

# Validation of genomic tools to improve production efficiency, health resilience and the carbon footprint of beef production

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## Abstract

Genomic tools and accuracy of molecular breeding values (MBVs) for economically important traits continue to improve and are being applied in commercial crossbred beef cattle. Genomic breed composition and retained heterozygosity of an individual animal can be used to further improve female fertility, stayability, lifetime productivity and calf health resilience. But this is just the first step. Within specific crossbred populations, researchers at Livestock Gentec have used large numbers of cattle phenotypes and genotypes, combined with advanced statistical genomic analyses to generate MBVs for 18 traits with moderate to moderately-high accuracy (0.35 to 0.60). This accuracy is equivalent to 10 to 20 progeny records. These MBVs are economically balanced into multi-trait profit indices such as the Replacement Heifer Profit Index Score and the Feeder Profit Index. The use of these genomic tools will improve the sustainability of beef production by improving profitability, lowering the carbon footprint, and improving an animal's ability to adapt to changing environments. The following paper outlines the validation of these genomic tools and their potential benefits.

**Key words:** beef, genomic tools, fertility, carcass quality, carbon footprint

## Introduction

Sustainable beef production is highly influenced by fertility, feed efficiency, feed intake, growth and carcass quality, and these traits are key focus areas identified in Canada's 2020-2024 National Beef Strategy.<sup>31</sup> Historically, the relative value of traits to the commercial cow-calf sector have been stated as the "10:2:1 rule of thumb", where fertility traits are 10x more important than carcass traits and 5x more important than growth traits.<sup>30,37</sup> Even when the calves are retained to slaughter, the relative value of traits is 2:1:1. This simple organization of traits recognizes that the heritability of traits increases as we move from fertility (low) to growth and feed efficiency (moderate) to carcass (moderately-high) traits. It also recognizes that in a crossbreeding production system, fertility and health resilience traits are more influenced by non-genetic effects (such as dominance, epistasis, and retained heterozygosity), though additive genetic effects are still important for improving fertility and longevity. The latter point is clearly illustrated by the improvement in the genetic merit for dairy cow longevity that has been observed in Ireland and the United States in the past two decades, due to less aggressive selection pressure on milk yield which modified cow size and increased body fatness.<sup>12</sup>

All major breed associations have expected progeny differences (EPDs) for numerous growth (e.g., birth weight, weaning weight, milk, residual gain), maternal (e.g., calving ease, heifer pregnancy, docility, foot and leg scores, stayability) and carcass traits, however, phenotypic records and EPDs are sparse for feed efficiency and feed intake. They also have all-purpose indexes for production of terminal calves and replacement heifers, and maternal indexes for selection of improved daughter productivity. Genetic trends published by the American Angus Association (<http://www.angus.org/Nce/GeneticTrends.aspx>) clearly show that growth and carcass traits have increased dramatically over the last 50 years (1972-2022). In fact, yearling weight has increased linearly ( $R^2 = 0.99$ ) at 3 lb per year (1.36 kg per year), and is projected to reach a mature cow weight of 1,650 to 1,750 lb (748 to 794 kg) by 2050. This is assuming a 2021 Angus breed average yearling weight for heifers of 838 lb (380 kg) and yearling weight being 53 to 56% of cow mature weight at a body condition score of five on a nine-point scale.<sup>32</sup> At the same time, feed intake has increased at 0.054 lb DM/day/year (0.024 kg DM/day/year). Unfortunately, heifer pregnancy, which is defined as the increased chance of a sire's daughters becoming pregnant as first-calf heifers during a normal breeding season, has remained relatively constant over the same period. Similarly, calf crop percentage in Canada and the United States has remained constant at 82-84% for over 30 years, with 10-13% potential calves lost due to female infertility and a further 4-5% to perinatal deaths,<sup>1,2,36</sup> despite major advances in nutrition and health management. This level of calf crop percentage does not indicate a "biological limit", but rather represents system inefficiency related to suboptimal management, compounded by the lack of selective breeding to maintain or improve retained heterozygosity and heterosis<sup>11, 17</sup> and suboptimal selection indexes for fertility, longevity and lifetime productivity that do not include both additive and non-additive genetic effects, particularly in crossbreeding production systems.

Researchers at Livestock Gentec, University of Alberta (Edmonton, Canada) have developed a suite of genomic prediction tools that include genomic evaluations for feed efficiency traits,<sup>18</sup> genomic prediction of breed composition (gBC)<sup>4</sup> and retained heterozygosity (gRHET).<sup>11</sup> It also includes construction of multiple trait selection scores based on gRHET and MBVs for feed efficiency and growth for commercial crossbred replacement heifers, and feed efficiency, growth and carcass MBVs for bulls producing feeder cattle with improved profitability.<sup>24</sup> These indexes referred to as the Replacement Heifer Profit Index Score™ (RHPI Score™) and the Feeder Profit Index™ (FPI™) require evaluation against independent on-farm data collected under various management and environmental conditions to

ensure producer confidence and quantify effects on growth, feed efficiency, carcass quality and economic benefits. This paper summarizes the evaluations of RHPI and FPI using “real-world” commercial on-farm and packing plant data, and their impact on replacement heifer fertility and carbon footprint, and on feeder profitability.

## Materials and methods

All animals were cared for according to the guidelines outlined in the Canadian Council on Animal Care.<sup>16</sup> Experimental procedures were evaluated and approved by the Animal Care and Use Committees at the University of Alberta and Lacombe Research and Development Centre.

## Evaluation of RHPI score

Over five years from 2018 to 2022, 1,544 commercial crossbred heifers from 10 Alberta herds were transported to Olds College (Alberta, Canada) at 7-13 months of age (mean = 9.7 mon; standard deviation [SD] = 1.4 mon) and tested for growth and feed efficiency following standardized procedures.<sup>8,9</sup> They were fed a high-silage diet (83.0% barley silage, 12.2% rolled barley grain, 3.8% protein supplement, 1.0% dry distillers' grain plus solids; as fed basis) over a 50 to 81-day test period. Heifers were DNA-sampled at the end of test, and samples sent to Neogen Canada (Edmonton, AB, Canada) for genotyping using the GGP ULD single nucleotide polymorphism (SNP) panel (~35k SNPs). Following the test, heifers were returned to their herds of origin two to four months before the start of the breeding season. Only replacement heifers exposed to natural breeding were included in this study, thus excluding 213 heifers bred by artificial insemination, 124 heifers sold for revenue before their first breeding season, and 299 heifers with incomplete or no records kept on first-parity calving. Fertility records on the remaining 908 replacement heifers (58.8%) included breeding dates, pregnancy diagnosis, first calf birth dates and weights, and first calf weaning dates and weights.

All genotypes were quality controlled for SNP markers with unknown position, located on sex chromosomes, monomorphic as well as with < 90% genotype call rate, minor allele frequency (MAF) < 0.05, and an absence of Hardy-Weinberg equilibrium ( $P < 10^{-6}$ ). In addition, samples with call rate < 90% were excluded. After the genomic quality control, a total of 35,438 SNP markers remained. Genomic breed composition (gBC) was estimated based on the SNP genotypes using the ADMIXTURE software<sup>7</sup> and a Purebred Reference Population containing 5,520 animals with 50k SNP genotypes from 14 major breeds including Black Angus, Red Angus, Charolais, Simmental, Hereford, Limousin, Gelbvieh, Salers, Maine Anjou, Shorthorn, Holstein, Brown Swiss, Jersey and Galloway. Genomic retained heterozygosity for each individual was calculated based on Dickerson<sup>23</sup> and expressed as  $gRHET = 1$  minus the sum of squares of each breed fraction.

Commercial heifer MBVs were generated using a training reference data set containing 1,323 replacement heifers born from 2004 to 2021 in two research herds, and followed for their performance from birth through feed efficiency testing, and then for 1 to 14 parities. Research heifers were from two herds: Lacombe Research and Development Centre (LRDC, Alberta, Canada), and Roy Berg Kinsella Research Ranch (KIN, Alberta Canada). These heifers had been measured for growth and feed efficiency starting at 8-10 months of age following standardized procedures,<sup>8,9</sup> and then measured for body weight and

ultrasound backfat thickness at pre-breeding, pregnancy evaluation and weaning. Pregnancy diagnosis, calving and weaning data, and culling disposition and date were recorded on more than 10,000 mating opportunities. Historically, the LRDC herd consisted of Black Angus-Hereford cows crossed with Hereford and Black Angus bulls, and Red Angus-Hereford cows mated to Charolais, Maine-Anjou and Red Angus bulls. More recently, black-coated crossbred cows were mated to black Simmental and black Angus bulls, and red-coated crossbred cows mated to red Simmental and Red Angus bulls. This has resulted in a mean gBC of 60%, 20%, 6%, 4% and 3% for Angus, Hereford, Charolais, Simmental and Maine Anjou, respectively. Mean herd gRHET is 0.37 with a coefficient of variation (CV) equal to 55.5%, indicating high variation in cow herd heterosis. The KIN cow herd is much more crossbred and consists of Angus, Hereford, Charolais, Simmental, Brown Swiss, Gelbvieh, Galloway and Limousin (44%, 14%, 7%, 7%, 5%, 5%, 4%, and 4%, respectively). Mean cow herd gRHET is 0.73 with a CV of 12.3%.

The Replacement Heifer Profit Index (RHPI) was developed based on the multiple trait selection index theory<sup>13, 22</sup> and generated for each animal based on the MBVs, accuracy of MBVs, variance components, heritability, genetic and phenotypic correlations across traits, and economic weights of each trait for a cow-calf production and marketing system. The RHPI Score<sup>TM</sup> included both non-additive (gRHET) and additive genetic effects (RHPI), and was developed to select replacement heifers with an increased chance of becoming pregnant during their first normal breeding season, and then to produce a calf every year, while improving feed efficiency, longevity and controlling production costs. It is expressed as  $RHPI\ Score^{TM} = gRHET, \% + ((-25 \times MBV_{BW}) + (8 \times MBV_{WNWT}) + (-10 \times MBV_{RFI}) + (-11 \times MBV_{DUR}) + (-19 \times MBV_{PBWT}) + (14 \times MBV_{PBBF}) + (-13 \times MBV_{AFC}) \times 0.20$ . Traits in the index are birth weight (BW), 200-day weaning weight (WNWT), residual feed intake (RFI), feeding event duration (DUR), pre-breeding body weight (PBWT), pre-breeding backfat thickness (PBBF) and age at first calving (AFC).

The RHPI Score was generated for each commercial heifer and then classified into two RHPI Scoregroups: Below ( $\leq 48.4$  score) and Above average ( $> 48.4$  score). Commercial heifer performance data from birth through feed efficiency testing were subjected to an analysis of covariance using PROC MIXED in SAS.<sup>35</sup> Main effects included age of dam (2-15 years), RHPI Score group (Below or Above average) and contemporary group which included herd, year and pen. Heifer open rate across herds was subjected to Chi Square analysis.

## Evaluation of the FPI

Two data sets were used to evaluate MBVs and FPI against actual performance, and these data sets were not included in the reference or training data set for genomic predictions. The first independent data set included 441 crossbred feeder steers (sires unknown) tested for average daily gain (ADG), average daily dry matter intake (DMI), metabolic mid-point body weight (MWT) and feedlot residual feed intake (RFI) using the GrowSafe® Feed Intake System at Olds College (Olds, AB, Canada). The second data set included 137 bulls with 1,894 crossbred feeder progeny records for carcass quality traits and sire assigned based on 50k SNP genotypes. Sires were purebred and included Angus, Simmental, Charolais and Hereford (13.8 progeny per sire). Feeders were custom fed a high rolled barley grain diet at Alberta feedlots following a standardized health, management and feeding program, and all finished cattle processed through Cargill's

High River facility (AB, Canada). Performance data collected included management, feeding and health program information, feedlot name and location, Canadian Cattle Identification and visual tag numbers, feedlot entry date and weight, sickness and treatment records, and finished date and weight. Carcass quality data taken by a certified grader (Canadian Cattle Grading Agency) included slaughter date, hot carcass weight (HCW), yield grade (YG) and quality grade (QG). Other detailed carcass data taken by the in-plant Computer Visions System included ribeye area (CREA), average grade fat (AFAT), marbling (CMAR), and lean meat yield (LMY).

Input cost and carcass income data were also collected and included feeder buy prices based on monthly price-weight slide equations for heifers and steers ( $R^2 > 0.95$ ) derived from 5 years (2018-2022) of weekly price and weight data from various auction markets in Alberta.<sup>14</sup> Feeder cost equaled feeder buy price multiplied by feeder weight (\$/cwt); buying and transportation cost equaled \$10.15 CDN/head; induction costs are for veterinary care and medicines and were set at 3% of feeder costs; feeding costs (\$ CDN/lb weight gain); implant costs were defaulted to \$10 CDN/head.<sup>15</sup> Individual carcass base price (\$ CDN/cwt), discounts (\$ CDN/cwt) and premiums (\$ CDN/cwt) were based on Cargill's pricing grid.

Thus, net return was calculated as follows:

Net return = carcass income (\$ CDN/head) – total costs (\$ CDN/head), where carcass income, \$ CDN/head = (base price, \$ CDN/cwt ± YG discount or premium, \$ CDN/cwt) ± (QG discount or premium, \$ CDN/cwt) ± (HCW discount or premium, \$ CDN/cwt) × (HCW, lb/100); total cost, \$ CDN/hd = feeder cost + buying and transportation cost + induction costs + feeding costs + implant costs.

Sire and feeder progeny MBVs were generated from a reference population containing > 15,000 growth and feed efficiency and > 8,400 carcass quality phenotypes from crossbred commercial beef cattle that had been used to train the genomic predictions (MBVs) for 18 traits (Livestock Gentec, University of Alberta, Edmonton, Canada). This reference population also contains genotypes of various SNP panels (GGP 50k v1-3, GGP ULD 35k, GGP 100k, GGP HD 770k SNP) that were subjected to quality control and then imputed to 50k, 100k and to sequence (57 million SNPs). Numerous studies have been published using this Reference Population for genomic predictions.<sup>3,4,5,6,11,18,19,21,29,38,39</sup> Sire and feeder genotypes were also used to estimate genomic

breed composition (gBC) using the ADMIXTURE software<sup>7</sup> and a Purebred Reference Population described previously. The FPI was based on the multiple trait selection index theory,<sup>13,22</sup> and generated for each animal based on the MBVs of the traits, accuracy of MBVs, variance components, heritability, genetic and phenotypic correlations across traits and economic weights of each trait for a beef on beef production and marketing system for calves destined for western Canadian feedlots. Trait MBVs and relative emphasis in the FPI were RFI (-42), post-wean ADG (+20), HCW (+16), AFAT (+13), LMY (+7) and CMAR (+2).

Feeder MBVs for growth and feed efficiency were associated with actual feeder performance (n = 441), and sire MBVs (137 sires) for carcass traits were associated with actual mean progeny carcass quality using a regression analysis (PROC GLM of SAS).<sup>35</sup> Similarly, relationships of the FPI to net return were conducted using a regression analysis. A positive and greater coefficient of determination ( $R^2$ ) is an indicator of validated MBVs. The linear effect (b ± standard error) indicates how much a phenotype or carcass net return is expected to change given one-point change in the MBV or the index.

## Results and discussion

### Evaluation of the RHPI Score

In commercial heifers, the mean accuracy for age at first calving MBV was low (0.11) while growth and feed efficiency MBVs had moderate accuracy values (Table 1). These accuracy values are low due to the small number of observations in the fertility reference population, and fertility traits typically have low accuracy. Mean gBC was 55%, 29%, 4%, 3% and 2% for Angus, Simmental, Maine Anjou, Hereford and Gelbvieh, respectively (Table 2). Mean gRHET was 0.48 (CV = 36.1%). Interestingly, heifers sold for revenue before their first breeding season (n = 124) were slightly different in breed composition (50%, 35%, 3%, 4% and 3% Angus, Simmental, Maine Anjou, Hereford and Gelbvieh, respectively) and gRHET (0.50), indicating that producers favored Angus heifers, but not heifers with higher gRHET.

Commercial heifers with Above average RHPI Score were heavier at birth (5.3%), weaning (2.6%), and 365-days of age (1.2%), and were more genomically diverse (gRHET, 0.587 vs. 0.383) as compared with Below average scoring heifers (Table 2). This is expected due to the high weighting being placed on retained heterozygosity in the RHPI Score and the positive effects of retained heterozygosity and heterosis on preweaning growth,

**Table 1:** Mean accuracy and standard deviation (SD) of molecular breeding values (MBVs) for index traits from 1,511 commercial heifers.

| Trait MBV  | MBV accuracy |      |              |
|--|--------------|------|--------------|
|  | Average      | SD   | Range        |
| Heifer birth weight, lb                              | 0.17         | 0.11 | 0.04 to 0.38 |
| 200-day weaning weight, lb                           | 0.23         | 0.05 | 0.05 to 0.32 |
| Residual feed intake adjusted for backfat, lb DM/day | 0.17         | 0.02 | 0.04 to 0.24 |
| Feeding event duration, min/day                      | 0.26         | 0.02 | 0.06 to 0.34 |
| Pre-breeding weight at first parity, lb              | 0.31         | 0.03 | 0.07 to 0.40 |
| Pre-breeding backfat thickness, in                   | 0.27         | 0.02 | 0.06 to 0.35 |
| Age at first calving, day                            | 0.11         | 0.06 | 0.02 to 0.23 |

**Table 2:** Least square means ( $\pm$  standard error) for performance traits, and open rate in crossbred beef heifers from 10 Alberta cow-calf herds classified as below or above average for the Replacement Heifer Profit Index Score™

| Traits                                  | Below average<br>RHPI Score | Above average<br>RHPI Score | Significance<br>level |
|---|-----------------------------|-----------------------------|-----------------------|
| Number of replacement heifers           | 359                         | 549                         |                       |
| Black and Red Angus, fraction of 1      | 0.717 $\pm$ 0.016           | 0.431 $\pm$ 0.015           | < 0.001               |
| Simmental, fraction of 1                | 0.103 $\pm$ 0.019           | 0.360 $\pm$ 0.017           | < 0.001               |
| Maine Anjou, fraction of 1              | 0.040 $\pm$ 0.005           | 0.054 $\pm$ 0.005           | < 0.001               |
| Gelbvieh, fraction of 1                 | 0.029 $\pm$ 0.006           | 0.037 $\pm$ 0.005           | 0.041                 |
| Hereford, fraction of 1                 | 0.025 $\pm$ 0.004           | 0.028 $\pm$ 0.004           | 0.217                 |
| Retained heterozygosity, fraction of 1  | 0.383 $\pm$ 0.012           | 0.587 $\pm$ 0.012           | < 0.001               |
| Birth weight, lb                        | 76 $\pm$ 1.7                | 80 $\pm$ 1.4                | 0.003                 |
| Wean weight, lb                         | 571 $\pm$ 7.1               | 581 $\pm$ 6.5               | 0.029                 |
| 205-day wean weight, lb                 | 604 $\pm$ 6.5               | 620 $\pm$ 6.0               | < 0.001               |
| 365-day weight, lb                      | 900 $\pm$ 9.1               | 911 $\pm$ 8.5               | 0.101                 |
| Off-test backfat thickness, in          | 0.21 $\pm$ 0.01             | 0.20 $\pm$ 0.01             | 0.023                 |
| On-test ADG, lb/day                     | 2.18 $\pm$ 0.04             | 2.16 $\pm$ 0.04             | 0.432                 |
| On-test feed intake, lb DM/day          | 16.5 $\pm$ 0.2              | 16.5 $\pm$ 0.2              | 0.553                 |
| Feed Conversion Ratio, lb feed/lb gain  | 8.02 $\pm$ 0.27             | 7.98 $\pm$ 0.25             | 0.839                 |
| On-test RFI, lb DM/day                  | -0.13 $\pm$ 0.18            | -0.20 $\pm$ 0.18            | 0.671                 |
| On-test feeding event duration, min/day | 122 $\pm$ 3.0               | 116 $\pm$ 2.8               | 0.004                 |
| Number of heifers exposed to breeding   | 359                         | 549                         |                       |
| Number open (not pregnant)              | 84                          | 75                          |                       |
| Number of heifers calving               | 275                         | 474                         |                       |
| Open rate, %                            | 23.4                        | 13.7                        | < 0.001               |
| Age at first calving, day               | 730 $\pm$ 3.8               | 729 $\pm$ 3.4               | 0.509                 |
| First calf birth weight, lb             | 68 $\pm$ 2.0                | 70 $\pm$ 2.0                | 0.186                 |
| First calf wean weight, lb              | 487 $\pm$ 9.0               | 490 $\pm$ 8.0               | 0.673                 |

<sup>a</sup> Score  $\leq$  48.4 are defined as below average, while those  $>$  48.4 are above average.

weaning weight and pre-breeding body weight are well documented.<sup>11,25,26,27,28</sup> Recently, Zimmermann et al.<sup>40</sup> quantified the direct effect of heterosis on mature cow weight as 33.7  $\pm$  5.7 lb (15.3  $\pm$  2.6 kg). Heifer with Above or Below average scores were similar in residual feed intake (RFI) and feed conversion ratio (FCR), though feeding event daily duration was 4.9% lower for Above average heifers. Lower feeding event duration is phenotypically ( $r_p = 0.24$ ) and genetically ( $r_g = 0.21$ ) associated with lower RFI (efficient) in beef heifers.<sup>33,34</sup>

The overall open rate was 17.5%, with Below and Above average heifers having open rate of 23.4% vs. 13.7%, respectively (Table 2). Age at first calving, and first calf birth and weaning weights were similar between Below and Above average scoring replacement heifers. Further delineation of open rates seems

to indicate that there is a threshold at a score  $>$  40 (Figure 1), however, Basarab et al.<sup>11</sup> has shown a linear response of 2-percentile points in pregnancy rate per female exposed to breeding for each 10% change in retained heterozygosity. In the present study there was a 35% difference in mean gRHET (0.383 vs. 0.587) and a 9.7-percentile difference in open rate between Below and Above average heifers, thus indicating a slightly higher difference in open rate than expected (7-percentile points), and highlights the need for validation studies with fertility records on more commercial heifers.

These results show that Above average scoring heifers produced nine more calves per 100 replacement heifers exposed to natural breeding. This is worth \$14,175 CDN from increase weaned calf income when valued at \$3.15 CDN/lb (\$6.94/kg) for

500 lb (226.8 kg) calves (Alberta Beef Producers Weekly Feeder Prices, April 12, 2023). It is also worth an additional \$8,550 CDN (\$950 CDN/heifer) from not having to replace nine heifers, and assuming a moderate 20% replacement rate (<https://www.beefmagazine.com/breeding/weighing-costs-buying-or-raising-replacement-heifers>). This would come at a cost of \$3,000 CDN to genotype 100 heifers (\$30 CDN/GGP ULD SNP panel), or a six-to-one return on investment (gross income = \$19,725 CDN, cost = \$3,000 CDN). The cost of \$950 CDN/heifers accounts for all cost plus selling the cull replacement heifer. Other benefits may include improve health resilience of calves and a lower carbon footprint of beef production. Veterinary students at the University of Calgary monitored health events from birth to weaning and identified an increase in all-cause morbidity and mortality from 10% in high gRHET calves to 15% in low gRHET calves (n = 500;  $P < 0.02$ ).<sup>20</sup> The odds ratio for a morbidity and mortality event in a calf with gRHET < 0.5 compared to gRHET  $\geq 0.5$  was 2.4 (confidence interval: 1.17-4.93;  $P = 0.018$ ). A life cycle assessment of greenhouse gas (GHG) emissions from high vs. low gRHET herds (mean = 56.3, SD = 6.2 vs. mean = 30.0, SD = 13.6) revealed that the total GHG reductions from maintaining a high hybrid vigor herd was 639 kg CO<sub>2</sub>e/youthful animal slaughtered, worth \$32 CDN assuming \$50 CDN/t CO<sub>2</sub>e. Greenhouse gas emissions included enteric CH<sub>4</sub>, manure N<sub>2</sub>O, manure CH<sub>4</sub>, cropping N<sub>2</sub>O and energy CO<sub>2</sub> and are based on procedures described by Basarab et al.<sup>10</sup> This suggests that breeding for and maintaining a high hybrid vigor cow herd using genomic tools would be one of the most beneficial management practices for reducing the carbon footprint of beef production.

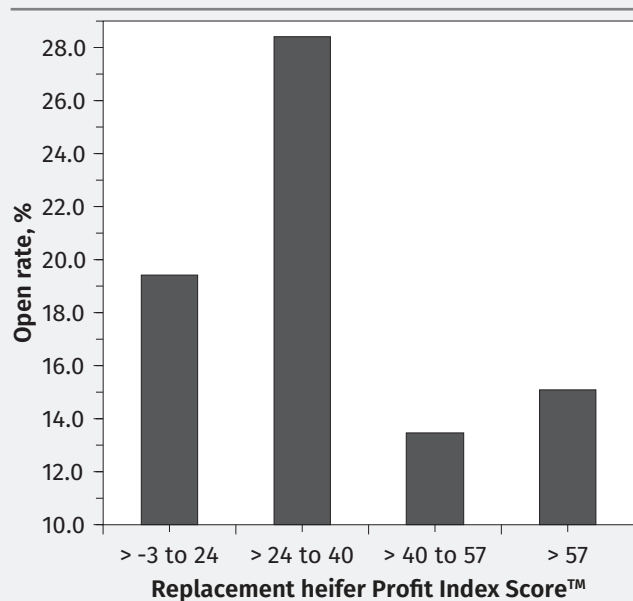
## Evaluation of the MBVs and FPI

Mean accuracy of sire MBVs for all post-weaning traits considered in the index were moderately-high (0.48 to 0.63) with the exception of lean meat yield (0.34; Table 3). Post-weaning daily gain, feed intake and feed efficiency MBVs were positively and linearly related to their actual phenotypes ( $R^2 = 0.18$  to 0.32; Figure 2A-C), indicating moderate reliability of MBVs. For example, each one-unit change in MBV for feed intake resulted in a change

in progeny feed intake of 1.9 lb DM/day (0.86 kg DM/day), and feed intake MBVs accounted for 31.8% of the inter-animal variation in average daily feed intake. Similarly, the RFI MBVs accounted for 19.3% of the inter-animal variation in RFI, and each 0.5 unit decrease in the MBV for RFI resulted in an improved feed efficiency of 1.05 lb DM/day (0.48 kg DM/day), worth about \$0.147 CDN/day assuming feed costs of \$0.14 CDN/lb DM (\$0.31 CDN/kg DM) or about \$22 CDN/feeder over a 150-day finishing period.

Sire MBVs for hot carcass weight, grade fat, lean meat yield and marbling were positively and linearly related to the mean progeny carcass performance ( $R^2 = 0.11$  to 0.60; Figure 3A-D). Sire MBVs for hot carcass weight only accounted for 10.8% of

**Figure 1:** Open rates in crossbred replacement heifers from 10 cow-calf herds from Alberta with different Replacement Heifer Profit Index Score™ ( $P = 0.0003$ , n = 908)

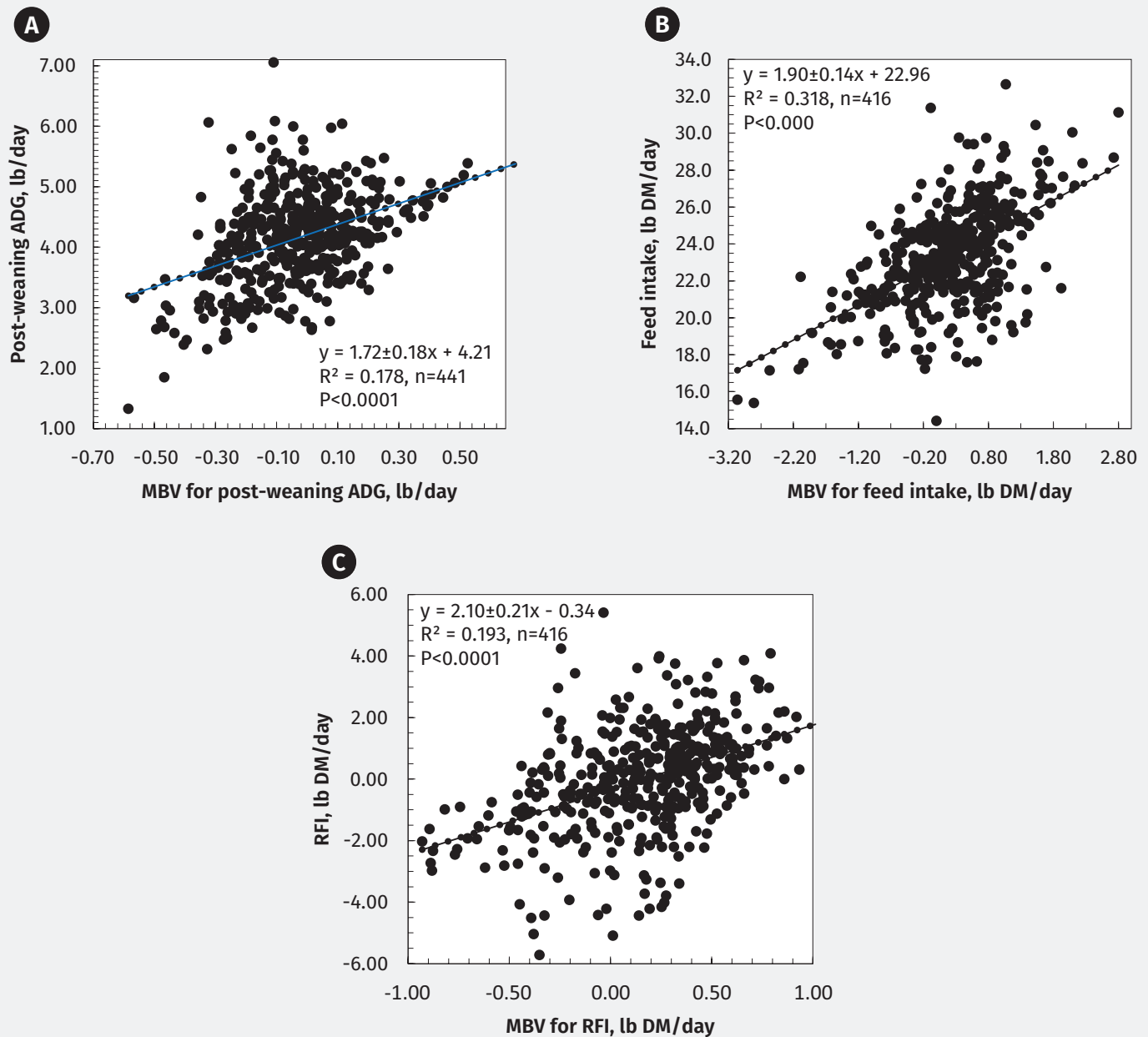


**Table 3:** Descriptive statistics for mean sire molecular breeding values (MBVs) and accuracy values for growth, feed efficiency and carcass traits (137 sires)

| Traits                               | Sire MBVs |       | Range           | Accuracy |       |
|--------------------------------------|-----------|-------|-----------------|----------|-------|
|                                      | Mean      | SD    |                 | Mean     | SD    |
| Post-weaning ADG, lb/day             | -0.013    | 0.075 | -0.260 to 0.302 | 0.398    | 0.091 |
| Feed Intake, lb DM/day               | 0.148     | 0.362 | -1.056 to 1.003 | 0.431    | 0.094 |
| Residual feed intake, lb DM/day      | 0.099     | 0.163 | -0.403 to 0.586 | 0.368    | 0.083 |
| Hot carcass weight, lb               | -0.49     | 15.7  | -53.8 to 43.8   | 0.576    | 0.124 |
| Carcass grade fat, in                | 0.017     | 0.049 | -0.127 to 0.133 | 0.564    | 0.124 |
| Carcass ribeye area, in <sup>2</sup> | -0.18     | 0.62  | -1.59 to 1.37   | 0.631    | 0.124 |
| Lean meat yield, %                   | -0.44     | 0.87  | -2.82 to 1.51   | 0.336    | 0.077 |
| Marbling <sup>a</sup>                | 5.6       | 27.8  | -59.8 to 121.7  | 0.579    | 0.124 |

<sup>a</sup> Marbling is a measure of intramuscular fat where trace marbling or less = 100 to 299 (Canada A quality grade), slight marbling = 300 to 399 (Canada AA quality grade), small to slightly abundant = 400 to 499 (Canada AAA quality grade) and slightly abundant or more marbling = 500 to 999 (Canada Prime). AMSA marbling score: 0 = devoid, 100 = practically devoid, 200 = traces, 300 = slight, 400 = small, 500 = slightly abundant, 600 = moderately abundant.

**Figure 2 A-C:** Relationships of growth and feed efficiency MBVs to actual performance in an independent validation data set of crossbred steers.



the variation in mean progeny performance, and this may have been due to the low variability in the trait (CV = 6.1% for slaughter heifers; CV = 7.5% for slaughter steers). Despite this one exception, all other sire trait MBVs had moderate-high reliability ( $R^2 = 0.329$  to  $0.599$ ), indicating that these MBVs will produce a reliable multi-trait selection index for selecting bulls that produce more profitable feeder cattle. Other factors influencing reliability were standardized feeding and management, resulting in high quality feed efficiency and carcass data, proper definition of contemporary groups and selection of a moderate sized training population with > 15,000 feed efficiency and > 8,400 carcass phenotypes and genotypes with a high degree of genetic relationship to the target population.

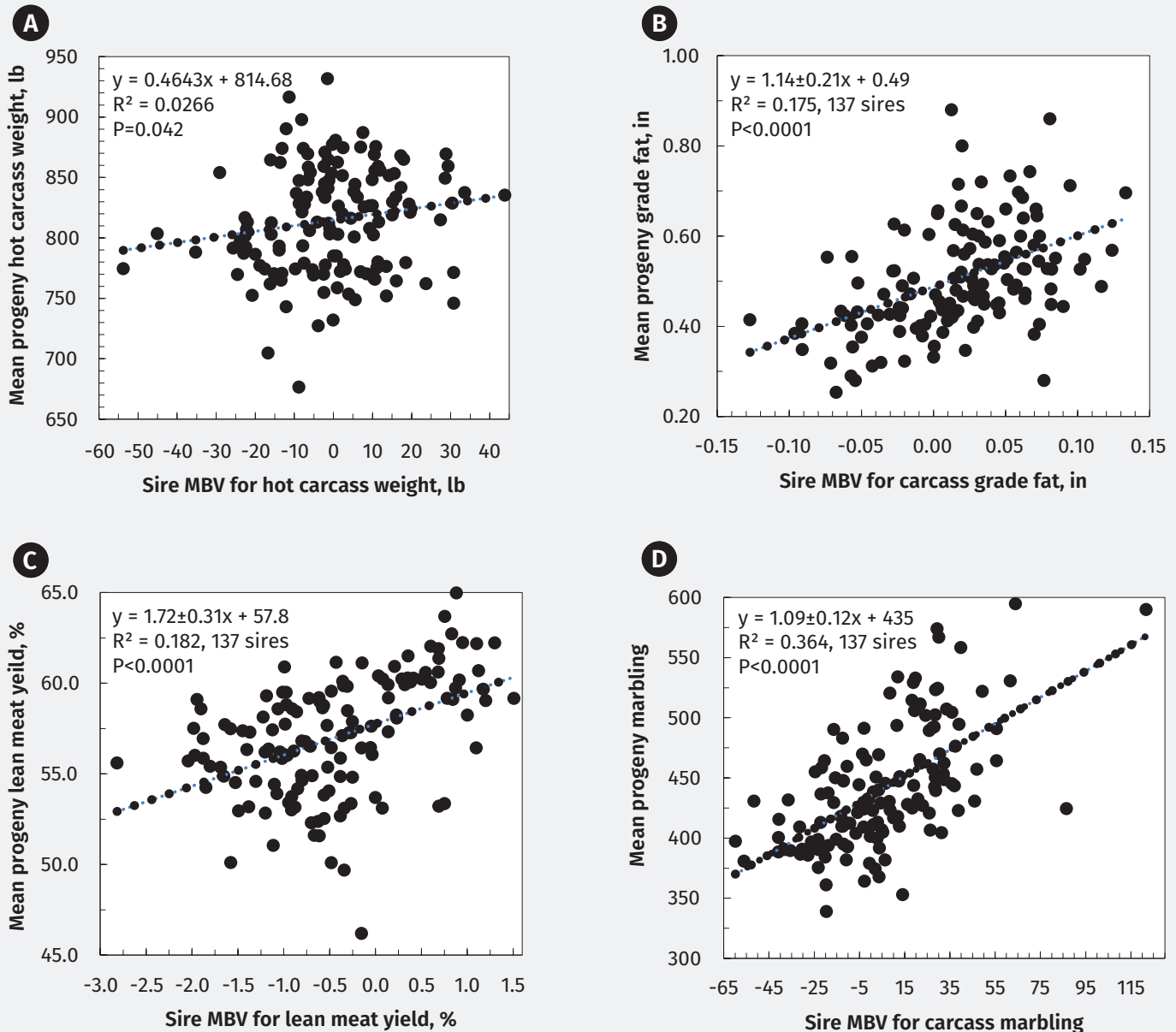
The FPI which included sire MBVs for RFI, post-wean ADG, HCW, AFAT, LMY and CMAR, was linearly related to carcass net income (linear effect =  $1.54 \pm 0.44$ ,  $P = 0.0006$ ). Thus, each

100-point change in the sire's FPI equaled \$154 CDN per feeder in net income. Potential difference between 3 high (+50) FPI sires and 3 lower (-50) FPI sires each producing 60 feeder calves over 3 years could be as high as \$9,240 CDN in net income, at a cost of \$270 CDN for genotyping the 6 sires (\$45 CDN/sire for GGP-100k SNP panel). Breakeven on genotyping costs would require at least a 10-point differential in the 2 bulls being compared and then using the selected bull for 3 years (10 points x \$1.54 CDN/index point x 3 years of bull use).

## Conclusions

The non-additive genetic effect, as identified by retained heterozygosity, is an essential component of any replacement heifer scoring system, as it has been shown to increase calving and weaning rate, decrease replacement heifer requirements and increase net income for commercial cow-calf producers.

**Figure 3 A-D:** Relationships of sire carcass MBVs to mean progeny carcass quality in an independent validation data set of 137 sires and 1,894 crossbred feeder progeny (13.8 progeny/sire).



Including both dominance and additive variance in the genomic analysis for longevity, stability and lifetime productivity traits may further improve the prediction of female fertility. The sire Feeder Profit Index, which included only the additive genetic effects, was effective in predicting net income in crossbred feeder progeny. Accuracy would be further improved above 0.65 for all index traits by increasing number of sires and progeny with genotypes and high-quality phenotypes.

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