

# Genomic Selection Decisions

Technical breakout session focuses on genomic tools to aid selection.

by *Kasey Brown*, associate editor, & *Nicole Lane*, editorial intern

**W**hile the 2015 Beef Improvement Federation (BIF) symposium's theme was "Expanding Focus," several technical breakout sessions presented by BIF's formal committees allowed attendees to dive deeper into specific topics. The session featuring advancements in selection decisions covered topics of feed efficiency, heterosis in across-breed expected progeny differences (AB-EPDs), genomics of bovine respiratory disease and how whole-genome sequencing will affect selection decisions in the future. The symposium was hosted June 9-12 in Biloxi, Miss.

## A quicker way to assess efficiency

A genetic trait that can help cattle producers increase efficiency and improve the bottom line is worth selecting for, according to Kelli Retallick of Kansas State University. Retallick presented her research on methods to better select for feed efficiency.

She reported that if a producer could increase feed efficiency by 10%, they could grow profits by as much as 43%.



PHOTOS BY NICOLE LANE

► Kelli Retallick evaluated 5,606 total animals, including 3,212 steers and 2,394 heifers, using data from the U.S. Meat Animal Research Center at Clay Center, Neb., and breed associations. Using ADG, ADFI and postweaning gain data, the calves were evaluated using the 35-day test and the traditional 70-day test.

Currently, BIF standards for testing for feed efficiency take 91 days to collect data. Retallick investigated a method that would cut the testing time to 56 days, increasing testing ability and cutting costs on selecting for feed efficiency.

Two parameters were used to derive genetic expression of feed efficiency — average daily gain (ADG) and average daily feed intake (ADFI). By using these

two parameters as guidelines, a moderately heritable feed efficiency trait was determined.

Research supports the idea that a shorter 35-day intake test (56 days with prep time) could be more economical than the current 70-day test (91 days with prep time). However, there has been concern that it would lower the accuracy of the test. Retallick increased selection intensity to compensate for the estimated loss in accuracy. Her work showed that this shorter test could be a cost-efficient and precise way to select for feed efficiency.

Retallick evaluated 5,606 total animals, including 3,212 steers and 2,394 heifers, using data from the U.S. Meat Animal Research Center (USMARC) at Clay Center, Neb., and breed associations. Using ADG, ADFI and postweaning gain data, the calves were evaluated using the 35-day test and the traditional 70-day test.

Using ADG, ADFI and postweaning gain as parameters to create an unrestricted selection index, she found that cost was lower in the shorter test, and the index resulted in a higher heritability for both gain and intake.

"Using our unrestricted linear index with our postweaning gain also allows for maximum genetic progress to be made for feed efficiency," said Retallick.

She concluded that a 35-day intake test is long enough to test ADFI without losing accuracy, and the test can be combined with postweaning gain data to test for feed efficiency. Also, her research showed that the shorter test can save a producer \$27 per head per week when testing for feed efficiency. If this test became the new industry standard, it would cut the current time used to test animals for feed efficiency in half, freeing up space for more animals to be tested per year and helping producers more accurately select for feed-efficient animals.

— by *Nicole Lane*

## Heterosis and EPDs for crossbreeding

Commercial producers are often encouraged to capitalize on the genetic strengths of different breeds to optimize their cow herd. This can be a difficult task when EPDs from the different breeds don't match up and across-breed adjustment factors aren't

always available for some of the economically valued traits.

Matt Spangler of the University of Nebraska shared his research on across-breed calving ease EPD adjustment factors. The goal of his work was to learn how to create an across-breed EPD for calving ease direct (CED) and calving ease maternal (CEM).



PHOTO BY TROY SMITH

► Matt Spangler suggested that an updated delivery model be required for EBVs for calving difficulty and other traits that don't fall on a normal distribution pattern to expand the number of across-breed EPDs that can be made available to producers.

"Currently we have this information for birth weight, but birth weight is an indicator trait, not an economically relevant trait," Spangler said. "Calving ease is an economically relevant trait, so we would like to be able to develop adjustment factors to tackle that."

Spangler studied this by evaluating breed-specific heterosis for the seven commonly used beef breeds in the United States (Angus, Hereford, Red Angus, Charolais, Gelbvieh, Simmental, Limousin) and the composite MARC III (¼ Angus, ¼ Hereford, ¼ Pinzgauer, ¼ Red Poll). By creating a population of animals that represented these breeds and frequent crosses, Spangler collected data to provide a heterosis summary.

This type of data can be used to estimate the effect a trait will have in specific crossbreeding scenarios. He concluded that heterosis still exists, use of biological type in breeding systems is warranted, and we need to revisit breed-specific heterosis again.

When attempting to compare calving ease EPDs across breeds, Spangler described it as comparing apples and oranges. This is due to

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the different models that breed associations use to provide birth weight EPDs. When scaling differences between breeds the variety of models makes creating an EPD or estimated breeding value (EBV) nearly impossible.

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— by Nicole Lane

### BRD genomic testing

Researchers have a similar problem as cattlemen in that genetic testing is expensive. This makes economically important research, like that of determining genomic traits for bovine respiratory disease (BRD), difficult. Larry Kuehn, research geneticist with USDA Agricultural Research Service and USMARC, explained an alternative — DNA pooling.



► Larry Kuehn shared research that is working to identify SNPs associated with severe lung lesions in fed beef cattle. The research team sampled 11,520 lungs from a Nebraska processing plant, and the majority of lungs came from cattle raised without antibiotics.

Kuehn said DNA pooling offers an alternative, though limitations must be taken into account.

The cost of testing 96 animals with a high-density DNA profile is \$14,880, but testing a pool of 96 animals costs \$155. The data need extra imputations when pooled, but it does present a significant cost savings.

Pooling DNA has opened up more research opportunities at USMARC, including studies on lung lesions, diseases like BRD, foot rot, pinkeye, bovine viral diarrhea, bloat, pregnancy detection and more.

He shared research that is working to identify single-nucleotide polymorphisms (SNPs) associated with severe lung lesions in fed beef cattle. The research team sampled 11,520 lungs from a Nebraska processing plant, and the majority of lungs came from cattle raised without antibiotics.

He admitted that the research isn't at a producer-application level for national cattle evaluation yet, but results are useful from a research perspective. Seven SNPs achieved genome-wide significance at the 5% level, and 84 SNPs achieved a false discovery rate of 5% or less. Near-significant SNPs were found for tissue repair and regenerations, tumor suppression, control of organ size and immunity.

“We reduced the cost of genotyping by exploiting sample pooling of extreme animals, and we identified SNPs that might be useful to reduce BRD complex and reliance on antibiotics,” Kuehn explained.

He highlighted a future study that will look at feedlot BRD, and said he hoped that the lung and feedlot project will produce complementary results to keep moving forward.

— by Kasey Brown

### Genome sequencing's impact on selection decisions

In the last 15 years, the cost of sequencing 1 million base pairs has dropped from more than \$5,000 to 5¢, said Jared Decker, assistant professor and beef genetics specialist at the University of Missouri.

That intense price drop illustrates the journey of genomic sequencing, and opportunities abound. Genomic sequencing has hit some rocky patches since the 1970s. The available technology wasn't always up to par, or assumptions didn't always reflect the data or biology, Decker explained. In 2009, the bovine reference genome sequence assembly was published, genomic predictions were implemented in the dairy industry and the entire DNA was taken into account. Angus Genetics Inc. (AGI) implemented genomic predictions in 2010, followed by several other breeds in 2012.

With the great leaps in technology, Decker highlighted some options of future opportunity with genome sequencing. Imputation is on the near horizon. He gave the example of mile markers vs. points of interest on a road trip. With enough background data, those “mile markers” could



► Jared Decker highlighted opportunities with genome sequencing now available due to leaps in technology.

be predicted from the data at those “points of interest.” He said scientists can infer 11 million markers from a 50,000-SNP chip. A finer scale and more precise analysis allows scientists to identify SNP regions associated with a specific trait.

Decker predicted more types of SNP chips or panels, including higher-density panels focusing on functional variants for research, and lower-density panels focusing on functional variants for prediction. Additionally, he added that genomic predictions would be based on causal variants or closely linked variants, which could lead to lower cost and more precise predictions.

He mentioned genomic “surveillance” of influential sires. Breed associations could sequence a sire when he reaches a certain number of progeny equivalents, which would mean progeny, grand progeny and farther down. This could lead to early identification of possible functional variants, both good and bad — like embryonic lethals. This could also help manage inbreeding based on shared negative variants.

Decker explained that genomic sequencing is in the upward trend, deemed the “slope of enlightenment,” and he concluded that there are many possibilities.

— by Kasey Brown



**Editor's Note:** The 2015 BIF Annual Convention was hosted by Mississippi State University and the Mississippi Extension Service June 9-12 at the Beau Rivage Casino and Hotel in Biloxi. The Angus Journal and LiveAuctions.tv provide comprehensive online coverage of the event at www.BIFconference.com. Visit the Newsroom for summaries, proceedings, PowerPoints and audio of the sessions; the Awards page for announcements of award winners; and the Photos page for photo galleries of the tour.