Genetic Analysis of Receiving Weight, Ultrasound Back Fat, Ultrasound Rib Eye Area, Ultrasound Percent Intramuscular Fat and Bovine Respiratory Disease in Feedlot Cattle

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ABSTRACT: Crossbred steer calves (n = 2,870) were received at a commercial feedlot in Southeastern Colorado. Upon arrival, weight (REC), ultrasound back fat (UBF), rib eye area (UREA) and intramuscular fat (UIMF) measures were collected. Animals treated for BRD received a treatment code (TRT) of 1 while animals not treated received a 0. Univariate sire model heritability estimates were calculated for TRT, REC, UBF, UREA and UIMF. Genetic correlations were calculated using bivariate sire models. Heritability estimates for TRT were (0.17 ± 0.08), REC (0.48 ± 0.08), UREA (0.49 ± 0.08), UBF (0.15 ± 0.05) and UIMF (0.33 ± 0.07). Genetic correlations varied between TRT and REC (0.62 ± 0.20), UREA (0.11 ± 0.22), UBF (-0.31 ± 0.31) and UIMF (0.06 ± 0.24). Results suggest that BRD resistance is heritable and related to initial feedlot body weight and back fat thickness.
Keywords: beef cattle; bovine respiratory disease; immunity

Introduction

Bovine respiratory disease (BRD) is perhaps the single most costly disease facing the beef industry. Costs associated with this disease have been shown to be upwards of $700 million each year and the disease has been shown to contribute to 28% of feedlot deaths (NASS (2011)). The nature of BRD is multifaceted caused by a variety of bacterial/viral infections that are aggravated by environmental conditions. Microscopic organisms such as Infectious Bovine Rhinotracheitis, Bovine Viral Diarrhea, Bovine Respiratory Syncytial Virus and Parainfluenza-3 have been shown to be the causative organisms of BRD (Urban-Chmiel et al. (2012)). Given the complexity of this disease, stemming the incidence of BRD has been largely unsuccessful. Although current figures show more than 95% of feedlots vaccinate their cattle against the BRD complex, prevalence has remained unchanged in the past 30 years (Gifford et al. (2012); APHIS, (2013)).

Selection for disease resistance is an alternative method to reduce economic losses. Before selection schemes can be implemented, the genetic variation within populations and any potential genetic antagonisms with other traits (Golden et al. (2000)) must be understood. Information such as weight and ultrasound measurements as well as immunological parameters collected upon arrival in the feedlot have been shown to possess phenotypic relationships with BRD susceptibility later in the feeding period (Montgomery et al. (2009); Holland et al. (2010); Speidel et al. (2013)). These studies have indicated that phenotypic relationships exist between BRD treatment and weight, ultrasound back fat, ultrasound rib eye area and ultrasound percent intramuscular fat. Understanding the genetic relationships between these traits would allow producers to either select for BRD resistance or more appropriately manage their cattle prior to the feeding period to help minimize BRD incidence. Therefore, in an effort to characterize the genetic relationships between BRD and receiving weight and ultrasound observations, the objective of this study was to estimate genetic parameters, specifically heritability and genetic correlations, between each of these five receiving traits.

Materials and Methods

Animal Procedures. All animal procedures were approved by Colorado State University's Animal care and use committee. Crossbred steer calves (n = 2,870) were received at a Southeastern Colorado commercial feedlot from a single source ranch over a sequential two-year period. Year one consisted of 1,551 calves at an estimated 204 d of age (70 d post-weaning). Year two consisted of 1,318 calves at an average 233 d of age (96 d post-weaning). Each year, cattle were received over a three-day period, and to minimize stress were housed overnight in feedlot receiving pens with hay and water until processed the next day. Processing in both years consisted of tagging calves with a radio frequency identification tag, visual identification tag and lot tag. Measures were collected on all receiving traits, including calf weights and ultrasound measurements consisting of loin eye area, backfat and percent intramuscular fat.

Health Management. Steer health was monitored daily by feedlot personnel. Animals identified as sick or lame were relocated to sick pens located at Colorado State University's South Eastern Colorado Research Center immediately adjacent to the commercial feed yard for additional symptom evaluation. Animals that presented multiple clinical signs consisting of lethargy, depression, nasal and optical discharge, cough and/or a rectal temperature greater than 39.7° C were assumed to be affected by BRD. Treatment for BRD was administered according to the commercial feedlot guidelines. Steers exhibiting a rectal temperature below 39.7° C between d 5 and d 7 were returned to their respective pens; steers with temperatures above 39.7° C on d 7 received an additional BRD treatment

and were monitored at 5 d increments. Steers in the study that were treated for BRD received a score of 1 while those not treated received a score of 0

Pedigree. Calves in the study were the result of multiple sire breeding pastures. Sire identification was performed via DNA sampling of both sire and progeny using a commercial DNA lab. A sparse historical pedigree was obtained from the ranch of origin and used to construct a 5-generation pedigree starting with the sires of animals in the study. In this 5-generation pedigree, dam information was extremely scarce. Therefore, for the purpose of estimating heritability and genetic correlation a sire model was used to best describe the flow of genetic material from one generation to next.

Statistical analyses. Two analyses were performed. First single trait heritability estimates were calculated for BRD treatment (TRT), receiving weight (REC), ultrasound back fat (UBF), ultrasound rib eye area (UREA) and ultrasound percent IMF (UIMF) using a univariate sire model. Second, genetic correlations were calculated between TRT and each of the ultrasound indicators using three separate bivariate sire models. Given the binary nature of TRT, a probit threshold link function was used to convert the observations to the continuous underlying scale (Gianola and Foulley (1983)). Contemporary group consisting of ranch unit of origin, commercial feedlot pen and year was included as the sole fixed effect for each trait. The random effect of sire was included in each model to estimate direct additive genetic effects and was assumed to be continuous. Both univariate and bivariate models were implemented using the statistical software package ASREML (Gilmour et al. (2009)).

Results and Discussion

Summary statistics for TRT, REC, UBF, UREA and UIMF are shown below in table 1. A treatment score was assigned to all animals in the population. If an animal was treated for BRD they received a score of 1 otherwise they received a score of 0. Across the both years, 792 animals received treatment for BRD leaving 2078 having received no treatment. A wide range of weight and ultrasound observations existed in the data set. This may be due to a range in animal age, however with no birth dates available, except on a small subsample, it was not possible to determine the age of individual animals. However, calves from years one and two were assumed to be approximately 70 and 96 days post-weaning, respectively.

Contemporary group definitions were formed on the basis of commercial feedlot pen, ranch unit of origin and year. Formation of contemporary groups in this manner resulted 12 unique group definitions. There were an average of 239 animals per group with minimum and maximum numbers of 90 and 310, respectively.

Table 1. Summary statistics for bovine respiratory disease treatment (TRT), receiving weight (REC), ultrasound rib eye area (UREA), ultrasound back fat (UBF) and ultrasound percent intramuscular fat (UIMF).

Item	N	Mean	SD	Min	Max
TRT	2,870	0.28	0.45	0	1
REC[1]	2,864	221.74	24.34	151	336
UREA[1]	2,854	40.13	5.42	21.48	63.81
UBF[1]	2,845	2.79	0.76	0.25	12.19
UIMF[1]	2,859	3.32	0.64	0.87	8.79

[1]REC, kg; UREA, cm^2; UBF, mm; UIMF, percent

Table 2. Heritability and genetic correlations (± s.e.) for bovine respiratory disease treatment (TRT), receiving weight (REC), ultrasound rib eye area (UREA), ultrasound back fat (UBF) and ultrasound percent intramuscular fat (UIMF).

Item	Heritability[1]	Correlation[2]
TRT	0.17 ± 0.08	
REC	0.48 ± 0.08	0.62 ± 0.20
UREA	0.49 ± 0.08	0.11 ± 0.22
UBF	0.15 ± 0.05	-0.31 ± 0.31
UIMF	0.33 ± 0.07	0.06 ± 0.24

[1]Heritability estimates reported for each of the traits were obtained from single trait sire models.
[2]Genetic correlations reported were from bivariate sire models with TRT and REC, UREA, UBF and UIMF.

The final pedigree used in the evaluation consisted of 548 sires, of which 309 had progeny with data. Of the sires with progeny with data, 237 (77%) had more than two progeny. The average number of progeny per sire was 7.57 (SD = 6.9) with a minimum of one and a maximum of 60.

Estimates of heritability reported in Table 2 were calculated for TRT, REC, UBF, UREA and UIMF using univariate sire models. Heritability for TRT was found to be 0.17 ± 0.08. Previous literature estimates have shown heritability for BRD treatment to range from 0.06 to 0.25 (Muggli-Cockett et al. (1992); Snowder et al. (2005); Snowder et al. (2007)). The heritability calculated in this study was in the upper end of this range. Estimates for REC, UBF, UREA and UIMF were moderate ranging from 0.15 ± 0.05 for UBF to 0.49 ± 0.08 for UREA. Ultrasound back fat heritability was low when compared to yearling ultrasound back fat heritability estimates. This may be a function of the low variability observed in UBF observations (Table 1).

Genetic correlations between TRT and REC, UBF, UREA and UIMF are also reported in Table 2. Virtually no genetic relationship was found between TRT and UIMF, (r_g = 0.06 ± 0.24). Similarly, Snowder et al. (2007) reported genetic correlations of similar magnitude when looking at the relationship between TRT and marbling score. Holland

et al. (2010) also had similar findings when looking at the phenotypic relationship between IMF and TRT in feedlot heifers.

The correlation between TRT and UREA (0.11 ± 0.22) in this population was low and not different from zero when standard errors were considered. Snowder et al. (2007) found correlations between TRT and carcass rib eye area of similar magnitude. Contrary to the findings presented here, they found a negative relationship between TRT and rib eye area, however considering the standard errors of the estimates both were no different than zero.

The genetic correlation between TRT and UBF was found to be -0.31 ± 0.31. This suggests that as 12th rib fat depth at receiving increases, animals are less likely to be treated for BRD. This estimate is much larger than the estimate reported by Snowder et al. (2007) between TRT and adjusted carcass fat of -0.08. Comparable results have been reported on a phenotypic level between UBF and BRD incidence (Holland et al., 2010).

Perhaps the most interesting genetic relationship is between TRT and REC. A genetic correlation of 0.62 ± 0.20 was found between the two traits suggesting that cattle with heavier initial body weights were more likely to be treated for BRD. Snowder et al. (2007) found no relationship between TRT and hot carcass weight while Montgomery et al. (2009) found animals with decreased body weights to be more likely to be treated for BRD on a phenotypic level.

It was expected that this relationship between TRT and REC would be similar to that reported by Montgomery et al. (2009) where larger animals would be less susceptible to BRD. The value found in this study contradicted our preconceived notions. Our findings may be explained by the fact that in this data set birth dates of the animals were not available from the originating ranches and as such we could not calculate age of the animal at receiving. Perhaps if we were able to adjust weight for age of the animal, this relationship would have been different.

The relationship between UBF and TRT is also puzzling. Our results suggest that as animals had greater fat thickness at receiving, they were less likely to be treated for BRD. Fat deposition occurs last in the relative order of tissue growth (Berg and Butterfield, 1976). As these animals are early in their growth phase, averaging 83 d post weaning, it would not be expected for them to be depositing back fat especially prior to the feeding period. Perhaps animals with greater fat thickness at receiving have extra energy reserves for immune response and stress management (C. C. L. Chase, South Dakota State University, Brookings, SD, personal communication).

Conclusion

Results from this study show that genetic variability exists with respect to treatment for BRD in this population of cattle suggesting that resistance to BRD can be selected. The results also indicate genetic relationships exist between treatment for BRD and initial receiving weight and initial backfat thickness. The genetic correlation between TRT and REC was moderately high and positive, suggesting that higher initial body weights are indicative of BRD treatment. This relationship needs to be further studied to determine if age of the animal has an effect on this relationship. The genetic correlation between TRT and UBF was moderate and negative indicating that animals with surplus energy stores were more resistant to BRD. Additional work needs to be completed to further evaluate the relationship between these traits, and additional immune response values to outline the genetic variability associated with BRD resistance.

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