

GENOMICS: Where are we going?

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Genomics. This term has become a popular buzzword within the beef industry. But what does it mean? Genomics is analyzing the entire DNA of an animal. Rather than focusing on a specific gene or segment of DNA, in genomic applications we generate data across all of the cattle chromosomes (strands of DNA inherited as a unit). Cattle have approximately 20,000 genes spread over 29 pairs of chromosomes plus the sex chromosomes, and in genomics we try to account for these 20,000 genes. In genomic predictions we estimate the effects of thousands of DNA variants spread across the cattle chromosomes using data from animals with both DNA data and trait records. We then validate these genomic predictions and use them to predict the genetic merit of newly genotyped animals. These genomic predictions are combined with traditional pedigree-based EPDs to create genomic-enhanced EPDs. By adding in this genomic information,

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EPDs become more reliable and precise, especially for animals with few progeny records.

In December of 2014 the AICA launched their genomic-enhanced EPDs. Where are we going next? Future directions can be summed up in three words: fewer, more, and targeted.

FEWER

Breed associations typically launch genomic-enhanced EPDs once a thousand animals are genotyped. Typically, these initial genomic-enhanced EPDs are based on 50,000 DNA variants. Once a breed has genotyped several thousands of animals, a second DNA panel with fewer variants is added as an additional option for breeders to use. This second panel contains about 10,000 DNA variants and is often referred to as an LD panel. In a process called imputation, we can use the patterns at the 10,000 genotyped DNA variants to infer the remaining 40,000 DNA variants that were not genotyped. This process of imputation is very accurate, and for the price of 10,000 variants we can obtain the same prediction accuracy as genotyping all 50,000 variants. Thus, one of the future directions in Charolais genomic predictions and genomic-enhanced EPDs will be a LD panel with fewer DNA variants. This lower-cost panel will allow breeders to genotype more animals.

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MORE

In many instances, a genomic prediction is a self-improving technology (exceptions include hard to measure traits like disease resistance). As long as breeders continue to collect and report performance records, the young animals that we genotype today become the animals used to retrain our genomic predictions in the future. “My message has always been and will continue to be that a breed association will be as strong as the performance database it can build and maintain,” stated Dr. Robert Williams, outgoing Director of Breed Improvement. He continued, “We work to keep breeders focused on reporting phenotypic data for a multitude of traits. Genomic prediction will only be as reliable as the phenotypic databases used to build the genomic estimates.” Thus, the more animals that are genotyped and correctly phenotyped, the more precise genomic predictions become.

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In addition to genotyping more animals, researchers are also collecting more DNA data on influential sires. As part of a USDA-funded fertility research project and with support from the Charolais association, researchers at the University of Missouri have sequenced the entire DNA of 244 sires, 12 of which are Charolais sires. When we sequence the entire DNA of an animal we produce data on 2.5 billion base pairs of DNA,

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not just the variable positions included in a SNP panel. Based on the sequence data at the University of Missouri, we have identified 50 million DNA variants. Of these 50 million DNA variants, at least 20 million are variable in Charolais cattle. The 1000 Bull Genomes Project, a group of international scientists who are sharing sequencing data, has also sequenced 33 Charolais animals. Using these millions of DNA variants, researchers will study in more detail cattle genetics and genomics.

TARGETED

With more animals and more DNA variants, researchers will have the ability to hone in on the important variants influencing

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genetic variation within and between breeds. The DNA panels currently used in genomic prediction use DNA variants that are evenly spaced along cattle's DNA. These variants serve as mile markers along the chromosomes of cattle. These mile markers help us track segments of DNA, but it is the points of interests within the segments that actually cause

differences between animals. These points of interests are functional or causal variants, the variants that actually change the content or abundance of a protein. If we can include not only the mile markers, but also the points of interests in our genomic predictions, these more targeted panels should improve the performance of genomic predictions and the EPDs they enhance.

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Genomic technologies and applications will continue to improve, and acceptance of the technology will continue to increase. Dr. Williams observed that genomic-enhanced EPDs have increased breeder awareness regarding the value of genetic tools and the role these tools will play in the future. As we use these new technologies, it is essential that we do the basics right: use economically relevant traits (e.g. calving ease) not indicator traits (e.g. birth weight) for selection decisions, select for optimums not just maximums, have a breeding objective and use selection indexes to reach that objective. Breeders focused on profit and customer satisfaction will recognize the benefits of genomic technologies and will find methods to incorporate genomics into their operation. Williams concluded, “Genomic predictions increase accuracy, which not only leads to improved genetic trend, but also greater trust in genetic values.”