THE CALIFORNIA COMMERCIAL BEEF CATTLE RANCH PROJECT

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SUMMARY

The overall objective of this project was to develop a genotyped, phenotyped population to permit the assessment of different DNA-enabled approaches for predicting the genetic merit of Angus sires on commercial beef ranches. Approximately 5,400 progeny conceived in natural-service, multiple sire breeding pastures on 3 commercial cow-calf ranches in Northern California from 2009-2011 were assigned to a single herd bull using SNP data. The number of calves born per sire per calf drop varied greatly, ranging from 0 in ~ 7% of bull seasons to 64. The total adjusted 205d weight per bull per calf drop was almost totally explained by prolificacy (R^2=0.98), and showed little correlation (R^2=0.09) with average calf weaning weight per sire. Over 4,000 offspring were followed through the feedlot, and processing plant to obtain carcass data. Progeny data from the bulls' first calf crop were used to calculate commercial ranch genetic (rEBV) evaluations for the bulls. These rEBVs were then compared to breed association (bEBV) EBV and genomic predictions (gMBV). The rEBV was the most predictive of future progeny performance, with the bEBV and Angus-trained gMBV having similar predictive ability.

BACKGROUND

Genomic breeding values have emerged as a promising technology for providing more accurate breeding values for selection candidates in cattle populations. However, relative to successes in the dairy industry, its adoption in the commercial beef industry remains sluggish. While the value proposition associated with using this technology in the stud sector may have some merit in improving the accuracy of selection (Van Eenennaam *et al.* 2011), there are numerous practical difficulties associated with using this technology in commercial settings and the feasibility and value association with collecting DNA samples from commercial beef cattle remains uncertain.

MATERIALS AND METHODS

A project was conducted to derive a population of Angus sires with high density (50K) genotypes, purchased as yearlings and used as herd bulls in multi-sire breeding pastures with predominantly Angus commercial cows in Northern California, concomitant with phenotyped progeny from which to assess the accuracy of Angus genomic predictions for traits measured in a commercial setting. A small number of South Devon, Hereford and Red Angus bulls were also used on these ranches. The cow to bull ratio was approximately 25:1 and breeding took place in fenced pastures. Bulls underwent a breeding soundness exam prior to the breeding season and were then assigned to breeding groups. Bulls remained in the same breeding group unless they were injured or in inadequate condition based upon the judgment of experienced personnel working on the cooperating ranches. Approximately 5,400 progeny born in 2009-2011 on 3 commercial cow-calf ranches were sire-identified to herd bulls using DNA information from tail hair collected at the time of weaning weight data collection. Weaning weights were adjusted for sex, cow age and calf age according to Beef Improvement Association recommendations except that age ranges were wider than this guide due to practical constraints associated with calves going to summer pastures where they were not accessible for weighing. Carcass data and a meat sample were collected on over 4000 carcasses for DNA confirmation of the animal's identity by comparing the genotype of the meat sample to that which was obtained from hair samples

collected on all calves at weaning.

SIRE PROLIFICACY

Birthdate records were collected on 5,940 individually identified calves enrolled in the trial. DNA samples were collected on 5,382 (90.6%) calves and of these 5,272 (98%) were assigned to an individual sire. Bulls present for a full breeding season siring at least one calf (n=263) produced 19.2±13.1 progeny per calf drop, ranging from 1 to 64 (Table 1). Bulls with reduced breeding seasons due to injury or lack of condition (n=33) produced fewer calves (9.1±8.5) compared to full breeding season bulls (19.2±13.3) progeny (P<.01). Prolificacy was by far the main driver of total weight weaned per sire. The total adjusted 205d weight per bull per calf crop was related (P<.01) to the number of calves (220±1.8 kg increase for each calf) explaining 98 percent of the variation in sire weight weaned per calf crop, and showed little relation (R^2=0.09) with mean adjusted progeny weaning weight per sire.

Table 1. Average bull age at the beginning of the breeding season, and number of calves produced per bull on 3 commercial ranches in Northern California during 2009-2011[1]

Ranch	Year	Season	# Bulls/ season	Mean bull age years (± SD)	Total # calves	Per bull		
						Min # calves	Max # calves	Mean # calves (± SD)
A	2009	Spring	18	3.8 ± 1.2	353	3	47	19.6 ± 13.4
		Fall	19	4.7 ± 0.8	113	1	29	16.1 ± 10.0
	2010	Spring	22	3.6 ± 0.9	346	1	47	18.2 ± 14.2
		Fall	19	4.5 ± 1.0	328	1	48	17.3 ± 12.6
	2011	Spring	17	3.9 ± 1.1	402	4	53	23.6 ± 13.6
		Fall	19	5.4 ± 0.7	286	1	33	15.0 ± 9.2
B	2009	Spring	8	4.6 ± 3	141	1	45	17.6 ± 17.0
		Fall	10	5.1 ± 2.5	214	10	50	21.4 ± 11.4
	2010	Spring	8	3.4 ± 1.4	142	3	30	17.8 ± 8.4
		Fall	12	5.1 ± 2.7	247	4	44	20.5 ± 11.4
	2011	Spring	4	4.6 ± 1.7	110	18	42	27.5 ± 11.0
		Fall	12	5.3 ± 2.9	266	3	51	22.2 ± 15.2
C	2009	Fall	30	4.2 ± 1.1	642	2	54	21.4 ± 13.8
	2010	Fall	27	4.6 ± 1.3	567	1	52	21.0 ± 13.0
	2011	Fall	38	5.4 ± 1.8	573	1	64	15.1 ± 16.1
A	2009-11	All	114	4.0 ± .2	2150	1	53	18.8 ± 1.2
B	2009-11	All	54	4.8 ± .2	1120	1	51	20.8 ± 1.8
C	2009-11	All	95	4.8 ± .2	1782	1	64	18.7 ± 1.4
A,B,C	2009-11	All	263	4.4 ± 1.7	5052	1	64	19.2 ± 13.3

[1] Table values are for bulls present for entire breeding seasons. Thirty three additional bulls were used for only a portion of the breeding season due to injury or other issues (data not shown).

Bulls produced a similar average number of progeny across ranches (18.8±1.2, 20.7±1.8, 18.7±1.4, P=.63), years (19.6±0.4, 19.2±1.4, 17.9±1.4, P=.68), and season (20.3±1.5, 18.3±0.9, P=.27). The most calves born from any single bull in one day was 11 from exposure to these naturally-cycling, unsynchronized females. The more prolific bulls sired more early calves (day 1-21 of the calving season) than low prolificacy bulls. There were also bulls that sired no calves. For each time a bull had an opportunity to breed cows in any given season, there was a 7.3% chance that he would produce no calf. This value is similar to the 6.0% reported by Holroyd *et al.* (2002) in an Australian study looking at the prolificacy of natural service *Bos indicus* bulls.

Scrotal circumference (SC) EBVs were positively related to prolificacy (P<0.01). Repeatability of prolificacy for full season bulls with data for more than one breeding season was 0.43 ($\pm$0.08). This is similar to the repeatability values of 0.43-0.69 reported by Holroyd *et al.* (2002). There was a trend (P=.14) for older bulls to sire an increased number of progeny. Although most bulls in the study were Angus a small number of South Devon, Hereford and Red Angus bulls were also used on these ranches. The calves that were sired by South Devon (n=217) and Hereford (n=145) bulls were on average 20.4 kg and 16.4 kg heavier than Angus-sired calves at weaning presumably due in part to heterosis in these herds with high-grade Angus commercial females. Irrespective of hybrid vigor, prolificacy was the main driver of total calf weight weaned per sire.

These retrospective data do not indicate specific bull management practices to enhance prolificacy, other than perhaps attention to SC EBV in commercial bull selection. Measuring scrotal circumference has consistently been reported as a useful method for assessing reproductive function in bulls (Burns *et al.* 2011). Previous work suggested a separate multiple-sire breeding pasture for yearling bulls would be advantageous as yearling bulls in mixed-aged sire groups sired few if any progeny (Van Eenennaam *et al.* 2007).

BULL SELECTION: GENOMIC (gMBV), BREED (bEBV), and RANCH (rEBV) EBV

Criteria for bulls used in this analysis (N=89) were Angus breed background, availability of a DNA sample for high density genotyping, and verified progeny phenotyped for weaning weight and carcass traits produced in the first season of data collection and at least one subsequent season. Genomic breeding values (gMBV) for weaning weight, carcass weight, ribeye area, backfat thickness and marbling were derived from single breed (Angus) and multi-breed training populations obtained from collaborators at Iowa State University/University of Missouri-Columbia (Weber *et al.* 2012b), and the US Meat Animal Research Center (Weber *et al.* 2012a), respectively. The gMBV were compared to Angus breed association breeding values (bEBV) available for bulls at the time of purchase, and single-season ranch breeding values (rEBV) derived from one season of progeny phenotypic data (n=1785). Using selection index theory, the distribution of future progeny performance was estimated for each EBV as normally distributed with a mean of one-half the bull's EBV and a variance of $(1-0.25*h^2*r^2)$ times the phenotypic variance of the trait, where h^2 is the trait heritability and r is the EBV accuracy. The likelihood of the observed adjusted progeny performance in future seasons (n=4108) was estimated for each EBV and then EBV were ranked on this likelihood estimate for each sire.

The frequency at which each EBV was found at a given rank was compared against that which would be expected given a random assortment using a chi-square test. EBVs were not ranked randomly (P<0.05); in general the rEBV was the most predictive EBV and differences between the rank of Angus-trained gMBV and bEBV were non-significant. This suggests that commercial ranch genetic evaluations based on a single season of data (i.e. progeny testing) are more predictive than either the currently available gMBV or traditional pedigree-and phenotype-based breed association bEBV. Weaber (2005) found rEBV for herd sires derived from one season of phenotypic progeny testing generated value by improving the response to selection for targeted traits. The return on investment that results from such progeny testing was found to be greatly influenced by the cost of parentage determination. If the cost of SNP genotyping continues to decrease, the use of DNA-based parentage to develop rEBV may offer commercial producers a cost-effective approach to obtain genetic evaluations on commercial and ranch-developed bulls.

HEIFER SELECTION

Commercial producers frequently have no EBV information upon which to base their replacement heifer selection decisions, and DNA testing offers an appealing approach to provide previously-absent selection criteria. Traits that are of the most economic value to self-replacing

herds are low heritability reproductive traits including age at first calving, reproductive success and replacement rate (Roughsedge *et al.* 2005). Research results suggest that large numbers of records will be required to obtain accurate DNA tests for low heritability traits (Goddard 2009). Further, such tests are the most difficult to validate as there is a paucity of cattle populations with sufficient phenotypic data to estimate the accuracy of new genetic tests for those traits. The value of using DNA information in making replacement heifer selection decisions will depend upon the information available at the time of selection, the accuracy (r) explained by the test, and the selection intensity (i.e. proportion of available heifers that are selected). The latter will be dependent upon the calving and replacement rates. In the absence of accuracy estimates it is not possible to model the value such tests might have for heifer selection. In practice, selection for replacement heifers is frequently driven by age and size as heifers that are born later in the calving season are too immature to be cycling in time for the first potential breeding season. This criterion tends to put indirect selection on fertility (i.e. selects for heifers that were conceived in the first estrus cycle). Additionally phenotypic considerations (feet, legs, udders, reproductive tract score, and pelvic area measurements) are likely to enter heifer selection decisions, further reducing selection intensity. In this study calves born during the first 21 days of the calving season were not randomly distributed among sires in multi-sire breeding pastures: highly prolific sires produced more early calves and hence their descendants were overrepresented in replacement heifers.

TECHNICAL DIFFICULTIES

During the course of this trial we encountered numerous technical difficulties of maintaining data integrity. Although in the field or at weaning we married the electronic ID and DNA barcode electronically, errors sometimes occurred emphasizing the need for a single "foolproof" DNA collection and animal identification system. Additionally in five consecutive Ranch A calf cohorts, the carcass misidentification rate in the processing plant ranged from 3.5 to 19.3%, with an average misidentification rate of 10.8% (Weber *et al.* 2012b). In this study paternity assignment of sampled calves using a 99 SNP panel was very high, but despite concerted efforts in working with the commercial producers DNA samples were not collected on 9.4% of the progeny with birth records. These considerations may influence whole herd results in commercial settings.

ACKNOWLEDGEMENTS

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