Association Between Reproduction and Preweaning Growth Traits and ELISA Scores for Paratuberculosis in an Angus-Brahman Multibreed Herd of Cattle

M.A. Elzo, *PhD*[1], **D.O. Rae,** *DVM, MPVM*[2], **S.E. Lanhart,** *BS*[2], **J.G. Wasdin,** *BS*[1], **W.P. Dixon,** *BS*[1], **J.L. Jones**[1]
[1]*Department of Animal Sciences, University of Florida, Gainesville, FL 32611-0910*
[2]*Department of Large Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville, FL 32610-0136*

Introduction

Genetic evaluation of animals for reproduction and production traits in beef cattle relies on models that account for environmental and genetic effects in the records used to perform computations. Records are assumed to come from healthy animals. This assumption is likely to be appropriate for acute or subacute infectious diseases that have short subclinical stages, where sick animals can be easily identified, and their records 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.

One chronic incurable disease of cattle and other ruminants with subclinical stages that 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 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 of this research 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.

Materials and Methods

Animals belonged to the Angus-Brahman multibreed herd of the University of Florida. The herd used a diallel mating strategy. Reproduction, weight and ELISA score data were collected from 430 purebred and crossbred cows (79 Angus, 79 3/4 A 1/4 B, 47 Brangus (5/8 A 3/8 B), 105 1/2A 1/2B, 57 1/4A 3/4B 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 3/4 A 1/4 B, 75 Brangus, 195 1/2A 1/2B, 95 1/4A 3/4B, 110 B) produced by mating 70 sires to the 430 cows indicated above. 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.

Detection of paratuberculosis.

Blood was sampled from the coccygeal vein of cows in late May each year. Serum was separated, stored and later evaluated by ELISA using a *Mycobacterium paratuberculosis* Antibody Test Kit. The assay was performed according to the manufacturer specifications. The ELISA sample to positive (S/P) ratios were transformed into four scores using the S/P categorization of Collins (2002): 0 = negative, 1 = suspect, 2 = weak positive and 3 = positive for serum antibodies to MAP.

Statistical analysis.

Cow (GL, CI, TO and WC) and calf (BW and WW) traits were analyzed with single-trait linear model methodology using multibreed models with a homogeneous variance-covariance structure that accounted for environmental, additive genetic and non-additive genetic effects. Models differed 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 be uncorrelated, with mean zero and a common variance. Computations were carried out with procedure MIXED of SAS. Means of predicted trait val-

ues (option OUTPRED) were plotted against breed group of cow by ELISA score using procedure GPLOT.

Results

Regression estimates of cow and calf traits on ELISA scores 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.

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.

Significance

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 effects 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 as indicators in populational genetic evaluation models.

Environmental Sampling for the Detection of *Mycobacterium Avium* subspecies *Paratuberculosis* in Dairies in Texas

Mario A. Villarino, *DVM, PhD*[1] , **G. Thomas**[2] and **E.R. Jordan,** *PhD*[1]
[1]*Texas Cooperative Extension, The Texas A&M University System, Dallas, TX*
[2]*Johne's Testing Center, University of Wisconsin, Madison, WI*

Introduction

Johne's disease (JD) is a chronic debilitating intestinal disease of ruminants, caused by the infectious agent *Mycobacterium avium* subspecies *paratuberculosis* (MAP). JD is widely disseminated in dairy farms and known to cause considerable economic loss. Recently, interest in the detection of clinical and subclinical manifestations of the disease and MAP has created interest in developing cost efficient methods for its detection. The culture of soil samples contaminated with MAP (called environmental samples) offers an economic, easily performed, detection technique on dairy farms. The objective of this investigation was to conduct environmental testing on two dairies (E and W; n=>2500) in Texas known to have clinical cases of JD and previous isolations of MAP from fecal cultures.

Materials and Methods

We collected a series of environmental samples during 2004-2005 (summer and winter) from holding pens, alleyways, sedimentation ponds and water from washing the milking parlor. To evaluate the repeatability of our findings, we conducted serial sampling of water from washing the milking parlor (slurry) from five different pens (A, B, C, D and E) after milking (Dairy E)

Results

The cultures of soil samples (40) were detected positive in only one case (Dairy E). Contrary, samples collected from water from washing the milking parlor were detected positive to MAP 80% of the time (n=20; both dairies). Samples from only two different pens (C and D) were detected positive.

Significance

Our results indicate variation in MAP dissemination in wash water, independent of age, lactation, milk production and seroprevalence of the cattle sampled.