

BY THE NUMBERS

by Kelli Retallick-Riley, AGI president

Genomic Selection in the United States: Where It Has Been and Where It Is Going

Is the promise of genomic selection realized?

This summer at the World Congress on Genetics Applied to Livestock Production, I presented the American Angus Association's success story with genomic selection with the topic: "Genomic selection in the United States: where it has been and where it is going?"

Conference attendees were in awe at this story. The talk ended with the simple question, is the promise of genomic selection being realized?

Sharing the message

The American Angus Association is the largest beef breed association in the world with more than 300,000 annual registrations. The demand for Angus genetics has been one of the strongest in the United States, with Angus capturing considerable market share in the beef industry. Undoubtedly, some of this success has been driven by genetic improvement programs offered by the Association.

In 1957 the Association launched the Angus Herd Improvement Records (AHIR®) program to facilitate the necessary data capture for genetic improvement. The first estimated breeding values on American Angus cattle were published in the *Group 1 Report-Sire*

Evaluation Report in 1974. Since that time, significant changes to genetic evaluations have taken place.

Genomic selection may be one of the most notable changes. Making its Angus debut in late 2009, genomic selection has been making headlines ever since — most recently being that of the millionth Angus animal being added to Angus's genomic database in July 2021. While this milestone was certainly celebrated, the success of genomic testing in American Angus has come about through a series of improvements and commitment from Angus breeders.

Looking back

The first Angus genomic-enhanced expected progeny differences (GE-EPDs) were introduced late 2009, a first for the U.S. beef industry. At this same time, the Association moved to the industry's first weekly genetic evaluation. This was a major change from the previous biannual evaluation schedule, and it enabled breeders to utilize genomic information more quickly.

The first models to include genomic information into the Angus EPD was with a multistep approach described by Steve Kachman in 2008. With this approach, genomic

information was included into the genetic evaluation by 1) computing molecular breeding values then, 2) fitting these molecular breeding values into genetic models as correlated traits. The challenge to this method was the reliance on training populations and the need for systematic recalibrations with additional genotypes and phenotypes.

This led the Association to work toward methods allowing for more real-time inclusion of genomic information. Several groups had been researching ways to utilize genotypes to estimate genomic relationships (pedigree combined with genomics) among animals, rather than predicting molecular breeding values to eliminate the need for recalibration.

Current evaluation

July 7, 2017, the Association deployed an updated evaluation: single-step genomic evaluation. Employing single-step was once again a first for a major U.S. breed. The new single-step model eliminated the need for recalibration, and on average, increased the ability to predict future progeny

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performance for growth traits by 50% compared to the multistep method. Genetic trends from single-step more closely mimicked genetic trends from traditional models (without genomics) supporting previous genetic trends with multistep were overestimated (Lourenco, 2018). The move to single-step was monumental for the entire U.S. beef industry.

Promise of genomic testing

The effect of genomic selection can be analyzed through standardized genetic progress. Standardizing allows for direct comparison among traits with different units (i.e., pounds vs. inches).

Figure 1 illustrates standardized genetic progress prior (2001-2009) to and presently (2010-2021) influenced by genomics for EPD traits with high economic relevance. Genetic progress for growth and carcass traits have accelerated in favorable directions with the inclusion of genomics and the exception of maternal milk and marbling. The downward trend in backfat is favorable when considering carcass yield. The pattern in maternal milk could be explained by breeder selection pressure working to find an optimal herd level. Marbling EPD has not seen acceleration with genomics. This could be explained by several high genetic bulls for marbling being culled from the Angus population due to lethal genetic conditions in 2008.

Increased EPD accuracy allows Angus genetics users to purchase bulls with less risk. This risk can be assessed in terms of the number of progeny equivalents added to an individual when genotyped. In Angus, genotyping a non-parent animal is equivalent to an animal producing, on average, 20 progeny depending on the trait.

Table 1 : Number of progeny equivalents for each trait included in the Association's genetic evaluation.

EPD Trait	Progeny equivalent	EDP Trait	Progeny equivalent
Calving ease direct	25	Pulmonary arterial pressure	17
Calving ease maternal	19	Hair shed score	8
Birth weight	23	Heifer pregnancy	17
Weaning weight	27	Maternal milk	35
Yearling weight	22	Mature weight	14
Yearling height	15	Mature height	9
Dry Matter Intake	11	Carcass weight	14
Scrotal Circumference	13	Marbling score	10
Docility	11	Ribeye area	16
Foot claw set	13	Backfat thickness	13
Foot angle	13		

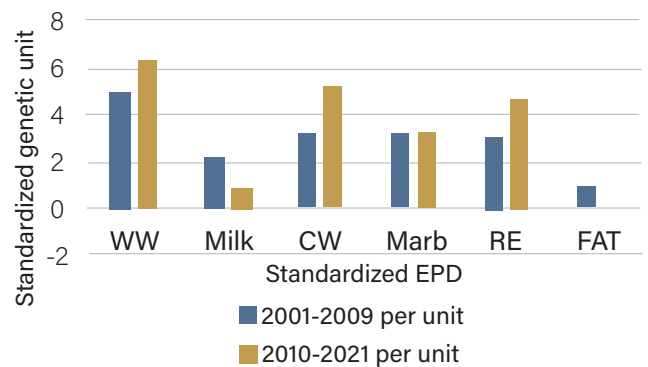
This increased accuracy has driven the demand for genomic-tested Angus bulls. Table 1 describes the number of progeny equivalents for each trait included in the Association's genetic evaluation.

Conclusion

The future of genomic selection appears bright. Yearly, more than one-half of Angus registrations are being genotyped. Price reductions have made widespread testing affordable. Sophisticated methodology has improved prediction accuracy and reliability of genetic predictions, increasing trust. Based on the number of genotypes being submitted, many breeders have made genomic testing a standard operating procedure on farm.

However, even with increased genomic testing, one thing remains certain. Angus would not have witnessed nearly as much success if it weren't for the members'

Figure 1: Standardized genetic progress made prior (2001-2009) to and presently (2010-2021) influenced by genomics for EPD traits with high economic relevance in the U.S. beef industry including weaning weight (WW), maternal milk (Milk), carcass weight (CW), marbling score (Marb), ribeye area (RE) and backfat (BF).



commitment to collection of accurate phenotypic data.

Without the actual phenotypes supporting this genomic engine, the American Angus Association genetic evaluation would certainly run out of gas. [A](#)

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Editor's note: References: Lourenco, D. A. L., Tsuruta, S. Fragomeni, B. O., Masuda, Y., Aguilar, I., et al. (2018) 11th Proc. World. Cong. Appl. Livest. Prod., Auckland, New Zealand.