



By the Numbers

► by *Sally Northcutt, Angus Genetics Inc.*

Incorporating genomics into genetic evaluation

The Beef Improvement Federation (BIF) hosted a genetic prediction workshop in Kansas City, Mo., Dec. 12-13, 2013. Sally Northcutt, American Angus Association director of genetic research, presented the Association's experience in incorporating genomics into genetic evaluation procedures. In this month's column we share the proceedings to that presentation.

Introduction

Genomic-enhanced expected progeny differences (GE-EPDs) are computed on a weekly basis at the American Angus Association. Angus Genetics Inc. (AGI) is a subsidiary of the Association that facilitates the implementation of DNA technology and the infrastructure for the weekly national cattle evaluation (NCE). AGI personnel receive results from two companies providing genotyping services.

The process

The DNA samples are received from Angus breeders and anonymously barcoded to associate the American Angus Association animal identity before forwarding samples to company laboratories for extraction and genotyping. Companies return single-nucleotide polymorphism (SNP) genotypes in A/B format to AGI, and breeders are

encouraged to anticipate a four-week turnaround for results to be incorporated into the weekly EPDs.

Any genotypes, as well as phenotypic trait data, received by AGI 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.

AGI geneticists, in conjunction with Association information systems personnel, oversee receipt and application of SNP genotypes into NCE procedures. Initially, the received SNPs are directed through parentage validation procedures conducted in-house to review any parentage conflicts for corrections to the Association database. Specific SNP effects are used in a 50K prediction algorithm to generate molecular breeding values for NCE traits. AGI and Zoetis scientists maintain a long-term collaboration to facilitate research, calibration efforts, and derivation of SNP effects for the purposes of genomic-enhanced EPDs. Genotypes are warehoused at the Association for reference and future calibration efforts.

Genomic impact on the EPDs

In the Association's 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 and the phenotypic data at the American Angus Association.

Table 1 presents the genetic correlations between the phenotypic records and the 50K molecular breeding value predictions. The genetic correlations effectively range from 0.60 to 0.70, except for milk and heifer pregnancy.

December 2013 marks the third calibration release for the 50K prediction since February 2011.

Available traits that include genomic results

Breeders and users of Angus genetics are strongly encouraged to use EPDs as the genetic improvement tool of choice, because EPDs account for all the available information on an animal, such as individual measures, progeny data, pedigree and genomic results.

Several considerations regarding genomic results merit special mention. The multi-trait genetic evaluation for mature weight and height includes the genomic prediction for only mature weight, because there is a high correlation between the molecular breeding values for mature weight and height. Likewise, the calving ease NCE that includes calving score and birth weight phenotypes incorporates genomic results for calving ease direct only. The residual average daily gain (RADG) values provided in the weekly genetic evaluation include the genomic indicator for dry-matter intake (DMI) rather than the genomic test result for residual feed intake (RFI).

The number of genotypes for use in the 50K prediction is expected to exceed 50,000 registered Angus animals by early 2014. Results are incorporated into at least 15 EPDs, which are then components of the selection index suite. Angus producers have appreciated the simplicity of this approach to incorporating genomics into the Association's NCE.

EMAIL: snorthcutt@angus.org

Editor's Note: "By The Numbers" is a column by Association performance programs staff to share insights about data collection and interpretation, National Cattle Evaluation (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 the Association at 816-383-5100.

Table 1: Genetic correlations between 50K predictions (n=38,981) and the American Angus Association phenotypic database, December 2013

Trait	Genetic correlation
Calving ease direct	0.63
Birth weight	0.66
Weaning weight	0.56
Yearling weight (gain)	0.67
Milk	0.38
Yearling height	0.73
Yearling scrotal	0.77
Dry-matter intake	0.73
Docility	0.65
Heifer pregnancy	0.49
Mature weight	0.71
Carcass weight	0.58
Marbling	0.66
Ribeye area	0.68
Fat	0.64

Source: S.L. Northcutt (2013). BIF Genetic Prediction Workshop, Kansas City, Mo.