Volume 13, Issue 4
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MISSISSIPPI
BCIA
BEEF CATTLE IMPROVEMENT ASSOCIATION

- May 12—BQA, Tadlock Stockyard, Forest
- May 12—Hinds County Extension and NRCS Field Day
- May 19—Alfalfa Hay Production Demo, Newton
- May 21—MS/LA Beef and Forage Field Day, Tylertown
- May 21—Beef Unit Filed Day, MSU campus
- May 26—BQA, Simpson County Livestock Pavilion, Mendenhall
- June 14-17— BIF Conference, Manhattan, KS
- October 13-15—MSUES Artificial Insemination School, MSU
- November 10—BCIA Bull and Heifer Sale, Raymond

Inside this issue:

Using Genetics to Improve Animal Welfare

Have you heard the old saying that a country with plenty of food resources has many problems, but a country without food only has one problem? Over the last few years, our country has been on what some call, a food revolution. With the eruption of social media from Facebook to Snapchat and everything in between—people are becoming more aware of food. In fact, Instagram, reports that food is one of the most common tags used when describing a picture (#food).

Our interest in food goes well beyond stimulating our taste buds. Based on results from the 2011 National Beef Quality Audit consumers are also interested in where their food comes from and how it is raised. With the average American consumer 3-4 generations removed from the family farm or ranch and an abundant amount of misinformation about agriculture technologies the average consumer is confused. In addition, we're presented with a conundrum— the public appreciates the values held by farmers and ranchers, but are uncertain about farming and ranching practices. We in the agriculture community can talk about the safety of our products and how we are regulated by strict standards set by the United States government. However, most people are skeptics of them, too.

Skeptical antagonisms

There are several things that we do in the cattle industry that consumers, for the most part, dislike—mostly because they do not understand. They are not generally in favor of growth promoting implants, antibiotics, feeding GMO-derived plant materials, and basic veterinary procedures, such as dehorning and castration. Farmers and ranchers do share one BIG attribute with consumers; we are all for proper animal welfare. How can we avoid the use of antibiotics, and provide animal welfare to sick animals? How can we remain judicious to environmental concerns without the uses of implants? Genetics!

Upcoming Genetic Technologies

Animal breeders around the world are working on identifying new genetic markers that can help us identify animals who are less prone to being sick and need less antibiotics. Multiple breeds have health-related genomic research being conducted for Bovine Respiratory Disease (BRD), pinkeye prevalence, and even prolapse occurrences. Some breed associations, like the American Hereford Association are working on genetic programming technologies that can help seedstock producers use horned genetics and remove the chances of having horned calves (think of sex sorting semen—but sorting for genes).

What Does this Mean?

Even though, we may be many years before this technology can be implemented on a commercial, wide-scale level, the possibilities are endless. As seedstock producers it is important to embrace the ideals of your breed associations and work with them to submit both phenotypic and genotypic data on ALL your animals. As we look for scientific validation on these genetic processes, it is also important that our lawmakers are aware of what you do a s a producer and how you are playing a role in the genetic improvement of the beef industry. These genetic tools will inevitably help us do a better job with selection and breeding decision and improve animal welfare.

The Random Shuffle of Genes—Putting the E in EPD

By: Jared Decker, PhD—University of Missouri Extension

Summary: Why are EPDs imprecise for young animals? How can genomics be used to track the random shuffle of genes?

Even though expected progeny differences (EPDs) have been used by the beef industry for over 40 years, many misconceptions still exist. Occasionally we will hear a producer say something like, "I bred my cows to a low birth weight bull, but I had a couple of large calves." What the producer does not realize is that this is to be expected based on the inheritance of complex or continuous traits. Let's look at this more closely.

A calf inherits about 50% of its DNA from its sire, with the other 50% coming from its dam. Each sperm that is produced by a sire is a random sample of that sire's chromosomes and genes. Cattle have 30 pairs of chromosomes. So, when a sperm is produced, it is similar to flipping 30 coins. If we label the chromosomes the sire inherited from his father as blue/paternal and the chromosomes inherited from his mother as pink/maternal, there are 1,073,741,824 possible combinations of the sire's paternal and maternal chromosomes. And, this number ignores the swapping of parts between paternal and maternal chromosomes in a biological process called recombination. So, the number of possible chromosome combinations is in the billions! We often state this as progeny receive a random sample of the sire's genes, and with billions of possible combinations no two sperm are exactly alike (the same is true for eggs produced by the dam).

Think for a moment about your favorite set of full siblings (brothers or sisters with the same parents). Perhaps this is the celebrity family with a reality television show, your brothers and sisters, your children, or your favorite set of embryo flush mate calves. The dissimilarity between these siblings may be striking, for example, one may be short and the other tall, one may have light hair and the other dark hair, or one may be laid-back and the other excitable. The similarities between siblings are due to shared environment and shared genes. The dissimilarities between siblings are due to differences in environment and genes which are not shared. Siblings share 50% of their DNA on average, but in humans this can vary from about 40% to 60%.

If we assume random mating and that the parents are unrelated, we can show mathematically that the breeding value variation (i.e. EPD variation) observed between a set of full siblings (calves with the same parents) will be half of the breeding value variation observed in the population. Even if our assumptions about random mating and unrelated parents do not hold up in real populations of cattle, the variation between full siblings will still be quite substantial. Research in Brown Swiss, Holstein, and Jersey dairy cattle provides evidence that the variation between full siblings is very close to, if not greater than, one half of the population's genetic variance (the variation in EPDs or breeding values.

The EPDs reported by breed associations can be thought of as one half of the sire's breeding value plus one half of the dam's breeding value plus the Mendelian sampling term (EPD_calf=1/2 EPD_sire+1/2 EPD_dam+Mendelian Sampling). The Mendelian sampling term represents a calf's difference from the average of the parent's breeding values. This difference is due to the random sample of genes and chromosomes that the calf inherited. When a calf is born, we have no data, so we assume this Mendelian sampling term is zero and the EPD is reported as the parent average. As we gain more data about the calf and the calf's eventual progeny, we are better able to estimate this Mendelian sampling term and the EPD accuracy increases and the EPD estimate either increases or decreases.

Unfortunately, in the past embryo transfer flush mates have been marketed by some seedstock producers as containing identical genetics. The only cattle that share identical genetics are identical twins and clones (but even clones do not share short segments of DNA, i.e. mitochondrial DNA). Because birth weight and weaning weight data from embryo transfer calves are not typically used in national cattle evaluation (as the calves are reared by recipient dams not the biological dam), the flush mates have identical EPD profiles early in life. These EPD predictions remain identical until data on the flush mates' progeny is recorded. These identical EPD profiles are simply the parent average EPDs. Like all parent average EPDs, these EPDs are not precise (reported as EPD accuracy) because the EPD estimation equations do not have data to predict the gene variants inherited from the sire and dam. In other words, without data the EPD equations are not able to predict the Mendelian sampling term, the random set of genes inherited as a result of gene segregation and shuffle. Traditionally, EPDs for flush mates have not changed until data about the progeny of the flush mates were recorded.

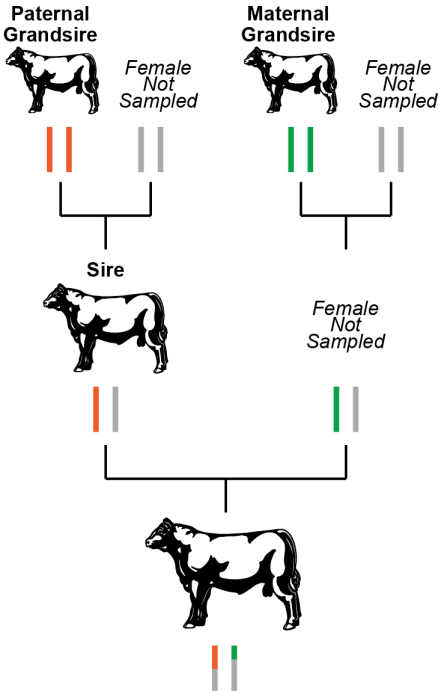
With new genomic technology the Mendelian sampling term can now be estimated for flush mates and other progeny. Genetic tests that provide genotypes on thousands of DNA variants enable an estimation of which set of genes an animal actually inherited. Genomic testing provides an estimate of the Mendelian sampling term and the genetic merit associated with the inherited variants. This information is then combined with the traditional pedigree EPDs to produce more reliable genomic-enhanced EPDs. In a roundabout way, this technology is tracking which bits of the sire's and dam's chromosomes were inherited. In a slightly different approach used by the dairy breeds and by the Santa Gertrudis beef breed, the pedigree relationship information used to calculate EPDs is supplemented with genomic relationship information. Shared DNA variants are used to estimate how closely related two animals are, in other words their genomic relationship. This procedure can tell whether a calf is more closely related to its paternal grandsire or its paternal granddam, thus tracking the

Genes: Continued

inheritance of the sire's chromosomes and identifying the Mendelian sampling term. See Figure below for an example based on real world data. Based on averages, we would expect a calf to share 25% of its genes with any of its grandparents. But, due to the random shuffle of genes and chromosomes, this percent can vary greatly. Whether genomic data is used to produce a genomic prediction or supplement the relationship estimates, both of these approaches increase the accuracy of the EPD as they provide data that allows the Mendelian sampling term to be estimated.

It is important to remember that EPD stands for expected progeny difference. Expected refers to a statistical expectation, which means a prediction or average. Thus an EPD is the predicted average difference between a sire's calves and the EPD base. EPDs predict averages, because for a large group of calves the Mendelian sample term approaches zero. An individual calf can have a very different genetic merit from the sire (a large Mendelian sample term) due to the random sample of genes it inherited.

In conclusion, a calf shares 50% of its DNA with its sire and 50% of its DNA with its dam. On average, two full siblings also share 50% of their DNA. But, which DNA variants are shared between a parent and a calf or two full sibling calves at birth is unknown. Because of this parent average EPDs are used for young calves. It is only when more data are collected that we are able to estimate this random sample of genes (i.e. the Mendelian sampling term). Genomics provides information that enables the Mendelian sampling term to be estimated. Genomic-enhanced EPDs use DNA information to estimate the random sample of genes inherited from the parents and result in more accurate and reliable EPDs for young animals. The random shuffle of genes and chromosomes puts the expected in EPDs. *From ebeef.org, accessed April 1, 2016.*



We still have room on the van to BIF in Manhattan, Kansas!
Contact Cobie to reserve your spot!

April 2016 — Management Calendar

GENERAL

Watch for grass tetany, particularly on lactating cows grazing lush pastures. Feed a high magnesium mineral supplement to cows on ryegrass/tall fescue pastures. Provide proper free-choice minerals and fresh water at all times. Maintain at least 4" average stubble height on winter annual pastures to avoid overgrazing. Fertilize cool-season grasses according to soil tests if not done by February. Locate hybrid bermudagrass sprigs for planting next month. Spray to control little barley, buttercup, and other winter annual weeds. Plan summer fly control before fly population buildup. Consider vaccination for anaplasmosis and/or pinkeye. Vaccinate all calves more than three months old for blackleg (7-way). Consider marketing cull cows.

SPRING CALVING - January, February, March

Dip navels, identify, castrate, dehorn, and implant calves as appropriate at birth. Acquire quality herd sires with performance information from reputable sources. Make sure that calving ease sires are selected for breeding to heifers. Conduct breeding soundness exams and make sure bulls are in good condition in advance of spring breeding. Vaccinate all open cows and heifers for vibriosis, leptospirosis, and IBR at least 30 days before breeding. Consult with a veterinarian for BVD recommendations for the local area. Cows need to be in moderate to good condition to rebreed early. Place cattle with the highest nutritional needs (lactating first-calf heifers and cows) on the highest quality grazing and hay. Supplement the cow herd as needed according to forage test results. Start breeding heifers about a month before the cow herd.

FALL CALVING - October, November, December

Remove bulls 283 days prior to the end of the desired calving season (mid-March to end the calving season around late December). Keep bulls in a small pasture traps with effective fences. Feed bulls to start the next breeding season in good condition. Observe the cow herd for returns to standing heat. Castrate and dehorn late calves or those missed in early working.

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Membership Application

Name:_____

Address:_____

City:_____

County:_____ State:_____ Zip:_____

Phone:_____ Email:_____

(Check one) Seedstock:____ Commercial:____

Cattle breed(s):_____

Completed applications and $5 annual dues or $100 lifetime dues payable to Mississippi BCIA should be mailed to:

Mississippi Beef Cattle Improvement Association
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