



By the Numbers

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Moving toward single-step evaluation: A new way to include genomic results

In 2010, the American Angus Association and Angus Genetics Inc. (AGI) launched their first run of genomic-enhanced expected progeny differences (GE-EPDs). It propelled the Association into a new era of genetic evaluation. Since then, breeders have been through five routine calibrations, where the impact of an animal's genotype on its EPD was determined.

The training population used in these calibrations now exceeds 100,000 animals, and genomic testing includes more than 260,000 animals. Although the technology has become mainstream, the incorporation of genomic data into genetic evaluation is an evolving science. Researchers continually look for more accurate and efficient ways to utilize the data.

A different way of handling genomics

The current deployment of genomics into EPD calculations involves a two-step process. Step 1 involves using the genomic data to predict molecular breeding values (MBVs), which quantify how the changes in an animal's individual genotype affect its performance. This is determined through the "calibration" as described earlier.

This MBV is then incorporated as a correlated trait into the Association's genetic evaluation to predict GE-EPDs, which is Step 2. Although AGI and the Association were using the most sophisticated and accurate approach available, different methodologies for using genomics in a more effective and appropriate way have since been developed.

Working in collaboration with research professionals at the University of Georgia, the

Association and AGI are looking to implement a new procedure known as *single step*. The basis of this change is that single step is able to handle all the genotype, pedigree and performance data simultaneously, providing the most current GE-EPDs possible for breeders with the appropriate emphasis on all sources of information. With single step, every EPD will fully leverage all the genotype, performance and pedigree information available each week.

Quantifying differences in pedigree relationships

The difference between a single-step genomic evaluation and a traditional pedigree-based EPD is how genetic relationships between animals are

determined. With the traditional pedigree-based approach, the relationships between animals are determined by pedigree alone. Pedigree would dictate all full sibs, for example, would have a genetic relationship to one another of 0.5, and the relationship between grandparent and grandprogeny would be 0.25.

Understanding the way DNA is inherited, we know there will be variation in these relationships. Real relationships between animals can be quantified with SNP data known as an animal's genomic relationship. The genomic relationship between animals will be different than the pedigree relationship. The pedigree relationship will have all flushmates being equally related, where the genomic relationship will identify variation in their relationship to each other.

The genius of the single-step method is that it uses both the pedigree and genomic data, where available, to determine the relationships among genotyped and ungenotyped animals.

Genotyping has revealed that parents can share common alleles with one another and, subsequently, a marker allele passed down to an offspring from the dam, for example, may also be present in the sire's genetic makeup. This means an offspring could possess more than 50% of genes located in the sire's genotype because of the random draw of received alleles.

If a calf gets 50% of its markers from its dam, but 10% of these markers overlap with those markers in the sire's genotype, then the calf still has a 50% genomic relationship with its dam, but is actually 60% genomically related to its sire. Then if the sire is exceptionally good or bad for a trait based on performance records and progeny data turned in to the Association, the calf's EPD would follow this trend, as well.

For instance, if a sire is exceptional for a trait like marbling based on progeny data reported, and this particular calf is 60% related to this sire, the calf's marbling EPD will increase based on the fact it is more related to the sire that performs genetically well for marbling. Of course, the EPD system is more complicated as the relationships amongst all animals are considered simultaneously.

Seeing differences with single step

Incorporating the genotypes in this manner will result in some changes the producer needs to be aware of. First of all, the training population and routine calibration involving registered-Angus seedstock will no longer be necessary. This means producers will not see EPDs fluctuate due to an annual calibration. Genotypes will be incorporated continuously into the evaluation. As a result,

Selecting for more tender beef

Providing consumers with a consistent, tender product leads to satisfied customers and increased demand. The most direct way to label a sire *genetically* tender is to eat his progeny; however, this is an expensive and time-consuming endeavor.

With the advancement in genomics, discovering sires genetically superior for tenderness is more attainable. In fact, alongside incorporation of the single-step method, the Association will simultaneously release a tenderness expected progeny difference (EPD). This selection tool is derived using both genotype information and Warner-Bratzler Shear Force (WBSF) phenotypes collected on Angus cattle.

Tenderness EPDs will be released as part of the weekly evaluation, with a lower EPD representing a lower WBSF score, indicating more tender beef. It is important for breeders to keep in mind that the closer your animals are related to the animals in the database with WBSF data, the better the prediction accuracy will be for your individual animals.

The Association will continue to actively pursue increasing the number of WBSF records in the Angus database. With additional records, AGI will be better able to explain the genetic variation associated with tenderness, which, in turn, will increase the validity of EPD predictions across the population.

EPDs are more likely to move up or down in a much less dramatic fashion.

This transition is similar to the transition producers experienced when the Association moved to weekly rather than biannual genetic evaluations. Instead of holding data out of the NCE until the next biannual evaluation, data were incorporated into the evaluation weekly. As a result, a bull's EPDs no longer changed as much from run to run; rather, EPDs moved in a more continuous manner each week. It could be described as EPD creep instead of EPD jump.

Sires will re-rank after the initial incorporation of single step. Even though changes will occur, producers must keep in mind this new method is a more accurate way of predicting the effects genotypes have on performance. While some animals will not see as much change as others, EPDs will likely fluctuate across the board, particularly for animals that have already been tested.

The amount of influence genomic information will have on EPD predictions in the future will be dependent on how many animals have been tested in the pedigree. With this new method, an animal with several past generations already genotyped will see a greater impact of genomics on their EPD compared to an animal who is the first generation to be tested in its pedigree.

A third change will be seen in the way genomic results are reported to members. Currently, producers testing individual animals receive genomic percentile ranks, ranking individuals to the rest of the tested population. These ranks can be calculated when genomic effects are estimated using a two-step process with MBV calculation. However, the genomic results will no longer be configured as a separate trait, and genomic percentile ranks will no longer be made available.

Producers will have access to the most accurate selection tools available, GE-EPDs, which take into account the genotype information along with performance and progeny data.

Moving forward

Using single step will increase abilities to accurately predict EPDs for use in selecting and mating Angus cattle. While changes will be experienced, the Association is confident this is the best direction for a national cattle evaluation to take. No changes in the way DNA is collected, samples are submitted or handled at the lab will take place. This is simply a difference in the way the genomic results are incorporated into the evaluation.

The AGI team welcomes any questions as the Association moves through this process.

