By the Numbers

► by **Dan Moser,** *Angus Genetics Inc.*

The science behind the numbers

Partnerships with research community keep Angus genetic evaluation on the cutting edge.

Long-standing priority

The American Angus Association has enjoyed long-term, productive collaborations with land-grant universities and other research organizations since early in our history. According to Keith Evans' book *A Historic Angus Journey: The American Angus Association, 1883-2000,* one of the reasons Saint Joseph, Mo., was selected as the location for the Association's headquarters was its proximity to four major agricultural research universities. A search on Google Scholar for research papers related to "Angus cattle" will return nearly 60,000 results.

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That collaboration between Association staff and the research community benefits our members in a number of ways. Some of the resulting research directly impacts the methods and procedures used weekly in the Angus genetic evaluation. Examples of this include our methods for incorporating genomics into genetic evaluation, procedures for combining carcass and ultrasound data, and calculations of residual average daily gain (RADG) expected progeny differences (EPDs).

Much of this research is presented to peer-reviewed journals, where other qualified scientists must approve the work as correct and relevant before it is selected for publication. Through engagement with top scientists in the field, and publication of procedures in peer-reviewed journals, Association staff members keep our genetic evaluation program the most up-to-date, accurate and unbiased program in the beef industry.

GE-EPDs

One example of a beneficial research collaboration is between the research teams of Angus Genetics Inc. (AGI) and Zoetis. Scientists from both organizations, with support from university researchers, work together to update the models and parameters used to calculate Angus genomically enhanced expected progeny differences (GE-EPDs).

The process of genomic calibration begins with Zoetis scientists accessing a file of unidentified records, with individual animals' EPDs (calculated without genomic information) and DNA marker genotypes. The Zoetis team selects the markers that have greatest statistical significance for each trait, and estimates the effect of each significant marker on each trait. The molecular breeding value (MBV) for each animal is simply the sum of marker effects for each trait. When genomic test results are provided to breeders after testing, the percent rank scores indicate how the animals compare to the population of tested Angus cattle for a particular trait, based on genomic testing alone.

The process used by Zoetis to select significant markers and estimate the effects on each trait is described in an article by Boddhireddy and other Zoetis and AGI scientists, published in the *Journal of Animal Science* in 2014.

The method currently used to incorporate genomic test results into Angus GE-EPDs was first suggested by Steve Kachman, professor in the Department of Statistics at the University of Nebraska, in 2008. Kachman's paper from a genetic prediction workshop, sponsored by the Beef Improvement Federation (BIF), described how molecular breeding values could be included in GE-EPD calculation simply by analyzing those values as correlated traits, just as weaning weight is used as a correlated trait to increase accuracy of yearling weight EPDs. Scientists from AGI and the University of Georgia, our genetic evaluation software provider, created the necessary programs to incorporate Kachman's method into the Angus genetic evaluation.

A key component of GE-EPD calculation using the Kachman model is estimation of the genetic correlations between the performance data and the molecular breeding values. That work is done by AGI research geneticist Lizhen Wang. The correlations for each trait determine the relative weighting of genomic information, compared to pedigree information, performance of the animal and performance of their progeny.

Those correlations provide an independent validation of the work done by Zoetis scientists. If the estimation of marker effects by the Zoetis research team is not accurate, the correlations between genomics and data will be lower than expected, and the relative weighting of genomics in the evaluation will be lower.

Over four calibrations, correlations between our data and the MBVs have been consistent and similar or slightly higher than those estimated in other breeds and species, indicating the marker selection and estimation of effects have been conducted accurately.

Carcass trait evaluation using ultrasound data

The current genetic evaluation for carcass characteristics using ultrasound data, carcass data and genomics is the result of several long-term research efforts supported by the American Angus Association and the Angus Foundation.

In the 1980s, scientists at Cornell University, Iowa State University (ISU) and Kansas State University began experimenting with the use of medical ultrasound equipment to measure carcass traits in live beef cattle. Paramount to this research effort was a collaborative relationship between the Association and ISU, where advanced models to predict intramuscular fat from ultrasound images were developed. The concept of centralized ultrasound processing labs was established through this collaboration.

In 2007, BIF recommended in its guidelines that carcass and ultrasound data be analyzed jointly with multiple-trait models and that EPDs be published on the carcass-trait scale. In response, the Association sought the help of Mike MacNeil, at the time a research geneticist at the USDA Agricultural Research Service (ARS) research laboratory in Miles City, Mont. MacNeil estimated the genetic correlations necessary to combine the Association's carcass and ultrasound data into one set of carcass EPDs, an approach that continues today.

RADG

The residual average daily gain EPD provided in the Angus genetic evaluation is another example of a collaboration between the research community and the Association staff. In the early 2000s, the Angus Foundation supported a number of research projects on feed efficiency at the University of Illinois, North Carolina State University and ISU. At the same time, individual breeders and test stations began collecting significant amounts of feed intake data on Angus cattle.

To develop a selection tool for feed efficiency, the Association again turned to MacNeil for help. He developed a mathematical model to identify animals with the genetic potential to gain more efficiently, using existing measures of feed intake, weight gain and body composition. The concept of RADG as a selection tool was based on the recommendation of Bob Koch and co-workers at the University of Nebraska, Oklahoma State University and the USDA ARS in a landmark 1963 paper.

Future efforts

Today, collaboration between the research community and your Association continues. The Angus Foundation has supported a number of promising research efforts in a variety of areas relevant to seedstock and commercial beef production. Examples include studies of genetic adaptation to regional environmental challenges, such as high-altitude disease and fescue toxicity.

Recently, AGI and the University of Georgia worked together on a project to evaluate a new method of incorporating genomic information into the weekly Angus genetic evaluation. This methodology, called Single-Step, uses genomic markers to redefine pedigree relationships among animals, adding accuracy to their EPDs, while eliminating the need to re-estimate marker effects on a regular basis.

As new opportunities arise to advance the science of cattle breeding, the Association will continue to collaborate to improve the sustainability and profitability of your business, and that of your customers.

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Publications describing methodology used in the Angus genetic evaluation

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