SORTING GATE

Genomic testing: What's the value to commercial bull buyers?

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As evidenced by the development of the next-generation vaccines that are being used to combat the coronavirus, genomics, which is the study of all of an organism's genes, is having an effect on our lives and our livelihoods. Animal agriculture has benefited, as well.

Though expected progeny differences (EPDs) have been used by commercial bull buyers for decades, advancements in genomic testing and genetic evaluation have greatly enhanced these traditional selection tools. Exactly what value is derived from purchasing a nonparent registered Angus bull that has been tested with Angus GS[SM] or HD50K™ for Angus? Answering this question requires a brief review of biology, as well as an overview of genomic testing and the current methods of genetic evaluation.

Back to biology

As depicted in Fig. 1, base pairs are a component of the building blocks (nucleotides) of the familiar DNA double helix, with adenine (A) pairing with thymine (T), and cytosine (C) pairing with guanine (G). The bovine genome consists of an astounding 3 billion base pairs spread across 30 pairs of chromosomes.

The vast majority of these 3 billion base pairs are identical within all cattle, which is what makes them cattle and not some other species. However, differenc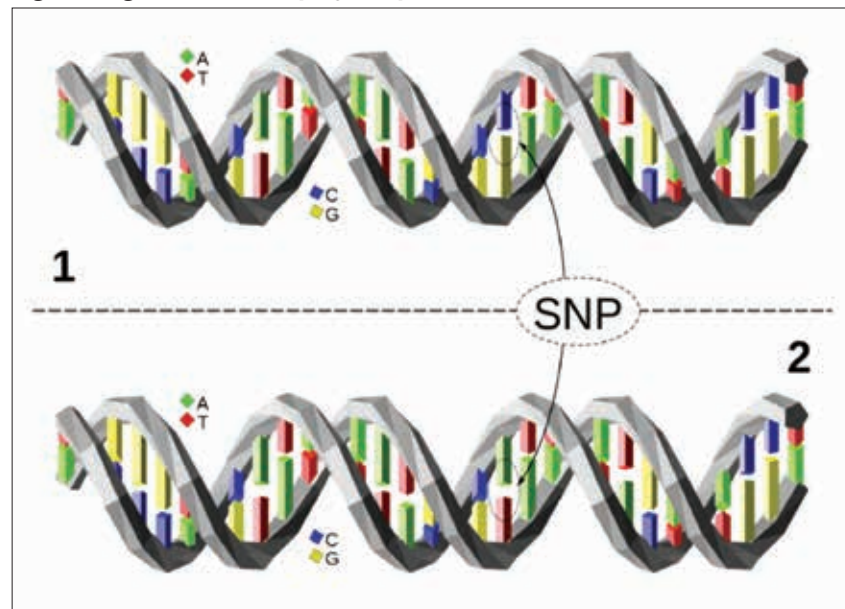es, like that shown between two animals in Fig. 1, do exist. These differences, where one base pair is commonly substituted for another at a specific position, are termed single-nucleotide polymorphisms, or SNPs (pronounced "snips").

Whereas the base pairs that are identical for all cattle define the bovine species, the differences in base pairs, or SNPs, help define the differentiation found within the species for a multitude of characteristics, ranging from physical appearance (color, height, weight, musculature, skeletal structure) to how efficiently an animal metabolizes energy or how effectively it responds to a challenge to its immune system.

Genomic testing

Genomic arrays are used to isolate SNPs that are known to be of interest within a population. In the case of Angus cattle, breeders can submit blood, tissue, hair or semen

Fig. 1: Single-nucleotide polymorphism, or SNP

SOURCE: Wikipedia (model by David Eccles).

Table 1: Angus database, as of Jan. 29, 2021

Phenotype	No. of records
Birth wt.	9,202,115
Weaning wt.	9,710,750
Yearling wt.	4,723,244
Heifer calving ease	1,749,941
Carcass measures	127,310
Ultrasound measures[1]	2,446,962
Feed intake	30,442
Docility	337,708
Scrotal circumference	1,037,225
Heifer pregnancy	121,826
Mature cow wt.	231,917
Foot scores[2]	109,576
Pulmonary arterial pressure (PAP) scores[3]	19,321
Hair shed scores	16,038

[1] Used to predict carcass measures.
[2] Foot angle and claw set.
[3] Includes yearling high-altitude, weaning high-altitude and yearling moderate-altitude scores.

SOURCE: American Angus Association, 2021.

samples for testing on either the Neogen Angus GS or the Zoetis HD50K for Angus array. These arrays isolate more than 50,000 SNPs from the 3 billion base pairs found in cattle that, through statistical analysis, have displayed an association with traits reported in the weekly Angus genetic evaluation.

Before, after genomics

Prior to the use of genomics, information used by the Angus genetic evaluation consisted of all known pedigree relationships between animals, as well as all available phenotypic measures of performance (weights, heights, etc.). The product of this statistical evaluation was an EPD for each animal for each trait where data was present. As they do now, these EPDs estimated, on average, the genetic value that would be transmitted from an animal to its progeny for each respective trait.

Each EPD is associated with an accuracy value, which will range between 0 and 1. Accuracies measure the reliability of an EPD estimate by reflecting both the quantity and type of information (the animal's own performance, the performance of half-sibs, the performance of progeny, etc.) that was used in its calculation.

Because the goal of an EPD is to predict how the average offspring of an animal will perform for any given trait, it should come as no surprise that high accuracies are only achieved with the inclusion of a significant number of progeny records. This means that the EPDs on a young sire that doesn't yet have any progeny are not as accurate as those for a sire with numerous progeny records. This translates to increased risk.

By incorporating genomics in today's Angus genetic evaluation, the relationships between animals are much better defined. As an example, because full siblings are expected to have 50% of their genes in common, a 50% relationship would have been assumed in a pre-genomic evaluation. However, due to the way in which genes are inherited from the parents, it is not surprising for full sibs to actually share anywhere from 38% to 61% of

their DNA. This is the reason that some full siblings bear a stronger resemblance than others.

The use of genomics allows us to determine, by comparing SNPs in common, which full siblings are more genetically related for individual traits. In fact, genomics allows for all relationships within the population to be better defined.

If a newly tested animal is determined to have a strong genomic relationship to animals that excel for growth to a year of age, the yearling weight EPD of this newly tested animal will increase even though the pedigree relationships between animals may be quite distant.

An additional benefit of genomic information is that it allows for a better characterization of genetic differences for traits that are difficult or expensive to measure. For example, by determining genomic relationships between an animal that has no direct carcass measures on their progeny with

animals that have a significant number of progeny carcass records, we are able to gain some information about the genetic potential for carcass merit for the animal in question.

The bottom line

As displayed in Table 1 (see page 38), the database of the American Angus Association holds millions of phenotypic records along with the genotypes of more than 900,000 Angus cattle. By testing a young, unproven bull with Angus GS or HD50K for Angus, this vast database is fully leveraged to enhance the accuracy of his EPD predictions for all traits.

How much accuracy is achieved? As illustrated in Table 2, the EPDs of an unproven animal that incorporate a genomic test have the same degree of accuracy as if they

Table 2: Progeny equivalents (PE) associated with the inclusion of genomics

Trait	PE
Calving ease direct	26
Birth wt.	23
Weaning wt.	27
Yearling wt.	23
Dry-matter intake	12
Yearling ht.	17
Scrotal circumference	15
Docility	12
Claw set	10
Foot angle	10
Heifer pregnancy	17
Calving ease maternal	20
Maternal milk	36
Mature wt.	15
Mature ht.	15
Carcass wt.	15
Carcass marbling	11
Carcass ribeye	17
Carcass fat	14

Carcass trait PE equate to actual carcass harvest data, not ultrasound equivalents.

already had progeny records on anywhere from 10 calves to 36 calves, depending upon the trait. As much value as genomic tests provide, it is important to note that the continued collection of phenotypic data is necessary to maintain an accurate genetic evaluation.

The purchase of an unproven bull always carries a certain degree of risk for a commercial cow-calf enterprise. Though EPDs have always served as a risk management tool, EPDs that incorporate a genomic test further reduce this risk.