

ECONOMIC VALUE OF GENOMIC SELECTION IN A VERTICALLY INTEGRATED BEEF CATTLE PRODUCTION SYSTEM

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SUMMARY

Two genetic evaluations were carried out for a vertically-integrated beef production operation running a 600 cow Charolais purebred herd providing terminal sires for a 10,000 commercial cow herd to determine the effect of genotyping on accuracy of genetic predictions, rate of genetic gain, and discounted revenue for breeding sires. Genetic evaluation A included phenotypes from purebred and crossbred offspring and a pedigree containing purebred relationships as well as sire-calf relationships for crossbred calves derived from parentage assignment. Genetic evaluation B contained the same information as A, with the addition of 9K genotypes for purebred and crossbred animals. Genotyping resulted in an 11.9% increase in the average accuracy (R_{TI}) of the estimated breeding values (EBV) over parentage assignment alone. Gene flow methodology was used to estimate the cumulative discounted expressions (CDE) resulting from the selection of a genetically superior purebred (PB) and commercial (CM) sire. Additional discounted revenue derived from the increased accuracy due to 9K genotyping in genetic evaluation B was \$465 for a CM sire, and \$10,355 for a retained PB sire. The cumulative net present value (CNPV) over a 20 year planning horizon was \$9,400,910 and \$17,930,183 for scenario A and B, respectively, assuming 25% of the CM progeny were assigned parentage or genotyped annually at a cost of \$15/parentage assignment or \$35/9K genotype. These estimates assume the value from genetic improvement is returned to the enterprise. In this scenario genotyping PB selection candidates and some proportion of CM progeny resulted in a positive return on investment over parentage assignment alone.

INTRODUCTION

Adoption of genomic technology in the beef cattle industry provides an opportunity to accelerate genetic gain and increase income (Meuwissen *et al.* 2013). In a vertically integrated production system there is opportunity to capture additional profit generated from genotyping by implementing a genetic evaluation using some combination of phenotypes, pedigree information, and genotypes (Aguilar *et al.* 2010). Increased genetic gain from genotype information results from an increase in the accuracy of the prediction of genetic merit and the reduction of generation interval through genomic selection on young unproven sires (Todd *et al.* 2014). The objective of this study was to compare the accuracy of genetic evaluations obtained from pedigree relationships derived from parentage with those obtained when using ~9K genotypes. A secondary objective was to calculate the estimated additional economic returns associated with the accelerated genetic gain in both scenarios. Inference was to a genetic evaluation program for a vertically-integrated, two-tiered beef cattle production system producing Charolais terminal sires for 10,000 commercial cows.

MATERIALS AND METHODS

Data used in this study consisted of records from a Charolais purebred herd combined with feedlot and carcass performance records from their crossbred calves finished at a common feeding facility. Historic pedigree information (n=8,361 pedigree records) was available for the purebred

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herd. During the course of three years, 568 purebred Charolais bulls and 8,776 crossbred calves were genotyped using a combination of the GeneSeek Genomic Profiler LD (26k) v.1.1-4 and HD (76k) SNP arrays, which allowed for the reconstruction of sire-calf pedigree relationships. There were 8,549 SNP markers common to all animals in the evaluation after trimming for call rate (≥ 0.90) and removing markers on sex chromosomes. Phenotypes collected from purebred Charolais bulls included birth weight (BW), weaning weight (WW), GrowSafe (GrowSafe Systems, Ltd, Airdrie, AB Canada) dry matter intake (DMI), average daily gain (ADG), ultrasound 12TH rib fat depth (URFAT), ultrasound intramuscular fat percentage (UIMF), and ultrasound ribeye area (UREA). Phenotypes collected from crossbred calves finished in the feedlot included WW (collected at feedlot arrival), DMI, 12th rib fat depth (FAT), marbling score (MARB) determined by image analysis (VBG 2000 E+V, Oranienburg, Germany), and carcass ribeye area (REA).

Pedigree-based and genomic EBVs were estimated using the single-step approach to simultaneously evaluate genotyped and non-genotyped animals with pedigree information. Inclusion criteria for purebred sires to be evaluated in this study were a recorded pedigree relationship, a genotype, ultrasound and DMI records, and at least one recorded crossbred calf. For evaluations where crossbred carcass traits were available, ultrasound indicator traits were analyzed in a bivariate animal model (MacNeil *et al.* 2010). Beef Improvement Federation (BIF) EBV accuracies were calculated using standard errors derived from single-step GBLUP according to BIF guidelines (2015).

$$BIF_{acc} = 1 - \sqrt{\frac{\text{Prediction error variance}}{\text{Additive genetic variance}}} \quad [1]$$

This accuracy was then transformed to an approximation of the correlation between the true and estimated breeding value (R_{TI}):

$$R_{TI} = \sqrt{1 - (1 - BIF_{acc})^2} \quad [2]$$

The average accuracy in each genetic evaluation was also used to estimate the expected genetic gain in profit per year ($\Delta G_{\$yr}$) using economic index coefficients for each trait:

$$\Delta G = \sum_{j=1}^n \alpha_j I R_{TI_j} \sigma_{A_j} \quad [3]$$

Where α_j equals the economic value for trait j (\$/marketed crossbred carcass), I equals the selection intensity of PB or CM bulls, R_{TI_j} equals the average accuracy for trait j , σ_{A_j} equals the additive genetic standard deviation for trait j . Selection intensities were chosen to create a replacement rate that would maintain the current population structure.

The gene flow method of Hill (1974) was utilized to estimate the cumulative discounted expression (CDE) resulting from the selection of a genetically superior CM or PB sire using the population structure, age classes, and selection intensity for a combined 600 cow nucleus herd and 10,000 commercial cow production system as described (Van Eenennaam *et al.* 2011). A discount rate of 5% and a 20 year planning horizon was used to determine the present value resulting from the future expression of production traits after selection decisions have been made. The discounted revenue derived from CM sires was estimated as:

$$\$CM = \frac{\Delta G \times CDE_{CM} \times \text{No. of commercial cows}}{\text{No. of yearling commercial bulls retained}} \quad [4]$$

Similarly, the discounted revenue derived from PB sires was estimated as:

$$\$PB = \frac{\Delta G \times CDE_{PB} \times \text{No. of commercial cows}}{\text{No. of PB sires retained}} \quad [5]$$

In addition, cumulative net present value (CNPV) over a 20 year planning horizon was calculated using the accuracies and resulting rate of genetic gain, along with the internal rate of return (IRR).

RESULTS AND DISCUSSION

Table 1 displays the population structure and breeding system assumptions used in this study.

Table 1. Population structure and system parameters commercial (CM) and purebred (PB).

Parameter	Assumed Value
No. of PB bull calves born each year	231
PB bull:cow ratio	1:25
No. of PB cows	600
No. of PB bulls selected each year	10 (4.3%, $i = 2.11$)
No. of bulls selected as CM bulls	154 (69.7%, $i = 0.50$)
CM bull:cow ratio	1:20
No. of CM cows	10,000
Age structure of PB bulls (2 to 4 yr)	0.41, 0.33, 0.26
Age structure of CM bulls (2 to 5 yr)	0.34, 0.27, 0.22, 0.17
Age structure of cows in CM herd	0.2, 0.18, 0.17, 0.15, 0.12, 0.09, 0.05, 0.03, 0.01

Average accuracy of EBVs for the traits included in the genetic evaluation are shown in Table 2 for the 248 purebred Charolais bulls that were included in this comparison. Genetic evaluation A and B contained the same pedigree and phenotypes, but genotypes were added to genetic evaluation B. The addition of genotypes to the genetic evaluation resulted in an 11.9% increase in the average accuracy over parentage assignment alone.

Table 2. Accuracy (R_{TI}) of Genetic evaluation. Evaluation (A) contained phenotypes from purebred and crossbred animals and a pedigree derived from SNP parentage assignment and (B) with the addition of 9K SNP genotypes

Trait ¹	Accuracy of Genetic Evaluation	
	A	B
D2H	0.474 ±0.008	0.490 ±0.005
DMI	0.569 ±0.018	0.648 ±0.006
FAT	0.628 ±0.008*	0.749 ±0.008*
HCW	0.602 ±0.009	0.721 ±0.005
MARB	0.621 ±0.011*	0.712 ±0.005*
REA	0.666 ±0.008*	0.725 ±0.004*
UFAT	0.597 ±0.003*	0.606 ±0.006*
UIMF	0.661 ±0.002*	0.712 ±0.002*
UREA	0.630 ±0.004*	0.655 ±0.003*
WW	0.699 ±0.006	0.711 ±0.004
YG	0.635 ±0.009	0.745 ±0.004

*Bivariate model with carcass traits evaluated with ultrasound indicator trait.

¹D2H = days to harvest, FAT = carcass backfat thickness, MARB = camera-based marbling score, UFAT = ultrasound backfat thickness, UIMF = ultrasound intramuscular fat, UREA = ultrasound ribeye area.

The discounted revenue from genetic evaluation is shown in Table 3. Additional discounted revenue derived from accuracy due to genotyping in genetic evaluation B was \$465 per CM sire. If 154 CM sires are retained each year (69.7%, $i = 0.50$) as breeding males that produce commercial offspring, then the annual economic return becomes \$71,610 on an enterprise basis.

Increased discounted revenue derived from genotyping for PB sires was \$10,355. If 10 PB sires are retained as herd sires (4.3%, $i = 2.11$) this value becomes \$103,550 on an enterprise basis. The total discounted revenue derived from genotyping is then \$175,160 for the enterprise per year. Additionally, the CNPV derived from estimates of genetic gain in \$/PB bull in both genetic evaluations was estimated over the first 20 years of selection. Assuming a cost of \$15/parentage test and \$100 or \$45 in phenotyping costs for PB and CM animals, respectively, the initial investment

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for scenario A was \$591,880. Assuming a cost of \$35/test for the GGPLD and the same phenotyping costs, the initial investment for scenario B was \$778,760 (Table 3).

Table 3. Discounted revenue per year and cumulative net present value (CNPV) for purebred (PB) and commercial (CM) sires in genetic evaluation scenarios A and B.

Genetic Evaluation	Income/expense source	N	Expense	Income	Total
A	CM progeny phenotyping (\$100/hd)	1875	\$187,500		
	PB bull phenotyping (\$100/hd)	231	\$23,100		
	Parentage (\$15/hd)	2106	\$31,590		
	Startup cost		\$591,880		
	20 year CNPV				\$9,400,910
	20 year internal rate of return				9.2%
B	CM progeny phenotyping (\$100/hd)	1875	\$187,500		
	PB bull phenotyping (\$100/hd)	231	\$23,100		
	Genotyping (\$35/hd)	2106	\$73,710		
	Startup cost		\$778,760		
	20 year CNPV				\$17,930,183
	20 year internal rate of return				16.3%
Difference in CNPV after 20 yr					\$8,529,273

This example assumes 25% of the CM progeny and 100% of the PB males were assigned parentage or genotyped each year of the 20 year period. Scenarios A and B reach breakeven value after 12 and 10 years of selection, respectively. Scenario B also generates approximately \$8,529,273 additional cumulative revenue over 20 years. These economic returns may be inflated as they were based on single trait accuracies which may be overestimated as they did not account for information that might be provided from correlated traits.

The CNPV estimate suggests a positive return on investment can be derived from 9K genotyping young PB selection candidates and a portion of the CM progeny in this two-tiered beef cattle production system as compared to a genetic evaluation using a pedigree containing purebred relationships and sire-calf relationships for crossbred calves based on parentage analysis alone.

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