Proceedings, The Range Beef Cow Symposium XXI
December 1, 2 and 3, 2009, Casper, WY

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USING INFORMATION TO MAKE INFORMED SELECTION DECISIONS

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INTRODUCTION

The information available to beef cattle producers for making selection decisions is constantly increasing. It is not unusual to open a sale catalog and quickly become overwhelmed with a plethora of data ranging from Expected Progeny Differences (EPD) to actual weights and ultrasound measurements, to marker panel results, and even within herd subjective scores and ratios for a variety of traits. Not all information is equal in the context of advancing the genetic potential of the next generation. Furthermore, some of this information is rapidly changing in terms of reporting styles and usefulness in distinguishing genetic differences between animals. Consequently, it is critical to understand the differences between sources of information, their limitations, and in some cases, their future potential.

BACKGROUND

The first EPDs were released to the US beef cattle industry approximately three decades ago, and have allowed for considerable genetic change, particularly with regard to growth and carcass traits. Now the list of available EPDs has grown to include things such as heifer pregnancy, docility, calving ease, and some measures of input (i.e. the Red Angus maintenance energy EPD). Not only has the list of available EPDs grown, but the tools from which producers can use to make selection decisions has also grown to include economic index values and molecular- based tools such as marker panels.

One challenge with currently available information is the disparity between respective breed associations in information collected, reporting styles, and advancements in technology adoption. There is no doubt that industry-wide progress could be made at a faster rate if some level of uniformity was achieved. This paper is not designed to be an all-inclusive discussion of what is available by breed, but rather an industry-wide look at the current tools we have a directions we need to go.

AN EXPANDING TOOL BOX

Bio-economic Index Values

Economic index values are one tool the US beef industry adopted for the purpose of multiple-trait selection. A bio-economic index (H) is simply a collection of EPDs that are relevant to a particular breeding objective, whereby each EPD is multiplied by an associated

economic weight (a). For example, the economic index value H can be written

$H = EPD_1a_1 + EPD_2a_2 + EPD_3a_3 + ...,$

where EPDs 1, 2, and 3 are multiplied by their corresponding economic weight and summed. Consequently, a high index value does not necessarily mean that an animal excels in all EPD categories given that superiority in trait can compensate for inferiority in other traits depending on how the EPDs are weighted in the index. A high index value should be thought of as excelling in the ability to meet a breeding objective. These index values do not have a measure of accuracy directly associated with them because each EPD is weighted differently in the index and it is not statistically possible to weight the accuracy values. Like EPDs, they can easily change overtime with the addition of new information (i.e. progeny records) as the component EPDs change. It is important to note, however, that before proper use of an index can be ensured, a breeding objective must be clearly identified. For example, the use of an index such as the American Angus Association's Dollar Beef ($B) in an enterprise that retains replacement heifers can lead to adverse effects, given that sire selection pressure has been placed on terminal traits via $B.

The majority of economic index values are rigid (i.e. not catered to individual enterprises). A much more desirable method would use individualized index values where the bull with the highest index value may differ from one herd to the next, depending on how the animal fits the specific needs of each enterprise. While this would lead to more accurate identification of parents for the next generation, it becomes a challenging metric to use for advertisement purposes in the seedstock industry, which probably explains why this more fluid method of multiple-trait selection has not been exploited by the majority of breed associations. For example, it is possible to advertise that a bull is in the top 1% of the breed for $B, but if an index parameters are partially defined by the prospective bull buyer or semen user the most desirable bull for that producer may not be the best for other producers. There are two primary cases to the contrary. One would be the interactive Terminal Sire index produced by the International Charolais Association, and another would be the decision support program developed at Colorado State University. However, for these types of tools to be truly effective, they must constantly be updated in light of novel traits that will potentially become the focus of selection programs in the future (i.e. metrics of efficiency, end-product healthfulness, disease susceptibility, etc.).

Molecular Information: Paternity and Simply Inherited Traits

Molecular based tools are another source of information that has received considerable attention by producers throughout the beef industry and by both the academic community and private sector. These tools initially came in the form of candidate genes but have now grown to the inclusion of multiple markers called Single Nucleotide Polymorphisms (SNP). The use of molecular information has grown from simple applications such as identifying animals that are carriers of the red allele to identifying animals that are carriers of lethal genetic defects, to paternity assignment, and a growing number of diagnostic tests for a suite of complex traits ranging from reproduction to carcass.

Genotyping to determine parentage allows for a sire to be correctly linked to a corresponding

calf. The identification of an animal's sire via DNA marker technology can be advantageous in multi-sire breeding pastures, or for ascertaining if a calf is the product of an artificial insemination (AI) mating or a clean-up bull. This promotes knowledgeable culling and breeding decisions by determining which sire(s) are contributing the most (or least) to a particular breeding objective. In the case of commercial ranch settings, for example, it may be beneficial to determine the sire that is responsible for calving difficulties.

Because paternity identification is a process of excluding potential sires on the basis of their genotype, it is important that DNA from all possible sires be included in paternity tests. It will be more difficult to definitively make paternity assignments on closely related bulls in a multiple-sire breeding pasture, given they are likely to share a similar genotype. Although microsatellites have typically been the marker of choice for paternity analysis, the use of SNP markers is becoming more common for a number of reasons including their abundance, high potential for automation, low genotyping error rates, and ease of standardization between laboratories.

Although identifying carriers of genetic defects is a rather simple application of DNA technology, it is an important tool when making mating decisions. We know that afflicted anjmals can only arise if two carrier animals are mated. In this scenario there exists a 25% chance that the corresponding calf will have the defect. Unfortunately this added information has been used as the primary selection tool whereby carrier animals are automatically discarded. If a producer potentially has carrier females, then carrier bulls should be avoided. However, if this is not the case, then it could be beneficial to use the best available bull, regardless of his status as a carrier. As an industry we have the ability to make informed decisions based on science concerning this issue and not throw away animals that are superior across the remainder of their genome because they have a flaw that we can effectively manage around.

Molecular Information: Complex Traits

Several advancements in this technology have occurred with regard to complex traits (i.e. production, carcass, and reproduction traits) including the number of markers included in a given panel, reporting styles of the results, the number of traits for which a diagnostic test exists, and recently, the inclusion of this information for the first time in National Cattle Evaluation (NCE) in the Angus breed.

The promise of the inclusion of marker information into EPD calculations holds three primary benefits:

1. Increased accuracy for young animals (i.e. yearling bulls), which is particularly beneficial when selecting on traits that are measured late in life (e.g., stayability)
2. Shortened generation intervals
3. EPD values for novel traits (i.e. efficiency, end-product healthfulness, disease susceptibility) that may have, at best, sparse collection of phenotypes

The uncertainty surrounding early predictions of genetic merit arise as a result of Mendelian sampling. Every animal is passed a random sample of alleles from each parent, half coming from the dam and half from the sire. We have an estimate of the average effect of what was passed from parent(s) to offspring in the form of pedigree estimates, but the certainty with

which we know this estimate is correct (i.e., the accuracy) is low. As more information is collected, such as an individual's own record and data from progeny, accuracy increases. For lowly heritable traits like measures of reproduction, it can take a considerable number of offspring to reach high BIF accuracy levels, given that the BIF scale is more conservative than true accuracy (r) as illustrated in Table 1. To calculate r in the context of progeny test sires the following equation can be used where *n* is the number of progeny:

$$r = \sqrt{\frac{nh^2}{4 + (n-1)h^2}}$$

To convert BIF accuracy to true accuracy (r) the following equation can be used:

$$r = \sqrt{1 - (1 - BIF)^2}$$

Table 1. Approximate number of progeny needed to reach accuracy levels (true (r) and the BIF standard) for three heritabilities (h^2).

Accuracy		Heritability Levels		
r	BIF	h^2 (0.1)	h^2 (0.3)	h^2 (0.5)
0.1	0.01	1	1	1
0.2	0.02	2	1	1
0.3	0.05	4	2	1
0.4	0.08	8	3	2
0.5	0.13	13	5	3
0.6	0.2	22	7	4
0.7	0.29	38	12	7
0.8	0.4	70	22	13
0.9	0.56	167	53	30
0.999	0.99	3800	1225	700

One primary benefit of molecular information is that it can be garnered much earlier in life (before a phenotypic record can be collected). This knowledge can, in part, reveal a portion of the black box that is Mendelian sampling in young animals. This results in higher accuracy values for young animals, which potentially increases the use of these younger animals in seedstock systems, thus decreasing the generation interval. The equation below predicts the rate of genetic change per year and is dependant on selection intensity, the accuracy of selection, genetic variation, and the length of the generation interval. From this it is apparent that if the generation interval is decreased this will lead to faster genetic change given that generation interval is in the denominator of the equation.

$$\frac{[(\text{Accuracy of Selection}) * (\text{Selection Intensity}) * (\text{Genetic Standard Deviation})]}{\text{Generation Interval}}$$

However, the magnitude of these benefits will depend on the proportion of variation explained by a given marker panel. At present, the best objective source of information regarding this is the National Beef Cattle Evaluation Consortium (NBCEC) website (www.nbcec.org). Admittedly, these results can be cumbersome to utilize and represents yet another reason why these MBVs should be incorporated into EPD calculations. However, in the context of these molecular results being disjoined from EPDs it is critical to understand how to interpret independent validation results. Pertinent information from this website includes: population, trait, regression coefficient (b) and the p-value (p). The population defines what breed(s) were used to validate the test. If the test was validated in *Bos taurus* animals then it is possible that the test will not explain the same proportion of variation in *Bos indicus* animals. The trait defines what the test was validated for. If it is a metric of efficiency like residual feed intake (RFI) then it will explain how the trait is defined. The b and p values can be more confusing. Generally a p-value of less than 0.05 suggests that the test is a statistically significant predictor of differences in phenotypes. The regression coefficient is equal to the regression of phenotypes for the trait of interest on the molecular score. It explains the units of change in the phenotype that would be expected for a one unit change in the molecular score (i.e. MBV). Ideally these b values should be 1. For example, if two animals have molecular scores for RFI of -1.5 and 1.0, respectfully, the difference between those scores is 2.5. Normally we would expect that, on average, these two animals' phenotypes would differ by 2.5 lb of RFI. However if the regression coefficient is 0.4 then we would expect their phenotypes to differ by 1 lb (2.5*0.4).

Without the seamless integration of this technology into EPD calculations, we find ourselves in the current context of being faced with two disjoined pieces of information: traditional EPD and marker panel results. In this scenario, it is impossible to directly compare EPDs to marker panel results even if the results come in the form of Molecular Breeding Values (MBVs). This is because the molecular scores only explain a portion of the additive genetic variation. Further, some of the marker panel results have a metric of accuracy associated with them. At the current time, this metric is not comparable to the Beef Improvement Federation (BIF) accuracy value associated with EPDs simply due to differences in the way they are computed. While it is logical that the accuracy value of a MBV should be related to the proportion of additive genetic variation explained by the test there is not a standardized metric that is being used. Thallman et al. (2009) analyzed different methods of calculating this proportion for MBVs in light of the fact that there is not a standardized method and recommended the use of the square of the additive genetic correlation between the MBV and the trait of interest.

In contrast to the thought process of DNA marker panel results being a separate and disjoined piece of information, these test results should be thought of as a potentially useful indicator that is correlated to the trait of interest. As such, the MBV can be included in NCE as a correlated trait following methods of Kachman (2008). Other methods have been proposed including using large (50,000+) SNP panels to form a genomic relationship matrix that could allow for known relationships between animals based on genotypes across SNP loci. Combining these sources of information, molecular tools and traditional EPDs, has the potential to allow for the benefits of increased accuracy and increased rate of genetic change as discussed earlier.

MacNeil et al. (2009) utilized Angus field data to look at the potential benefits of including both ultrasound records and MBVs for marbling as correlated traits in the evaluation of carcass marbling score. MacNeil and colleagues used a 114 SNP marker panel that was developed using 445 Angus animals and calculated to have a genetic correlation (r) of 0.37 with marbling (i.e. the test explained $(0.37)^2 = 0.137$ or 13.7% the additive genetic variation). For animals with no ultrasound record or progeny data, the marker information improved the BIF accuracy of the Angus marbling EPD from 0.07 to 0.13. Assuming a heritability of 0.3 for marbling, a BIF accuracy of 0.13 is equivalent to having approximately 5 progeny carcass records on a young animal or an ultrasound record on the individual itself. In this particular study, both ultrasound records and MBVs were found to be beneficial indicators of carcass marbling. The genetic correlation between MBVs and ultrasound was found to be 0.25. Some breeds have begun to integrate this technology and it is likely that more will do so in the future. In July of 2009, the American Angus Association entered into an agreement with IGENITY® to develop Marker Assisted EPDs (MA-EPDs) by integrating DNA marker results into their NCE. These MA-EPDs will be implemented beginning in the fall of 2009.

CONSIDERATIONS

Current marker panels are likely to work best in the populations where discovery occurred, but will potentially decrease in predictive power as the target population becomes more genetically distant from the discovery population (de Roos et al., 2008). This however has yet to be thoroughly tested in beef cattle populations although there are existing projects that are currently working to answer this question (Pollak et al., 2009). Below is an example of scenarios where the discovery population is close to the target population and progresses to more distant populations.

Discovery	Target	
Angus	Angus	Closest relationship
Angus	Charolais	↓
Angus	*Bos indicus*	Most distant relationship

Marker panels are likely to become larger in the future with the possibility of whole genome selection (WGS). Currently, genome selection in beef cattle is in its infancy. Although preliminary data from the dairy industry look promising (VanRaden et al., 2009), the structure of the beef industry offers unique challenges. It is not known how well this approach will work in beef cattle with its diversity of breeds, diverse sector-specific selection goals, and less extensive phenotype and data collection resources. A final issue is the fact that fruitful integration of this information into genetic prediction requires all entities to work in concert including breed associations, seedstock producers, scientists, extension personnel, and commercial testing companies. This, unfortunately, is no small task. Current NBCEC projects are designed to explore many statistical and computational caveats related to the integration of this information and also to bring all critical parties together to work towards successful integration of molecular information (Pollak et al., 2009).

CONCLUSION

Although there is a considerable amount of information from which to make selection decisions, it is clear that some sources are more desirable than others if the goal is genetic improvement. It is likely that the list of genetic selection tools will continue to expand in the short term as this arena is far from stagnant. Although the goal is the consolidation of information into one of two basic forms, EPDs and economic index values, it is likely that there will be several intermediate steps in an effort to quickly commercialize technology that will create confusion. For those who have not yet adopted thirty-year-old technology such as EPDs, the inherent selection mistakes that have been made in the past will only be exacerbated in the future when the accuracy of genetic predictions of young animals is increased. And, as molecular-based EPDs are developed for phenotypes not usually measured the need to utilize EPD technology will be even greater.

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