Recent Developments in Genetic Evaluations and Genomic Testing[1]

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The majority of genetic evaluations for beef cattle are carried out by breed associations. These associations use a variety of genetic evaluation providers and methods to calculate their EPDs, and as a result there are different EPDs reported for different breeds. This means that it is sometimes challenging to compare data from different evaluations. Within a breed EPDs can be directly compared; however, this is not true when comparing across different breeds as an EPD from one breed evaluation is not directly comparable to an EPD from another evaluation. Historically this has been resolved by using "across-breed" EPD adjustment factors that are developed by the Meat Animal Research Center (MARC), available at http://beefimprovement.org. The eBEEF page (http://www.ebeef.org) has links to some across breed EPD calculator worksheets developed by Kansas State University and Oklahoma State University.

To help improve the comparability of EPDs from different breeds, twelve breed associations (Chianina, Gelbvieh, Limousin, Maine-Anjou, Red Angus, Simmental, Shorthorn, Canadian Simmental, Canadian Gelbvieh, Canadian Limousin, Canadian Angus, and Canadian Shorthorn) have been collaborating under the umbrella of International Genetics Solutions (IGS) to leverage a multibreed database that enables the calculation of EPDs on a common base. This allows commercial producers to directly compare the genetic merit of animals in this genetic evaluation system regardless of breed composition. The cumulative IGS database includes approximately 16 million total animal records, 100,000 genotypes, and over 340,000 new animals are added annually.

Whole-herd recording

One feature of this IGS collaboration is that many of the participating breed associations require or strongly encourage whole-herd (also called inventory-based) recording. Historically, many genetic evaluations for beef breeds were based on progeny weaned and/or registered and did not require data to be submitted on females that failed to reproduce or whose progeny were not registered. By contrast, inventory-based reporting requires collection of annual reproductive records on every inventoried female within a herd so that some record exists for each animal in the herd, regardless of whether they produced progeny in that year.

According to the Beef Improvement Federation (BIF), the objective of inventory-based or whole herd recording (WHR) is "to accumulate reproductive and certain performance data on all animals in a breed. It does not, however, seek to control which animals will be registered. That remains a decision of individual breeders. With WHR,

[1] This fact sheet was developed based on an article written by the author for Western Livestock Journal 2016 Bull Buyer's Guide. Used with permission.

performance records (or disposal codes) are required on all calves produced by each breeder, but whether any or all of those calves receive registration papers is the breeder's decision." This enables the collection of phenotypes relevant for the development of EPDs for important traits such as heifer pregnancy and stayability which would otherwise be difficult to produce with incomplete data. It also helps to remove selection bias from genetic evaluations which results from only obtaining a select subset of data from superior animals.

Genomic Testing

The incorporation of DNA information into genetic evaluations has been a stepwise evolution since the first genetic tests for cattle were released in the early 2000s. The goal of including genomic information in genetic evaluation is to increase the accuracy of predicting genetic merit for breeding animal candidates. Initially, results were presented independently of beef breed genetic evaluations (i.e. EPDs). This was not an ideal situation as it resulted in two pieces of information about the same trait, and, if the results differed, it was unclear which result was "correct". This changed with the incorporation of DNA test results into National Cattle Evaluations.

For breeders to make the best use of genomic data, it needs to be combined with traditional sources of information (i.e. phenotypes and pedigrees) into traditional genetic evaluations. The main advantage of including genomic information in EPDs is that it improves the accuracy of EPDs on young animals where there is little other information upon which to base genetic merit estimates. This increase in accuracy is dependent upon how much of the genetic variation is explained by the genomic information. In other words, the usefulness of the test is proportional to how well it predicts the true genetic merit of an animal.

The lower the correlation (r) between the test and the true genetic merit of an animal, the more possible change there is in the ranking based upon that test. This is analogous to low accuracy interim EPDs where the possible change in the EPD value is high for low accuracy EPDs. Accuracy (ACC) is the reliability that can be placed on the EPD; ACC ranges from .00 to 1.0. An accuracy close to 1.0 indicates higher reliability. In many breeds, accuracies that are listed as letters (e.g. "PE", "I") are given to young bulls with very little available information. Breed association EPDs are typically associated with Beef Improvement Federation (BIF) accuracies. This BIF ACC measure is very conservative, and it takes a lot of progeny records to increase the BIF ACC. Reranking is uncommon among bulls with high accuracy EPDs as there is less possible change associated with well-proven bulls.

EPDs with low accuracy are still the single best tool for selecting on the trait of interest; however, they are associated with wide margins of possible change. To explain this concept, consider two bulls that have low accuracy EPDs of 0 and +3, but the possible change at that accuracy is 4. This means that it is likely that the second bull is better than the other by 3 units, but it is possible the first bull's EPD will improve by up to 4 units with more data, and likewise the second bull's EPD could change plus or minus 4 units. It is therefore possible that the rank of these two low accuracy bulls could flip with more information. Low accuracy estimates are associated with increased possibilities for changes and reranking.

Production sale catalogs and breed associations often provide breed average EPDs against which to compare a specific bull's numbers. It is important to consider that, although this is useful information, most commercial herds select bulls that are not the breed average. However, since 87.5% of the genetics of a calf crop is determined by the previous three sire generations, it is

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possible to obtain a general sense of a commercial herd's standing for additive genetic merit by evaluating the EPDs of the herd sires used in the recent past.

Incorporation of genomic information into National Cattle Genetic Evaluations

Breed associations have made an effort to invest in developing large phenotyped and genotyped "training" populations to enable the development of genomic prediction equations. Basically, the effect of each genetic marker on the trait of interest is estimated, so that when a new animal is genotyped the effect of each marker it inherited can be summed to get a genetic merit estimate based on genomic data. Bigger training populations allow for the development of more accurate tests. Many breeds now have tens of thousands of genotyped animals in their databases (see Table 1).

Currently, the incorporation of genomic information into genetic evaluations is statistically complex, and often involves a multistep approach that requires 1) traditional genetic evaluation with an animal model, 2) estimation of the marker effects and development of the prediction equation, and 3) a blending of those two pieces of information using a variety of approaches to develop a GE-EPD.

Ultimately, breed associations are working to move to a simpler "single step method" to calculate their genomic-enhanced EPDs and provide a better prediction of true genetic merit. Single-step approaches incorporate all pedigree, genotype, and phenotypic information available from both genotyped and non-genotyped animals into a single, simultaneous evaluation. This is important as usually only a select subset of superior animals is genotyped, and this leads to bias in genomic predictions.

Including information from non-genotyped animals with phenotypes in genetic evaluation helps to correct for this bias. This process uses a lot of computer power, and if there are a large number of records in the breed association database, it can take a long time.

There are two main groups working on improving single-step methodology in the United States. One is the University of Georgia and the other is Iowa State University in collaboration with a private company, Theta Solutions, LLC. They differ in their approach to weighting the individual markers in the genomic prediction equation. Choosing an optimal method for weighting the genomic predictions can have a substantial impact on the accuracy of the resulting EPDs. This is a rapidly evolving area of research and it is likely that most breed associations will have moved to a single step genomic evaluation to produce genomic-enhanced EPDs by the end of 2016.

There are a number of breed associations working on developing a suite of novel traits for genetic evaluations (see Table 1). There are also several large USDA-funded grants that are working to develop training populations for hard-to-measure, novel traits. These include traits such as feed efficiency, susceptibility to bovine respiratory disease complex, and fertility. These large projects require thousands of genotyped animals with observations on these novel traits. It is anticipated that their results will allow for more traits to be added to the list of GE-EPDs in the future.

What genomic tests are available?

Genomic testing is available through breed associations who have partnered with two companies that provide genotyping services; Zoetis and Neogen/GeneSeek (see Table 1). There are several types of tests which differ mainly by the number of genetic markers that are included in the test. There are the so called high-density chips which have somewhere between 50,000-150,000 single nucleotide polymorphism, or SNP, markers on a single assay. It has been found that SNP chips containing more than 50,000 markers show minimal improvement in the genetic variation explained over the 50K chip. For example,

in Holsteins an 800,000 SNP chip only increased the reliability of dairy bull proofs by 0.4% as compared to a 54,000 marker chip.

There are also some lower-density chips that are less expensive and can be used for "imputation," which is a process designed to fill in missing genotypes using information on relatives to achieve a density similar to the high density chip (e.g. Zoetis® i50K and GeneSeekLD). Finally, there are tests that involve a small number of markers that are used for a specific purpose such as parentage, coat color, polled status or genetic defect testing.

Producers typically need to work with their breed associations to order genomic testing in order to ensure the results are included in the breed association's records and genetic evaluation. The cost for the tests that are used in genetic evaluation is ~ $75-90 for the high-density chips, and $45-55 for the low-density imputation chips. Typically, the breed associations obtain either molecular breeding values or direct genotypes from the service provider and work to include that genomic information in genetic evaluation. This produces genomic-enhanced EPDs (GE-EPD), which have improved accuracy due to the inclusion of the genomic information in the EPD calculations.

There are also a number of tests available for simple genetic conditions such as horned/polled, coat color or genetic abnormalities. The costs of these tests vary and there are a number of laboratories providing these tests. Stand-alone tests for parentage vary from $18-30 and for other simple genetic conditions range from $22-$45. Many of these simple genetic tests can be purchased less expensively as an add-on to the higher density genotyping tests.

Testing for commercial cattle
There are several tests that are being marketed for use on commercial cattle that are not directly part of a breed

association genetic evaluation program. In a commercial setting producers often have few criteria (performance records, pedigree, parentage or EPDs) upon which to base their selection decisions. Unfortunately there are not yet any independent, peer-reviewed papers in the scientific literature documenting the field performance of any of these tests for commercial cattle.

GeneMax
There are two products exclusively distributed by Angus Genetics Inc. (AGI) and marketed by Zoetis® and designed for animals that are at least 75% Black Angus. These include GeneMax Advantage ($39) and GeneMax Focus ($17). The first test involves tens of thousands of markers and is marketed as a heifer selection and mating tool that ranks heifers for net return using three economic indices (Cow Advantage: Predicts differences in profitability due to heifer development, pregnancy and calving, and sale of weaned progeny; Feeder Advantage: Predicts differences in net return of feeder calf progeny due to growth, feed efficiency and CAB carcass merit; Total Advantage: Predicts differences in profitability from genetic merit across all economically-relevant traits captured in Cow and Feeder Advantage index scores). It also identifies genetic outliers for cow cost, docility, marbling and tenderness, and also includes parentage information if the sires have been 50K or i50K tested by Zoetis®. The second, less expensive test utilizes fewer genetic markers and is marketed to provide genomic predictions for feedlot gain and marbling, in addition to sire assignment. These two tests are only intended for use on unregistered, commercial Angus animals. As such, GeneMax predictions do not contribute to Angus breed association GE-EPDs.

Igenity Breed-Specific Tests
There are also two Angus-specific heifer selection tests available from Igenity; Angus Silver ($25) which includes calving ease maternal, heifer pregnancy, docility, milk, average daily gain,

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marbling and Igenity Angus Gold ($40), which additionally includes birth weight, mature weight, residual average daily gain, weaning weight, tenderness, ribeye area, back fat thickness and carcass weight. These two tests can be directly ordered through Igenity. Additionally, there are two breed-specific heifer replacement tests for Red Angus and Gelbvieh that can be ordered through the corresponding breed association. The Red Angus Herd Navigator ($25) test provides results on all traits for which RAAA calculates EPDs, Red Angus' HerdBuilder and GridMaster Indices, and parent verification if the potential sires have been tested with the RA50K test. Due to the breed-specific nature of this test, the Herd Navigator should only be used on females that are at least 75 percent Red Angus. The Gelbvieh Maternal Edge Female Profile ($26) is a low-density panel to be used by producers as a sorting tool for Gelbvieh-influenced commercial females. It includes calving ease, maternal calving ease, weaning weight, yield grade, marbling, and carcass weight.

PredicGEN
PredicGEN ($19.50) is a test marketed by Zoetis® as "a heifer selection tool for straight-bred or crossbred British/Continental animals that are less than 75% Black Angus". The carcass traits predicted include marbling score, USDA yield grade, grid merit and tenderness. According to the Zoetis technical bulletin, 10,000 animals with recorded carcass data were included in the training population. Reported outcomes for internal validation showed a correlation (r) of 0.31, 0.34, 0.45 for tenderness, yield grade and marbling phenotypes, respectively. Data is reported back on a normally distributed 0 to 100 scale, with a mean of 50 based on Zoetis'® database of 20,000 genotyped animals.

Igenity Gold and Silver
The Igenity Gold and Silver tests, which include approximately 1000 markers associated with 13 traits of interest and some randomly spaced markers, are being marketed by Neogen® as "DNA profiles for crossbred and purebred cattle." A single prediction equation is used for each trait to give the score or molecular breeding value, irrespective of the breed makeup of the animal being tested. The silver test ($25) evaluates six traits (calving ease maternal, stayability, residual feed intake, average daily gain, tenderness, marbling), and the gold test ($40) includes an additional 7 traits (birth weight, calving ease direct, heifer pregnancy, docility, milk, ribeye area and back fat thickness). According to the Neogen brochure, the development of these tests involved large populations with phenotypic data and/or expected progeny differences (EPDs) comprising tens of thousands of animals that represent various biological types. The six main datasets used to form the training data set for this test were from six breed associations: Black Angus, Hereford, Gelbvieh, Limousin, Red Angus, and Simmental. Data is reported back on a 1 to 10 scale.

These tests were developed with input from researchers at Iowa State University. Unpublished data (Saatchi and Garrick, personal communication) suggests that this reduced SNP panel (~2,300 markers) gives purebred genetic merit estimates of ~ 80-90% of the accuracy of the 50K SNP chip for the six breeds in the training data set. The accuracy drops when utilized in a crossbred commercial cattle population, and the correlation between the test result and the true breeding value (r) is approximately ~ 0.3 when estimating the genetic merit of commercial crossbred animals. The correlation is likely to be even lower in animals comprised of breeds that were not in the original training set. The lower the correlation (r), the more possible inaccuracy there is in the ranking based upon that test.

Summary
The application of genomics to improve the accuracy of EPDs is a rapidly developing field. There are ongoing

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improvements in genotyping and sequencing technologies, statistical methods to increase the correlation between genomic predictions and true genetic merit, and the computing systems to handle the large datasets associated with animal breeding. One thing still remains true in the genomic age and that is the need to collect accurate phenotypic records. It is essential to ensure performance data, pedigree, and DNA information are recorded and reported accurately. Genomic predictions will only be as reliable as the data upon which they are based. Although it might seem like the genomics era could signal the end of performance recording, the opposite is true. Now more than ever, it is important that producers accurately report data, and ensure that animals which are genotyped are correctly identified so that their information can contribute towards improving the accuracy of the genomic predictions of the future.

Table 1. Summary of Breed Association Updates

	No. Animals genotyped	Genomic-enhanced EPDs?	Genotype provider	Genetic evaluation provider	New traits in development
Angus	160,000	Y	GeneSeek Zoetis	AGI[2]	Feed intake EPD has been implemented, feet and leg phenotypes being collected, PAP score (indicator of brisket disease), adaptability-heat stress/fescue tolerance
Brahman	400	Y (for tenderness)	GeneSeek Zoetis	ABRI[3]	Plan to roll out GE-EPDs for all traits in current evaluation by mid to late 2016
Brangus	4,316	Y	GeneSeek Zoetis	LGS[4]	Fertility and end product indexes, stayability, docility, feet and leg scoring system
Beef Master	400	Target 2016		LGS	Plan to deploy maternal and terminal indexes in Spring 2016
Charolais	2136	Y	GeneSeek	AGI	Developed static terminal index
Gelbvieh	3880+	Y	GeneSeek	IGS	Revamping Stayability definition to require a calf be born every year (more indicative of actual reproductive performance).
Hereford	>20,000	Y	GeneSeek	ABRI[2]	Carcass weight EPD, heifer calving rate, sustained cow fertility, feed intake, docility
Limousin	5660	Y	GeneSeek	IGS	Feed intake/efficiency, maternal data: breeding, udder score, body condition scoring and mature weights
Maine-Anjou	~1000	Not yet		IGS	
Red Angus	13700	Y	GeneSeek Zoetis	IGS	Feet and leg scoring genomic data incorporated into threshold traits, feed intake, and environmental stress
Santa Gertrudis	3,320	Y	GeneSeek	LGS	Tenderness EPDs have been implemented, have developed two indexes for growth and carcass. Introducing 3 new EPDs, with April 2016 being the target date for release, Heifer Pregnancy, Breed Back, and Scrotal Circumference
Shorthorn	940	Target 2016		IGS	
Simmental	25,296	Y	GeneSeek	IGS	Multibreed: Stayability and Heifer Pregnancy

[2] Angus Genetics Inc. http://www.angus.org/agi [3] Agricultural Business Research Institute https://abri.une.edu.au
[4] Livestock Genetic Services, LLC

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