ASSOCIATION BETWEEN REPRODUCTION AND PREWEANING GROWTH TRAITS AND ELISA SCORES FOR PARATUBERCULOSIS IN AN ANGUS-BRAHMAN MULTIBREED HERD OF CATTLE

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SUMMARY

Genetic evaluation for production traits assume that records come from healthy animals. Records from animals suffering from chronic diseases with long subclinical stages may be difficult to identify, thus likely to be included in genetic evaluations, and disease effects not accounted for. One such disease is paratuberculosis. A common diagnostic test for paratuberculosis is ELISA. Regression estimates of four cow and two calf traits on ELISA scores (0 = negative to 3 = positive) were obtained. Regressions indicated that cows with greater ELISA scores tended to stay open longer, to have larger weight losses from December (pre-calving) to September (weaning), and to have calves with lower birth and weaning weights than cows with lesser ELISA scores.

INTRODUCTION

Genetic evaluation of animals for reproduction and production traits in beef cattle assumes that records come from healthy animals. This assumption is likely to be appropriate for acute infectious diseases with short subclinical stages, where records from sick animals can be easily identified and excluded from genetic evaluations. However, for chronic infectious diseases with long subclinical stages, it may be difficult to accurately identify sick animals. Their records are likely to be included in genetic evaluations, and losses in performance due to subclinical disease effects will not be accounted for.

A chronic incurable disease of cattle and other ruminants with subclinical stages that may last for years is paratuberculosis. Paratuberculosis is caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP). A commonly used serological test to detect subclinical paratuberculosis is ELISA. The purpose of ELISA is to detect antibodies against MAP in the serum of infected animals. This test is primarily a herd-screening tool, and it can detect approximately 50% of infected animals. In spite of its low sensitivity, Elzo *et al.* (2006) found significant associations between ELISA scores for paratuberculosis and several cow and calf traits in a multibreed herd of beef cattle. The next step was to evaluate these associations from a genetic evaluation perspective, i.e., to quantify the association between individual traits of interest and ELISA scores.

The objective was to obtain regression estimates of gestation length (GL), calving interval (CI), time open (TO), weight change of cow (WC) from late November (pre-calving) to September (weaning), birth weight of calf (BW), and weaning weight of calf (WW) on ELISA scores for paratuberculosis in an Angus-Brahman multibreed herd of beef cattle.

MATERIAL AND METHODS

Detection of paratuberculosis. Blood was sampled from the coccygeal vein of cows in late May every year using a collection tube with a 3.8 cm, 18 gauge needle. Serum was separated, stored at -6.7 ºC, and later evaluated by ELISA using a *Mycobacterium paratuberculosis* Antibody Test Kit from IDEXX Laboratories, Westbrook, Maine. This kit had 50% sensitivity (detection of infected animals) and a 99% specificity (detection of non-infected animals).

The ELISA sample to positive (s/p) ratios were transformed into four scores using the S/P categorization of Collins (2002):
a) 0 = negative, for s/p ratios from zero to 0.09: antibodies to MAP were not detected; b) 1 = suspect, for s/p ratios from 0.10 to 0.24: low level of serum antibodies but above normal background levels;
c) 2 = weak positive, for s/p ratios from 0.25 to 0.39: low level of serum antibodies to MAP, but above the standard cutoff for a positive test;
d) 3 = positive, for s/p ratios from 0.40 to 10.00: moderate to high level of serum antibodies to MAP.

Animals, feeding, and management. Animals belonged to the Angus-Brahman multibreed herd of the University of Florida, USA. The herd used a diallel mating strategy. Reproduction, weight, and ELISA score data were collected from 430 purebred and crossbred cows (79 Angus, 79 ¾ A ¼ B, 47 Brangus (5/8 A 3/8 B), 105 ½A ½B, 57 ¼A ¾B, and 63 Brahman) produced by the mating of 97 maternal grandsires and 287 maternal granddams. Growth data were collected from 733 purebred and crossbred calves (133 A, 155 ¾ A ¼ B, 75 Brangus, 195 ½A ½B, 95 ¼A ¾B, 110 B) produced by mating 70 sires to 430 cows.

Cows were synchronized in March, artificially inseminated twice, and then exposed to a natural service bull for 60 days. Calves were born from mid December to mid March, and weaned in September. Cows and calves were kept on bahiagrass pastures, supplemented in Winter (bermudagrass hay, cottonseed meal, and molasses), and free access to minerals. During calving cows were separated into two groups by their ELISA scores: low-risk (0 1) and high-risk (2, 3).

Statistical analysis. Cow (GL, CI, TO, and WC) and calf (BW and WW) traits were analyzed using single-trait multibreed models with homogeneous variance-covariance structure (Koonawootrittriron et al., 2004). Models varied by trait. Common fixed effects to all traits were: year (Y), age of dam (A), sex of calf (S), Brahman fraction of sire and dam, and heterosis of dam and calf. Additional fixed effects fitted per trait were: a) Y*A, pre-calving weight of cow, BW, and current year ELISA score (CYES) for GL; b) BW and previous year ELISA score (PYES) for CI and TO; c) GL, BW, WW, PYES, and CYES for WC; d) GL, GL*S, and CYES for BW; and e) Y*A, Y*S, age at weaning, and CYES for WW. Random effects were: a) sire and dam for GL, BW, and WW; and b) residual for all traits. Random effects were assumed to have zero mean, common variance, and be uncorrelated. Computations were carried out with procedure MIXED of SAS. Means of predicted trait values (OUTPRED) were plotted against breed group of cow by ELISA score using GPLOT.

RESULTS AND DISCUSSION

Table 1 contains regression estimates of cow and calf traits on ELISA scores. These regression estimates indicate that cows with greater ELISA scores tended to have: a) longer times open, suggesting that these cows had diminished fertility; b) larger weight losses from December (pre-calving) to September (weaning), suggesting poorer weight maintenance ability; and c) calves with smaller birth and weaning weights, suggesting that they provided a lower level of nutrition to their calves than cows with lower levels of antibodies. Regression estimates for gestation length and calving interval on ELISA scores were non-significant, but in the expected direction.

Figures show mean predicted values for cow and calf traits plotted against breed group of dam for each ELISA score. Despite the small dataset available, predicted breed group means were generally as expected given the overall regression estimates, i.e., predicted breed group means for cows with greater ELISA scores tended to be larger for positive regressions, and smaller for negative regressions than cows with lesser ELISA scores.

Table 1. Regression estimates of cow and calf traits on ELISA score for paratuberculosis from linear model analyses for individual traits in an Angus-Brahman multibreed herd

	Cow traits				Calf traits	
	Gestation length	Calving interval	Time open	Weight change	Birth weight	Weaning weight
ELISA score	-0.3292	1.7988	4.3137	-2.6433	-0.5659	-2.3381
SE	0.4042	1.5792	1.5671	1.3716	0.2577	1.0747
P > |t|	0.4165	.2553	.00063	0.0548	0.0294	0.0303
No. records	484	448	268	637	485	709
No. sires	52	60	42	60	52	70
No. cows	246	211	153	290	246	292

Gestation Length

Calving Interval

Time Open

Weight Change

Birth Weight

Weaning Weight
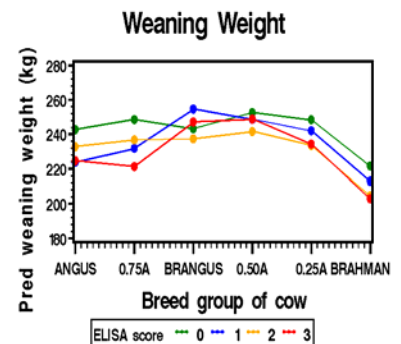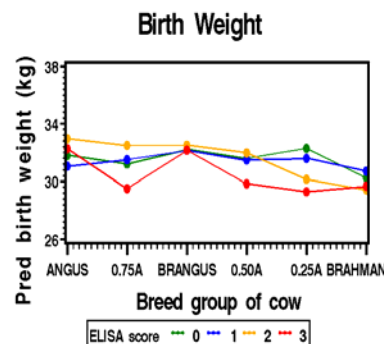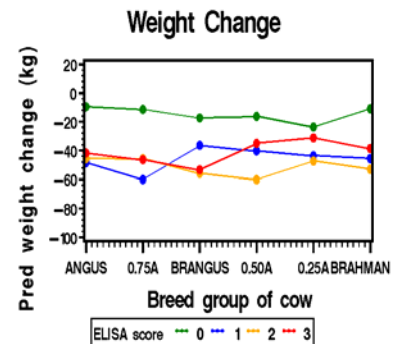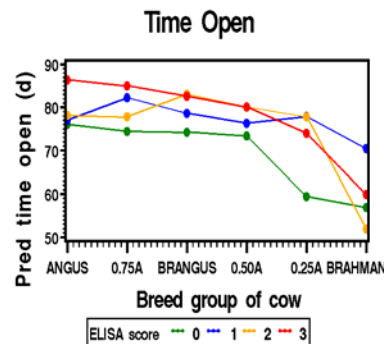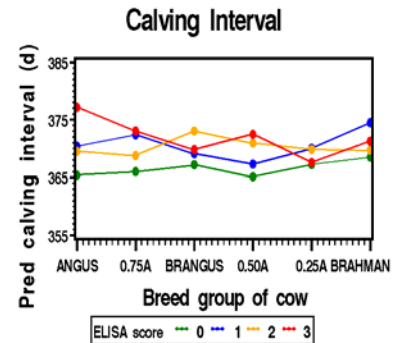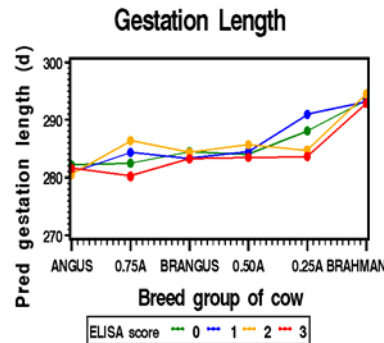
CONCLUSIONS

Insofar as ELISA scores are an indicator of subclinical paratuberculosis, results here suggest that ELISA scores could be used to account for effects of this disease on cow and calf traits. Inclusion of ELISA scores in genetic evaluation models would help eliminate biases due to subclinical paratuberculosis on cow and calf traits. In areas where paratuberculosis is endemic, tests for paratuberculosis, such as ELISA, should be routinely applied and become integral components of the record of an animal. This would permit their values to be included in genetic evaluation models.

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