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Using cow carcass weight to select efficient cows in UK

Getinet M. Tarekegn[1], Harriet Bunning[2,]*, Marco Winters[2], Raphael Mrode[1,3], Mike Coffey[1]
[1]*Scotland's Rural College, Easter Bush Campus, Roslin Institute Building, EH25 9RG, UK;* [2]*Agriculture and Horticulture Development Board, Middlemarch Business Park, Siskin Parkway East, Conventry, CV3 4PE, UK;*
[3]*International Livestock Research Institute (ILRI), Naivasha Road, Nairobi, Kenya P.O.Box 30709*
*Corresponding author: *Harriet.Bunning@ahdb.org.uk*

Abstract

Breeding more efficient cows is important for both increased profitability and reduced environmental impact. Therefore, there is a need to estimate genetic merit for feed intake of cows. While direct measurement of feed intake is difficult, maintenance requirements which accounts for one third of the energy intake of a cow, can be adequately approximated using body weight. Mature cows are not usually weighed, but abattoirs do collect carcass weights of cull cows. Carcase weight varied between 268 kg and 400 kg. Heritability estimates of carcass weight, conformation and fat class of mature cows were calculated. Mature cows between 1 095 and 7 301 days of age were included in the study. A total of 4 721 cows with weight phenotypes were included, born between 1997 and 2020. A mixed linear animal model was fitted considering the cow, parity of the cow's dam, number of calvings per cow, breed and season of birth as fixed effects and coefficient of heterosis and recombination loss estimated from four breed groups as covariate effects. The study cows were traced back up to five generations in the pedigree that include 67 641 animals in total. The heritability estimates were generated using ASReml. The estimated heritabilities were 0.64 ± 0.01, 0.49 ± 0.10 and 0.44 ± 0.01 for carcass weight, carcass fat and conformation, respectively. The moderate to high heritability estimates observed in this study indicates there is cull cow carcass weight genetic variation to allow for genetic improvement and that when data for direct feed intake is limited, this trait in the meantime could be used as a proxy for cow feed intake and consequently, predicted methane emissions.

Key word: Carcass trait, Genetic parameter, Heritability, Mature cow

Introduction

Compared to historic breeding goals which focussed on increased production alone, increasing milk yield in dairy and growth rates in beef, modern breeding goals aim to increase overall efficiency and increasing production per unit of input. The impact of selection for increased production levels can be seen across dairy and beef across the globe. For example, in the past 50 years, the annual milk yield per cow increased from 1 000 kg to >11 000 kg in Canada and from 4 000 kg to ~12 000 kg in US (Cole et al., 2023). In the same period in the US, beef production increased by 25%, even while the number of cattle destined for beef production decreased by 6%, the latter percentage has been countered by a more than 30% increase in average cattle (mainly steers and heifers) weights (USDA, 2019).

However, the positive genetic correlations between both milk yield and growth rates with animal size (e.g. cow) (Ouataha et al., 2021) imply that selection focussed on production has increased the average mature cow size across beef and dairy (Rowan, 2022). Although these heavier cows have some benefits, including less ketosis, metabolic, infectious, and other diseases than lighter cows (Frigo et al., 2010), they also have increased feed requirements (Liinamo et al., 2012), meaning they cost more to feed and have a greater environmental impact (IPCC, 2019). For example, in dairy production, feed accounts up to 60% of the operating cost (European Commission, 2013). On the other hand, animals that consume more feed tend to produce more methane (CM4) on a daily basis (Crompton et al., 2011; de Haas et al., 2014). These all imply that our previous selection goals may have led to less efficient cows.

In order to breed for efficiency, a measure of cow size can be included as a trait in a selection index. Various strategies are used to measure cow size. Both liveweight and linear body measurements have been also used as selection indices for beef production in different countries like New Zealand, Australia and US. The use of some measures of body size and other linear body measurements instead of liveweight are used whenever there is absence of liveweight data (Haile-Mariam et al., 2014) as there are situations where animals do not have either liveweight records or any linear body measurements. This absence of liveweight records is very common for cows. However, interestingly abattoirs in countries like UK collect records for carcass traits of the animals slaughtered. These records can be used as a proxy for cow feed intake and consequently to predict methane emissions, liveweight prediction, genetic parameters estimation to help understand the genetic merits for cow size for efficient cows and evaluate breeding values of the carcass traits that can be later utilized for selection and improvement purposes by considering the traits in the selection index. In this preliminary study we estimated heritabilities for carcass weight, carcass conformation and carcass fat for mature cows of different breeds combined in UK.

Materials and methods

In this study, cows that include multiple beef, dairy and cross breeds with age in days above 1 095 days were considered as mature cows (Figure 1). Carcass traits that include carcass weight, carcass conformation and carcass fat were evaluated. Carcass conformation and fat were scored as the EUROP carcass classification (EEC Regulation N.1208/81 and N.2930/81; details present at Englishby et al., 2016). Carcass weight varied between 268 kg and 400 kg, defined based on the mean and standard deviation (µ ± SD) of extracted data, were considered in the study (Table 1). This range of the carcass weight is equivalent to the liveweight between 487 kg and 727 kg in an assumed killing out percentage of 0.55. The box plot distribution of the carcass weight by breed, parity of the cow's dam and number of calvings per cow is presented at the figure below (Figure 2). Heritability estimates of carcass weight, conformation and fat class of the mature cows (n = 4 721) were evaluated. These animals were born between 1997 and 2020 (Figure 3). Mixed linear animal model was fitted as follows considering sources of the cows, parity of the cow's dam, number of calvings per cow, breed and season of birth as fixed effects. In addition, heterosis and recombination loss estimates generated from four breed groups were fitted as covariate effects.

$$Y_{ijklmnopqr} = \mu + S_i + P_j + C_k + B_l + Se_m + H_{1n} + \ldots + H_{6n} + R_{1p} + \cdots + R_{6p} + a_q + e_{ijklmnopqr}\,, \qquad (1)$$

where, $Y_{ijklmnopqr}$= the analysed trait; µ = the overall mean; S_i is i^{th} source of the cows; P_j = j^{th}parity of the cow's dam (j = 1, …, 7; parities > 7 merged into the 7th parity); C_k is k^{th} number of calvings per cow (k = 1, …, 10; number of calvings > 10 were merged in to 10th calving); B_l is l^{th} breed (l = LIMX, CH, SMX, BRBX, AAX, HEX, BBX, BF, HF, LIM, HFX and HO); Se_m = m^{th} is season of birth of the cows (m = March–May, June–August, September–November, and December–February); H_{1-n} is estimates of coefficient of heterosis generated from four breed groups considered as covariate effect in the model; R_{1-n} is estimates of coefficient of recombination loss generated from four breed groups considered as covariate effect in the model; $a_q$is the random additive genetic effect of cow q with var (a), ~ ND (0, $\boldsymbol{A}\delta_a^2$), where ND is normally distributed, δ_a^2 is the additive genetic variance, $\boldsymbol{A}$ is the additive relationship matrix using pedigree information that was traced back five generations for 67641 animals in total; and $e_{ijklmnopqr}$ is the random residual variance with var (e), ~ IND (0, δ_e^2), where δ_e^2 is the residual genetic variance. The variance components were estimated using ASReml (Gilmour et al., 2015), and used to evaluate heritability estimates as:

$$h^2 = \delta_a^2/(\delta_a^2 + \delta_e^2) \qquad (2)$$

The coefficient of heterosis (Het) and recombination loss (Rec) were calculated for all animals using the formulae derived by VanRaden and Sanders (2003):

$$Het = 1 - \sum_{k=0}^{n} Sire_i \ x \ Dam_j \qquad (3)$$

$$Rec = 1 - \sum_{k=0}^{n} (Sire_i^2 + Dam_j^2)/2 \qquad (4)$$

where, $Sire_i$ and Dam_j are the proportion of breed i and breed j in the sire and dam, respectively

Table 1. Descriptive statistics of carcass weight by breed

Breed*	N	µ±SD	Max.	Min.
HF	738	319.26 ± 31.60	399.8	268.2
LIM	695	338.97 ± 33.84	399.9	269.5
HFX	673	320.48 ± 32.88	399.7	268.1
BRBX	736	348.20 ± 32.83	400.0	268.2
HEX	766	326.30 ± 33.57	399.3	268.3
AAX	734	330.38 ± 34.84	399.9	268.4
BBX	798	342.97 ± 32.62	399.9	269.3
HO	738	322.53 ± 32.62	399.8	268.3
CH	435	351.65 ± 34.23	400.0	268.1
BF	664	314.58 ± 29.78	398.1	268.1
LIMX	791	338.95 ± 33.14	400.0	268.1
SMX	796	334.82 ± 33.75	399.8	269.1

*LIMX=Limousin cross; CH=Charolais; SMX=Simental cross; BRBX=British Blue Cross; AAX=Aberdeen Angus Cross; HEX=Hereford Cross; BBX=Belgian Blue cross; BF=British Friesian; HF=Holstein-Friesian; LIM=Limousin; HFX=Holstein-Friesian cross; HO=Holstein; Max= maximum; Min=minimum

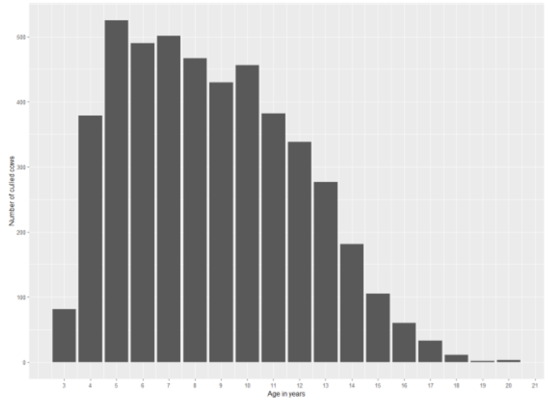

Figure 1. Distribution of culled mature cows by age at slaughter

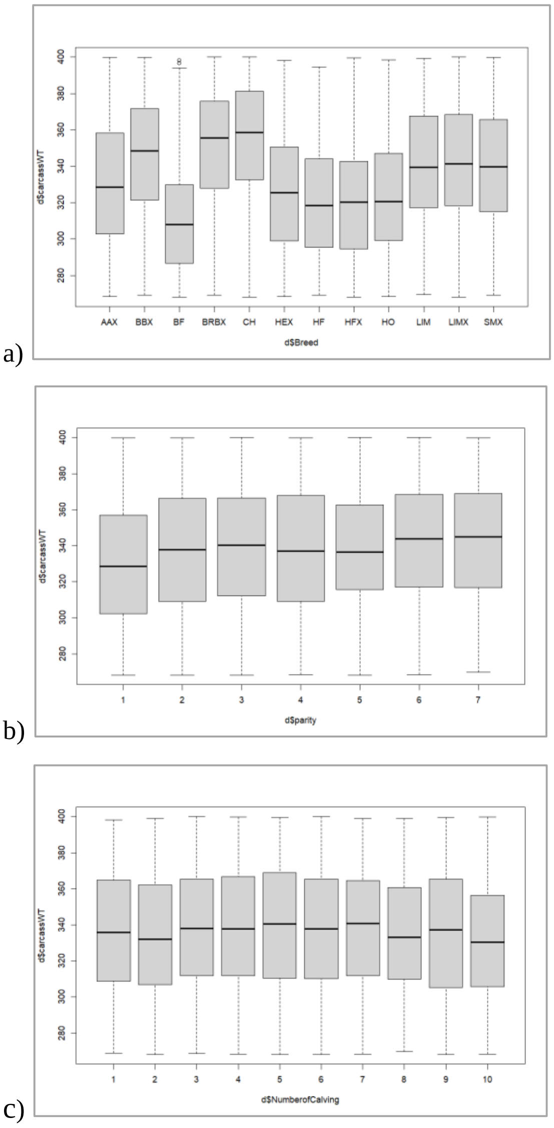

Figure 2. Distribution of carcass weight by: a) breed; b) parity of the cow's dam; c) number of calvings per cow

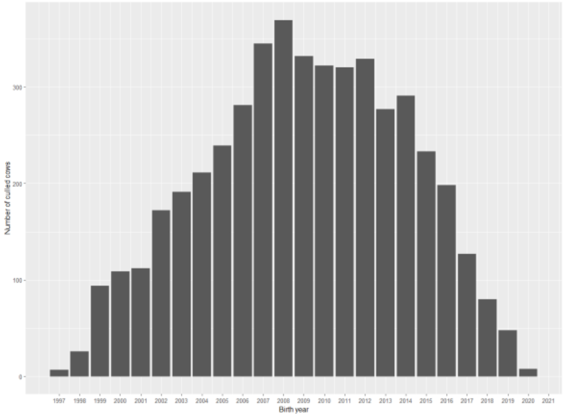

Figure 3. Distribution of culled mature cows by year of birth

Results and Discussion

The average carcass weight considering all breeds was 332.42 ± 33.0 kg. The breakdown of average carcass weight by breed is present in the table (Table 1). It is not a surprise that the beef origin mature cows showed heavier carcass weight over the dairy type, as carcass weight reflects lifetime growth (Pabiou et al., 2011a) and lifetime growth varies between breeds and breed types. Heritability estimates of the carcass traits are depicted in the table (Table 2). The result indicated high heritability estimate ($h^2 = 0.64$) for carcass weight of mature cows, followed by carcass fat ($h^2 = 0.49$) and carcass conformation ($h^2 = 0.44$). The genetic parameter estimates for carcass conformation and carcass fat obtained in the present study go in line with the previous studies reported for other cattle populations (Kause et al., 2015; Pabiou et al., 2009, 2011b). Similarly for carcass weight, comparable heritability estimate was reported for Black cattle in Japan ($h^2 = 0.70$) (Hoque et al., 2006) and Charolais sire groups in Ireland ($h^2 = 0.65$) (Hickey et al., 2007). Whereas, in breed specific evaluation of the beef breeds, moderate heritabilities were reported for carcass weight (h^2 = 0.39 to 0.48), for conformation (h^2 = 0.30 to 0.44) and carcass fat (h^2 = 0.29 to 0.44) in Finland (Kause et al., 2015).

Table 2. Heritability (h^2) and standard error (SE) estimates of carcass traits of mature cows

Trait	Variance components		$h^2 \pm SE$
	δ_a^2	δ_e^2	
CWT[1]	664.778	375.357	0.64 ± 0.01
CC[2]	30.9875	38.6982	0.44 ± 0.01
FC3	22.6136	23.5714	0.49 ± 0.10

[1]CWT=Carcass weight; [2]Carcass conformation; [3]FC=Fat class; δ_a^2= Additive variance; δ_e^2= Residual variance; h^2 = heritability; SE=Standard error

However, compared with the current study lower and wider range of estimates of heritability were reported for carcass traits (carcass weight: h^2 = 0.24 to 0.42; conformation: h^2 = 0.08 to 0.34; fat score: h^2 = 0.16 to 0.40) for Irish beef herds that included heifers, steers and young bulls (Englishby et al., 2016) where the highest heritability estimate was observed for heifers (age in days: 420 to 970 days) compared to steers and young bulls. Similar range of heritability estimates for carcass conformation and fat were previous reported for sire groups of eight beef breeds in Irland (Hickey et al., 2007) unlike to the highest heritability estimates (Carcass conformation: h^2 = 0.78; carcass fat: 0.63) for pooled data of dairy and beef breeds still in Irland in later study (Pabiou et al., 2009).

In the current study we observed that the carcass traits evaluated are highly heritable and this suggests in helping to improve and maximize the response to selection if the carcass traits are considered in the breeding program. However, we pooled the data set from different breeds together that may shadow to provide full picture of breed specific evaluation as there is huge variation between breeds on the heritability estimates of these traits (Hickey et al., 2007; Pabiou et al., 2009; Englishby et al., 2016).

Overall, to our knowledge evaluating genetic parameters for mature cows is the first work that could provide insights on the importance of this group of animals for efficient cow selection specially when data for direct feed intake is limited. Moreover, the carcass traits for this group of animals demonstrated high heritability and may encourage to use for the purpose of genetic evaluation in the breeding programs. However, evaluating these traits for each breed separately could help to provide breed specific estimates for effective breed specific breeding management decision. It is also important to note that the carcass data collected in UK abattoirs can serve as a proxy of cow liveweight prediction and feed intake.

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