

HERITABILITIES AND GENETIC CORRELATIONS OF ULTRASOUND-MEASURED RIBEYE AREA WITH OTHER PERFORMANCE TRAITS IN BRANGUS CATTLE¹

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Summary

Heritabilities and genetic correlations for ultrasound-measured ribeye area and fat thickness, as well as growth traits and scrotal circumference, were determined using performance records of 1613 Brangus calves born from 1987 to 1990. Moderate heritabilities of .39 for weaning and .40 for yearling ultrasound-measured ribeye area indicate that selection to change these traits should be effective. The positive, and generally large, genetic correlations between ultrasound-measured ribeye areas and growth traits indicate that genetic change of these traits can be made in tandem. The low heritability (.14) of fat thickness, the small amount of fat, and the lack of variation would make it very difficult to change the genetic ability of animals to deposit fat.

(Key Words: Heritability, Genetic Correlation, Ultrasound-measured Traits, Growth, Scrotal Circumference, Brangus Cattle.)

Introduction

Ultrasound technology has been proposed as a means of evaluating ribeye area and fat thickness of young breeding stock. Determining the best age to obtain these measurements was our first step and was reported in the Cattlemen's Day Report in 1991. The second step in determining the usefulness of ultrasound measurements was to estimate the genetic parameters of these traits and their genetic relationships with other traits.

Experimental Procedures

Real-time ultrasound equipment was used to measure weaning and yearling ribeye area and yearling fat thickness from 2101 calves born at the Brinks Brangus Ranch, Eureka, KS from 1987 through 1990. Editing the data for completeness and restricting calf age to between 160 and 250 days at weaning and 320 to 410 days at yearling scan dates resulted in the number of observations shown in Table 1, which were used in these analyses. Calves were sired by 59 bulls, were out of 814 dams, and were from 121 weaning contemporary groups formed on the basis of sex, age (not more than 90 days difference in birth date), pre-weaning management (creep vs. no creep), and weaning scan date. Weaning contemporary groups were then subdivided according to post-weaning management and yearling scan date, resulting in 151 yearling contemporary groups.

Calves were born and birth weights taken in both the fall and spring of each year. Weaning data were collected at an average age of 204 days. After weaning, bulls were placed in an on-farm, 140-day performance test, whereas heifers were placed on a growing program. Yearling data were collected at an average age of 361 days.

Of the 1613 calves with weaning data, 378 were in full-sib groups (ranging from 2 to 11 per mating), largely as a result of embryo transfer (ET). All recipient cows were Brangus, and the ET calves were used in calculating the direct heritabilities and genetic

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correlations. In subsequent editing, the ET calves were deleted, thus eliminating ET recipient cows from the analysis to obtain the maternal heritabilities. A derivative-free, restricted-maximum-likelihood procedure was used with a full numerator relationship matrix in a mixed-linear-animal model. The model included contemporary group and age of dam (2, 3, 4, 5, 6-10, and > 10 yr) as fixed effects; measurement-age to regress all records to an equal age basis; and individual animal, maternal, and permanent maternal environment as random effects.

Results and Discussion

Heritabilities and genetic correlations of birth weight, weaning weight, post-weaning gain, yearling weight, frame score, and scrotal circumference (Table 2) are generally within the range of previous literature reports for within-herd analysis, except that birth weight heritability was .75, whereas other estimates average approximately .45. The heritabilities obtained for ultrasound-measured weaning and yearling ribeye areas were .39 and .40, respectively, with a genetic correlation of .66 between them. These estimates indicate a moderate amount of genetic influence on these traits and that most of the genes affecting weaning ribeye area also affect yearling ribeye area. The genetic correlations between ultrasound-measured

ribeye areas and weight-growth traits were all positive and generally moderate to high, with the exception of weaning ribeye area and post-weaning gain (.06). The genetic correlations obtained between yearling frame score and ribeye area at weaning (.18) and for yearlings (.01) were positive and very low. Similar small, positive, genetic correlations were obtained between ultrasound-measured ribeye areas and scrotal circumference. Scrotal circumference had positive genetic correlations with all measures of growth and a moderate negative (-.33) correlation with fat thickness. The heritability (.14) of ultrasound-measured yearling fat thickness was very low, and cattle averaged only .17 in. with little variation (standard deviation of .07 in.), indicating that genetic differences in ability to deposit fat were probability not expressed at this age and level of nutrition. Genetic correlations between fat thickness and weaning and yearling ribeye areas, as well as frame score, were positive but small. The maternal heritability for both ultrasound-measured ribeye areas was .01, indicating no maternal influence on these traits. The maternal heritability of fat thickness (.10) was low, although nearly equal to the direct heritability, indicating that preweaning maternal environment and an individual animal's own fattening ability have almost equal effects on yearling fat thickness.

Table 1. Number of Observations, Means and Standard Deviations of Data Analyzed for Each Trait

Trait	n	Mean	SD
Birth wt, lb	1583	85	13
Weaning wt, lb	1613	548	85
Weaning Ribeye are, in ²	1613	6.9	1.2
Yearling wt, lb	1296	904	176
Post-weaning gain, lb	1296	346	151
Yearling frame score	325	7.4	.87
Scrotal circumference, cm	373	34.3	2.7
Yearling ribeye area, in ²	1296	10.0	2.1
Yearling fat thickness, in	1111	.17	.07

Table 2. Heritabilities and Genetic Correlations^a of Traits Analyzed for Brangus Cattle

Trait ^b	BW	WW	WRE	YW	PWG	FRA	SC	YRE	FAT
BW	.75								
WW	.52	.48							
FRE	.26	.68	.39						
YW	.54	.90	.42	.44					
PWG	.38	.50	.06	.88	.31				
FRA	.46	.47	.18	.67	.71	.42			
SC	.37	.07	.04	.23	.38	.20	.48		
YRE	.17	.29	.66	.38	.43	.01	.06	.40	
FAT	.52	-.17	.19	-.53	.44	.14	-.33	.12	.14

^aHeritabilities are on the diagonal and genetic correlations are below the diagonal.

^bBW = birth weight, WW = weaning scan weight, WRE = weaning ultrasound ribeye area, YW = yearling scan weight, PWG = post-weaning gain, FRA = yearling frame score, SC = yearling scrotal circumference, YRE = yearling ultrasound ribeye area, FAT = yearling ultrasound twelfth-rib fat thickness.