat covering the carcass, as well as within the thoracic cavity of the carcass. Scores of 1 for CC and CF represent poor conformation and low fat cover, respectively, and a score of 15 represents the opposite (Englishby et al., 2016). Days postcalving at slaughter were collapsed into 0 to 49 d, 50 to 99 d, . . . , 300 to 349 d, and finally 350 to 400 d.

Contemporary group for live weight and BCS was defined as herd-year-season of calving developed using an algorithm used for most of the genetic evaluations in Ireland (Berry et al., 2013); only contemporary groups with at least 10 records were considered further when

the difference in calving date between the start and end of the contemporary group was no longer than 30 d. The BCS and live weight data from a total of 33,242 cows remained. Contemporary group for the linear scores was herd-date of scoring. Three different contemporary groups for slaughter were defined as per the national genetic evaluations: (1) herd-year-season of slaughter where herd here was the herd the cow resided in immediately before slaughter, (2) previous herd-year-season of slaughter where previous herd represented herd the cow resided in before its last herd (to account for the cows that moved herds for a fattening period before slaughter which is common in Ireland), and (3) processing plant-by-date of slaughter. Each contemporary group had to have at least 10 records to be considered further.

Of the cows with live weight and BCS phenotypes, 2,344 also had linear type trait data for the 6 body-related traits (postediting). All linear score data from herd-dates, where at least 1 cow had a recorded live weight and BCS measure, were retained. Furthermore, to increase the quantity of linear score data included in the analyses, herd-dates with at least 20 records and where there was at least 1 paternal half-sib to a cow with a live weight and linear score were also retained. Linear score data were available on 29,592 animals in total. These data were used to estimate the (co)variance components between the linear scores and both live weight and BCS when supplemented with live weight and BCS records from 15,806 cows residing in the herds that had at least 1 cow linearly assessed. Of the data set of 44,069 cows used to estimate the covariances between the linear scores and both live weight and BCS, 3,333 of these cows had been slaughtered in large contemporary groups, and thus also had carcass information included in the analysis. Carcass data from an additional 34,951 contemporary animals slaughtered in the same herd-year-season of slaughter were also used for the estimation of (co)variance components.

### **Estimation of Genetic Parameters**

Variance components for each trait were estimated using univariate animal linear mixed models in ASReml (Gilmour et al., 2009); a total of 40,174 live weight and BCS records from 15,806 cows were used in the estimation of the respective variance components with linear type traits data and carcass information available on 29,592 and 38,284 cows, respectively. Genetic and phenotypic correlations between recorded live weight and BCS with the 6 linear type traits and 3 carcass traits were estimated using a series of bivariate animal linear mixed models in ASReml (Gilmour et al., 2009). The

animal linear mixed models fitted to the live weight, BCS, linear type, and carcass data were as follows:

$$Y1 = HYS_c + HTD + Stage \times Parity + Het \\ + Rec + a + pe + e,$$

$$Y2 = HTD + Stage + Month + Het + Rec + a + e,$$

$$Y3 = HYS_s + HYS_{ps} + PD + Stage \times Parity \\ + Het + Rec + a + e,$$

where  $Y1$  represents live weight or BCS,  $Y2$  represents 1 of the 6 linear type traits, and  $Y3$  represents 1 of the 3 carcass traits;  $HYS_c$  is herd-year-season of calving;  $HTD$  is the contemporary group of herd  $\times$  date of assessment or weighing;  $Stage$  is the stage of lactation;  $Month$  is the calendar month of first calving;  $Het$  is the heterosis coefficient;  $Rec$  is the recombination loss coefficient;  $HYS_s$  is the herd-year-season of slaughter;  $HYS_{ps}$  is the previous herd-year-season of slaughter;  $PD$  is the meat processing plant  $\times$  date of slaughter;  $a$  is the random additive genetic effect,  $N(0, \mathbf{A}\sigma_a^2)$ , where  $\sigma_a^2$  is the additive genetic variance and  $\mathbf{A}$  is the numerator relationship matrix;  $pe$  is the random permanent environmental effect,  $N(0, \mathbf{I}\sigma_{pe}^2)$ , where  $\sigma_{pe}^2$  is the permanent environmental variance and  $\mathbf{I}$  is the identity matrix; and  $e$  represents the residual term, where  $N(0, \mathbf{I}\sigma_e^2)$ , with  $\sigma_e^2$  representing the residual variance and  $\mathbf{I}$  an identity matrix. In a follow-up series of analyses, BCS was also included as a covariate in the statistical model for live weight so as to adjust live weight to a common BCS as it is known to contribute to animal live weight (Berry et al., 2006, 2011).

### Genetic Evaluations

A series of different genetic evaluations were undertaken to estimate breeding values for all animals with live weight and BCS records. Live weight or BCS records of animals used in the estimation of the variance components were not considered either in the genetic evaluation itself or the subsequent validation. The first genetic evaluation to predict genetic merit for live weight was a  $7 \times 7$  multitrait model that included live weight, stature, angularity, body depth, chest width, rump width, and VBCS. The second genetic evaluation to predict genetic merit for live weight was a  $4 \times 4$  multitrait evaluation which included live weight, carcass weight, CC, and CF score. The third genetic evaluation

for live weight included all type traits and carcass traits in the same evaluation. In all instances, no phenotypic live weight data were included in the evaluation, but all linear and carcass data used in the national genetic evaluations were used. Linear type trait data from 246,848 cows were included for the relevant genetic evaluation, and carcass data from 2,464,153 cows were included for the relevant genetic evaluation. The statistical models used were those used for the estimation of variance components in the present study, and the estimated variance components in the present study were those used in the subsequent genetic evaluation. Live weight EBV and associated reliability estimates for all animals were generated for all 3 genetic evaluations. The same process of 3 genetic evaluations was replicated to estimate breeding values for BCS.

### Validation Analyses

Live weight and BCS data from 17,436 cows not used in the estimation of variance components were retained for use in quantifying the relationship between EBV from the aforementioned multitrait genetic evaluations for live weight and BCS with phenotypic live weight and BCS; all records were from contemporary groups of herd-year-season of calving with at least 10 records. The association between phenotypic live weight or BCS (dependent variable) with the corresponding EBV for live weight or BCS was determined using linear models. Fixed effects included in all models were contemporary group of calving, herd-date of weighing and scoring, parity, stage of lactation, and the 2-way interaction of stage-by-parity. Estimated breeding values for live weight or BCS were included as a continuous effect in all models as well as in 2 interactions with parity and stage of lactation. The different approaches to calculating each EBV were included individually in the model and the regression coefficients estimated. Furthermore, the partial correlation between both live weight and BCS with its respective EBV were also quantified; adjustment factors were as previously described for the statistical model of analysis, namely contemporary group, parity by lactation stage, heterosis, and recombination loss.

## RESULTS

Summary statistics for the different traits of interest including heritability estimates are in Table 1. The heritability of all traits was between 0.19 (BCS) and 0.50 (live weight), with the range in heritability estimates for the 6 type traits varying from 0.23 (angularity) to 0.48 (stature). The heritability of the carcass traits

**Table 1.** Number of records (N), sample population mean, genetic SD ( $\sigma_g$ ), and heritability estimates ( $h^2$ ) for the traits analyzed

Trait	N	Mean	$\sigma_g$	$h^2$ (SE)
Producer recorded				
Live weight (kg)	40,174	541.4	33.27	0.50 (0.02)
BCS <sup>1</sup>	40,174	2.947	0.13	0.19 (0.01)
Linear type (1–9 scale)				
Stature	29,592	5.778	0.80	0.48 (0.02)
Angularity	29,592	5.571	0.66	0.23 (0.02)
Body depth	29,592	5.173	0.56	0.24 (0.02)
Chest width	29,592	4.985	0.69	0.25 (0.02)
Rump width	29,592	5.138	0.66	0.26 (0.02)
VBCS <sup>2</sup>	24,981	4.678	0.83	0.33 (0.02)
Carcass				
Weight (kg)	44,025	288.9	19.89	0.47 (0.03)
Conformation <sup>3</sup>	44,025	2.77	0.41	0.25 (0.03)
Fat <sup>3</sup>	44,025	6.21	0.65	0.20 (0.02)

<sup>1</sup>Scale of 1 (thin) to 5 (fat).

<sup>2</sup>Visual BCS.

<sup>3</sup>Scale of 1 (poor conformation and low fat cover) to 15 (excellent conformation and high fat cover).

varied from 0.20 (CF) to 0.47 (carcass weight). Repeatability estimates (SE in parenthesis) for live weight and BCS were 0.70 (0.005) and 0.35 (0.007), respectively.

## Correlations

The phenotypic and genetic correlations between the linear type traits with both live weight and BCS are in Table 2, as are the correlations between the carcass traits and both live weight and BCS. The phenotypic and genetic correlation between BCS (as recorded using visual and tactile appraisal) and live weight was 0.40 (0.01) and 0.34 (0.06), respectively. The phenotypic correlations between the type traits and live weight varied from 0.20 to 0.29 with the exception of stature (0.41)

and angularity (−0.08). Angularity had a phenotypic correlation of −0.16 with BCS, and the phenotypic correlation between VBCS (i.e., linear type trait assessed visually) and BCS (as scored by producers) was 0.27. The phenotypic correlations between the carcass traits with both live weight (0.00 to 0.21) and BCS (0.12 to 0.17) were, at best, weak. Adjusting live weight phenotypically for differences in BCS had minimal effect on the estimated phenotypic correlations (Table 2).

With the exception of the genetic correlation between angularity and live weight (−0.28), the absolute genetic correlations between each of the remaining 5 type traits and live weight varied from 0.43 (body depth) to 0.68 (stature). Once adjusted phenotypically for differences in BCS, the genetic correlations varied from −0.11 to 0.74 (Table 2). The genetic correlation between angularity and BCS was −0.79 (Table 2), and the genetic correlation between VBCS and BCS was 0.90. Once adjusted phenotypically for differences in BCS, the genetic correlation between angularity with live weight was −0.11, although the genetic correlation between VBCS and adjusted live weight remained moderate at 0.42. A strong genetic correlation (0.81) existed between carcass weight and live weight, with the genetic correlation between both CC and CF with live weight being  $\leq|0.24|$ . The genetic correlations between BCS and the 3 carcass traits varied from 0.07 (CC) to 0.62 (carcass weight).

The phenotypic and genetic correlations among the type traits, among the carcass traits, and between the type and carcass traits are in Table 3. The type traits were weakly phenotypically correlated with CC and CF, although the phenotypic correlations between the type traits and carcass weight varied from −0.16 to 0.33. Genetically, some type traits (i.e., stature, chest

**Table 2.** Genetic (SE in parentheses) and phenotypic<sup>1</sup> correlations between the different linear type traits and carcass traits with both live weight [unadjusted (raw) or adjusted phenotypically to a constant BCS (adjusted)] and BCS

Trait <sup>2</sup>	Score interpretation		Phenotypic			Genetic		
			Live weight		BCS	Live weight		BCS
	Low	High	Raw	Adjusted		Raw	Adjusted	
STA	Short	Tall	0.41	0.44	0.00	0.68 (0.03)	0.74 (0.03)	−0.13 (0.08)
ANG	Coarse	Sharp	−0.08	−0.02	−0.16	−0.28 (0.06)	−0.11 (0.05)	−0.79 (0.05)
BD	Shallow	Deep	0.20	0.19	0.02	0.43 (0.05)	0.43 (0.05)	−0.03 (0.09)
CW	Narrow	Wide	0.29	0.22	0.17	0.64 (0.04)	0.52 (0.05)	0.63 (0.06)
RW	Narrow	Wide	0.27	0.25	0.06	0.61 (0.05)	0.58 (0.05)	0.31 (0.08)
VBCS	Thin	Fat	0.26	0.21	0.27	0.44 (0.07)	0.42 (0.05)	0.90 (0.03)
CWT	Light	Heavy	0.21	0.18	0.15	0.81 (0.04)	0.70 (0.05)	0.62 (0.07)
CC	Poor	Excellent	0.00	−0.03	0.17	0.24 (0.09)	0.08 (0.09)	0.07 (0.01)
CF	Thin	Fat	0.00	−0.02	0.12	−0.04 (0.11)	−0.15 (0.10)	0.44 (0.11)

<sup>1</sup>Standard error of all phenotypic correlations was  $\leq 0.02$ .

<sup>2</sup>STA = stature; ANG = angularity; BD = body depth, CW = chest width; RW = rump width; VBCS = visual body condition score, CWT = carcass weight, CC = carcass conformation score, CF = carcass fat score.

**Table 3.** Genetic (above diagonal; SE in parentheses) and phenotypic<sup>1</sup> (below diagonal) correlations among and between the linear type traits and carcass traits

Trait <sup>2</sup>	STA	ANG	BD	CW	RW	VBCS	CWT	CC	CF
STA		0.40 (0.05)	0.45 (0.05)	0.23 (0.05)	0.49 (0.05)	0.09 (0.06)	0.57 (0.05)	-0.31 (0.08)	-0.40 (0.07)
ANG	0.18		0.52 (0.05)	-0.24 (0.07)	0.04 (0.07)	-0.50 (0.06)	-0.38 (0.08)	-0.71 (0.06)	-0.44 (0.07)
BD	0.31	0.36		0.59 (0.04)	0.47 (0.05)	0.08 (0.07)	0.17 (0.08)	-0.44 (0.06)	-0.28 (0.08)
CW	0.22	-0.06	0.52		0.59 (0.05)	0.74 (0.04)	0.53 (0.05)	0.24 (0.07)	0.17 (0.10)
RW	0.30	0.08	0.31	0.40		0.30 (0.06)	0.56 (0.07)	0.23 (0.09)	-0.02 (0.11)
VBCS	0.08	-0.23	0.17	0.48	0.22		0.25 (0.05)	0.10 (0.07)	0.13 (0.06)
CWT	0.33	-0.16	0.18	0.27	0.18	0.11		0.61 (0.05)	-0.25 (0.06)
CC	-0.11	-0.20	-0.08	0.12	0.02	0.04	0.47		-0.03 (0.06)
CF	-0.10	-0.15	-0.04	0.10	0.01	0.04	0.35	0.29	

<sup>1</sup>Standard error of all phenotypic correlations was  $\leq 0.03$ .

<sup>2</sup>STA = stature; ANG = angularity; BD = body depth; CW = chest width; RW = rump width; VBCS = visual body condition score; CWT = carcass weight; CC = carcass conformation score; CF = carcass fat score.

width and rump width) were moderately correlated (0.53–0.57) with carcass weight; the genetic correlation between CF with both angularity and VBCS was -0.44 and 0.13, respectively.

### Validation

The regression coefficients when phenotypic live weight or BCS was regressed on their respective EBV that were predicted using information on type traits alone, carcass traits alone, or both type traits and carcass traits are in Table 4; also included are the partial correlations between phenotypic live weight and the EBV for live weight, as well as the partial correlations between phenotypic BCS and the EBV for BCS. Figures 1 and 2 describe the influence of parity and stage of lactation on the regression coefficients of both phenotypic liveweight and phenotypic BCS on their respective EBV. The expectation of the regression coefficient is 1, and although the coefficient was 1 across all data for live weight predicted from type traits, it was less than 1 when the EBV was estimated from just the carcass data. Nonetheless, the regression coefficients became larger as lactation stage progressed (Figure 2) and in older parity animals (Figure 1). A similar trend was observed when relating phenotypic BCS to EBV for BCS across stages of lactation and parities, albeit the regression coefficients were negative for all stages of lactation and younger parity cows when the EBV were predicted using just the carcass data.

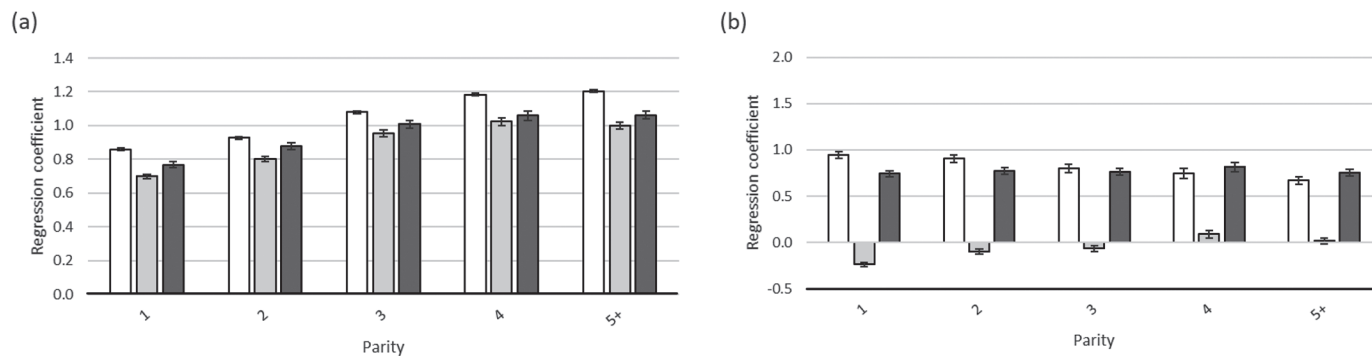
## DISCUSSION

Accurate estimates of genetic merit are fundamental to genetic gain (Rendel and Robertson, 1950). Furthermore, confidence among breeders and producers on how these genetic evaluations translate into phenotypic difference is crucial for achieving penetrance (Ramsbottom et al., 2012; Ring et al., 2021). Despite the moder-

ate heritability of both live weight and BCS (Berry et al., 2003; Vallimont et al., 2010; Banos and Coffey, 2012), the relatively low availability of phenotypes for use in genetic evaluations challenges the ability to achieve a high accuracy of selection. Using data from genetically correlated traits within the framework of a multitrait genetic evaluation is a strategy to increase the accuracy of selection for the goal trait; the cost of such a strategy can be minimal if phenotype observations on these correlated traits already exist. Data on linear type traits and carcass traits are generally freely available, and the hypothesis of this study was that (some of) these traits should correlate with live weight and BCS, and thus be informative in genetic evaluations. Also of interest was if these associations persisted across parities and stages of lactation. Heritability estimates for the different traits investigated in the present study are in line with international estimates (Veerkamp and Brotherstone, 1997; Vallimont et al., 2010; Banos and Coffey, 2012) as well as estimates of the same traits in other Irish cattle population (Berry et al., 2003, 2004; Pabiou et al., 2012). Similarly, the moderate to strong phenotypic and genetic correlations among the linear type traits themselves are consistent with those documented elsewhere for dairy cows (Berry et al., 2004; Banos and Coffey, 2012). There is a paucity of estimates of correla-

**Table 4.** Regression coefficients (b; SE in parentheses) and partial correlations (r) between phenotypic live weight and BCS with the EBV for each trait when estimated in a multitrait model using observations on just linear type traits, just carcass traits, or a combination of both

Observation	Live weight		BCS	
	b	r	b	r
Type traits	1.00 (0.014)	0.38	0.83 (0.021)	0.22
Carcass traits	0.84 (0.010)	0.43	-0.10 (0.015)	-0.02
Type + carcass traits	0.91 (0.012)	0.40	0.76 (0.017)	0.25



**Figure 1.** Regression coefficients ( $\pm 1$  SE) per parity for the regression of phenotypic (a) live weight and (b) BCS on EBV predicted from just linear type trait information (white bars), just carcass trait information (light gray bars), and both linear type traits and carcass information (dark gray bars).

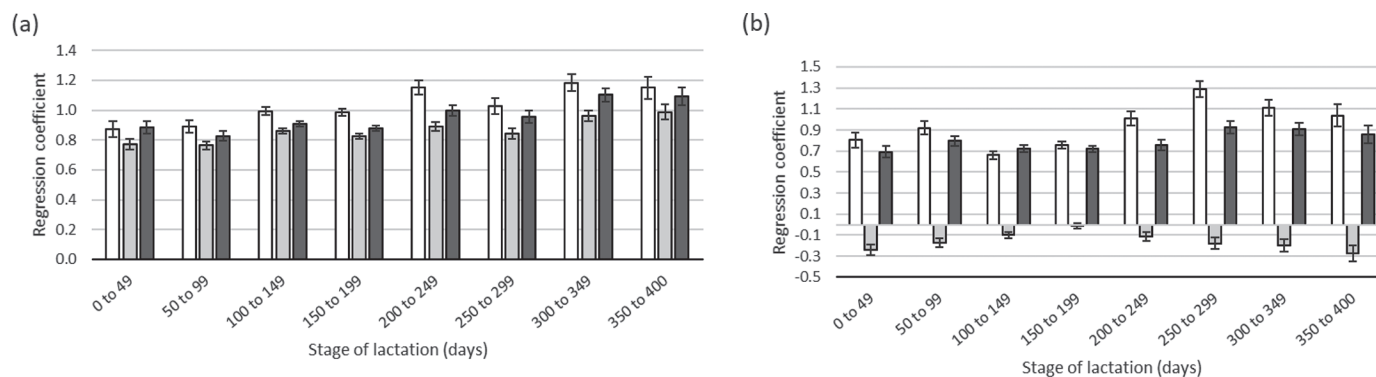
tions between the linear type traits and carcass traits in dairy cows, although estimates of phenotypic and genetic relationships between linear scores and carcass traits have been published in beef cattle (Conroy et al., 2009; Pabiou et al., 2012; Berry et al., 2019). Although the objective of the present study was not to quantify the usefulness of predicting cow carcass traits from linear assessments in live cows, the results from the present study demonstrated some predictive ability, as evidenced by the moderate genetic correlations between some of the linear type traits and the carcass traits.

The observed moderate to strong genetic correlations between many of the body-related linear type traits and live weight have already been documented in other dairy cow populations (Berry et al., 2004; Vallimont et al., 2010; Banos and Coffey, 2012). These moderate correlations were not surprising given that the body-related traits reflect biometric characteristics of the animal. Only Coyne et al. (2019) estimated genetic correlations between carcass traits and live weight in cows, although their study had a mixture of dairy and beef

cows and the live weight measure was within 7 d of the carcass weight measure. The mean (median) number of days between when the live weight was recorded and the cow slaughtered in the present study was 921 (575) days. Irrespectively, the genetic correlation of 0.81 between carcass weight and live weight in the present study was not much weaker than the genetic correlation of 0.99 reported by Coyne et al. (2019) between the same traits.

### Pros and Cons of Linear Type Trait Scores Versus Carcass Measures

The (potential for) readily accessible routine data on large populations of animals for both suites of predictor traits is a particular advantage for multitrait evaluations of live weight and BCS. The fact that the body-related linear scores (Brotherstone, 1994; Veerkamp et al., 2002; Berry et al., 2004) and carcass traits in cull cows (Coyne et al., 2019) are moderately heritable, and are genetically correlated with live weight and BCS



**Figure 2.** Regression coefficients ( $\pm 1$  SE) per stage of lactation for the regression of phenotypic (a) live weight and (b) BCS on EBV predicted from just linear type trait information (white bars), just carcass trait information (light gray bars), and both linear type traits and carcass information (dark gray bars).

(Table 2), imply that the coheritability (i.e., product of the square root of the heritability of both traits and the genetic correlation between them; Falconer and Mackay, 1996) with live weight or BCS is also moderately high. Individually, however, both suites of traits have their own particular pros and cons, and the relative importance of each argument for and against may also vary by population, or indeed over time. Of course, the main disadvantage of both strategies is that they are only a reflection of 1 moment in time, and are thus not useful for cow management purposes. Another disadvantage is that the reliability of EBV for the goal traits cannot be greater than the proportion of the genetic variance explained by the predictor traits. The type traits combined explained 91% and 70% of the genetic variance in live weight and BCS, respectively, and the corresponding percentages explained by the carcass traits was 89% and 49%.

Because linear type trait data are already collected as part of the service herdbooks offer, the data are already available with the cost of data acquisition incurred elsewhere; however, as the adoption of genomic evaluations intensifies globally, subsidization of linear assessments of first crop daughters of new AI bulls may erode. Although linear assessments can be undertaken for any parity, it is generally only first parity records that are included in national genetic evaluations, meaning the data are available early in life. This is particularly important as generation intervals in dairy cattle shorten (García-Ruiz et al., 2016) with the adoption of genomic evaluations. The traits scored and the phenotypic value represented by a given score for an individual linear trait in a given breed is consistent across jurisdictions, enabling Interbull to provide international genetic evaluations for each trait; therefore, these can subsequently be used to generate estimates of genetic merit for live weight even for animals with no information in a given country (Mark et al., 2007). International genetic evaluations directly for VBCS and angularity scored during the linear assessment actually already exist, both of which are strongly genetically correlated with BCS scored using tactile and visual cues (Table 2), and have been proven to be associated with phenotypic BCS scored on farm using the data mined in the present study (Berry and Kelleher, 2021). It is also important to note that because the linear type traits describe the morphological profile of the cow, it is possible to focus on particular characteristics of the animal (e.g., shorter animal but holding width and depth constant) when attempting to change live weight without necessarily having to indiscriminately select on live weight.

One shortcoming of linear type scores as an information source for use in genetic evaluations is that they

tend to only be scored in registered cows and, even at that, there can be selection bias in which animals are actually presented for assessment (Ring et al., 2018); preferential treatment of potential candidate bull dams could also bias the evaluations. Although linear assessment is undertaken in multiple breeds, harmonization across breeds of what traits are scored is lacking, but also the phenotypic value reflected by a given score of a trait can differ by breed, thus often making them not comparable across breeds. The subjective nature of linear assessment means that the scores can contain (random) error. Nonetheless, interclassifier differences in mean score and range of scores can be adjusted for in genetic evaluation models. For example, Banos and Coffey (2012) provided an equation for predicting phenotypic live weight in Holstein-Friesian dairy cows from linear score data; a 1-unit difference in scored stature, chest width, body depth, or angularity would translate into a mean error in predicting live weight in multiparous cows of 9.9, 9.1, 6.0, and 5.1 kg, respectively.

In an attempt to minimize the subjective nature of linear assessment and the range in the scale used by individual classifiers, Brotherstone (1994) rescaled the variance per classifier to a common variance. Veerkamp et al. (2002) estimated the genetic correlation between the scores for a given linear type trait (21 traits in total were investigated) for each of 18 professional classifiers of Holstein-Friesian primiparous cows with the scores of related animals from the other 17 classifiers. Even though the genetic correlations between classifiers were generally strong for the body traits (stature, rump width, and BCS were represented), some of the genetic correlations between an individual classifier and all others combined differed from 1 (Veerkamp et al., 2002); this was less of an issue for stature. Furthermore, interclassifier differences in heritability estimates for the same linear trait were also evident, suggesting issues with consistency of scoring for some classifiers (Veerkamp et al., 2002). It should nevertheless be noted that linear scores could potentially be objectively measured with developments in video and image capture along with associated downstream analytical techniques (Bewley et al., 2008), thereby mitigating some of the shortcomings. Nonetheless, should such a technology be used, it may be better to directly predict live weight and BCS rather than proxies.

Unlike linear type scores, which are generally only available on a specific segment of the dairy cow population, carcass information can be available on all culled animals (i.e., excludes cows that died on farm or were euthanized). Most of the carcass traits are objectively measured (e.g., video image analysis; Pabiou et al., 2011) as opposed to the subjective nature of linear type



traits. The carcass traits measured and the scale of measurement are the same across all breeds, although some of the traits measured, as well as their definition or scale (e.g., CC), can vary by jurisdiction. Nonetheless, although it is possible to generate carcass data for cull cows, these data are not always available for genetic evaluations. This could be due to a multitude of factors such as no data transfer between the meat processing plants and the genetic evaluation database, or the lack of an animal identification system to relate the phenotypic record to the animal, its pedigree, and its influencing environmental effects.

Although no international genetic evaluation currently exists for carcass traits in dairy cattle, this certainly does not preclude it from happening in the future. Similarly, international genetic evaluations for live weight are not outside the realm of possibility. Akin to the approach undertaken for the international fertility genetic evaluations in dairy cattle (Jorjani, 2007), countries would not necessarily have to submit exactly the same trait, but could instead submit data from correlated traits clustered by similarity to the carcass goal trait of interest. Exercises similar to the present study applied to other populations can help inform the best selection of such traits.

A big disadvantage of using carcass data is the delay in the acquisition of the data because it is only available on culled animals; this has implications for generating estimates of genetic merit for the cow herself (e.g., a bull dam) as well as the sire. Of the carcass data used in the present study, 12, 13, 14, 14, and 47% were from parity 1, 2, 3, 4, and 5+ cows, respectively. Nonetheless, once a sufficiently large reference population of genotyped and phenotyped animals are available, then genomic evaluations for carcass measures (or better still, live weight predicted from carcass measures) can mitigate this shortcoming.

Genetic evaluations rely on removing as much nuisance influences to the phenotypic variability as possible, ensuring that the EBV are independent of such effects; 1 model feature that has a large contribution to phenotypic variability is contemporary group. A contemporary group is a set of animals that have had an equal opportunity to perform (van Bebber et al., 1997); examples of contemporary groups in dairy cattle include herd-year-season of calving or herd-date of assessment or slaughter. Many cull cows are not directly sold off the dairy farm, but instead undergo a finishing period on another farm or unit to achieve a desired CF cover. Where cull cows are directly sold to meat processing plants from the dairy farm, they often undergo a fattening regimen, which can be specific to individual (groups of) animals. For example, 1 cow may be dried

off early and fattened on an energy-rich diet, and a contemporary cow in better condition may not need any fattening period. Being able to properly account for these animal-specific differences in the statistical model for genetic evaluations (i.e., definition of contemporary group of animals that were truly treated the same) can be challenging, thus influencing the EBV and any correlated traits.

### Exploitation Strategy

Irrespective of the challenges from the subjectivity of data (i.e., linear scores) or properly accounting for animal-specific treatments before slaughter (i.e., carcass data) along with other limitations, results from the present study clearly demonstrated the moderate genetic correlations between (some of) these traits with both live weight and BCS, which subsequently translated into phenotypic differences. Of particular interest in the present study was the contribution in predicting live weight using carcass records over and above that predicted using the linear type trait observations as previously advocated (Vallimont et al., 2010; Banos and Coffey, 2012), or if the carcass traits were, in themselves, a better predictor of cow live weight. Although the correlation between phenotypic live weight and live weight EBV predicted using carcass data was slightly stronger than that predicted using linear type traits data, the regression of phenotypic live weight on its EBV deviated to a greater extent from 1 in the former, with the effect of a joint estimation from both linear type trait data and carcass data being somewhere in between. Hence, there appeared to be little benefit of carcass records in predicting genetic merit for live weight over and above that already captured by the linear type traits; nonetheless, in the absence of linear type trait data, carcass records could be a good alternative. The correlation between the EBV for live weight predicted from just linear type traits data versus those predicted just for carcass data was 0.72.

Although carcass records contributed to the prediction of genetic merit, and subsequently phenotypic live weight, their usefulness in the prediction of BCS was less apparent (Tables 2 and 4). Unexpectedly perhaps, the weak genetic correlation between BCS and CF reflected the difference in definition of the 2 traits. The BCS is a measure of fat depth, generally along the lumbar and tail head region of the cow, and CF is a measure of the cover (as opposed to the depth) of fat across the entire carcass as well as within the thoracic cavity. Nonetheless, based on a genetic analysis of 5,172 growing animals of different sexes, Kelly et al. (2019) reported a genetic correlation of 0.84 between

CF (as measured in the present study) and ultrasound fat depth measured at the third lumbar vertebrae and 13th thoracic rib on live animals within 30 d of slaughter. This suggests that CF, in growing beef cattle at least, somehow reflects (indirectly) fat depth. Reasons for the apparent discrepancy in the present study include that the present study was on dairy cows, and that of Kelly et al. (2019) was on growing beef cattle. Moreover, the number of days between the ultrasound measure and the CF measure was <30 d in the study of Kelly et al. (2019), all undertaken by a single operator and originating from 1 farm with consistent herd management. In contrast, there was, on average, 921 d between the BCS measure and CF measure in the present study, and the BCS measures were both subjective and undertaken by many operators. Moreover, the cows originated from many different herds, were slaughtered at different stages of lactation, and were also likely exposed to different management strategies that could not be properly accounted for in the statistical model; such management strategies are likely to influence CF more than either carcass weight and conformation, thus having a lesser effect on the genetic correlation between carcass weight and live weight (the latter also recorded objectively). This was substantiated by the opposite (i.e., negative) association between phenotypic BCS and EBV for BCS when derived using just carcass data; the association was positive in older animals, reflecting the age of animal that contributed most to the carcass data.

Also of note was how the relationship between EBV for live weight and BCS with the respective phenotype differed both by parity (Figure 1) and stage of lactation (Figure 2). The increase in regression coefficients of phenotypic live weight on EBV for live weight as parity increased from first to third parity was most likely due to cows getting heavier from first to second to third parity, and remaining relatively stable thereafter (Berry et al., 2005). Little difference in regression coefficients of phenotypic BCS on EBV for BCS by parity was evident, although the regression coefficient was closest to the expectation of 1 for younger animals when predicted using the linear type traits; the linear type traits are scored on first parity animals. Generally, the weakest associations with both phenotypic live weight and BCS in very early lactation was likely attributable to the actual variability in the observed phenotype immediately postcalving, which may have been influenced by periparturient factors such as dystocia (Berry et al., 2007a) or metabolic diseases. Fifty-five percent of the linear assessments were undertaken between 100 and 199 d of lactation, coinciding with the period when the regression of phenotypic live weight on EBV for live weight predicted from the linear traits was closest to

the expectation of 1. Irrespective, however, of the variability in regression coefficients of phenotype on EBV across parities and stage of lactations, most did not deviate from 1, with the exception of BCS predicted from the carcass traits.

In conclusion, observations for both linear type traits and carcass traits are useful sources of information in the prediction of live weight and BCS in dairy cows. Although the strength and degree of association differed by stage of lactation and parity, prediction of live weight was more accurate than that for BCS. Moreover, live weight can be equally well predicted using linear type trait data or carcass data; in contrast, it is not recommended to predict BCS in dairy cows from carcass data alone. The implications of having more accurate estimates of genetic merit for live weight and BCS include the opportunity to accelerate genetic gain in both efficiency of production and resilience. Though considerable resources are being expended on the development of sophisticated technologies and approaches to predicting both efficiency and resilience measures, their adoption will be initially slow; the strategy proposed within, at the very least, can help bridge the gap in time until such technologies are widely used, with the resulting predictions being integrated into available genetic evaluations.

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