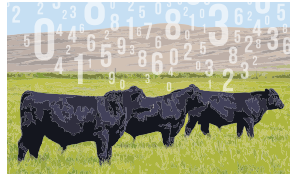


# BY THE NUMBERS



by Dan W. Moser

## Genomic progeny counts

*What they mean, and what they don't.*

Recently, a member asked me an excellent question about genomic progeny counts. He observed a pair of young full-brother bulls. Both had been genotyped for the genetic evaluation, and neither had yet recorded progeny performance records for any trait. The only difference in the bulls from a data standpoint was that one bull had 17 genomic progeny — that is, 17 sons or daughters with genomic profile test results. The full brother had no genomic progeny, yet had practically identical expected progeny difference (EPD) accuracy for all traits. The breeder was surprised that the 17 genomic progeny hadn't increased the accuracy of their sire's EPDs. I suspect many Angus breeders would have been similarly surprised.

### Why count genomic progeny?

The American Angus Association began reporting genomic progeny counts on *angus.org* in 2015. Breeders observed that bulls' EPD accuracy increased along with the number of genomic progeny, and requested that information be provided, like it was with several dairy cattle breeds.

At the time, our genetic evaluation used a multi-step genomic approach, where genotypes obtained from genomic testing were converted to molecular breeding values (MBVs). Those MBVs were then incorporated into the evaluation

models as correlated traits, additional information beyond the animal's measurements and its progeny.

That approach, while the best available technology at the time, did tend to slightly overestimate accuracy of EPDs as a result of progeny genotypes. The multi-trait methodology also introduced a degree of bias into the evaluation, where animals' EPDs were slightly overestimated if only their most favorable progeny were genotyped.

Those were some of the reasons Angus Genetics Inc. (AGI) began investigating single-step genomic evaluation, and implemented that methodology in the Angus genetic evaluation in July 2017.

In reality, if an animal is genotyped, genotypes from their progeny add no new information about the parent to the evaluation. Each offspring of an animal will receive a random half of each parent's genetic material. Genomic testing reveals which progeny received the most favorable genetic material for a particular trait among a group of half-siblings. But for every offspring receiving a better-than-average contribution from their parent, a half-sibling inherits an equally unfavorable draw of the parent's genetics. By using genotypes to better define pedigree relationships instead of estimating MBVs, no bias is created even if only the best progeny of a sire or dam are genotyped.

In contrast, if a parent animal is not genotyped, genomic testing of their progeny can add significant information about the parent, especially if the parent also has no progeny performance records for a trait. In effect, genomic testing of a large group of progeny informs the genetic evaluation of the parent's genotype. When an ungenotyped sire or dam has their first progeny genotypes added to the genetic evaluation, that animal's EPDs can change in a similar manner as if the animal itself was genotyped. The amount of change depends on how much other information is available for that animal and trait. A sire with many progeny records may not change at all when progeny are genotyped, but when no sire genotype and no progeny records are available for a trait, the change in EPD may be noticeable, and the increased accuracy might be significant.

For ungenotyped animals, genomic progeny counts can indicate the impact of that information on EPD accuracy and potential for future change in EPDs. However, once an animal itself is DNA tested, only progeny performance records add accuracy to EPDs, not progeny genotype counts.

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