Evaluation of fixed sources of variation and estimation of genetic parameters for incidence of bovine respiratory disease in preweaned calves and feedlot cattle[1,2]

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ABSTRACT: The primary objective of this study was to estimate variance components and heritability of bovine respiratory disease (BRD) incidence in beef calves before weaning and during the finishing phase. The second objective was to investigate the impact of BRD incidence and treatment frequency on performance and carcass traits. Bovine respiratory disease is the biggest and most costly health challenge facing the cattle industry. The 2 populations used consisted of 1,519 preweaned calves and 3,277 head of feedlot cattle. The incidence rate of BRD in preweaned calves was 11.39%, and among treated cattle, 82.1% were treated once, 13.9% were treated twice, and 4.0% were treated 3 times or more. The incidence of BRD ($P = 0.35$) and the number of treatments ($P = 0.77$) had no significant effect on weaning BW. Heritability estimates of the entire preweaned population for BRD resistance and number of treatments were 0.11 ± 0.06 and 0.08 ± 0.05, respectively. The genetic correlation estimates for BRD incidence with weaning BW and birth BW were low (-0.02 ± 0.32 and 0.07 ± 0.27, respectively). The same estimate for the number of BRD treatments with weaning BW and birth BW was 0.25 ± 0.35 and 0.30 ± 0.27, respectively. The observed BRD incidence rate for feedlot cattle was observed at 9.43%. Incidence of BRD significantly ($P < 0.01$) decreased overall and acclimation ADG by 0.06 ± 0.01 kg/d and 0.28 ± 0.03 kg/d, respectively. Carcass traits were also significantly ($P < 0.05$) affected by BRD incidence; untreated cattle had a 9.1 ± 1.7-kg heavier HCW. Results were similar in the analysis of treatment frequency. The heritability estimate of BRD incidence and the number of treatments were 0.07 ± 0.04 and 0.02 ± 0.03, respectively. Estimates of genetic correlations of BRD incidence with production traits were -0.63 ± 0.22 for acclimation ADG, -0.04 ± 0.23 for on-test ADG, -0.31 ± 0.21 for overall ADG, -0.39 ± 0.21 for final BW, -0.22 ± 0.22 for HCW, -0.03 ± 0.22 for LM area, 0.24 ± 0.25 for fat, and -0.43 ± 0.20 for marbling score. Similar results for the number of treatments and production traits were -1.00 ± 0.68 for acclimation ADG, -0.04 ± 0.39 for on-test ADG, -0.47 ± 0.41 for overall ADG, -0.66 ± 0.40 for final BW, -0.58 ± 0.45 for HCW, -0.12 ± 0.38 for LM area, 0.42 ± 0.50 for fat, and -0.32 ± 0.37 for marbling score. Because of the high economic cost associated with BRD incidence, even these modest estimates for heritability of BRD resistance should be considered for incorporation into beef cattle breeding programs.

Key words: bovine respiratory disease, cattle, disease

INTRODUCTION

Bovine respiratory disease (**BRD**) is the most prevalent and economically devastating health concern of the cattle industry (USDA NAHMS, 2000). The overall cost to the industry has been estimated as \$750 million per year (Griffin, 1997). A single treatment for BRD has been estimated to cost \$15.57 (Faber et al., 1999) due to expenses related to pharmaceutical products and supplies, whereas total associated costs of BRD treatment as it relates to loss of production and decreased carcass value have been reported at \$92.26 (McNeill et al., 1996). Taking steps to ensure preven-

tion is extremely important because of the possibility of an epidemic outbreak and compounding economic ramifications that BRD presents. Prevention of BRD is best accomplished through vaccination and management, specifically paying close attention during periods of increased stress, such as weaning and shipping.

Cattle of all ages can be affected by respiratory disease; however, they are most susceptible during the decay of passive immunity in young calves, weaning time, and entrance into the feedlot because cattle are introduced to a wide range of stress and pathogens (Muggli-Cockett et al., 1992). These 3 factors converge in the typical beef production system at nearly the same time. Common viral agents that are implicated in BRD include infectious bovine rhinotracheitis, bovine viral diarrhea virus, bovine respiratory syncytial virus, and parainfluenza type 3. In addition, bacterial strains associated with BRD include *Mannheimia hemolytica, Pasteurella multocida, Hemophilus somnus*, and mycoplasma (Ellis et al., 2001; Plummer et al., 2004).

Heritability estimates for resistance to BRD have previously been reported in preweaned calves by Muggli-Cockett et al. (1992; $h^2 = 0.10$) and Snowder et al. (2005; $h^2 = 0.00$ to 0.26). In feedlot cattle, Snowder et al. (2006) estimated heritability of BRD resistance between 0.04 and 0.08, with an estimate of 0.18 when the heritability was calculated on the continuous scale underlying the binomial distribution. In addition, the incidence rate of BRD has been reported at 14.4% (USDA NAHMS, 2000), and lung lesions prevalent at slaughter have been observed between 29.7 and 77% (Wittum et al., 1996; Bryant et al., 1999; Thompson et al., 2006). Bovine respiratory disease is a growing concern because disease incidence has been increasing (Babcock et al., 2006), and corresponding deaths of infected cattle have increased from 52.1% in 1994 to 61.5% in 1999 (USDA NAHMS, 2000).

The primary objective of this study was to estimate variance components and the associated heritability of BRD resistance in young beef calves before weaning and during the finishing phase, using health records of cattle fed in a typical feedlot environment. The second objective was to investigate the impact of BRD incidence and treatment frequency on performance of preweaned calves and performance and carcass traits of feedlot cattle.

MATERIALS AND METHODS

All animal protocols were approved by the Iowa State University Committee on Animal Care before this study was performed.

Preweaned Calves

Performance, sire identification, and health records for calves born from spring 1997 to fall 2006 were obtained from the Iowa State University Teaching Farm located in Ames, IA. Calves that did not have an oppor-

tunity to experience BRD (e.g., died shortly after birth) were removed from the data set. The preweaned data analyzed within this study were obtained from 1,519 head of cattle with known purebred sires. The majority of this cowherd is composed of purebred Angus and Simmental cattle, with some crossbreds between these breeds calving in the spring and fall periods. Spring and fall calving cows are maintained in separate herds, and calves in both seasons are provided a creep ration (corn- and oat-based). Spring cows are grazed on pasture throughout the lactation phase, whereas fall cows are exposed to pasture part of the lactation phase and are then moved onto drylots during part of this time period.

Feedlot Cattle

The feedlot cattle data analyzed within this study were obtained from 3,277 head of cattle with known Angus sires as described in Schneider et al. (2009). Performance, carcass, sire identification, and health records for cattle enrolled from 2003 to 2006 were obtained from the Tri County Steer Carcass Futurity (**TCSCF**). This organization is designed to relay information regarding the performance, carcass, and economic components of retained ownership back to the cow/calf consignors for use as decision tools in their operations. Typical management of cattle in TCSCF feedlots is to sort into 2 slaughter groups approximately 35 d apart based on visual appraisal and actual performance.

Preweaned Calves Health Management

The health protocols were consistent across years, with calves receiving vaccination for Clostridia, *Hemophilus somnus*, infectious bovine rhinotracheitis, bovine viral diarrhea virus, bovine respiratory syncytial virus, and parainfluenza type 3 by 200 d of age. Common symptoms associated with BRD include breathing difficulty such as noisy or rapid breathing, coughing, decreased appetite, lethargy, droopy ears, eye discharge, fever, nasal discharge, open-mouthed breathing, and death. Diagnosis of disease classification was maintained by the farm manager across years.

Feedlot Cattle Health Management

The health protocols in place are determined by each particular feedlot; however, guidelines established by the TCSCF organization ensure that optimal health standards are applied to each feedlot setting. Clinical symptoms common in cattle with BRD are fever, breathing difficultly, coughing, nasal and ocular discharge, droopy ears, lethargy, and decreased appetite. Health records from each feedlot were examined to establish disease classifications of diagnosis for each treated animal. Diagnosis of BRD can be complicated due to the wide range of symptoms as well as the difficulties of distinguishing between other diseases. Thus,

Table 1. Significance tests for fixed sources of variation for growth traits in preweaned calves and feedlot cattle by type of bovine respiratory disease (BRD) measurement used

Item[1]	n	Preweaned calves–model fixed effect[2]					
		TRT	CG	Sex	BWT	AgeW	BoDam
BRD incidence							
Weaning weight	954	0.35	<0.01	<0.01	<0.01	<0.01	<0.01
NoTrt							
Weaning weight	954	0.77	<0.01	<0.01	<0.01	<0.01	<0.01
		Feedlot cattle–model fixed effect[3]					
		TRT	CG	SD(CG)	Sex	DelWt	
BRD incidence							
Acclimation ADG	3,244	<0.01	<0.01	<0.01	0.01	<0.01	
On-test ADG	3,189	0.72	<0.01	<0.01	<0.01	<0.01	
Overall ADG	3,189	<0.01	<0.01	<0.01	<0.01	<0.01	
Final BW	3,206	<0.01	<0.01	<0.01	<0.01	<0.01	
NoTrt							
Acclimation ADG	3,244	<0.01	<0.01	<0.01	0.01	<0.01	
On-test ADG	3,189	0.68	<0.01	<0.01	<0.01	<0.01	
Overall ADG	3,189	<0.01	<0.01	<0.01	<0.01	<0.01	
Final BW	3,206	<0.01	<0.01	<0.01	<0.01	<0.01	

[1]BRD incidence = untreated (100) vs. treated (200), NoTrt (number of treatments): 100 = nontreated cattle, 200 = cattle treated once, 300 = cattle treated twice, 400 = cattle treated 3 or more times; acclimation ADG = early feeding period; on-test ADG = late feeding period; overall ADG = total feedlot period; and final BW = last BW before slaughter.

[2]TRT = BRD incidence or NoTrt; CG = contemporary group; sex = bull, steer, or heifer; BWT = BW at birth; AgeW = age of calf at weaning time; BoDam = breed of dam.

[3]TRT = BRD incidence or NoTrt; CG = contemporary group; SD(CG) = final slaughter date within contemporary group; sex = steer or heifer; DelWt = BW upon delivery to feedlot.

guidelines used in this study for defined BRD treatment are representative of typical standards used by feedlot managers across the cattle industry.

Statistical Analysis

For these analyses, records from cattle that died during the monitoring period were retained in the data sets for preweaned cattle (n = 1,519) and feedlot cattle (n = 3,277). The binary classification for respiratory treatment was defined as treated (BRD incidence = 200) or untreated (BRD incidence = 100). For the analysis of number of treatments (**NoTrt**), animals were classified as 100 for untreated cattle, 200 for cattle treated once, 300 for cattle treated twice, and 400 for animals treated 3 or more times (indicating cattle chronically ill with respiratory problems).

Preweaned Calves Statistical Analysis

The MIXED procedure (SAS Inst. Inc., Cary, NC) was used to estimate the effects of BRD on weaning BW. The data set evaluated for weaning BW was reduced to 954 animals because of missing data (Table 1). Bovine respiratory disease incidence is defined as a binary classification of 100 for untreated and 200 for treated cattle (based on at least 1 treatment for respiratory reasons). The number of BRD treatments (NoTrt) was defined as the following: 100 if cattle were never treated for BRD, 200 if cattle were treated once

for BRD, 300 if cattle were treated twice for BRD, and 400 if cattle were treated 3 times or more (thought to be suffering from chronic illness with BRD).

The following model was used to estimate the effect of BRD on weaning BW:

$$y_{ijklmn} = \text{TRT}_i + \text{CG}_j + \text{Sex}_k + \text{BWt}_n + \text{AgeW}_n + \text{BoDam}_l + \text{Sire}_m + \varepsilon_{ijklmn},$$

where y_{ijklmn} = weaning BW measured on calf n, in treatment classification i, in contemporary group j, of sex k, of breed of dam l, and from sire m; TRT_i = fixed effect of BRD incidence i or NoTrt i; CG_j = fixed effect of contemporary group j (based on calving season and birth year of cattle); Sex_k = fixed effect of sex k (bull, steer, or heifer); BWt_n = linear effect of birth BW of calf n; AgeW_n = linear effect of age at weaning of calf n; BoDam_l = fixed effect of breed of dam l (Angus, Simmental, or crossbred); Sire_m = random effect of Sire_m with $\text{Sire}_m \sim N(0, \sigma_s^2)$; ε_{ijklmn} = random residual effect of animal n with $\varepsilon_{ijklmn} \sim N(0, \sigma_\varepsilon^2)$.

Genetic parameters were estimated using a sire model within MTDFREML (Boldman et al., 1995). Three different analyses were conducted: estimates based on records from the entire population (n = 1,519), estimates based only on purebred Angus records (n = 484), and estimates based on purebred Simmental records (n = 655). In all cases, a 3-generation sire, maternal grandsire pedigree was constructed from data provided by the American Angus Association and the Ameri-

can Simmental Association. In total, there were 303 sires and maternal grandsires within the pedigree file, of which there were 110 sires with direct progeny records (Angus = 68 sires with an average 10.0 progeny per sire, range 1 to 79; Simmental = 42 sires with an average of 20.0 progeny per sire, range = 1 to 144). The pedigree included 22 inbred animals with an average inbreeding coefficient of 3.20%. The model used within MTDFREML for each trait was as follows: $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$, where $\mathbf{y}$ = vector of observations; $\mathbf{b}$ = vector of fixed effects, $\mathbf{a}$ = vector of random additive sire effects, which utilizes the numerator relationship matrix among sires; $\mathbf{e}$ = vector of residuals. The incidence matrices relating observations to fixed effects and random animal are $\mathbf{X}$ and $\mathbf{Z}$, respectively. Fixed effects included in the analysis of BRD incidence and number of treatments were contemporary group (based on calving season within year) and breed of dam, along with a linear covariate of individual birth BW. Similar fixed effects were included in the analysis of birth BW except that the linear covariate of birth BW was removed and the effect of sex at birth was added. The analysis of weaning BW included similar fixed effects as the analysis of BRD incidence and number of treatments with an additional fixed effect of sex at weaning and a linear covariate of age at weaning.

The MTDFREML program was run on performance traits in English units until convergence, defined as when the variance of the simplex of −2 logL was less than 1×10^{-9}. After initial convergence was attained, 2 restarts were preformed to ensure global convergence. The results were then converted to metric units for reporting purposes. For single trait models, variance component estimates were used to calculate heritability as the ratio of $(4 \times V_S)/V_P$, where V_S, sire variance, and V_P, phenotypic variance, were estimated from MTDFREML (Falconer and Mackay, 1996), the SE of the heritability reported by MTDFREML was also multiplied by 4 as a result of running a sire model analysis. Bivariate models were utilized to estimate genetic correlations for BRD with weaning and birth BW. Bivariate model SE of the genetic correlation for incomplete data was calculated as described by Kachman and Van Vleck (2007). Phenotypic correlations were calculated using the CORR procedure of SAS.

Feedlot Cattle Statistical Analysis

We were interested in estimating the effect of BRD on acclimation ADG (early feeding period; initial 4 to 6 wk), on-test ADG (late feeding period; end of acclimation period until slaughter), overall ADG (total feedlot period), and final BW. We were also interested in the effect of BRD on the carcass traits of HCW, LM area (**LMA**), subcutaneous fat cover (**fat**), and marbling score (**MarbS**; 2.00 = practically devoid[00]; 3.00 = traces[00]; 4.00 = slight[00]; 5.00 = small[00]; 6.00 = modest[00]; 7.00 = moderate[00]; 8.00 = slightly abundant[00]; 9.00 = moderately abundant[00]; 10.00 = abundant[00]).

The final analysis model was developed using PROC MIXED of SAS, and was as follows:

$$y_{ijklmn} = \mathrm{TRT}_i + \mathrm{CG}_j + \mathrm{Sex}_k + \mathrm{DelWt}_n$$
$$+ \mathrm{SD}_l(\mathrm{CG}_j) + \mathrm{Sire}_m + \varepsilon_{ijklmn},$$

where y_{ijklmn} = the trait measured on calf n, in treatment classification i, in contemporary group j, of sex k, in slaughter date l nested within contemporary group j, and from sire m; TRT_i = fixed effect of BRD incidence i or NoTrt i; CG_j = fixed effect of contemporary group j (based on group of cattle that entered feedlot together and fed together through the feedlot phase); Sex_k = fixed effect of sex k (steer or heifer); DelWt_n = linear covariate effect of the delivery BW of calf n; $\mathrm{SD}_l(\mathrm{CG}_j)$ = fixed effect of final slaughter date l nested within contemporary group j; Sire_m = random effect of Sire_m with $\mathrm{Sire}_m \sim \mathrm{N}(0, \sigma_s^2)$; ε_{ijklmn} = random residual effect of animal n with $\varepsilon_{ijklmn} \sim \mathrm{N}(0, \sigma_\varepsilon^2)$. The above model was used for the analysis of all performance traits. For the analysis of carcass measures, similar fixed effects were fitted; however, the linear effect of DelWt was replaced with the linear effect of age at slaughter in days.

Genetic parameters were estimated using a sire model within MTDFREML (Boldman et al., 1995). A 3-generation sire, maternal grandsire pedigree was constructed from data provided by the American Angus Association. In total, there were 973 sires and maternal grandsires within the pedigree file, of which there were 432 sires with direct progeny records. Sires had an average of 7.6 progeny per sire (range 1 to 73) in the feedlot. The pedigree included 295 inbred animals with an average inbreeding coefficient of 1.63%. The model used within MTDFREML for each trait was as follows: $\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$, where $\mathbf{y}$ = vector of observations; $\mathbf{b}$ = vector of fixed effects; $\mathbf{a}$ = vector of random additive sire effects, which utilizes the numerator relationship matrix among sires; $\mathbf{e}$ = vector of residuals. The incidence matrices relating observations to fixed effects and random sire effect are $\mathbf{X}$ and $\mathbf{Z}$, respectively. Fixed effects included in the analysis of BRD incidence and number of treatments was contemporary group (based on group of cattle that entered feedlot together and fed together through the feedlot phase) along with a linear covariate of individual delivery BW. Similar fixed effects were included in the analysis of genetic parameter for performance traits with the addition of sex to the model for acclimation ADG, whereas sex and slaughter date nested within contemporary group were added to the analysis of on-test ADG, overall ADG, and final BW. Fixed effects included in the analysis of HCW, LMA, fat, and MarbS were contemporary group, sex, slaughter date nested within contemporary group, and a linear covariate of individual age at slaughter.

The MTDFREML program was ran on performance and carcass traits in English units until convergence, defined as when the variance of the simplex of −2 logL was less than 1×10^{-9}. After initial convergence was

attained, 2 restarts were performed to ensure global convergence. The results were then converted to metric units for reporting purposes. For single trait models, variance component estimates were used to calculate heritability as the ratio of $(4 \times V_S)/V_P$, where V_S, sire variance, and V_P, phenotypic variance, were estimated from MTDFREML (Falconer and Mackay, 1996); the SE of the heritability reported by MTDFREML was also multiplied by 4 as a result of running a sire model analysis. Bivariate models were utilized to estimate genetic correlations for BRD with performance and carcass traits. Bivariate model SE of the genetic correlation for incomplete data were calculated as described by Kachman and Van Vleck (2007). Phenotypic correlations were calculated using the CORR procedure of SAS.

RESULTS AND DISCUSSION

Preweaned Calves

Bovine respiratory disease was observed at a rate of 11.39% (n = 173) across all years. The greatest incidence (59.6%) of disease occurred during the fall of 2005, and the least incidence (0.0%) was detected in the fall of 1999 and 2000 and spring of 1998. Mean birth and weaning BW were 39.9 kg (SD = 5.8) and 252.2 kg (SD = 45.5), respectively. The average age at weaning was 176 d (SD = 26), and the average age of first treatment was 118 d (SD = 41). Among cattle treated for BRD, 82.1% were treated once, 13.9% were treated twice, and 4.0% were treated 3 times or more. There was a death rate of preweaned calves of 1.38% (21 head). The population consisted of 28.0% bulls, 24.6% steers, and 47.5% heifers.

The significance of BRD incidence or the number of BRD treatments in conjunction with the other effects in the model on weaning BW is presented in Table 1. Neither BRD incidence nor NoTrt had a significant effect on weaning BW ($P = 0.35$ and $P = 0.77$, respectively). This result indicates that BRD infection may not have been severe enough to reduce performance or that treatment for BRD-stricken cattle was effective in combating disease.

Feedlot Cattle

Mean delivery BW to the feedlot for this population was 286 kg (SD = 42) and mean on-test BW was 342 kg (SD = 48). Acclimation, on-test, and overall ADG averaged 1.56 (SD = 0.59), 1.47 (SD = 0.28), and 1.48 (SD = 0.23) kg/d, respectively. A greater ADG for the acclimation period may be explained by the fact that initial BW included within the calculation is greatly affected by shrinking related to transportation. The average age upon delivery was 291 d, (SD = 56), and mean final BW was 535 kg (SD = 48). The average HCW was 328 kg (SD = 30), the mean LMA was 79.7 cm^2 (SD = 6.64), the mean fat was 12.0 mm (SD = 3.31), and the mean MarbS was 5.53 (SD = 0.87).

Feedlot Cattle Performance Traits

The average incidence of BRD across all years was 9.43% with 309 animals treated at least once. Among treated cattle, 47.9% were treated once, 36.6% were treated twice, and 15.5% were treated 3 times or more. In total, 48 head (1.46%) of cattle died during the feeding phase, 62.5% of which were attributed to respiratory causes. The BRD incidence rate observed in this study is within the smaller range of previous reports of 5 to 50% (Gardner et al., 1999; Snowder et al., 2006) and could be attributed to the excellent management standards and predelivery protocols in place or may indicate that the exposure to pathogens associated with BRD was minimal in the present study.

The effects of BRD incidence or number of treatments on measures of feedlot performance traits are presented in Table 1. The effects of clinical BRD on cattle performance were similar to the results reported in Schneider et al. (2009). Least squares means estimates for production traits on which BRD incidence had a significant effect are presented in Table 2. Feedlot cattle diagnosed with BRD had significantly ($P < 0.01$) less ADG during the acclimation period (1.22 ± 0.03 vs. 1.50 ± 0.02 kg/d); however, no significant effect was observed on ADG during the on-test period ($P = 0.72$). The length of the acclimation period averaged 37 d in the current study. This time period represents the most critical period because most BRD incidences occurred during or directly after this time period within the population under study. Overall ADG was adversely affected ($P < 0.01$) by treatment for BRD; treated cattle gained 0.06 ± 0.01 kg/d less BW when compared with untreated cattle. These results indicate that BRD incidence has a detrimental effect on ADG, especially early in the finishing period. In addition, because cattle that were treated for BRD have a decreased reduction in ADG when considering the entire feedlot phase compared with the acclimation period, perhaps cattle properly treated for BRD are able to more closely match the performance of untreated cattle after the effects of infection have been minimized.

The number of treatments revealed similar results to the analysis of BRD incidence; significant effects on acclimation ADG ($P < 0.01$) and overall ADG ($P < 0.01$) were observed for treatment numbers. As expected, cattle that were never treated had greater estimates for ADG for both time periods. Cattle treated once or twice did not differ significantly for acclimation ADG ($P = 0.40$) or overall ADG ($P = 0.79$), but were significantly greater than cattle treated 3 times or more ($P < 0.10$; data not shown).

Feedlot Cattle Carcass Traits

The effects of BRD incidence and NoTrt on carcass traits are presented in Table 3. Carcasses from cattle treated had lighter HCW (9.15 ± 1.68 kg; $P < 0.01$) compared with healthy cattle (Table 2). This result

Table 2. Least squares means for performance and carcass measures of cattle diagnosed with bovine respiratory disease (BRD) and those considered healthy

Item[1]	Untreated	SE	Treated	SE	Diff[2]	SE
BRD incidence						
Acclimation ADG,** kg/d	1.50	±0.02	1.22	±0.03	0.28	0.03
Overall ADG,** kg/d	1.45	±0.01	1.39	±0.01	0.06	0.01
Final BW,** kg	527.0	±1.5	515.8	±2.3	11.1	2.0
HCW,** kg	319.6	±1.2	310.4	±1.9	9.1	1.7
Fat,** mm	12.35	±0.14	11.43	±0.23	0.91	0.21
MarbS[3]*	5.59	±0.04	5.49	±0.06	0.11	0.05

[1]BRD incidence = untreated (100) vs. treated (200). Acclimation ADG = early feeding period; overall ADG = total feedlot period; final BW = last BW before slaughter; fat = subcutaneous fat cover; and MarbS = marbling score.

[2]Diff = untreated minus treated.

[3]2.00 = practically devoid[00]; 3.00 = traces[00]; 4.00 = slight[00]; 5.00 = small[00]; 6.00 = modest[00]; 7.00 = moderate[00]; 8.00 = slightly abundant[00]; 9.00 = moderately abundant[00]; 10.00 = abundant[00].

*$P \leq 0.05$; **$P \leq 0.01$.

may be explained by the effect of BRD incidence on ADG, which subsequently leads to lighter final BW at a constant age. Treated cattle were also leaner (11.43 ± 0.23 mm vs. 12.35 ± 0.14 mm; $P < 0.01$) and had smaller marbling scores (5.49 ± 0.06, small[49] vs. 5.59 ± 0.04, small[59]; $P < 0.05$). The distribution of USDA quality grades assigned to carcasses illustrated that 80.9% of cattle never treated for BRD received the Choice category or better. This is a definite advantage when compared with cattle in the other number of treatment categories (1 = 72.2%; 2 = 71.1%; 3+ = 72.2%). This result may have a profound effect on the profit potential for feedlots when marketing under value-based systems. The effect of number of treatments on HCW, fat, and MarbS were generally similar to those reported by Schneider et al. (2009). With regard to each trait, the values associated with HCW, fat, and MarbS generally decreased as the number of treatments increased.

Preweaned Genetic Parameters

Genetic parameter estimates from single trait analysis of measures for respiratory disease, weaning BW, and birth BW are presented in Table 4. Heritability estimates for BRD incidence and number of treatments were 0.11 ± 0.06 and 0.08 ± 0.05, respectively. These estimates are similar to those reported by Muggli-Cockett et al. (1992; h^2 = 0.10) and Snowder et al. (2005; h^2 = 0.00 to 0.26) in preweaned calves. Estimates of heritability for birth and weaning BW were 0.67 ± 0.14 and 0.49 ± 0.16, respectively. Selection for decreased BRD incidence during the preweaning period may be possible based on the heritability estimates obtained from this population.

When the data were subset by breed, the estimate of heritability for BRD incidence in purebred Angus calves was 0.10 ± 0.11 and was 0.02 ± 0.06 in purebred Sim-

Table 3. Significance tests for fixed sources of variation for carcass traits in feedlot cattle by type of bovine respiratory disease (BRD) measurement used

Item[1]	n	Feedlot cattle–model fixed effect[2]				
		TRT	CG	SD(CG)	Sex	AgeS
BRD incidence						
HCW	3,184	<0.01	<0.01	<0.01	<0.01	<0.01
LMA	3,184	0.22	<0.01	<0.01	<0.01	<0.01
Fat	3,184	<0.01	<0.01	<0.01	<0.01	0.02
MarbS	3,184	0.04	<0.01	<0.01	<0.01	<0.01
NoTrt						
HCW	3,184	<0.01	<0.01	<0.01	<0.01	<0.01
LMA	3,184	0.13	<0.01	<0.01	<0.01	<0.01
Fat	3,184	<0.01	<0.01	<0.01	<0.01	0.02
MarbS	3,184	<0.01	<0.01	<0.01	<0.01	<0.01

[1]BRD incidence = untreated (100) vs. treated (200); NoTrt (number of treatments): 100 = nontreated cattle, 200 = cattle treated once, 300 = cattle treated twice, 400 = cattle treated 3 or more times; LMA = LM area; fat = subcutaneous fat cover; and MarbS = marbling score.

[2]TRT = BRD incidence or NoTrt; CG = contemporary group; SD(CG) = final slaughter date within contemporary group; sex = steer or heifer; and AgeS = day of age at slaughter.

Table 4. Variance component and heritability estimates for health, performance, and carcass traits obtained from single trait sire model analysis[1]

Item[2]	n	V_A	V_P	h^2
Preweaned calf genetic component				
Entire population				
BRD[3] incidence	1,519	88.9	789.5	0.11 ± 0.06
NoTrt	1,519	119.1	1,478.2	0.08 ± 0.05
Birth BW, kg[2]	1,516	19.8	29.7	0.67 ± 0.14
Weaning BW, kg[2]	954	421.3	852.2	0.49 ± 0.16
Angus only				
BRD incidence	484	78.4	805.3	0.10 ± 0.11
NoTrt	484	117.9	1,621.2	0.07 ± 0.10
Simmental only				
BRD incidence	655	12.9	803.3	0.02 ± 0.06
NoTrt	655	0.0	1,587.5	0.00 ± 0.06
Feedlot cattle genetic component				
BRD incidence	3,277	57.7	775.4	0.07 ± 0.04
NoTrt	3,277	55.1	2,594.6	0.02 ± 0.03
Acclimation ADG, $(kg/d)^2$	3,244	0.129	0.232	0.56 ± 0.08
On-test ADG, $(kg/d)^2$	3,189	0.0248	0.0459	0.54 ± 0.09
Overall ADG, $(kg/d)^2$	3,189	0.0220	0.0327	0.67 ± 0.09
Final BW, kg[2]	3,189	676.2	950.7	0.71 ± 0.10
HCW, kg[2]	3,213	479.7	672.6	0.71 ± 0.10
LMA, $(cm^2)^2$	3,213	21.34	37.01	0.58 ± 0.08
Fat, mm[2]	3,213	3.15	9.28	0.34 ± 0.07
MarbS[2][4]	3,213	0.403	0.598	0.67 ± 0.09

[1]V_A = additive genetic variance; V_P = phenotypic variance (total variance); h^2 = heritability.

[2]Entire population = all animals; BRD incidence = untreated (100) vs. treated (200); NoTrt: 100 = non-treated cattle, 200 = cattle treated once, 300 = cattle treated twice, 400 = cattle treated 3 or more times; birth BW = BW at birth; weaning BW = BW of cattle at weaning time; Angus only = Angus calves; Simmental only = Simmental calves; acclimation ADG = early period of feedlot; on-test ADG = late period of feedlot; overall ADG = total feedlot period; fat = subcutaneous fat cover; and MarbS = marbling score.

[3]BRD = bovine respiratory disease.

[4]2.00 = practically devoid[00]; 3.00 = traces[00]; 4.00 = slight[00]; 5.00 = small[00]; 6.00 = modest[00]; 7.00 = moderate[00]; 8.00 = slightly abundant[00]; 9.00 = moderately abundant[00]; 10.00 = abundant[00].

mental calves. These results indicate that selecting for BRD resistance may be more feasible in Angus cattle within this population compared with the Simmental breed. Possible differences in the heritability estimates between breeds are likely due to breed differences observed in terms of additive genetic variances, rather than phenotypic variances (Table 4). Within this population the additive genetic variance for Angus cattle is considerably larger with relatively similar estimates for phenotypic variance seen between both breeds.

Phenotypic and genetic correlations among BRD incidence, number of BRD treatments, weaning BW, and birth BW were estimated from records on the entire population (Table 5). The phenotypic correlations between all traits were low, ranging between −0.04 and −0.00. The genetic correlation estimates for BRD incidence with weaning BW and birth BW were low (−0.02 ± 0.32 and 0.07 ± 0.27, respectively). However, slightly greater genetic correlation estimates were obtained for the number of BRD treatments with weaning BW and birth BW (0.25 ± 0.35 and 0.30 ± 0.27, respectively). These estimates of genetic correlations between number of BRD treatments and BW traits may have implications for selection decisions. Selection for reduced birth BW is favorable for reduced number of treatments; however, selection for increased weaning weights may

lead to an increased number of treatments for BRD in preweaned calves.

Feedlot Cattle Genetic Parameters

Genetic parameter estimates from single trait analysis of respiratory disease, performance, and carcass traits are presented in Table 4. The heritability estimate for BRD incidence was 0.07 ± 0.04, which was similar to the reports of Snowder et al. (2006 and 2007; $h^2 = 0.04$ to 0.08). Analysis of number of treatments for BRD revealed a heritability estimate of 0.02 ± 0.03. The results of this study agree with conclusions of Snowder et al. (2006), in that developing a selection program with an emphasis on BRD resistance may be challenging but is possible. The heritability of BRD incidence estimated within this study was observed with a disease rate of 9.43%, which is approaching the lower end of the incidence expectation, and there is evidence that as incidence rate is increased, heritability estimates are increased (Snowder et al., 2006).

Heritability estimates for all production traits were moderate to strong (Table 4). Estimates for performance traits ranged from 0.54 to 0.71, and carcass traits ranged from 0.34 to 0.71. In comparison with the heritability estimates from the American Angus Asso-

Table 5. Phenotypic (r_p) and genetic (r_g) correlations among 2 measures of bovine respiratory disease (BRD) incidence with performance traits and carcass traits estimated for a bivariate sire model

| Item[1] | Trait[2,3] | | | |
| | BRD incidence | | NoTrt | |
	r_p	r_g	r_p	r_g
Weaning BW	−0.04	−0.02 ± 0.32	−0.02	0.25 ± 0.35
Birth BW	−0.03	0.07 ± 0.27	−0.00	0.30 ± 0.27
Acclimation ADG	−0.19	−0.63 ± 0.22	−0.20	−1.00 ± 0.68
On-test ADG	−0.06	−0.04 ± 0.23	−0.06	−0.04 ± 0.39
Overall ADG	−0.14	−0.31 ± 0.21	−0.14	−0.47 ± 0.41
Final BW	−0.11	−0.39 ± 0.21	−0.11	−0.66 ± 0.40
HCW	−0.09	−0.22 ± 0.22	−0.09	−0.58 ± 0.45
LMA	−0.03	−0.03 ± 0.22	−0.02	−0.12 ± 0.38
Fat	−0.07	0.24 ± 0.25	−0.07	0.42 ± 0.50
MarbS	−0.05	−0.43 ± 0.20	−0.06	−0.32 ± 0.37

[1]Weaning BW = BW of cattle at weaning time; birth BW = BW at birth; acclimation ADG = early period of feedlot; on-test ADG = late period of feedlot; overall ADG = total feedlot period; fat = subcutaneous fat cover; and MarbS = marbling score.

[2]BRD incidence = untreated (100) vs. treated (200); NoTrt (number of treatments): 100 = nontreated cattle, 200 = cattle treated once, 300 = cattle treated twice, 400 = cattle treated 3 or more times.

[3]Phenotypic correlations were calculated as a ratio of phenotypic covariance estimates to the product of respective phenotypic SD estimates.

ciation (2007) for HCW (0.30), fat (0.25), LMA (0.28), and MarbS (0.36), the estimated heritability estimates from this study are greater. One possibility for this result is the consistency with which all cattle are fed and managed by the TCSCF organization. Based on the increased heritability estimates for production and carcass traits in this analysis, the selection of breeding stock used by cattle producers within this management system is extremely important and the potential to increase production and beef quality due to genetics exists.

Phenotypic and genetic correlations were estimated among BRD incidence or number of BRD treatments with all performance and carcass traits evaluated within this study (Table 5). Phenotypic correlations between all reported traits with BRD incidence and number of BRD treatments were poorly correlated and ranged between −0.20 and −0.02.

Moderate estimates of genetic correlations were estimated between BRD incidence and acclimation ADG (−0.63 ± 0.22), overall ADG (−0.31 ± 0.21), and final BW (−0.39 ± 0.21). However, the genetic relationship of BRD incidence and on-test ADG was −0.04 ± 0.23. Generally, similar genetic relationships were estimated between the number of BRD treatments and the above performance traits (Table 5). However, there was a more extreme estimate of the genetic correlation between number of treatments and acclimation ADG (−1.00 ± 0.68); this estimate warrants further investigation in new populations. The only known estimates of genetic correlation of BRD incidence are with ADG from the entire feedlot phase of 0.08 ± 0.07 (Snowder et al., 2007). When considering the SE for the estimate

of genetic correlation for BRD incidence with overall ADG, the results from this study are similar.

Genetic correlations tended to be greater for the number of treatments as compared with BRD incidence when carcass traits were analyzed (Table 5). Hot carcass weight, LMA, and fat ranged from −0.22 to 0.24 for BRD incidence and −0.58 to 0.42 for number of treatments. The estimate for genetic correlations with BRD incidence and number of treatments with marbling score were −0.43 ± 0.20 and −0.32 ± 0.37, respectively. This is a more favorable genetic correlation of BRD incidence with MarbS than Snowder et al. (2007) reported (0.09 ± 0.13).

Overall Conclusion

This study utilized field data from preweaned cattle from the Iowa State University Teaching Farm and from typical Midwest feedlots. Results indicate that the incidence of BRD has negative effects on important performance and carcass traits. Furthermore, the number of times cattle are treated has adverse effects on performance and carcass traits. Though the heritability estimate for BRD was small, results here illustrate that breeding programs could be developed to incorporate BRD resistance into selection programs for improving cattle health to ultimately increase profit potential. In addition, this study indicates that selection for BRD resistance may have little to favorable effect on HCW, LMA, and fat due to the low genetic correlation estimates and large SE. Favorable genetic correlations exist for acclimation ADG, overall ADG, final BW, and MarbS with either health measure. Further research

on the selection for reduced BRD incidence are warranted due to the benefits to cattle producers not only in terms of reduced disease incidence but also in regard to increasing performance and carcass quality from a genetic merit perspective.

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