Extension demonstration project outcomes: Industry adoption and translation of project deliverables

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Unfortunately, the amount of feed intake data available to U.S. beef breed associations is spars compared to the amount of data available for growth traits. This makes traditional pedigree-based genetic evaluation for feed intake or efficiency challenging. However, progress in this trait complex could be made as we know that dry matter intake and various "efficiency" traits would respond favorably to selection. Table 1 below depicts the heritability (on the diagonal) and genetic correlations (on the off diagonal) of several feed efficiency traits.

Table 1. Heritabilities and genetic correlations for feed efficiency traits[1].

	ADG	DMI	RFI	G:F
ADG	0.26	0.56	-0.15	0.31
DMI		0.40	0.66	-0.60
RFI			0.52	-0.92
G:F				0.27

[1]Adapted from Rolfe et al. (2011).

Although EPD for traits related to the cost of production are limited, some EPD do currently exist to select for partial efficiency. Examples of those are detailed below.

	Bull A	Bull B
Residual average daily gain	-0.1	0.05
Residual feed intake	-0.3	0.0
Maintenance energy	0	10

Residual average daily gain (Angus)- Calves sired by bull B should gain 0.15 pounds per day more when fed the same amount of feed during the post weaning phase.

Residual feed intake (Gelbvieh)- Calves sired by bull A would consume 0.3 lbs of feed per day less on average than calves sired by bull B to gain the same amount of weight.

Maintenance energy (Red Angus)- Daughters from bull B should require 10 Mcal/month less energy for maintenance. If average hay quality is 0.86 Mcal/lb. this equates to 11 lb. less forage per month.

Even though some EPD do exist for components of efficiency, feed intake phenotypes are expensive to collect and thus for the foreseeable future, wide-spread collection of individual intake data in the seedstock sector will remain sparse at best. Moreover, residual gain and residual feed intake are not phenotypes per se, but rather restricted selection indices. Although these residuals are biologically intriguing, they are

suboptimal at generating response to overall profitability given that they only allow for improvement in either gain or feed intake and not both traits simultaneously.

Selection Methods for Efficiency

In terms of guidelines for the U.S. beef industry to follow relative to genetic selection for improved feed efficiency, Nielsen et al. (2013) recommend an index-based approach. From a total life-cycle perspective, maintenance energy costs are estimated to be about 70% of the total energy intake in the beef production system. Thus a primary goal must be to decrease maintenance energy requirements while not reducing output. This means that profitable selection decisions must contemplate multiple traits simultaneously. Using selection index values will be very beneficial to achieve the overall goal of improved profitability. If constructed correctly, multiple-trait index tools can account for antagonisms that may exist between feed intake and other economically relevant traits, including cow-herd centric traits.

Hazel (1943) first introduced the selection index equations to calculate index coefficients (b) for each of the selection criteria:

$$\mathbf{b} = \mathbf{P}^{-1}\mathbf{Gv}$$

where **P** is a n x n matrix of the phenotypic (co)variances among the n traits measured and available as selection criteria, **G** is a n x m matrix of the genetic (co)variances among the n selection criteria and m objective traits, and **v** is an m x 1 vector of economic values for all objective traits.

Rolfe et al. (2011) estimated selection response for three feed efficiency related phenotypes and four different selection indices (Table 2). From these results it is clear that an economic index approach to selection is the most desirable.

Table 2. Expected response (selection intensity*lbs) to selection based on several criterion[1].

Selection Criterion[2]	Direction	DMI Response, lbs.	Gain Response, lbs.
DMI	Down	-125.0	-11.91
GAIN	Up	+57.98	+16.54
G:F	Up	-60.63	+5.29
I_1	Down	-98.33	+4.19
I_2	Down	-84.88	0
I_3	Down	-27.34	+11.91
I_4	Down	0	+16.98

[1] Adapted from Rolfe et al. (2011).

^{2} DMI= Dry matter intake; GAIN = Weight gain; G:F = Gain to feed ratio; I_1 = Phenotypic RFI; I_2 = Genetic RFI; I_3= Economic index including DMI and Gain; I_4=Economic index including Gain and RFI.

The improvement of efficiency is inherently a multiple-trait issue and thus the development and utilization of indexes to select for the most profitable animals is critical. An interactive example of such an index is available at www.beefefficiency.org. The interactive tool enables the user to calculate residual average daily gain, residual feed intake, and index three from table 2.

Although Rolfe et al. (2011) illustrated that an economic index based approach was superior to single trait selection when considering both feed intake and gain, a more comprehensive approach is to consider feed intake as a cost in existing economic selection indices such as Angus's $B or Simmental's TI, therefore considering traits such as carcass merit, feed intake, carcass weight, survival, and other traits as dictated by the complete breeding objective. This approach is currently being implemented by several U.S. beef breed associations, in part enabled by the massive number of phenotypes generated through the USDA-NIFA funded project National Program for Genetic Improvement of Feed Efficiency in Beef Cattle that has provided phenotypes and genotypes to these associations at no cost.

The importance of feed intake in a terminal index is well documented. In example, Ochsner et al. (2016) assumed a terminal breeding objective for Beefmaster cattle whereby all calves were born from mature cows, retained through the feedlot phase and sold on a grid-based system. The five objective traits considered for the terminal index included hot carcass weight (HCW), marbling score (MS), ribeye area (REA), 12th-rib fat (FAT) and feed intake (FI), with the latter representing the only expense related phenotype among the objective traits. Relative economic values for the terminal objective traits HCW, MS, ribeye area REA, FAT, and FI were 91.29, 17.01, 8.38, -7.07, and -29.66, respectively. This illustrates that sale weight, in this case hot carcass weight, and feed intake are drivers of profitability. Selection criteria for both indices were selected from the ten EPD currently reported by BBU. The suite of BBU EPD included: birth weight (BWT), WWd, WWm, 365-day yearling weight (YW), scrotal circumference (SC), ultrasound ribeye area (UREA), ultrasound 12th-rib fat (UFAT), ultrasound rump fat (URUMP), ultrasound intramuscular fat percentage (UIMF) and total maternal (TM). Selection criteria considered for the terminal index were YW, UREA, UFAT and UIMF. The accuracy of this index (r_{HI}) was estimated to be 0.50. If additional economically relevant traits could be added to the suite of selection criterion, such as an EPD for FI, this accuracy would increase. In the context of feed intake, this will require additional phenotyping efforts supported by a genomics approach.

A Genomics Approach

Genomic information, in the form of Single Nucleotide Polymorphisms (SNP), has always held the promise to increase the accuracy of Expected Progeny Differences (EPD).

This promise has finally been realized for those breeds that incorporate this information into their EPD calculations. One key advantage to genomic predictors (i.e. Molecular Breeding Values (MBV)) is that this information can be garnered early in the life of the animal thus enabling an increase in the accuracy of EPD particularly on young animals, which have not yet produced progeny. The benefit of the inclusion of genomic predictions into EPD estimates is proportional to the amount of genetic variation explained by the genomic predictor.

Genomic-enhanced EPD were first estimated for carcass traits and then evolved to other production traits for which EPD already existed. This is due to the need for phenotypes to develop (train) the genomic prediction equations. Consequently, genomic tests for "novel" traits such as different measures of efficiency require a significant effort in order to build large resource populations of animals with both phenotypes and genotypes. In this case, strategic genotyping and phenotyping could have an economic advantage over routine collection of very costly phenotypes.

The underlying question commonly asked by producers is "does it work?". It is critical to understand that this is not a valid question, as the true answer is not binary (i.e. yes or no). The important question to ask is "how well does it work?", and the answer to that question is related to how much of the genetic variation the marker test explains. The magnitude of the benefits will depend on the proportion of genetic variation (%GV) explained by a given marker panel, where the %GV is equal to the square of the genetic correlation multiplied by 100.

Combining these sources of information, molecular tools and traditional EPD, has the potential to allow for the benefits of increased accuracy and increased rate of genetic change. Increased rate of genetic change can occur by increasing the accuracy of EPD, and thus the accuracy of selection, and by decreasing the generation interval. This decrease in the mean generation interval could occur particularly for sires if they are used more frequently at younger ages given the increased confidence in their genetic superiority due to added genomic information.

Figures 1 and 2 illustrate the benefits of including a MBV into EPD (or Estimated Breeding Value (EBV) which is twice the value of an EPD) on accuracy (BIF scale) when the MBV explains 10 or 40% of the genetic variation (GV), which is synonymous with r^2 values of 0.1, and 0.4. The darker portion of the bars shows the EPD accuracy before the inclusion of genomic information and the lighter colored portion shows the increase in accuracy after the inclusion of the MBV into the EPD calculation. As the %GV increases, the increase in EPD accuracy becomes larger. Additionally, lower accuracy animals benefit more from the inclusion of genomic information and the benefits decline as the EPD accuracy increases. Regardless of the %GV assumed here, the benefits of including genomic information into EPD dissipate when EPD accuracy is between 0.6 and 0.7. On the other hand, when %GV is 40, an animal with 0 accuracy could exceed 0.2 accuracy with genomic information alone. This would be comparable to having approximately 7 progeny for a moderately heritable trait like feed intake. It should be noted that although a SNP panel that only explains 10% of the GV would be considered poor for weight traits,

if phenotypes do not exist, a panel of this efficacy would be beneficial.

Figure 1. Increase in accuracy from integrating genomic information that explains 10% of the genetic variation into Estimated Breeding Values (EBV).
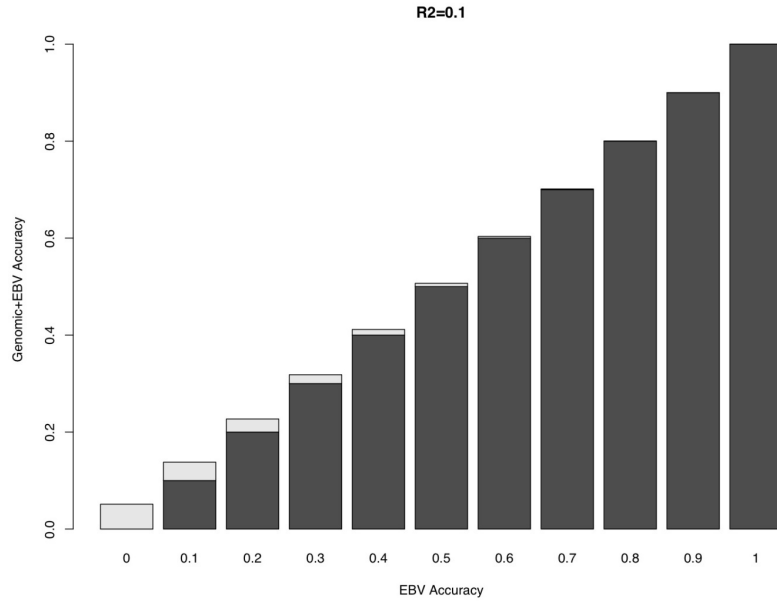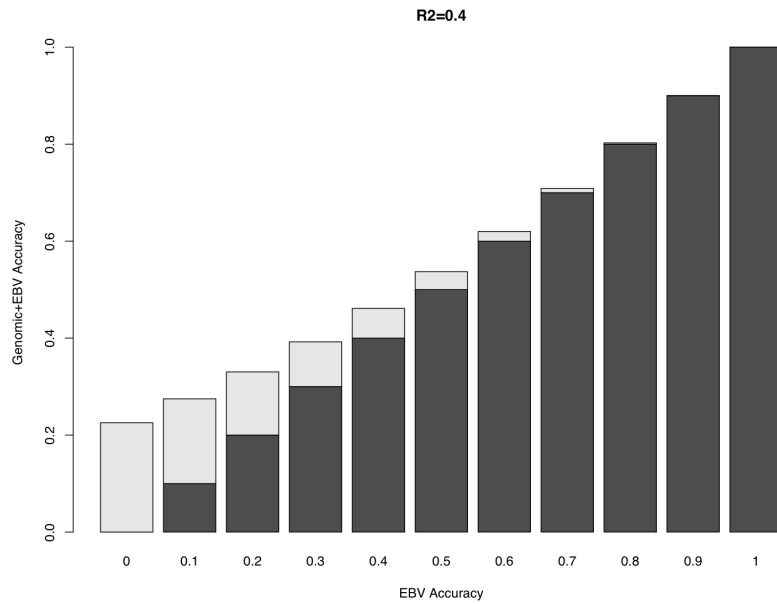

Figure 2. Increase in accuracy from integrating genomic information that explains 40% of the genetic variation into Estimated Breeding Values (EBV).

Current efforts

A USDA-NIFA funded project, National Program for Genetic Improvement of Feed Efficiency in Beef Cattle, to develop genomic predictors for feed intake/efficiency using dense single nucleotide polymorphism (SNP) panels (50,000 and 770,000 SNPs). To do this requires the collection of feed intake records from thousands of animals that are genotyped with either the 50K or 770K (HD) SNP assays across multiple breeds in order to develop genomic predictors that are accurate and robust across cattle populations. Table 3 contains initial genome-wide association results from this project (Saatchi et al., 2014). Four populations of cattle involving over 5,000 animals were used for a genome-wide association study (GWAS) of different feed efficiency related traits. The heritability estimates (h2) represent the proportion of phenotypic variation explained by the SNPs. Although all estimates suggest that these traits are moderately heritable, differences in parameter estimates exist between the resource populations likely due to differences in population size, structure (e.g., the number of contemporary groups, degree of relatedness among animals, etc.), and data collection methods.

Table 3. Genomic heritability estimates for ADG, MBW, RFI and DMI[1]

Population[2]	N	SNP Density	ADG h^2	MBW h^2	RFI h^2	DMI h^2
HH	847	HD	0.27	0.50	0.45	0.41
USMARC	1,160	50K	0.30	0.47	0.49	0.35
SM x AN	1,444	HD	0.23	0.38	0.32	0.27
AN	1,580	HD	0.19	0.49	0.21	0.35

[1] ADG = Average daily gain, MBW = mid-test metabolic body weight, RFI = Residual feed intake, DMI = dry matter intake.
[2] HH=Hereford cattle fed at Olsen Ranches, USMARC=F_1^2 composites from the Meat Animal Research Center Cycle VII, SM x AN=Legacy Simmental x Angus animals fed at the University of Illinois, AN=Angus cattle fed at Circle A and the University of Missouri.

Saatchi et al. (2014) also identified regions of the genome that appear to harbor large effect quantitative trait loci (QTL). Given the complex nature of these traits (the fact they are controlled by numerous genes), a large effect QTL was considered as a locus explaining greater than 1% of the additive genetic variation. A total of 5, 5, 17, and 10 of these large effect QTL were identified for ADG, DMI, MBW and RFI, respectively. Some of the QTL identified had substantially larger effects than might have been expected. For instance, a QTL in Angus explained over 10 and 14% of the additive genetic variation in DMI and MBW, respectively. No QTL identified for RFI explained greater than 2.5% of the additive genetic variation. These QTL regions were generally breed specific, further illustrating why genomic predictors are not easily transferable across breeds.

In 2009, the concept of an integrated project focused on the development and translation of genomic selection tools in beef cattle was initiated as a collaboration between the National Beef Cattle Evaluation Consortium, the University of Nebraska-Lincoln, the U.S. Meat Animal Research Center, and the seven largest U.S. beef breed associations. This project, called the Weight Trait Project (WTP) due to the initial focus on weight traits, has served as the industry demonstration project for the before mentioned USDA-NIFA project. The WTP has engaged 24 seedstock producers from seven states representing the following U.S. beef breeds: Angus, Hereford, Red Angus, Charolais, Gelbvieh, Limousin, and Simmental. Through this demonstration project, these producers were able to nominate herd bulls that were used via AI to breed cows either at the U.S. Meat Animal Research Center or the Rex Ranch. The corresponding progeny were then feed in individual feed intake facilities and genotyped with the BovineSNP50v2 beadchip. All sires were genotyped with the HD assay (770K). All corresponding phenotypes have been provided to the respective beef breed associations. Over 770 calves were produced with complete feed intake data representing 63 sires.

Summary

Results from this project illustrate that by using either the 50K or 770K SNP assay, the genomic heritability estimates of traits related to feed efficiency are in general agreement with heritability estimates from the scientific literature using phenotypes and pedigree information. The fact that these traits are moderately heritable and that the SNP assays can explain large proportions of the phenotypic variation suggest that genetic progress in these traits can be made by using genomic selection. However, this study further illustrates the breed specific nature of genomic predictors and thus caution should be used if attempting to use a genomic predictor in a population that is distantly related to the training population (e.g., across breeds). The continued collection of feed intake phenotypes will be required to refine and retrain genomic predictions overtime. To this end, strategic phenotyping and the use of multiple-trait GWAS models are needed to ensure that genotyped populations represent the larger target population and that information can be borrowed from more densely recorded traits such as the plethora of weight phenotypes (e.g. post weaning gain) currently available.

In terms of delivering tools and information to the beef industry for use in National Cattle Evaluation, this project has provided both phenotypes and genotypes to beef breed associations, initial predication equations to three beef breed associations, and online resources for the calculation of an economic-based efficiency index. For those breeds that relatively recently began including feed intake into current indices, many of the phenotypes were provided by this project. Next steps will need to include expanding the number of breeds for which prediction equations are developed, and exploring the utility of a newly developed assay with putative functional content (GGPF250).

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