

Improvement of cow feed efficiency using molecular breeding values for residual feed intake - The “Kinsella Breeding Project”

C. Ekine-Dzivenu¹, E. C. Akanno¹, L. Chen¹, L. McKeown^{1,2}, B. Irving¹, L. Baker³, M. Vinsky³, S. Miller⁴, Z. Wang¹, J. Crowley¹, M. Colazo⁵, D. Ambrose⁵, M. Juarez³, H. Bruce¹, M. D. MacNeil⁶, G. Plastow¹, J. Basarab^{1,2}, C. Li^{1,3} & C. Fitzsimmons^{1,3}

¹ *Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, T6G 2P5*

² *Alberta Agriculture and Forestry, Lacombe Research Centre, 6000 C&E Trail Lacombe, AB, Canada, T4L 1W1*

³ *Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, 6000 C&E Trail, Lacombe, AB, Canada T4L 1W1*

cfitzsim@ualberta.ca, changxi.li@agr.gc.ca (Corresponding Authors)

⁴ *Angus Genetics Inc. (AGI), St. Joseph, Missouri*

⁵ *Alberta Agriculture and Forestry, 7000 - 113 Street, Edmonton, AB, Canada T6H 5T6*

⁶ *Delta G 145 Ice Cave Rd, Miles City, Montana 59301*

Summary

Genomic selection for feed efficiency in beef cattle offers an opportunity to reduce feed costs and greenhouse gas (GHG) emission while increasing profitability and environmental sustainability in beef production. In the beginning of 2013 at the University of Alberta Roy Berg Kinsella Research Ranch, Kinsella, Canada, a project for selection of improved feed efficiency, i.e. low residual feed intake (RFI), using molecular breeding values (MBVs) in a multiple trait selection index was initiated. It involves three beef cattle populations namely, Kinsella beef composite herd (KC) which was split into efficient and control herds, purebred Angus (AN), and purebred Charolais (CH). Preliminary assessment of genetic trends after two years of selection showed that average estimated breeding values (EBV) for RFI in the three beef cattle populations changed favorably. The KC-Efficient herd had a lower average EBV for RFI of 0.026 ± 0.015 Kg DMI/d in comparison to 0.044 ± 0.017 Kg DMI/d in the control herd and 0.056 ± 0.013 Kg DMI/d in the base efficient herd from 2013. Average EBV for RFI in the Angus population decreased from 0.065 ± 0.02 to 0.053 ± 0.023 Kg DMI/d and that for Charolais from 0.118 ± 0.025 to 0.039 ± 0.026 Kg DMI/d. Demonstration of the results achieved, especially in the longer term, will help support the adoption of genomic technology in combination with RFI and increase farm profits due to reduced feed input costs in cow-calf and feeder cattle operations in Canada.

Keywords: genomic selection, molecular breeding value, selection index, efficient

Introduction

The single largest expense in most commercial beef production enterprises is the

provision of feed. Feed costs account for 50-70% of the total costs of beef production (Cattle Fax, 2017), while 50-70% of greenhouse gas (GHG) production from beef cattle is generated from mature cows (Beauchemin *et al.*, 2010; Basarab *et al.*, 2012). Feed cost for maintenance is estimated to represent at least 60-65% of the total feed requirement for a cowherd, with considerable variation between animals (Montano-Bermudez *et al.*, 1990; Parnell *et al.*, 1994). Genomic selection for improved feed efficiency in beef cattle herds offers an opportunity to reduce feed cost and GHG emissions, while increasing profitability and environmental sustainability of beef production. The aim of the “Kinsella Breeding Project” at the Roy Berg Kinsella Research Ranch, is to demonstrate the use of genomic technologies and residual feed intake (RFI) to breed for improved cow feed efficiency, and to serve as a catalyst to increase the uptake of RFI and genomics as a means to increase profit for cow-calf and feedlot operations.

Material and methods

The project uses three beef cattle populations, namely the Kinsella beef composite (KC), purebred Angus (AN), and purebred Charolais (CH), all maintained at the Roy Berg Kinsella Research Ranch, Alberta, Canada. Within the KC cattle population, a herd of 420 crossbred cows was randomly divided into two equal groups (control vs. efficient) based on calving interval, age, and mature weights. Replacement yearling bulls and heifers for the KC efficient population were tested in a GrowSafe System[®] to determine their RFI. Efficient replacement heifers (10-20% per year) and bulls (25% per year) were selected based on a multi-trait maternal index (MPI), which included RFI and direct and maternal weaning weights (WWTd, WWTm). Determinants of economic profitability were obtained from the beef industry and used to establish economic weightings that maximize profitability on these traits in the selection index. The efficient animals were ranked on the index after independent culling for high birth weight and low yearling weight. For the top ranking bulls, final selection was made by visualizing their conformation to ensure that bulls with undesirable conformation attributes would not be selected as breeding animals. The molecular breeding values (MBVs) of potential replacements (bulls and heifers) were predicted based on a Genomic Best Linear Unbiased Prediction (GBLUP) procedure for all traits except WWTd and WWTm. The GBLUP was performed within each of KC, AN, and CH herds with the genomic relationship matrix constructed from the SNP markers of the BovineSNP50k chip using the first method described by VanRaden (VanRaden, 2008). The reference population used in the GBLUP had approximately 1500 Kinsella beef cattle and the MBVs were predicted using ASReml 4.0 (VSN International Ltd., Hemel Hempstead, UK) (Gilmour *et al.*, 2015). Estimated Breeding values (EBVs) for WWTd and WWTm were obtained with a numerator relationship matrix defined based on the pedigree. Accuracies of the MBVs and EBVs were calculated using the formula by Gilmour *et al.* (2015) as follows:

$$(1)$$

where σ_e is the standard error reported with the breeding value for each individual, F is the inbreeding coefficient, R is the diagonal from the relationship matrix and σ_a^2 is the additive genetic variance of the trait. MBVs and EBVs were then incorporated into the multi-trait selection index.

Replacements for the KC control herd were selected using phenotypic information for lower birth weight and higher yearling weight as well as for greater average daily gain from birth to one year of age, with no emphasis on RFI. Replacement occurred at the same rates as the efficient herd.

Due to the relatively small population sizes of the purebred herds (AN=182, CH=124), they were treated as the initial efficient herd and no control groups were created. Replacement animals in the Angus herd were selected each year based on the MPI, similar to the efficient KC animals, while replacement animals in the Charolais herd were selected based on a feedlot profitability index (FPI), which included RFI, average daily gain (ADG), carcass marbling (CMAR), lean meat yield (LMY), average backfat thickness (AFAT), and hot carcass weight (HCW).

After two years of selection, genetic trends across years were evaluated for the three populations based on average EBV for each of the economically important traits considered (RFI, RFIF, ADG, DMI, BWT, WWT, HCW, REA, AFAT, LMY, CMAR), using a univariate animal model. The model for RFI, RFIF, ADG and DMI included a fixed effect of gender and a linear covariate of test age in days, random effects of batch (combination of year of birth and feedlot test pen), and the direct genetic effect of the animal. The same model was used for HCW, REA, AFAT, LMY, CMAR but had animal slaughter age in days in place of test age. The model for BWT and WWT included fixed effects of gender, year of birth, and dam age in years, and random effects of direct genetic effect of the animal and maternal effects. Additive genetic relationship matrix (A-matrix) from the pedigree and actual measured phenotype data of all animals including the calves were used to estimate breeding values (EBV), as implemented in ASReml 4.0 (VSN International Ltd., Hemel Hempstead, UK) (Gilmour *et al.*, 2015). Realized genetic gain in the KC population was measured by comparing the trait EBVs of calves from the efficient and control herds both within and between generations, while progress realized in the Angus and Charolais herds was measured by comparing the trait EBVs of calves from one generation to the next with RFI values re-calculated based on combined data across years. T-tests were used to determine whether average trait EBVs of the calves were significantly different between the efficient and control groups or years.

Results and discussion

Average EBVs and standard errors (SE) are presented in Table 1 for the 2013 and 2015 born KC control and efficient calves and in Table 2 for Angus and Charolais calves. The genetic trend shows favorable progress made on breeding values for RFI across the three populations. The 2015 KC-Efficient herd had a lower average EBV for RFI of 0.026 ± 0.015 Kg DMI/d in comparison to 0.044 ± 0.017 kg DMI/d for the 2015 control herd and 0.056 ± 0.013 Kg DMI/d for the 2013 efficient herd (Table 1). The average EBV of RFI for Angus and Charolais also decreased across years from 0.065 ± 0.02 to 0.053 ± 0.023 kg DMI/d in the Angus population and from 0.118 ± 0.025 to 0.039 ± 0.026 kg DMI/d in the Charolais population (Table 2). Changes were also observed for other traits included in the selection indexes. As expected in short term selection, changes for RFI EBVs were relatively small (Tables 1 and 2) and was significant only in the Charolais herd (Table 2).

Table 1. Genetic trends (average EBV by year of birth \pm SE) for the KC control and efficient populations for feed efficiency and carcass traits.

Traits	2013			2015		
	Control (N=159)	Efficient (N=167)	P-value	Control (N=165)	Efficient (N=165)	P-value
RFI	0.038 \pm 0.013	0.056 \pm 0.013	0.3376	0.044 \pm 0.017	0.026 \pm 0.015	0.4473
RFIF	0.034 \pm 0.011	0.041 \pm 0.012	0.6616	0.032 \pm 0.015	0.014 \pm 0.013	0.3635
ADG	-0.005 \pm 0.003	-0.005 \pm 0.003	0.9530	0.011 \pm 0.003	0.018 \pm 0.003	0.1383
DMI	-0.015 \pm 0.027	0.030 \pm 0.034	0.3011	0.089 \pm 0.024	0.079 \pm 0.027	0.7789
BWT	-0.232 \pm 0.609	-0.203 \pm 0.613	0.9735	1.409 \pm 0.645	0.636 \pm 0.638	0.3953
WWTd	-3.762 \pm 1.238	0.086 \pm 1.188	0.0256	2.281 \pm 1.311	-1.040 \pm 1.143	0.0571
HCW	-3.668 \pm 1.931	-3.168 \pm 2.159	0.8629	5.208 \pm 1.658	-3.005 \pm 1.273	0.0001
REA	-0.896 \pm 0.511	-1.001 \pm 0.486	0.8826	-0.058 \pm 0.473	-1.545 \pm 0.34	0.0112
AFAT	-0.215 \pm 0.091	-0.193 \pm 0.076	0.8525	0.28 \pm 0.088	0.244 \pm 0.101	0.7903
LMY	0.066 \pm 0.127	0.041 \pm 0.12	0.8879	-0.471 \pm 0.129	-0.503 \pm 0.121	0.8547
CMAR	0.636 \pm 1.528	1.932 \pm 1.64	0.5634	1.292 \pm 1.758	-4.105 \pm 1.881	0.0368

RFI (Kg, DMI/d) = residual feed intake, RFIF (Kg, DMI/d) = residual feed intake adjusted for ultrasound backfat thickness measured at the end of feedlot test, ADG (Kg/d) = average daily gain, DMI (Kg/d) = dry matter intake, BWT (lb) = birth weight, WWTd (lb) = weaning weight direct, HCW (Kg) = hot carcass weight, REA (cm²) = rib eye area, AFAT(mm) = average back fat thickness, LMY (%) = lean meat yield, CMAR = carcass marbling.

Table 2. Genetic trend (average EBV by year of birth \pm SE) for the Angus and Charolais populations for feed efficiency and carcass traits.

Traits	Angus			Charolais		
	2013 (N=191)	2015 (N=172)	P-value	2013 (N=84)	2015 (N=106)	P-value
RFI	0.065 \pm 0.02	0.053 \pm 0.023	0.6842	0.118 \pm 0.025	0.039 \pm 0.026	0.0277
RFIF	0.063 \pm 0.02	0.041 \pm 0.022	0.4487	0.102 \pm 0.023	0.008 \pm 0.028	0.0111
ADG	0.022 \pm 0.005	0.007 \pm 0.005	0.0292	0.014 \pm 0.01	-0.004 \pm 0.009	0.2041
DMI	0.142 \pm 0.048	0.139 \pm 0.046	0.9686	0.177 \pm 0.041	0.08 \pm 0.051	0.1391
BWT	2.331 \pm 0.643	0.661 \pm 0.605	0.0593	-1.728 \pm 0.922	-2.004 \pm 0.803	0.8213
WWTd	-1.826 \pm 2.24	0.841 \pm 2.944	0.4715	3.487 \pm 4.321	-6.766 \pm 4.232	0.0917
HCW	7.166 \pm 2.544	5.08 \pm 2.076	0.5256	3.32 \pm 2.221	-1.297 \pm 1.581	0.0923
REA	-0.312 \pm 0.127	-0.484 \pm 0.103	0.2954	-1.434 \pm 0.509	-2.568 \pm 0.439	0.0937
AFAT	-0.098 \pm 0.091	-0.142 \pm 0.1	0.7476	0.173 \pm 0.15	-0.343 \pm 0.09	0.0036
LMY	0.06 \pm 0.078	0.012 \pm 0.072	0.6571	-0.487 \pm 0.153	-0.272 \pm 0.13	0.2879
CMAR	6.342 \pm 2.942	6.05 \pm 3.551	0.9495	15.051 \pm 3.019	9.129 \pm 2.56	0.1364

RFI (Kg, DMI/d) = residual feed intake, RFIF (Kg, DMI/d) = residual feed intake adjusted for ultrasound backfat thickness measured at the end of feedlot test, ADG (Kg/d) = average daily gain, DMI (Kg/d) = dry matter intake, BWT (lb) = birth weight, WWTd (lb) = weaning weight direct, HCW (Kg) = hot carcass weight, REA (cm²) = rib

eye area, AFAT(mm) = average back fat thickness, LMY (%) = lean meat yield, CMAR = carcass marbling.

However, results should be interpreted with some caution as the tests for differences between average EBVs might be too liberal since the EBVs for the different traits were derived from a single trait animal model and they may be correlated. Moreover, the accuracies of genomic prediction for RFI and other traits ranged from 0.32 to 0.75, which may contribute to the small genetic gains along with a relatively short selection period. As the project progresses, realized genetic gains are expected to improve with more selected replacements in the herds and with increases in genomic prediction accuracies as more phenotypic data is collected in the reference population.

List of References

- Basarab, J., V. Baron, Ó. López-Campos, J. Aalhus, K. Haugen-Kozyra & E. Okine, 2012. Greenhouse gas emissions from calf- and yearling-fed beef production systems, with and without the use of growth promotants. *Anim 2*: 195-220.
- Beauchemin, K.A., H.H. Janzen, S.M Little, T.A. McAllister, & S.M. McGinn, 2010. Life cycle assessment of greenhouse gas emissions from beef production in western Canada: A case study. *Agric. Syst.* 103(6):71-379. doi: 10.1016/j.agsy.2010.03.008.
- Cattle Fax. 2017. 2017 Reduction to cow costs? Issue 9 | vol. XXXXIX. [Online] Available https://www.cattlefax.com/uploaded_images/88832138-7cf8-4109-84f3-1b2ed5bb7c30.pdf.
- Gilmour, A., B. Gogel, B. Cullis, S. Welham, & R. Thompson, 2015. ASReml user guide release 4.1 structural specification. Hemel Hempstead: VSN International Ltd.
- Montano-Bermudez, M., M. K. Nielsen, & G. H. Deutscher, 1990. Energy requirements for maintenance of crossbred beef cattle with different genetic potential for milk. *J. Anim. Sci.* 68:2279–2288.
- Parnell, P. F., R. M. Herd, D. Perry, & B. Bootle, 1994. The Trangie experiment—Response in growth rate, size, maternal ability, reproductive performance, carcass composition, feed requirements and herd profitability. *Proc. Aust. Soc. Anim. Prod.* 20:17–26.
- VanRaden, P. M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91:4414–4423.