By the Numbers

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Increasing prediction accuracy

The American Angus Association Aug. 8 began accepting birth weights earlier for genetic evaluation. This enhancement was made possible with the implementation of the genetic evaluation system launched in July. Historically, birth weights recorded prior to weaning weight submission were held out of the evaluation until the subsequent weaning weights were turned in.

Why update

One of the many advancements to Angus's genetic evaluation this summer included incorporating additional trait relationships between birth, weaning and yearling weights. These relationships were added to the growth model to start using birth weight data prior to weaning weight submission.

Although a positive genetic correlation was not fit between birth weight and growth prior to July 7, the expected progeny differences (EPDs) were positively correlated due to animals being recorded for both traits, and the underlying phenotypes are correlated. The animals that had been previously genotyped were subject to a positive correlation between the genomic scores among birth and growth traits.

Weaning weights were never recorded for some animals, such as those that died at or shortly after birth, and this valuable data never entered the evaluation. In addition, the models will now take advantage of a calf's weaning information to make a more accurate birth weight (BW) EPD prediction for producers unable to capture a birth weight on a calf within 24 hours, but who do submit a weaning weight. In addition, young sires will be better evaluated, as members will no longer have to wait six to eight months before birth weights on the sire's first calf crop enter the evaluation. This cuts down on the lag time between a young sire producing calves and adding that information to the database, potentially making that information available one breeding season earlier.

To take advantage of the benefits of using birth weights earlier, it is imperative to fit the correlations between these biologically related traits. The strength of the relationship among birth, weaning and yearling weight were estimated directly out of the Association's member-submitted data. Analysis of these traits showed positive genetic correlations exist among these traits — meaning as one trait moves in either direction, the other trait moves in that same direction.

By not fitting these correlations, the models were ignoring the biological relationship, which attributed to some larger changes in BW EPDs as progeny data flowed into the evaluation.

Benefits

As birth weights enter the evaluation, there is potential for all the growth EPDs to adjust and add accuracy. For example, as birth weights are added on a sire group that is below average compared to its respective contemporaries, a downward trend in BW EPD will be witnessed. If no weaning weight data has been submitted on the sire group, producers will also see a slight downward trend in weaning weight (WW) and yearling weight (YW) EPDs because of the positive correlation among these traits. Producers must remember, though, as data come into the evaluation, if a bull is truly a low-birth-weight, high-growth bull, the progeny data will overwhelm these correlations.

While these updates coincide with the incorporation of a new genomic methodology, changes seen in BW EPDs are not a response to a change in the genomic data. Rather, changes are due to the statistical growth model updates discussed above.

Being able to utilize birth weight data earlier does affect the accuracy of the genomic component of the EPD. The true value of single-step genomic evaluation is that it uses all information continuously every week, in a sense recalibrating itself each time, keeping the genomic components as current as possible. Holding the birth data points out until weaning weight submission would limit the power of single step. Using every data point available by fitting these correlations allows for the single-step genetic evaluation to be as current as possible to make the best estimates of genetic merit.

Result

The correlation between birth weight and weaning weight is less than 0.30, while the weaning weight-postweaning gain correlation is nearly 0.50. While these correlations are far from one-to-one relationships, producers have still witnessed EPD changes since these relationships have been added.

A concern among breeders is by fitting these correlations, the new EPD system will not reveal "spread bulls" at the same rate. To investigate this, we did an analysis of 32,252 2015-born non-parent bulls. Other birth years for non-parent animals would identify similar birth and growth trends. In this case, spread bulls were determined to be animals who ranked in the top 5% within this sample of 2015-born non-parent sires for both BW and YW EPD.

In the old system (evaluation previous to July 7) to be in the top 5% for both BW and YW EPD, the animal would need to be ≤-1.7 on BW EPD and ≥117 on YW EPD. Out of the 32,000+ animals in this data subset, only 25 animals fit this scenario, with an average BW EPD of -2.4 and an average YW EPD of 121.

With the new single-step (SS) EPDs, animals in the top 5% for both BW and YW EPD in this population would have a BW EPD ≤-1.5 and a yearling weight EPD ≥132. There were five animals that fit this scenario with an average BW EPD of -2.1 and an average YW EPD of 136.

Within the population of 32,251 2015-born non-parent bulls, spread bulls under either multi-step (MS) or SS are relatively rare (<1 in 10,000), but was more common under MS.

To investigate how these ratios looked when animals get more data, a further 3,945 bulls with EPD accuracy for both BW and YW greater than 0.7 were used in a similar analysis. Within this proven bull population, two bulls met the spread criteria (-2.4 BW and 113 YW) under SS where one bull met the criteria (-3.0 BW and 110 YW) with MS.

It would appear that once bulls have more accuracy behind their BW and YW EPD, the frequency of spread bulls is similar. While it is a bit more rare to find a bull that fits this definition of spread in young bulls, it is still possible. There are still many sires in the Angus breed that a have below-average BW EPD and an above-average YW EPD. Within the top 200 sires in terms of registrations, there were 94 that had both above-average SS EPD for YW and below-average SS EPD for BW.

The ultimate goal of these additions to the growth model is to more closely predict the genetic merit of young sires to where these bulls will be once they are progeny-tested. This will give the commercial marketplace a higher degree of confidence in the genetics marketed by Angus breeders as the genetic potential of the Angus seedstock population to produce cattle that perform closer to what those initial EPD predictions state. This ultimately induces even more confidence in the Angus genetic evaluation than what was already apparent.

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