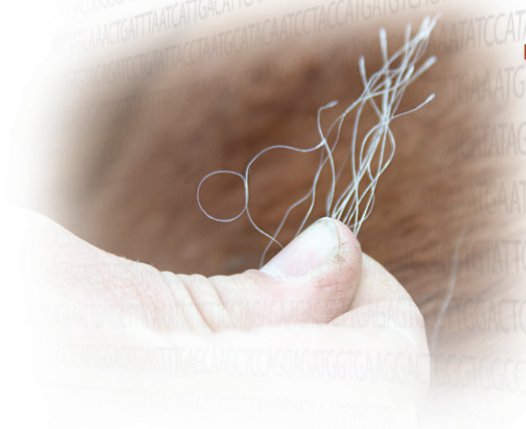
Genomics and the Rancher



A look at how genomics will affect the cattle industry.

by ***Troy Smith***

It takes time and observation to evaluate how a new technology will influence beef cattle production at the ranch level. According to a pair of animal scientists making presentations at the 2011 Range Beef Cow Symposium in Mitchell, Neb., that's the case for genomics — the study of genes and their function in order to understand how they influence differences among living beings.

Colorado State University Extension Beef Specialist Jack Whittier and University of Nebraska Geneticist Matt Spangler talked about how information gathered through DNA testing of beef cattle applies to genetic improvement through selection of seedstock. Their take-home message was that information from DNA testing is not a replacement, but an enhancement, for tried and true tools for genetic selection.

According to Whittier, samples of an animal's DNA are evaluated for SNPs (single nucleotide polymorphisms called "snips") or "markers" known to be associated with genes influencing the expression of particular production traits. The association between SNPs and phenotypic traits of interest has been established through extensive statistical comparisons of DNA libraries with databases representing populations of animals with known performance.

"As new SNP information is discovered," explained Whittier, "the statistical models are 'trained' or 'validated' to assure that accurate predictions are valid."

At the time of the symposium, Whittier said, two primary companies have the technology to test beef cattle for genetic defects, parentage, coat color, horned/polled traits and numerous performance traits. DNA samples can be evaluated and genetic merit predicted for traits such as carcass tenderness, marbling, yield grade, ribeye area and others. With validated tests, predictions can be made regarding an animal's performance, even when that animal has little or no phenotypic data in the database. (For information about Hereford genomic testing, see "Hereford DNA Q&A" on Page 16.)

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Whittier reminded the audience of the importance phenotypic data has played in evaluating an animal's genetic worth as a parent. All available information about an individual and its relatives is combined to create a genetic profile for comparison to other individuals of the same breed.

PHOTO BY BECKY HARRELL

DNA vs. progeny testing

Expected progeny difference (EPD) values, used for at least 25 years to evaluate an individual's genetic merit, are based on the actual performance of individual sires and their progeny. While important, Whittier called the collection of progeny data both time-consuming and expensive.

"It's slow. Progeny testing takes three to four years and a bull is at least 5 years old before his first evaluation is available. And progeny testing costs about $25,000 per bull," Whittier explained, adding that only one in eight to 10 bulls "graduate" from progeny testing.

Whittier said marker-assisted selection, based on sampling and evaluating DNA for SNPs, offers savings of time and resources needed to test large numbers of progeny. And now, genomic information derived from DNA testing for gene markers is being integrated with traditional EPDs, resulting in marker-assisted or genomic-enhanced EPDs (GE-EPDs) for economically important traits. Whittier likened GE-EPDs to the application of more rigorous analysis of nontraditional player statistics in Major League Baseball, as depicted in the film "Moneyball."

"Predictors like marker-assisted EPDs, or molecular breeding values for economically relevant traits, may allow cattle producers a better way to identify valuable animals, using 'player statistics' coupled with DNA markers," said Whittier.

A fair question to ask is why development of genomic predictions seems to have focused more on heavily recorded traits, such as growth, rather than desirable but "novel" traits like disease susceptibility or measures of efficiency. According to Nebraska's Matt Spangler, development of genomic tests depends on existing phenotypes used to "train" the markers.

"Training is simply determining if there is an association between each marker and the trait of interest, and quantifying that effect. Consequently, the first genomic tests focused on those traits for which vast phenotypic resources exist," explained Spangler, noting that current U.S. Department of Agriculture (USDA)-funded research projects are focused on the novel traits previously mentioned.

Another question producers commonly ask is whether DNA testing really works. However, Spangler said the more appropriate question is, "How well does it work?" The answer,

he says, is related to how much genetic variation for a specific trait is explained by a marker test.

A very useful application of genomics has been for identification of genetic defects. Coupled with DNA testing for parentage, this has provided for the identification and removal from the breeding population of animals that carry specific defects. A step beyond that is to apply genomics to selection for more complex traits. Spangler said collection of DNA information, which can be accomplished at a young age, affords an improved prediction of an animal's genetic potential.

Blending with EPDs

But rather than looking at DNA test results as separate and disjoined pieces of information, Spangler sees greater value when genomic information is incorporated in national cattle evaluation and the calculation of EPDs. The real benefit derived from combining molecular tools and traditional EPDs is improved accuracy of prediction. Marker-assisted EPDs, through their increased accuracy, can provide for an increased rate of genetic change through selection.

When more information is added to the calculation, an EPD value may go up or down, explained Spangler, adding, "When you genotype animals, the accuracy will always go up."

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A limitation to current application of marker-assisted selection is that marker panels work best in the populations where training occurs but potentially decrease in predictive power as the target population becomes more genetically distant from the training population. Erosion in accuracy is likely to occur, over successive generations, if panels are not retrained. What this means is that genomic predictions developed for one breed cannot be effectively applied to other breeds.

Spangler expects more breed associations to incorporate genomic information into their EPD calculations. And he believes methodology for applying the technology to crossbred or composite cattle is critically needed. He believes widespread adoption hinges on the rate at which commercial bull buyers recognize the added value of increased EPD accuracy and show their willingness to pay for it.

"There still is a need to collect and routinely record phenotypic information by seedstock producers," stated Spangler, "and commercial producers need to realize that EPDs and economic index values are the currency of the realm for beef cattle selection. Genomic technology only makes these tools stronger; it does not replace them." **HW**

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