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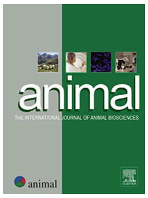

Formulation of a decision support tool incorporating both genetic and non-genetic effects to rank young growing cattle on expected market value

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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 predict 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 composed of three carcass-related traits [i.e., 1) carcass weight, 2) carcass conformation and 3) carcass 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 all 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 [**PVs**]). 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; the correlation coefficients almost doubled in strength when total merit was based on PV-based estimates as compared to the breed solutions alone. Including phenotypic live-weight data, collected during the animal's life, strengthened the predictive ability of the indexes further. Based on the results presented, the proposed indexes may fill the void in decision support when purchasing or selling cattle. In addition, given the dynamic nature of indexes, they have the potential to be updated in real-time as information becomes available.

Implications

A large proportion of cattle are traded every year for beef production, yet there are few decision-support tools which aid in the identification of superior animals for beef harvesting. The current study presents the framework for novel decision-support tools that ranks growing cattle based on their predicted carcass revenue potential. As the indexes presented are not for breeding purposes, the animal's total merit for a given trait was calculated using not only their additive and non-additive genetic effects but also non-genetic effects. Thus, ensuring more informed data-driven decision-support is provided to cattle traders.

Introduction

Individual animal ranking on beef breeding indexes is widely used to support decisions for selecting candidate parents of the next generation (Berry et al., 2019). In the absence of genotype-by-environment interactions, the progeny of genetically superior animals are, on average, expected to 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

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index values, if economic-based, still provide an indication of the expected profit of that animal and therefore have the potential to be utilised when trading cattle prior to harvesting. Despite this potential, there is a void in the literature available relating to the possibility of incorporating breeding index values into such a decision support tool framework. The applicability of such breeding indices for live animals destined for slaughter are, however, limited in that: 1) they are constructed solely from an animal's additive genetic merit without cognisance of either the non-additive genetic effects (e.g., heterosis) or the non-genetic effects (e.g., dam parity) and 2) the indexes often include traits that become redundant to the expected profit of a growing animal itself once born (e.g., genetic merit for stillbirth).

Both non-additive genetic effects and non-genetic effects are known to impact the performance of growing cattle. Gregory et al. (1978) carried out extensive research into heterosis values in beef cattle and reported that crossbred calves were weaned 7.4% heavier than purebred calves. Connolly et al. (2016) documented that third parity cows produced progeny carcasses 1.1 kg heavier than progeny from second parity cows; furthermore, progeny from second parity cows had, on average, 2.04 kg heavier carcasses than progeny from primiparous cows. McHugh et al. (2014) reported that up to the point of weaning, male 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 cognisance of both additive and non-additive genetic effects as well as contributing non-genetic effects. Such an index has the potential to be targeted towards beef-finishing systems to aid not only in the purchase of animals destined for slaughter but also for better aligning animals to different production and finishing systems; with modifications, the index could also be used by beef processors when agreeing flat prices for cattle prior to slaughter.

Material and methods

Data

Three separate phenotypic data sets used in the Irish national genetic evaluations were obtained from the Irish Cattle Breeding Federation (**ICBF**). The first data set 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 data set 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 data set 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 three life-stage points, namely between the ages 250 days up to 350 days old (adolescent), between 350 days up to 450 days old (adult) and between 450 days up to 550 days old (finisher). The three data sets 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. Heterosis and recombination coefficients were available for all animals, estimated using the methodology reported by VanRaden and Sanders (2003). For the genetic evaluation of docility, only a single general heterosis covariate was included in the model while when the genetic evaluation was for the carcass traits a separate individual and dam heterosis covariate was considered for both dairy × beef cross and beef × beef cross (since more breed crosses existed).

Genetic evaluations

Genetic evaluations were run for the three suites of traits using the Mix99 software suite (Mix99 Development Team, 2015) 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 24×24 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 3×3 multi-trait evaluation which included the traits weanling docility assessed by producers or trained professionals, separately, and producer-scored docility of the dam; only the producer-scored 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. Although the calving genetic evaluation was a 9×9 multi-trait evaluation, only random effect solutions were retained for a subset of the three relevant traits, namely calving mortality, calving difficulty and gestation length. The statistical models used in the respective genetic evaluations are summarised in Supplementary Material S1 and Supplementary Table S1.

Production value estimation

Genetic evaluations in Ireland use genetic groups (stratified by breed) 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 as follows: 1) using just the breed effect solutions, 2) using the animal's additive genetic merit combined with the breed effect solutions (EBV) and 3) to estimate an animal's production value (**PV**) using the breed, additive genetic merit as well as the non-additive and non-genetic effects from the respective genetic evaluations as described in Supplementary Material S2.

Index development

The Irish national beef Terminal index comprises eight traits including three calving traits (i.e., difficulty, gestation length and mortality), feed intake, docility and three carcass traits (i.e., weight, conformation and fat) (Supplementary Table S2); 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 (Supplementary Table S2) 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 five economically important traits, namely docility, feed intake, carcass weight, carcass conformation and carcass fat (Supplementary Table S2).
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 economically important traits, namely carcass weight, carcass conformation and carcass fat (Supplementary Table S2).

Index validation

A subset of animals from the national beef bull performance test centre at Tully, Co. Kildare, Ireland, was identified to validate each of the constructed indexes. The validation population consisted of 374 steers and 500 young bulls that were slaughtered between the years 2016 and 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) and Kelly et al. (2019).

Price (€) per kg of carcass weight was determined using the EUROP beef classification grid scores (Englishby et al., 2016). The EUROP classification system describes the carcass conformation as well as the fat cover outside and in the thoracic cavity of a carcass and ranges from E (excellent conformation) to P (poor conformation) and 1 (very low fat) to 5 (very high fat), respectively (Englishby et al., 2016); both metrics, along with other external factors (e.g., supply and demand), are used by Irish abattoirs in determining carcass price per kg. The price per kg for different carcass conformation score by fat score credentials is summarised in Supplementary Table S3. To generate the animal's total carcass value, price per kg was multiplied by their carcass weight. Given the on-going promotion of animal live-weight recording, especially in Ireland, the carcass genetic evaluations were rerun seven times while the docility genetic evaluation was rerun twice to reflect the scenario where additional information (e.g., live-weight phenotypes) becomes available as the animal grows; all phenotypic records belonging to all other animals not pertaining to the validation population were also included in each genetic evaluation scenario. The first scenario of the carcass and docility national genetic evaluations contained all phenotypes of the validation animals to determine the upper threshold of predictive ability. In the next scenario, 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. A subset of 459 animals within the validation population was identified as having live-weight phenotypes recorded at three different age categories. Therefore, for the third, fourth, and fifth scenario of the carcass national genetic evaluations, a single live-weight record pertaining to the validation population subset was included, separately, for the age category 250 days up to 350 days ($n = 459$), 350 days up to 450 days up ($n = 459$) or 450 days up to 550 days ($n = 459$), respectively (Supplementary Table S4). For the sixth scenario of the carcass national genetic evaluations, two live-weight records pertaining to the subset of validation animals that spanned from 250 days to 450 days were included ($n = 459$). For the final scenario of the national carcass genetic evaluation, the phenotypes of animals within the validation population that had a live-weight record for each of the three age categories spanning from 250 days to 550 days were included ($n = 459$).

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. Using SAS 9.4 software (SAS Institute Inc., Cary, NC), the least squares 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 LSM for age at slaughter); no multiple-comparison correction was undertaken when comparing the different LSM.

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 estimated. The statistical test proposed by Steiger (1980) 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 animal's total merit for a given trait as summarised in Supplementary Material S3.

Results

The mean performance of animals ranked on their national beef Terminal, Calf and Harvest index values is shown in Table 1. 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 shown in Table 2. 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 the exception of 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 shown in Table 2. With the exception of carcass weight and feed intake, the regression coefficient was always closer to 1 for the total merit derived using PVs relative to the total merit estimated using just breed, although it was 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 from 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 PVs, 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 shown in Table 3. Regardless of the index, or how it was formulated (i.e., breed effects only, EBVs, or PVs), 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). Of all the traits, carcass conformation was the most strongly correlated with each of the indexes evaluated.

Table 1
The mean index value, least square means and SE (within parenthesis) of beef females within the top and bottom 25% when ranked on their Irish national Terminal (Terminal), Calf and Harvest index values, separately.

Item	Rank	Means (SE)		
		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 (days)	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}

^{a,b,c} Values within a row with different superscripts indicate a significant difference of $P < 0.05$.

Correlations with revenue metrics

The correlations between each of the three indexes with both the total carcass value and price per kg are shown in Table 4. 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 per 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 carcass revenue as the number of live-weight records available for each individual included in the genetic evaluation changed are shown in Table 5. 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 4, 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 days 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 days of age. Partial correlations were either 0.18 between carcass value and Calf index or 0.23 between the Harvest index and carcass value regardless of the number of live-weight records

Table 2
Partial and within-sex correlations between the three formulations of an individual beef female's total merit (i.e., just breed effects (Breed), then breed plus the additive genetic merit (EBV), then breed plus the additive, non-additive and non-genetic effects in the form of production value estimates (PV)) for a given trait and the corresponding realised 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.

Trait		Correlations			Regression ($n = 874$)	R-square
		Partial ($n = 874$)	Steer ($n = 374$)	Young bull ($n = 500$)		
Carcass weight	Breed[1]	0.16^{a}	0.03^{a}	0.26^{a}	0.94 (0.24)	0.64
	EBV[2]	0.36^{b}	0.33^{b}	0.40^{b}	1.27 (0.09)	0.70
	PV[3]	0.40^{c}	0.40^{c}	0.42^{b}	1.26 (0.09)	0.72
Carcass conformation	Breed[1]	0.51^{a}	0.55^{a}	0.49^{a}	1.20 (0.09)	0.72
	EBV[2]	0.64^{b}	0.65^{b}	0.66^{b}	1.09 (0.05)	0.78
	PV[3]	0.64^{b}	0.66^{b}	0.66^{b}	1.09 (0.05)	0.78
Carcass fat	Breed[1]	0.40^{a}	0.46^{ab}	0.37^{a}	1.14 (0.12)	0.61
	EBV[2]	0.42^{a}	0.44^{b}	0.44^{b}	1.10 (0.09)	0.64
	PV[3]	0.47^{b}	0.47^{a}	0.49^{c}	1.03 (0.08)	0.65
Feed intake	Breed[1]	0.35^{a}	0.38^{a}	0.35^{a}	1.08 (0.10)	0.53
	EBV[2]	0.37^{a}	0.40^{a}	0.35^{a}	0.84 (0.08)	0.52
	PV[4]	0.38^{a}	0.42^{a}	0.36^{a}	0.83 (0.08)	0.53
		Partial ($n = 438$)	Steer ($n = 122$)	Young bull ($n = 316$)	Regression ($n = 438$)	R-square
Docility	Breed[1]	−0.01^{a}	0.00^{a}	−0.01^{a}	1.61 (0.73)	0.49
	EBV[2]	0.14^{b}	0.15^{b}	0.14^{b}	0.67 (0.16)	0.51
	PV[5]	0.14^{b}	0.14^{b}	0.15^{b}	0.67 (0.16)	0.51

^{a,b,c} Within each trait, values within a column with different superscripts indicate a significant difference of $P < 0.05$.

[1] Breed included breed effects.

[2] EBV included breed and additive genetic merit effects.

[3] PV included breed, additive genetic merit, heterosis, twin, dam dairy breed fraction, dam age and parity interaction, dam permanent environment effects.

[4] PV included breed, additive genetic merit, heterosis, twin, dam dairy breed fraction and dam age and parity interaction effects.

[5] PV included breed, additive genetic merit, heterosis, recombination, sex and dam parity effects.

Table 3
Partial correlations between three indexes calculated using formulations of an individual beef female's total merit (i.e., just breed effects (Breed), then breed plus the additive genetic merit (EBV), then breed plus the additive, non-additive and non-genetic effects in the form of production value estimates (PV)) and the realised phenotypic values for 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[2]	0.21	0.53	-0.43	−0.24	0.01
Calf	Breed[1]	0.12^{a}	0.49^{a}	−0.44^{ab}	−0.39^{a}	−0.04^{a}
	EBV	0.29^{b}	0.57^{b}	−0.44^{a}	−0.25^{b}	0.02^{b}
	PV[3]	0.33^{c}	0.56^{b}	−0.40^{b}	−0.22^{c}	0.00^{ab}
Harvest	Breed[1]	0.15^{a}	0.49^{ab}	−0.45^{a}	−0.35^{a}	−0.01^{ab}
	EBV[2]	0.35^{b}	0.53^{a}	−0.39^{b}	−0.12^{b}	0.05^{a}
	PV[4]	0.39^{c}	0.50^{b}	−0.35^{c}	−0.09^{c}	0.02^{b}

^{a,b,c} Within each index, values within a column with different superscripts indicate a significant difference of $P < 0.05$.

[1] Breed: only breed effects were included within the index.

[2] EBV effects included within the index were breed and additive genetic merit effects.

[3] PV effects included within the index were breed, additive genetic merit, heterosis, twin, dam dairy breed fraction, dam age and parity interaction (as well as just dam parity for the docility trait), dam permanent environment, recombination and sex effects.

[4] PV effects included within the index were breed, additive genetic merit, heterosis, twin, dam dairy breed fraction, dam age and parity interaction, dam permanent environment effects.

Table 4
Partial and within-sex correlations between the three indexes calculated using formulations of an individual beef female's total merit (i.e., just breed effects (Breed), then breed plus the additive genetic merit (EBV), then breed plus the additive, non-additive and non-genetic effects in the form of production value estimates (PV)) and the realised total carcass value as well as the price/kg based on the quality pricing grid payment structure common to Ireland.

Indexes	Sub-components	Total carcass value			Price/kg		
		Partial ($n = 874$)	Steer ($n = 374$)	Young bull ($n = 500$)	Partial ($n = 874$)	Steer ($n = 374$)	Young bull ($n = 500$)
Terminal	EBV[2]	0.29	0.29	0.32	0.54	0.63	0.51
Calf	Breed[1]	0.20^{a}	0.18^{a}	0.22^{a}	0.50^{a}	0.58^{a}	0.46^{a}
	EBV	0.36^{b}	0.35^{b}	0.42^{b}	0.58^{b}	0.65^{b}	0.57^{b}
	PV[3]	0.40^{c}	0.38^{c}	0.45^{c}	0.57^{b}	0.64^{b}	0.55^{b}
Harvest	Breed[1]	0.22^{a}	0.15^{a}	0.29^{a}	0.50^{ab}	0.58^{ab}	0.48^{ab}
	EBV[2]	0.41^{b}	0.40^{b}	0.48^{b}	0.53^{a}	0.62^{a}	0.51^{a}
	PV[4]	0.44^{c}	0.44^{c}	0.49^{b}	0.50^{b}	0.60^{b}	0.48^{b}

^{a,b,c} Within each index, values within a column with different superscripts indicate a significant difference of $P < 0.05$.

[1] Breed: only breed effects were included within the index.

[2] EBV effects included within the index were breed and additive genetic merit effects.

[3] PV effects included within the index were breed, additive genetic merit, heterosis, twin, dam dairy breed fraction, dam age and parity interaction (as well as just dam parity for the docility trait), dam permanent environment, recombination and sex effects.

[4] PV effects included within the index were breed, additive genetic merit, heterosis, twin, dam dairy breed fraction, dam age and parity interaction, dam permanent environment effects.

included in the genetic evaluation, 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 days, 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 of the Harvest index). When only including one live-weight record in

Table 5
Partial correlations across a sub-set of 459 validation animals between the three indexes constructed using three formulations of an individual beef female's total merit (i.e., just breed effects (Breed), then breed plus the additive genetic merit (EBV), then breed plus the additive, non-additive and non-genetic effects in the form of production value estimates (PV)) and the realised total carcass value when varying numbers of live-weight phenotypes were included in the estimation of each index; obs = number of live-weight phenotype records taken at each specific time point included in each genetic evaluation scenario.

			Age of live-weight phenotype recording (days)				
			250–350	350–450	450–550	250–450	250–550
Indexes	Sub-components	(obs = 0)	(obs = 1)	(obs = 1)	(obs = 1)	(obs = 2)	(obs = 3)
Terminal	EBV[2]	0.30^{a}	0.36^{b}	0.36^{bc}	0.39^{d}	0.37^{c}	0.39^{d}
Calf	Breed[1]	0.18^{a}	0.18^{a}	0.18^{a}	0.18^{a}	0.18^{a}	0.18^{a}
	EBV	0.38^{a}	0.44^{b}	0.43^{bc}	0.46^{de}	0.44^{cd}	0.46^{e}
	PV[3]	0.41^{a}	0.46^{b}	0.46^{bc}	0.49^{d}	0.47^{c}	0.49^{e}
Harvest	Breed[1]	0.23^{a}	0.23^{a}	0.23^{a}	0.23^{a}	0.23^{a}	0.23^{a}
	EBV[2]	0.47^{a}	0.54^{b}	0.55^{b}	0.58^{c}	0.56^{d}	0.59^{c}
	PV[4]	0.51^{a}	0.57^{b}	0.58^{b}	0.61^{c}	0.59^{d}	0.62^{c}

^{a,b,c,d} Values within a row with different superscripts indicate a significant difference of $P < 0.05$.

[1] Breed: only breed effects were included within the index.

[2] EBV effects included within the index were breed and additive genetic merit effects.

[3] PV effects included within the index were breed, additive genetic merit, heterosis, twin, dam dairy breed fraction, dam age and parity interaction (as well as just dam parity for the docility trait), dam permanent environment, recombination and sex effects.

[4] PV effects included within the index were breed, additive genetic merit, heterosis, twin, dam dairy breed fraction, dam age and parity interaction, dam permanent environment effects.

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 days 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, with premium prices being paid for better conformed carcasses with optimal fat cover; evidence of this relationship also existed in the present study (Table 3) with carcass conformation having the strongest positive correlation with the proposed indexes whereas carcass fat had the strongest negative correlation with the proposed indexes. 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 (Department of Agriculture, Food and the Marine, 2018); combined this represents almost 40% of the prime animals that are eventually harvested. 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 (approximately 730 days old; Berry et al., 2017). 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 cognisance 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 (Connolly et al., 2016). 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 (Judge et al., 2019) but also whether the animal will be finished as a bull or steer (Connolly et al., 2016). 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 (Cole and VanRaden, 2018). 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) suggested that, within reason, carcass weight and dressing percentage are largely reflected by breed type. For this reason, the present study investigated the relationship between the five performance phenotypes and just the breed solutions of an animal. 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 2), 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. Furthermore, a post hoc analysis was undertaken to investigate the benefit of the inclusion of the additive genetic merit in the estimation of PVs; when correlating the Calf index based on PVs without the additive genetic component, the correlation was only 0.27 between the index and the carcass revenue. Therefore, including the additive genetic effect in the PVs is beneficial to prediction. It is currently a legal requirement to record the breed of all animals in Ireland. 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) which improves the ability to not only predict animal breed composition more accurately (Judge et al., 2017) but can also (in)validate parentage (Purfield et al., 2015) on a greater number of (commercial) animals, thus improving the precision of prediction.

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). 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 penalised 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). 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.

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) but also that the expression of non-additive genetic effects of a sire is a function of (the genotype of) its mate. Nevertheless, using beef breed composition estimates of heterosis, DeRouen et al. (1992) estimated that significant non-additive effects in the form of heterosis were associated with both hot carcass weight and retail yield (trimmed boneless retail yield) for all crosses investigated with the exception of Charolais × Hereford cross. Similarly, Gregory et al. (1978) reported significant heterosis effects for various beef carcass traits such as steer slaughter weight, carcass weight and retail yield. Therefore, it makes sense to consider the influence of heterosis 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 estimation of PVs (Table 4). Moreover, if genomic data were used in the estimation of the proposed indexes, it is possible that regions expressing dominance could be identified providing more granularity than simple global estimates of heterosis based on pedigree information; these estimates could be easily incorporated into the index framework presented here.

Index deployment

In its simplest form, once the decision is made to not retain an animal for breeding, the index published for an animal could graduate from being the Terminal index value (includes calving performance) at the national genetic evaluation immediately post-calving, to the Calf index coinciding with the first national genetic evaluation after the birth of the animal. As the Harvest index is targeted towards older animals, to avoid confusion it would be more beneficial for it to be published as the animal nears the expected harvest date. A 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. The economic weights applied to each trait used in the present study were the same for all indexes and were those from the Irish breeding indexes (Crosson et al., 2006) which are based on current day costs and prices. Greater certainty on carcass value may exist when purchasing an animal to be harvested in the very near future. Liu et al. (2019) developed the methodology for forecasting pig prices and, although the research was not in cattle, similar challenges exist across both sectors in capturing particular influential factors within the prediction models. For instance, one of the main challenges was factoring in price data that, albeit follows a cyclic trend throughout a specific time-frame, the cycle is never identical (Liu et al., 2019); this is an especially regular occurrence in seasonal production systems, common in Ireland, by which many animals are ready for processing at a similar period of the year. In such a period when price forecasting is available for deployment, the economic values used in the decision support tool could be adapted to be more dynamic and linked to projected costs and values; the economic values used could even differ by index or the time horizon until projected slaughter date which could also be used to account for known seasonal variability in prices and costs.

The benefit of including a single live-weight phenotype in the genetic evaluation for improving the accuracy of predicting carcass value was clear (Table 5), 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 coupled with the strong genetic correlation that exists among live-weight records at different life-stages (McHugh et al., 2011). The results from the present study suggest that in the development of live-weight recording schemes, perhaps it is more beneficial to get excellent quality phenotypes recorded once, rather than multiple recordings. Live-weight phenotypes are also often recorded at livestock auctions in Ireland immediately prior to sale. Thus, provided the data infrastructure was in place for the immediate uploading of the live-weight phenotypes, these information sources could be integrated via selection index methodology to (rapidly) improve the estimate of the final index value of an animal, much like the ad hoc blending approach used in two-step genomic evaluations (e.g., VanRaden et al., 2019). Subsequently, cattle traders would have access to up-to-date index values on the animals at the point of sale.

Dynamic indexes of the future

Given the accelerating developments in the internet of things (**IoT**), animal level sensors for measuring different characteristics (Johnsen et al., 2019; colostrum immunoglobulin in saliva), biomarkers for growth (Ibeagha-Awemu and Zhao, 2015; epigenetics), as well as the associated systems for traceability like blockchain (Makhdoom et al., 2018), 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., live-weight phenotype) in order to provide reliable estimates. Blockchain technology offers the potential to include considerably more traits (e.g., animal health and remedies administered) and, in doing so, offers 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.

Linking IoT with application programming interfaces could provide an excellent route to market for such an index. Several hundred animals can be traded in livestock auctions on a given day. These animals are usually booked in the day before. Live-weight phenotypes are often recorded at livestock auctions in Ireland immediately prior to sale. If such weights were recorded when the animals arrive at the livestock auction, these information sources could be integrated via selection index methodology into the final index estimate of an animal. 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 radio-frequency identification (**RFID**) tags, those on the filtered list could then be visually inspected the following day and their respective transaction index studied. It is acknowledged that such an integrated system would be heavily reliant on a robust infrastructure that would facilitate the transfer of such data. Furthermore, with the increasing pressure to be compliant with general data protection regulations, users of such transaction indexes may need to be given the option to 'opt-in' and therefore provide permission for each animal's transaction index value to be advertised. In Ireland, however, many producers partake in governmental schemes that encourage data collection and, within such schemes, consent is given to ICBF to use the data pertaining to the animals. Despite the two aforementioned obstacles, the two proposed indexes have the capability of utilising 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.

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 minimise the stress on animals with obvious welfare and biosecurity benefits as well as potential cost savings for both parties in the transaction. Moreover, a brokerage system would further facilitate the transaction of animals if the movement of traders becomes limited.

Conclusion

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 sale of live animals for harvest, 2) including non-additive genetic effects in the prediction of total genetic merit and 3) including relevant (and available) non-genetic effects in the prediction of eventual carcass value. 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.

Supplementary materials

Supplementary data to this article can be found online at https://doi.org/10.1016/j.animal.2020.100077.

Ethics approval

Not applicable.

Data and model availability statement

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). The data used in this study cannot be made available by the authors as they are managed by a third party, Irish Cattle Breeding Federation. Requests for data can be made to Irish Cattle Breeding Federation, Highfield House, Shinagh, Bandon, Co. Cork.

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Declaration of interest

Not applicable.

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References

Albertí, P., Panea, B., Sañudo, C., Olleta, J., Ripoll, G., Ertbjerg, P., Christensen, M., Gigli, S., Failla, S., Concetti, S., 2008. Live weight, body size and carcass characteristics of young bulls of fifteen European breeds. Livestock Science 114, 19–30. https://doi.org/10.1016/j.livsci.2007.04.010.

Berry, D.P., Cromie, A.R., Judge, M.M., 2017. Rapid communication: large exploitable genetic variability exists to shorten age at slaughter in cattle. Journal of Animal Science 95, 4526–4532. https://doi.org/10.2527/jas2017.2016.

Berry, D.P., Amer, P.R., Evans, R.D., Byrne, T., Cromie, A.R., Hely, F., 2019. A breeding index to rank beef bulls for use on dairy females to maximize profit. Journal of Dairy Science 102, 10056–10072. https://doi.org/10.3168/jds.2019-16912.

Bolormaa, S., Pryce, J.E., Zhang, Y., Reverter, A., Barendse, W., Hayes, B.J., Goddard, M.E., 2015. Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. Genetics, Selection, Evolution 47. https://doi.org/10.1186/s12711-015-0114-8.

Cole, J.B., VanRaden, P.M., 2018. Symposium review: possibilities in an age of genomics: the future of selection indices. Journal of Dairy Science 101, 3686–3701. https://doi.org/10.3168/jds.2017-13335.

Connolly, S.M., Cromie, A.R., Berry, D.P., 2016. Genetic differences based on a beef terminal index are reflected in future phenotypic performance differences in commercial beef cattle. Animal 10, 736–745. https://doi.org/10.1017/S1751731115002827.

Crosson, P., O'Kiely, P., O'Mara, F.P., Wallace, M., 2006. The development of a mathematical model to investigate Irish beef production systems. Agricultural Systems 89, 349–370. https://doi.org/10.1016/j.agsy.2005.09.008.

Crowley, J.J., McGee, M., Kenny, D.A., Crews Jr., D.H., Evans, R.D., Berry, D.P., 2010. Phenotypic and genetic parameters for different measures of feed efficiency in different breeds of Irish performance-tested beef bulls. Journal of Animal Science 88, 885–894. https://doi.org/10.2527/jas.2009-1852.

Department of Agriculture, Food and the Marine, 2018. AIM Bovine Statistics Report 2018. AIM division. Department of Agriculture, Food and the Marine, Dublin, Ireland.

DeRouen, S.M., Franke, D.E., Bidner, T.D., Blouin, D.C., 1992. Direct and maternal genetic effects for carcass traits in beef cattle. Journal of Animal Science 70, 3677–3685. https://doi.org/10.2527/1992.70123677x.

Englishby, T.M., Banos, G., Moore, K.L., Coffey, M.P., Evans, R.D., Berry, D.P., 2016. Genetic analysis of carcass traits in beef cattle using random regression models. Journal of Animal Science 94, 1354–1364. https://doi.org/10.2527/jas.2015-0246.

Eriksson, S., Nasholm, A., Johansson, K., Philipsson, J., 2004. Genetic relationships between calving and carcass traits for Charolais and Hereford cattle in Sweden. Journal of Animal Science 82, 2269–2276. https://doi.org/10.2527/2004.8282269x.

Gregory, K.E., Cundiff, L.V., Koch, R.M., Laster, D.B., Smith, G.M., 1978. Heterosis and breed maternal and transmitted effects in Beef Cattle I. Preweaning traits 1, 2, 3, 6, 7. Journal of Animal Science 47, 1031–1041. https://doi.org/10.2527/jas1978.4751031x.

Ibeagha-Awemu, E.M., Zhao, X., 2015. Epigenetic marks: regulators of livestock phenotypes and conceivable sources of missing variation in livestock improvement programs. Frontiers in Genetics 6, 302. https://doi.org/10.3389/fgene.2015.00302.

Johnsen, J.F., Chincarini, M., Sogstad, Å.M., Sølverød, L., Vatne, M., Mejdell, C.M., Hänninen, L., 2019. Salivary IgG levels in neonatal calves and its association to serum IgG: an observational pilot study. Translational Animal Science 3, 589–593. https://doi.org/10.1093/tas/txz001.

Judge, M.M., Kelleher, M.M., Kearney, J.F., Sleator, R.D., Berry, D.P., 2017. Ultra-low-density genotype panels for breed assignment of Angus and Hereford cattle. Animal 11, 938–947. https://doi.org/10.1017/S1751731116002457.

Judge, M.M., Pabiou, T., Conroy, S.F., Fanning, R., Kinsella, M., Aspel, D., Cromie, A.R., Berry, D.P., 2019. Factors associated with the weight of individual primal carcass cuts and their inter-relationship in cattle. Translational Animal Science 3, 1593–1605. https://doi.org/10.1093/tas/txz134.

Kelly, D., Murphy, C., Sleator, R.D., Judge, M., Conroy, S., Berry, D., 2019. Feed efficiency and carcass metrics in growing cattle. Journal of Animal Science 97, 4405–4417. https://doi.org/10.1093/jas/skz316.

Liu, Y., Duan, Q., Wang, D., Zhang, Z., Liu, C., 2019. Prediction for hog prices based on similar sub-series search and support vector regression. Computers and Electronics in Agriculture 157, 581–588. https://doi.org/10.1016/j.compag.2019.01.027.

Makhdoom, I., Abolhasan, M., Abbas, H., Ni, W., 2018. Blockchain's adoption in IoT: the challenges, and a way forward. Journal of Network and Computer Applications 125, 251–279. https://doi.org/10.1016/j.jnca.2018.10.019.

McHugh, N., Evans, R.D., Amer, P.R., Fahey, A.G., Berry, D.P., 2011. Genetic parameters for cattle price and body weight from routinely collected data at livestock auctions and commercial farms. Journal of Animal Science 89, 29–39. https://doi.org/10.2527/jas.2010-3044.

McHugh, N., Cromie, A.R., Evans, R.D., Berry, D.P., 2014. Validation of national genetic evaluations for maternal beef cattle traits using Irish field data. Journal of Animal Science 92, 1423–1432. https://doi.org/10.2527/jas.2013-6658.

MiX99 Development Team, 2015. MiX99: A software package for solving large mixed model equations. Biometrical Genetics, Natural Resources Institute Finland (Luke). Jokioinen, Finland.

Purfield, D.C., Bradley, D.G., Evans, R.D., Kearney, F.J., Berry, D.P., 2015. Genome-wide association study for calving performance using high-density genotypes in dairy and beef cattle. Genetics Selection Evolution 47. https://doi.org/10.1186/s12711-015-0126-4.

Steiger, J.H., 1980. Tests for comparing elements of a correlation matrix. Psychological Bulletin 87, 245–251. https://doi.org/10.1037/0033-2909.87.2.245.

VanRaden, P.M., Sanders, A.H., 2003. Economic merit of crossbred and purebred US dairy cattle. Journal of Dairy Science 86, 1036–1044. https://doi.org/10.3168/jds.S0022-0302(03)73687-X.

VanRaden, P.M., Bickhart, D.M., O'Connell, J.R., 2019. Calling known variants and identifying new variants while rapidly aligning sequence data. Journal of Dairy Science 102, 3216–3229. https://doi.org/10.3168/jds.2018-15172.

Wiggans, G.R., Cole, J.B., Hubbard, S.M., Sonstegard, T.S., 2017. Genomic selection in dairy cattle: the USDA experience. Annual Review of Animal Biosciences 5, 309–327. https://doi.org/10.1146/annurev-animal-021815-111422.