

Rapid Communication: Variance component estimates for Charolais-sired fed cattle and relative economic impact of bovine respiratory disease¹

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ABSTRACT: Variance components were estimated and relative economic importance of bovine respiratory disease (BRD) was derived from 3 yr of performance, morbidity, and mortality data collected from a single beef cattle finishing operation. One thousand one hundred eighty nine of 12,812 Charolais-sired calves were treated for BRD during the finishing period. Weaning weight (WW), DMI, days to harvest (D2H), HCW, yield grade (YG), and marbling score determined by image analysis (MARB) were collected to quantify the economic impact associated with treatment for BRD. Observed means and (co)variances for carcass and production traits were used to simulate populations of 10,000 healthy and 10,000 BRD treated calves. A bio-economic model was developed to derive the economic value associated with the incidence and number of treatments for BRD during the finishing period. Carcasses from healthy calves were worth \$58.28 more on average compared to calves treated at least once for BRD. Heritability estimates for BRD were 0.15 when the trait

was measured as number of treatments (0 to 4), and 0.14 when measured as incidence (0 or 1). The model indicated that D2H had the lowest relative economic importance in this system, with a cost of \$1.91 per head for each additional day on feed. Furthermore, the relative economic value of BRD morbidity was approximately 10.65 greater than D2H when recording the BRD phenotype as the number of BRD treatments. The economic values of HCW, WW, and DMI were 11.47, 5.15, and 3.61 times more important than D2H, respectively. This indicates BRD morbidity has the second greatest relative economic value in this system, with a one percent increase in morbidity associated with an average loss of \$2.08 per head. These results indicate that BRD morbidity can have an equal or greater economic importance when compared to carcass and production traits during the finishing period. Further, this indicates the opportunity exists to increase the genetic merit for profitability during the finishing period by incorporating BRD incidence into terminal-sire selection indexes.

Key words: Bovine respiratory disease, economic model, relative economic value, variance components

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INTRODUCTION

Bovine respiratory disease (**BRD**) is heritable and economically important in the feedlot industry in the United States (Snowder et al., 2005; Berry, 2014). The

cost of prevention, treatment, and loss of performance from BRD has been estimated to account for approximately 7% of the total cost of production from weaning to packing (Griffin, 1997). Multiple studies have quantified the total economic discounts on finished carcasses resulting from decreases in performance after an animal was treated at least once for BRD (Bureau et al., 2001; Cernicchiaro et al., 2013). Treatment of BRD at least once during finishing results in a 1.3% to 5.3% lighter HCW, a 7.5% to 26.5% lower yield grade (**YG**), and a 2.4% to 5.3% lower marbling score (**MARB**; Gardner et al., 1999; Schneider et al., 2009; Garcia et al., 2010; Cernicchiaro et al., 2013; Pardon et al., 2013). However, there are few applied examples available that demonstrate the economic impact of incorporating health traits

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into terminal-sire selection indexes focused on profit during finishing. Previous results from bio-economic simulation indicated that BRD may have an equal or greater relative economic value compared to carcass traits during the finishing phase (Van Eenennaam and MacNeil, 2011).

The primary objective of this study was to estimate genetic parameters and the relative economic value of BRD in Charolais-sired feedlot cattle. Because estimation of variance components for health traits typically proceeds from modeling the affliction as either a threshold or binary trait (Collie, 1992; McGuirk, 2008), a secondary objective was to compare these alternative models for BRD.

MATERIALS AND METHODS

Animals and Data Collection

There were 12,812 total animals observed during the finishing period over 3 yr, with 1189 animals treated for BRD at least once during finishing. All animals were fed a similar finishing ration and managed under common conditions at a single feedlot. All animals in this study were owned by the commercial cooperator and under the supervision of a practicing veterinarian. All animals were Charolais-sired with pedigree relationships derived from either traditional pedigree recording in a 3 generation pedigree or by genotyping with the GeneSeek GGP_LD (20k or 26k v1.1-v4) SNP array. All animals were characterized by 18,121 SNP markers after trimming for minor allele frequency (0.05) and quality (95% non-missing); an adequate density to accurately represent the genomic relationship matrix (Rolf et al., 2010).

To compare phenotyping strategies, BRD was recorded as both a binary trait indicating incidence (0 or 1) and as a categorical trait with thresholds indicating the number of treatments for BRD (0 to 4). Weaning weight (**WW**) was recorded for every animal on arrival at the feedlot. The trait DMI was recorded on a subset of the population for a minimum of 30 d ($n = 1803$) using the GrowSafe™ System Ltd. (Airdrie, AB, Canada). The trait ADG was calculated as the difference between WW and the latest recorded live weight divided by the number of days between measurements ($n = 10,038$). Measures of YG and MARB determined by image analysis were collected at slaughter ($n = 7911$). Means and (co)variances from these records were used to model the average carcass price differential associated with treatment for BRD.

Heritability of Bovine Respiratory Disease

Variance components were estimated for BRD and ADG using a 2-trait threshold-linear model with a single-

step Bayesian approach implemented in THRGIBBS1F90 (Tsuruta and Misztal, 2006). This implementation relies on Gibbs sampling to estimate posterior means. All phenotyped animals were genotyped and additional pedigree relationships from ancestors without genotypes were incorporated into the relationship matrix using the single-step approach (Legarra et al., 2014). Variance components were estimated in a 2-trait model (BRD and ADG) using BRD modeled either as a binary or categorical trait. The underlying distribution for the bivariate linear-threshold animal model is assumed:

$$\begin{pmatrix} y_{ADG} \\ I_{BRD} \end{pmatrix} \sim N \left(\begin{pmatrix} X\beta_{ADG} + Zu_{ADG} \\ X\beta_{BRD} + Zu_{BRD} \end{pmatrix}, I \otimes R \right)$$

Where β are fixed effects including ranch of origin, weaning date, and sex; u are breeding values; X and Z are incidence matrices that link data with respective effects; and R is the residual covariance matrix. The response for BRD was modeled with the following distribution:

$$\begin{aligned} f(y_{BRD} | I_{BRD}) &= \prod_{i=1,nd} f(y_{i_{BRD}} | I_{i_{BRD}}) = \prod_{i=1,nd} \\ &1(I_{i_{BRD}} < t_1)1(y_{i_{BRD}} = 1) + \\ &1(t_1 < I_{i_{BRD}} < t_2)1(y_{i_{BRD}} = 2) + \\ &1(t_2 < I_{i_{BRD}} < t_3)1(y_{i_{BRD}} = 3) + \\ &1(t_3 < I_{i_{BRD}} < t_4)1(y_{i_{BRD}} = 4) + \\ &1(t_4 < I_{i_{BRD}})1(y_{i_{BRD}} = 5) \end{aligned}$$

where t_0 to t_4 are thresholds that define the 5 categories of response. All prior distributions were assumed flat. Further details on the underlying assumptions of threshold-linear models were presented in detail by Varona et al. (1999b). The R package ‘mcgibbsit’ (<https://cran.r-project.org/web/packages/mcgibbsit>) was used to determine the length of the burn-in period and minimum chain length needed to obtain stationary chains of independent samples to estimate the total number of Gibbs samples required for the cumulative distribution function of the 0.025 quantile to be estimated within ± 0.0125 , with a probability of 0.95 for all genetic parameters (Raftery and Lewis, 1995). Within THRGIBBS1F90, a single chain of 50,000 iterations was used to calculate posterior means with the first 10,000 iterations discarded as burn-in and every 10th sample stored for post-analysis. These parameters met the recommended diagnostics from the ‘mcgibbsit’ results as described by Raftery and Lewis (1995). The remaining samples were used to calculate posterior means to estimate variance components and heritability with the program POSTGIBBSF90 (Tsuruta and

Misztal, 2006). Variance components were also estimated for ADG using a single-trait model as a basis for comparison to the threshold-linear model using single-step average-information REML (**AI-REML**) implemented in AIREMLF90 (Misztal, 2008).

Relative Economic Value of Bovine Respiratory Disease

The relative economic value of BRD was derived by evaluating a model of profit with respect to percent BRD incidence as well as other traits relevant to profit in a typical feedlot finishing operation. Phenotypic means and (co)variance structure from actual performance data with recorded incidence of BRD were used to model traits including WW, DMI, days to harvest (**D2H**), HCW, YG, and MARB. The means and (co)variance structure from observed healthy and BRD treated calves from the 3 carcass traits were used to simulate 2 populations of 10,000 healthy calves and 10,000 BRD afflicted calves. The opportunity cost of mortality is imbedded in the difference in total revenue generated from each population. The mean number of treatments for BRD was used to simulate a random exponential distribution with categorical treatments from 1 to 4. The distribution of treatments was then sampled at the mean incidence of BRD for the population (9.3%) to randomly assign either a healthy or BRD affected phenotype to each animal in the simulation.

The simulated carcasses were priced using a typical carcass grid to model the carcass price penalty and cost associated with the incidence and number of treatments for BRD. A profit equation was developed with income and cost elements of carcass price, feed price, fixed cost of finishing, and cost of BRD treatment to derive an economic weight for BRD at the mean percentage of BRD incidence in a typical feedlot operation. Costs accounted for in the model included calf purchase cost (\$3.20 kg⁻¹), feed cost (\$0.0935 kg⁻¹), fixed cost or yardage fee (\$0.45 hd⁻¹d⁻¹), and treatment cost for BRD (\$26 hd⁻¹). Mortality cost was included in the model using the observed 6.3% death rate of animals treated at least once for BRD. Mortality cost was included in the model by assuming dead calves incurred feed cost for 133 d and received an average of 1.6 treatments for BRD before death. Profit equations were adapted from previous attempts to simulate an economic system (Ponzoni and Newman, 1989; Tang et al., 2011) to model the finishing phase of the production system.

$$\text{Total income} = \text{HCW} \times \text{carcass grid price}$$

$$\text{HCW} = [\text{WW} + (\text{ADG} \times \text{D2H})] \times \text{Dressing\%} \\ \text{(DP)}$$

$$\text{Finishing cost} = \text{calf purchase cost} + \text{feed cost} + \text{fixed cost} + \text{BRD treatment cost}$$

$$\text{Calf purchase cost} = \text{WW} \times \text{feeder calf price} \\ (\$/\text{kg})$$

$$\text{Feed cost} = \text{D2H} \times \text{DMI} \times 1/\% \text{DM} \times \text{feed price} \\ (\$/\text{kg})$$

$$\text{Fixed cost} = \text{D2H} \times \text{fixed cost of finishing}$$

$$\text{BRD treatment cost} = \text{number of treatments} \\ \times \text{BRD treatment cost}$$

$$\text{Profit} = \text{total income} - \text{finishing cost}$$

Parameters assumed or calculated from the data were: DP = 62%; Feeder Calf Price = \$3.20/kg; Feed price = \$0.0935/kg; % Dry matter (%DM) = 55%; Fixed cost of finishing = \$0.45 hd⁻¹d⁻¹; and Cost of BRD treatment: \$26 hd⁻¹.

Percent incidence of BRD, WW, D2H, YG, MARB, and DMI were independently deviated one unit from their respective mean to estimate the change in profit (economic value) when all other traits are held constant (MacNeil et al., 1994). The economic value for HCW was calculated by perturbing DP a small amount and dividing the resulting change in profit by the change in HCW that occurred between the simulations. Relative economic values for breeding purposes were calculated by multiplying the economic value by the estimated genetic standard deviation for each trait. The absolute value of each relative economic value was then divided by the trait with the smallest relative economic value to generate a relative importance.

RESULTS AND DISCUSSION

Estimates of variance components and genetic parameters derived from the 3 models that were used in evaluating BRD and ADG are shown in Table 1. Variance component estimates for ADG were similar across the 3 models. Heritability estimates for ADG were nearly identical for the 2 Bayesian models. The heritability estimates for both BRD and ADG were marginally greater when BRD was modeled as a categorical trait indicating number of treatments. It is generally acknowledged that susceptibility/resistance to BRD is heritable (Snowder et al., 2005; Berry, 2014), but there are challenges to address when drawing conclusions about the underlying genetic distribution. Previous estimates using both traditional pedigree information and SNP genotypes also suggest it is a lowly heritable trait, with estimates ranging from 0.02 to 0.29 depending on the breed, technique of analysis, and

Table 1. Variance components for bovine respiratory disease (BRD) and ADG using a Bayesian/Gibbs sampling approach and average-information REML (AI-REML). There were 10,038 animals with recorded ADG with 748 animals treated for BRD at least once

Component	# of TRT TL-Gibbs ¹			Binary TL-Gibbs ²			AI-REML ³
	2.5 percentile	Mean	97.5 percentile	2.5 percentile	Mean	97.5 percentile	
σ_g^2 -ADG	0.040	0.046	0.052	0.041	0.046	0.051	0.040 ± 0.003
σ_e^2 -ADG	0.121	0.126	0.131	0.122	0.126	0.131	0.131 ± 0.027
h^2 -ADG	0.314	0.365	0.418	0.316	0.365	0.412	0.304 ± 0.004
σ_g^2 -BRD	0.081	0.132	0.187	0.066	0.136	0.226	–
σ_e^2 -BRD	0.739	0.878	1.030	0.967	1.005	1.043	–
h^2 -BRD	0.090	0.150	0.216	0.065	0.135	0.226	–
r_u ADG-BRD ⁴	-0.098	0.059	0.270	-0.200	0.106	0.345	–

¹Bayesian model with BRD recorded as a categorical trait indicating number of treatments (0 to 4). Components estimated in a 2-trait threshold-linear model with BRD and ADG with associated 95% credibility interval.

²Bayesian model with BRD recorded as a binary trait (0 or 1) indicating incidence of treatment. Components estimated in a 2-trait threshold-linear model with BRD and ADG with reported associated 95% credibility interval.

³Single-trait model for variance components of ADG using AI-REML with reported standard error.

⁴Genetic correlation between BRD and ADG.

method used to model the phenotype (Lyons et al., 1991; Snowden et al., 2005; Taylor et al., 2010; Neiberger et al., 2014). Practical results suggest that different models lead to slightly different estimates of heritability and variance components (Neiberger et al., 2014). Simulated studies estimating variance components for both binary and categorical models have been shown to produce similar heritability estimates indicating that either model can be appropriately utilized to estimate the heritability of BRD (Varona et al., 1999a,b). Further, characterizing the BRD phenotype is not standardized across research studies and facilities (Abdallah et al., 2016), and a significant number of animals likely go undiagnosed in commercial systems. In the present system, there were 45 animals that died from morbidity associated with BRD before morbidity was diagnosed or treated. Heritability estimates for BRD also have been found to differ among breeds (Snowden et al., 2005), likely due to differences among breeds in allele frequencies at or near causative loci.

Economic value, relative economic value, and importance relative to D2H for the traits in the economic simulation are shown in Table 2. The smallest (absolute value) relative economic value was observed for D2H, and it was used as the basis for calculating the relative importance of the other traits that were included in the breeding objective. The cost of 1 additional day to finishing averaged \$1.91 per head. Calves treated at least once for BRD were on feed for an average of 2.6 d longer than untreated calves. The trait HCW had the highest relative economic value in this system with 11.47 times the importance of D2H for breeding purposes. This is in line with other terminal-sire selection indexes which reflect a relatively high importance for final carcass weight (Amer et al., 1998; Barwick and Henzell, 2005). Morbidity associated with the number of treatments for BRD had the

2nd highest relative economic value in this system with approximately 10.65 times the importance of D2H. A 1 percent increase in the mean incidence of BRD resulted in an average decrease in profit of \$2.08 per head. Van Eenennaam and MacNeil (2011) found BRD to have the highest relative economic value in a simulated terminal-sire index with 37.7 times the importance of YG. This previous study simulated a commercial straightbred Angus enterprise and the economic values were expressed on that basis. Among other differences between the studies, the difference in probability of mortality between afflicted and healthy animals was greater in the earlier study, as was the cost to diagnose and treat BRD (\$44 vs. \$26), which resulted in a higher relative economic value. In the

Table 2. Economic value, genetic standard deviation (SD), relative economic value, and relative importance to days to harvest (D2H) for bovine respiratory disease (BRD) modeled as a categorical trait indicating number of treatments as well as for other production traits in the economic model

Trait	Economic value (\$)	Genetic SD	Relative economic value	Relative importance to D2H ¹
BRD (% incidence)	-2.08	38.83	-80.96	10.65
HCW (kg)	5.11	17.04	87.17	11.47
YG ²	-66.14	0.21	-13.59	1.79
MARB ³	0.72	34.14	24.50	3.22
DMI (kg)	-46.34	0.59	-27.43	3.61
D2H (d)	-1.91	3.97	-7.60	1.00
WW ⁴ (kg)	-3.20	12.24	-39.14	5.15

¹The relative importance was calculated as the absolute value of the relative economic value divided by the smallest relative economic value (D2H).

²Yield grade.

³Camera marbling score.

⁴Weaning weight.

present study, the mean incidence of BRD was lower but still resulted in a high relative economic value during the finishing period due to the combined effect on decreased final carcass price and increased finishing cost.

This study highlights the economic importance of BRD in commercial settings using phenotyping strategies that fit within typical feedlot management practices. The demonstrated relative economic importance of BRD justifies attempts to develop genomic predictions and incorporate this trait into terminal-sire selection indexes with profit as the breeding objective.

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