

Improving Cattle Health Genetically

by **KATIE GAZDA**, editorial intern

Animal health is synonymous with animal welfare, Mark Enns of Colorado State University (CSU), told attendees of the 43rd annual Beef Improvement Federation (BIF) symposium in Bozeman, Mont. A picture of a sick animal is automatically associated with improper treatment to an unknowing member of the public.

What the public doesn't realize, however, is that the producer also associates animal health with animal welfare. We want to see a sick animal just as much as the average consumer, Enns said.

Enns opened Thursday's second general session, which focused on genetics and animal health. In today's genetically focused industry, he said, it is highly beneficial for beef breeders to select for health traits. By selecting for these traits, cattlemen stand to gain as an industry from reduced costs of production, lower treatment and mortality rates, and an

overall decline in poor performance associated with sick cattle.

In regard to health, we have historically focused on management: low-stress handling, vaccination, and early treatment of disease. We have given environment and performance the majority of our attention, and we have generally ignored genetic improvement in health, Enns said. In doing this, we have limited ourselves from additional possibilities that could ultimately benefit our industry.

Selection typically focuses first on the "low-hanging" fruits — those that are easily picked. Expected progeny differences (EPDs) for traits such as birth weight, weaning weight, milk, etc., have been heavily utilized. However, there are other economically relevant and hard-to-evaluate traits, such as health, that could improve profitability of production.

In terms of cattle health, Enns described three disease classes that provide opportunity for improvement through genetic selection:

- diseases that result from a defect in genetic composition;
- diseases that result from nontransmittable environmental challenges; and
- vector-related diseases.

The industry has had overwhelming selection success against genetic defects and a good bit of success in environmental diseases. Unfortunately, there has been little to no success with regard to vector-related diseases. But, Enns asked, have we tried hard enough?

Enns explained the impediments to genetic progress, including an absence of selection tools, a lack of knowledge concerning hard-to-evaluate traits (such as health), and a general lack of focus.

He described research performed at the CSU beef unit to study high-altitude, or "brisket," disease in beef cattle. He determined a genetic variation and heritability of pulmonary arterial pressure (PAP), which can be used to predict an animal's likelihood of developing brisket disease at high altitude. The unit began

applying downward selection pressure to PAP scores in the early 1990s. Consequently, it has significantly reduced death loss in the herd.

Selection for health traits does in fact work when you have a way to evaluate it, Enns said.

He concluded that there is evidence genetic variation does exist for health traits in beef cattle populations and, if utilized correctly, can benefit the industry. However, in order to do that, the industry must first develop the necessary tools to make the selection successful.

Lastly, in a world focused on monetary value, we must determine the level of economic importance that these hard-to-evaluate traits hold.

To listen to this presentation and to view the PowerPoint and the proceedings paper that accompanied it, visit the Newsroom at www.BIFconference.com.



Integrating Molecular Data Into NCEs

by **TROY SMITH**

Serious cattle breeders of all stripes seek tools for genetic selection. Commercial cow-calf producers want tools for mitigating risk when choosing which bulls to buy. Seedstock breeders — the suppliers of those bulls — want tools that hasten genetic progress.

Expected progeny difference (EPD) values are widely used tools for genetic selection, but they will become even more valuable, according to University of Nebraska animal scientist Matt Spangler.

"Genomic information holds the promise to not only increase the accuracy of EPDs, but also to add new and novel traits to our suite of traits

included in national cattle evaluations," Spangler stated during the 43rd annual Beef Improvement Federation (BIF) symposium in Bozeman, Mont.

Inclusion of DNA marker information into EPD calculations promises three primary benefits, according to Spangler:

1. increased accuracy of prediction for young animals (before a phenotypic record can be collected);
2. shortened generation intervals; and
3. calculation of EPD values for novel traits.

Examples of novel traits might include feed efficiency, disease susceptibility, end-product healthfulness, or other traits for which there is little if any collection of phenotypes.

Spangler noted how numerous commercial DNA tests (marker panels) are available for complex traits. A given trait may be influenced by many genes, however, and there still exists considerable confusion among producers regarding the efficacy of DNA tests.

To help remedy that, said Spangler, the Weight Trait Project was begun in 2009 to investigate the reliability of marker-based predictions across beef breeds. It also provides a data resource helpful for determining methodology for incorporation of genomic information into national cattle evaluation calculation, with marker-assisted EPD values as the goal.

The Weight Trait Project will continue as part of a \$5 million USDA grant-funded

national research effort. This five-year project represents a collaborative effort among multiple land-grant universities, several breed associations and the USDA-Agricultural Research Service, with the U.S. Meat Animal Research Center, Clay Center, Neb., as the project hub.

To listen to this presentation and to view the proceedings paper and the PowerPoint that accompanied it, visit the Newsroom at www.BIFconference.com.

BIF's 43rd Annual Research Symposium and Annual Meeting was hosted June 1-4 on campus at Montana State University, Bozeman, Mont.



Genetics of vaccine response

While beef cattle breeders have successfully developed expected progeny difference (EPD) values for a large number of traits, genetic prediction for animal health remains undeveloped. Speaking during the Beef Improvement Federation's 43rd Annual Research Symposium in Bozeman, Mont., South Dakota State University geneticist Michael Gonda explained research targeting development of a DNA test that producers could use to select for healthier cattle.

Gonda has sought to measure individual animal response to vaccination against bovine viral diarrhea (BVD) by checking blood antibody levels. His study also looked at how vaccine response might differ among calves by different sires. Results suggest a link between sire and calf vaccination response — strong evidence that the response was at least par-

tially controlled by genetics.

Gonda's research team also tested whether a polymorphism in the leptin gene was associated with vaccine response. The leptin gene has been associated with carcass and growth traits. The objective was to determine whether producers might have inadvertently selected for lower disease immunity when making selections based on this leptin polymorphism. However, results suggest there is no association with BVD vaccine response.

Gonda said the study represents just a first step toward development of a DNA test for vaccine response. Some questions remain unanswered.

"One question is whether measurement of antibodies explains all of the vaccine response. My guess is that it does not, and other factors are involved," Gon-

da said. "I want to build a resource population to collect phenotypes that can be used for DNA testing."

Gonda also wants to determine the genetic correlation between vaccine response and disease susceptibility, as well as the correlation to other economically important traits. He hopes to determine which DNA markers are associated with vaccine response. After discovery, these associations will need to be confirmed in an independent gene mapping population. The next task, Gonda said, will be to develop a selection tool based on DNA markers.

To listen to this presentation and to view the PowerPoint and the proceedings paper that accompanied it, visit the Newsroom at www.BIFconference.com.

— by Troy Smith