



Evaluating “Single-Step” Methodology for Genomic Selection

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Single-Step Evaluation in the American Angus Association: The American Angus Association have been incorporating genomic information into their National Cattle Evaluation (NCE; performed by Angus Genetics, Inc.) since 2011. In that time, they have accumulated well over 300,000 animals with high-density genotypes; over 50,000 genotypes imputable for each animal. Originally, these genotypes were incorporated into the NCE using a multi-step (MS) approach. Under this methodology, a molecular breeding value (MBV) was derived from the genotypes using an external prediction equation. Then, the MBV was incorporated into the NCE as a correlated trait using standard multi-trait methodology with a genetic correlation estimated between the MBV and the trait of interest. This method required the derivation of the MBV prediction equation (from a commercial partner) and a calibration step to estimate the genetic correlation between the MBV and the traits. Both of these steps were intensive and could take several months to complete.

As an alternative, Angus Genetics, Inc. began evaluating a single-step (SS) approach using algorithms and software developed by the University of Georgia. In this approach, genomic information is directly incorporated into the evaluation by replacing pedigree relationships with relationships derived by similarities in animal genotypes. As such, no prediction equation or calibration step is required.

The U.S. Meat Animal Research Center Germplasm Evaluation Program (USMARC GPE; Figure 1) was used to determine whether EPDs from MS or SS approaches were more accurate and/or reflected higher or lower levels of bias. The program has sampled 213 Angus sires in its lifespan and of these, 143 are genotyped with high-density arrays. Most of the bulls used in the program have at least 10-12 progeny. The GPE program is used to derive annual across-breed EPD adjustment factors and, as such, EPDs for birth eight, weaning weight, yearling weight, maternal weaning weight (milk), marbling score, ribeye area, backfat depth, and carcass weight are produced using internal data from USMARC. This data was not part of the Angus NCE. We evaluated correlations between the EPDs from GPE and the Angus EPDs from SS and MS to determine which system was more accurate. We also produced Angus-specific regressions of performance on EPD to examine the potential for bias in the system.

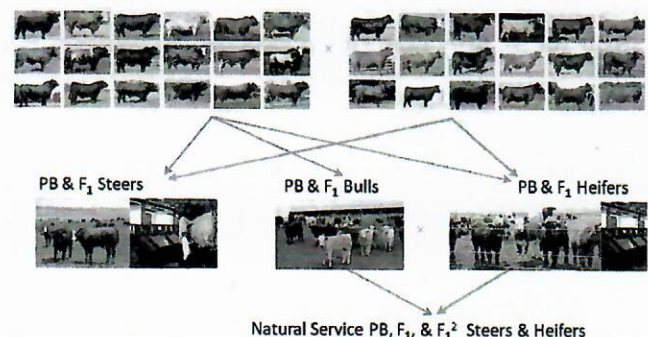


Figure 1. Germplasm evaluation population structure

Results of Analysis: Table 1 contains the correlations between EPDs produced at USMARC and EPDs from SS, MS, or a non-genomic (NG) analysis from the Angus database.

Table 1. Correlations between EPDs derived at USMARC and EPDs from the American Angus Association derived with Single-step (SS), Multi-Step (MS) or Non-genomic (NG) methodologies.

TRAIT	ALL BULLS IN GPE			BULLS WITH GENOTYPES		
	SS	MS	NG	SS	MS	NG
Birth weight	0.60	0.59	0.60	0.64	0.63	0.63
Weaning weight	0.43	0.43	0.43	0.39	0.39	0.38
Yearling weight	0.52	0.51	0.52	0.39	0.39	0.38
Maternal milk	0.40	0.40	0.40	0.27	0.26	0.26
Carcass weight	0.35	0.32	0.35	0.26	0.22	0.26
Marbling score	0.51	0.44	0.49	0.56	0.49	0.55
Ribeye area	0.27	0.24	0.22	0.28	0.24	0.22
Backfat depth	0.42	0.24	0.38	0.44	0.25	0.40

Correlations from SS were consistently higher relative to MS. In several cases, NG EPDs had higher correlations than MS. The clearest advantage of SS was observed for carcass traits, which have less actual data in the Angus NCE.

While not shown, regression coefficients for carcass traits were less than one for MS which indicates that MS may have over-predicted performance differences. Regression between SS and NG were very similar for all traits, indicating the SS is not changing the scale observed when no genomic information contributes to the NCE.

These results indicate that the change to SS evaluation results in bull rankings that are more similar to those produced in the independent GPE data set. These results are consistent with internal evaluations for weight traits by Angus Genetics, Inc. Based on the regression results, the MS approach may have been overestimating differences in carcass data.

Because of these and other internal results, Angus Genetic, Inc. adapted the SS approach in their NCE and has been delivering weekly EPDs using this method since July 2017.

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