

Rapid Communication: Large exploitable genetic variability exists to shorten age at slaughter in cattle¹

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ABSTRACT: Apprehension among consumers is mounting on the efficiency by which cattle convert feedstuffs into human edible protein and energy as well as the consequential effects on the environment. Most (genetic) studies that attempt to address these issues have generally focused on efficiency metrics defined over a certain time period of an animal's life cycle, predominantly the period representing the linear phase of growth. The age at which an animal reaches the carcass specifications for slaughter, however, is also known to vary between breeds; less is known on the extent of the within-breed variability in age at slaughter. Therefore, the objective of the present study was to quantify the phenotypic and genetic variability in the age at which cattle reach a predefined carcass weight and subcutaneous fat cover. A novel trait, labeled here as the deviation in age at slaughter (DAGE), was represented by the unexplained variability from a statistical model, with age at slaughter as the dependent variable and with the fixed effects, among others, of carcass weight and fat score (scale 1 to 15 scored by video image analysis of the carcass at slaughter). Variance components for DAGE were estimated using either a 2-step approach

(i.e., the DAGE phenotype derived first and then variance components estimated) or a 1-step approach (i.e., variance components for age at slaughter estimated directly in a mixed model that included the fixed effects of, among others, carcass weight and carcass fat score as well as a random direct additive genetic effect). The raw phenotypic SD in DAGE was 44.2 d. The genetic SD and heritability for DAGE estimated using the 1-step or 2-step models varied from 14.2 to 15.1 d and from 0.23 to 0.26 (SE 0.02), respectively. Assuming the (genetic) variability in the number of days from birth to reaching a desired carcass specifications can be exploited without any associated unfavorable repercussions, considerable potential exists to improve not only the (feed) efficiency of the animal and farm system but also the environmental footprint of the system. The beauty of the approach proposed, relative to strategies that select directly for the feed intake complex and enteric methane emissions, is that data on age at slaughter are generally readily available. Of course, faster gains may potentially be achieved if a dual objective of improving animal efficiency per day coupled with reduced days to slaughter was embarked on.

Key words: age at harvest, beef, genetic, heritability

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INTRODUCTION

Interest is rapidly intensifying in the efficiency of modern-day cattle production systems and their repercussions on the environment (Opio et al., 2013).

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Many alternative management strategies have been advocated to improve efficiency (Hristov et al., 2013). Breeding solutions to improve feed efficiency and reduce the associated environment footprint have also been proposed (Berry and Crowley, 2013; Berry et al., 2015). Most (reviews of) experiment studies on the potential of breeding to improve both feed and environmental efficiency, however, have focused on direct selection for such traits, usually over a specific period of the life cycle of the animal. For example, improvements in feed efficiency in beef cattle have generally focused on genetic parameters for feed efficiency traits

within a certain time period, usually in a growing animal (Berry and Crowley, 2013). Similarly, genetic studies on enteric methane emissions in beef cattle, although few in number, have been limited to a specific period of time in the lifetime of an animal (Donoghue et al., 2016). Such a strategy of focusing on direct selection for efficiency or environmental load per day continues despite the known contribution of other strategies to improve both efficiency statistics at a systems level (Berry et al., 2015). Reproductive rate, for example, is known to influence beef herd feed conversion efficiency and environmental efficiency (Berry et al., 2015) as is the total lifetime DMI of the offspring (Berry et al., 2015). Therefore, reducing the number of days on feed (i.e., fewer days from birth to slaughter) could be one strategy to improve animal-level and herd-level feed and environmental efficiency. If achieved through breeding within the confines of a holistic breeding goal, then any possible unfavorable correlated effects on other measured traits could be negated.

The objective of the present study was to quantify the potential to breed for animals that are ready for slaughter at a younger age. The approach taken was similar to the concept of residual feed intake (**RFI**), often used for depicting differences in daily feed efficiency (Berry and Crowley, 2013). In the present study, we estimated what we termed deviation in age at slaughter (**DAGE**), which is the deviation in age at slaughter of each animal relative to its contemporaries for the same carcass weight and subcutaneous carcass fatness.

MATERIALS AND METHODS

Information on slaughter date as well as carcass characteristics was available from 10,213,447 cattle slaughtered between the years 2010 and 2016, inclusive. Carcass-related information included carcass weight, carcass conformation, and subcutaneous carcass fat cover score. Carcass conformation and fat score are based on mechanical grading and were recoded to a scale of 1 (poor conformation; little fat cover) to 15 (excellent conformation; large fat cover) for use in the present study. Estimated breeding values for carcass weight, carcass fat score, and feed intake from the April 2017 Irish national genetic evaluation were available. Estimated breeding values for carcass weight, carcass fat score, and feed intake in Ireland are generated from a multitrait, multibreed genetic evaluation.

Animals that moved from one herd to another more than twice in their lifetime were not further considered in the present study. Furthermore, only animals that resided in the same herd for all of the 200 d prior to slaughter were retained. Only animals with a known sire and dam were retained. Using the breed composition of the dams, whether the slaughtered animal was

born into a dairy herd or a beef herd was determined. Only singleton animals that were slaughtered as heifers, steers, or young bulls (termed “gender” from here on in) were retained for further analysis; all carcasses are classified as heifers, steers, or young bulls at slaughter, but this was confirmed by the animal not appearing as either a sire or dam in the national pedigree database. A final set of edits was also imposed to improve the integrity of the data and included discarding records from carcass weights of <100 or >800 kg as well as animals recorded as having been slaughtered at <12 or >36 mo of age. A total of 2,400,948 records remained.

An algorithm was invoked to assign to contemporary groups, animals of the same gender (i.e., bull, steer, and heifer) and similar age purchased into the same herd (from which they would be eventually slaughtered from) in relatively close proximity in time. Age of the animal when it was purchased into the herd was categorized into 90-d intervals. Initially, animals of the same gender and 90-d age bracket purchased into the same herd (from where they would be directly slaughtered) within 10 d of each other were grouped into the same contemporary group. If the number of records within any contemporary group was <10, then adjacent contemporary groups in time from the same herd were merged if the number of days between the start date of one contemporary group and the end date of the other contemporary group was <30. Subsequently, only contemporary groups with at least 5 animals were retained for further consideration. Following all edits, a total of 570,053 records from 35,174 contemporary groups in 9,780 herds remained. These data were used for all subsequent analyses with the exception of the estimation of variance components, which was based on randomly selected large (i.e., >10 records) contemporary groups; this data set consisted of 67,031 animals in 5,574 contemporary groups from 1,624 herds.

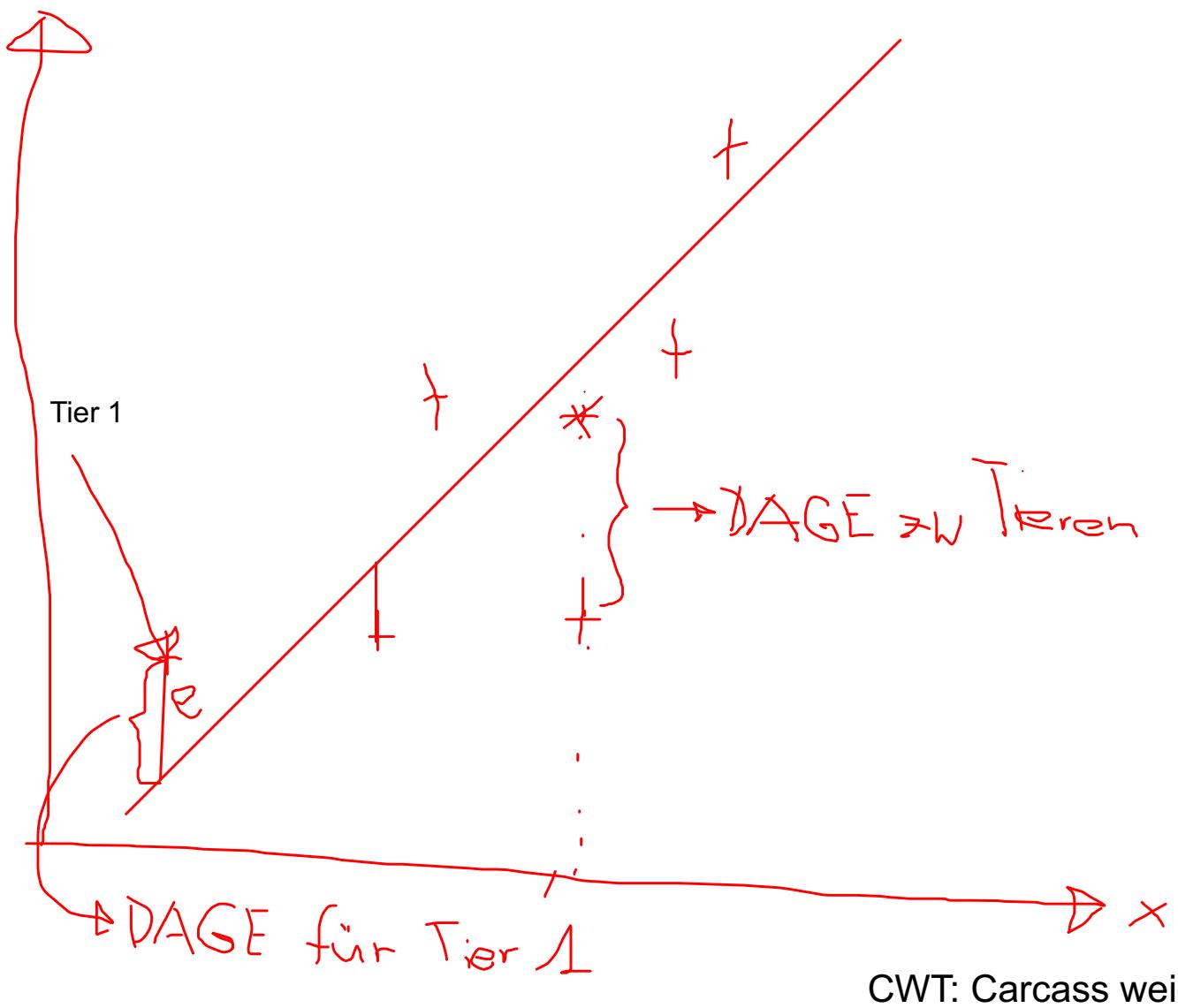
Statistical Analyses and Covariance Component Estimation

Deviation in age at slaughter was initially generated for each animal using a phenotypic model and was defined as the residuals from the fixed effects linear model

$$\text{age} = \text{CG} + \text{GENDER|CWT} + \text{GENDER|CFAT} + e, \rightarrow \text{DAGE} \sim Z [1]$$

in which age represents age at slaughter (d); CG is the contemporary group; GENDER = bull, steer, or heifer; CWT is the carcass weight; CFAT is the carcass fat; and *e* is the residual (here representing DAGE). Deviation in carcass weight (**DCWT**; kg) was defined as the residuals from model [1] but with the variable representing

Y AGE = Age at slaughter



Modell in Gleichung 1:

$$\text{age} = \underline{\text{CG}} + \text{GENDER|CWT} + \text{GENDER|CFAT} + e \rightarrow \text{DAGE}$$

Tiere mit gleichem Wert für CG, GENDER und CFAT

age at slaughter and the variable representing carcass weight interchanged. Higher order polynomials on carcass weight and carcass fat, although improving the fit to the data ($P < 0.001$), did not noticeably alter the relationship with age across the parameter space of carcass weight and carcass fat score represented in the data set. Animals were stratified into 3 groups based on either DAGE or DCWT. The mean phenotypic performance and EBV (from the April 2017 national genetic evaluations) per stratum for a range of traits were estimated.

Residual and genetic variance components for both traits were estimated using linear mixed models in ASReml (Gilmour et al., 2009). The model fitted varied by dependent variable but for DAGE was

$$\text{DAGE} = \text{CG} + \text{Het} + \text{Rec} + \text{Parity} + \text{herd_source} + \alpha + e, \quad [2]$$

in which DAGE is expressed in days, CG is the contemporary group, Het is the general heterosis coefficient of the animal as a class variable (0%, >0% and $\leq 10\%$, $>10\%$ and $\leq 20\%$, ..., $>90\%$ and $<100\%$, and 100%), Rec is the recombination loss as a class effect (0%, >0% and $\leq 10\%$, $>10\%$ and $\leq 20\%$, $>20\%$ and $\leq 30\%$, $>30\%$ and $\leq 40\%$, $>40\%$ and $\leq 50\%$, and $>50\%$), parity represents the parity of the dam (1, 2, 3, 4, and 5+), herd_source is whether the animal was born in a dairy herd or a beef herd, α is the direct additive genetic effect, and e is the random residual term. In a supplementary analysis, DAGE was replaced by DCWT and the variance components estimated using the same model

Variance components for adjusted age at slaughter or adjusted carcass weight were also estimated in a single step using the following model:

$$\text{age} = \text{CG} + \text{GENDER|CWT} + \text{GENDER|CFAT} + \text{Het} + \text{Rec} + \text{Parity} + \text{herd_source} + \alpha + e, \quad [3]$$

in which age represents the age at slaughter (d); CG is the contemporary group; GENDER = bull, steer, or heifer; CWT is the carcass weight; CFAT is the carcass fat; Het is the general heterosis coefficient of the animal as a class effect; Rec is the recombination loss as a class effect; parity represents the parity of the dam; herd_source is whether the animal was born into a dairy herd or a beef herd; α is the direct additive genetic effect; and e is the random residual term. In a supplementary analysis, the variables Age and CWT in model [3] were interchanged.

Breeding values for all 4 traits (i.e., DAGE and DCWT using either a 1-step or a 2-step approach) were estimated using the entire edited data set of 570,053 individuals in the Mix99 software suite (MiX99 Development Team, 2015). The variance components and statistical models used were those derived in the present study.

RESULTS

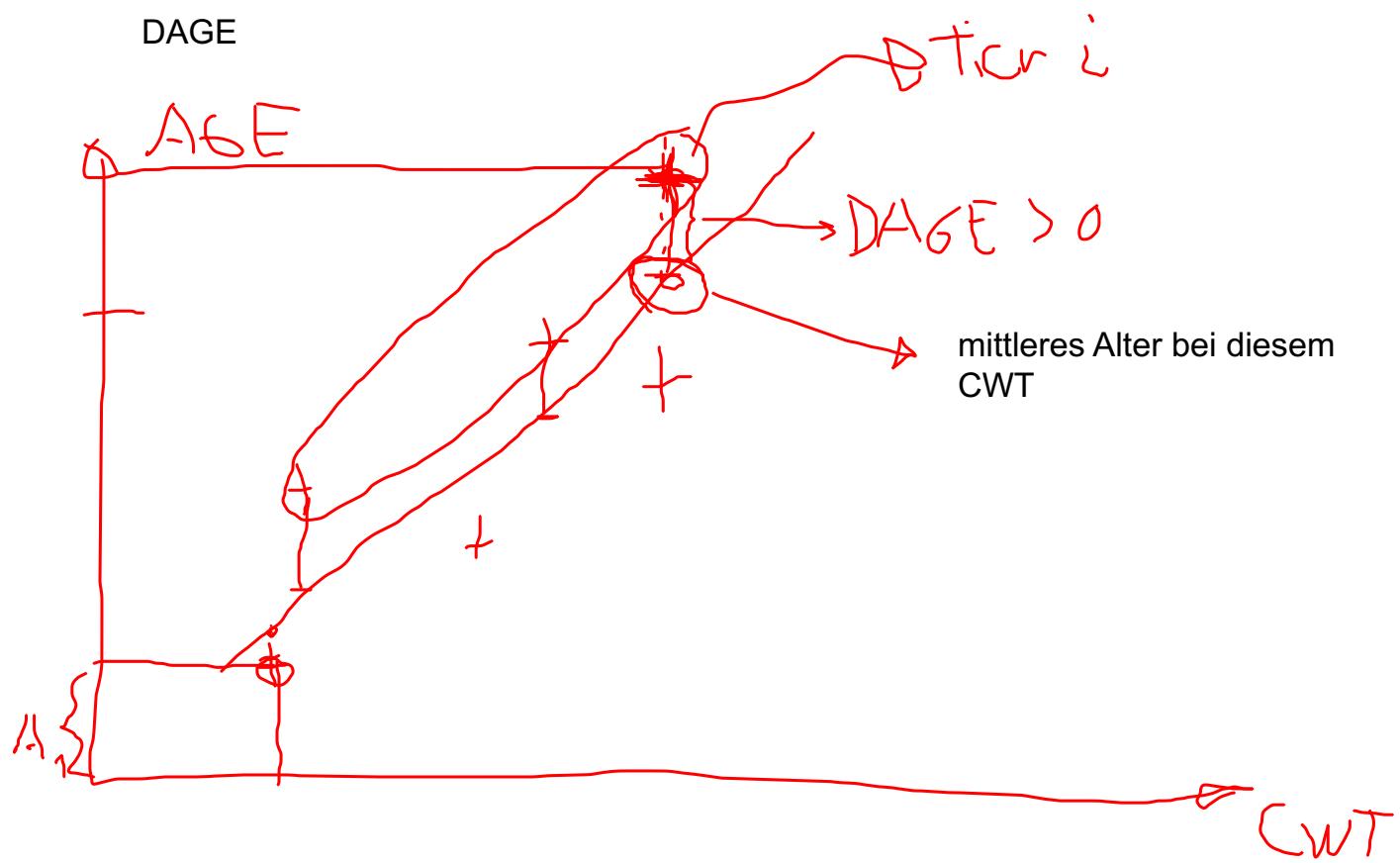
The mean age at slaughter in the entire edited data set was 730 d; the mean carcass weight of the entire data set was 354 kg. Deviation in age at slaughter and DCWT were both normally distributed. The proportion of the phenotypic variation in age at slaughter accounted for by the model that included contemporary group, gender, and the interaction between gender and both carcass weight and carcass fat across the entire data set was 91%. The phenotypic SD in DAGE across the entire data set was 44.2 d; the mean was, as expected, 0. The phenotypic SD in DAGE for bulls, steers, and heifers was 36.5, 44.8, and 52.7 d, respectively.

The proportion of the phenotypic variation in carcass weight accounted for the model the included contemporary group, gender, and the interaction between gender and both age at slaughter and carcass fat across the entire data set was 79%. The phenotypic SD in DCWT across the entire data set was 28.1 kg; the associated phenotypic SD in bulls, steers, and heifers was 31.6, 26.7, and 25.0 kg, respectively. As expected, the correlation between DAGE and carcass weight was 0, as was the correlation between the DCWT and age at slaughter. The correlation between DAGE and DCWT was -0.24.

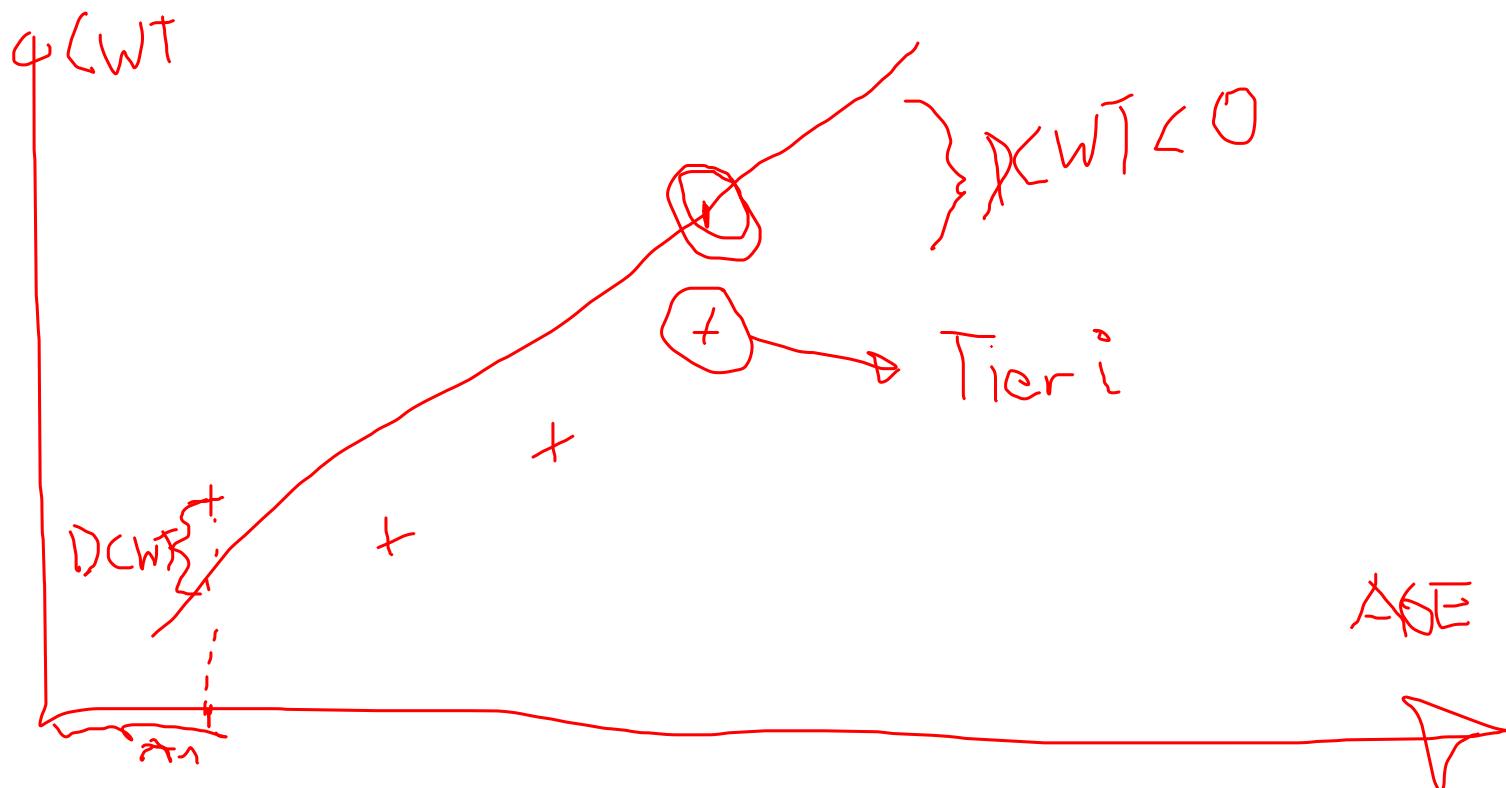
The mean performance and EBV for animals stratified on DAGE or DCWT are shown in Table 1. Animals divergent for DAGE differed by 94 d in actual age of slaughter, and when adjusted to a common carcass weight and carcass fat score (i.e., DAGE), the difference was still 90 d. The similarity in statistics between mean age at slaughter and mean DAGE of animals divergent for DAGE was because the difference in mean carcass weight and carcass fat score of the divergent groups was biologically small, although statistically significantly different ($P < 0.001$; Table 1). Of note, however, was that based on the EBV for feed intake, shorter DAGE animals are expected to eat, on average, 0.12 kg DM/d more than their longer DAGE counterparts. A 58-kg difference in carcass weight (even after adjusting for age at slaughter and other nuisance factors), on average, existed between animals divergent on DCWT.

Irrespective of whether estimated using a 1-step or 2-step approach, progeny from dairy herds had, on average, 8.8 to 9.7 d (SE 1.4) longer DAGE. Progeny from parity 1 dams had, on average, 2.7 to 2.8 d (SE 0.4) longer DAGE compared with second parity dams, which, in turn, were similar to progeny from later parity dams. When estimated using either a 1-step or a 2-step approach, progeny from dairy herds had, on average, 8.1 to 8.6 kg (SE 1.2) lighter DCWT. The mean DCWT of progeny from different dam parities was similar, varying from -0.93 (progeny from first parity dams) to 1.2 kg (progeny from parity 4 dams).

DAGE



DCWT



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Table 1. Number of records and raw means for deviation in age at slaughter (DAGE), age at slaughter (Age), deviation in carcass weight (DCWT), carcass weight (CWT) and carcass fat (CFAT) as well as EBV for carcass weight (EBV_{CWT}), carcass fat (EBV_{CFAT}), and DMI (EBV_{DMI}) for strata of DAGE and DCWT

| Trait | Stratum | Scale | No. of records | DAGE | Age | DCWT | CWT | CFAT | EBV_{CWT} | EBV_{CFAT} | EBV_{DMI} |
|-------|---------|--------------|----------------|--------------|--------------|-------------------|--------------|-----------------|---------------------------|----------------------------|---------------------------|
| DAGE | Short | <15 d | 179,576 | -44 (0.1) | 693 (0.3) | 8.92 (0.064) | 356 (0.1) | 6.49 (0.004) | 19.54 (0.051) | 0.00 (0.001) | -0.10 (0.001) |
| | Average | -15 to 15 d | 221,078 | 0 (0.1) | 715 (0.3) | 0.62 (0.058) | 353 (0.1) | 6.28 (0.003) | 13.65 (0.046) | -0.05 (0.001) | -0.11 (0.001) |
| | Long | >15 d | 169,399 | 46 (0.1) | 787 (0.3) | -10.27 (0.066) | 353 (0.1) | 6.40 (0.004) | 12.95 (0.052) | -0.06 (0.001) | -0.22 (0.001) |
| DCWT | Light | < -10 kg | 198,706 | 12 (0.1) | 729 (0.3) | -28.58 (0.033) | 328 (0.1) | 6.38 (0.004) | 7.46 (0.046) | 0.06 (0.001) | -0.25 (0.001) |
| | Average | -10 to 10 kg | 176,040 | -1 (0.1) | 732 (0.3) | -0.06 (0.035) | 347 (0.1) | 6.44 (0.004) | 13.59 (0.049) | -0.03 (0.001) | -0.12 (0.001) |
| | Heavy | >10 kg | 195,307 | -11 (0.1) | 728 (0.3) | 29.14 (0.033) | 386 (0.1) | 6.33 (0.004) | 24.82 (0.046) | -0.15 (0.001) | -0.05 (0.001) |

Genetic Parameters and EBV

The genetic SD and heritability for DAGE estimated using the 2-step approach were 15.1 d and 0.26 (SE 0.02), respectively; the values when estimated using the 1-step approach were 14.2 d and 0.23 (SE 0.02), respectively. The genetic SD and heritability for DCWT in the 2-step approach were 18.4 kg and 0.46 (SE 0.02), respectively; the values when estimated using the 1-step approach were 19.1 kg and 0.51 (SE 0.02), respectively.

The distribution of individual animal DAGE EBV (where EBV accuracy was >0.70) per breed for a selection of the main breeds is shown in Fig. 1; only animals recorded to be $\geq 87.5\%$ of that breed were considered. The mean EBV of these high-reliability animals for Angus ($n = 1,069$), Charolais ($n = 3,600$), Limousin ($n = 2,953$), Hereford ($n = 327$), Holstein-Friesian ($n = 1,449$), and Simmental ($n = 417$) was -19.3, -15.3, 4.7, -25.6, 14.0, and -17.9 d, respectively. Within breed, the correlation between high accuracy (i.e., >0.70) DAGE EBV estimated using the 1-step or 2-step approach was 0.93; the within-breed correlation between DCWT EBV estimated using the 1-step or 2-step approach was 0.92. The correlation between EBV for DAGE and DCWT both estimated using the single-step approach was -0.35.

DISCUSSION

The importance of efficient and environmentally benign animals has been discussed at length elsewhere (e.g., Opio et al., 2013). Most mitigation breeding strategies investigated to date, however, have focused on direct selection for (daily) feed efficiency, and this has always been confined to only a limited period of the animal's life. Direct genetic selection for net feed efficiency (in cattle) suffers from both a lack of high accuracy of selection and an inability to achieve a high

intensity of selection. Such a drawback owes itself to the high cost associated with direct measurement of individual animal feed intake on a sufficiently large population. Therefore, breeding programs that exploit readily accessible data on heritable and pertinent traits could be a useful tactic to more easily improve animal and system efficiencies. Selection for reduced age at slaughter without any indirect consequences on other important traits is one such option. It is important, for example, that any reduction in age at slaughter is not accompanied by lighter carcasses or carcasses with insufficient fat cover to meet retailer specifications. Achieving both objectives in the present study was accomplished by generating a novel phenotype that depicted the difference in age at slaughter, in days, relative to the population mean given the animal gender (i.e., bull, steer, or heifer) and both the animal's carcass weight and fat cover. To our knowledge, such an approach has never been previously investigated in any species. Using data from 1,324 feedlot cattle, however, Speidel et al. (2016) did document variance components for the animal age, phenotypically adjusted to a common live weight; Speidel et al. (2016) reported a heritability of 0.58 ± 0.08 for days to reach 513 kg estimated using a repeatability model.

Several cattle-based studies that estimate variance components for carcass weight (phenotypically) adjust for age at slaughter (Crews et al., 2003; Berry and Evans, 2014); nongenetic studies have also applied the same approach where differences in carcass performance characteristics between "treatments" (e.g., animal genotype) has been confined to the evaluation of carcass weight adjusted to a common age at slaughter (Clarke et al., 2009). Such an approach, however, is not statistically equivalent to a model with age at slaughter as the dependent variable and carcass weight as an independent variable. This can be clearly illustrated by the fact



Figure 1. Distribution of deviation in age at slaughter (estimated using a 1-step approach) for purebred Hereford (thin continuous line), Charolais (dotted thin black line), Angus (dashed thin black line), Holstein-Friesian (thick black line), Limousin (thick gray line), and Simmental (thick dashed line)

that the regression of carcass weight on age at slaughter in a simple linear regression model may be defined as

$$\hat{\beta}_{\text{Age, CWT}} = \text{cov}(\text{CWT}, \text{Age}) / \text{var}(\text{CWT}),$$

in which $\hat{\beta}_{\text{Age, CWT}}$ is the linear regression coefficient of age at slaughter on carcass weight, $\text{cov}(\text{CWT}, \text{Age})$ is the covariance between carcass weight and age at slaughter, and $\text{var}(\text{CWT})$ is the phenotypic variance in carcass weight. The regression coefficient of age at slaughter on carcass weight, however, in a simple linear regression may be defined as

$$\hat{\beta}_{\text{CWT, Age}} = \text{cov}(\text{CWT}, \text{Age}) / \text{var}(\text{Age}),$$

in which $\hat{\beta}_{\text{CWT, Age}}$ is the linear regression coefficient of carcass weight on age at slaughter, $\text{cov}(\text{CWT}, \text{Age})$ is the covariance between carcass weight and age at slaughter, and $\text{var}(\text{Age})$ is the phenotypic variance in age at slaughter. Hence the regression coefficients will be identical only if the variance in carcass weight is equal to the variance in age at slaughter. Therefore, the approach proposed here through DAGE is not equivalent to genetic evaluations and statistical models applied heretofore.

The Concept of Deviation in Slaughter Age

The idea behind DAGE as used in the present study stems from the now commonly used concept of RFI in research studies as a measure of net feed efficiency over a certain period of time (Berry and Crowley, 2013). Residual feed intake values per animal are represented by the residuals from, usually a least squares regression of feed (or energy) intake on various energy sinks such as metabolic live weight and growth rate, as is the case for growing animals (Berry and Crowley, 2013). Although RFI itself is not commonly explicitly represented in cattle

breeding goals, and much discussion exists on the usefulness of such (Berry and Crowley, 2013), quantifying the extent of (phenotypic and genetic) variability in RFI is extremely useful as a measure of the potential to improve. Experimental analyses of animals divergent for RFI can also be useful in the elucidation of biological, including genetic, mechanisms governing differences in RFI.

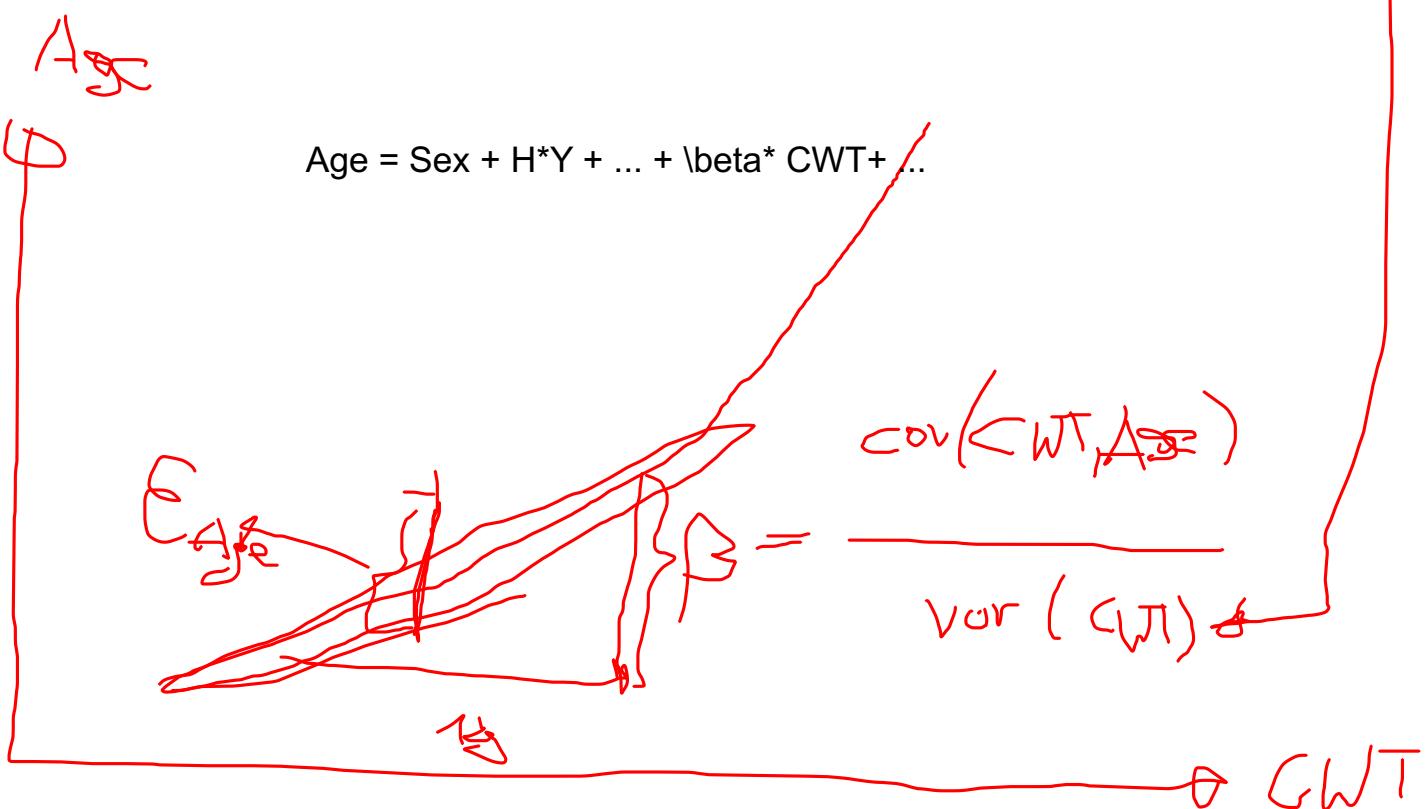
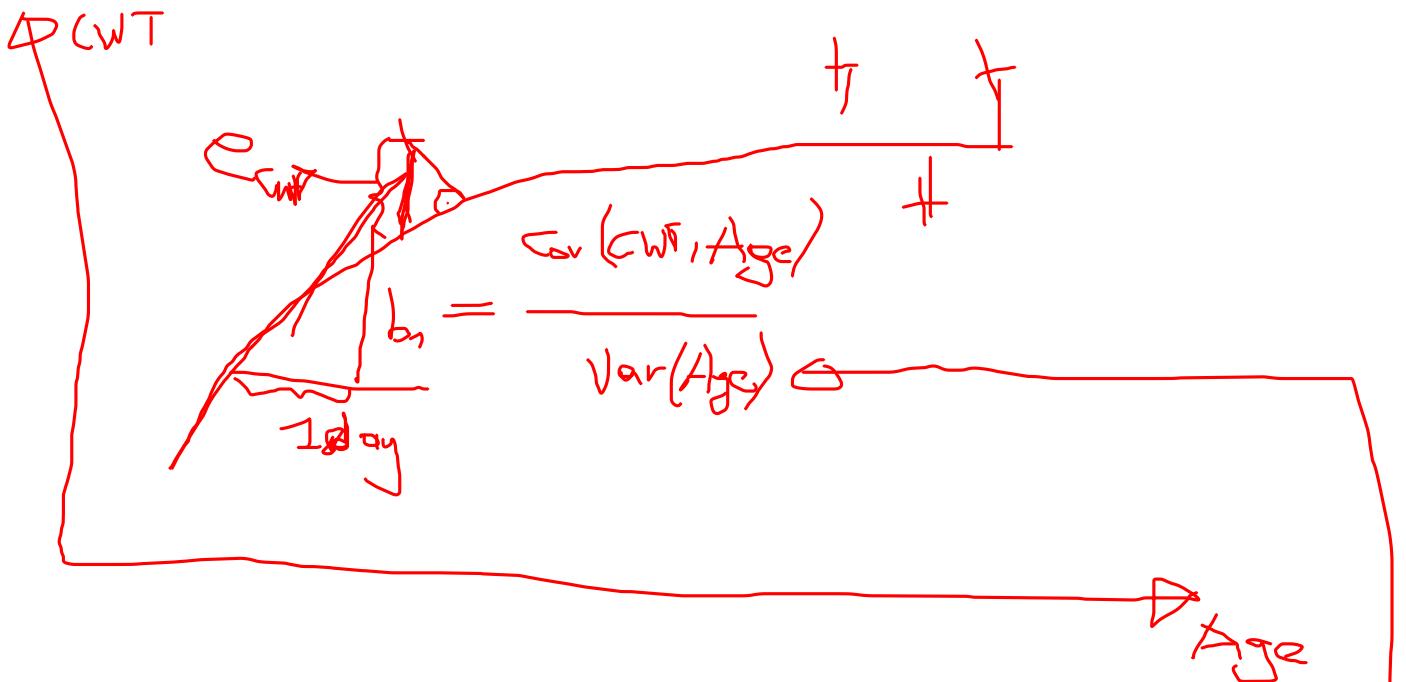
Results from the present study clearly show considerable phenotypic and genetic variability in DAGE. The goal of DAGE itself is not to identify animals slaughtered at the youngest age but instead animals slaughtered at a younger age relative to their carcass weight and carcass fat score. Therefore, although animals with a large proportion of continental beef bloodline are expected to be, on average, slaughtered at an older age, they are also expected to have, on average, heavier carcasses and, therefore, could still have favorable DAGE. A comparable phenomenon is expected with genetic evaluations or experimental studies that adjust the observed animal carcass weight for the respective difference in age at slaughter (Crews et al., 2003; Clarke et al., 2009). Biologically, however, DAGE and DCWT represent different traits, as evidenced by the weak phenotypic correlation but also the weak correlation between the respective EBV.

Direct comparison of variability in traits measured in different units and/or with different mean population values can be difficult. Houle (1992) proposed the coefficient of genetic variation (i.e., the genetic SD divided by the population mean) as a measure of evolvability; the units of the measure in the numerator and denominator cancel, making the coefficient of variation unitless and using the sample population mean as the denominator therefore scales the variability to the mean. The coefficient of genetic variation for RFI (using population mean intake as the denominator) is 0.05 (Berry and Crowley, 2012); the coefficient of genetic variation for DAGE estimated using the 1-step approach (using mean age at slaughter as the denominator) was lower at 0.02. Nonetheless, although the coefficient of genetic variation for DAGE is relatively low, biologically, the (within-breed) genetic SD in DAGE of 14.1 d (1-step analysis) is substantial. Based on a similar analysis of 1,324 Angus, Charolais, and Charolais-crossbred feedlot cattle, Speidel et al. (2016) reported a genetic SD of 18.7 d to reach 513 kg live weight, again substantiating the existence of considerable biological variability in traits depicting age for a certain (slaughter) weight.

Although the potential exists to improve DAGE as well as the traits evaluated by Speidel et al. (2016) through breeding, further management benefits could be achieved by understanding the biological factors governing the observed variability; one such scenario could entail deep phenotyping of animals of the same breed genetically divergent for DAGE. Furthermore,

Aktuelle ZWS für CWT mit gemischem linearen Modell:

$$\underline{\text{CWT}} = \text{Sex} + H^*Y + \dots + b_1 * \text{Age} + b_2 * \text{Age}^2 + u + e$$



Bis jetzt immer univariat, also single Trait

Was passiert bei Multi-trait?

$$\begin{aligned} \text{CWT} &= \text{fix1} + b1 * \text{Age} + b2 * \cancel{\text{Age}^2} + u + e \\ \text{Age} &= \text{fix2} + \cancel{\beta_1 \text{CWT}} + u + e \end{aligned} \quad \left. \begin{array}{l} \text{Multi-varianz} \\ \Rightarrow \text{kein LMME} \end{array} \right.$$

Reaction Norm

$$\begin{aligned} [\text{CWT}] &= \text{fix1} + u + e \\ [\text{Age}] &= \text{fix2} + u + e \end{aligned}$$

→ Ver-Lor nur linear

considerable differences among herds in the present study exist in DAGE; the SD of contemporary group effects for DAGE in the 1-step analysis was 139 d. Therefore, potential also exist to decipher why, in some contemporary groups, animals are slaughtered at considerably younger age than in other contemporary groups; because these contemporary group effects were estimated using the 1-step model, the effects should be independent of the other factors in the statistical model including breed and genetic merit of animal.

Reducing Age at Slaughter through Breeding

As already alluded to, considerable genetic variability exists in DAGE. Therefore, the accuracy of selection and the intensity of selection are the 2 remaining factors that affect genetic gain per generation using single trait selection; the covariances between DAGE and other traits in a breeding objective affect its genetic gain within the framework of a larger breeding objective. It is a legal requirement in several countries to record date of birth and date of death (i.e., here, death equates to culling) in all animals. Hence, age at slaughter should be available for all slaughtered animals. Therefore, other animal-centric-level information required for inclusion in a genetic evaluation includes the pedigree of the animal as well as the relevant fixed effects and, in particular, contemporary group. National animal traceability systems currently in place in many countries can relatively easily be exploited in the generation of such contemporary groups. The relatively high heritability of DAGE implies that large progeny group sizes are not a necessity to achieve a high accuracy of selection. For example, using selection index theory and a heritability of 0.24 (i.e., 1-step heritability of DAGE), an accuracy of selection based solely on progeny information for that single trait would be 0.70 with just 16 progeny records. Because the phenotype is not sex linked and the necessary data are generally plentiful, strict editing criteria (e.g., large contemporary groups) can be imposed with minimal impact on accuracy of selection.

Practical Implications of Improving Efficiency per Day or Efficiency per Lifetime

Deviation in age at slaughter as defined in the present study (or deviation in age to a given live weight; Speidel et al., 2016) has a role in breeding objectives to select for more efficient animals. For example, feed intake in the Irish cattle breeding objective is based on an EBV for daily feed intake, and the economic value is the cost of that feed summed across the average number of days the animal eats up to slaughter, and this value is constant for all animals; therefore, the

breeding objective does not consider the number of days each animal eats prior to slaughter. Deviation in age at slaughter attempts to rectify this shortcoming.

The genetic SD for RFI in growing Irish cattle has been reported to be 0.58 kg/d; the mean feed intake and live weight of these animals were 10.7 kg/d and 546 kg, respectively (Berry and Crowley, 2012). Therefore, the mean feed intake of the genetically elite 20% of individuals for RFI is expected to be 0.81 kg/d less relative to the population mean. Assuming a feeding period of 365 d (and constant genetic variance), this equates to a lesser feed intake of 296 kg in the most efficient 20% relative to the population mean. The genetic SD for DAGE in the present study was 14.2 d, or in other words, the 20% most genetically elite for DAGE are expected to be slaughtered, on average, (14.2×1.4) 19.8 d younger than the population mean. Assuming a 19.8 d (i.e., 14.2×1.4) feed intake of 10.7 kg/d, this equates to 212 kg less feed per year; based on a finishing diet feed value per kilogram DM of €0.20, this equates to a potential saving of €42.40 on feed costs. Table 1, however, suggests that animals with shorter DAGE are expected to eat more per day, on average, than their later DAGE contemporaries; the correlation between the 1-step DAGE EBV and the national EBV for feed intake was -0.21, substantiating that superior DAGE animals eat more per day, but still, considerable exploitable variability exists independent of daily feed intake. Nonetheless, if considered within the framework of a total merit index, any repercussions of expected genetic change in a trait such as feed intake from selection on a correlated trait (e.g., DAGE) can be negated. More importantly, however, is the fact that achieving such gains in lifetime feed efficiency can be achieved with little or no additional recording over and above the data that are already available, thus ensuring a shift in the population mean. Furthermore, animals that are slaughtered at a younger age may require less capital resources such as labor and feedlot space; the latter will facilitate a greater turnover rate. Selection for daily feed intake in growing animals, however, has potential additional benefits for the entire system over and above its contribution to the efficiencies in slaughtered animals. Although based on only 2 study populations, which were limited to dairy cattle, daily feed intake in lactating cows and growing heifers are genetically correlated (Nieuwhof et al., 1992; Berry et al., 2014), implying that favorable changes in daily feed intake in growing animals should, on average, translate to favorable changes in lactating dairy cows; the impact on the cow herd of shortening DAGE in growing animals is unknown.

Conclusions

A novel phenotype was derived in the present study to depict the variability that exists among cattle in the age at slaughter standardized to a common carcass weight and fat score. This trait is different than what is often evaluated in beef cattle genetic evaluations where the dependent variable is carcass weight and one of the independent variables is age at slaughter or where the dependent variable is age at weighing and one of the independent variables is live weight (Speidel et al., 2016). Considerable (heritable) variability was shown to exist in this novel phenotype, which could be relatively easily exploited through breeding. The impact of incorporating such a trait in a breeding objective is shorter days to slaughter without necessarily reducing the genetic merit of other traits included in the breeding objective. The benefit is potentially fewer days on feed, which will impact not only feed efficiency but also, potentially, the environmental footprint per unit output.

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