

# BIF Headlines

BIF explores new frontiers in genetic predictions.

by Barb Baylor Anderson, Mathew Elliott & Troy Smith

**B**eef Improvement Federation (BIF) committees bring together the thought leaders of the industry to explore and critique concepts that could lead to improvements in beef production, evaluation and end product. As beef industry leaders from around the world gathered in Calgary, Alta., Canada, June 30-July 3 for the 2008 annual meeting and research symposium, the organization's six standing committees focused on incorporating DNA into cattle evaluation, whole-genome selection, current application of expected progeny differences (EPDs) and predictive indexes, and the future of the organization itself, among other issues.

Following are a few highlights of material presented in committee. Angus Productions Inc. (API) is providing online coverage of the event at [www.bifconference.com](http://www.bifconference.com). From the site you can access summaries of the sessions, as well as proceedings papers, PowerPoint presentations and audios.

API's online coverage is made possible through sponsorship by BioZyme Inc. and its continuing support of the Angus Foundation and by the generous producers listed on the Seedstock Directory page. For more information about BIF, visit [www.beefimprovement.org](http://www.beefimprovement.org).

## Incorporating DNA tests into genetic evaluation

DNA tests can be incorporated into genetic evaluation, but they need to be incorporated into something that makes sense, that can sit alongside current approaches, and that is practical and flexible. Stephen Kachman, University of Nebraska-Lincoln, shared his thoughts regarding the process during the Genetic Prediction Committee breakout.

"The objective is to evaluate the genetic potential of an animal with traditionally phenotypic and pedigree information and then incorporate DNA information — molecular breeding values (MBVs) and marker information," he said, noting the work of the National Beef Cattle Evaluation Consortium (NBCEC) and others.

Currently, producers rely on phenotypic records of traits of interest, indicator traits, pedigrees and parameter estimates from reference herds that all factor into EPDs. But phenotypic data are limited and difficult to collect, he said, which opens the door to complementary sources of information, like DNA.

DNA information has evolved from single markers to several markers to thousands of markers and even sequence data summarized into marker scores," Kachman said. "It provides flexibility in handling evolving molecular and statistical technologies."

Kachman reviewed four models for measuring the accuracy of traits — a phenotypic model, a full model using phenotypic and marker information from

various companies, a marker-only model and a reduced model that will allow for the evolution of marker scores while keeping the computational and memory requirements within reason.

Accuracy increases in sires and progeny when you add marker data to phenotypic information, he said. The reduced model showed the greatest accuracy.

"With just marker information, accuracy is greatest in an individual that is genotyped. Accuracy in others is minimal. With actual genetic parameters, you get the best EPDs," he said. "The solution is a reduced model with EPD and residual components."

Kachman reviewed the economic analysis that supported his recommendations.

"We are capturing a large portion of the information that is out there for sires and progeny. We can get pretty darn close," he said. "Once an individual has been genotyped, there is minimal benefit in terms of accuracy to genotyping relatives. The greatest benefit from genotyping is for animals with limited phenotypic information."

In calculating interim EPDs, Kachman takes the EPD from the current evaluation based on the average of the parental EPDs, and adds new information typically based on an individual's own adjusted record deviated from the adjusted records of its contemporaries. The new information is given a weight and added to the individual's current EPD to produce an interim EPD.

A marker score interim EPD is adjusted in the same way as a phenotypic record. Using the appropriate weight, the adjusted marker

score is added to the current EPD to produce a marker score interim EPD. Kachman said the weight will be a function of the genetic variances and covariances.

"The methodology is in place and is based on a robust and familiar statistical foundation. We can compute EPDs, accuracies and interim EPDs and make them available as before," he said. "This is an extension of the current approach to genetic evaluation. We can make use of lessons already learned and not go back to square one to handle issues."

Kachman said the industry still needs estimation of genetic parameters and resource populations for estimation of genetic parameters.

"We need to look at reporting criteria and evaluate the effect of selective reporting. We have to determine the criteria for determining when a marker score is ready to be included. We don't want to add noise to our evaluation," he said. "We also need to evaluate the tradeoff between computational requirements and model complexity and consider software development. The models are similar, but they will need some modification for the future."

— by Barb Baylor Anderson

## Traditional and marker-assisted evaluation

While the transition from traditional beef cattle evaluation to genomics tools has long been discussed, geneticist Denny Crews said he believes it is time to move forward.



Denny Crews

Crews, then at Agriculture and Agrifoods Canada Research Centre, addressed Thursday's general session at the BIF symposium, offering praise for progress made through EPD-driven selection based on pedigree and phenotypic evaluation programs. However, he said he foresees much additional benefit from what he calls "phenomics" — DNA marker-assisted evaluation.

"Traditional cattle evaluation programs are mature. The resulting EPDs work. Producers use them. They believe in the system," Crews stated. "But traditional programs, which evolved mostly on a breed-specific basis, have limitations. For the most part, EPDs are not comparable across breeds."

Crews said EPDs are most useful in selection for or against traits which:

- ▶ relate to a direct benefit or cost;
- ▶ are easily and cheaply measured;
- ▶ are based on high data density to improve accuracy;
- ▶ have few genetic antagonisms;
- ▶ can be measured early in an animal's life;
- ▶ have a high degree of genetic variation; and
- ▶ have several indicators.

Crews said incorporation of DNA markers should enhance evaluation programs by increasing accuracy. Marker-assisted evaluation should be particularly beneficial for selection for traits that are difficult, excessively time-consuming, or costly to evaluate through phenotypic data collection (progeny testing). Examples include economically relevant traits (ERTs) such as disease resistance and feed efficiency.

Crews noted danger in publishing separate and disparate EPDs and DNA test results.

"We need to focus on an optimal combination, representing economically important traits," he advised. "We'll get a more accurate total evaluation."

— by Troy Smith

## Producers can gauge residual feed intake and more

By studying traits such as residual feed intake (RFI), producers can help reduce cost of gain while improving yield and quality grades; increase gain value; and decrease yardage costs. That was the message delivered by Allison Sunstrum of GrowSafe Systems Ltd. during the Producer Application Committee breakout.

GrowSafe's Feedlot Challenge features multiple RFID (radio frequency identification) tags and readers in close proximity. Normally, she explained, that is an issue because multiple readers cancel each other out.

"When the animals enter a lot, they are tagged with electronic ID tags," she explained. "We have RFID antennas molded into each bunk, and animal feed supply is automatically recorded when they eat. The tag measures individual intake and behavior data."

The tag records the frequency at which the animal feeds, the amount of feed it eats and the amount of time the animal stands at the bunk and doesn't eat. Such information is of great value because the remote support studying the data may help identify illness before even the best cowboys, Sunstrum said.

Along with measuring feed intake, Sunstrum said tags record the amount of water animals drink and performance information. One of the newest traits of the GrowSafe system is the ability to mark an animal with spray paint for a particular reason.

While capturing the water data, daily weights are recorded and sent back to the GrowSafe center at midnight. After 30 days of information input, regressions can be used to predict future performance, identify poor performers and start predicting an optimal end point or the point at which it is no longer economical to feed. The GrowSafe system then spray-paints animals on their backs when they are ready to be marketed. The system can be modified to identify optimal shipping dates by pen, load lots or individuals.

"Sickness identification is another aspect of the system," Sunstrum said. With two weeks of data, it can begin to identify illness, which is changing the way feedlots using the system ride their pens.

"We really don't know what the value of this is," she added. "And we also don't know if there's going to be a change in performance due to early intervention, but we think there must be."

She cited an example of when the water intake data would have identified an animal as being ill Jan. 9. The animal was visually identified as sick and pulled on the 19th, treated and moved to the home pen Jan. 23, pulled Jan. 24, treated hard for another three days, given a week to recover and then railed. Over that eight days, the animal had lost almost 150 pounds (lb.).

Sunstrum said GrowSafe will be focusing efforts at looking at growth curves and trying to identify when cattle move from Select to Choice. She said they are seeing in their data a growth curve that grows very, very fast then stops. These cattle are typically overfed and become the YG 4s, but if identified and harvested optimally, they would be the best cattle.

Sunstrum said she would like to work with breed associations in the future to incorporate what they are finding into selection indexes.

— by Mathew Elliott

## Select for profit when selecting traits

Producers focused on single-trait selection should select for profit, said Dorian Garrick, Iowa State University. Garrick spoke during the Genetic Prediction Committee breakout.

"Start with a goal with a purpose for change. Look at your breeding objectives. What do you need to change, and how much emphasis should those changes receive?" he asked. "Then, for the selection process, determine how and when you will measure traits, what you will do with the good cows and who you will use as mates. Perform the economic analysis and, finally, ask 'If we do all of this, how much more profit will we see?'"

Garrick acknowledged coming up with an index to measure traits in beef cattle is a challenge.

"Over the years people have tried to come up with indexes for cattle, but it is not the

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same natural process for putting together an index as it is for dairy and sheep,” he said. “The preferred characterization for selecting traits is to separate the economic measures from the production — the economically relevant traits (ERTs) versus the indicator traits that do not directly affect profit, but are correlated to those traits that do.”

Garrick proposed identifying traits as part of objectives for improvement, using procedures to predict traits that matter and placing them in the breed’s sire summary.

“Breed associations are doing a disservice if they do not share the right information with their clients. The more information in the catalog, the more disservice you do to selection,” he said. “I like the idea of single-trait selection on an index. While you may need to take other things into account ... you will get faster progress and profit.”

An EPD can be used to construct EPDs for all the factors producers want to improve



**Dorian Garrick**

to meet the objectives. Then, Garrick said, take those numbers and multiply them by economic weight to get their dollar ending value.

“If I was looking at a dollar value, I would want a one-sentence description of what it is trying to achieve,” he said. “Tell me what the goal is and the list of traits to get

that. Identify the ERTs that influence the goals. Make the list as small as possible, but account for all that is important and then derive the economic values. Ask yourself, ‘If I select on this index, how will my cows change in 20 years time?’”

Garrick encouraged producers to think wider about various real-life circumstances for different breeds, crosses and management systems.

“Users must be comfortable and believe they have sound information,” he said. “We are good on production, slightly good on reproduction, but not so much on animal health or beef healthfulness. In this molecular era, I would like to see the trends on production traits come down at the expense of new traits going up, such as improving iron concentration and calf survival.”

— by Barb Baylor Anderson

### The 2,000-Bull Project makes strides toward validation of whole-genome selection

Recent advances in technology, including the 50K SNP chip, are making it possible to now promote the use of whole-genome selection (WGS) technology as a genetic decision tool. Mark Thallman of the U.S. Meat Animal Research Center (USMARC), Clay Center, Neb., talked about validation of the technology through the “2,000-Bull Project” during the Emerging Technologies Committee breakout session.

“The technology is unproven, but it looks promising. A lot of work still needs to be done so we can make it work,” Thallman said. “The problem is that WGS gives the breeder thousands of genetic markers, and you can’t interpret it to make an informed selection decision. It needs to be merged into the genetic evaluation system to have value, and we need a training body of data to work with to try and bring it into being.”

That’s where the 2,000-Bull Project has value. Thallman said he and several other researchers can pursue WGS validation for three primary reasons:

**Technology.** “Massive technological advances have occurred in genotyping beef markers. The 50K SNP (single-nucleotide polymorphism) chip is powerful technology for us with 50,000 SNP markers across the bovine genome. Multiple breeds were used for SNP discovery,” Thallman said. “Working effectively together to provide this tool will revolutionize the beef industry and change the way we do DNA work.”

**Training data.** USMARC has developed a powerful resource population of more than 3,000 pedigreed cattle with extensive phenotypes that were genotyped using the 50K chip. Traits include feed intake, heifer development, carcass data, age at puberty, pregnancy rate, maternal performance, calving and growth traits and more. Thallman said the information provides a good resource for a training data set.

**People.** Breed association personnel and the scientific community collaborated in August 2007 to design the 2,000-Bull Project, which was structured to include a representative number and sampling of bulls from each of 16 breeds, Thallman explained. USMARC will run the 50K chip on those 2,000 sires.

Breed associations are responsible for selecting sires to be

included and providing semen. Selection is based on such criteria as making sure the bulls represent their breed, are current candidates for selection, possess high-accuracy genetic predictions, are influential within their breeds and are broadly representative of each breed’s bloodlines. Objectives of the 2,000-Bull Project include:

- ▶ extending genetic predictions from MARC phenotypes to industry bulls;
- ▶ developing and delivering EPDs for traits not typically reported;
- ▶ development and use of commercial genotyping of additional animals with the 50K chip;
- ▶ validation of the effectiveness of WGS using EPDs from the 2,000 bulls relative to USMARC data on common traits;
- ▶ improving EPD accuracy for common traits; and
- ▶ determining to what extent training data must be of the same breed as WGS is applied.

As of the July BIF symposium, USMARC had semen for 1,300 of the bulls, and had run the 50K chip on the training data, which had generated 150 million genotypes. Analysis of the training data was under way. Thallman said they expected to begin running the 50K chip on the 2,000 bulls in August 2008.

“We have a lot of work to do, but we are excited so far,” he said. “We don’t know if whole-genome selection will work ... We may need more than 50,000 markers, patents may restrict some use of the technology, and we need to develop complex computational methods to extract value. We hope our first results will be useful, but the statistics will evolve for a number of years. We might as well be prepared for change to be part of our lives.”

Thallman said USMARC will continue to collect training data, including data for difficult-to-measure traits.

“It is too early to make any conclusions, but it is appropriate we think about the possibilities,” he said. “I am confident of substantial new opportunities for the seedstock industry, it will still be important to contribute to heterosis, and pedigrees and phenotypes will continue to be important.”

— by Barb Baylor Anderson