By the Numbers

► by *Association staff*

Genomic-enhanced EPDs

Recent changes to the weekly genetic evaluation related to genomic trait tests may affect the expected progeny differences (EPDs) and accuracies published, even for animals that were previously tested. These changes in EPDs and accuracies are influenced by necessary modifications to correlations between the genomic test results and the American Angus Association's phenotypic database. These genetic correlations have been re-estimated for both company products [Igenity 384 (Ig384) and Zoetis (formerly Pfizer) HD 50K] offered through Angus Genetics Inc. (AGI).

Genetic correlations between genomic results and trait phenotypes

Through AGI research and development, a genetic relationship is calculated between the values obtained from the genomic test results from both companies and the phenotypic data at the American Angus Association. Table 1 presents the genetic correlations, by trait, that have been estimated in this process to date.

As genomic-tested animals entering the weekly evaluation EPDs become further removed from the training or reference animals used in deriving the genetic predictions, the genetic correlations need to be re-estimated. Igenity correlations were re-estimated by AGI using the current pool of approximately 17,000 test results for Ig384 animals. Previous correlations based on training animals dated back to spring 2010, representing only 5,400 genotypes. With the additional volume of animals tested over time and their distance from the training population, the genetic relationship between the genomic test result and the phenotypic data tends to decrease and is reflected in Table 1.

Zoetis HD 50K correlations depicted in Table 1 are a result of the 2012 collaborative recalibration project between the AGI and Zoetis research teams. During this project, existing 50K genotypes were used to retrain the genomic computations for each trait. Then genomic results, or molecular breeding values, were recomputed under this new calibration representing nearly 12,000 animals in comparison with 2,400 used in the initial Zoetis HD 50K results. The Zoetis scientists provided recalibrated genomic values and AGI re-estimated the genetic relationships with the actual performance data in the Association database (see Table 1).

Recalibration over a larger number of current animals, on the average, provides similar or greater genetic correlations than the initial results reported for the Zoetis HD 50K in 2010. Benefits of the Zoetis HD 50K recalibration include similar or higher accuracy for EPDs on young animals or those with limited or no phenotypic data. Also, there is an increased representation of Angus genetics in the genomic prediction population, and retraining to a more current population provides genetic predictions that are more relevant to today's Angus genetics. The use of updated genomic results through this process also causes EPDs to change on young, unproven animals that had low accuracies in the initial training population. In contrast, higher-accuracy animals in training tend to be less affected by the recalibration of their genomic results.

Interpreting the genetic correlations

Typically, there are two measures used to report the relationship of a genomic test and phenotype: the genetic correlation and percent of additive genetic variance accounted for by the test. These two measures are related and can be transformed equally. The genetic correlation is the square

CONTINUED ON PAGE 168

Table 1: Genetic correlation between genomic results and phenotypic traits of interest (American Angus Association data), by genomics company

	Igenity 384 (Ig384)	Zoetis HD 50K
Calving ease direct	.34	.61
Birth weight	.42	.64
Weaning weight	.38	.54
Yearling weight	.34	.66
Dry-matter intake (component of RADG)	.27	.59
Yearling height	.24	.70
Yearling scrotal	.23	.73
Docility	.18	.67
Milk	.21	.38
Mature weight	.39	.51
Carcass weight	.27	.57
Carcass marbling	.34	.63
Carcass rib	.29	.63
Carcass fat	.22	.53

To learn more about available genomic tests, go to *www.angus.org/AGI/default.aspx.*

Table 2: Weekly evaluation traits with genomic data included in American Angus Association weekly EPDs

Trait EPD	Igenity	Zoetis
Calving ease (CED)	X	X
Calving ease maternal (CEM)		
Heifer pregnancy (HP)		
Growth (BW WW YW Milk)	X	X
Residual avg. daily gain (RADG)	X	X
Docility (DOC)	X	X
Yearling scrotal/height (SC, YH)	X	X
Mature weight (MW)	X	X
Carcass (CWT MARB RIB FAT)	X	X

CONTINUED FROM PAGE 167

root of the percent additive genetic variance and, conversely, the percent additive genetic variance is the squared value of the genetic correlation.

For example, if the genetic correlation between the genomic result and the phenotypic measure is .60, then the genomic result explains 36% of the additive genetic variance. Simply stated, the more genetic variance a test explains, the more impact it will have on your EPDs and accuracies for that trait. Angus breeders must consider these relationships and then make the best choice for their breeding programs and traits of interest.

Available traits that include genomic results

Use the EPDs to make the most informed selection decisions among animals. The EPDs should be considered the genetic improvement tool of choice, since EPDs account for all the available information on an animal, such as individual measures, progeny data, pedigree and genomic results. The details below will help you gauge the areas where genomics are having the most impact by trait.

In American Angus Association genetic evaluations, the genomic results are incorporated into the EPDs as a correlated trait. Table 2 summarizes the traits impacted by genomic results. Both companies' genomic results are included in the calculations for the traits as indicated.

Residual average daily gain (RADG) EPDs include genomic results for dry-matter intake. Company information for tenderness and RFI are not part of any EPD calculations. Also, heifer pregnancy (HP) EPDs do not include genomic results.

EPDs, profile scores and percentile ranks

As a reminder, if you are making selection decisions for traits that have an EPD provided by the Association, then the EPDs should be considered the selection tool of choice. The EPD and accuracy account for all sources of information available on the animal of interest (e.g., pedigree, own record, weights/measures, genomic results). Using EPDs and genomic scores separately leads to double counting information and will lessen selection efficiency.

Table 3 describes by trait the Igenity profile score (1-10) and Zoetis percentile rank (1-100) systems to assist in establishing direction of interest for each trait.

Igenity profile scores are presented on a 1-to-10 scale, which reflects the animal's genetic potential for a particular trait based on the combination of the DNA markers analyzed. Higher scores are not necessarily most desirable, as illustrated in Table 3.

Table 3: Establishing direction for Igenity profile scores and Zoetis percentile ranks

	Igenity score 'Favorable'	Zoetis percentile 'Favorable'
Calving ease direct (more unassisted)	10	1%
Calving ease maternal	10	1%
Birth weight (lighter)	1	1%
Weaning weight	10	1%
Yearling weight	10	1%
ADG postweaning	10	
Milk (more maternal milk in daughter calves)	10	1%
Carcass marbling	10	1%
Carcass rib (larger)	10	1%
Carcass fat (leaner)	1	1%
Carcass weight (heavier)	10	1%
Dry-matter intake (eat less)	1	1%
RFI (lower feed intake than predicted)	1	1%
Tenderness (more tender)	10	1%
Docility (more docile)	10	1%
Yearling height (more hip height)	10	1%
Scrotal (larger size)	10	1%
Mature weight (larger cow weight)	10	1%
Mature height (more cow height)	10	1%
Heifer pregnancy	10	1%

For the Zoetis HD 50K percentile rankings, a lower value indicates a more favorable ranking for the trait. The percentile ranking format, ranging from 1% to 100% in integer increments, is similar to that used in EPD percentile rankings. For example, a smaller numeric percentile ranking for birth weight and carcass fat indicates an expectation of lighter calves and leaner carcasses.

Importance of phenotypic performance data. Genomic results are used as indicator traits in the evaluations to compute EPDs. Genomics do not completely describe the variation in the traits of interest. Breeders sometimes ask if it is no longer necessary to collect weights and measures (e.g., weaning weights, scan data, carcass measures). On the contrary, phenotypic measures collected by Angus breeders continue to be an important part in further development of improved genomic panels and the refinement of this technology over time, not to mention an important component in EPD calculation.

Conclusion

Angus breeders must consider the available genomic options and then make the best choice for their breeding programs to impact traits of interest. Genomic results are a way to enhance the current selection tools, to achieve more accuracy on predictions for younger animals, and to characterize genetics for traits where it's difficult to measure the phenotype.

Through the evolution of these technologies, we plan to keep breeders advised of progress in the development of genomic EPDs. These updates, when available, will be provided on *www.angus.org*. To learn more about available genomic tests, go to *www.angus.org/AGI/default.aspx*.

Editor's Note: *"By The Numbers" is a column by Association performance programs staff to share insights about data collection and interpretation, NCE, genetic selection and relevant technology and industry issues. Sally Northcutt is director of genetic research for the American Angus Association. If you have questions or would like to suggest a topic for a future column, contact Northcutt, Bill Bowman or Tonya Amen at 816-383-5100.*