Breeding Objectives Indicate Value of Genomics for Beef Cattle

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Introduction

Genomics may have much to offer in the implementation of breeding objectives. Advantages of genomic prediction include increased accuracy of expected progeny differences (EPDs) for traits that have been components of routine genetic evaluations. Perhaps more importantly, genomic prediction makes it possible to include traits that are too costly or too difficult to measure, and traits that are measured too late in life or are sex-limited such that candidates for selection cannot have EBV with high accuracy at the time when selection decisions are made. Genomically enhanced EPDs may also allow for a marked reduction in generation interval, thus accelerating the annual rate of genetic improvement. Here, the value of genomic prediction, on a trait-by-trait basis, is extended to explore the contribution of genomic prediction to selection for a multi-trait breeding objective indicative of economic merit. A simple two-trait objective indicative of feed efficiency is illustrated first, followed by objectives for terminal and maternal strains of Angus.

Key words: multi-trait, selection, genomics

Materials and Methods

A breeding objective (O) reflects the functional relationship between breeding values (BV) of biological traits and profit (for example, $O = a_1BV_1 + a_2BV_2 + a_3BV_3 ...$; where a_i is economic value of the ith economically relevant traits). Implementing a breeding objective depends on a genetic evaluation system such that: $\hat{O} = a_1EPD_1 + a_2EPD_2 + a_3EPD_3 ...$ By definition economic values are the change in profit that is expected from a single unit change in the associated trait, holding all other traits constant. The outcome of this calculation can be thought of as an EPD for "profit."

Three distinct objectives are evaluated: 1) feed efficiency, a linear transformation of the ratio of postweaning average daily gain to feed intake; 2) a terminal objective based on work for the Circle A Angus Sire Alliance; and 3) a maternal objective also for Angus. The conceptual model employed to incorporate genomic information into multiple-trait economic breeding objectives is shown in Figure 1. True genetic values for each of n, possibly correlated traits, are the cause of differences in both genomic and phenotypic estimated breeding values gEBV and pEBV, respectively. The separate EBVs are then merged (blended) as a function of their respective accuracies to produce an EPD for

each of the n traits. Finally, for each animal the sum of products of economic weights and EBV is calculated to predict its economic value.

A series of differing accuracies of the EBV components of the feed efficiency objective was evaluated. Shown here are results calculated for accuracies of the EBV quartet $[_p\text{EBV}_1, _g\text{EBV}_1, _p\text{EBV}_2, _g\text{EBV}_2]$ of [0.50, 0.00, 0.61, 0.00], [0.50, 0.40, 0.61, 0.40], [0.50, 0.60, 0.61, 0.60], [0.60, 0.40, 0.70, 0.40], and [0.60, 0.60, 0.70, 0.60].

For the terminal sire objective, economic weights were calculated by simulation based data from Angus calves born during a 4-month spring calving season and weaned at an average age of 192 days. After weaning, the calves were fed a diet of moderate energy density for an average of 106 d before transport to a feedlot for finishing. Daily feed intake of individual animals was measured in contemporary groups of 96 steers using a Calan Broadbent Feeding System. A stepwise series of five diets that increased in energy density was used throughout the finishing period. Harvest date was determined to target a contemporary group to average ½ inch fat depth at the 12-13 rib and/or to avoid discounts for under- and over-weight carcasses. The afternoon before harvest, steers were weighed and then transported overnight to the packing plant for harvest and collection of carcass data. Carcass data included: harvest date, hot carcass weight, marbling score, fat depth, LM area, and percentage kidney, pelvic and heart fat. The terminal breeding objective is described by statistics presented in Table 1.

The maternal objective considered Angus as a specialized dam line used in a 2-breed rotation crossbreeding system wherein income was derived from calves sold at weaning. Here the simulation described progression of the cows through their life cycle as a function of age-specific mortality and reproduction. As with the terminal objective, spring-born calves were weaned at 192 days of age. The maternal breeding objective is described by statistics presented in Table 2.

For each breeding objective two scenarios were simulated: 1) where the accuracies of both the phenotypic and genomic EBV were as presented in Tables 1 and 2; and 2) where the accuracies of the genomic EBV were = 0.0. Accuracy estimates for the phenotype-based EPD were from a 2015 Angus national cattle evaluation for 2014 bulls that were not genotyped. Thus, the accuracies of the EBV were approximately those available for choosing among yearling bulls.

Finally, the "Breeder's equation": $R = h\sigma_a i$, wherein, R = response to selection, h = square root of heritability or accuracy, σ_a = genetic standard deviation, and i = selection intensity was used to assess selection response as a function of changes in accuracy due to the addition of genomic information to traditional phenotype-based predictions of genetic merit.

Results and Discussion

The five scenarios analyzed for the feed efficiency objective reflect meaningful circumstances. In scenarios 1-3, accuracies of the $_p$EBV equal the square roots of the corresponding heritability estimates. Thus, the EBV are assumed to be based only on individual performance records. In scenarios 4 and 5, the accuracies of the $_p$EBV were increased to reflect the addition of records from sibs. Accuracies of the $_g$EBV

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were selected to reflect no genomic information (scenario 1), modest accuracy $_g$EBV (scenarios 2 and 4), and higher accuracy $_g$EBV (scenarios 3 and 5). Higher accuracy $_p$EBV were not considered as it is thought to be unlikely that greater levels of accuracy could be attained prior to the time selection decisions are typically made. Adding genomic information improved accuracy of the feed efficiency EPD when only the individual phenotypes were available. However, as the accuracy of phenotypic information contributing to the feed efficiency EPD increased, the value of genomic information became negligible.

For individual traits in the terminal objective, selection response is increased through the use of genomic predictors by 9% to 41% with the least effect on birth weight and the greatest effect on dry matter intake. In general, these effects were greater on postweaning traits that are less frequently recorded and (or) monitored with indicator traits. For individual traits in the maternal objective, selection response is increased through the use of genomic predictors by 12% to 76% with by far the greatest effects on stayability and heifer pregnancy, traits that are unobserved on bull candidates for selection at the time when the selection decisions are typically reached.

Use of breeding objectives allows consequences of incorporating genomic information to be translated into economic terms. Assume the classical pyramid paradigm for flows of genetic and economic signals in the beef industry. Conceptually, the industry is divided into two segments. One is a seedstock or stud breeding sector wherein data recording and subsequent genetic evaluation facilitate genetic improvement that results in enhanced profitability for the commercial producers that form the second segment. These commercial producers benefit from the selection decisions that have been made by stud breeders and reward them for the enhanced genetic merit of the stock that they sell for use in commercial production. Here, assume that in the seedstock segment 5% of bulls and 30% of heifers are retained for breeding. The value of incorporating genomic information into EBVs that are components of multiple-trait breeding objectives for Angus cattle is illustrated in Figure 2. Other things being equal, these results indicate selection response for economic merit would be increased 1.25- and 1.56-fold by including genomic information in the EBV in the two objectives, respectively. In economic terms, adding genomic information to the prediction of EBV yields $11.55 for the terminal index and $50.85 for the maternal objective. If an individual terminal sire were to produce 60 commercial progeny, then the expected net increase would total $346.50 and a maternal sire producing 15 replacement females add $326.00 to the bottom line of the cow-calf producer.

Implications
Genomically enhanced EBVs are more accurate predictors of merit than traditional EBV and these increases in accuracy can yield economic returns in commercial production that are more than sufficient to offset the cost of genotyping by the seedstock producers.

Table 1. Estimates of mean (μ), phenotypic standard deviation (σ), heritability (h^2), economic weights ($\partial P/\partial t$), and accuracies for traits (t) included in an Angus terminal sire-breeding objective

Trait	μ	σ	h^2	$\partial P/\partial t$	Relative value, %	Accuracy[a] $_g$EBV	Accuracy[a] $_p$EBV
Birth weight, lb	77.9	11.0	0.41	-0.85	8.8	0.68	0.76
Weaning weight, lb	427	86.9	0.23	0.41	25.4	0.56	0.66
Average daily gain, lb	2.90	0.40	0.36	47.40	16.9	0.66	0.60
Feed intake, lb/day	20.2	2.20	0.41	-10.02	21.1	0.74	0.56
Marbling score[b]	5.8	1.00	0.26	13.54	10.3	0.67	0.59
Yield grade	3.4	0.70	0.22	-35.28	17.4	0.65	0.57

[a] $_g$EBV = genomic EBV; $_p$EBV = phenotypic EBV.
[b] 4.0 = Slight[00]; 5.0 = Small[00]; etc.

Table 2. Estimates of mean (μ), phenotypic standard deviation (σ), heritability (h^2), economic weights ($\partial P/\partial t$), and accuracies for traits (t) included in a breeding objective for an Angus specialized dam line

Trait	μ	σ	h^2	$\partial P/\partial t$	Relative value, %	Accuracy[a] $_g$EBV	Accuracy[a] $_p$EBV
Stayability, %	55.1	16.2	0.21	8.00	50.6	0.58	0.37
Heifer pregnancy, %	91.0	22.6	0.14	1.61	11.6	0.45	0.31
Calving ease (d), %	85.5	28.6	0.12	1.90	16.0	0.62	0.65
Calving ease (m), %	-		0.13	1.90	16.7	0.32	0.46
Weaning weight (d), lb	564.7	109.1	0.30	0.086	4.4	0.56	0.66
Weaning weight (m), lb	-		0.14	-0.023	0.8	0.36	0.51

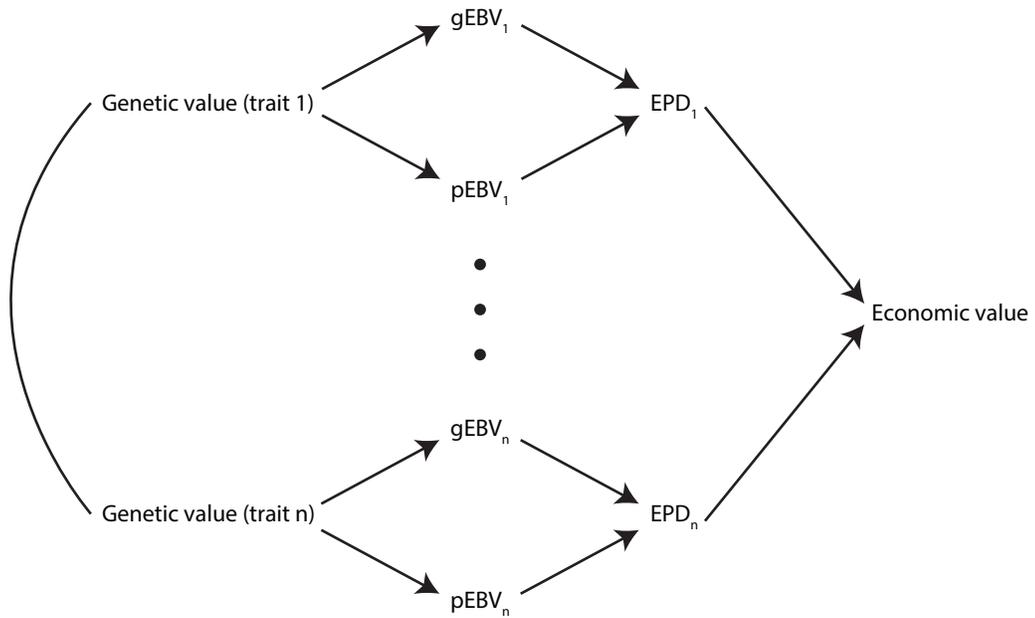[a] $_g$EBV = genomic EBV; $_p$EBV = phenotypic EBV.

Figure 1. Conceptual model employed to incorporate genomic information into multiple-trait economic breeding objectives.
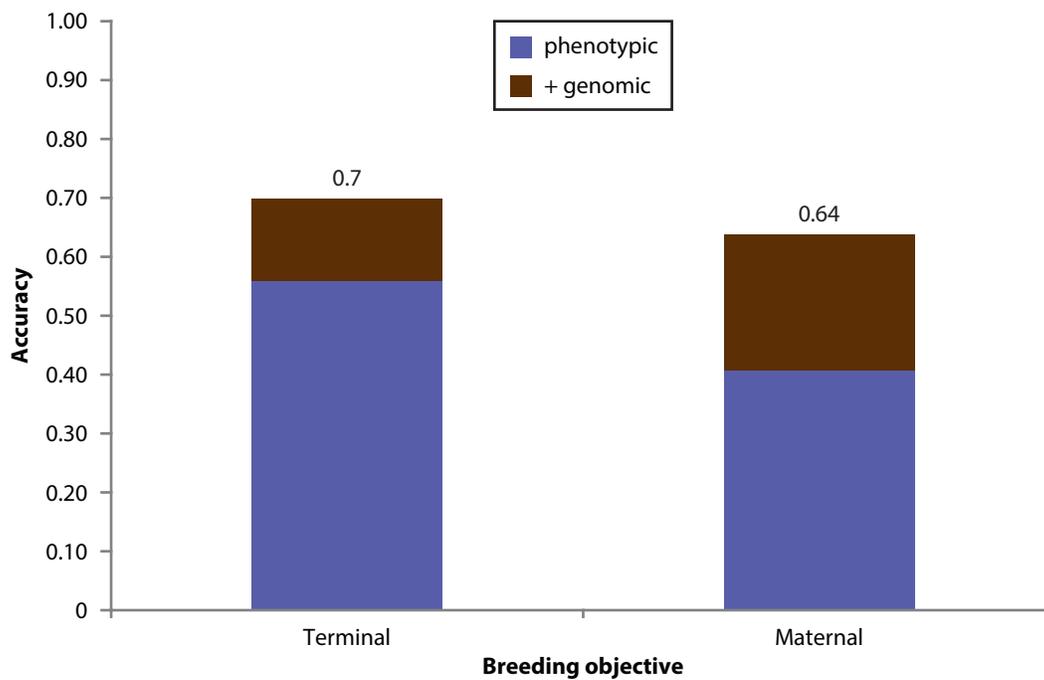

Figure 2. Effect of adding genomic information to traditional phenotype-based EBV on the accuracy of breeding objectives for selection of beef cattle as specialized sire (terminal) and dam (maternal) lines.