Using Genomics to Affect Cow Herd Reproduction

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Introduction
It should be common knowledge that fertility is the most economically relevant suite of traits in beef cattle production, followed in order by growth and carcass merit. The relative importance of fertility compared to other traits is roughly double for non-integrated firms, which the overwhelming majority of commercial cow-calf producers would be classified as.

To further illustrate the importance of fertility, a pragmatic view of efficiency in beef cattle as proposed by Dickerson (1970) is detailed below.

[Dam Weight*Lean Value of Dam + No. Progeny*Progeny Weight*Lean Value of Progeny]
- [Dam Feed*Value of Feed for Dam + No. Progeny*Progeny Feed*Value of Feed for Progeny].

The income component is comprised of output from harvesting the dam (or fraction of the dam accounting for death loss) and from harvesting progeny (again, accounting for death loss). The feed cost component accounts for the input of feed energy. The number of progeny per dam is in both components and, thus, increasing number of progeny will increase efficiency. *By simply increasing number of progeny per dam, through either selection, heterosis from crossing, or better management, we will increase efficiency of production* (Nielsen et al., 2013).

The challenge of improving fertility at the commercial level via genetics is two-fold:
1) How do producers select sires that will enhance their daughters' reproductive ability?
2) How do producers make educated decisions relative to the heifers that are retained as replacements?

These are the two decisions that need to be made at the commercial cow/calf level. Throughout the remainder of this paper, the current state of genomics and options and opportunities for commercial cattle producers to improve fertility through genetic tools will be detailed and discussed.

What do we know about the genetic control of female fertility?
Heritability (h^2) estimates of several reproductive traits are listed in Table 1 as reported in a review paper by Cammack et al. (2009). Many of these traits can be classified as lowly heritable. However, in some cases studies have reported much larger heritability estimates than the perceived bound of 0.10 generally associated with female fertility traits. Particularly for binary (yes/no) traits, the incidence rate (or success rate) can greatly influence the estimates of heritability. As the incidence rate approaches 50%, heritability estimates will likely become larger than cases where the incidence rate is more extreme.

Table 1. Summary of heritability estimates (h^2) for commonly used reproductive traits in beef cattle[1].

Trait	h^2	No. of references
Age at first calving	<0.10	2
	0.20-0.30	3
Age at puberty	<0.10	1
	0.10-0.20	3
	0.40-0.50	4
	>0.60	3
Calving date	<0.10	4
	0.20-0.30	3
	0.40-0.50	1
Calving rate	<0.10	1
	0.10-0.20	1
Calving success	<0.05	1
	0.05-0.10	1
Calving to first insemination	<0.10	2
Days to calving	<0.10	2
First-service conception rate	<0.10	1
	0.20-0.30	1
Heifer pregnancy	<0.20	1
	0.20-0.30	1
Number of calves	<0.10	2
	0.10-0.20	2
	0.30-0.40	1
Pregnancy rate	<0.10	4
	0.10-0.20	4
	0.20-0.30	4
Probability of pregnancy	<0.10	1
	0.10-0.20	1
	0.20-0.30	3
	0.50-0.60	1
Scrotal Circumference	0.20-0.40	3
	0.40-0.50	8
	0.50-0.80	3

[1]Adapted from Cammack et al., 2009.

Selecting sires to alter reproductive performance

For commercial herds, roughly 85% of gene flow or genetic changes made are due to the sires used over the past 4 years. Consequently, sire selection is a critical component of improving commercial level reproductive performance. Table 2 details a listing of reproductive traits that are included in beef cattle genetic evaluations in several countries.

Table 2. Example of countries with reproduction traits as part of beef genetic evaluation systems[1].

Trait	Country[2]
Scrotal circumference	AU, NZ, SA, NA, AR, UK, IR, BR, FR, US, CA, ME
Days to calving	AU, NZ, SA, NA
Heifer pregnancy	US, VE, BR
Heifer calving success	FR
Age at 1st calving	IR, UK, BR
Calving interval	IR, DE, UK
Stayability/productive life	US, CA, VE, UK, FR, BR

[1]Adapted from Johnston (2014).
[2]AU = Australia; NZ = New Zealand, BR = Brazil; VE = Venezuela; UK = United Kingdom; IR = Ireland; SA = South Africa; FR = France; US = United States; CA= Canada; DE = Denmark; AR = Argentina; NA = Nambia; ME = Mexico.

Unfortunately, most of these traits are lowly heritable, sex-limited (bulls will not have records themselves), or simply indicator traits (e.g., scrotal circumference) and thus yearling bulls will have EPD for these traits that are relatively low in accuracy. The inclusion of genomic information into EPD has aided in increasing accuracy for these traits. Since the American Angus Association's implementation of genomic-enhanced EPD in 2009, there has been considerable evolution in terms of adoption of this technology by the beef industry. In the past few years several beef breed associations have deployed this technology with several others quickly nearing this milestone.

The past seven years have illustrated the speed at which the technology, and our knowledge of it, has changed. Although perhaps "common knowledge" now, there have been considerable changes and advancements over a very short period of time that have greatly enhanced our ability to utilize this technology. We know that the inclusion of Molecular Breeding Values (MBV) into National Cattle Evaluation can add accuracy to EPD, particularly for young animals. Figure 1 illustrates this benefit when the MBV explains 40% of the genetic variation (GV; squared genetic correlation). 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.
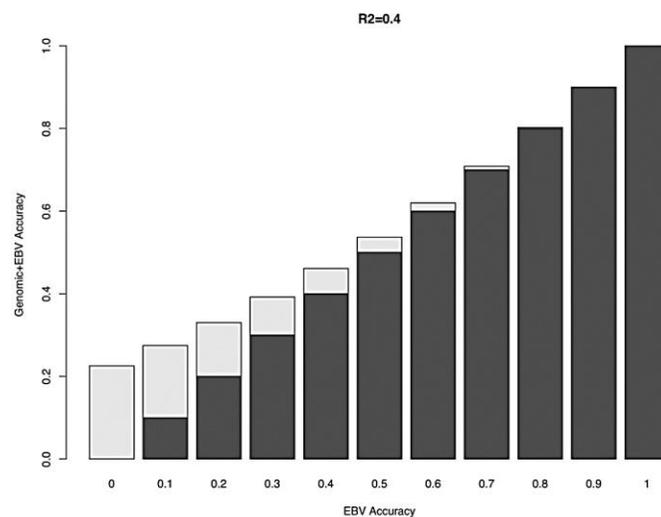

Figure 1.

Essentially this means that yearling bulls can have an accuracy associated with various EPD as if they had already sired several (10-30 depending on the trait) offspring. Buying bulls that have genomically-enhanced EPD offers a powerful tool for commercial producers to identify bulls that truly fit their breeding programs, particularly for lowly heritable traits such as fertility.

We also know the limitations of using MBV derived in one breed to predict the genetic merit of animals in a different breed, even closely related breeds (i.e. Angus trained and used in Red Angus; Kachman et al., 2013; Table 2). The fact is that the population of animals used to develop the DNA marker test must be representative of the population it will be used to predict in. As an example, a genomic test built using Angus cattle will not perform well if trying to predict the genetic merit of Hereford cattle.

Table 3. Estimated genetic correlations and standard errors for within-breed trained MBV for Angus, Hereford, and Limousin[1], evaluated in evaluation populations of each of four breeds[2]

	Weaning weight MBV		
Breed	Angus	Hereford	Limousin
Angus	**0.36±0.07**	0.14±0.08	-0.06±0.08
Red Angus	0.16±0.16	0.09±0.16	0.25±0.16
Hereford	0.04±0.21	**0.42±0.18**	0.27±0.21
Limousin	0.02±0.09	0.23±0.09	**0.40±0.08**

[1]Animals in the pedigree of the field data evaluation population were excluded from training; [2]genetic correlations and their standard errors are in bold characters when the MBV was evaluated in the breed in which it was trained. Adapted from Kachman et al., 2013.

Genomic applications for commercial cattle producers
Listed below is a description of several tests that are being marketed for use in commercial cattle that are not directly part of a breed association genetic evaluation programs (Van Eenennaam, 2016). Unfortunately, independent, peer-reviewed papers in the scientific literature documenting the field performance of any of these tests for commercial cattle do not exist.

GeneMax
There are two products exclusively distributed by Angus Genetics Inc. (AGI) and marketed by Zoetis® and designed for animals that are at least 75% Black Angus. These include GeneMax Advantage and GeneMax Focus. The first test involves tens of thousands of markers and is marketed as a heifer selection and mating tool that ranks heifers for net return using three economic indices (Cow Advantage: Predicts differences in profitability due to heifer development, pregnancy and calving, and sale of weaned progeny; Feeder Advantage: Predicts differences in net return of feeder calf progeny due to growth, feed efficiency and CAB carcass merit; Total Advantage: Predicts differences in profitability from genetic merit across all economically-relevant traits captured in Cow and Feeder Advantage index scores). It also identifies genetic outliers for cow cost, docility, marbling and tenderness, and also includes parentage information if the sires have been tested using either the 50K or i50K offered by Zoetis®. The second test utilizes fewer genetic markers and is marketed to provide genomic predictions for feedlot gain and marbling, in addition to paternity testing. These two tests are only intended for use on unregistered, commercial Angus animals.

Igenity Breed-Specific Tests

There are also two Angus-specific heifer selection tests available from Igenity; Angus Silver which includes calving ease maternal, heifer pregnancy, docility, milk, average daily gain, and marbling and Igenity Angus Gold, which additionally includes birth weight, mature weight, residual average daily gain, weaning weight, tenderness, ribeye area, back fat thickness and carcass weight. These two tests can be directly ordered through Igenity. Additionally, there are two breed-specific heifer replacement tests for Red Angus and Gelbvieh that can be ordered through the corresponding breed association. The Red Angus Herd Navigator test provides results on all traits for which the Red Angus Association of America (RAAA) calculates EPD, the RAAA HerdBuilder and GridMaster Indices, and parent verification if the potential sires have been tested with the RA50K test. Due to the breed-specific nature of this test, the Herd Navigator should only be used on females that are at least 75 percent Red Angus. The Gelbvieh Maternal Edge Female Profile is a low-density panel to be used by producers as a sorting tool for Gelbvieh-influenced commercial females. It includes calving ease, maternal calving ease, weaning weight, yield grade, marbling, and carcass weight.

PredicGEN

PredicGEN is a test marketed by Zoetis® as "a heifer selection tool for straight-bred or crossbred British/Continental animals that are less than 75% Black Angus". The carcass traits predicted include marbling score, USDA yield grade, grid merit and tenderness. Results are reported back on a normally distributed 0 to 100 scale, with a mean of 50 based on Zoetis'® database of 20,000 genotyped animals.

Igenity Gold and Silver

The Igenity Gold and Silver tests, which include approximately 1,000 markers associated with 13 traits of interest and some randomly spaced markers, are being marketed by Neogen® as "DNA profiles for crossbred and purebred cattle." A single prediction equation is used for each trait to give the score or molecular breeding value, irrespective of the breed makeup of the animal being tested. The silver test evaluates six traits (calving ease maternal, stayability, residual feed intake, average daily gain, tenderness, marbling), and the gold test includes an additional 7 traits (birth weight, calving ease direct, heifer pregnancy, docility, milk, ribeye area and back fat thickness). According to the Neogen brochure, the development of these tests involved large populations with phenotypic data and/or expected progeny differences (EPD) comprising tens of thousands of animals that represent various biological types. The six main datasets used to form the training data set for this test were from six breed associations: Angus, Hereford, Gelbvieh, Limousin, Red Angus, and Simmental. Data is reported back on a 1 to 10 scale.

An often overlooked test (that costs less than any of the above mentioned tests) is a simple parentage (or paternity) test. Simply knowing the true sire of commercial animals is beneficial and can inform keep/cull decisions.

Practical considerations

For commercial producers wishing to increase heifer pregnancy rates, or reduce the rate of culling of older females due to reproductive failure, a genomic test to aid in heifer selection is undoubtedly appealing. However, consider the scenario below.

Assume a genomic test explains 16% of the genetic variation for heifer pregnancy (meaning the test has a correlation (r) of 0.4 with the true breeding value). This is similar to what has been estimated in purebred, seedstock data (correlations range between 0.3 and 0.5 for fertility related traits). Further assume the heritability of heifer pregnancy is 0.1 (from Table 1 above). This means the hypothetical genomic test would explain 1.6% of the phenotypic differences between animals in their ability to conceive as heifers.

Van Eenennaam and Drake (2012) modeled the breakeven cost of testing all 45 potential replacement heifers born per 100 cows (weaning rate = 90%; 50% female) per year in a commercial herd with a replacement rate of 20%. To select replacement heifers a multiple-trait maternal selection index was developed that included maternal, pre-weaning performance, post-weaning performance, and carcass traits. It was further assumed that the producer was retaining ownership through the feedlot and marketing the cattle on a value based grid.

A hypothetical DNA test with an intermediate accuracy (0.3) with regard to the selection objective was then modelled. The breakeven cost of testing replacement heifers was approximately $24 per test. As the accuracy of the test increases, the breakeven cost will decrease. Interestingly, if the producer did not retain ownership they would have captured less than $10 of the total value, with the majority of the value being realized by post-weaning genetic improvement (i.e. feedlot/carcass traits).

These hypothetical examples, using realistic estimates of the accuracy of genomic tests for commercial cattle within breed, minimally cast some doubt on the economic return of testing commercial replacement heifers. Particularly given the overall importance of sire selection to the genetic improvement of commercial herds. Moreover, it has been shown multiple times that predicting the genetic merit of crossbred animals, particularly when they may contain breeds that were not represented in the training population used to build the DNA marker panel, is problematic and results in much lower accuracies.

A Path Forward
The use of "traditional" genetic selection tools and methods in the U.S. beef cattle industry to improve reproductive success is poor, at best. The development and use of proper crossbreeding systems is far from pervasive, the use of fertility EPDs in bull selection often takes a back seat to growth and carcass merit, and the utilization of economic selection indices seems to meet with skepticism due, in part, to confusion surrounding how they are developed. Although the above statements may be controversial to some, I cannot think of three action items that would lead to more progress in reproductive performance than the three listed below:

1) The commercial cow-calf industry needs to utilize composite or F_1 females. The majority of commercial producers should breed these to an unrelated terminal sire breed. Larger commercial producers may take advantage of scale and serve as a multiplier, focusing on the production of commercial replacement females. Data has shown that heterosis has a sizable impact on cumulative weaning weight over cow's lifetime—and these estimates are nearly doubled for *indicus* F1 females.
2) Commercial bull buyers should utilize the currently available reproductive EPDs previously detailed in this paper. Buying bulls with genomically-enhanced EPD will add accuracy to bull buying decisions.
3) Commercial bull buyers should also utilize economic selection indices that correctly match their breeding objectives.

The three action points above are not "sexy", but will have far greater impact per units of investment than using DNA marker panels to select replacement females given the current limitations of related to cost and accuracy of predicting non-pedigreed crossbred animals. This is not to say that genomics will not play an important role through marker-assisted management in the future as the technology matures but the utility of genomics will be marginalized relative to fertility until the lower handing fruit detailed above is fully exploited.

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