

Uses of DNA information on Commercial Cattle Ranches

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For the past two years we have been collecting DNA, performance and carcass data from all of the calves produced by approximately 2,500 crossbred cows and 120 Angus bulls located on four large Northern California commercial cow-calf operations. This sample collection is part of a USDA-funded project entitled “**Integrating DNA information into beef cattle production systems.**” The overall objective of this project is to develop a large phenotyped and genotyped population to use as a resource to compare different approaches to predict the genetic merit of commercial beef bulls. The research objectives are to compare the current means of genetic prediction of herd sires, which include breed association-derived expected progeny differences (EPDs) with DNA-assisted genetic predictions, and “commercial ranch” genetic evaluations based on offspring performance under field conditions. Additionally, we are interested in exploring the costs and benefits associated with DNA testing in the beef cattle industry.

VALUE OF DNA TESTS FOR PARENTAGE DETERMINATION

In the commercial cow-calf sector, the principal determinants of income are the number of sale animals and the value per sale animal. Most commercial producers sell their calves at weaning or shortly thereafter. Their financial returns are therefore very closely tied to the number of calves produced. A bull has two qualities of value to producers. One is his ability to impregnate cows, and the second is having genes for superior performance to pass on to his offspring. The latter is predicted by EPDs. However, the former is hard if not impossible to predict, and if a bull sires no calves then his EPD values are irrelevant.

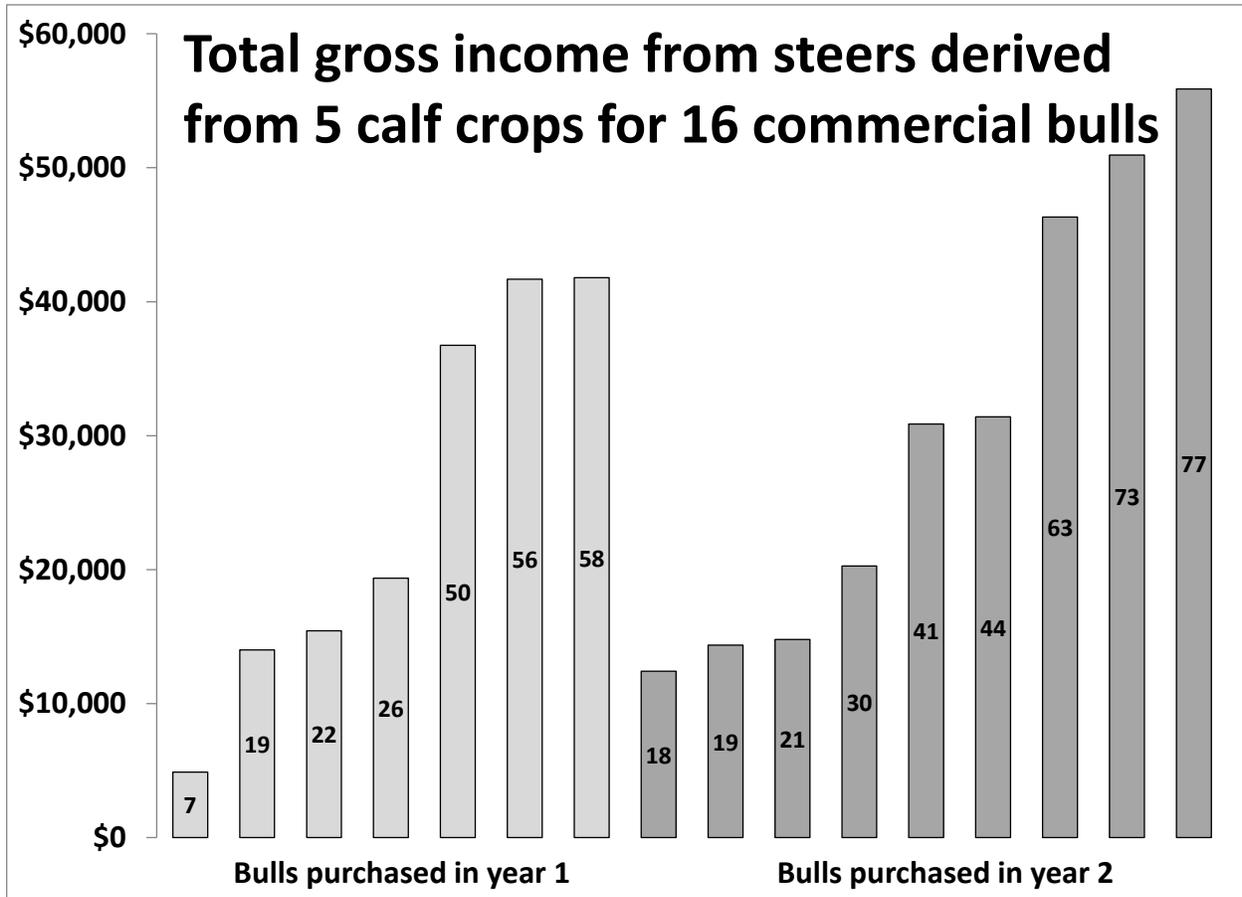
Recently we compiled data on all steer progeny derived from two cohorts of commercial bulls purchased in successive years on one of the commercial ranches in our study. Both year groups were comprised of apparently healthy bulls that had passed a breeding soundness examination. Both year groups served in multisire breeding pastures for 5 consecutive breeding seasons. Having multiple sires present with a group of cows has a number of benefits including higher fertility, precluding sire failure, and reducing the calving interval. It also minimizes the number of pastures needed, thereby facilitating better pasture management (Van Eenennaam et al., 2007).

We used a DNA parentage panel to assign the paternity of each calf to a bull. Offspring were sold at an average age of 10 months to a commercial feedlot, and although the ranch did not retain ownership, they participated in a program that required selection for specific carcass attributes and rewarded carcass quality with a premium paid back to the producer. The average gross return including the quality premium derived from the steer progeny of each sire was \$721 and did not differ greatly among the bulls, but the total gross revenue derived from all male offspring of each bull ranged from \$4,881 to \$55,889 due to differences in sire prolificacy (Figure 1). This huge discrepancy in calf numbers shows how certain bulls in a team may disproportionately influence affect profit.

VALUE OF DNA TESTS TO IMPROVE THE ACCURACY OF EPDs

Genetic improvement on commercial ranches is largely realized through the purchase of bulls from seedstock producers. There may be some value in using DNA testing to improve the accuracy of identifying above-average herd sires. However, producers would want this information at the time of purchase and so DNA testing costs have typically been paid by the seedstock producer, and recouped by an increased price at the time of bull sale. Until recently, DNA tests results (stars, scores, MVPs) have been presented in sire catalogs as a piece of information separate from EPDs. This has led to confusion especially when the two sources of information offered contradictory information regarding a bull’s genetic merit for a given trait. This has often begged the question of which to use. Sometimes it has led to the belief that one must be incorrect (Spangler and Van Eenennaam, 2010).

Figure 1. Total gross revenue (number of male calves sired shown inside the bars) derived from all of the steer progeny produced by two cohorts of yearling bulls purchased in successive years. Both groups served in multisire breeding groups for 5 breeding seasons on a US commercial ranch. Offspring were marketed at an average of 314 days of age to the feedlot, and an additional carcass-based quality premium was paid to the commercial producer.



The DNA testing industry has matured from marker tests involving a handful of markers explaining a relatively modest amount (0-10%) of the genetic variation in the target trait, to panels involving hundreds or thousands of markers. This is an exciting development because many of the production traits of interest to beef cattle producers are likely to be controlled by a large number of genes. High density panels containing more than 50,000 (50K) markers, or panels of several hundred of the best markers derived from the high density panels, are likely to be more predictive than previous commercial test offerings. It stands to reason that as the number of markers included in the test increases, so will the proportion of genetic variation explained by the test.

The proportion of genetic variation explained by a test provides producers with a way to quantitatively evaluate the merit of commercial products. Factors that affect this include the number of animals and records that were present in the “training” population used to develop the test. Larger training populations result in better DNA tests. It is also easier to develop accurate DNA tests for traits with high heritability as compared to traits with low heritability. Tests that are developed in one breed have generally not worked well in other breeds, with the exception of the test for tenderness. Because many factors can influence the accuracy of DNA tests, it is important to develop estimates of the accuracy of DNA tests currently on the market. Independent estimates are not available for many traits. Absence of this metric is a major deficiency in the information that is available to producers to evaluate the utility of including DNA tests in their selection system (Van Eenennaam, 2010).

DNA tests can be used much more effectively when they are incorporated into and presented as EPDs. Such an approach is appealing as it presents results in a format that is familiar to producers, and it eliminates the choice that is implicitly associated with the current practice of publishing traditional EPDs and marker information separately. The promise of using DNA information to improve the accuracy of EPDs on young animals is starting to be realized, at least for Angus cattle. First there was an agreement between Angus Genetics Inc. (AGI) and IGENITY to calculate genomic-enhanced expected progeny differences (GEPDs) for multiple carcass traits using American Angus Association carcass and ultrasound data. Then, in November 2010, AGI announced an agreement to similarly accept Pfizer Animal Genetics' High-Density 50K test results for incorporation into GEPDs.

Knowledge of the amount of genetic variation associated with the test is also required to incorporate DNA test information into EPDs. Ideally this value is high, such that DNA tests results can help improve the accuracy of EPDs. Some estimates are available for Angus cattle (Table 1). The Igenity estimates were developed in the US Angus population, whereas the Pfizer estimates were developed in the Australian Angus population. To incorporate Pfizer HD 50K data in the American Angus EPDs, these estimates will need to be calibrated in the US Angus population (Van Eenennaam, 2011).

Table 1. Percentage of genetic variation associated with different DNA tests for various traits. "na" means no estimate is publicly-available or published. h^2 = trait heritability.

Trait	h^2	Igenity® Angus Profile		Pfizer HD 50K for Angus		
		Included	% Genetic variation ¹	Included	% Genetic variation ²	% Genetic variation ³
Average Daily Gain	0.28	X	na	X	30	1-10
Net/residual Feed Intake	0.39	X	na	X	12	0
Dry matter intake	0.39			X	11	4-5
Tenderness	0.37	X	na	X	26	na
Calving Ease (Direct)	0.10			X	22	6
Birth weight	0.31			X	28	12-16
Weaning Weight	0.25			X	32	12-19
Yearling Weight	0.60	X	na			
Calving ease (maternal)	0.10	X	na	X	40	4
Milking Ability	0.25			X	27	10-14
Heifer Pregnancy	0.20	X	na			
Stayability	0.10	X	na			
Docility	0.37	X	na			
Yield grade	0.64	X	na			
Carcass weight	0.39	X	29	X	29	6-13
Backfat thickness	0.36	X	25	X	40	14-19
Ribeye area	0.40	X	34	X	29	10-20
Marbling score	0.37	X	42	X	34	4-11
Percent choice		X	na			

¹ MacNeil, M. D., S. L. Northcutt, R. D. Schnabel, D. J. Garrick, B.W. Woodward, and J. F. Taylor. 2010. Genetic correlations between carcass traits and molecular breeding values in Angus cattle. 9th World Cong. Genet. Appl. Livest. Prod. Leipzig, Germany. August, 2010.

<http://www.kongressband.de/wcgalp2010/assets/pdf/0482.pdf>

² Pfizer Animal Genetics. 2010. Technical Summary.

<http://www.pfizeranimalgenetics.com/sites/PAG/Documents/50K%20Tech%20Summary.pdf>

³ Animal Genetics and Breeding Unit (AGBU). 2010. Evaluation of Pfizer Animal Genetics HD 50K MVP Calibration. http://agbu.une.edu.au/pdf/Pfizer_50K_September%202010.pdf

As mentioned previously, independent estimates of the amount of genetic variation associated with DNA tests are not available for all breeds and tests on the market. Breeds other than Angus are also going to have to derive these genetic estimates for any DNA test targeted to be used in that breed. To date, data suggest that tests developed for one breed are unlikely to work very well in another. Even within Angus, tests trained in North American Angus were associated with less genetic variation when used in the Australian/New Zealand Angus population (Table 1), and required regional recalibration for that population and production system. Although there is a lot of work to be done, this move towards incorporation of DNA information into National Cattle Evaluation (NCE) aligns with the Beef Improvement Federation (BIF) guiding philosophy which reads: *“BIF believes that information from DNA tests only has value in selection when incorporated with all other available forms of performance information for economically important traits in NCE, and when communicated in the form of an EPD with a corresponding BIF accuracy. For some economically important traits, information other than DNA tests may not be available. Selection tools based on these tests should still be expressed as EPD within the normal parameters of NCE.”*

These genetic tests target a suite of traits ranging from fertility and longevity to growth and carcass merit. A question that often arises in conversations with producers is “What is the value of these tests?” The answer to that question depends on what the tests are being used for. Some breeders are just listing the results as an additional source of information in sale catalogs. If this adds value, increasing the animal’s sale price beyond the cost of the test, then this makes economic sense. Other people are using tests to make culling or selection decisions on traits that are not currently in breed EPDs (e.g. feed efficiency or tenderness). Working out whether this pays is a little more complicated.

While estimates of genetic merit for new traits may have value, the amount of emphasis to put on them is dependent on their economic value to the commercial producer. For example, should you eliminate animals from your herd based solely on a poor feed efficiency DNA test result? That depends partly on how accurate the test is at predicting superior versus inferior animals. The more accurate a test is, the more opportunity there is to accelerate genetic improvement. This decision also depends on the importance of feed efficiency versus all the other traits contributing to your overall profitability.

One way to make this decision is to develop a “selection index” that weights all traits on their relative economic importance. Indexes consider both the “input” or expense side and the “output” or income side of selection decisions and enable cattle producers to make balanced selection decisions, taking into account the economically-relevant growth, carcass and fertility attributes of each animal to identify which animals are the most profitable for their particular commercial enterprise. Melton (1995) suggested that US cow-calf producers should have a relative economic emphasis of 47% on reproduction, 24% on production, and 30% on carcass traits whereas producers in an integrated system should have a relative economic emphasis of 31% on reproduction, 29% on production and 40% on carcass traits. This relative emphasis will depend on how much the value derived from genetic gain in carcass traits is shared with the producer in the integrated system. If the value of genetic improvement for carcass traits is not paid back to the producers making the selection decisions, there is no economic value to them for continuing to emphasize carcass performance at the expense of reproduction or production.

VALUE OF DNA TESTS TO IMPROVE COMMERCIAL BULL SELECTION

The response to selection and therefore the value associated with a particular DNA test is dependent upon how much that test information improves the accuracy of genetic evaluations at the time of selection, and the value of a unit of genetic improvement. To determine that value I recently did a simulation study to determine the value of DNA tests to increase the accuracy of commercial beef bull selection (Van Eenennaam et al., 2010) I used selection indexes to estimate the value derived from using information from a hypothetical DNA test to increase the accuracy of selection. I expressed these values on a per DNA test basis.

In order to do this simulation study I had to make a number of assumptions about where and how the DNA tests were used. I modeled an example where the seedstock breeder was incurring the

costs of DNA testing to improve the accuracy of bull selection. In this example the seedstock tier consisted of a closed nucleus of 600 breeding females. It was assumed that in the absence of DNA test information, EPDs on young, untested bulls were informed by their own performance records, along with those of their sire, dam and 20 paternal-half sibs.

Each year the top 8 bulls were selected to be stud sires, and 125 (remaining bulls from the top half of the calf crop) were made available for sale to commercial producers. Commercial sires were then used to sire four calf crops at a mating ratio of 25 females: 1 male (i.e. they were exposed to a total of 100 cows). DNA test information was combined with performance records to increase the accuracy of EPDs. This increased \$Index selection response 20-41% over that obtained with performance recording alone, depending upon the traits included in the breeding objective.

The value derived from using DNA test information to enable more accurate selection of genetically-superior commercial bulls ranged from AU\$61-135 per bull. Assuming that the entire bull calf crop (n = 267) was tested and that the top half of the bulls (n=125) were sold as commercial sires, the breakeven value of the genetic gain derived from DNA testing ranged from **\$30-67** per DNA test depending upon the market being targeted. These values assumed commercial producers were willing to pay a price premium for genetically-superior bulls, and some form of industry vertical integration or profit sharing between sectors such that the rewards for improvement in processor traits (e.g. dressing %, marbling score, etc.) were transferred along to commercial producers and breeders. The value of DNA tests to improve traits of direct value to commercial cattle enterprises (e.g. fertility) would be less than this value. For example, 69% of the returns from including DNA data in commercial sire selection for an integrated system index were derived from traits that generate a direct return to processors (e.g. marbling score).

These values were based on using a relatively powerful hypothetical DNA test panel that accurately predicted ALL of the traits in the selection index. DNA tests are most valuable for traits that are not routinely recorded before selection decisions are made. For example, a DNA test accounting for 50% of the genetic variation in a trait like feed efficiency for which EPDs do not exist is likely be more valuable than a DNA test accounting for 50% of the variation in an easily measured trait like weaning weight.

VALUE OF DNA TESTS TO IMPROVE REPLACEMENT HEIFER SELECTION

The cow-calf industry could benefit greatly from tests that accurately predict maternal performance. It has been proposed that DNA information be used to select replacement commercial females, most of which have no EPD information. The value of testing heifers will depend upon the cost of the test relative to the return on investment, the accuracy of the test, and how many heifers are being selected relative to the number available from which to select. I calculated that the breakeven cost of testing all of the potential replacement heifers in a commercial herd with a replacement rate of 20% (i.e. selecting 20 heifers) from the 45 potential replacement heifers born per 100 cows per year using a DNA test with an index accuracy (i.e. correlation between the test result and the true genetic merit) of 0.25 was less than **\$5** per test, using the assumptions outlined in the previous example and assuming that the commercial producer was not performance recording his females (i.e. had no other data upon which to base heifer replacement decisions). This low value is due in part to the fact that commercial cows do not produce very many progeny, and so the value derived from spending money on improving the genetic merit of females is spread over few offspring relative to bulls.

It should be noted that unless DNA tests have high accuracy, they should ideally be used in conjunction with available phenotypic data. And here is the quandary when developing tests for replacement female selection. Traits that are of the most economic value to cow-calf producers for replacement heifer selection are low heritability reproductive traits including age at first calving, reproductive success and replacement rate. Research suggests that very large numbers of records will be required to obtain accurate DNA tests for low heritability traits. Further such tests are the most difficult to evaluate as there are few cattle populations with sufficient phenotypic data to enable estimation of the accuracy of DNA tests for these traits. However as most commercial producers have no EPD information upon which to base their replacement heifer selection decisions, even moderately powerful tests will provide previously-absent criteria upon which to base selection decisions.

VALUE OF DNA TESTS FOR GENETIC DEFECTS

DNA information can also be used to test for simply-inherited traits including coat color, horned-status, and recessive genetic defects. There are a large number of genetic abnormalities in cattle occurring in a variety of breeds. These defects have had a significant impact on specific cattle populations. Naturally-occurring recessive genetic defects are common in all species, including humans. The average human carries approximately 2,000 deleterious recessive alleles, of which one to two are thought to be lethal. Recessive conditions only become evident when certain lines of cattle are used very heavily, such that both cows and bulls have common ancestors in their pedigree, thereby allowing a rare genetic defect to become homozygous in their offspring.

Genetic defects are often propagated as a result of specific trait selection. In dogs it has been noted that each of the top 50 breeds has one aspect of breed type that predisposes the breed to a genetic disorder. For example bull dogs are prone to airway obstruction syndrome, and King Charles spaniels are affected by a reduced-size malformation of the skull. Perhaps the most famous example of a genetic defect in 20th century beef breeding was “snorter” dwarfism which became an issue in Angus and Hereford cattle during the 1940s and 1950s. This genetic defect was uncovered as a result of strong selection pressure for animals with small stature. Ultimately the cause of this mutation was traced back to a bull named St. Louis Lad, born in 1899. A 1956 survey of Hereford breeders in the USA identified 50,000 dwarf-producing animals in 47 states.

The Angus breed has recently had to manage three recessive genetic conditions. These include two lethal conditions Arthrogyposis Multiplex (AM; “Curly Calf Syndrome”), and Neuropathic Hydrocephalus (NH). The first is caused by a chromosomal deletion that occurred in Rito 9J9 of B156 7T26 (AAA Registration No. 9682589; born 10/29/1979). The second occurred as a result of a single DNA base pair mutation in his grandson, the widely-used GAR Precision 1680 (AAA Registration No. 11520398; born 9/6/1990). The widespread use of this superior carcass trait bull spurred on by an increased selection emphasis on carcass traits increased the probability of this bull showing up on both sides of many Angus pedigrees, thereby uncovering the presence of any recessive lethal mutations. The third condition is a non-lethal autosomal genetic defect called Congenital Contractural Arachnodactyly (CA; “Fawn Calf Syndrome”) that is caused by a ~54,450 base pair deletion.

Genetic tests for AM, NH, and CA became available 1/1/2009, 6/15/2009 and 10/4/2010, respectively. The speed with which these genetic tests were developed is testament to the power of having access to the bovine genome sequence information, and is perhaps the greatest success story of genomics never told. The proactive response of the breed association in making genotypes available also helped to rapidly and transparently address the problem (Table 2).

CONCLUSION

The advent of molecular information in the form of both tests for simply inherited traits and complex traits has created both excitement and confusion. The lag between discovery and application has been decreased, allowing for technology to be rapidly delivered to industry. In some cases this has caused confusion surrounding the methods for incorporating this technology into breeding schemes. DNA marker tests results should not be used to replace traditional selection based on EPDs and economic index values, but rather should be seen as providing an additional source of information from which to predict genetic merit. When included in the estimation of genetic predictions, DNA information provides valuable information on young animals which could improve the accuracy of genetic predictions. DNA testing holds the greatest promise for economically-relevant traits which are too expensive to measure, and for which no good selection criteria exist (e.g. residual feed intake or reproduction). Commercial companies have started to offer genetic tests for such traits. Meaningful incorporation of these traits into national cattle evaluations will be required to make the best use of DNA information, and such efforts will call for further collaboration between DNA companies, producers, scientists, and breed associations.

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Table 2. Dates that Arthrogryposis Multiplex (AM; “Curly Calf Syndrome”), Neuropathic Hydrocephalus (NH), and Congenital Contractural Arachnodactyly (CA; “Fawn Calf Syndrome”) were recognized as recessive genetic defects, and subsequent availability of genetic tests and American Angus Association registration cutoff dates. Only the animals from carrier parents are required to be tested.

DATE	AM	NH	CA
Recognized as genetic defect	November 15, 2008	June 12, 2009	July 14, 2010
Commercial test becomes available	January 1, 2009	June 15, 2009	October 4, 2010
Number of carriers recorded (current as of March 2011)	34,653	32,193	5,088
HEIFERS: Must test & all can register if born before or on	December 31, 2011	June 14, 2012	October 4, 2013
HEIFERS: Only non-carriers can be registered if born on or after	January 1, 2012	June 15, 2012	October 5, 2013
BULLS: Must test & all can register if born before or on	December 31, 2009	June 14, 2010	October 4, 2011
BULLS: Only non-carriers can be registered if born on or after	January 1, 2010	June 15, 2010	October 5, 2011

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