**Formulation of a decision support tool incorporating both genetic and non-genetic effects to rank young growing cattle on expected market value1**

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**ABSTRACT**

While breeding indexes exist globally to identify candidate parents of the next generation, fewer tools exist that provide guidance on the expected monetary value of young animals. The objective of the present study was therefore to develop the framework for a cattle decision support tool, which incorporates both the genetic and non-genetic information of an animal, and in doing so better informs the potential market value of an animal, whatever the age. Two novel monetary indexes were constructed and their predictive ability of carcass value was compared to that of the Irish national terminal breeding index typical of other terminal indexes used globally. A constructed Harvest index was comprised of three carcass-related traits (i.e., weight, conformation and fat each weighted by their respective economic value) and aimed at purchasers of animals close to harvest; the second index, termed the Calf index, also included docility and feed intake (weighted by their respective economic value) thus targeting purchasers of younger calves for growing (and eventually harvesting). Genetic and non-genetic fixed and random effect model solutions from the Irish national genetic evaluations underpinned the indexes. The two novel indexes were formulated using three alternative estimates of an animal’s total merit for comparative purposes: 1) an index based solely on the animal’s breed solutions, 2) an index which also included within-breed animal differences and, 3) an index which, as well as considering additive and non-additive genetic effects, also included non-genetic effects (referred to as production values [PV]). As more information (i.e., within breed effects and subsequently non-genetic effects) was included in the total merit estimate, the correlations strengthened between the two proposed indexes and the animal’s calculated carcass market value, almost doubling in strength when comparing the total merit estimates based on just breed to the PV-based estimates. Including phenotypic live-weight data, collected during the animal’s life, strengthened the predictive ability of the indexes further. Results from the present study suggest that the proposed indexes may fill the void in decision support regarding the transaction of cattle and demonstrate the dynamic nature of the indexes whereby they have the potential to be updated in real-time as information becomes available.

**Keywords:** beef, cattle trading, blockchain, carcass, transaction

**INTRODUCTION**

 Individual animal ranking on beef breeding indices are widely used to support decisions for selecting candidate parents of the next generation ([Amer et al., 2001](#_ENREF_4); [Berry et al., 2019](#_ENREF_6)); in the absence of genotype-by-environment interactions, the progeny of genetically superior animals are, on average, expected perform better than the progeny of genetically inferior animals if exposed to the same management conditions. Breeding index values are available in some countries for all cattle from birth irrespective of whether they can even become parents (e.g., steers); these index values, if economic-based, still provide an indication of the expected profit of that animal. The applicability of such breeding indices for live animals destined for slaughter are, however, limited in that: 1) they are constructed solely from estimates of the additive genetic merit of the animal for a selection of traits without cognizance of either the non-additive genetic effects (e.g., heterosis), or the non-genetic effects that impact the animal’s phenotypic performance (e.g., dam parity), and 2) the indexes often include traits which become redundant to the expected profit of a growing animal itself once born; an example is genetic merit for calving difficulty or gestation length which does not impact the profit of a growing animal once born, over and above the phenotypic expression of the trait.

 Both non-additive genetic effects and non-genetic effects are known to impact the performance of growing cattle. [Gregory et al. (1978)](#_ENREF_17) carried out extensive research into heterosis values in beef cattle and reported that crossbred calves were weaned 7.4% heavier than purebred calves while also reaching puberty 9.4 d younger than purebred calves. Furthermore, [Connolly et al. (2016)](#_ENREF_10) documented that progeny carcass weight from third parity cows was 1.1 kg heavier than second parity cows with the progeny carcasses from second parity cows being 2.04 kg heavier than progeny from primiparous cows; similarly, the value of carcasses from twin cattle were worth € 28.79 less than carcasses from singletons ([Connolly et al., 2016](#_ENREF_10)). [McHugh et al. (2014)](#_ENREF_28) reported that up to the point of weaning, males calves grew 0.17 kg per day faster than female calves. Given that such heterosis and environmental effects exist, then these effects should be incorporated into tools to rank animals on expected profit.

The objective of the present study was to formulate a decision support index which is capable of predicting the lifetime revenue of animal for harvest taking cognizance of both additive and non-additive genetic effects as well as contributing non-genetic effects. The index has the potential to be targeted towards beef-finishing systems to aid in the purchase of animals destined for slaughter; with modifications, the index could also be used by beef processors when agreeing flat prices for cattle prior to slaughter.

**MATERIALS AND METHODS**

Data used in the present study were collected prior to October 2018 and originated from the Irish Cattle Breeding Federation (ICBF) national database, Bandon, Co. Cork, Ireland (<http://www.icbf.com>).

***Data***

Three separate phenotypic datasets used in the Irish national genetic evaluations were obtained from the ICBF. The first dataset contained calving performance phenotypes on 20,847,261 individual animals for calf mortality, gestation length and calving difficulty; the associated pedigree file included 25,504,740 animals. The second dataset contained docility performance phenotypes on 3,012,970 individual animals, which were either scored subjectively by the farmer or by a trained professional; the associated pedigree file included 6,163,517 animals. The third dataset contained data on 24 traits, namely those related to feed intake, live-weight and carcass-related related traits on 13,126,903 individual animals; the associated pedigree file included 18,078,810 animals. The phenotypes in the performance data included live-weight measurements taken at 4 life-stage points, namely between the ages 150 d and 250 d old (weanlings; 150-250 d), between 251 d and 350 d old (adolescent; 251-350 d), between 351 d and 450 d old (adult; 351- 450 d), and between 451 d and 550 d old (finisher; 451-550 d). The three datasets represent the three suites of multi-breed multi-trait genetic evaluations undertaken in Ireland to derive estimated breeding values (EBVs) for calving performance, docility and carcass merit.

***Genetic Evaluations***

Genetic evaluations were run for the three suites of traits using the Mix99 software suite ([MiX99 Development Team, 2015](#_ENREF_30)) to generate both fixed and random effect solutions for all traits included in the Irish beef cattle terminal index. The carcass genetic evaluation was a 24 x 24 multi-trait evaluation. Fixed and random effect solutions for carcass weight, carcass conformation (i.e., the muscularity score of the carcass; Englishby et al., 2016) , carcass fat (i.e., subcutaneous fat cover and fat in the thoracic cavity; Englishby et al., 2016), feed intake as well as all live-weight age categories were generated for use in the present study. The docility genetic evaluation was a 3 x 3 multi-trait evaluation; only the weanling docility fixed and random effects solutions were retained for use in the present study as this is the trait included in the national terminal index. The calving genetic evaluation was a 9 x 9 multi-trait evaluation which included traits such as calving mortality, calving difficulty and gestation length. The statistical models used in the respective genetic evaluations are summarized in Appendix 1.

***Production value estimation***

Genetic evaluations in Ireland use pedigree groups for the estimation of breed effects. In the present study, however, breeds were fitted as separate covariates. This facilitated the estimation of animal total merit for a given trait using three alternative formulations. The first formulation estimated the total merit of each animal for a given trait using just the breed effect solutions; following this, total merit of an animal was estimated using the animal’s additive genetic merit combined with the breed effect solutions (EBV); the third approach in the estimation of an individual’s total merit for a given trait was to estimate an animal’s production value (PV) using the fixed and random solution coefficients from the respective genetic evaluations. The PV’s were calculated as:

$$Carcass traits and Feed intake PV\_{abcdefghz}= \sum\_{a=1}^{4}b\_{1}heterosis\_{a}+\sum\_{b=1}^{16}b\_{2}breed\_{b}+ b\_{3}EBV\_{c}+b\_{4}twin\_{d}+b\_{5}dam dairy fraction\_{e}+b\_{6}dam age\_{f}|dam parity\_{g}+b\_{7}dam pe\_{h}$$

$$Docility PV\_{abcgijz}=b\_{1}heterosis\_{a}+\sum\_{b=1}^{16}b\_{2}breed\_{b}+ b\_{3}EBV\_{c}+b\_{4}dam parity\_{g}+ b\_{4}sex\_{i}+b\_{5}recombination\_{j}$$

where $heterosis\_{a}$ = the heterosis coefficient *a*; $breed\_{b}$ = covariate representing the proportion of 16 breeds *b* in the animal *z* (i.e., Aberdeen Angus (AA), Aubrac (AU), Blonde D’Aquitaine (BA), Belgian Blue (BB), Charolais (CH), Friesian (FR), Hereford (HE), Holstein (HO), Jersey (JE), Limousin (LM), Piemontese (PI), Montbelliarde (MO), Parthenais (PT), Salers (SA), Shorthorn (SH) and Simmental (SI); $EBV\_{c}$ = the estimated breeding value for trait c of animal *z*; $twin\_{d}$ = whether or not the animal was a twin; $dam dairy fraction\_{e}$ = dam dairy-breed proportion coefficient *e*;$ dam age\_{f}|dam parity\_{g}$ = the interaction between dam age *f* and the dams *g*th parity (i.e., 1 to 7, inclusive) for the carcass traits and feed intake or just the dams *g*th parity for docility;$ dam pe\_{h}$= permanent environment effect of *h*, animal *z*’s dam; $sex\_{i}$ = sex which was male or female for the docility PV; $recombination\_{j}$ = recombination coefficient *j* and all of *b1-b7* are the associated regression coefficients from the respective national genetic evaluation.

***Index development***

The Irish national beef terminal index comprises 8 traits including three calving traits (i.e., difficulty, gestation and mortality), feed intake, docility and three carcass traits (i.e., carcass weight, carcass conformation and carcass fat) (Table 1); this index, populated with the relevant EBVs, was used as the base scenario from which two additional variants of the index were compared. The economic weights applied (Table 1) were the same for all three indexes evaluated in the present study. The two novel indexes proposed in the present study were:

1. The Calf index - developed to provide support in purchasing young animals to be reared and eventually harvested. The Calf index comprised 5 traits namely docility, feed intake, carcass weight, carcass conformation and carcass fat (Table 1); therefore the index did not incorporate calving-related traits.
2. The Harvest index was an adaption of the Calf index in that feed intake and docility were omitted leaving only the three carcass-related traits, namely carcass weight, carcass conformation, carcass fat (Table 1).

***Index Validation***

A subset of animals was identified to validate each of the constructed indexes. The validation population consisted of 374 steers and 500 young bulls, all of which originated from the national beef bull performance test center at Tully, Co. Kildare, Ireland. All validation animals were slaughtered between the years 2016 to 2018, inclusive; therefore, phenotypic data for carcass weight, carcass conformation, and carcass fat as well as feed intake were available. Details on the test protocols (e.g., diet) and the feed intake phenotypes have been described in detail by [Crowley et al. (2010)](#_ENREF_11) and [Kelly et al. (2019)](#_ENREF_25).

Despite carcass price per kg being available from the abattoirs, in order to counteract seasonal fluctuations in price, a Quality-Based Pricing grid was recreated to reflect the current pricing structure used by abattoirs throughout Ireland. Price (€) per kg of carcass weight was determined using the EUROP beef classification grid scores ([Englishby et al., 2016](#_ENREF_14)); the price per kg for different carcass conformation score by fat score credentials are summarized in Supplementary Table 1. Price per kg was multiplied by the carcass weight of the animal to generate a carcass value per animal. Prior to validation, the carcass genetic evaluations were rerun seven times while the docility genetic evaluation was rerun twice. Both the carcass and docility national genetic evaluations which contained phenotypes for the validation animals (as well as all other animals) were run as a measure of the upper threshold for predictive ability. In the next iteration, all phenotypic data of the validation animals were masked in both the carcass and docility national genetic evaluations and the fixed and random effects model solutions re-estimated. For the third, fourth, fifth and sixth iteration of the carcass national genetic evaluations, a single live-weight record of the validation animals was included separately for the age category 150 d up to 250 d (n = 168), 250 d up to 350 d (n = 459), 350 d up to 450 d up (n = 459) or 450 d up to 550 days (n = 459), respectively (Table 2). For the final iteration of the national carcass genetic evaluation, the phenotypes of animals within the validation population who had a live-weight record for each of the three age categories that spanned from 250 d to 550 d were included (n = 459); phenotypes of all other animals not in the validation population were also included in the seventh genetic evaluation iteration.

***Statistical analyses***

 Animals were ranked into four strata of equal sizes separately based on their national terminal, Calf or Harvest index value. The mean Irish national terminal, Calf and Harvest index values of the animals within the top and bottom 25 % strata were calculated. Least square means (LSM) were calculated for the three carcass traits (i.e., weight, conformation and fat), feed intake, carcass revenue, price per kg and age at slaughter whilst adjusting for the following: 1) gender (i.e., steer or young bull), 2) age at slaughter (with exception to age at slaughter), 3) heterosis, 4) dam heterosis, 5) dam parity and, 6) carcass weight (only included when estimating the least squares means for age at slaughter).

The correlations between the three alternative formulations of an individual animal’s total merit for a given trait and the corresponding phenotypic values for each trait were estimated; spearman correlations were used to estimate within-gender correlations but also partial correlations adjusted for gender. Spearman correlations between each phenotypic value as well as carcass revenue and price per kg with the whole range of different indexes and scenarios evaluated were also estimated. The statistical test proposed by [Steiger (1980)](#_ENREF_37) was used to test the difference between the correlation coefficients. Multiple linear regression models in the validation animals were used to regress the phenotypes for carcass weight, carcass conformation, carcass fat score, feed intake, and docility on the three alternative definitions of an individual animals’ total merit for a given trait using the models:

$$Carcass traits\_{abcd}=\sum\_{a=1}^{2}HY\_{a}+ gender\_{b}+\sum\_{c=1}^{3}age^{c} +TM\_{d}+e$$

$$Feed intake\_{ebcd}= HYSfi\_{e}+ gender\_{b}+\sum\_{c=1}^{3}age^{c} +TM\_{d }+e$$

$$Docility\_{fbcd}= HYSdoc\_{f}+ gender\_{b}+\sum\_{c=1}^{2}age^{c}+TM\_{d}+e$$

where $HY\_{a}$ = the class effect of herd-year contemporary group of slaughter and the previous herd in which the animal spent the longest time in; $HYSfi\_{e}$= the class effect of herd-year-season contemporary group of the feed intake; $HYSdoc\_{f}$ = the class effect of herd-year-season contemporary group of docility; $gender\_{b}$ = fitted as a class effect whether the animal a steer or a young bull;$ age^{c}$ = the age of the animal (linear, cubic and quadratic for the three carcass traits and feed intake and linear and cubic for docility); $TM\_{d}$ = the total merit estimate; *e* = residual.

**RESULTS**

The mean performance of animals ranked on their national beef terminal, Calf, and Harvest index values is in Table 3. Although not always significant (i.e., P > 0.05), the mean performance of the bottom 25 % of animals tended to get progressively worse shifting from ranking on the terminal index to ranking on the calf index and from the calf index to the harvest index; similarly, the mean performance of the top 25 % of animals tended to get better shifting from using the terminal index to rank animals versus using the calf index and from using the calf index to using the harvest index. The carcass value of the top 25% of animals ranked on the harvest index was superior (P < 0.05) to that of the top 25 % ranked on the terminal index. This was predominantly due to the heavier (P < 0.05) carcass weight of the top 25 % of animal ranked on the harvest index relative to the top 25 % ranked on the terminal index.

***Relationships with phenotypic performance***

The correlations between the alternative formulations of total merit of an individual animal for a given trait and the corresponding phenotypic values for that trait are in Table 4. As more information was included in the calculation of the total merit (i.e., from just breed effects to inter- and intra-breed effects, to then also include non-genetic effects), the partial correlations between the estimate of total merit for a given trait and the respective phenotypic value typically strengthened. The correlations between the estimate of total merit for a given trait using just breed solutions and the corresponding phenotypic values were consistently weaker (P < 0.05) relative to when the total merit estimate included inter- and intra-breed effects, as well as when including non-genetic effects (with exception to feed intake and the within steer group for carcass fat). Furthermore, the correlations between the phenotypic values for both carcass fat and carcass weight (with the exception of the young bull group) and the relative total merit formulated using PVs were stronger (P < 0.05) compared to when formulating the total merit using just EBVs.

The regression coefficients of the phenotypic value for all five traits on the three formulations defining an individual’s total merit for that trait after accounting for age, sex and contemporary group effects are in Table 4. With the exception of carcass weight and feed intake, the regression coefficient was always closer to 1 for the total merit derived using PVs, although not always different to when the total merit was estimated from just EBVs. With the exception of feed intake, the least amount of variation explained by the multiple linear regression model was when total merit was defined solely on breed effects (ranging from 49% (docility) to 72% (carcass conformation)) relative to EBV or PV estimates; irrespective of whether the total merit for feed intake was based on just breed or PV, the regression models explained 53% of the variation.

The partial correlations between the three indexes and their different constructions with each of the phenotypic values for the component traits are in Table 5. Regardless of the index, or how it was formulated (i.e., breed effects only, EBV, or PV), there was little to no relationship between either of the indexes and docility, with correlations ranging from -0.04 (the Calf index calculated using only breed solutions) to 0.05 (the Harvest index calculated using the EBV solutions). Irrespective of the formulation of the three indexes, phenotypic carcass fat and feed intake were both negatively correlated (i.e., the desired direction) with each of the three indexes (from -0.45 to -0.35 and from -0.39 to -0.09 for carcass fat and feed intake, respectively; Table 5). Of all the traits, carcass conformation was the most strongly correlated with each of the indexes evaluated.

***Correlations with revenue metrics***

The correlations between each of the three indexes with both the total carcass value and price per kg are in Table 6. The national terminal (breeding) index, which is the Irish industry standard for beef breeding, was moderately correlated with carcass value and price per kg. For the Calf index, the correlations with carcass value strengthened as more information was included in the calculation of the index (P < 0.05); the same was true for the Harvest index (P < 0.05; with the exception of in young bulls). In fact, the strength of the correlations almost doubled (P < 0.05) when either index was formulated using PVs compared to when it was formulated using just breed effects. The strongest correlations were between price per kg and the Calf index when formulated on either EBVs or PVs relative to using just breed solutions (P < 0.05). The correlations were strongest between price/kg and the Harvest index formulated using EBVs relative to the index calculated using PVs (P < 0.05).

***Including live-weight data in the genetic evaluations***

The partial correlations between the three indexes with the carcass revenue as the number of live-weight records available for each individual included in the genetic evaluation changed are in Table 7. Where no live-weight records were included in the genetic evaluations, partial correlations between the indexes and carcass value followed the same trend (i.e., strengthened as more information was included in the calculation of the index; P < 0.05) as described in Table 6, albeit with a small number of animals included.

The correlations between the national terminal index and carcass value strengthened (P < 0.05) from 0.30 to 0.36 with the inclusion of one live-weight phenotype recorded between 250 to 450 d of age; the correlation further strengthened (P < 0.05) to 0.39 if the live-weight included in the genetic evaluation was recorded between 450 to 550 d of age. The correlations did not differ (P > 0.05) regardless of the number of live-weight records included in the genetic evaluation, partial correlations were either 0.18 between carcass value and Calf index or 0.23 between the Harvest index and carcass value, provided the indexes were formulated using just breed solutions. In comparison to when no live-weight phenotypic data on the validation animals were included in the genetic evaluation, the inclusion of one live-weight record strengthened (P < 0.05)the correlations between carcass value and both the Calf and Harvest index formulated using PVs or EBVs; between the ages of 250 to 450 d, the correlations did not differ (i.e., P > 0.05) regardless of when the live-weights were recorded or indeed the number of live-weight phenotypes included in the genetic evaluation (with exception to the Harvest index). When only including one live-weight record in the genetic evaluation, the strongest correlations (P < 0.05) existed between the Calf index formulated using PVs and the carcass value when the live-weight of an older animal was included (450 to 550 d of age); the same was true for the Harvest index (P < 0.05). Provided there was an older animal’s live-weight record included in the genetic evaluation, there was no further benefit to the inclusion of multiple live-weight records.

**DISCUSSION**

The main revenue source for beef producers is carcass value, which is a function of both carcass price and carcass weight; carcass price itself is a function of the carcass conformation and fat grade. Almost a quarter of a million calves are sold younger than 6 weeks of age at Irish livestock auctions annually, with a further quarter million sold younger than 12 months of age ([DAFM, 2018](#_ENREF_12)). The mean age of Irish cattle at harvest is 730 days ([Berry et al., 2017](#_ENREF_5)). Thus the ability of producers to predict the future carcass value of an animal at sale can be extremely difficult due to many of the animals being sold at such a young age relative to their age at harvest. Hence, the motivation for the present study was to develop a tool that could predict an animal’s potential carcass value and therefore aid in the decision-making process when purchasing animals; this was particularly true where the animal was young and thus the visible expression of genetic differences in weight and conformation is expected to be poor. In doing so, the aim of the present study was also to determine whether there was a benefit from taking cognizance of not only the within-breed additive genetic merit of an individual, but also the non-additive genetic and non-genetic effects, both of which are known to contribute to the eventual carcass phenotype ([Gregory et al., 1978](#_ENREF_17); [McHugh et al., 2014](#_ENREF_28); [Connolly et al., 2016](#_ENREF_10)). Nonetheless, a caveat in estimating an animal’s future carcass value using *a priori* predictions, especially at such a young age, is that such predictions will never be extremely accurate due to the number of factors that are associated with differences in carcass value, some of which will not be known at the time of prediction. For instance, not only does age at harvest have a big impact of carcass performance ([Warren et al., 2008](#_ENREF_40); [Judge et al., 2019](#_ENREF_21)), but also whether the animal will be finished as a bull or steer ([Clarke et al., 2009](#_ENREF_8); [Connolly et al., 2016](#_ENREF_10)). Thus, the carcass value predictions from the two proposed indexes are simply to assist in comparing candidate animals for purchase rather than an absolute prediction of carcass value *per se*.

***Why not just use a breeding index in the transaction of animals?***

Subjective evaluation of an animal’s visible characteristics, and their likely association with animal value, has been fundamental to livestock improvement since the beginning of livestock domestication ([Simm, 1998](#_ENREF_36); [Cole and VanRaden, 2018](#_ENREF_9)). A general feeling among some is that knowledge of the breed (combinations) of an animal is sufficient to predict its future carcass merit. In fact, whilst investigating the between-breed differences of 15 European cattle breeds, [Albertí et al. (2008)](#_ENREF_3) suggested that, within reason, carcass weight and dressing percentage is largely reflected by breed type. For this reason, the present study investigated the relationship between the 5 performance phenotypes and just the breed solutions of an animal and, although positive correlations did exist between the trait phenotypes and the respective total merit based on just breed solutions (with the exception of docility; Table 4), exploiting the known within-breed variability in EBVs and non-genetic effects (i.e., the PVs) improved the partial correlation prediction accuracy by 0.09 (feed intake) to 14 (docility) times that of using the breed solutions alone. It is currently a legal requirement to record the breed of all animals in Ireland; the proportion of animals with a recorded sire is also increasing. Thus, it is possible to estimate the within-breed genetic potential of an animal over and above the breed effects. This is especially true given the growing uptake of genotyping in cattle ([Wiggans et al., 2017](#_ENREF_41)) which improves the ability to not only predict animal breed composition more accurately ([Judge et al., 2017](#_ENREF_20)), but can also (in)validate parentage ([Purfield et al., 2015](#_ENREF_35)) on a greater number of (commercial) animals, thus improving the precision of prediction.

[Amer et al. (2001)](#_ENREF_4) originally proposed an Irish beef breeding objective that would have the potential to simplify the decision-making process when selecting beef bulls for use on beef females by means of summarizing their breeding values into a single index. This index was further revised to form the Irish national terminal index for beef cattle (Connolly et al., 2016); [Berry et al. (2019)](#_ENREF_6) outlined a terminal index for the selection of beef bulls for use on dairy females, which was similar to the beef terminal index differing only in the relative economic weights. Animals excelling in the terminal index have been documented to produce, on average, heavier, more conformed carcasses when compared to their lower genetic merit contemporaries ([Connolly et al., 2016](#_ENREF_10)). Despite this, as calving performance-related traits (i.e., dystocia, gestation length and calf mortality) represent approximately 25 % to 50 % of the relative emphasis within the terminal indexes, it is possible that animals of potentially superior carcass merit will be penalized owing to their expected poorer calving performance. This is because of the known positive genetic correlations between calving difficulty and carcass weight in cattle (Berry et al., 2019), as well as between calf birth weight and calving difficulty ([Eriksson et al. (2004)](#_ENREF_15). However, when purchasing calves or weanlings solely for eventual harvest, it is not logical to consider an individual’s merit for calving traits (since the animal is already born). This prompted the development of both the Calf and Harvest indexes in the present study to satisfy the void in decision support tools for the transaction of animals for harvest, or in other words, those that will never become parents. Breeding indexes are still relevant in the transaction of candidate parents of the next generation.

The Irish national terminal breeding indexes, like all other cattle indexes globally are solely based on the individual animal’s additive genetic merit for the component traits. This in part is not only due to the difficulty in estimating non-additive genetic effects ([Bolormaa et al., 2015](#_ENREF_7)), but also that the expression of non-additive genetic effects of a bull is a function of (the genotype of) its mate. Nevertheless, using genotypic and phenotypic data from beef cattle, [Bolormaa et al. (2015)](#_ENREF_7) estimated that 10 % and 18 % of phenotypic variance for intra-muscular fat (i.e., marbling) and carcass retail beef yield (i.e., salable beef yield; kg), respectively, was explained by dominance variance. Furthermore, [Akanno et al. (2018)](#_ENREF_1) reported that two SNPs were associated with an increased level of marbling in heterozygote individuals relative to homozygous individuals. As the non-additive genetic merit of an animal can be theoretically estimated once born ([Bolormaa et al. (2015)](#_ENREF_7); dominance variance), it makes sense to consider this influence in the prediction of performance. This is especially true given that the prediction of carcass value improved once the non-additive and non-genetic effects were considered in the total merit estimation (i.e., PVs; Table 6).

***Consideration of the costs of production***

Although both of the new proposed indexes facilitate the prediction of relative carcass value, they are targeted at different end-users. The Calf index is directed towards producers who specialize in purchasing young calves for the purpose of growing and either finishing themselves, or selling to specialized finisher facilities. In such an index, consideration must also be given to both docility and feed intake especially given that feed costs are the largest variable input costs in cattle production ([Montano-Bermudez et al., 1990](#_ENREF_31)). The phenotypic SD for feed intake among the animals in the present study was 1.76 kg DM/day while the SD for the Calf PV index was €69.14; given the correlation of -0.22 between the two, animals in the top 20% of the population for Calf PV were expected to eat, on average, 0.54 kg DM/d less than the average animal who was eating 13.09 kg DM/d; this represents a difference of 0.31 SD units. Assuming a constant differential of 0.31 SD over a 120-d finishing period, this saving would be expected to accumulate to a reduction in feed intake of 65.20 kg DM and, based on a cost of € 0.29 / kg DM, this equates to a saving of almost € 20 per animal (just over the finishing period). The SD for feed intake, however, does not remain consistent across the animal’s lifetime. From a review of the literature in cattle, as well as from data used in the present study, the published SD for DMI of growing cattle was plotted against age in Figure 1 ([Myers et al., 1999](#_ENREF_32); [Wang et al., 2006](#_ENREF_39); [Kelly et al., 2010a](#_ENREF_22); [Kelly et al., 2010b](#_ENREF_24); [Kelly et al., 2011](#_ENREF_23); [Khan et al., 2012](#_ENREF_26); [Durunna et al., 2013](#_ENREF_13)). A linear regression line was subsequently fitted to the data regressing the SD of DMI on age with regression model being:

$$SD\_{DMI} = 0.6975+ 0.0018 x age$$

Assuming the calculated relative difference of 0.31 SD units in DMI between the top 20% of animals on PV versus the those average on PV remains the same throughout life, it was possible to estimate the expected kg DM difference in DMI per day from the linear regression model solutions for each day of age (Figure 2). Animals in the present study were, on average, 548 days of age at harvest (at the end of their test). Therefore, if purchased at 248 days of age (i.e., 300 days of feeding), it is estimated that animals in the top 20 % stratum would eat just under 132 kg DM less than the average, equating to a saving of € 38; assuming a price of € 0.29 per kg of DM. If the animals were, however, only purchased 100 d prior to harvest, the saving would only be € 14.41.

***Index deployment***

 In its simplest form, the index published for an animal could graduate from being the terminal index value (includes calving performance) at the national genetic evaluation immediately post conception, to the calf index coinciding with the first national genetic evaluation after the birth of the animal. While the Harvest index value of an animal can easily be calculated concurrently with that of the calf index value (by simply removing the contribution of both the docility and feed intake measures), the actual Harvest index value could be published as the animal nears it expected harvest date. Nevertheless, such a naïve system would consist of a re-estimation of index values concurrent with the release of each national genetic evaluation which, in most cases, is only 3 to 6 times annually. An additional shortcoming of the proposed indexes within the present study is the number of traits considered is limited, which here is simply a function of the data available for genetic evaluations.

Given the accelerating developments in the internet of things (IoT; Al-Fuqaha et al., 2015), animal level sensors for measuring different characteristics (Johnsen et al., 2019; colostrum immunoglobulin (IgG) in saliva), biomarkers for growth (Ibeagha-Awemu and Zhao 2015; epigenetics), hormone surveillance (Nebbia et al., 2011; growth hormone detection), as well as the associated systems for traceability like blockchain ([Makhdoom et al., 2018](#_ENREF_27)), there is massive potential to improve, not only the dynamic nature of the indexes, but also the completeness and validity of the data contributing to the index values. While one of the current limitations of the present study is the incorporation of only a few traits in the overall index, there is also a reliance on producers to accurately record the data (e.g. calving difficulty score) in order to provide reliable estimates. Blockchain technology offers the potential to include considerably more traits (e.g., animal health and remedies administered, prediction of IgG consumed after birth, number of animal movements) and, in doing so, offer a system to ensure data integrity, thus improving the credibility of the data used in the evaluations. Such data could include information on the animal that spans from their healthcare history to movements, thus providing a full traceability report that can be verified by the different peers. The two proposed indexes have the capability of utilizing more information and being integrated into IoT systems to provide updated predictions of carcass value and details of provenance as the uptake in the technology intensifies. The outcome is more accurate (dynamic) predictions of not only carcass value but also the potential costs of production; for example, did the young calf receive sufficient IgG from colostrum.

The benefit of including a single live-weight phenotype in the genetic evaluation for improving the accuracy of predicting carcass was clear (Table 7), although the benefit of additional live-weight records was minimal; the relatively low return in prediction accuracy with additional live-weight records is most likely due to the high heritability of live-weight in cattle ([Nephawe et al., 2004](#_ENREF_34); [McHugh et al., 2011](#_ENREF_29)) coupled with the strong genetic correlation that exists among live-weight records at different life-stages ([McHugh et al., 2011](#_ENREF_29)). Live-weight phenotypes are often recorded at livestock auctions in Ireland immediately prior to slaughter. These information sources could be integrated via selection index methodology into the final index estimate of an animal, much like the ad hoc blending approach used in two-step genomic evaluations (e.g., VanRaden et al., 2019).

Linking IoT with application programming interfaces (APIs) could provide an excellent route to market for such an index. Several hundred animals can be traded in livestock marts on a given day. These animals are usually booked in the day before. Prospective purchasers of cattle could download all registered animal details the day before the sale onto their mobile devices. Animals could be filtered for personal preferences such as breed type, genotype status or age. Using the animal RFID tags, those on the filtered list could then be visually inspected the following day and their respective transaction index studied. Potential then exists for the prospective purchaser to score the animal on quality or other metrics (e.g. docility, defects). While these data can be uploaded to the cloud for later integration into genetic evaluations, the scoring system can also be used by the auction for scheduling the sale time of animals to minimize conflicts but also used to alert the prospective purchaser of the location and time of the next sale.

Another possibility entirely could be the introduction of a brokerage system, whereby an intermediate party could link potential sellers to buyers and *vice versa* based on their criteria, without the animals needing to visit an intermediary location. This direct farm-to-farm movement would minimize the stress on animals with obvious welfare and biosecurity benefits as well as potential cost savings for both parties in the transaction.

**CONCLUSION**

Selection indexes have revolutionized animal breeding by providing decision-support to assist in the identification of genetically superior animals as candidate parents of the next generation. The Calf and Harvest indexes proposed in the present study are a simple evolution of existing selection indexes by 1) focusing on just the traits pertinent to the live animals, 2) including non-additive genetic effects in the prediction of total genetic merit and 3) including also relevant (and available) non-genetic effects in the prediction of eventual carcass value. A simplistic approach to incorporate inter-animal differences in the cost of production was also demonstrated. The end result of such developments is a more accurate prediction of eventual carcass value. Inclusion of live-weight data on the animal itself also improves the accuracy of prediction thus providing an incentive for recording data; while the present study was limited to only traits already considered in the national terminal indexes, the rapid developments in IoT and blockchain facilitates the recording and storage of additional data with less opportunity for manipulation.

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**TABLES**

Table 1: Component traits of the different indexes evaluated, including the traits units of measurement, genetic standard deviation (SD) and economic weighting

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | Indexes |  |  |  |  |
| Component trait | National Terminal | Calf | Harvest | Units | Genetic SD | Economic weight |
| Calving difficulty | 🗸 | - | - | % | 0.158 | -€4.65 |
| Calving mortality | 🗸 | - | - | 0 to 1 | 0.038 | -€5.34 |
| Gestation length | 🗸 | - | - | Days | 3.020 | -€2.25 |
| Docility | 🗸 | 🗸 | - | 1 (very quiet) to 5 (very difficult) | 0.365 | €17.03 |
| Feed intake | 🗸 | 🗸 | - | Kg DM per lifetime | 0.667 | -€38.63 |
| Carcass weight | 🗸 | 🗸 | 🗸 | Kg | 15.419 | €3.14 |
| Carcass Conformation | 🗸 | 🗸 | 🗸 | EUROP scaleE (best) to P (worst) | 0.644 | €14.77 |
| Carcass Fat | 🗸 | 🗸 | 🗸 | 1 (leanest) to 15 (fattest) | 0.679 | -€7.86 |

Table 2: Phenotypic records included in each individual carcass genetic evaluation iteration, whereby phenotypes encompass the traits carcass weight, carcass conformation, carcass fat and, feed intake phenotypic records. Live-weight phenotypes were recorded at 4 different age-points of the animals.

|  |  |  |
| --- | --- | --- |
| Genetic evaluation iteration | Phenotypes | Live-weight (d) |
| 150-250 | 250-350 | 350-450 | 450-550 |
| 1 | 🗸 | 🗸 | 🗸 | 🗸 | 🗸 |
| 2 | - | - | - | - | - |
| 3 | - | 🗸 | - | - | - |
| 4 | - | - | 🗸 | - | - |
| 5 | - | - | - | 🗸 | - |
| 6 | - | - | - | - | 🗸 |
| 7 | - | - | 🗸 | 🗸 | 🗸 |

Table 3: The mean index value, least square means and standard error (within parenthesis) of animals within the top and bottom 25% when ranked on their Irish national terminal, Calf and Harvest index values, separately

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  | Means (SE) |
|  | Rank |  | Terminal | Calf | Harvest |
| Index Value (€) | Bottom 25 % |  | 103.24 (2.47)a | 232.30 (2.92)b | 254.16 (2.93)c |
| Top 25 % |  | 246.92 (1.32)a | 406.70 (1.67)b | 408.76 (1.66)b |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| Carcass revenue (€) | Bottom 25 % |  | 1497 (13.35)a | 1483 (12.81)a | 1463 (12.48)a |
| Top 25 % |  | 1688 (13.20)a | 1716 (12.87)a | 1723 (12.26)a |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| Price per kg | Bottom 25 % |  | 4.07 (0.01)a | 4.07 (0.01)a | 4.07 (0.01)a |
| Top 25 % |  | 4.19 (0.01)a | 4.19 (0.01)a | 4.18 (0.01)a |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| Carcass weight (kg) | Bottom 25 % |  | 366.95 (2.94)a | 363.73 (2.83)ab | 358.63 (2.75)b |
| Top 25 % |  | 401.75 (2.91)a | 408.62 (2.85)ab | 411.15 (2.70)b |
|  |  |  |  |  |  |
| Carcass conformation | Bottom 25 % |  | 9.28 (0.09)a | 9.24 (0.09)a | 9.27 (0.09)a |
| Top 25 % |  | 11.21 (0.09)a | 11.19 (0.09)a | 11.04 (0.09)a |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| Carcass fat | Bottom 25 % |  | 7.39 (0.09)a | 7.34 (0.09)a | 7.25 (0.09)a |
| Top 25 % |  | 6.00 (0.08)a | 6.00 (0.09)a | 6.14 (0.09)a |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| Feed intake(kg DM) | Bottom 25 % |  | 13.31 (0.11)a | 13.37 (0.11)a | 13.21 (0.11)a |
| Top 25 % |  | 12.57 (0.11)a | 12.55 (0.11)a | 12.89 (0.11)b |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| Age at slaughter (d) | Bottom 25 % |  | 572.61 (4.18)a | 576.34 (4.16)ab | 586.90 (4.04)b |
| Top 25 % |  | 545.71 (4.14)a | 541.09 (4.22)a | 534.86 (4.09)a |

Different superscripts across the indexes for each trait indicate a difference (p < 0.05)

**Table 4:** Partial and within-sex correlations between the three formulations of an individual’s total merit (i.e., just breed effects, inter- and intra-breed effects (EBV) or production value estimates (PV)) for a given trait and the corresponding phenotypic values for the trait. Regression coefficients, standard errors (within parenthesis), and coefficient of determination of each traits phenotype regressed on the respective three variant estimates

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | Correlations |  |  |
|  |  | Partial (n=874) | Steer (n=374) | Ybull (n=500) | Regression (n=874) | R-square |
| Trait |  |
| Carcass weight | Breed  | 0.16a | 0.03a | 0.26a | 0.94 (0.24) | 0.64 |
| EBV | 0.36b | 0.33b | 0.40b | 1.27 (0.09) | 0.70 |
| PV | 0.40c | 0.40c | 0.42b | 1.26 (0.09) | 0.72 |
|  |  |  |  |  |  |  |
| Carcass conformation | Breed  | 0.51a | 0.55a | 0.49a | 1.20 (0.09) | 0.72 |
| EBV | 0.64b | 0.65b | 0.66b | 1.09 (0.05) | 0.78 |
| PV | 0.64b | 0.66b | 0.66b | 1.09 (0.05) | 0.78 |
|  |  |  |  |  |  |  |
| Carcass fat | Breed  | 0.40a | 0.46ab | 0.37a | 1.14 (0.12) | 0.61 |
| EBV | 0.42a | 0.44b | 0.44b | 1.10 (0.09) | 0.64 |
| PV | 0.47b | 0.47a | 0.49c | 1.03 (0.08) | 0.65 |
|  |  |  |  |  |  |  |
| Feed Intake | Breed  | 0.35a | 0.38a | 0.35a | 1.08 (0.10) | 0.53 |
| EBV | 0.37a | 0.40a | 0.35a | 0.84 (0.08) | 0.52 |
| PV | 0.38a | 0.42a | 0.36a | 0.83 (0.08) | 0.53 |
|  |  |  |  |  |  |  |
|  |  | Partial (n=438) | Steer (n=122) | Ybull (n=316) | Regression (n=438) |  |
|  |  |  |  |  |  |  |
| Docility | Breed  | -0.01a | 0.00a | -0.01a | 1.61 (0.73) | 0.49 |
| EBV | 0.14b | 0.15b | 0.14b | 0.67 (0.16) | 0.51 |
| PV | 0.14b | 0.14b | 0.15b | 0.67 (0.16) | 0.51 |

Different superscripts between the different estimations of total merit for each trait separately indicate a difference (p < 0.05)

Table 5: Partial correlations between three indexes calculated formulations of an individual’s total merit (i.e., just breed effects, inter- and intra-breed effects (EBV) or production value estimates (PV)) and the three carcass traits (weight, conformation and fat), feed intake and docility

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Indexes | Sub-components | Carcass weight (n = 874) | Carcass conformation (n = 874) | Carcass fat (n = 874) | Feed intake  (n = 874) | Docility (n = 438) |
|
| Terminal | EBV | 0.21 | 0.53 | -0.43 | -0.24 | 0.01 |
|
|  |  |  |  |  |  |  |
| Calf | Breed | 0.12a | 0.49a | -0.44ab | -0.39a | -0.04a |
|  | EBV | 0.29b | 0.57b | -0.44a | -0.25b | 0.02b |
|  | PV | 0.33c | 0.56b | -0.40b | -0.22c | 0.00ab |
|  |  |  |  |  |  |  |
| Harvest | Breed | 0.15a | 0.49ab | -0.45a | -0.35a | -0.01ab |
|  | EBV | 0.35b | 0.53a | -0.39b | -0.12b | 0.05a |
|  | PV | 0.39c | 0.50b | -0.35c | -0.09c | 0.02b |

n = number of animals included in analysis

Different superscripts between the three different formulations of the indexes for each trait separately indicate a difference (p < 0.05)

 **Table 6:** Partial and within-sex correlations between the three indexes calculated using formulations of an individual’s total merit (i.e., just breed effects, inter- and intra-breed effects (EBV) or production value estimates (PV))and the simulated quality pricing carcass value as well as the price/kg based on the quality pricing grid payment structure common to Ireland where n = number of animals

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | Quality Pricing Carcass Value |  | Price/kg |
| Indexes | Sub-components | Partial (n=874) | Steer (n=374) | Ybull (n=500) |  | Partial (n=874) | Steer (n=374) | Ybull (n=500) |
| Terminal | EBV | 0.29 | 0.29 | 0.32 |  | 0.54 | 0.63 | 0.51 |
|  |  |  |  |  |  |  |  |  |
| Calf | Breed | 0.20a | 0.18a | 0.22a |  | 0.50a | 0.58a | 0.46a |
| EBV | 0.36b | 0.35b | 0.42b |  | 0.58b | 0.65b | 0.57b |
| PV | 0.40c | 0.38c | 0.45c |  | 0.57b | 0.64b | 0.55b |
|  |  |  |  |  |  |  |  |  |
| Harvest | Breed | 0.22a | 0.15a | 0.29a |  | 0.50ab | 0.58ab | 0.48ab |
| EBV | 0.41b | 0.40b | 0.48b |  | 0.53a | 0.62a | 0.51a |
| PV | 0.44c | 0.44c | 0.49b |  | 0.50b | 0.60b | 0.48b |

Different superscripts between the three different formulations of the indexes for each trait separately indicate a difference (p < 0.05)

Table 7: Partial correlations across a sub-set of 459 validation animals between the three indexes constructed using formulations of an individual’s total merit (i.e., just breed effects, inter- and intra-breed effects (EBV) or production value estimates (PV)) and the simulated carcass value; n = number of live-weight phenotype records taken at each specific time points included in each genetic evaluation iteration

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|   |   |   | 250-349 d | 350-449 d | 450-549 d | 250-449 d | 250-549 d |
| Indexes | Sub-components | (n = 0) | (n = 1) | (n = 1) | (n = 1) | (n = 2) | (n = 3) |
| Terminal | EBV | 0.30a | 0.36b | 0.36b | 0.39c | 0.37d | 0.39c |
|  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |
| Calf | Breed | 0.18a1 | 0.18a1 | 0.18a1 | 0.18a1 | 0.18a1 | 0.18a1 |
| EBV | 0.38a2 | 0.44b2 | 0.43bc2 | 0.46de2 | 0.44cd2 | 0.46e2 |
| PV | 0.41a3 | 0.46b3 | 0.46bc3 | 0.49d3 | 0.47c3 | 0.49e3 |
|  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |
| Harvest | Breed | 0.23a1 | 0.23a1 | 0.23a1 | 0.23a1 | 0.23a1 | 0.23a1 |
| EBV | 0.47a2 | 0.54b2 | 0.55b2 | 0.58c2 | 0.56d2 | 0.59c2 |
| PV | 0.51a3 | 0.57b3 | 0.58b3 | 0.61c3 | 0.59d3 | 0.62c3 |

Different superscripts indicate a difference (p < 0.05) between the correlation coefficients within row (letters) and within each index (1,2,3)

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**Figure 1:** Standard deviation of dry matter intake (kg/d) corresponding to the reported age of animals in [Khan et al. (2012)](#_ENREF_26) (orange diamond), [Myers et al. (1999)](#_ENREF_32) (purple triangle), [Wang et al. (2006)](#_ENREF_39) (orange square), [Durunna et al. (2013)](#_ENREF_13) (purple square), [Kelly et al. (2010a)](#_ENREF_22) (light blue diamond), [Kelly et al. (2011)](#_ENREF_23) (blue diamond), ([Kelly et al., 2010b](#_ENREF_24))(navy diamond), average feed intake SD using Tully feed intake performance data when ranked on age (pink circle) and, the present study (green diamond) as well as equation of the line



Figure 2: The accumulating difference in the standard deviation of dry matter intake (kg of DMI) between animal in the top 20% for the Calf index and the average as the animal ages.

**APPENDIX**

Statistical models used in the carcass, docility and calving genetic evaluations were as follows:

$$Carcass trait\_{abcdefghijklm}= \sum\_{a=1}^{4}heterosis\_{a}+\sum\_{b=1}^{16}breed\_{b}+ \sum\_{c=1}^{3}age^{c}+ twin\_{d}+byr\_{e}+ abattoir CG\_{f}+\sum\_{g=1}^{2}HY\_{g}+dam fraction\_{h}+dam age\_{i}|dam parity\_{j}+dam pe\_{k}+ animal\_{l}+residual\_{m}$$

$$Feed intake\_{abcdenhijlm}= \sum\_{a=1}^{4}heterosis\_{a}+\sum\_{b=1}^{16}breed\_{b}+ \sum\_{c=1}^{3}age^{c}+ twin\_{d}+byr\_{e}+ HYS\_{n}+dam fraction\_{h}+dam age\_{i}|dam parity\_{j}+ animal\_{l}+residual\_{m}$$

$$Liveweight\_{abcdegphijkqlm}= \sum\_{a=1}^{4}heterosis\_{a}+\sum\_{b=1}^{16}breed\_{b}+ \sum\_{c=1}^{3}age^{c}+ twin\_{d}+byr\_{e}+ \sum\_{g=1}^{2}HY\_{t}+HY\_{p}+dam fraction\_{h}+dam age\_{i}|dam parity\_{j}+dam pe\_{k}+sex\_{q}+ animal\_{l}+residual\_{m}$$

$$Docility\_{abcrsjqlm}= heterosis\_{a}+\sum\_{b=1}^{16}breed\_{b}+ \sum\_{c=1}^{2}age^{c}+recombination\_{r}+HYS\_{s}+dam parity\_{j}+sex\_{q}+ animal\_{l}+ residual\_{m}$$

$$Calving difficulty and mortality\_{aeuijkqlm}= \sum\_{a=1}^{4}heterosis\_{a}+byr\_{e}+HYS\_{u}+dam age\_{i}|dam parity\_{j}+dam pe\_{k}+sex\_{q}+ animal\_{l} + residual\_{m}$$

$$Calving gestation\_{aevijkqlm}= \sum\_{a=1}^{4}heterosis\_{a}+byr\_{e}+HYS\_{v}+dam age\_{i}|dam parity\_{j}+dam pe\_{k}+sex\_{q}+ animal\_{l} + residual\_{m}$$

$Carcass trait\_{abcdefghijklm}$ = carcass traits (i.e., weight, conformation and fat); $Feed intake\_{abcdenhijlm}$ = feed intake trait; $Liveweight\_{abcdegphijkqlm}$ = live-weights recorded between the ages 150 d and 250 d old (weanlings), between 251 d and 350 d old (adolescent), between 351 d and 450 d old (adult), and between 451 d and 550 d old (finisher); $Docility\_{abcrsjqlm}$ = docility phenotypes; $Calving difficulty and mortality\_{aeuijkqlm}$ = calving difficulty and mortality traits; $Calving gestation\_{aevijkqlm}$ = calving gestation; $heterosis\_{a}$ = heterosis coefficient *a*; $breed\_{b}$ = covariate representing the proportion of 16 breeds *b* in the animal (i.e., Aberdeen Angus (AA), Aubrac (AU), Blonde D’Aquitaine (BA), Belgian Blue (BB), Charolais (CH), Friesian (FR), Hereford (HE), Holstein (HO), Jersey (JE), Limousin (LM), Piemontese (PI), Montbelliarde (MO), Parthenais (PT), Salers (SA), Shorthorn (SH) and Simmental (SI); $age\_{c}$ = age of the animal (linear, quadratic and cubic for all traits except for docility which included linear and quadratic age) at the time of slaughter for carcass traits (i.e., weight, conformation, fat, feed intake recording for feed intake trait, or docility scoring for docility trait;$ twin\_{d}$ = whether or not the animal was a twin; $byr\_{e}$ = birth year of theanimal *l*; $abattoir CG\_{f}$ = the covariate representing the abattoir contemporary group *f* coefficient of animal *l*; $HY\_{g}$,$ HY\_{t}$ $HYS\_{n}$, $HYS\_{s}$, $HYS\_{u}$ and $HYS\_{v}$ = contemporary group coefficient of 1) herd-year *g* (carcass traits; including contemporary group coefficient for herd that animal *l* was harvested in and the previous herd that animal *l* spent the most time in), 2) herd-year *t* (live-weights; including contemporary group coefficient for herd that animal *l*’s live-weight was recorded in and the previous herd that animal *l* spent the most time in), 3) herd-year-season *n* of feed intake recording, 4) herd-year-season *s* of docility recording, 5) herd-year-season *u* of calving and, 6) herd-year-season *v* of gestation; $dam fraction\_{h}$ = dam dairy breed fraction coefficient *h*;$ dam age\_{i}|dam parity\_{j}$ = the interaction between dam age *i* and the dams *j*th parity (i.e., 1 to 7, inclusive) for all traits with exception to docility whereby just the dams *j*th parity is modeled;$ dam pe\_{k}$= permanent environment effect of *k*, animal *l*’s dam; $sex\_{q}$ = sex which was male or female docility, otherwise, bull, steer or heifer; $recombination\_{t}$ = recombination coefficient

**SUPPLEMENTARY MATERIAL**

**Supplementary Table 1:** Quality based pricing grid displaying cent (€) per kg corresponding to the EUROP carcass classifications and fat grade awarded to the carcass

|  |  |
| --- | --- |
|   | EUROP Classification |
| Fat grade | E+ | E= | E- | U+ | U= | U- | R+ | R= | R- | O+ | O= | O- | P+ | P= | P- |
| 1- | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 382 | 376 | 370 | 364 | 358 | 352 |
| 1= | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 382 | 376 | 370 | 364 | 358 | 352 |
| 1+ | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 382 | 376 | 370 | 364 | 358 | 352 |
| 2- | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 382 | 376 | 370 | 364 | 358 | 352 |
| 2= | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 382 | 376 | 370 | 364 | 358 | 352 |
| 2+ | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 382 | 376 | 370 | 364 | 358 | 352 |
| 3- | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 388 | 382 | 376 | 370 | 364 | 358 |
| 3= | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 388 | 382 | 376 | 370 | 364 | 358 |
| 3+ | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 388 | 382 | 376 | 370 | 364 | 358 |
| 4- | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 388 | 382 | 376 | 370 | 364 | 358 |
| 4= | 442 | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 400 | 388 | 376 | 370 | 364 | 358 | 352 |
| 4+ | 436 | 430 | 424 | 418 | 412 | 406 | 400 | 394 | 394 | 382 | 376 | 370 | 364 | 358 | 352 |
| 5- | 418 | 412 | 406 | 400 | 394 | 388 | 382 | 376 | 376 | 364 | 358 | 352 | 346 | 340 | 334 |
| 5= | 418 | 412 | 406 | 400 | 394 | 388 | 382 | 376 | 376 | 364 | 358 | 352 | 346 | 340 | 334 |
| 5+ | 418 | 412 | 406 | 400 | 394 | 388 | 382 | 376 | 376 | 364 | 358 | 352 | 346 | 340 | 334 |