

## **Carcass EPDs at a glance**

The American Angus Association's weekly carcass expected progeny differences (EPDs) are composed of the typical pieces one would expect in a national cattle evaluation (NCE),

but they also include genomic results if available. Every week the full NCE for carcass traits is conducted for the most timely, up-to-date genetic predictions computed on nearly 2 million animals.

## **Multiple inputs**

Sources of information include harvest data, ultrasound scans (bulls, heifers, or steers) genomic results and associated pedigree information. Fig. 1 illustrates the components and serves as a reminder that the evaluation includes animals with varying sources of data present.

The harvest data traits (carcass weight, ribeye, marbling and fat) are the economically relevant traits for which the resulting EPDs will be expressed. Ultrasound data and genomic results serve as indicator traits. Established genetic relationships between the indicator and carcass traits affect the EPDs and accuracy.

The beauty of using the genomic data as an indicator trait is that animals at a young age can have carcass trait EPDs prior to scanning. For example, Fig. 2 presents an Angus calf out of registered parents that have

EPDs. Prior to the calf's genomic profile, the EPDs were simply a parental average EPD, or interim EPD, with a 0.05 accuracy level.

This calf (of any age) then has a genomic



Fig. 2: Animal with interim EPDs (old) vs. carcass EPDs resulting from genomic profile (new)

OLD	СѠТ	MARB	RE	FAT
EPD	l+15	l+.79	l+.41	I001
Acc	.05	.05	.05	.05
NEW	CWT	MARB	RE	FAT
EPD	+18	+.71	+.50	+.004
Acc	.30	.38	.35	.28

Fig. 3: Dam with scan record and scan progeny (old) vs. carcass EPDs resulting from addition of genomic profile (new)

OLD	CWT	MARB	RE	FAT
EPD	+12	+.46	+.08	008
Acc	.21	.25	.31	.24
NEW	CWT	MARB	RE	FAT
EPD	+12	+.86	+.13	+.024
Acc	.28	.37	.38	.30

result reported through Angus Genetics Inc. (AGI) and the American Angus Association. The weekly carcass EPD result is an EPD with accuracies ranging from 0.28 to 0.38,

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depending on the carcass trait.

Unlike the phenotypic data (carcass, ultrasound) the genomic result required no contemporaries to enter the genetic evaluation. Thus, the genomic profile can be incorporated from animals of any age.

For animals that already have an EPD in the carcass evaluation, the genomic results still have an effect on the carcass traits. EPDs

may move up, down or stay the same, and the accuracies increase on animals where there is not extensive data reported for the animal as a parent thus far.

In Fig. 3, the animal is a dam with her own scan record from a proper contemporary group and 11 scanned progeny. With her own record and progeny information, the marbling accuracy is 0.25 (OLD). After her profile results are included in the weekly NCE carcass evaluation, her marbling accuracy improves to 0.37. (NEW)

Mixed model methodology to generate EPDs is not trivial, but can be referenced in the guidelines for the Beef Improvement Federation (*www.beefimprovement.org*). With efficient software routines and highspeed computers, the computational step to generate weekly carcass EPDs is straightforward.

Weekly carcass evaluations with genomic results included in the analysis are part of the evolution to provide Angus breeders with rapid, accurate selection tools for genetic improvement.

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**Editor's Note:** "By the Numbers" is a column by Association performance programs staff to share insights about data collection and interpretation, the NCE, genetic selection, and relevant technology and industry issues.

## An evolution in carcass selection tools

*Incorporating molecular breeding values in the Angus NCE.* 

The American Angus Association has collected data for genetic evaluation of marbling, longissimus muscle area, subcutaneous fat depth and carcass weight since 1974. Each genetic evaluation captures information from a variety of sources to produce a unified national cattle evaluation (NCE) for these economically relevant traits (ERTs).

Carcass data were either from an Association-sponsored sire evaluation program or submitted directly to the Association by members who had obtained the data using a variety of commercial and private services. Yearling Angus bulls and heifers were scanned by certified technicians using ultrasound.

Molecular breeding values (MBV) evaluated herein were produced specifically for Angus cattle by Igenity.® These MBV were calculated as multimarker compound covariate prediction equations using a single panel of SNP that provided whole-genome coverage.

The MBV were incorporated into the NCE as correlated traits. Genetic correlations of MBV with the economically relevant carcass traits ranged from 0.50 to 0.65.

These results show MBV to be useful indicators of ERTs in Angus cattle. Their incorporation into conventional systems for NCE allows breeders to efficiently and unambiguously use the results. However, highly accurate genetic evaluations continue to require collection of phenotypic data for the economically relevant traits.

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