What weighting should be given to BRD resistance in selection decisions?

Alison L. Van Eenennaam, and Michael D. MacNeil

Department of Animal Science, University of California, Davis, CA; and USDA, Agricultural Research Service, Miles City, MT, respectively

Introduction

Multiple-trait selection indexes should include all of the economically-relevant traits that influence the profitability of beef cattle production. They provide an economic evaluation of the genetic differences among sires, and an objective way to determine likely differences in the profitability of progeny from different sires. In contrast to the swine, poultry, sheep, and dairy cattle industries, in which economic indexes are a critical component of selection strategies, the US beef industry has made little use of selection indexes (Garrick and Golden, 2009). Some breed associations have produced and published generalized indexes for their breeders, but details concerning the criteria and relative economic weights are not readily available. Wide disparities in the costs of production and different marketing strategies exist throughout the US, making it unlikely that the economic values used in these generalized indexes are universally applicable. However, correlations among breeding objectives that incorporate local prices conditions are generally quite high, making an approximate index perhaps a preferable option to no index at all.

As DNA testing becomes more comprehensive and encompasses a larger number of traits, it will provide a selection tool for traits where no other information or selection criteria exist. There are many economically-relevant traits in this category including cow and feedlot feed efficiency, and disease resistance (Pollak, 2005). This will enable the development of more comprehensive selection indexes that include all of the economically-relevant traits of relevance to U.S. beef production systems. One of the most important of these is likely to be feedlot health.

Almost all US cattle are finished in feedlots. At any one point in time there are around 13.6 million US cattle on feed, and 26 million head were fed in 2009. In the United States, 1.4% of all feedlot cattle perish before reaching harvest weight and of those, the majority are due to bovine respiratory disease (**BRD**). Indeed, more feedlot cattle die from BRD than all other diseases combined, and this trend is increasing. (Lonergan et al., 2001) Bovine respiratory disease accounts for 29% of all US cattle industry deaths and causes annual losses of more than one million animals and $692 million (National Agricultural Statistics Service 2006).

There is growing interest in selective breeding of domestic livestock for enhanced disease resistance. Disease-resistant animals contribute to sustainability goals in that they have improved health, welfare, and productivity (Stear et al., 2001). Understanding the genetic basis for susceptibility has become an increasingly important target for research, especially with the availability of genome sequence. BRD resistance represents an obvious target for selective breeding programs. However as with any trait selection emphasis needs to be weighted by its effect on profitability relative to other economically-important traits. **The objective of this paper was to calculate the weighting that should be given to selection for BRD resistance in a multi-trait selection index for Angus terminal sires.**

Materials and Methods

Methods were based on those outlined in MacNeil (2005) for the development of breeding objectives for terminal sires in U.S. beef production systems. All herd level economic statistics were modeled for a 1000–cow-calf enterprise and retained ownership was assumed. All progeny of terminal sires were harvested and so no economic value was associated with maternal traits. Only phenotypes for weaning weight, feedlot average daily gain, feed intake, USDA yield grade, marbling score and BRD incidence (%) contributed to the breeding objective. The feedlot phase was divided into three periods. The first period (backgrounding) was terminated at a weight-constant end point of 850 lb. The second (growing) and third (finishing) periods were of 50 and 100 days duration, respectively. The genetic parameter estimates and phenotypic characterization used to develop the terminal sire index were those used to develop the Angus Sire Alliance Index detailed in MacNeil and Herring (2005), although the liveweight and carcass prices were updated in 2008, as detailed in Table 1.

Weaned calf weight (lb)	$/lb	Quality/Yield Grade	$/100lb
< 350	1.21	Prime	28.07
351-400	1.15	High Choice	5.53
401-450	1.09	Choice	0
451-500	1.04	Select	-10.20
501-550	1.01	Standard	-20.20
551-600	0.96		
>600	0.92	Yield Grade 1	3.00
Carcass weight (lb)	$/100lb	Yield Grade 2	2.00
Base price	155.95	Yield Grade 3	0.00
<550	-15	Yield Grade 4	-10.20
>950	-15	Yield Grade 5	-20.20

Table 1. Prices, premiums and discounts used in developing the multi-trait selection index for Angus terminal sires.

To parameterize the model to include BRD, the following was assumed: 1) All BRD occurred when calves were moved to the feedlot phase at weaning; 2) the fixed cost of feedlot phase was unchanged; 3) a dead calf incurred no feed costs; 4) there was a 10% mortality from BRD (Holland et al., 2010; Reinhardt et al., 2009) 5) there was a 13% reduction in ADG (1.3 lbs/d) for the first phase of feeding (weaning to 850 lbs; (Holland et al., 2010); 6) final yield grade was reduced by 0.1 (Garcia et al., 2010; Reinhardt et al., 2009); and 7) the cost to diagnose and treat a BRD calf was $44 (Randall Raymond DVM, Simplot Land and Livestock, personal communication).

To obtain the genetic standard deviation for BRD incidence the following calculations were made. The phenotypic variance of the binomial at a mean incidence of 10% was calculated to be $p(1-p) = 0.09$. A binomial scale heritability of 0.07 (Snowder et al., 2006) was applied to get a genetic variance of 0.0063, or a genetic standard deviation of 0.0794. Transforming from decimal to a percentage resulted in a genetic standard deviation of 7.94.
Economic values were calculated by performing bio-economic simulations using a modified version of the computer software described by MacNeil (1994). The main modification was that harvest phenotypes were generated stochastically, and steers were valued based on a multivariate normal distribution of marbling, yield grade, and carcass weight. In separate simulations, the phenotypes for each of the economically relevant terminal sire traits were changed by one unit. The difference between simulated profit with a phenotype perturbed by one unit and profit in the baseline simulation was taken to be the economic value for that trait (Table 2). The results are

expressed on enterprise basis, rather than per cow exposed or progeny produced. To provide some indicator of the relative magnitude of the economic values, each economic value was multiplied by the corresponding trait genetic standard deviation to give the relative economic value (REV). To simplify trait comparisons, each REV was divided by the REV for the trait with the smallest value (i.e. yield grade in this index), and the absolute value of that calculation is shown as "Relative Importance" in Table 2.

Results

Table 2. Enterprise economic values, relative economic value, and relative importance of economic values for traits in the terminal sire breeding objective.				
Trait (unit)	Economic Value ($)	Genetic SD	Relative economic value (REV)	Relative Importance (relative to YG)
BRD incidence (%)	-8424.7	7.94	-66892	37.7
Weaning wt. (lb)	241.4	41.76	10081	5.7
Feed Intake (lb/d)	-5811.8	1.41	-8195	4.6
Feedlot ADG (lb/d)	27654.5	0.24	6637	3.7
Marbling score	8926.0	0.51	4552	2.6
Yield Grade	-5379.2	0.33	-1775	1

Selection index methodology is designed to weight traits by their economic merit. Following Henderson (1963), the appropriate terminal sire selection index weighting for EPDs the economically-relevant traits listed in Table 2 would be the economic value for each trait. The REVs suggest that to maximize the profitability of the commercial production system modeled in this study, BRD incidence should be very heavily emphasized in terminal sire selection, followed by a relatively uniform emphasis on weaning weight, postweaning average daily gain and feed intake, and less emphasis should be placed on marbling score and yield grade.

This emphasizes the economic importance of BRD on feedlot profitability. It should be noted that other potential benefits were not considered in these calculations. These include reduced shedding and transmission of pathogens from resistant hosts, and externalities like improved animal welfare and public support for the decreased use of antibiotics in food animal production.

The values derived in this study were for terminal sire selection. There is a higher relative importance of maternal traits compared to feedlot and carcass traits, when the goal is to produce herd replacements. Melton (1995) suggested that US cow-calf producers keeping replacement heifers and selling calves at weaning should have a relative economic emphasis of 47% on reproduction, 24% on growth, and 30% on carcass traits, whereas producers in an integrated system should have a relative economic emphasis of 31% on reproduction, 29% on production, and 40% on carcass traits. This relative emphasis will depend on how much the value derived from genetic gain in feedlot and carcass traits is shared with the producer in the integrated system.

Discussion

Our preliminary data based on this terminal sire selection index suggest that there would be considerable value associated with the successful development of DNA tests to enable selection for BRD resistance. This index was developed to maximize the profitability of the entire industry as though it were one vertically integrated production system. In reality, even though nearly all US calves go through the feedlot and are sold on a carcass quality basis, most commercial producers market their calves at weaning or shortly thereafter. Ninety percent of US cattle operations (692,050) have fewer than 100 head, and most sell their cattle at auction prior to feedlot entry. Consequently, producer financial returns are tied very closely to the number of calves, a function of reproduction, and less to feedlot performance and health, and even less to carcass traits. To incentivize the inclusion of BRD resistance in selection decisions, a mechanism analogous to a calf preconditioning bonus would be needed to equitably share some of the value derived from reduced feedlot disease incidence and to compensate breeders and producers for reduced selection emphasis on other economically-relevant traits.

There are a number of issues that will need to be addressed in the development of DNA tests for BRD resistance. The first is that disease resistance heritabilities tend to be low, especially under field conditions. There a number of reasons for this including suboptimal diagnosis (e.g. not all sick animals are identified and healthy animals may be incorrectly diagnosed as ill), and some susceptible animals will appear resistant to a disease when in fact they have not been exposed to the disease agent (Bishop and Woolliams, 2010). These factors add environmental noise to field data. Field studies therefore likely underestimate heritability, and thus also undervalue the potential gains that could be made by breeding for disease resistance (Allen et al., 2010).

Evidence that BRD susceptibility/resistance is under genetic control is demonstrated by breed differences in BRD morbidity and mortality, the fact that BRD prevalence in unweaned calves and feedlot cattle is heritable, and the finding of genomic regions that have been shown to be associated or "linked" with BRD incidence. Prior to entry into the feedlot, the incidence of BRD in weaned calves varied by breed from a low of 10% in Angus to a high of 35% in Pinzgauer (Snowder et al., 2006). Mortality also differs by breed, ranging from 0.1% in Braunvieh cattle to 8.9% in Red Poll cattle. Susceptibility differs among various breeds, ranging from 28% in Braunvieh to 73% in Hereford. Heritability estimates also suggest there is a genetic underpinning of the disease. The heritability estimate for feedlot animals was 0.18, when adjusted to an underlying continuous scale (Snowder et al., 2006).

BRD susceptibility is most likely a complex genetic trait governed by the effects of many genes. This suggests a large number of cases and controls will be needed to detect all of these variants and so datasets for disease resistance marker discovery will need to be comprised of observations on several thousands of individuals (Amos et al., 2011).

On the positive side, obtaining markers that track disease resistance loci relies on "linkage disequilibrium" (LD) between DNA makers and the causative loci. Fortunately cattle have long stretches of LD and it is thought that the new generation of high density SNP arrays (e.g. Affymetrix Bovine 650K, Illumina Bovine 770K HD SNP Array) will provide adequate coverage of the bovine genome to track loci that are associated with disease susceptibility (Allen et al., 2010). It is also hoped that these high density arrays will enable the development of tests that can work across multiple-breeds.

With the less dense (i.e. 50,000 SNP) marker panels, a marker associated with a trait in one breed was not associated in the same way in another breed (Figure 1A). The reason for this is that the SNP marker could be located a "long way" from the gene and so in some breeds it was not associated or "linked" with the variant of the gene causing a given phenotype. By increasing the number of SNP markers to > 700,000, markers are more closely spaced and there is a greater likelihood of finding SNPs that are close to the gene (red markers in Figure 1B), and hence the marker will "work" in both breeds.
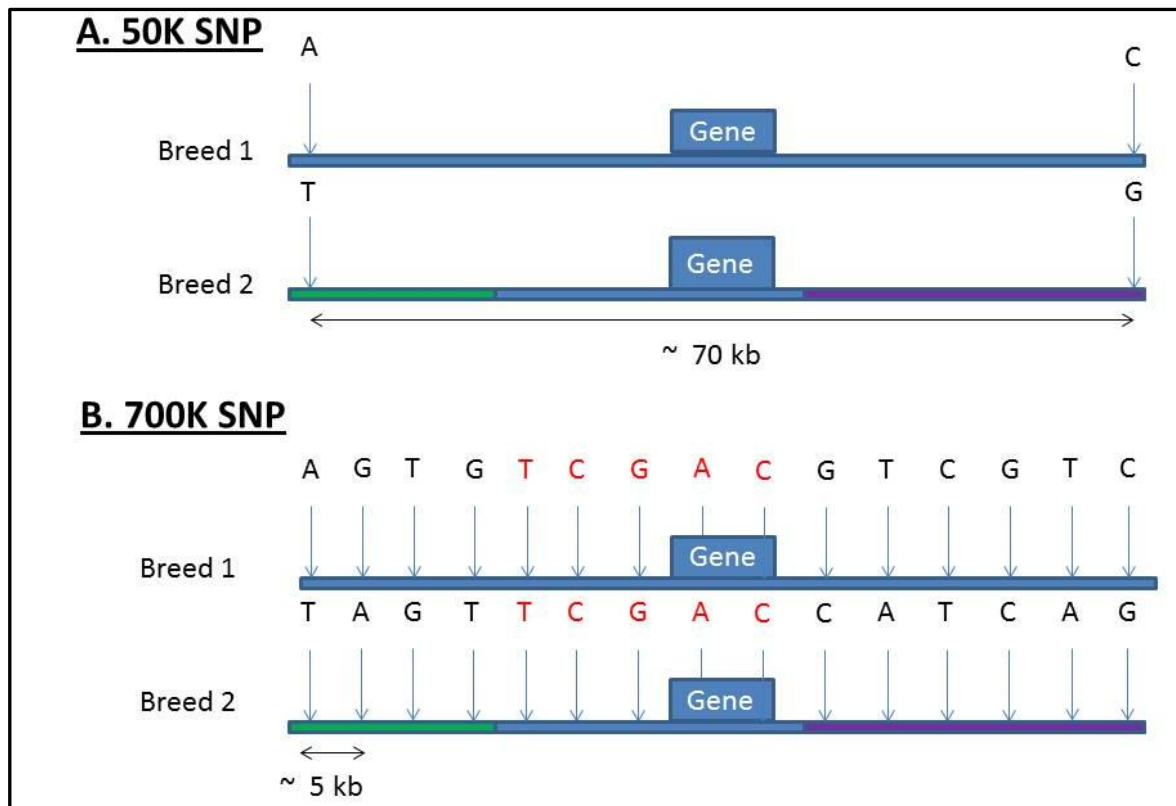

Figure 1. Marker location relative to the gene of interest in two breeds when using (**A**) the 50K SNP marker panel (markers spaced at 70 thousand base pair (70 kb) intervals), or (**B**) the high-density 700K SNP marker panel (markers spaced at approximately 5 thousand base pair (5 kb) intervals).

In cattle it has been estimated that SNPs need to be spaced less than 10 kb apart to show consistent LD phase across breeds (de Roos et al., 2008). These high density bovine marker panels also provide an opportunity for multiple *Bos taurus* breeds to pool information and records. Developing large multi-breed training data sets for disease phenotypes may collectively improve the accuracy of tests for all breeds, more than any single breed can do on its own due to the larger number of combined records. These high density bovine marker panels also provide an opportunity for breeds to pool information and records (Figure 2).

In dairy cattle, selection programs have been developed to take advantage of genetic variability in mastitis resistance, despite the fact that the heritability of clinical mastitis is low and mastitis resistance has an adverse correlation with production traits (Rupp and Boichard, 2003). Likewise chicken breeders have long used breeding to improve resistance to avian lymphoid leucosis

complex and Marek's disease (Stear et al., 2001). Recent developments in molecular genetics and genotyping platforms offer a unique opportunity to use modern genomic tools to manage the future health of beef cattle. Developing large multi-breed training data sets for disease phenotypes may collectively improve the accuracy of tests for all breeds, more than any single breed can do on its own due to the larger number of combined records. Reducing the considerable animal morbidity, mortality and economic losses associated with BRD will require the simultaneous development of DNA tests to enable the selection of resistant animals, and the incorporation of this trait into breeding objectives of relevance to U.S. beef production systems.
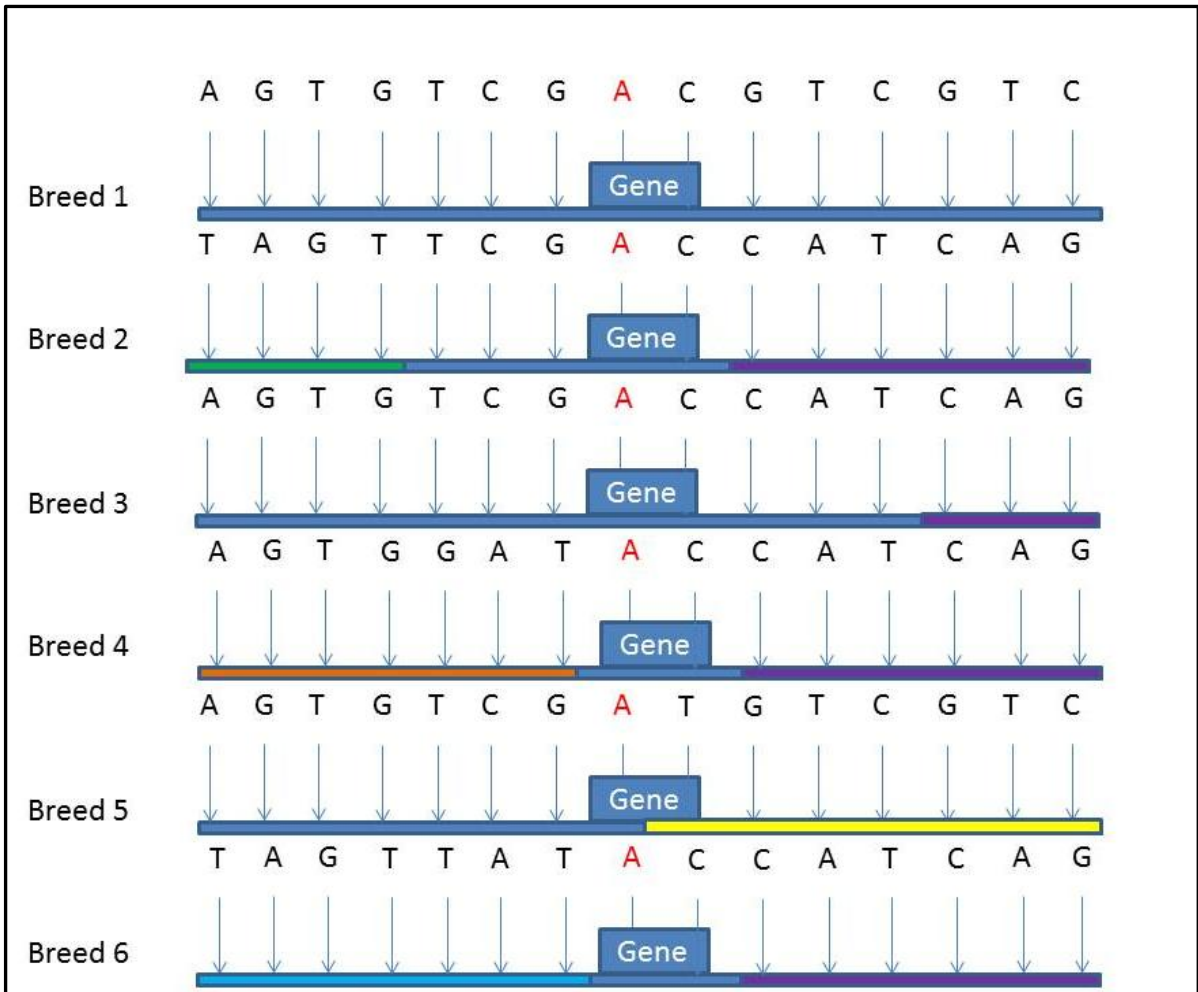

Figure 2. High density SNP marker panels may enable the discovery of the causal mutations underlying genetic variation (i.e. red "A" SNP located in the gene).

"We now stand at a defining moment in the history of agriculture wherein we can use modern genomic tools to subtly influence the future evolution of the animals we have farmed for thousands of years." (Allen et al., 2010)

Acknowledgements

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