

BY THE NUMBERS

by Kelli Retallick-Riley, AGI president

Genomic Selection: The Good and the Potentially Bad?

While genomic testing has proved beneficial, AGI researches effects on genetic diversity.

We often speak of the benefits of genomic selection — the added accuracy and increased rate of genetic progress come to mind. The American Angus Association is no stranger to either of these. Just look at your genetic trends. Figure 1 shows the current genetic trend for the Marbling expected progeny difference (EPD). Producers can see notable changes in genetic progress as the trend becomes much steeper in recent years. Overlay that with the amount of genetic testing that has been taking place, and you must give some credit to the increased use of genomic selection.

Unintended consequences

Even with all the positives, one could still wonder what is lurking on the other side. Decreasing the genetic diversity of the breed could be one possible consequence of genomic selection. Other cattle populations like U.S. Holstein have seen their rate of inbreeding increase over the years while their use of genomic selection grows. Increased inbreeding has the potential to affect fitness and decrease performance for economically important traits like fertility and growth.

Inbreeding generally arises due to the mating of closely related animals,

which leads to a greater likelihood of offspring having two copies of the same variant (homozygous) AA or BB. Prediction of a pedigree-based inbreeding coefficient uses a set equation to distinguish ancestral inbreeding based on pedigree relationships. Genomic inbreeding uses genotypes to detect the percentage of the genome covered by the same, homozygous variant.

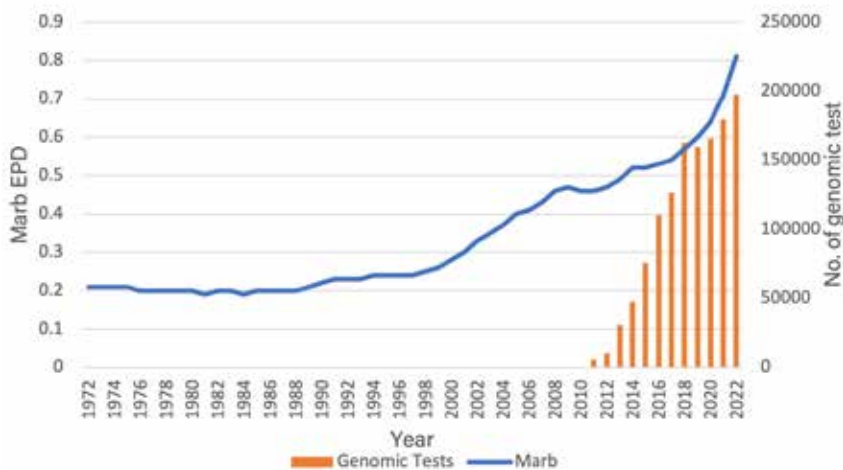
In most cases, genomic inbreeding is more precise. Take full sibs — based on pedigree, the inbreeding coefficients on all siblings would be equal. Yet we know full sibs will not receive the exact same genetic material from their parents, and therefore can differ for genomic inbreeding.

With these factors in mind, Angus Genetics Inc. (AGI), thanks to funding contributions from the Angus Foundation, set out to understand what genomic selection has done to the genetic diversity of the Angus breed.

The data

The study focused on quantifying both the pedigree and genomic inbreeding levels. In total, 569,364 animals born from 1969 to 2019

Figure 1: Marbling EPD genetic trend vs. number of genomic tests submitted per year



Continued on page 40

were included in the analysis. To specifically focus on the effects of genomic selection, 26,149 sires and 135,548 dams born between 2000 and 2017 were split into two groups for analysis. These groups were identified as animals born before genomic selection (2000-2009) and after genomic selection (2010-2017).

Figure 2 shows the number of genotyped sires and dams by birth year. The number of genotyped parents has been on an upward trajectory since the advent of genomic testing. The slight decline in recent years is a function of when the data was captured. Only animals that had a reported progeny into the evaluation at the time the data was pulled in early 2019 were included in this study.

The results


Both pedigree and genomic inbreeding remained relatively constant before and after the advent of genomic selection, only increasing by approximately 2%.

The yearly rate of inbreeding accumulation remained similar in sires pre- and post-genomics; and for females, it decreased significantly.

This supports that even with the advent of genomic selection, the genetic diversity in the American Angus population has been conserved. The diversity in environments and breeding objectives is probably partly

responsible for this continued conservation. It could also be argued that because a larger proportion of the Angus population is now being genotyped, we are just starting to capture the full variation of the population.

While the outcome may be brighter than what some may have expected, it must be noted within certain breeding schemes, inbreeding coefficients could be higher due to selection pressures. It is important to utilize all tools when making breeding decisions.

At AGI, we will continue to monitor this rate of inbreeding and the potential effects inbreeding, even inbreeding within parts of the genome, could possibly have on the outcome of production, maternal, management and carcass traits. 

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Editor's note: Research completed by Lozada-Soto, E.A., et al. (2021) <https://doi.org/10.1186/s12711-021-00644-z>

Figure 2: Number of genotyped sires and dams by birth year.

