

Considerations for Multi-breed Herds

Stayability and evaluation tools for multi-breed herds discussed.

by **Raney Lovorn**, editorial intern, & **Troy Smith**, field editor

Cattle breeders are wise to apply selection pressure for cow herd stayability, according to Scott Speidel, Colorado State University research geneticist.

“It’s an efficiency trait,” he told attendees of the 2015 Beef Improvement Federation Annual Convention June 9-12 in Biloxi, Miss. Speaking during a committee breakout session, Speidel talked about heterosis effects on stayability.



► Citing data from multi-breed studies, Scott Speidel said an increase in heterosis, or hybrid vigor, corresponds with an increase in stayability. Looking at the heterosis effect on females even younger than the typical 6-years-of-age threshold, researchers also determined that the heterosis effect increases with age end point.

Speidel explained that stayability is not the same as cow longevity. Rather, stayability is one of many factors that contribute to a beef cow’s ability to remain as a productive member of a breeding herd. More specifically, noted Speidel, stayability is a measure of reproductive efficiency.

As tools for genetic selection, expected progeny difference (EPD) values for stayability predict the probability that a sire’s daughters will remain in the breeding herd and deliver a calf each year until 6 years of age. Age 6 is considered to be the threshold at which a beef female has produced enough calves to recover her cost. Explaining that it accounts for 53%-77% of the value of most maternal indexes, Speidel called stayability a significant contributor to economic efficiency.

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hybrid vigor, corresponds with an increase in stayability. Looking at the heterosis effect on females even younger than the typical 6-years-of-age threshold, researchers also determined that the heterosis effect increases with age end point. Heterosis increased stayability in 3-year-olds by 5.4% and in 4-year-olds by 9.2%. In cows 5 and 6 years old, heterosis increased stayability by 10.9% and 12%, respectively.

“The literature suggests that heterosis can account for as much as a 38% increase in stayability, depending on the breed crosses involved,” added Speidel.

Speidel spoke Thursday, June 11, at a joint session of the Cow Herd Efficiency and Adaptability Committee and the Live Animal, Carcass and End Product Committee.

— by *Troy Smith*

Challenges to multi-breed evaluation

Establishing an EPD to bridge gaps between breeds and allow for maximization of potential genetic improvement in crossbred cattle is a difficult task. Wade Shafer and Larry Kuehn addressed the potential of using the Germplasm Evaluation Program (GPE) at the U.S. Meat Animal Research Center (USMARC) at Clay Center, Neb., to help make multibreed evaluation a reality.

“We want to merge multiple breed databases together. Structures are different, and we need a lot of cooperation to get

multi-breed done, as we know,” Kuehn said. “Estimation cost relation parameters are a lot of our problem now.”



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The problem comes when the data arrives in the system and, although they have the data to estimate the EPD, they cannot input the information in a way that would put the breeds in the same contemporary group and allow them to easily compute the EPD, Kuehn continued.

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The current structure of the GPE at the moment is to use seedstock females and cross them with samples of purebred bulls to simulate one diallel cross, Kuehn said, to investigate the quantitative traits associated with crossbreeding.

“We are producing useful data for things like parameterization of breed differences that we release every year, as far as for the across-breed EPD program,” Kuehn said. The data have been used for several graduate student projects to establish breed differences and current heterosis estimates.

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analysis of their 40,000 animal pedigrees from the research herd using all of the cycles and GPE data available. The information is then adjusted using a regression coefficient to put the solution on an industry scale, Kuehn explained.

Problems are associated with this data because it works on EPDs and cycles from bulls that were breed impacters more than 40 years ago. Their information needs to be phased out of the equation as their influence diminishes, Kuehn said.

“The proposal that we are talking about today is to use breed differences from the GPE to parameterize the multibreed model currently in use,” Kuehn said, “We can basically preadjust the data for the breed composition, and we need to consider where the programs are different and how to accommodate the difference.”

— by Raney Lovorn

Help in making the decision

Despite advances in selection technologies, producer use of technology as a whole has been poor, according to Matt Spangler, University of Nebraska. Spangler addressed the need for decision-support software to use as a tool for genetic selection in the beef industry.

When producers were asked who they turned to for help in making selection decisions, they went to everyone but resources like extension personnel, university faculty, scientists or other experts, Spangler said. They instead turned to individuals like close neighbors and family friends without access to information like professionals.

“Poor technology adoption is really related to the sum of a lot of underlying issues,” Spangler said. “Genetic prediction to the layperson seems very opaque.”

Because cattle genetics do not change as quickly or as visibly as traits such as weight or health, people often have a hard time understanding the changes they need to make, Spangler said.

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“Time is focused on routine day-to-day management, be it nutrition, be it reproduction, financial management, employee management or otherwise, and genetic selection decisions are made once a year at bull-buying time.”

Bull selection is a difficult process with a high number of complicated physical and economic variables, Spangler said. It is a lot to ask a producer to consider in the amount of time that they have while reading a standard bull sale catalog, he continued.

“The critical need is a web-based decision-support tool to aid in really combining all sources of information toward

sire-selection decisions that are economically focused and assistance in determining the value proposition of increased information content,” Spangler said. “That’s a fancy way of saying what is the value of me generating and potentially paying for additional phenotypes.”

Spangler maintained that although there are many partial solutions to the problem of bull selection, the multitude of half answers only further confuses producers.

The software all-in-one solution that Spangler proposed would include an economic index that caters to the individual producer and a report listing all of the best bull candidates at a particular sale based on their relative value.

“The benefits to this to the commercial producers I would hope would be obvious,” Spangler said. “The benefits to the seedstock sector as I mentioned can help clientele become more profitable.”

— by Raney Lovorn



Editor’s Note: Troy Smith is a freelance writer and cattleman from Sargent, Neb. 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, PowerPoint and audio of the sessions; the Awards page for announcements of award winners; and the Photos page for photo galleries of the tour.

SNP chips and sequence variation

The 1,000-bull genome-sequencing project is under way, and Warren Snelling, research geneticist for USDA Agricultural Research Service (ARS), explained that SNP chips have opportunities and challenges in explaining DNA sequence variation. He spoke to attendees of the technical breakout session on advancements in genetic prediction at the 2015 Beef Improvement Federation (BIF) Annual Convention in Biloxi, Miss., June 9-12.

Snelling said BovineHD linkage showed that the strong correlations among close SNP correlations dropped when there was increased separation between the SNPs. The BovineHD sequence accuracy was about 0.75, while typical accuracy for high-density 50K tests is greater than 0.95. He added that differences in minor allele frequencies limit the correlations between BovineHD and sequence variants.

Snelling explained a study looking at the linkage disequilibrium in Germplasm Evaluation Project (GPE) bulls. There were 176 sires with high-density (HD) genotypes, low-density (LD) genome and high-coverage exome sequence — of those, 123 were purebred bulls and 53 were F1 crosses. Bulls were tested with HD-HD, HD-nonsynonymous SNP (nsSNP) and nsSNP-nsSNP. When comparing high-LD pairs to moderate-LD pairs, moderate-LD pairs seemed to corroborate more frequently, each more than 70%, on the same chromosomes.

He proposed, “What if nsSNP-HD LD is typical of unknown quantitative trait loci (QTL) chip SNP LD?” Limited high QTL-SNP LD means few QTL may have strong correlations with any genotyped SNP. Much low-moderate QTL-SNP LD means most QTL may have weak to moderate correlations with many genotyped SNPs. Future research could include using sequence variants predicted to affect genes instead of standard chip SNP.

— by Kasey Brown, associate editor