

Updated Angus High Density (HD) 50K Genomic Predictions and Incorporation into Genetic Evaluation

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Introduction

Genomic-Enhanced Expected Progeny Differences (GE-EPDs) are computed during National Cattle Evaluation (NCE) conducted on a weekly basis for the American Angus Association[®] (AAA) by Angus Genetics Inc.[®] (AGI), a subsidiary of the Association. In addition to weekly evaluations, AGI also executes periodic updates to the calibration and weighting of genomics information with its research partner, Zoetis Genetics. These endeavors help insure that available information is most appropriately incorporated into Angus EPD and accuracy values to competitively empower the selection, mating and marketing activities of Angus breeders and commercial users of Angus genetics.

The Processes

DNA samples are received by AGI from Angus breeders and anonymously bar-coded to associate the AAA animal identity before forwarding samples to company laboratories for DNA extraction and genotyping. Companies return SNP genotypes to AGI, and any genotypes, as well as phenotypic trait data, received prior to close of business each Tuesday are included in the NCE weekly release on Friday mornings. Remaining DNA samples are returned to AGI by the genomics companies after genotyping and are archived at the Association headquarters. Breeders are encouraged to anticipate at least a four-week turnaround for results being incorporated into the weekly GE-EPDs.

AGI scientists, and Association information systems personnel, oversee receipt and application of SNP genotypes into GE-EPDs each week. Prior to incorporation in the NCE, SNP marker information is used to verify recorded pedigree information or help resolve any parentage exclusions. Specific SNP effects are then used in 50K prediction algorithms to generate molecular breeding values for each trait. AGI and Zoetis scientists collaborate on research, recalibrations, and to derive correlations between genomic predictions and expressed performance for use in genomic-enhanced EPDs. Genotypes are stored at the Association for reference and future recalibration efforts.

Genomic calibration updates encompass three general processes, including 1) classic genetic evaluation conducted by AGI without genomic information that yields traditional EPDs used for recalibration of marker effects, 2) recalibration or retraining of marker effects by Zoetis Genetics scientists using classic EPDs, Iowa State University GenSel software and Zoetis proprietary grouping technology for estimation and internal validation of marker effects, and 3) parameter

estimation by AGI to determine genetic correlations between genomic predictions and expressed performance that are used in weekly Angus NCE.

Depending upon the trait, the most recent version-four AGI calibration utilized HD 50K genotypes from upwards to 57,550 registered Angus animals. Notable adoption of HD genotyping by Angus breeders has enabled continuous competitive improvement in the accuracy and breadth of GE-EPDs for existing and additional traits.

Genomic Impact on EPDs and Accuracy Values

As implied earlier, in the AAA genetic evaluations, the molecular breeding values are incorporated into the EPDs using a correlated trait approach. Through AGI research and development, a genetic relationship is calculated between the values obtained from the genomic test results (genotypes and the calibration) and the phenotypic data at AAA.

Table 1 includes genetic correlations (r) between the phenotypic records and the HD 50K molecular breeding value predictions. The genetic correlations effectively range from .60 to .75, except for milk and heifer pregnancy (range from .35 to .45). September 2014 marks the fourth calibration release for the 50K predictions since February 2011.

Also included in Table 1 is the average accuracy value achieved by non-parents from verified pedigree and HD 50K information for each trait, as well as approximate progeny equivalent counts. The progeny equivalents represent the number of offspring with records of the associated trait, measured in valid contemporary groups, required in traditional genetic evaluation to achieve the same level of accuracy immediately provided by GE-EPDs that include HD 50K predictions and verified parentage. This information is intended to help communicate the benefits of the technology, given the time, difficulty and cost of traditional data collection. However, it is more important than ever for breeders to continue to collect and submit the full range of performance data, which is essential for future recalibrations of marker effects and achieving more proven levels of accuracy for young animals.

Genomic Results for Available Traits

Breeders and users of Angus genetics are strongly encouraged to use GE-EPDs as the selection, mating and marketing tools of choice, because they account for all available information on an animal, including individual performance measures, progeny data, pedigree and genomic results — and are clearly the most accurate predictions of genetic merit.

With the latest integration of genomic results, GE-EPDs for heifer pregnancy now better account for the effects of service sire on pregnancy rate. Heifer pregnancy EPDs are expressed in units of probability of pregnancy, with higher values indicating genetic merit for greater likelihood of being bred (pregnant) versus open (not pregnant) at the end of defined breeding

seasons. This inclusion of genomic information is estimated to deliver heifer pregnancy GE-EPDs and accuracy values for tested animals that are roughly equivalent to having 10 daughters with pregnancy test results contributing to traditional EPDs. The AAA, AGI and Zoetis thanks Angus breeders for contributing heifer breeding records that have enabled GE-EPDs for this important early life-cycle reproductive trait.

Several other considerations regarding genomic results merit special mention. The multi-trait genetic evaluation for mature weight and height includes only the genomic predictions for mature weight, because there is a high correlation between the molecular breeding values for mature weight and height. Likewise, calving ease maternal EPDs only include calving score and birth weight phenotypes, and genomic results for calving ease direct. The residual average daily gain (RADG) value includes genomic predictions for dry matter intake (DMI), rather than the genomic test result for residual feed intake (RFI). While genomic predictions are reported for tenderness, GE-EPDs are not available.

In conjunction with release of the HD 50K version-four genomic calibration, underlying genomic information used to derive GeneMax Advantage Scores and SMART Outlier reporting were also updated. This ensures the two products remain complementary beyond multi-sire parentage assignment in their use across the Angus seedstock, commercial cow-calf, and CAB supply chain. There are two components of the update to GeneMax Advantage Scores and SMART Outliers that may affect new reported results when contrasted with initial results, including: 1) use of more informative underlying marker effects, and 2) an expanded reference population of over 14,000 commercial Angus females now used for benchmarking. For more detailed information about these advancements, a separate “GeneMax Advantage Enhancement Update” is available.

Conclusion

Thanks to adoption by Angus breeders, the number of animals with genotypes for use in HD 50K predictions and GE-EPDs is expected to approach 100,000 registered Angus animals by early 2015. Genomic results incorporated into at least 15 GE-EPDs and used to verify parentage also provide added dependability to economic selection indexes for young Angus animals. This integration of genomics into GE-EPDs and Angus \$Value indexes simplifies use of genetic information across many traits for Angus breeders and their commercial customers.

Table 1. Angus heritability estimates, genetic correlations (r) between version four (V4) 50K predictions ($n=57,550$) and the American Angus Association phenotypic database (September, 2014), standard errors (SE), approximate accuracy (ACC) and progeny equivalents (PE) for tested non-parents (based on verified pedigree and HD 50K information).

Trait	AGI h²	HD 50K V4 r (SE)	HD 50K V4 ACC	HD 50K V4 PE
Calving Ease Direct (CED)	0.20	0.62 (.09)	0.31	21

Birth Weight (BW)	0.42	0.68 (.02)	0.37	13
Weaning Weight (WW)	0.20	0.56 (.02)	0.29	19
Yearling Weight (YW)	0.20	0.66 (.02)	0.32	22
Residual Average Daily Gain (RADG) ¹	0.31	0.74 (.03)	0.37	18
Yearling Height (YH)	0.50	0.74 (.01)	0.38	11
Scrotal Circumference (SC)	0.47	0.78 (.01)	0.41	14
Docility (Doc)	0.37	0.71 (.03)	0.33	12
Heifer Pregnancy (HP)	0.13	0.45 (.05)	0.14	10
Milk	0.14	0.36 (.01)	0.19	14
Mature Weight (MW)	0.37	0.68 (.02)	0.34	13
Carcass Weight (CW)	0.38	0.60 (.03)	0.30	10
Marbling Score (Marb)	0.45	0.67 (.03)	0.33	9
Ribeye Area (RE)	0.33	0.69 (.03)	0.30	11
Fat Thickness (FAT)	0.34	0.65 (.03)	0.31	12

¹Dry Matter Intake Component