



By the Numbers

► by *Shauna Rose Hermel*, editor

Angus to convert to single step July 7

July 7. That's the answer to the most-asked question in the Angus business today, announced Stephen Miller, director of genetic research for Angus Genetics Inc. (AGI). That's the day the American Angus Association plans to release its first national cattle evaluation (NCE) based on single-step methodology.

Peer review

Miller made the announcement June 1 during the technical breakout session focused on advancements in genomics and genetic predictions at the 2017 Beef Improvement Federation (BIF) Research Symposium and Convention in Athens, Ga. Miller discussed aspects of the current two-step method being used by the Association, single step, reasons for changing to the new methodology and what producers can expect with the July 7 analysis.

"I've been at Angus since September, and I can say this is the biggest thing that has happened to the Angus genetic evaluation since I've been there," Miller said, garnering a hearty laugh from the standing-room-only crowd of academia, cattlemen and allied industry. "Absolutely. 100%."

Nearly a decade ago, as the industry looked into how to incorporate genomics into genetic predictions, the Association adopted a model introduced during a 2008 BIF workshop by Steve Kachman, Miller explained. This two-step process requires periodic training — or calibration — of the SNP (single-nucleotide polymorphism) effects to the data to establish molecular breeding values (MBVs), which quantify how the changes in an animal's genotype affect its performance. These MBVs can then be incorporated into genetic evaluation as correlated traits to establish genomic-enhanced expected progeny differences (GE-EPDs).

Room to improve

"It was very timely, and it, I think, served the evaluation well," Miller said. However, there is room to improve.

One of the drawbacks of the two-step model is the lag time in inputting new known information into the database between calibrations. The Association has performed five such calibrations — the first, in 2010, based on 2,253 genotypes; the last, in 2016, based on 108,211. Without the move to

single step, the Association would be due for another that would encompass the nearly 350,000 Angus genotypes available.

"Each time you go through a calibration, there's some re-ranking," said Miller, explaining that the EPDs may "jump" as a volume of data is dumped into the system. "That's not desirable."

Another drawback of the two-step analysis is the growing complexity of the correlated MBVs fit into the analysis.

"If we do a genetic evaluation for carcass weight, we'd have one trait, but now we fit this correlated trait, which is the MBV [for carcass weight]," Miller explained. Because carcass weight and ribeye area are correlated, there's another correlation added to the carcass weight model, and then there are correlations for ultrasound values; for heifers, steers and bulls; and for the various genomic tests that have been accepted over time.

Advantages to single-step evaluation

- Eliminates the need for periodic calibration, allowing constant inflow of information into the database
- Simplifies the model, eliminating unnecessary correlations that add noise
- Allows incorporation of meaningful traits not previously incorporated, such as weaning weight and yearling, fat into the carcass model
- Allowed the Association to rebuild the carcass model, improving it significantly
- Eliminates a source of bias due to culling, because not all genotyped animals have progeny that are progeny-tested.
- Uses a more accurate relationship matrix based on actual genomic relationships of genotyped animals rather than pedigree estimates of inbreeding
- Eliminates yearling weight drift
- Increases accuracies

Single step simplifies the model, removing some of the correlations that were adding noise to the evaluation, Miller said. "We're only evaluating now the traits that we're actually interested in."

That actually frees up opportunity to add traits to improve the carcass model, said Miller.

"When we look at our carcass model, we had scan weight or weight at a year of age in our model, but we didn't have weaning weight," he explained. "Why would weaning weight be important? Well, the animals that go on to have a scan weight from weaning are not a random sample. Typically, producers might weigh all their calves at weaning, and the really light ones get culled, so there's a biased sample that goes on. If we don't fit weaning weight at the same time, we don't account for that pre selection bias."

The Association also added fatness to the single-step carcass model.

"There [are] different maturity patterns, and that ultrasound fat measurement at a year of age picks up differences in maturity, and we can add that in and fit that in the correlations," said Miller. "It gave us an opportunity to really rebuild the carcass trait model because of single step."

Better relationships

Single step also overcomes a source of bias inherent with the two-step model. Miller explains that the bias results from our normal selection process. He offered the example of a set of genotyped sons of a fictitious dairy bull, Xerox. Only the absolute best Xerox sons are used to produce daughters that are then included in the dairy evaluation.

"This is a source of bias in our system when we don't account for that all at the same time," Miller said. "With single step it's better because all the genotypes and all the phenotypes are in the model at the same time."

Driving single step is the better characterization of relationships, Miller noted. "We've got animals that just have pedigree; we've got animals that are genotyped; and amongst those genotyped animals, now we can get the relationship between them based on the genomic information."

He used as an example a set of six flush mates.

"If we didn't know anything about genomics, you'd say the relationship among them should be half," he explained, or 0.50. Based on the pedigree, which includes some inbreeding due to common sires, the relationship would be estimated at 0.59, but when you actually look at the genotypes of all

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six animals, the genetic relationships amongst the flush mates vary from 0.49 to 0.65.

“Some of those flush mates are more related to each other than others,” he explained, “and that’s essentially what’s driving the genomic prediction in single step.”

Proving different is better

What are the new numbers going to look like? It will be a noticeable change, Miller said. “We’re not giving you something that is 0.99 correlated. . . . It’s not going to be miniscule. Breeders are going to notice.”

He shared a table showing the correlation values comparing the Association’s current two-step evaluation and the values that will go into effect July 7 for the top 200 sires and the young sires (see Table 1).

“It’s the younger sires where we are going to see the differences. The genomics has a bigger impact on those animals,” he said.

It’s different, but is it better? Miller questioned, noting that AGI has spent the last six months running single step side-by-side with the two-step model, comparing how the evaluations differ to determine which provides the better genetic prediction.

As one consideration, they compared the genetic trends to the classic model, which doesn’t incorporate genomics. When they laid the genetic trend line for single step over the genetic trend line from the classic model, they were almost identical for all of the traits. However, there was a drifting in the genetic trend — upward for young sires and downward for older sires — resulting from the two-step model.

The yearling weight drift has become noticeable, as EPDs of high-accuracy older bulls have drifted down further than what the possible change values would suggest they could. A subset of 12 high-accuracy sires that lost an average of 2 pounds (lb.) per year from 2011 to 2017 in the two-step model, lost only 0.3 lb. per year with single step.

The comparison also revealed a gradual widening of the standard deviation for carcass weight that was an artifact of the genetic correlations fit between all the MBVs and the traits in that big model. Single-step fixes that problem. A narrower standard deviation will result in less spread among carcass weight EPDs.

As another proof, Larry Kuehn, a geneticist at the U.S. Meat Animal Research Center (USMARC) at Clay Center, Neb., ran correlations between the Association’s single-step and two-step evaluations and a separate evaluation using the USMARC’s germplasm evaluation. In almost every trait, single step

and two step were similar or single step was better, Miller said.

“That for us was kind of the light bulb [going] on that single-step is doing a better job than what we’re doing today,” Miller said.

As a third test, the AGI team did a single-step evaluation and a two-step evaluation as of the last calibration in 2016. They then analyzed which of the two models did a better job of predicting the phenotypes received since that evaluation.

“What we see is single step is always better than what multi-step was with our own data,” Miller said, discussing the growth traits. “That’s good news.”

“Our accuracies are higher, basically higher, for single step,” said Miller. “What’s behind that? We’ve got a lot more data in there. We know it is doing a better job at forward-predicting, so we expect the numbers to go up a bit, and that’s what we’re seeing with our accuracies.”

Other improvements

“While we’re making a major change, you might as well change a lot of things,” said Miller, noting that they have re-estimated the parameters that go into the Angus evaluation. He shared a table showing the heritabilities used with the two-step model and those used for single step (see Table 2). Many of the heritabilities are the same, but several, like dry-matter intake, are higher. Correlations among traits have also been re-estimated.

As of July 7, the Association will also begin to fit the correlation between birth weight and weaning weight to prepare for accepting birth weights alone in the evaluation as of Aug. 7.

“That’s really important for young sires,” Miller explained, “so someone can actually see their birth EPD based on their first crop of calves before they breed heifers to them again.”

The July 7 evaluation will also incorporate updated economic assumptions to calculate dollar value indexes (\$Values). Genomic percentile rankings will be provided and will be updated with the July 7 NCE.

With new methods; new parameters; a new carcass model incorporating preselection at weaning and difference in maturity; and new economic assumptions, expect some re-ranking Miller said, but also expect a better evaluation.



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Table 1: Correlations of EPDs derived through single step model for the top 200 sires and 2,417 young sires compared to the EPDs derived through the two-step model

Trait	Top 200 sires	2,417 young sires
Calving ease	0.92	0.85
Birth wt.	0.99	0.94
Weaning wt.	0.99	0.92
Yearling wt.	0.99	0.92
Milk	0.80	0.76
Mature wt.	0.69	
Yearling ht.	0.96	0.85
Scrotal	0.98	0.90
Heifer preg.	0.67	0.60
Carcass wt.	0.81	0.67
Marbling	0.86	0.85
Ribeye	0.82	0.80
Fat	0.73	0.64

Source: American Angus Association, Stephen Miller slide presentation, “Advancements in Emerging Technology” technical breakout, 2017 Beef Improvement Federation Research Symposium and Convention.

Table 2: Re-estimated heritability (h²) estimates and variance components increase prediction accuracy

Trait	Old h ²	New h ²
Calving ease direct	0.20	0.19
Birth wt.	0.42	0.43
Weaning wt.	0.20	0.20
Yearling wt.	0.20	0.24
Dry-matter intake	0.31	0.36
Yearling ht.	0.50	0.51
Scrotal	0.47	0.48
Docility	0.37	0.44
Heifer preg.	0.13	0.15
Milk	0.14	0.12
Mature wt.	0.37	0.37
Mature ht.	0.64	0.62
Carcass wt.	0.38	0.44
Marbling	0.45	0.48
Ribeye area	0.33	0.32
Fat thickness	0.34	0.33

Source: American Angus Association, Stephen Miller slide presentation, “Advancements in Emerging Technology” technical breakout, 2017 Beef Improvement Federation Research Symposium and Convention.