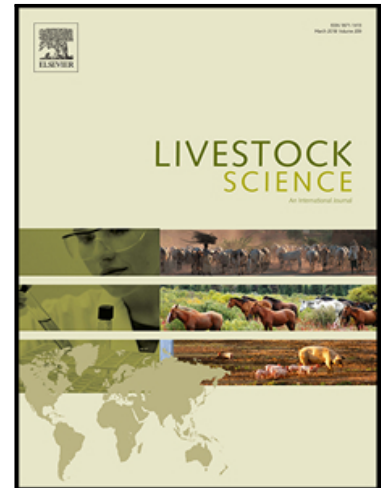


## Journal Pre-proof

The use of subjectively assessed muscular and skeletal traits on live cattle to aid in differentiation between animal genetically divergent in carcass kill out metrics

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PII: S1871-1413(19)30523-2  
DOI: <https://doi.org/10.1016/j.livsci.2020.103984>  
Reference: LIVSCI 103984



To appear in: *Livestock Science*

Received date: 12 April 2019  
Revised date: 28 February 2020  
Accepted date: 29 February 2020

Please cite this article as: D.P. Berry , J.M. Coyne , J. Doyle , R.D. Evans , The use of subjectively assessed muscular and skeletal traits on live cattle to aid in differentiation between animal genetically divergent in carcass kill out metrics, *Livestock Science* (2020), doi: <https://doi.org/10.1016/j.livsci.2020.103984>

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## HIGHLIGHTS

- Subjective measures of muscularity on live animal can predict, with some accuracy, genetic merit for kill out-related metrics
- The maximum accuracy of selection for kill out percent achievable from selection on the subjective assess development of hind quarter is 0.60
- Selection for increased muscularly, while increasing both live-weight and carcass weight simultaneously, with will increase the latter faster thus contributing to greater kill out percent

Journal Pre-proof

**The use of subjectively assessed muscular and skeletal traits on live cattle to aid in differentiation between animal genetically divergent in carcass kill out metrics**

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**ABSTRACT**

Subjective linear scoring of live beef cattle is routinely undertaken as part of breed society regulations or as part of national breeding programs; linear scores describe biological extremes of animals for a range of different traits reflecting muscularity, skeletal development, and functionality. The objective of the present study was to quantify the usefulness of these linear scores measured on live growing beef cattle to predict genetic merit for kill out (KO) percent and the difference between live-weight at slaughter and carcass weight (herein known as KO difference). The data used consisted of linear scores for 16 traits on up to 67,167 cattle as well as KO information on 31,827 cattle; 1,166 animals had records for both sets of traits. Variance components were estimated using univariate animal linear mixed models while covariance components between the linear scores and the KO traits were estimated using a series of bivariate sire linear mixed models. In an additional series of analyses, the KO metrics were adjusted phenotypically for differences in live-weight at slaughter through its inclusion as a covariate in the statistical model. Heritability estimates of the linear scores varied from 0.06 (width at pins) to 0.37 (development of hind-quarter); the heritability of KO percent and KO difference were estimated to be 0.53 and 0.37, respectively. Both the phenotypic and genetic correlations between the muscular type traits and KO percent were moderately positive, albeit the genetic correlations were stronger. The phenotypic correlations ranged from 0.27 (development of inner thigh) to 0.37 (development of hind quarter) while the genetic correlations varied from 0.40 (development of inner thigh and development of loin) to 0.60 (development of hind quarter); in all cases, adjusting for differences in live-weight at slaughter had minimal impact on the estimated correlations. With the exception of depth of rump, the phenotypic and genetic correlations between the skeletal traits with KO percent were all close to zero ( $\leq |0.24|$ ) irrespective of whether or not differences in live-weight at slaughter were accounted for. While the genetic correlations between the muscular traits and KO difference not adjusted for differences in live-weight at slaughter were all close to zero ( $\leq |0.30|$ ), the correlations strengthened ( $\geq |0.39|$ ) once adjusted to a common live-weight at slaughter. The opposite was true for the genetic correlations between the skeletal traits and KO difference. In all, the results suggest that the muscular linear scores assessed subjectively on live animals at, on average, 10 months of age are a useful genetic (and phenotypic) predictor of KO percent at, on average, 21 months of age, but also the quantity of live-weight that does not end up as carcass, once adjusted to a common live-weight.

**Keywords:** fifth-quarter, heritability, correlation, selection index

## 1. Introduction.

Data collection, whatever the phenotype, incurs a cost, and thus any additional useful information which can be garnered from the data should be welcomed. Linear classification of live cattle has been undertaken since the early twentieth century as a means of describing the physical characteristics of an animal on a linear scale from one extreme to another. While linear classification of dairy cattle is generally undertaken only on females in first lactation (i.e., 2 to 4 years of age; Berry et al., 2004; Veerkamp and Brotherstone, 1997), the majority of linear classification in beef cattle, at least in Ireland, are undertaken when the animal is between 6 and 16 months of age (Doyle et al., 2018). Furthermore, unlike in dairy cattle, linear classification in beef cattle is undertaken on both sexes. This information therefore provides a potentially rich early source of information on future performance metrics; this is especially true because linear scores on beef cattle are moderately heritable (Doyle et al., 2018) and do not require the animal to be sacrificed, a feature which is particularly important when measured on candidate parents of the next generation.

Linear type traits in beef cattle have heretofore been demonstrated, in a whole range of different populations and breeds, to be genetically correlated with animal live-weight (McHugh et al., 2012), average daily gain (Riley et al., 2002), feed intake and efficiency (Crowley et al., 2011), carcass weight (Pabiou et al., 2012) and carcass conformation (Berry et al., 2019) as well as individual carcass primal cuts (Berry et al., 2019). Little, however, is known of the usefulness in multi-trait genetic evaluations of including linear type trait information on young animals as predictors of genetic merit for kill out (KO) percent. Coyne et al. (2019) and Pariacote et al. (1998) both documented the presence of heritable genetic variability in KO in beef cattle. Coyne et al. (2019) proceeded to define a novel trait reflecting the difference, in kilograms, between the carcass weight and live-weight of an animal at slaughter. Coyne et al. (2019) termed this trait dressing difference (this trait will be termed KO difference in the present study) and stated that it is similar to the more familiar fifth quarter weight (Simões et al., 2005) except that KO difference includes the weight of the both the gut contents and blood. Like any slaughter trait, the actual KO percent or KO difference phenotype is not available until the animal is slaughtered, which is not obviously realistic for breeding animals. Even if based on information from relatives, waiting for the KO information from progeny delays genetic gain as the pursuit of high accuracy of genetic selection necessitates a longer generation interval, while shortening the generation interval can only be achieved with a relatively low accuracy of selection. The objective, therefore, of the present study was to quantify the information content of routinely recorded linear type traits on live animals within the framework of a multi-trait genetic evaluation for KO percent and difference. Should (some of) the linear type traits be informative, then they may be useful early predictors of the genetic merit for KO-related traits in

young candidate parents of the next generation. Furthermore, the moderate to high heritability of KO-related traits in young cattle (0.35 to 0.48; Coyne et al., 2019) implies that the true breeding value of an animal (e.g., at birth) is a relatively good reflection of its future phenotypic value and thus has merit in animal management and sale.

## 2. Materials and Methods

The data used in the present study were obtained from a pre-existing database managed by the Irish Cattle Breeding Federation (ICBF). Therefore, it was not necessary to obtain animal care and use committee approval in advance of conducting this study. The data and data editing procedures, as well as the justifications for such, are outlined in detail by Coyne et al. (2019) for the KO traits and by both Berry et al. (2019) and Doyle et al. (2018) for the linear type traits.

### 2.1. Kill out percent and kill out difference

Carcass data were available on 13,929,856 animals slaughtered between the years 2008 to 2018, inclusive; this represents the vast majority of slaughtered animals in Ireland during this time period. At least one live-weight record was also available on 3,308,415 of the animals with carcass data. Only bulls slaughtered between 14 and 24 months of age, and steers and heifers slaughtered between 14 and 36 months of age were retained. Animals in the present study were classified as having either been born in a dairy or beef herd; whether a herd was deemed to be dairy or beef was based on the breed composition of the cows in that herd (Ring et al., 2018). Only singleton animals with a known sire and at least one live-weight record within 7 days of slaughter were considered further; data on 126,366 animals remained. Animals that moved herds more than 4 times during their life-time or that resided for less than 70 days in the herd from which they were slaughtered were discarded. Kill out percent was defined as carcass weight divided by the final live-weight record of the animal (i.e., within 7 days of slaughter) and only animals with a KO percent between 40% and 70% were retained. Kill out difference was defined as the final live-weight record of the animal (i.e., within 7 days of slaughter) minus its carcass weight. Contemporary groups for the KO traits of herd-sex-year-season of slaughter were defined based on an algorithm used in the Irish national genetic evaluation (Berry and Evans, 2014; McHugh et al., 2014). Within each herd, animals of the same sex were clustered together based on the proximity of their slaughter dates ( $\leq 10$  days); if there were  $< 10$  animals in the initial cluster, then the group was amalgamated with an adjacent group. This process was repeated, until there was  $\leq 30$  days between the initial and final slaughter date for the group. Contemporary groups with less than 5 animals were removed. The final KO dataset consisted

for 31,827 animals (9,414 heifers and 22,413 steers) from 3,566 contemporary groups originating from 1,446 herds.

## 2.2 Linear type trait data

Individual animal records on 6 muscular and 10 other traits, which included skeletal linear traits, body condition score and docility, were available on 157,840 animals classified between 6 and 16 months of age during the 15-year period between 2004 and 2018. The 6 muscular traits, which were recorded on a 1 to 15 scale, included development of hind quarter, loin development, thigh width, development of thigh, width at withers, and width behind withers. The 10 other traits including skeletal traits, recorded on a scale of 1 to 10, were chest depth, chest width, height at withers, pelvic length, length of back, thickness of bone, body condition score, depth of rump, width at pins and width at hips. All animals had to have a sire known, and only data from herd-dates with at least 10 animals classified were retained. Contemporary groups for the linear type traits were defined as herd-date of assessment as per Doyle et al. (2018). Following edits, data were available on 70,074 animals in 1,126 herds. A total of 1,166 of these animals also had information on KO.

## 2.3 Non-additive genetic effects

A general coefficient of heterosis and the coefficient of recombination loss were calculated for each animal as:

$$1 - \sum_{i=1}^n \text{sire}_i \cdot \text{dam}_i \quad (\text{VanRaden, 1992})$$

and

$$1 - \sum_{i=1}^n \frac{\text{sire}_i^2 + \text{dam}_i^2}{2} \quad (\text{VanRaden and Sanders, 2003})$$

respectively where  $\text{sire}_i$  and  $\text{dam}_i$  are the proportion of breed  $i$  in the sire and dam, respectively. The heterosis coefficient for each animal was subsequently categorised into 0%, >0 and ≤10%, >10% and ≤20%, ... >90% and <100%, and 100%. The general recombination loss coefficient for each animal was categorised as 0%, >0 and ≤10%, >10% and ≤20%, >20% and ≤30%, >30% and ≤40%, >40% and ≤50%, and >50%.

## 2.4 Estimation of genetic and residual (co)variance components

The statistical model presented by Berry et al. (2019) was used for the estimation of the residual and genetic variance components for the linear type traits while the models described by Coyne et al. (2019) was used for the KO-related traits. All variance components were estimated using animal linear mixed models in the ASReml software suite (Gilmour et al., 2009). The fitted model for the linear traits was:

$$Y_{ijklmnp} = CG_j + \text{gender}_k * \text{age}_l + \text{heterosis}_m + \text{recombination}_n + \text{animal}_i + e_{ijklmnp}$$

where  $Y_{ijklmnp}$  is the linear score of animal  $i$ ,  $CG_j$  is the contemporary group  $j$  of herd-date of scoring,  $\text{gender}_k$  is the  $k$ th gender of animal  $i$  (male or female),  $\text{age}_l$  is the age  $l$  at linear classification,  $\text{heterosis}_m$  is the heterosis coefficient value  $m$  (0%, >0 and  $\leq 10\%$ , >10% and  $\leq 20\%$ , ... >90% and <100%, and 100%) of animal  $i$ ,  $\text{recombination}_n$  is the recombination coefficient value  $n$  (0%, >0 and  $\leq 10\%$ , >10% and  $\leq 20\%$ , >20% and  $\leq 30\%$ , >30% and  $\leq 40\%$ , >40% and  $\leq 50\%$ , and >50%) of animal  $i$ ,  $\text{animal}_i$  is the random direct additive genetic component of animal  $i$   $N(0, \mathbf{A}\sigma_a^2)$ , and  $e_{ijklmnp}$  is the random residual term  $N(0, \mathbf{I}\sigma_e^2)$  where  $\sigma_a^2$  is the additive genetic variance,  $\sigma_e^2$  is the residual variance,  $\mathbf{A}$  is the numerator relationship matrix and  $\mathbf{I}$  is an identity matrix. The fitted model to the two KO-related traits was:

$$y_{ijklmnop} = CG_j + \text{gender}_k * \text{age}_l + \text{heterosis}_m + \text{recombination}_n + \text{days}_o + \text{animal}_i + e_{ijklmnop}$$

where  $y_{ijklmnop}$  is either the KO percent or KO difference of animal  $i$ ,  $CG_j$  is the contemporary group  $j$  of herd-year-sex-season of slaughter,  $\text{gender}_k$  is the  $k$ th gender of animal  $i$  (bull, steer or heifer),  $\text{age}_l$  is the age  $l$  at slaughter,  $\text{heterosis}_m$  is the heterosis coefficient value  $m$  (0%, >0 and  $\leq 10\%$ , >10% and  $\leq 20\%$ , ... >90% and <100%, and 100%) of animal  $i$ ,  $\text{recombination}_n$  is the recombination coefficient value  $n$  (0%, >0 and  $\leq 10\%$ , >10% and  $\leq 20\%$ , >20% and  $\leq 30\%$ , >30% and  $\leq 40\%$ , >40% and  $\leq 50\%$ , and >50%) of animal  $i$ ,  $\text{days}_o$  is the number of days between the date of last recorded live-weight and the slaughter date of animal  $i$ ,  $\text{animal}_i$  is the random direct additive genetic component of animal  $i$   $N(0, \mathbf{A}\sigma_a^2)$ , and  $e_{ijklmnop}$  is the random residual term  $N(0, \mathbf{I}\sigma_e^2)$  where  $\sigma_a^2$  is the additive genetic variance,  $\sigma_e^2$  is the residual variance,  $\mathbf{A}$  is the numerator relationship matrix and  $\mathbf{I}$  is an identity matrix. In all instances, the pedigree of all animals was traced back to the founder population which was allocated to genetic groups based on breed.

The genetic correlations between the linear type traits and all of carcass weight, live-weight at slaughter and the KO-traits were estimated using a series of bivariate sire linear mixed models; fixed effects in the models were those described for the univariate analyses. In a supplementary series of analyses, the genetic correlations between the linear type traits and the KO traits were estimated with the latter adjusted phenotypically for differences in live-weight at slaughter through the inclusion of phenotypic live-weight at slaughter as a covariate in the mixed model.



### 3. Results

The number of records per linear type trait is in Table 1. The mean (median) age of the animals at linear assessment and at slaughter was 295 days (285 days) and 649 days (635 days), respectively; the mean age at slaughter for the bulls, steers and heifers was 538, 771 and 651 days, respectively.

The heritability of the muscular linear type traits (Table 2) varied from 0.24 (development of loin) to 0.37 (development of hind quarter); heritability estimates for the remaining linear type traits varied from 0.06 (width at pins) to 0.34 (height at withers). The heritability for KO percent and KO difference was 0.53 (0.03) and 0.37 (0.03), respectively. The phenotypic correlations between the muscular traits with both carcass weight and live-weight varied from 0.19 to 0.31 and from 0.10 to 0.23, respectively (Table 2); the respective ranges in genetic correlations were from 0.22 to 0.38 and from 0.00 to 0.24 (Table 2). The mean of the phenotypic correlations between the remaining linear scores and both carcass weight and live-weight was 0.29 and 0.43, respectively; the mean of the genetic correlations was 0.30 and 0.46, respectively (Table 2).

#### 3.1 Correlations with kill out traits

The phenotypic correlations between each of the linear type traits and both KO percent and KO difference are in Table 1; both the raw correlations (after adjustment for fixed and random effects in the model) as well as the correlations adjusted to a common live-weight at slaughter are presented. The correlations between the muscular type traits and KO percent ranged from 0.23 (width at withers) to 0.37 (development of hind quarter); adjusting for differences in live-weight at slaughter had minimal impact on the estimated correlations. The correlations between the skeletal traits and KO percent varied from -0.14 (thickness of bone) to 0.17 (width at hips) irrespective of whether or not live-weight at slaughter was adjusted for in the statistical model. While the unadjusted correlations between the muscular traits and KO difference were all close to zero (-0.07 to 0.07), following adjustment to a common live-weight at slaughter, they strengthened varying from -0.36 (development of hind quarter) to -0.22 (width at withers). In contrast, the phenotypic correlations between the skeletal traits and KO difference weakened, and in almost instances changed from positive to negative, once adjusted to a common live-weight at slaughter.

The genetic correlations between the muscular traits and both KO traits had the same sign, albeit stronger than their corresponding phenotypic correlations (Table 3); the exception was the correlations with unadjusted KO difference which were all close to zero phenotypically and genetically. A point of note is that the correlation between the type traits and KO difference

adjusted to a common live-weight is equivalent, albeit opposite in sign, to the correlation between that type trait with carcass weight adjusted to a common live-weight.

#### 4. Discussion

While several previous studies have reported genetic correlations between linear type traits in beef cattle with feed intake and efficiency (Crowley et al., 2011), live-weight (McHugh et al., 2012), and carcass merit (Pabiou et al., 2012), no study in cattle has reported on the phenotypic or genetic correlations between subjectively scored muscular traits in a multi-breed population of live beef cattle with subsequent KO metrics. Using a dataset of 18,479 young Irish cattle from 653 herds, Coyne et al. (2019) documented the contribution of genetic and non-genetic effects to differences in both KO percent and KO difference. Coyne et al. (2019) proceeded with discussing the importance of both metrics from an animal production perspective. The energetic cost of growing and maintaining a kilogram of live-weight, which eventually does not end up as saleable carcass, can be considerable, so therefore increasing carcass weight while minimising the remainder of live-weight is advantageous. While this is the objective of the KO percent trait, as a trait, it does not provide any information on the actual carcass weight itself as well as suffering from the mathematical properties of being a ratio trait and the known complications of such in breeding programs (Sutherland, 1965).

The two main factors hindering accurate genetic evaluations for either KO metric, and by extension, genetic gain, is a) routine access to sufficient data from which to generate accurate genetic evaluations, and b) the time lag required to obtain the phenotypes since the animal must be slaughtered in order to obtain information on KO. The latter also has implications for breeding programs since the animal must be sacrificed to generate the phenotype and thus, unlike traits like gestation length, calving difficulty or yearling weight, a KO phenotype on a candidate sire will not be available. Given the age at linear scoring and slaughter in the present study, linear score data are available, on average, almost one year earlier. The impact is a potentially shorter generation interval. This is particularly important in seasonal breeding systems, as exist in Ireland (Berry and Evans, 2014), especially those that adopt genomic selection. Calving in Irish dairy (Berry et al., 2013) and beef (Berry and Evans, 2014) herds peaks around March with breeding peaking in April and May; animals are slaughtered throughout the year (McHugh et al., 2010). Hence, having more accurate genetic evaluations based on phenotypic data on young genomically-tested bulls for a breeding season without necessarily having to wait for the slaughter data, can contribute to the bulls being used at least one year earlier. The importance of short generation intervals in accelerating genetic gain is well established (Rendel and Robertson, 1950).

#### **4.1. Muscularity traits**

While there is a general consensus that breeds of greater muscularity (e.g., continental type breeds) tend to kill out better than those breeds of traditionally poorer muscularity like the British breeds of Angus (Albertí et al., 2008; Coyne et al., 2019), the present study adjusted for such breed differences via genetic groups in the numerator relationship matrix; hence the correlations reported in the present study between the muscular traits and KO percent are all within breed. Nonetheless, even within breed, genetically more muscular animals had a superior KO percent and this was true even when adjusted to a common live-weight at slaughter. While selection for increased muscularity is expected to, on average, increase both live-weight and carcass weight (Table 2), it will, on average, increase carcass weight proportionally more as evidenced by the negative genetic correlation with KO difference, substantiated by the stronger genetic correlation with carcass weight than with live-weight (the genetic variance for both carcass weight and live-weight is similar). Genetically, in fact, 36% of the variability in KO percent was attributable to differences in just the development of hind quarter scored subjectively as a linear trait, on average, almost one year earlier than when the animal was slaughtered. Based on the parameters estimated in the present study, the accuracy of selection for KO percent and KO difference (adjusted to a common carcass weight) for a bull with just his own phenotypic record for development of hind quarter (most strongly genetically correlated with the KO traits) would be 0.37 and 0.36, respectively; having also phenotypic records for development of hind quarter on 10 progeny would increase the accuracy to 0.48 and 0.46, respectively. Hence, there is merit in using linear scores to help identify animals, at a young age, that excel genetically for KO traits.

#### **4.2 Skeletal traits**

The positive phenotypic correlations between the skeletal traits and unadjusted KO difference implies that animals with greater skeletal scores (i.e., larger framed animals) have a greater difference between their live-weight and carcass weight, or in other words, this larger frame is contributing to more matter which is not part of the eventual carcass. Interestingly, once adjusted for differences in live-weight at slaughter, the phenotypic correlations with KO percent were near zero implying that carcass weight and KO difference were both increasing at approximately the same rate which is not overly surprising given that the phenotypic correlations between the skeletal traits with carcass weight were similar to the correlations between the skeletal traits and live-weight (Table 2). This conclusion was further verified when the correlation between the skeletal traits and KO difference was adjusted to a common live-weight; the correlations weakened to all be close to zero (and mostly negative). Given that the trend in genetic correlations between the skeletal traits

and both KO traits (unadjusted or adjusted) correlations was similar to the respective phenotypic correlations, the conclusions drawn also apply to breeding programs. Selection for larger framed animals will result in heavier live-weight, consistent with reported elsewhere (Riley et al., 2002), but will also result in heavier carcasses, also reported elsewhere (Riley et al., 2002); the net impact is minimal effect on KO percent, yet a heavier KO difference. One trait which noticeably differed from the other skeletal trait was thickness of bone which was negatively genetically correlated with KO percent; while not different from zero ( $P>0.05$ ), it was different from some of the genetic correlations between the other skeletal traits and KO percent.

In conclusion, the moderate genetic correlations between the muscular linear scores and KO percent, coupled with their availability early in life and without the necessity to sacrifice the animals, point to their usefulness in a breeding program to help achieve accurate genetic evaluations for KO percent. Of course, the maximum accuracy achievable reaches a plateau depending on how much of the genetic variability in KO percent can be explained by difference in genetic merit for the linear traits. In the case of development of hind quarter, the maximum accuracy of selection for KO percent is 0.60 (i.e., the genetic correlation between development of hind quarter and KO percent).

#### **Funding**

This publication has emanated from research supported by a research grant from Science Foundation Ireland and the Department of Agriculture, Food and Marine on behalf of the Government of Ireland under the Grant 16/RC/3835 (VistaMilk).

#### **Conflicts of interest**

No conflicts of interest.

#### **Ethical approval**

No approval was required for this study as the genotype data used had been previously collected by the Irish Cattle Breeding Federation for commercial use.

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Table 1. Number of records (N), mean (raw standard deviation) as well as the phenotypic correlations between kill out percent (KO%) or kill out difference (KO diff) with each linear type trait either as raw correlations or partial correlations after adjusting for differences in live-weight at slaughter

Trait	N	Mean (SD)	Raw		Adjusted	
			KO %	KO diff	KO %	KO diff
<i>Muscular</i>						
Development of hind quarter	67162	8.24 (1.73)	0.37	-0.07	0.37	-0.36
Development of loin	67167	8.32 (1.75)	0.24	0.02	0.25	-0.24
Thigh width	67159	9.20 (2.37)	0.31	0.07	0.32	-0.33
Development of inner thigh	43871	10.28 (2.86)	0.27	-0.02	0.28	-0.28
Width at withers	51773	8.31 (1.83)	0.23	0.03	0.24	-0.22
Width behind withers	66733	7.58 (1.65)	0.30	0.01	0.31	-0.31
<i>Skeletal &amp; other</i>						
Width of chest	43876	5.78 (1.01)	0.10	0.23	0.12	-0.15
Depth of chest	43872	6.46 (0.98)	0.00	0.32	0.01	-0.05
Height of withers	67161	5.71 (1.23)	0.00	0.37	0.02	-0.05
Length of pelvis	51773	6.19 (1.05)	0.04	0.28	0.05	-0.08
Length of back	66729	6.45 (1.12)	0.07	0.29	0.09	-0.11
Width at hips	66726	5.58 (1.06)	0.15	0.23	0.17	-0.18
Thickness of bone	43876	5.69 (1.13)	-0.14	0.19	-0.13	0.11
Depth of rump	42235	6.06 (1.06)	0.01	0.40	0.03	-0.08
Width at pins	43873	4.95 (1.07)	0.10	0.06	0.11	-0.12
Body condition score	52536	5.07 (1.29)	0.16	0.11	0.17	-0.17

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Table 2. Genetic standard deviation (SD) and heritability estimates for each type trait as well as their phenotypic and genetic correlations (standard errors in parenthesis) with carcass weight and live-weight immediately prior to slaughter.

Trait	Genetic SD	Heritability	Carcass weight		Live-weight	
			Phenotypic	Genetic	Phenotypic	Genetic
<i>Muscular</i>						
Development of hind quarter	0.62	0.37 (0.01)	0.21 (0.02)	0.24 (0.07)	0.10 (0.02)	0.00 (0.08)
Development of loin	0.54	0.24 (0.01)	0.19 (0.02)	0.31 (0.08)	0.13 (0.02)	0.20 (0.09)
Thigh width	0.62	0.27 (0.01)	0.31 (0.02)	0.38 (0.07)	0.23 (0.02)	0.24 (0.08)
Development of inner thigh	0.59	0.27 (0.01)	0.23 (0.08)	0.28 (0.09)	0.14 (0.08)	0.15 (0.09)
Width at withers	0.52	0.25 (0.01)	0.19 (0.03)	0.22 (0.09)	0.13 (0.04)	0.16 (0.10)
Width behind withers	0.52	0.25 (0.01)	0.24 (0.02)	0.33 (0.08)	0.16 (0.02)	0.17 (0.08)
<i>Skeletal &amp; other</i>						
Width of chest	0.29	0.17 (0.01)	0.37 (0.06)	0.36 (0.10)	0.36 (0.07)	0.36 (0.10)
Depth of chest	0.29	0.19 (0.01)	0.34 (0.07)	0.52 (0.09)	0.38 (0.07)	0.57 (0.08)
Height of withers	0.47	0.34 (0.01)	0.35 (0.02)	0.44 (0.07)	0.40 (0.02)	0.52 (0.07)
Length of pelvis	0.39	0.25 (0.01)	0.29 (0.02)	0.48 (0.07)	0.32 (0.02)	0.54 (0.07)
Length of back	0.47	0.32 (0.01)	0.32 (0.02)	0.40 (0.07)	0.34 (0.02)	0.42 (0.07)
Width at hips	0.32	0.21 (0.01)	0.33 (0.02)	0.45 (0.07)	0.32 (0.02)	0.44 (0.08)
Thickness of bone	0.32	0.22 (0.01)	0.07 (0.08)	0.44 (0.09)	0.13 (0.08)	0.57 (0.08)
Depth of rump	0.30	0.18 (0.01)	0.43 (0.07)	0.61 (0.08)	0.48 (0.07)	0.58 (0.09)
Width at pins	0.19	0.06 (0.01)	0.16 (0.09)	0.42 (0.11)	0.13 (0.09)	0.48 (0.11)
Body condition score	0.34	0.16 (0.01)	0.20 (0.03)	0.18 (0.09)	0.18 (0.03)	0.13 (0.10)

Table 3. Genetic correlations (standard errors in parenthesis) between kill out percent (KO%) or KO difference (KO diff) with each linear type trait either as raw correlations or partial correlations after adjusting for differences in live-weight at slaughter

Trait	Raw		Adjusted for live-weight	
	KO %	KO diff	KO %	KO diff
<i>Muscular</i>				
Development of hind quarter	0.60 (0.06)	-0.33 (0.08)	0.60 (0.06)	-0.59 (0.06)
Development of loin	0.40 (0.08)	-0.02 (0.09)	0.41 (0.08)	-0.39 (0.08)
Thigh width	0.51 (0.07)	-0.03 (0.09)	0.51 (0.07)	-0.50 (0.07)
Development of inner thigh	0.40 (0.08)	-0.05 (0.09)	0.41 (0.08)	-0.39 (0.09)
Width at withers	0.43 (0.08)	-0.01 (0.09)	0.44 (0.07)	-0.40 (0.08)
Width behind withers	0.51 (0.07)	-0.11 (0.09)	0.52 (0.07)	-0.49 (0.07)
<i>Skeletal &amp; other</i>				
Width of chest	0.13 (0.11)	0.29 (0.11)	0.14 (0.11)	-0.15 (0.11)
Depth of chest	0.04 (0.11)	0.52 (0.09)	0.07 (0.10)	-0.06 (0.10)
Height of withers	0.02 (0.08)	0.48 (0.07)	0.04 (0.08)	-0.04 (0.08)
Length of pelvis	0.07 (0.09)	0.49 (0.08)	0.09 (0.09)	-0.07 (0.09)
Length of back	0.16 (0.08)	0.32 (0.08)	0.18 (0.08)	-0.17 (0.08)
Width at hips	0.22 (0.08)	0.31 (0.09)	0.24 (0.08)	-0.21 (0.09)
Thickness of bone	-0.11 (0.09)	0.61 (0.08)	-0.08 (0.10)	0.10 (0.10)
Depth of rump	0.34 (0.10)	0.42 (0.10)	0.36 (0.10)	-0.32 (0.10)
Width at pins	0.02 (0.13)	0.45 (0.12)	0.05 (0.13)	-0.03 (0.13)
Body condition score	0.22 (0.10)	0.04 (0.10)	0.21 (0.09)	-0.20 (0.09)