

Application of Genomic Information: The California Commercial Ranch Project

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The overall objective of this project is to develop a genotyped, phenotyped population to enable the evaluation of different DNA-enabled approaches for predicting the genetic merit of herd sires on commercial beef ranches. The research objectives are to compare the current means of genetic prediction of herd sires, which include the breed-based expected progeny differences (EPDs), DNA-assisted genetic predictions, and "commercial ranch" genetic evaluations based on the performance of offspring under field conditions. An additional objective is to determine the costs and benefits associated with the application of DNA-based technologies on commercial beef operations.

Four commercial ranches using predominately Angus sires and running a total of ~ 2400 cows are participating in this 4 year project. Blood and hair samples have been collected on the natural service bulls (45 from Ranch 1, 16 from Ranch 2, 40 from Ranch 3, and 26 from Ranch 4) siring 2009-, 2010-, and 2011-born calves and they have all been 50K genotyped. Calves sired by these bulls in multi-sire pastures are being DNA sampled for genotyping and individually identified using RFID tags prior to being shipped from each ranch and fed in large contemporary groups, until harvest. Feedlot in weights and individual carcass data will be collected on all animals, and DNA information will be used to assign progeny groups to sires. As of June 2011, we have collected 1448 birth weight, 3362 weaning weight, 2221 feedlot in-weight, and 2294 carcass records. Data collection will proceed through 2013 with the last of the 2011-born progeny scheduled to be processed in Q1, 2013. Progeny phenotypes, along with bull pedigrees, will be used to compute "commercial ranch" genetic evaluations for performance and carcass traits. In total, we will collect three complete years of data from all herds. We plan to compare genomic predictions derived from a variety of sources (e.g. US MARC multibreed population predictions, predictions based on the Angus Bull DNA repository developed by Jerry Taylor, University of Missouri) to the "commercial ranch" genetic evaluations. We have also run a small independent assessment of commercially-available genomic prediction products (Pfizer MVPs and IGENITY MBVs) to evaluate relative to this commercial ranch data.

Preliminary Sire Prolificacy and Gross Return Data

A bull has two qualities of value to commercial producers. One is the ability to impregnate cows, and the other is the ability to pass genes for superior performance to his offspring. In the absence of the former, the importance of the latter is moot. In large commercial ranches in Northern California, we have found that sire prolificacy varies dramatically among apparently healthy bulls that have undergone a breeding soundness examination¹. Recently we compiled data on all of the steer progeny derived from two cohorts of 16 bulls purchased in successive years that all served as herd sires for 5 breeding seasons in multi-sire breeding groups on one of the commercial ranches involved in this study (Figure 1). Offspring were marketed at an average of 314 days of age to the feedlot, and although the producer did not retain ownership he 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 but the total gross revenue derived from all male offspring of each bull ranged from \$4,881 to \$55,889 (Figure 1) due mainly to differences in sire prolificacy. This huge discrepancy in calf numbers shows how certain bulls in a multi-sire team may disproportionately influence herd genetics and affect profit².

¹ Van Eenennaam AL, Weaber RL, Drake DJ, Penedo MC, Quaas RL, Garrick DJ, Pollak EJ (2007) DNA-based paternity analysis and genetic evaluation in a large, commercial cattle ranch setting. *Journal of Animal Science* **85**, 3159-3169.

² Van Eenennaam AL, Drake DJ (2011) Where in the beef cattle supply chain might DNA tests generate value? *Animal Production Science*. Submitted.

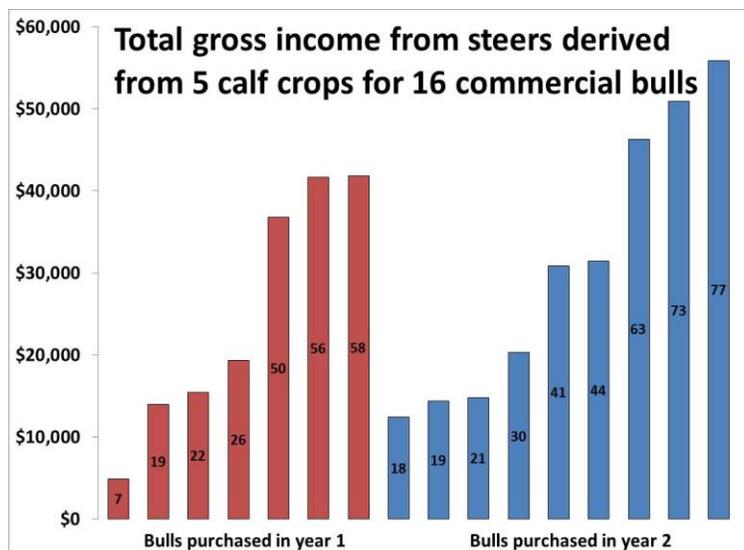


Figure 1. Total gross revenue (No. of steer progeny sired) derived from progeny produced by two cohorts of yearling bulls (■ born 2004; ■ born 2005). All bulls served as herd sires for 5 breeding seasons in multi-sire breeding groups on a commercial ranch in California. Offspring were marketed at an average of 314 days of age to the feedlot (DJ Drake, University of California, Davis, unpublished data).

Preliminary Assessment of Commercial Tests for Beef Cattle Production Traits

The objective of this study was to estimate the genetic correlation between DNA test results and target traits based on ranch genetic evaluations of herd bulls sourced from the Angus seedstock sector. Molecular

breeding values (MBV) from IGENITY (Duluth, GA) and HD 50K molecular value predictions (MVP®) from Pfizer Animal Genetics (Kalamazoo, MI) were obtained for 29 registered Angus bulls that had sired 1852 progeny with commercial cows on 3 northern California ranches. Each bull had at least 20 progeny weaning weight records or 10 progeny carcass records. Traits evaluated were weaning weight (WWT), ADG from feedlot entry to estimated feedlot final weight (derived from HCW/0.63), HCW, ribeye area (RE), and marbling score (MS). REML estimates of the genetic correlation between DNA test results and the target trait were obtained using a bivariate animal model with DNA test treated as a second trait.

Table 1. Genetic correlation (r) estimates between DNA test results and target trait being used by the American Angus Association® (AAA) to calculate genomic-enhanced EPDs, and estimates (\pm SE) derived from commercial ranch data. The percent additive genetic variance accounted for by the test is r^2 .

TRAIT	# Herd Bulls with ranch BIF accuracy > 0.05	# direct progeny in commercial ranch dataset	Pfizer HD 50K MVP		IGENITY MBV	
			American Angus Association® r estimate ³	Estimated r (\pm SE) from commercial ranch data ⁴	American Angus Association® r estimate ³	Estimated r (\pm SE) from commercial ranch data ⁴
WWT	29	1734	0.52	0.51 (0.17)	0.45	0.12 (0.22)
ADG (FEEDLOT)	28	341	n/a	0.10 (0.39)	n/a	-0.01 (0.42)
HCW	20	455	0.48	0.08 (0.28)	0.54	0.33 (0.27)
RE	23	455	0.60	0.57 (0.21)	0.58	0.35 (0.24)
MS	23	455	0.57	0.71 (0.17)	0.65	0.61 (0.19)

Genetic correlation estimates from this small preliminary dataset were generally positive and tended to be lower than the AAA values, although they were associated with large standard errors. As more records are added, these commercial ranch data will be used to assess genomic predictions from a variety of sources.



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³ Northcutt SL (2011) Genomic Choices. American Angus Association/Angus Genetics Inc. release.

<http://www.angus.org/AGI/GenomicChoiceApril2011.pdf> (Released 6 April 2011)

⁴ Weber KL, Van Eenennaam AL (2011). Independent assessment of commercial DNA tests for beef cattle production traits. 2011 American Society of Animal Science late-breaking research abstract session.