

ECONOMIC BENEFITS OF USING GENETIC SELECTION TO REDUCE THE PREVALENCE OF BOVINE RESPIRATORY DISEASE COMPLEX IN BEEF FEEDLOT CATTLE

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Abstract

The prevalence of bovine respiratory disease complex (BRDC) has remained unchanged for decades despite efforts to suppress the disease through prevention programs aimed at vaccination and metaphylaxis. An additional approach that focuses on host response to infection by the pathogens responsible for BRDC, through the selection of animals that are less susceptible to the disease, has been undertaken as part of the USDA funded “Integrated Program for Reducing BRDC in Beef and Dairy Cattle” with Dr. James Womack at Texas A&M University as the Project Director. This study, now beginning its fourth year, has found that estimates of heritability for susceptibility to BRDC were greater than 17% for a binary case-control definition of BRDC and greater than 29% for a semi-quantitative (clinical score) definition of BRDC in a commercial feedlot in Colorado. The higher heritability estimate for the more precise definition of BRDC was anticipated as heritability improves as accuracy of a measured phenotype (in this case the BRDC phenotype) improves.

The estimated annual rate of genetic gain due to selection on these phenotypes was estimated at 1.26% (case-control) and 2.08% (clinical scores). The economic cost of \$253.97 per BRDC feedlot steer was determined through the loss of carcass quality, death and treatment costs. When this value was combined with the 16.2% national prevalence of BRDC in the feedlot and the estimated reduced prevalence of BRDC (rate of genetic gain made by selecting to increase the proportion of cattle that are more resistant to disease), the feedlot industry could gain between \$13 and \$21.5 million per year

through the implementation of selection for cattle that are less susceptible to BRDC.

Introduction

Bovine respiratory disease complex is the result of viral and bacterial pathogens and is the leading cause of illness and death in feedlot cattle (USDA 2001, Gagea et al. 2006, Snowden et al 2006). The prevalence of bovine respiratory disease complex (BRDC) detected in feedlot cattle varies by year with a 15 year range of from 5% to 44%, and also by season, with higher prevalence rates in the fall and winter (Snowden et al 2005, Miles 2009). The average prevalence rate of BRDC was 16.2%, with virtually all feedlots (96.9%) reporting one or more cases between July 1, 2010 and June 30, 2011 (USDA 2011). Recent reports have indicated that greater than 60% of all cattle in the feedlot have lung lesions resulting from BRDC and many of these animals were undetected as suffering from an illness (Schneider et al. 2009). Of animals that showed noticeable signs of illness, BRDC was the most common cause (67% to 82%) of illness detected in feedlot cattle (Edwards 1996, USDA 2011). An estimated 1.4% of all feedlot cattle die from BRDC prior to harvest.

The high prevalence of BRDC in feedlot cattle has not fallen in spite of best management practices and vaccination programs (Gagea et al. 2006, Miles 2009). According to the USDA (2011), the majority of feedlots over 1,000 head used one respiratory vaccine to combat disease. Unfortunately, only about 25% of cattle were vaccinated for both the viral and bacterial pathogens associated with BRDC. Specifically, 96.6% of feedlots vaccinated for bovine viral diarrhea virus (BVDV), 93.7% vaccinated for infectious bovine rhinotracheitis virus (IBR), 85.1% vaccinated for parainfluenza 3 virus (PI3) and 89.5% of feedlots vaccinated for bovine respiratory syncytial virus (BRSV) (USDA 2011). Approximately 66% of feedlots used vaccines that incorporated BRDC bacterial pathogens *Hemophilus somnus* and *Mannheimia haemolytica* (previously named *Pasteurella haemolytica*) and 21.8% vaccinated against *Mycoplasma bovis*.

One strategy used to prevent or minimize an outbreak of BRDC is to treat cattle with an injectable antibiotic (metaphylaxis) for BRDC pathogens. Factors that heightened concerns of BRDC and caused feedlots to consider metaphylaxis included: cattle

with a poor appearance on arrival (88.4% of feedlots would consider metaphylaxis), the presence of one or more animals from the same source affected with BRDC (83.8%), the presence of BRDC affected cattle in the same pen (70.5%), or if cattle came from a sale barn (88.3%) (USDA 2011). In all, 59.3% of feedlots used metaphylaxis treatment for some cattle in the feedlot. Unfortunately this strategy, as well as vaccination, have collectively failed to reduce the prevalence of BRDC and further suggests that other approaches, such as focusing on the host response to pathogen challenges, may be helpful in reducing the prevalence. The use of new approaches, such as genomic selection, is supported by studies providing evidence that genetic factors are important in BRDC prevalence rates.

Although the environment and stress play a major role in BRDC infection rates, there is increasing evidence that susceptibility to BRDC is at least partially under direct genetic control. Differences in BRDC susceptibility have been found between cattle breeds and sire lines, and heritability estimates in the low to moderate range (0.04 to 0.21) have been reported for BRDC susceptibility in beef and dairy cattle (Lyons et al 1991, Muggli-Cockett et al. 1992, Snowden et al 2005, Heringstad et al. 2008, Schneider et al 2009, Neibergs et al 2013, Seabury et al 2014). This suggests that selecting for BRDC resistant cattle could have a substantial impact on BRDC prevalence (Snowden et al 2009). A limited number of quantitative trait loci related to bovine health, including resistance to BRDC, have been reported (Casas and Snowden 2008, Settles et al 2009, Zanella et al 2011). New tools are now available to investigate the role of genetics in diseases such as BRDC that were not available just a few years ago. These resources have now been harnessed to identify the bovine genomic regions associated with BRDC susceptibility so that breeding less susceptible breeding stock can be identified and utilized (Neibergs et al 2013, Seabury et al 2014). The identification of individual genetic differences in cattle that predispose them to enhanced susceptibility to BRDC serves as the basis for selecting cattle that are less likely to become ill as breeding stock. The development of genomic breeding values for sires that are less susceptible to BRDC is underway as part the ongoing USDA-funded multi-institutional research project "Integrated Program for Reducing BRDC in Beef and Dairy Cattle" (www.brdcomplex.org).

To adopt selection as a means of reducing BRDC in feedlot cattle, it must be feasible and profitable for the feedlot industry. The average cost per treatment for cattle with BRDC in feedlots over 1,000 head was reported as \$23.60 by the USDA (2011) but the average number of treatments given per affected animal was not provided. However, for U.S. cattle weighing less than 700 pounds, over 18% did not respond to their first treatment, 4% died, 14.9% were retreated and 2.3% were considered chronic and were subsequently shipped to slaughter prior to reaching a normal slaughter weight. For cattle weighing over 700 pounds, just over 13% did not respond to their first treatment, 3.6% died, 12.4% were retreated and 1.9% were considered chronic (USDA 2011). For light cattle weighing less than 700 pounds treated a second time, 63.1% of cattle responded to treatment, 13.3% died and 12% were treated a third time. For cattle heavier than 700 pounds that were retreated, 69.5% responded, 13.2% died and 17.1% were treated a third time (USDA 2011). Although the exact cost of BRDC to the beef industry is unknown, it has been estimated to be responsible for losses of over \$800 million annually and represents the single most economically important disease of cattle (Chirase and Green 2001, Snowden et al. 2006a, Gagea et al 2006). The aims of this study were to estimate the heritability of BRDC susceptibility in *Bos taurus* feedlot cattle at a commercial facility that did not treat cattle with metaphylaxis, estimate the rate of genetic change that would result from selection for cattle that were less susceptible to BRDC and determine the economic gain of selecting cattle for reduced BRDC susceptibility in the feedlot based on the estimated rate of genetic change.

Materials and Methods

Nine hundred ninety-five *Bos taurus* beef cattle were evaluated using the BRDC diagnostic criteria of McGuirk (2008) and determined to be either affected with BRDC (n=497) or to be unaffected (n=498). Animals' health statuses were defined by clinical signs of fever, cough, nasal discharge, and either ocular discharge or the ear position or head tilt scores (McGuirk 2008). For each clinical sign, a numerical value of 0 to 3 was assigned based on the severity of the clinical signs. Values for ocular discharge and ear position/head tilt were compared and the largest of these values was summed with all of the other clinical score values to reach a cumulative score. Animals with summed cumulative scores ≥ 5 were deemed

BRDC affected and animals with summed cumulative scores <5 were deemed unaffected. The mean clinical score for cases was 8.04 ± 1.23 and the mean score for controls was 2.06 ± 0.037 . All cases and controls were housed together in the same pens until harvest. Weights of animals at diagnosis, finished weights, days until harvest, treatment costs and estimated feed costs were provided for study animals. Treatment costs were based on a one-time injectable antibiotic treatment for BRDC as cattle were not retreated per the policy of the feedlot facility. The steers were marketed as a pen when they reached a finished weight. Six lots were shipped throughout the study period and were followed to processing where the carcasses were evaluated for yield and quality grade. Hot carcass weight was provided for all study animals.

Heritability estimates for BRDC susceptibility were obtained by GenABEL/GRAMMAR (GenABEL.org) from relationship matrixes obtained from genotypes of each animal derived from the Illumina BovineHD assay that contains 778,000 single nucleotide polymorphisms (SNPs). All cattle were steers and consisted of 908 Angus, 18 Charolais, 25 Hereford, and 44 Red Angus. To account for potential breed differences in susceptibility to BRDC, animal breed was fit as a fixed effect in the model used to obtain heritability estimates. Data were filtered for quality at both the animal and SNP level, such that animals with a genotyping success rate of less than 90% (n=63 animals), or SNPs that failed to genotype greater than 95% of the time or that had minor allele frequencies less than 1%, were removed. In addition, animals with ambiguous genetic gender identification (n=3) were removed leaving a total of 932 males and 678,895 SNPs for the analyses. Two different phenotypes for BRDC were used to estimate heritabilities. The first phenotype was a binary case-control phenotype where cases had McGuirk health scores ≥ 5 and controls had scores <5 and will be referred to as the 'case-control' phenotype. The second BRDC phenotype used numerical values of the McGuirk system (that ranged from 0 to 12) as a semi-quantitative phenotype and will be referred to as the 'clinical score' phenotype. The heritability estimate for the case-control phenotype was 17.7% and was 29.2% for the clinical score phenotypes. These estimates were similar to those estimated in previous studies and as estimated by investigators of

the BRDC-CAP for dairy calves (Lyons et al. 1991, Neiberger et al 2013, Seabury et al 2014).

To estimate the rate of genetic change, the equation described by Falconer (1989) was used:

$$\Delta BV / t = \frac{ir\sigma_a}{L}$$

where $\Delta BV/t$ is the rate of genetic change per year, which represents the reduction in BRDC prevalence in feedlot steers, i is the standardized selection intensity, r is the accuracy of selection, σ_a is the additive genetic standard deviation of the trait of interest, and L is the generation interval in years.

The following parameters were assumed to estimate the model. In a typical beef cow-calf operation, the annual cow culling rate is between 13% and 20%, so for this example, we used a cow culling average of 15%. If sexed-semen was not used and half of the calves were heifers, then 30% of the heifers would need to be retained to maintain a constant herd size. This corresponds to a standardized selection intensity coefficient of 1.16. The accuracy of selection was assumed to equal the square root of the heritability for BRDC (42% for case-control and 54% for clinical scores) that would be realized from phenotypic selection. This would form a conservative estimate for the accuracy of prediction of molecular breeding values for susceptibility to BRDC. The genetic standard deviation for BRDC prevalence was based on the following assumptions and calculations: BRDC prevalence in beef steers will vary between operations, seasonally and annually. The USDA (2011) average prevalence of BRDC for feedlot cattle of 16.2% (with a standard error of 1.4) was used as the BRDC prevalence rate. The binomial phenotypic variance of BRDC susceptibility with a prevalence rate of (p) can be calculated as $p(1-p)$ and, assuming that heritability is constant (independent of p), the additive genetic variance for a prevalence p is $VA = h^2p(1-p)$. Thus, for a heritability of 17.7% (case-control) or 29.2% (clinical score), the additive standard deviations for the prevalence rate of 16.2% are $\sigma_a = .1550$ and 0.1991 , respectively. The generation interval (L) for beef cows was estimated at 6 years. Biologically, the shortest possible generation interval is the sum of age at sexual maturity and gestation length, or approximately 2 years of age.

Results and Discussion

The rates of genetic change for the case-control phenotype was 1.26% with a BRDC prevalence rate of 16.2%. The rates of genetic change for the clinical score phenotype was even higher at 2.08% for BRDC as defined by clinical scores (Table 1).

Direct costs attributable to BRDC include declines in carcass quality, death losses, treatment and labor costs, and prevention costs. In this study, losses due to carcass quality and death, and costs for treatment were used to estimate direct costs. Prevention costs (vaccination and best management practices implemented at the feedlot) were identical between BRDC cases and controls and so were not estimated for this study. Labor costs for treating BRDC cases were not provided by the feedlot and so were not included in the direct costs. Table 2 presents the quality grades and death loss data for the cattle affected and unaffected with BRDC. The BRDC cases had a lower number of choice animals compared with healthy animals ($P=0.005$), but a similar number of select carcasses between cases and controls ($P>0.05$). The drop in carcass value shown in Table 2 reflects that the loss in quality grade of BRDC affected animals was not due to a simple slip of quality grade from choice to select, but a more extreme loss of carcass value to that of condemned (\$0 value), railers (carcasses with quality issues that result in a standard value) or animals that died prior to harvest (\$0 value). The average loss in value of BRDC cases compared to controls was \$162.78 per head in 2013.

The average treatment cost of the single BRDC treatment of an injectable antibiotic was \$41.32 per head. Because cases and controls were co-mingled, fed and harvested together, there was no difference ($P>0.05$) between cases and controls on rate of gain, hot carcass weight or yield grade. When treatment costs were combined with the losses due to carcass quality, the estimated total direct cost of each BRDC case in the feedlot was \$204.10.

The average feeder purchase price lost for the cases that died was distributed across all of the cases. This added an additional \$49.87 to the total cost per BRDC affected animal, bringing the total cost to \$253.97. In 2013, 9,131,500 heifers and 16,003,400 steers were harvested from U.S. feedlots that contained 1,000 or more head (<http://quickstats.nass.usda.gov/results/135554B0-FDB3-34F2-A5F9-8ADBF8-BAC18D>) for a total

Factors	Case-Control Phenotype	Clinical Score Phenotype
BRDC prevalence (USDA 2011)	16.2%	16.2%
Estimated heritability	17.7%	29.2%
Accuracy of selection	0.42	0.54
Selection intensity	1.16	1.16
Additive genetic variance	0.155	0.1991
Generation interval (years)	6	6
Rate of Genetic Change in BRDC susceptibility	1.26%	2.08%

Table 1. Factors Affecting the Rate of Genetic Change in Reducing BRDC Susceptibility

of 25,134,900 animals. With the most current national estimate of BRDC prevalence in feed lots of 16.2% (USDA 2011), 4,071,854 feedlot cattle were estimated to be affected with BRDC in 2013. A conservative estimate of the cost of BRDC to the feedlots (based on a single treatment cost, and loss of carcass value) was determined to be \$253.97 per animal or \$1.034 billion in total losses to the feedlot industry. With the current estimates of the rate of genetic gain (1-2%, see Table 1) that could be achieved through selection for cattle that were less susceptible to BRDC, the feedlot industry could realize gains between \$13,030,022 to \$21,509,877 per year based on 2013 costs and market prices, by selecting for cattle that are less susceptible to BRDC.

	Prime	Choice	Select	No Rolls	Condemned	Deads	Railers	Total
Case	16	240	181	10	2	26	17	492
Control	12	286	177	8	0	2	3	488
χ^2	1.26	8.11	0.04	0.46	na	285.27	64.57	980
P-value	>0.05	0.005	>0.05	>0.05	>0.05	0.000	0.000	>0.05

Table 2. Carcass Quality of Bovine Respiratory Disease Complex Cases and Controls

Conclusions

Genomic selection for health traits, such as BRDC, offers new approaches to reduce the prevalence of economically important diseases. New technologies allow the identification of cattle that are less susceptible to BRDC and the opportunity to select less susceptible breeding stock so that the next generation of feedlot cattle will be less likely to be affected with BRDC. The use of molecular breeding values in sires and elite dams has become common for cattle genotyped through commercial companies and/or breed associations. As part of the aims for the ongoing “Integrated Program for Reducing BRDC in Beef and Dairy Cattle” the genomic regions that are predictive of cattle that are less resistant to BRDC will become publicly available. These SNPs will then be

freely available to be placed on commercial genotyping platforms to benefit the beef and dairy industries. Molecular or genomic breeding values for susceptibility to BRDC can be computed for genotyped cattle so that selection decisions based on BRDC susceptibility may be made across the industry. The use of genomic selection offers significant opportunities to reduce BRDC prevalence and gain increased profitability in the beef feedlot industry.

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