Utilizing Molecular Information in Beef Cattle Selection

Matt Spangler, University of Nebraska-Lincoln and Alison Van Eenennaam, University of California-Davis

Molecular sources of information represent a rapidly developing technology with regards to beef cattle selection. Given the rapid commercialization of DNA marker panels, producers have been able to see changes first hand in reporting styles, panel sizes, and traits for which panels are available. Unfortunately, the power of this technology will only be fully exploited when it is seamlessly integrated into National Cattle Evaluations (NCE).

Utilization of Molecular Information to Date

DNA information has been effectively utilized to identify animals that are carriers of recessive alleles. This has been of particular interest for genetic defects, color, and horned/polled status. Prior to the advent of this technology the only way to test if a sire was a carrier of a particular genetic defect was to mate him to a given number of known carriers of the defect or an even greater number of his own daughters of unknown genotype. Even then definitive conclusions could only be drawn if he sired an afflicted calf. If all corresponding offspring were free of the defect, then it would be possible to assign a certain probability to the sire being a non-carrier with the probability being dependant on the number of calves born from a particular mating. DNA-marker technology has also proven very beneficial in determining parentage. More recently, SNP panels have been developed to test for a portion of the genetic merit of an animal for a variety of traits ranging from fertility and longevity, to growth and carcass merit.

Methods of Reporting (past and present)

Many of the early recording systems to relay marker panel results were categorical in nature. For instance, systems existed that provided one star for each favorable allele regardless of the proportion of variation explained by the marker. Others provided a 1-10 scale where genotypes were categorized by the impact they had on the trait of interest. Neither of these systems allowed for the inclusion of these results in NCE. More recently marker panel results have been reported as Molecular Breeding Values (MBVs). Although MBV is the term that is being used by the scientific community, DNA testing companies have created unique names to identify their respective products in the market place (i.e. Molecular Value Prediction [MVP] and Genetic Prediction Difference [GPD]).

Differences between MBVs and EPDs

EPDs provide an estimate of the genetic potential of an animal as a parent based upon ancestral information; his/her own records, and the records of his/her progeny. With this in mind, an EPD accounts for all the genes that affect a particular trait, regardless of the magnitude of their affect. While an EPD accounts for all of the additive genetic variation, the specific sources of the variation (genes) are unknown. Conversely, DNA marker tests reveal the genotype of an animal for specific DNA markers for a particular trait but, to date, do not account for all of the genetic variation. This is simply due to the fact that the markers or genes with the largest effects are the easiest to identify and become the logical candidates for inclusion in marker panels. The potentially infinite number of markers or genes with much smaller effects are more difficult to identify, and consequently have not been included in the development of marker panels.

The other caveat is the inherent difference between an EPD and an estimated breeding value (EBV). An EBV is the genetic merit of an animal whereas an EPD is the genetic merit of an animal as a parent given that an animal can only pass on a sample half of its alleles to the next generation. The relationship between the two is as follows:

$$EPD=1/2(EBV)$$

Although some DNA companies report results in a form that looks similar to an EPD in that it is reported in units of the trait, the values are EBVs based on molecular information. To determine how much better one animal is versus another as a parent, EBVs must be divided by two.

It is critical to understand that a desirable genetic test result with current commercially available panels is not always associated with a desirable EPD. For instance, it would be possible for an animal to be homozygous for the favorable allele for a DNA marker for marbling but still have a marbling EPD that is below breed average. This could occur because, although the animal has the favorable form of both alleles of one of the genes affecting marbling, it may have unfavorable alleles for numerous other unknown genes that affect marbling as well.

Accuracy

When DNA from an animal is submitted for a DNA-test, there is an accuracy associated with that result. Accuracy has multiple meanings. One definition is "degree or extent of freedom from mistake or error". Genotyping generally has a high level of technical accuracy or precision, meaning that there are rarely errors in the actual results of the DNA test. However, in animal breeding, accuracy refers to how well an estimate of the genetic merit (e.g. EPD, or DNA-test result) predicts the true genetic merit of an animal. One measure of this genetic prediction accuracy is the correlation (r) between a genetic merit estimate and the true genetic merit of that animal. Accuracy values can range from 0 (in which case the estimate has no relationship to an animal's true genetic merit) to 1 (in the theoretical situation where the estimated breeding value is equal to the true breeding value). In practice accuracy values never reach the theoretical limit of 1, although very high accuracy of extensively used AI sires can reach 0.99.

In some countries, the accuracy of a genetic prediction (EPD in the U.S.) is reported as the correlation between the estimated value and the "true" value. With progeny test information, this accuracy measure quickly attains a high value as progeny numbers exceed 20, especially for traits with moderate to high heritability. Traits that are lowly heritable, such as reproductive traits, require more progeny records to attain the same level of accuracy as a trait that is moderately to highly heritable.

The U.S. beef industry reports accuracy using standards suggested by the Beef Improvement Federation (BIF). The BIF accuracy scale is based on minimizing Prediction Error Variance (a measure of the magnitude of errors in predicting breeding values), rather than using *the correlation* between the estimated and true breeding value. BIF accuracies are more conservative than the simple correlation, in that they require more data (e.g. progeny records in the case of a bull evaluated from a progeny test) to achieve high accuracy values. Table 1 illustrates this point.

Table 1. Accuracies of estimated breeding values based on (A) the correlation with true breeding values (r), and (B) the BIF standard, and the number of progeny test records required to obtain these accuracy values for traits of low (0.1) and moderate (0.3) heritability.

		Number of Progeny Records Required	
Correlation (r)	BIF Accuracy	Low Heritability (0.1)	Moderate Heritability (0.3)
.1	.01	1	1
.2	.02	2	1
.3	.05	4	2
.4	.08	8	3
.5	.13	13	5
.6	.20	22	7
.7	.29	38	12
.8	.40	70	22
.9	.56	167	53
0.99	.93	1921	608
0.995	.99	3800	1225

The accuracy associated with EPDs increases as more information becomes available. Initially EPDs are derived from the average of animals' parents (called a pedigree estimate). Once an animal has a record, the accuracy of the EPD increases and continues to do so as the animal has recorded progeny. Unfortunately this takes time and for some economically relevant traits (ERTs) it is not possible for animals to have a record themselves or the record may occur very late in life (i.e. stayability). New metrics for estimating the "accuracy" of DNA tests have been developed based on the relationship between MBVs and the trait of interest, some of which are published by DNA testing companies to accompany marker panel results. It is critical to understand that at present, these values are not directly comparable to the BIF accuracy values associated with EPDs.

Example. Assume that a DNA test has a genetic correlation of 0.8 with the trait of interest. This would equate to a BIF accuracy of 0.40. For traits that are hard to measure or measured late in life this would be very beneficial. Seedstock producers could identify superior animals earlier in life and commercial producers who purchase unproven sires could reduce the risk associated with low accuracy values. However, if the genetic correlation between the molecular test and the trait of interest is low (0.02) then the value of using only the genetic test score for the purposes of selection is dramatically decreased, especially in the context of having available EPDs for the trait of interest. The greatest benefit in accuracy should come from the integration of DNA tests scores along with phenotypic records in the calculation of EPDs.

The reason that DNA tests are able to increase the accuracy of EPDs is that they have the ability to account for a phenomenon called "Mendelian sampling". This term is used to describe the random sampling that occurs when parents pass on a random sample of half of their DNA to their offspring. Every allele, good or bad, has an equal likelihood of being inherited. One could envision a scenario where an animal could receive only the most desirable alleles from both parents resulting in a large favorable Mendelian sampling effect or the exact opposite which could result in a large unfavorable sampling effect. Perhaps the best example of this is a set of flush mates. Although all of them have the same pedigree estimate, they may differ considerably in terms of their performance and ultimately their EPDs due to Mendelian sampling. This effect can be quantified using contemporary group deviations and is a measure of how much better or worse an animal is compared to the average of its parents. Mendelian sampling is the reason that performance records on the individual and its progeny are required to obtain accurate genetic predictions. Individual records provide some information on the sampling of alleles inherited by an animal, and progeny information provides even greater insight as to the sum of the additive effects that the animal is passing to the next generation. DNA tests have the potential to view into the black box of Mendelian sampling at birth and reveal what alleles an animal inherited.

The accuracy of a DNA test at predicting the true genetic merit of an animal is primarily driven by the amount of additive genetic variation accounted for by the DNA test. Thallman et al. (2009) found that the best predictor of this proportion was the square of the genetic correlation between the MBV and the trait of interest. The first generation of DNA tests for complex traits in beef cattle did not have high accuracies because the small number of markers included in these tests were associated with only a small proportion of the additive genetic variation for the trait of interest (Allan and Smith, 2008). As the number of informative markers in a DNA test increases so will the proportion of additive genetic variation explained by the test.

Since the first marker tests were developed, a large number of SNP markers have been identified in the bovine genome. As a result, companies have started to develop tests using multiple (10-200) SNPs to develop marker panels to predict an animal's genetic merit. In January 2010, Pfizer Animal Genetic announced the availability of a 50,000 marker DNA test for Angus cattle (http://www.pfizeranimalgenetics.com/Pages/HD50KRelease.aspx). As marker panels grow they track the inheritance of an increased number of genes, and if these genes are associated with genetic variability in the trait under selection then these tests will explain a larger proportion of the overall genetic variation for that trait.

What is the benefit of higher accuracy values on young sires? For the seedstock producer, it enables the selection of truly superior animals earlier in life and potentially decreases the number of animals to place on test. It also allows seedstock producers to supply clientele with a product that has less risk of change associated with it. The benefit to commercial producers lies in the ability to buy yearling bulls with more certainty surrounding their EPDs.

Example. Assume a commercial producer wants to purchase a calving ease bull for use on heifers. If a bull does not have a record of calving ease himself, the BIF accuracy might be 0.20.

Assume that the possible change[1] value associated with this accuracy level is 6 and that his published EPD is +5 (breed average in this case). In this situation, we would be 68% confident that this bull's "true" EPD for calving ease is between -1 and +11 realizing that for calving ease a larger number is more desirable since it is interpreted as the percentage of unassisted births. However, if the accuracy were higher (0.5) this would mean a small possible change value (4) so we would then be 68% confident that his true EPD would be between +1 and +9.

Increased accuracy values can aid in the selection of truly superior animals. For instance, if calving ease is a concern for a commercial producer who buys yearling bulls then there is an inherent risk that the bull's true genetic merit and his predicted genetic merit are not close. It would be advantageous to have more information from which to predict the genetic merit of yearling animals so that the predicted value was a closer estimate of the true value.

Example. Assume that two yearling bulls both have a calving ease direct EPD of +5 and that the possible change values associated with them are +6. In this scenario both bulls would be equally likely to be candidates for selection. However, assume that we were able to garner more information, in the form of a marker panel test, and thus increase the accuracy values of both bulls by joining the results of the marker panel and the information included in the EPD. Perhaps we would find that one bull is actually a -1 and the other bull's is a +11. In this case the two bulls seemed equally valuable based on their low accuracy EPDs but as the accuracy values increased and we were able to get a clearer picture of their true genetic potential as parents we found one bull is actually superior over the other. In this example, the difference between the two bulls is actually 12 or one bull is likely to have 12% fewer assisted births than the other. If multiple bulls were purchased with the same low accuracy EPDs (in this case +5) it could be argued that the average of the "true" values would still be close to +5 even though some are likely to be higher and some lower. However, for a trait like calving ease, it is advantageous to eliminate bulls that may create calving difficulty even if the average of an entire bull battery is acceptable.

Shorter Generation Interval

Combining phenotypic and molecular data, particularly for traits that cannot be measured early in life, can lead for faster genetic change. The factors that impact the rate of genetic change are the accuracy of selection, the genetic standard deviation, the selection intensity, and the generation interval. Generation interval is defined as the average parental age when the offspring are born. Typically this is six years of age in beef cattle. Genetic change per year can be derived by:

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

It is clear that if the generation interval were to decrease then the rate of genetic change would increase. For seedstock producers, the ability to use a yearling sire heavily due to increased confidence in his EPD could reduce generation interval and thus lead to faster genetic progress.

The benefits of including molecular information in the calculation of EPDs for yearling bulls will depend on the marker panel itself. The more genetic variation that is explained by the panel the larger the increase in accuracy. Marker panel results should be thought of as another phenotype, correlated to the trait of interest, which can be included in the genetic prediction. In other words, the addition of the DNA panel phenotype adds to the amount of information and consequently provides an increase in accuracy proportional to the amount of variation explained by the panel.

Paradigm of Disjointed Pieces of Information

Differences in reporting styles, between EPDs and molecular test results and even between DNA companies, have led to a plethora of confusion. There are seemingly two distinct pieces of information, marker panel results and EPDs, which due to the sources of information included in them can potentially be in disagreement. This has often begged the question of which to use. Sometimes it has led to the belief that one must be incorrect.

Benefits of Combining Molecular and Phenotypic Data

An obvious benefit of combining traditional phenotypic based EPDs and the results from marker panel results is less confusion. No longer would there be a question as to which one to use. However there are other, more quantitative benefits such as the potential to increase the accuracy of EPD predictions in young animals thereby potentially enabling a decrease in the generation interval leading to more rapid genetic change.

Methods of Combining MBVs and EPDs

Rather than thinking of DNA-marker panel results as being separate and disjointed pieces of information, test results should be thought of as an indicator trait that is correlated to the trait of interest. As such, the MBVs can be included in NCE as a correlated trait. In this scenario it will be important to estimate the heritability of the marker score and the genetic correlation between it and other production traits as well as the phenotypic variation of the marker score. Kachman (2008) suggested that marker scores (MBVs) have a number of advantages over using the marker panel data (genotypes) directly. Three primary advantages are:

1. It reduces the amount of data that must be processed when conducting a genetic evaluation.

[1] Possible change values are standard deviations and are a measure of risk associated with different accuracy values. Possible change values differ between breeds and between traits. Updated possible change values can be found on breed association websites.

2. Markers used in the test (panel) do not have to be identified.
3. It allows for advances in DNA tests and statistical methodology to be taken advantage of in a timely manner.

One major caveat to this approach is the need to clearly identify evolutions in marker panels. For instance, if company X has a marker panel for some trait that includes 50 SNPs and the panel is later updated to include 100 SNPs it is important to be able to identify which panel was used. Futhermore, the covariances between marker scores generated by different tests within a company and for tests between companies will need to be estimated given that there are likely differences in the amount of additive variance explained by the variety of tests that are either currently available or that will be available in the future. Other methods have been proposed including adjusting the additive variance of the trait of interest and the appropriate (co)variances for the amount of variation explained by the molecular source of information (Spangler et al., 2007), and using large (50,000+) SNP panels to form a genomic relationship matrix in place of the traditional pedigree based relationships that are currently used.

MacNeil et al. (2010) 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 score (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 (Table 1) 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 0.80, suggesting that these two were not explaining the same sources of variation and thus were both beneficial when included as correlated traits in the model.

In the context of utilizing marker panels that explain less that 100% of the additive genetic variation, collecting phenotypes is beneficial particularly at the nucleus level. Garrick (2007) illustrated an example of different selection schemes to improve carcass marbling using combinations of phenotypes and molecular information. Five possible selection schemes illustrated were as follows:

1. Measure carcass marbling scores on progeny test offspring of young bulls bred in the nucleus herd prior to their widespread use in the bull breeding herd (prior to use to produce seedstock for the multiplier and commercial levels).
2. Measure ultrasound IMF% on all yearling males in the bull breeding herd (nucleus herd).
3. Measure ultrasound IMF% on all offspring bred in the nucleus herd.
4. Genotype all young bulls in the bull breeding herd.
5. Genotype and measure IMF% on all males in the bull breeding herd.

In his example, Garrick assumed that the heritability of carcass marbling was 0.54 and the phenotypic and genetic standard deviations were 0.88 and 0.65, respectfully. Finally it was assumed that the heritability of IMF% was 0.50 and the genetic correlation between carcass marbling and IMF% was 0.72. Under these assumptions using a marker panel that accounted for 10% of the additive variation in place of collecting ultrasound information was less beneficial than collecting ultrasound information and even a panel that accounted for 50% of the variation was not more profitable than collecting IMF% in both sexes.

The American Angus Association has announced that they are going to develop "genomic-enhanced EPDs" by integrating IGENITY profile for Angus DNA marker results for carcass traits into their NCE (http://www.angus.org/Pub/Newsroom/Releases/AGI_Igenity_EPDs.html; Accessed 3/09/10). This development, along with the integration of DNA markers into tenderness breeding values reported by the Animal Genetics and Breeding Unit of the University of New England in Australia (Johnston et al., 2009), represent important milestones in the application of DNA testing in beef cattle.

A Model for the Flow of Data

Tess (2008) detailed a model for the evaluation of commercial marker panels (Figure 1) and the incorporation of different sources of information including DNA test information from multiple companies into NCE on an ongoing basis (Figure 2). In this model the National Beef Cattle Evaluation Consortium (NBCEC) serves as the independent source of validation. The evaluation of DNA tests includes:

1. The delivery of DNA samples from reference populations to the DNA testing company that developed the test.
2. The company genotypes the samples and calculated the molecular score.
3. The company communicates the molecular score to the independent validation entity.
4. The validation entity performs the statistical evaluation of the molecular scores using pedigree and phenotypic information from the reference population.
5. The results of the statistical analysis are communicated to the DNA testing company and to the public.

This model would allow for the calculation of covariances between the DNA test and the target trait, covariances between competing DNA tests, and covariances between the DNA test and non-target traits and finally the calculation of EPDs and associated accuracy values on the BIF scale.

Economics

DNA testing presents a marketing opportunity for bull sellers. Early adopters, those who have panel information sent to breed associations for inclusion in genetic evaluations, may have a competitive advantage over other seedstock producers who do not. This assumes that bull buyers are willing to pay more for yearling bulls with higher accuracy values. The process of collecting DNA samples and then paying for a diagnostic test for a particular trait represents an additional cost to the breeder. Some seedstock producers are currently DNA-testing their bulls to provide potential buyers with DNA information. The value of that information to the buyer is will be determined by the market.

If the value is deemed to be more than the cost of testing and is reflected in the bull purchase price, then the seedstock producer will have improved his/her bottom line.

DNA testing also presents an opportunity accelerate the rate of genetic progress through marker-assisted selection (MAS). The important question to ask regarding this application is "Does DNA testing increase the accuracy of the genetic prediction (e.g. EPD) of young animals sufficiently to justify its cost?" There is undoubtedly value associated with increasing accuracy. This is perhaps best reflected by the higher price of a straw of semen from a well proven AI bull, versus the price of semen from a low-accuracy, unproven bull with the same EPD values and by the risk associated with selecting an unproven bull by commercial producers. High accuracy of selection can almost always be achieved for a highly heritable trait like marbling, but accumulating the necessary data takes time, lengthening the generation interval, and is associated with increased costs. Likewise, generation interval can be shortened by the use of younger, less proven sires, but accuracy typically suffers under that scenario. Genetic tests have the potential to decrease the generation interval by improving the accuracy of genetic merit estimates associated with young sires.

The value of increasing accuracy will also depend on whether the trait in question is an economically relevant trait (ERT), and the availability and accuracy of existing genetic merit estimates. It may be that DNA-based approaches allow for the development of genetic merit predictions for economically relevant traits that are not currently part of beef cattle genetic evaluation programs (e.g. adaptability, feed efficiency). If these traits are ERTs, meaning traits that directly affect profitability by being associated with a specific cost of production or arevenue stream, then some estimate of genetic merit is better than none. However, the aggregate economic value of including that trait in selection decisions must outweigh the costs of obtaining the genetic estimate and associated effects on other economically relevant traits.

The economic benefits associated with MAS relative to the costs involved in running a small number of markers accounting for a modest amount of the genetic variance in a limited number of complex traits in beef cattle have not been well characterized from a scientific viewpoint, as evidenced by the lack of published results on this topic. However, the joint analysis of both phenotypic and molecular information has the potential to enhance the bottom line of both DNA testing companies and producers. Similar to ultrasound in the early 1990's, DNA technology is at a critical point. It seems reasonable to expect that if marker panels are included in NCE, they will eventually become a regular part of information collection for the seedstock industry, as has become the case for ultrasound data (Moser, 2008).

Other Considerations

There are other considerations associated with the use of DNA tests in beef cattle breeding that have not yet been fully addressed. One is the issue of breed differences with regard to allele frequency (Johnston and Graser, 2010). If a marker is found to have a large effect in one breed, but to the close to fixation (frequency close to 1) in another breed, then it is probably not worth applying selection pressure to increase the frequency of that marker in the second breed since most animals will already be homozygous for it.

Gene markers effects have also been found to vary between independent datasets and in breeds outside of those used for discovery (i.e. population where the markers were discovered). Marker panels are likely to work best in discovery populations and be less predictive of genetic merit in more genetically distant populations or breeds. Johnston and Graser (2010) found that markers which worked well in temperate breeds did not always work well in tropical breeds. This suggests that a test developed in an Angus discovery population, as in the following example, might be expected to work well in an Angus target population, but not in a Bos indicus target population.

1. Angus (discovery) -> Angus (target)
2. Angus (discovery) -> Charolais (target)
3. Angus (discovery) -> *Bos Indicus* (target)

This premise has yet to be thoroughly tested in beef cattle populations, although there are existing projects that are working to, at least in part, answer this question (Pollak et al., 2009). Another important consideration is genetic correlations that may exist between marker panels and secondary traits (i.e. non-target traits). Prior to using marker information for selection, it should be confirmed that the marker panel does not have undesirable correlations with other non-target traits.

Figure 1. Model for the evaluation of commercial DNA tests (Tess, 2008).

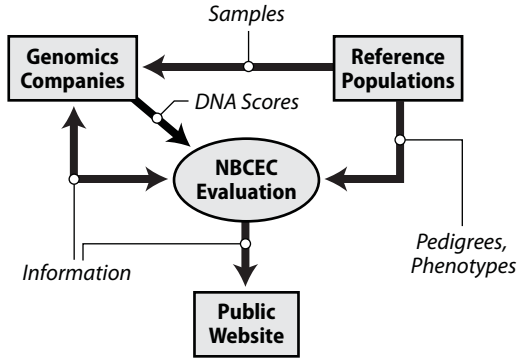
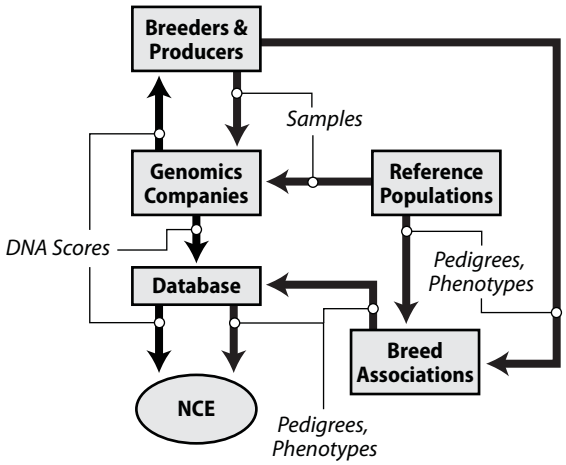


Figure 2. Model for the incorporation of DNA test information into national cattle evaluations (Tess, 2008).



The Future

Marker panels are likely to continue to grow in size and in the future it may even become cost-effective to obtain whole genome sequence on individual animals, i.e. sequence all 3 billion base pairs! These technology advances could enable selection decisions to be made solely on the basis of DNA information, an approach entitled "whole genome selection" (WGS). WGS is a form of MAS that uses thousands of markers distributed throughout the genome to make selection decisions. With WGS, thousands of animals that have phenotypes for a given trait are genotyped, and these data are then used to develop a prediction equation that predicts how well an unknown animal will perform for that trait based on its DNA genotype alone (Meuwissen et al., 2001). Currently genome selection in beef cattle is in its infancy. Although preliminary data coming from the dairy industry look promising (VanRaden et al., 2009), evaluation and validation of the technology for the beef industry will be required before adoption.

Some of the significant hurdles for the successful implementation of WGS in the beef industry include data suggesting large discovery populations (i.e. thousands) of genotyped and phenotyped cattle are going to be needed to make WGS prediction equations accurate in unrelated animals (Goddard, 2009). Additionally, it has been shown that DNA tests developed in one breed are considerably less predictive (i.e. do not work as well) when used in a different breed (de Roos et al., 2008). Given that there are numerous important beef cattle breeds with dozens of traits of economic importance, it is conceivable that beef cattle discovery populations for WGS will need to be very large. It is also likely that populations of animals will be needed to continually update the association between markers and traits of interest. The selection of young animals as parents based on their genotype will likely result in some SNP alleles becoming fixed. This will effectively decrease the proportion of genetic variation explained by a panel of DNA markers over time. In the absence of periodic reevaluation of SNP effects, it is possible that selecting young animals over several generations would have the effect of decreasing the accuracy of selection.

Summary

The advent of molecular information in the form of both tests for simply inherited traits and complex traits has created both excitement and confusion. The lag between discovery and application has been decreased, allowing for technology to be rapidly delivered to industry. In some cases this has caused confusion surrounding the methods for incorporating this technology into breeding schemes. DNA marker tests results should not be used to replace traditional selection based on EPDs and economic index values, but rather should be seen as providing an additional source of information from which to predict genetic merit. When included in the estimation of genetic predictions DNA information provides valuable information on young animals which could improve the accuracy of genetic predictions. DNA testing holds the greatest promise for economically-relevant traits which are too expensive to measure, and for which no good selection criteria exist (e.g. residual feed intake). Commercial companies have started to offer genetic tests for such traits. Meaningful incorporation of these traits into national cattle evaluations will be required to make the best use of DNA information, and such efforts will call for collaboration between DNA companies, producers, scientists, and breed associations.

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