National Beef Cattle Evaluation Consortium (NBCEC) White Paper - Delivering Genomics Technology to the Beef Industry

Introduction

Artificial selection of cattle has been practiced for centuries using a variety of methods and tools. Early selection was based on visual observations that eventually lead to the development of breeds. In efforts to improve production, selection was practiced on measured phenotypic traits with limited success depending on the heritability of the trait. The next big breakthrough in selection tools was the development of statistical methodologies and computer hardware, capable of handling large data sets, to estimate the breeding values of cattle, the tool known in the U.S. as Expected Progeny Differences (EPD). Widespread usage of EPDs in the seedstock and commercial beef sectors has lead to great increases in the genetic propensity of beef cattle for a variety of traits including calving ease, growth and carcass composition.

Expected Progeny Differences are data-driven computations and the accuracy of an individual EPD is based on the amount of information used to estimate that EPD for an individual. For this reason young, unproven bulls have EPDs with low accuracy values, indicative of a greater range of possible change as more data is collected on the bull. As more data is collected on a bull, particularly progeny information, his accuracy value rises and his possible change reduces. Given that commercial bull buyers do not have the advantage of seeing their natural service sires increase in accuracy (commercial records are not currently included in National Cattle Evaluations), tools that could increase yearling bull accuracies would be advantageous.

In the late 80's and early 90's technologies were beginning to develop that allowed access to the genetic code of living organisms. Based on these discoveries the beef industry soon developed genomic based predictors for a limited number of traits, initially reported as candidate genes. The appearance of these "markers" alongside EPDs in many sales catalogues created confusion among producers, in some cases, relative to making selection decisions. Which do I use: genomic-based predictors or EPDs? As genomics technology advanced it became increasingly tempting to visualize a day when a drop of blood or a hair follicle could be analyzed to tell us all we needed to know about an animal to make completely informed selection decisions. Despite considerable progress in the arena of genomics based selection tools over the past 20-plus years, including the mapping of the bovine genome, genomics has not developed into a standalone tool to replace EPDs.

It seems the more we know about bovine genomics the more questions we have about how to properly use the information in selection decisions. This white paper will establish how genomic information can be successfully utilized in selection programs, identify challenges associated with genomic technology and outline promising potentials for its future use.

Current Usage of Genomics Technology in Beef Cattle Selection

Parentage

A critical factor in estimating reliable EPDs is the proper determination of parentage. Errors in pedigree structure may have significant negative impacts on the reliability of genetic evaluation in which they are used and the potential genetic gains (Geldermann et al., 1986; Israel and Weller, 2000). Increases in misidentification of an animal's parentage results in progressively more biased estimates of genetic parameters and this bias severely compromises potential genetic gains from selection (Van Vleck, 1970; Senneke et al., 2004). Incorrect pedigree information, or the breaking of genetic ties, leads to a decreased estimate of heritability and incorrect estimates of EPDs particularly for individuals with incorrect parentage. By utilizing genomic technology to determine parentage these inaccuracies can be greatly diminished (Dodds et al., 2005). There are currently two methods being utilized to ascertain parentage; microsatellites and SNPs. Both methods provide a probability of parentage which is influenced by the sensitivity of the test and the relationship of the potential parents.

Utilizing genomics for parentage allows seedstock producers to manage multiple sire breeding pastures and settle AI/natural sire discrepancies when birth dates are inconclusive. Genomics parentage testing enables an increase in the amount of information used to estimate an animal's genetic merit thereby improving the accuracy of prediction of the estimate although not necessarily affecting the predicted value (Davis and DeNise, 1998). The use of genomics parentage testing to resolve the paternity of calves produced by multi-sire breeding systems with subsequent use of their pedigree and phenotypes in a progeny test genetic evaluation has been proposed (DeNise, 1999; Goddard and Goddard, 1997). More recently, genomically derived pedigree structures coupled with strategically collected performance records have been used to compute EPD for both seedstock and commercial producers (Weaber, 2005; Van Eenennaam et al., 2007).

Qualitative Traits (Identifying Carriers)

Markers for many qualitative traits (traits controlled by a single pair of genes that have simple recessive inheritance) such as coat color, horned/polled and a variety of genetic defects have been identified and are commercially available. This technology can now be used to identify cattle that are carriers of recessive genes facilitating selection against the carriers, if desired; or make more informed mating decisions. There are certainly some convenience and potentially economic benefits to producing an all polled calf crop or calves with a uniform coat color. However, the greatest value of these tests is to identify and manage lethal recessives; this technology has saved the beef industry countless dollars.

Historically, when lethal recessives were identified the common method of eliminating them from the population was an aggressive culling campaign, often eliminating entire lines of cattle. On November 15, 2008 the American Angus Association (AAA) recognized Arthrogryposis Multiplex (AM) as a genetic defect that had emerged in the breed and on June 12, 2009 the same determination was made for Hydrocephalus (NH). Within a relatively short time after each defect was identified, genomic markers were identified to clearly distinguish heterozygous (carrier) animals from those that were homozygous normal. Animals within the

affected lines could then be eliminated, without the complete elimination of a prominent line of Angus cattle. Genomic tests for most cattle breeds are available to identify deleterious recessive genes in their respective populations, thus generating immeasurable value to the beef industry.

Quantitative Traits

Commercially available tools have been developed to select cattle for quantitative traits (traits controlled by multiple pairs of genes and influenced by the environment). Breeding values based on genomics information for a variety of traits are now available from multiple commercial companies and can be used as selection tools. However, there is no evidence to suggest that these tools provide a better selection tool than EPDs and the likely best use of this information is to combine it with phenotypic information in a genetic evaluation to compute *genomically enhanced EPDs*.

There are four basic ways of combining genomic and phenotypic information into a single selection tool. The first method is to compute independent values, both EPDs and molecular breeding values (MBVs), and to then include both pieces of information in a selection index whereby each "trait" is weighted proportionally to the respective amount of genetic variation. A second approach is through genomic relationships whereby marker information is used to fit a genomic relationship matrix (relationship among animals at the Single Nucleotide Polymorphism (SNP) level) that is used to augment estimated relationships based on pedigree information. For this method it is necessary to know the actual SNP genotypes rather than having a marker score or MBV. This method is currently being used in dairy genetic evaluations. The first method deployed by the beef industry, and which is currently used by the AAA, is the correlated trait approach. MBV information is included in National Cattle Evaluation (NCE) as a correlated trait (Kachman, 2008), similarly to the way ultrasound information is utilized in a multiple trait model in the estimation of EPDs for carcass traits. As the genetic correlation between the indicator trait, MBVs in this case, and the trait of interest increases so does the EPD accuracy, particularly for younger (lower accuracy) animals. The final method is to treat MBVs as if they were external EPDs (EPDs from an animal that is external to the population or breed). This method is currently being used by the American Simmental Association and allows for MBVs to influence the accuracy of EPDs differently for each animal due to the relationship between the animal with the MBV and the training population.

The magnitude of the benefits will depend on the proportion of genetic variation (%GV) explained by a given marker panel, where the %GV is equal to the square of the genetic correlation multiplied by 100. Table 1 shows the relationship between the genetic correlations (true accuracy), %GV and Beef Improvement Federation (BIF) accuracy. BIF accuracy is the standard for all U.S. beef breeds. Table 2 summarizes the genetic correlations for the two tests that AAA currently utilizes.

Table 1. The relationship between true accuracy (r), proportion of genetic variation explained (%GV), and Beef Improvement Federation (BIF) accuracy.

r	%GV	BIF
0.1	1	0.005
0.2	4	0.020
0.3	9	0.046
0.4	16	0.083
0.5	25	0.132
0.6	36	0.200
0.7	49	0.286

Table 2. Genetic correlations (r_g) between traits and their genomic indicators used by the American Angus Association (by company).

Trait	Igenity r_g (384 SNP)	Pfizer r_g (50K SNP)
Calving Ease Direct	0.47	0.33
Birth Weight	0.57	0.51
Weaning Weight	0.45	0.52
Yearling Weight	0.34	0.64
Dry Matter Intake	0.45	0.65
Yearling Height	0.38	0.63
Yearling Scrotal	0.35	0.65
Docility	0.29	0.60
Milk	0.24	0.32
Mature Weight	0.53	0.56
Mature Height	0.56	0.56
Carcass Marbling	0.65	0.57
Carcass Ribeye Area	0.58	0.60
Carcass Fat	0.50	0.56
Carcass Weight	0.54	0.48

Although AAA was the first to augment their EPD with genomic information, several other breeds have shown interest in taking advantage of this technology. Saatchi et al., (2011a and 2012) has shown moderate to high genetic correlations between several traits of interest and MBV for Hereford and Limousin (carcass traits only). Kachman et al., (2012) used growth traits (weaning weight and yearling weight) to illustrate the efficacy of BovineSNP50 (50,000 SNP assay) based MBV when the MBV was evaluated in the same breed as training (process of developing prediction equations using significant SNP above some threshold) and when it was evaluated in a different breed than training. The authors showed that when the MBV is used in the same breed that it was trained in, typical genetic correlations were between 0.28 and 0.42. However, the same authors found that when a breed-specific MBV was used in a different breed, the genetic correlations clustered around zero. This shows the unfortunate breed specificity issues surrounding these tools, which leads to the current reality that these tests are breed

specific. This is consistent with other results that show the predictive power of MBV begin to erode as the genetic distance between the training and target (or evaluation) populations increase (Ibanez-Escriche et al., 2009; Toosi et al., 2010).

Challenges to Adoption of Molecular Information

An early, and ongoing, challenge relative to technology adoption is a general understanding and familiarity with genomics. To increase the knowledge base and aid in the adoption of genomics, an integrated project referred to as the Weight Trait Project (WTP) was initiated in 2009 as a means of educating the US beef industry about the utility of genomics tools and to build a resource population for development and evaluation of methodology for incorporating molecular information into NCE. Twenty-four seedstock producers from the Northern Plains region of the US were nominated by their respective breed associations to participate in the WTP. These seedstock producers represent Angus, Red Angus, Charolais, Gelbvieh, Hereford, Limousin, and Simmental. As part of the WTP, they collected hair samples on the natural service (NS) sires and other animals used in their herds as a source of DNA for genotyping and a wide array of phenotypic data are collected on the progeny. The population has evolved into a valuable resource for demonstrating the efficacy of genomically enhanced EPDs on traits of economic importance. Through this ongoing integrated effort, key technology adopters are able to learn by doing, using their own animals as a demonstration of genomic predictors and methodology.

Although genomic information has the potential to generate value for each sector of the beef cattle industry, it must have an economic driver outside of seedstock advertisement. The value distribution among sectors (seedstock, commercial, feedlot, processing) will differ depending upon marketing, with fully integrated operations having the greatest opportunity to claim the return on investment. Using genomic tests to increase the accuracy of selection in the nucleus seedstock sector has the potential to generate large returns throughout all sectors. Improving the accuracy of EPDs on elite young seedstock animals will accelerate the rate of genetic gain and impact the genetic merit of many descendants thereby amplifying the value of each unit of genetic improvement (Van Eenennaam et al., 2011). The economic value resulting from increases in productivity via improvements in net genetic merit may be captured by the beef industry through a variety of methods. Some of the improved economic value will be captured through improvements in sector specific economically-relevant traits (ERTs). Genetic improvements that result in improved production efficiencies through more successful reproduction (more calves per cow exposed), growth (more pay weight) and end product merit (value to consumers) yield improved revenue streams through the value chain based on existing pricing mechanisms in the market.

Genomic technologies, such as marker assisted selection (MAS), may also offer the opportunity to change the economic position of the beef industry through improved demand for beef products. Simulated selection strategies to improve meat tenderness via selection of bulls or bulls and replacement females with desirable MBV for Warner-Bratzler shear force (WBSF) reveal a potential mechanism to create a positive shift in beef demand. The shift in demand caused by improvement in tenderness, a trait where no direct pricing mechanism exists, results in consumers rewarding beef value chain participants with high prices for 'higher valued' products (Weaber and Lusk, 2007). Genomically enabled selection strategies at the seedstock level to

produce bulls used by the commercial sector may support higher testing costs due to the seedstock sector's ability to demonstrate and capture the value of improved genetic merit. In contrast, genetic tests for selection of animals in the commercial sector will need to be inexpensive, or have large returns, because commercial animals produce fewer descendants from which to recoup testing costs.

The feedlot sector could potentially use genomics information for marker-assisted management (MAM), although the slim margins associated with feeding cattle will impose a low ceiling on testing costs. Since the feedlot sector is a margin business, technology adoption in the feedlot sector is closely tied to demonstrated return on investment. At present, there appears to be limited value associated with using genomics tests to sort cattle on quality grade alone, especially given the variability of the Choice-Select spread. Tests that focus on only single trait management in a feedlot setting are not likely to capture enough value for the feedlot operator to pay for the test. It is anticipated that in the future tests will be developed for important feedlot profit drivers (e.g. disease resistance, feed efficiency) which impact multiple outcomes. These developments, along with the continued decline in genotyping costs, may lead to cost-effective approaches to feedlot MAM with favorably associated returns on investment in the future.

The cost and difficulty of obtaining sufficient phenotypes to develop accurate tests on difficult or expensive to measure traits should not be underestimated. However, if a large feedlot incentivized DNA collection and genotyping of animals prior to entry into the feedlot through breeder and producer partnerships and routinely collected feedlot phenotypes, large databases would soon accumulate. It may be that the combined value derived from using genomic test information for multiple purposes across several value chain sectors, in combination with the rapidly-declining cost of genotyping, will ultimately push the economics of genomics-based technologies over the tipping point towards more widespread industry adoption (Van Eenennaam, 2011).

At the current time the costs of genomics testing tend to exceed the value that is returned to any single sector. The current marketing structure is for seedstock producers to collect DNA for pedigree verification, genetic defect testing and possibly genomic enhanced EPDs and should pass that cost on through higher bull prices. Obtaining further genomics information results in re-collection and extraction of genomics information at additional costs to the new owner. Perhaps a better economic model could be developed so that cattle would be genotyped once early in life and genotypes shared among production sectors to derive the maximum value from the DNA collection and extraction costs incurred. Groups that can organize themselves to take advantage of the rapidly-declining cost of genotyping and capture the cumulative supply chain value derived from using genomics information for multiple purposes (traceability, parentage, genetic defects, selection, MAM, product differentiation), will be ideally positioned to fully realize the nascent potential of genomic information (Van Eenennaam and Drake, 2011).

Promising Future for Genomics Technology

Cattle Health

Other livestock industries have successfully incorporated selection for disease resistance into their breeding programs. 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. Likewise chicken breeders have long used breeding to improve resistance to avian lymphoid leucosis complex and Marek's disease. 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. Doing so will require the development of large multi-breed genotyped training data sets with disease phenotypes.

Bovine Respiratory Disease (BRD), also known as shipping fever or pneumonia, is the leading cause of illness and death for the backgrounding and feedlot cattle industries and is the most important cause of disease-related economic losses. Evidence that BRD susceptibility has a genetic component is demonstrated by breed differences in BRD morbidity and mortality, and the fact that BRD prevalence in pre-weaned calves and feedlot cattle has been reported to be heritable. One study found that the heritability of BRD incidence in feedlot animals was 0.18 (Snowder et al., 2006). There are some technical reasons why BRD heritabilities tend to be low under field conditions. These include 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 (viruses and opportunistic bacteria in the case of BRD). These confounding factors add environmental noise to field data which decreases heritability. Field studies therefore likely underestimate the true importance of genetics in BRD incidence, and thus also undervalue the potential gains that could be made by breeding for disease resistance.

Trying to understand the genetic potential of animals to remain healthy and free of BRD is the focus of a 5-year USDA-NIFI grant entitled "Integrated Program for Reducing Bovine Respiratory Disease Complex (BRDC) in Beef and Dairy Cattle." The goal of this program is to reduce the incidence of BRD in beef and dairy cattle by capitalizing on recent advances in genomics to enable novel genetic approaches to select for cattle that are less susceptible to disease. This effort, known as the BRD CAP (Coordinated Agricultural Project), involves a multi-institutional team led by Dr. James Womack at Texas A&M University, and involves research groups from Washington State University, University of Missouri, Colorado State University, New Mexico State University, and University of California, Davis. For more information on the BRD CAP see www.BRDComplex.org. Reducing the considerable animal morbidity, mortality and economic losses associated with BRD will require the simultaneous development of genomics 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.

Production

Beef producers have a reliable selection tool, in EPDs, to assist in selection decisions for many production traits. However, there are opportunities to improve the accuracy in these traits through the incorporation of genomic information into NCE. Genomic enhanced EPDs were first estimated for carcass traits and then evolved to other production traits for which EPDs already existed. This has worked quit well on a within breed basis.   MacNeil et al., (2010) utilized Angus field data to look at the potential benefits of including both ultrasound records and MBV for carcass traits in genetic evaluations. The MBV values were produced specifically for Angus cattle and provided to AAA by Igenity. The MBV were developed using genotypes and EPD from 1,710 Angus bulls. The genetic correlations between the MBV and carcass traits

are reflected in Table 2 above. Although the genetic correlations between the MBV and the economically relevant carcass traits are moderate, they are not perfect predictors.

Although within breed predictions look promising, some breeds do not have the luxury of immediately having thousands of genotyped animals for use in developing a breed-specific genomic test. Consequently, the use of a robust across-breed set of genomic prediction equations would be beneficial. There are two primary methods of constructing an across-breed training data set: Pool purebred animals from multiple breeds or use crossbred animals. The first option requires the use of de-regressed EPD (Garrick et al., 2009) as "phenotypes" for training similar to the within breed scenario with the exception of correcting for breed effects in the model. The second option requires the use of adjusted phenotypes to train the genomic predictors. Weber et al., (2012) and Kachman et al., (2012) both evaluated the efficacy of across breed genomic predictors derived from two training data sets: the USMARC Germ Plasm Evaluation Project (GPE), and the USMARC 2,000 Bull Project. Both authors showed moderate genetic correlations between MBV and growth traits using the 2,000 Bull MBV in multiple purebred beef breeds. Both authors also showed lower genetic correlations when using the GPE derived MBV for growth traits across multiple purebred populations. The difference between the two across-breed MBV is that the 2,000 Bull training population leverages more information, since the phenotypes are truly de-regressed EPD that include several progeny records, while the GPE MBV relies on adjusted phenotypes. So while more genotyped animals were used to train the GPE MBV, the amount of phenotypic information used in training was less. Kachman et al., (2012) concluded that developing MBV using a training population of a pooled group of purebred animals can produce reliable MBV if the breed in which the MBV is to be used is also contained in the training population (i.e. if the MBV is to be used in Charolais, Charolais animals must be represented in the training data).

While the majority of the effort thus far has focused on revenue, or output traits, given they are the most densely recorded and EPD already exist that can be used in training, there is a need to develop large populations of phenotyped animals to enable prediction of input traits such as feed intake and efficiency. Feed accounts for approximately 65% of total beef production costs and 60% of the total cost of calf and yearling finishing systems. The cow-calf segment consumes about 70% of the calories; 30% are used by growing and finishing systems. Of the calories consumed in the cow-calf segment, more than half are used for maintenance. During the growing and finishing phase of production, a 10% improvement in gain improved profit 18% while a 10% improvement in feed efficiency improved profit 43% (Fox et al, 2001). Other work suggests that improvements in efficiency have 7-8 times the economic impact of increases in daily gain (Okine et al., 2004).

The inability to routinely measure feed intake and feed efficiency on large numbers of cattle has precluded the efficient application of selection despite moderate heritabilities (h2 = 0.08-0.46). The objective of the 5 year USDA-AFRI funded project titled "National Program for Genetic Improvement of Feed Efficiency in Beef Cattle" (www.beefefficiency.org) is to sustainably reduce feed resources required to produce beef via the rapid development and deployment of novel nutritional, genomic and genetic improvement technologies. Additionally project participants aim to strengthen the international competitiveness of US agriculture and enable increased food production by increasing the animal protein produced without additional feed inputs and with a reduced greenhouse gas footprint. The project includes a large effort to

gather existing individual feed intake and composition records across the major US beef breed and back fill deficiencies in these represented breeds through collection of new records. The project will use high density SNP genotyping platforms to develop tools for MAS and MAM feed efficiency traits. The integrated project includes a large demonstration project, which leverages the animals in the WTP, to demonstrate the use of genomics tools and improvement of feed efficiency.

Reproduction

Traits that are of the most economic value to commercial, self-replacing herds are reproductive traits including age at first calving, reproductive success, and replacement rate (Roughsedge et al., 2005). These maternal traits are sex-limited, lowly heritable, and some are expressed quite late in life. This has precluded replacement heifer selection on these traits, and frustrated genetic progress. In fact, the antagonism between terminal and some maternal and calving traits may have led to negative progress, as positive selection on the terminal traits can result in negative selection on the maternal traits. It has been suggested that US cow-calf producers should have a relative economic emphasis of 47% on reproduction, 24% on growth, and 30% on carcass traits (Melton, 1995).

Given the economic importance of reproduction, it is crucial for commercial cow-calf producers to optimize reproductive performance in their herds. Because of the low heritability of most reproductive traits and limited access to reproduction EPDs (heifer pregnancy rate and stayability in a limited number of breeds) the commercial beef sector has attempted to maintain high reproduction rates through crossbreeding and improved management practices with very little emphasis on selection. Genomic testing offers an appealing approach to provide these previously-absent selection criteria.

Traits that have the greatest opportunity to see increased accuracy values are those with low heritability and little phenotypic data. Reproduction, in general, qualifies as having both low heritability and limited data in most breeds. Therefore, it stands to reason that if tests could be developed to explain a reasonably high portion of genetic variation, then a more effective selection tool (EPD) could be developed. However, in the complete absence of currently available EPDs, any gain at all through the use of genomics could be advantageous.

Despite the fact that genomics tests are ideally suited for low heritability traits for which there is no indicator trait or measurement that can be used for selection decisions, research suggests that genomics tests for low heritability traits will be the most challenging to develop. That is because a very large number of "training" records will be required to obtain accurate genomics tests for these traits. Additionally, such tests will also be the most difficult to validate as there are few cattle populations with sufficient phenotypic data from which to estimate the accuracy of new genetic tests (i.e. how well the test is working).

USDA-NIFA had a 2012 call for grant proposals aimed at using an integrated approach to improve the fertility of agriculturally-relevant animal species. The decision as to which projects will receive funding to achieve this missing link across all livestock/poultry species is expected in August 2012. There are multiple cattle/beef proposals under consideration for these five year projects with differing methodologies, but a similar goal of finding genomics tools to assist in the selection of beef cattle for improved reproductive performance.

Healthfulness of Beef

Since the mid 1970's the beef consuming public has cast a discriminating eye towards beef in regard to its healthfulness. Cattlemen can argue the validity of many of the claims against beef, and research supports beef as a healthy part of our diet, however, there are still areas for improvement and selection may be a means to that end.

Studies conducted by the National Beef Cattle Evaluation Consortium (Garmyn et al., 2011) have investigated the possibilities and potential consequences of altering the mineral and/or fatty acid composition of beef. This study concluded that altering beef's composition should not have an adverse affect on its palatability. Other studies have shown that genetic factors influence fatty acid composition (De Smet et al., 2004), so it stands to reason that if for genetic markers that impact fatty acid and mineral composition can be identifies then selection for improved beef healthfulness can be achieved. Developing a business model that will allow beef producers to capture potential added value is essential.

Summation

Clearly there is significant research underway to develop genomic tests for various economically-relevant traits of importance to the beef industry. As genomic 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 efficiency of feed utilization by the cow herd and growing animals, fertility, disease resistance and many other traits that have both a genetic component and economic relevance.

With an expanding number of EPDs being available to beef producers for selection decisions, multiple-trait selection indexes will need to be developed (and adopted) to appropriately weight these traits that influence the profitability of beef cattle production. Selection indexes provide an economic evaluation of the genetic differences among sires, and an objective way to determine likely differences in the profitability of progeny of 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 limited 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 in some cases. Development of tools for the selection of additional traits will necessitate the need for more comprehensive selection indexes that include all of the economically-relevant traits of importance to U.S. beef production systems.

The use of any tool to make selection decisions that is less than 100% accurate is a practice in risk management. As advancements continue to eliminate the "unknown" part of genetic evaluations then those risks are continuing to be reduced. When utilized responsibly a tool without error is a good thing, but in the case of abuse or misuse mistakes can be greater and occur at a faster pace. By establishing sound breeding objectives with a focus on profitability these potential pitfalls can be avoided.

Contributing Authors:

Darrh Bullock, University of Kentucky

Matt Spangler, University of Nebraska – Lincoln

Alison Van Eenennaam, University of California – Davis

Robert Weaber, Kansas State University

Reviewers:

Tom Field, University of Nebraska – Lincoln

Dorian Garrick, Iowa State University

John Pollak, Meat Animal Research Center - USDA

Citations

Davis, G. P. and S. K. Denise. 1998. The impact of genetic markers on selection. J Anim Sci 76:2331-2339.

DeNise, S. K. 1999. Using parentage analysis in commercial beef operations. Proc. Beef Improvement Federation 31st Annual Research Symposium and Annual Meeting, Roanoke, VA. pp 183-190.

De Smet, S., K. Raes, and D. Demeyer. 2004. Meat fatty acid composition as affected by fatness and genetic factors: A review. Anim. Res. 53:81–98.

Dodds, K.G., M. L. Tate and J. A. Sise. 2005. Genetic evaluation using parentage information from genetic markers. J Anim Sci 83: 2271–2279.

Fox D.G., Tedeschi L.O. & Guiroy P.J. (2001) Determining feed intake and feed efficiency of individual cattle fed in groups. In: *Proceedings of the 33rd Annual Beef Improvement Federation Annual Research Symposium and Annual Meeting*, pp. 80-98.

Garmyn, A. J., G. G. Hilton, R. G. Mateescu, J. B. Morgan, J. M. Reecy, R. G. Tait, Jr., D. C. Beitz, Q. Duan, J. P. Schoonmaker, M. S. Mayes, M. E. Drewnoski, Q. Liu, and D. L. VanOverbeke. 2011. Estimation of relationships between mineral concentration and fatty acid composition of longissimus muscle and beef palatability traits. J Anim Sci 89:2849-2858

Garrick, D. J., and B. L. Golden. 2009. Producing and using genetic evaluations in the United States beef industry of today. J Anim Sci 87: E11-18.

Garrick D. J., J. F. Taylor and R. L. Fernando. 2009. Deregressing estimated breeding values and weighting information for genomic regression analyses. Genet Sel Evol 41: 55.

Geldermann, H., U. Pieper and W. E. Weber. 1986. Effect of misidentification on the estimation of breeding value and heritability in cattle. J Anim Sci 63:1759-1768.

Goddard, M. E. and D. E. Goddard. 1997. Using DNA fingerprinting of extreme offspring to progeny test sires. Proceedings of the Association for the Advancement of Animal Breeding and Genetics 12:438-441.

Ibanez-Escriche, N., R. L. Fernando, A. Toosi, and J. C. Dekkers. 2009. Genomic selection of purebreds for crossbred performance. Genet Sel Evol 41:12–29.

Israel, C. and J. I. Weller. 2000. Effect of misidentification on genetic gain and estimation of breeding value in dairy cattle populations. J Dairy Sci 83:181-187.

Kachman S. 2008. Incorporation of marker scores into national cattle evaluations. Proc. 9th Genetic Prediction Workshop, Kansas City, MO, pp. 88-91.

Kachman, S. D., M. L. Spangler, G. L. Bennett, K. J. Hanford, L. A. Kuehn, W. A. Snelling, R. M. Thallman, M. Saatchi, D. J. Garrick, R. D. Schnabel, J. F. Taylor and E. J. Pollak. 2012. Comparison of within and across breed trained molecular breeding values in seven breeds of beef cattle. J Anim Sci (submitted).

MacNeil M. D., J. D. Nkrumah, B. W. Woodward and S. L. Northcutt. 2010. Genetic evaluation of Angus cattle for carcass marbling using ultrasound and genomic indicators. J Anim Sci 88: 517.

Melton, B. E. 1995. Conception to consumption: The economics of genetic improvement. Proc. Beef Improvement Fed. 27th Ann. Mtg. p 40-87, Sheridan, WY.

Okine E.K., J. Basarab, L. A. Goonewardene and P. Mir. 2004. Residual feed intake and feed efficiency: Difference and implications. In: *Florida Ruminant Nutrition Symposium*, pp. 27-38.

Roughsedge, T., P. R. Amer, R. Thompson, and G. Simm. 2005. Development of a maternal breeding goal and tools to select for this goal in UK beef production. J Anim Sci 81: 221-232.

Saatchi M., D. J. Garrick, J. Ward. 2011a. Accuracy of genomic breeding values in Hereford beef cattle using k-means clustering method for cross-validation. J Anim Sci 89 E-Suppl. 2: 59.

Saatchi, M., D. J. Garrick and J. F. Taylor. 2012. Genetic correlations between carcass traits and genomic breeding values in Limousin cattle. J Anim Sci 90 E-Suppl. 2: 66.

Senneke, S. L., M. D. MacNeil, L. D. Van Vleck. Effects of sire misidentification on estimates of genetic parameters for birth and weaning weights in Hereford cattle J Anim Sci 82:2307-2312.

Snowder GD, LD Van Vleck, LV Cundiff, GL Bennett. 2006. Bovine respiratory disease in feedlot cattle: Environmental, genetic and economic factors. J Anim Sci 84:1999-2008.

Toosi, A., R. L. Fernando, and J. C. M. Deckers. 2010. Genomic selection in admixed and crossbred populations. J Anim Sci 88:32–46.

Van Eenennaam, A.L. 2011. Beef translational genomics: Lessons from the literature. Association for the Advancement of Animal Breeding and Genetics. 19: 271-278.

Van Eenennaam, A. L., and D. J. Drake. 2011. Where in the beef cattle supply chain might DNA tests generate value? Anim Prod Sci 52(3) 185-196.

Van Eenennaam, A.L., van der Werf, J.H.J., and M. E. Goddard. 2011. The value of using DNA markers for beef bull selection in the seedstock sector. J Anim Sci 89: 307-320.

Van Eenennaam, A. L., R. L. Weaber, D. J. Drake, M. C. T. Penedo, R. L. Quaas, D. J. Garrick, and E. J. Pollak. 2007. DNA-based paternity analysis and genetic evaluation in a large, commercial cattle ranch setting. J Anim Sci 85:3159-3169.

Van Vleck, L. D. 1970. Misidentification and sire evaluation. J. Dairy Sci. 53:1697-1702.

Weber, K. L., R. M. Thallman, J. W. Keele, W. M. Snelling, G. L. Bennett, T. P. L. Smith, T. G. McDaneld, M. F. Allan, A. L. Van Eenennaam, and L. A. Kuehn. Accuracy of genomic breeding values in multi-breed beef cattle populations derived from deregressed breeding values and phenotypes. J Anim Sci (submitted).

Weaber, R. L. and J. L. Lusk. 2010. The economic value of improvements in beef tenderness by genetic marker selection. Amer. J. Agr. Econ. 92(5): 1456-1471

Weaber, R. L. 2005. A simulation study of replacement sire selection and genetic evaluation strategies for large commercial ranches. PhD Diss. Cornell Univ., Ithaca, NY.