geneSTream™
Genomics and Reproductive Technology Explained

Genomics 101

The era of genomics has given the cattle industry a wealth of information about how an animal can transmit their positive and negative genes to the next generation. Genomics gives us insight into the profitability potential of our animals and also identifies genes that we do not want to propagate for years to come. By understanding how genomic evaluations are derived and how you can use genomic data to make profitable and sustainable breeding decisions, you can wield the power that genomic data generates.

geneSTream™
Genomics and Reproductive Technology Explained

How do we get data from DNA?

You may have taken a biology class at some point that taught you a little bit about DNA which is the carrier of genetic information of all living things. Chromosomes are structures that contain DNA which is like a blueprint. Chromosomes are comprised of nucleotides including Adenine, Thymine, Guanine, and Cytosine. If we are looking at DNA sequences, we abbreviate those nucleotides to A, T, C, and G. In the structure of DNA, A's are always linked to Ts and Gs are always linked to Cs as shown in **Figure 1**.

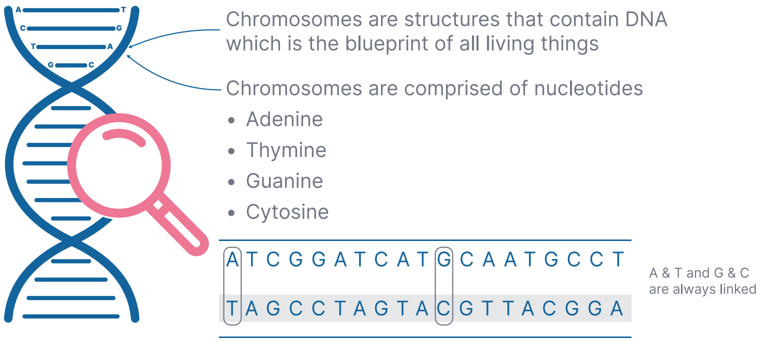


Figure 1

If we unwound a cow's DNA, we would see sequences similar to what you see in **Figure 2**. The bovine genome has about 2.7 billion nucleotides. As you can see, most of the sequence for the 2 cows is the same starting with "G, C, A". This is because 99% of the genome is identical between two individuals or two cows. When we talk about genomic testing animals, we often times talk about SNPs and how many SNPs are identified in a specific test. A SNP is a Single Nucleotide Polymorphism. In simple terms, it's a difference in the nucleotide makeup of an individual at a specific location. The SNPs show us the difference in the genetic makeup of the cow. In this example, the pink cow has an A at this location and the blue cow has a G. If we measure the phenotypes for these two cows or their performance such as how much milk they produce, we can identify the effect of the SNP or difference in the DNA sequence of the cows that is responsible for the difference in performance. When we genomic test individuals, we strategically select 6k-100k SNPs that are most informative for the breed we are investigating.

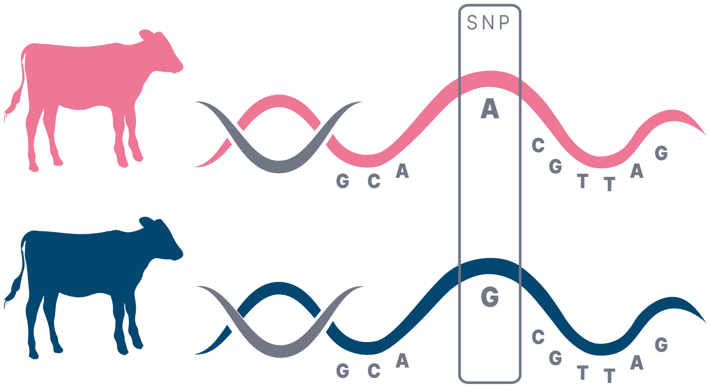


Figure 2

How do we get genomic data?

In order to genomic test an animal, we have to first take a tissue sample. DNA can be found in all tissue of an animal, but the ear sample provides an easy way to take the sample and store it in a TSU tube that can be easily utilized by our labs. The DNA is extracted from the tissue sample through a series of processes that removes other material found in the sample. The genetic variation at the DNA level is measured using a process called genotyping. As mentioned previously, we have to have DNA or genotypes of a group of animals along with their performance data to be able to determine the differences in the DNA sequence between individuals and what those differences will produce in terms of performance. This is what we call our reference population. After we extract the DNA from a tissue sample, we compare the DNA of the individual to our reference population so that we can predict the economic traits that are important to profitability such as production, type, health, and reproductive traits, as well as EcoFeed®.

How can you make genetic progress with genomic testing?

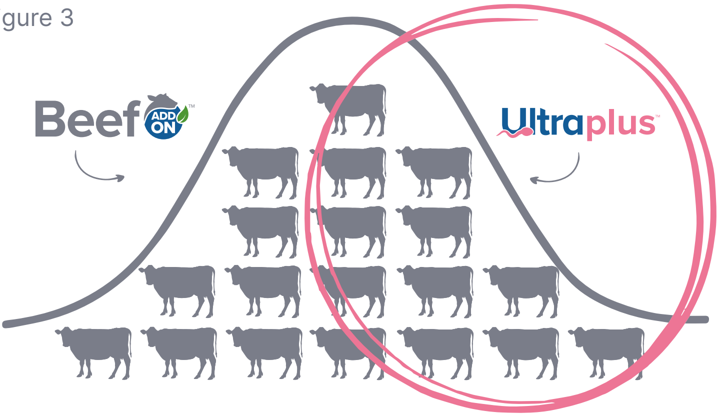
In the past, parent averages were used to predict progeny potential for traits like NM and TPI. This approach has a low accuracy in identifying the superior animals in a herd because it is only 30-40% reliable and it is only as reliable as the record keeping on the farm. Genomic predictions for traits like NM$ and TPI are typically 70% or higher in reliability. Also, many farms begin genomic testing and find they have a parent misidentification rate of over 20%. This increases the probability that you make the wrong breeding decision for example, breeding a female that you think has great genetics to sexed semen when she should be bred to beef. Genomics also influences generation interval. Generation interval is the average age of parents when their offspring is born. Shorter generation intervals will speed up genetic gain in a herd. If the best females can be selected to make replacements before they are breeding age, the generation interval of cow dams can be reduced.

How can you visualize the genetic potential of your herd with genomic data?

Genomic testing with Vision+™ provides commercial dairymen with valuable production, type, and health information along with EcoFeed® that allows you to rank your females based on genetic merit. If you genomic test your herd, the ranking of animals based on genetic merit will look similar to the bell shaped curve in **Figure 3** with your highest genetic merit females on the right hand side and your females with less genetic merit on the left hand side. This allows you to identify your best females to use to make replacements so you can breed them to Ultraplus High Purity™ semen. You can also make other important breeding decisions such as lower genetic value animals being utilized in a beef on dairy breeding strategy to extract more value out of the beef cross calf.

Customers that utilize Vision+™ genomic testing can view their genomic data in STrategy™, STgenetics® platform to demonstrate the benefits of STgenetics® Integrated Approach to promote profitability and sustainability. In STrategy™, you can view all of the genomic data generated for each animal in a grid format that allows you to view only the items or traits that are most important to you. In the Genetic Progress charts, you can view your progress over time for over 40 different traits.

Figure 3



In **Figure 4**, you can see the Genetic Progress chart for NM$ for one of our customers. On the lefthand side, you can see the NM$ value, and across the bottom, you can see the birth year of the females in the herd. The blue bars represent the average NM$ for females born in each birth year. This particular herd started genomic testing all of their heifer calves starting in 2018. You can see that they have made consistent genetic progress, yielding an average increase of over 370 Net Merit dollars in 5 years, by selecting females to make replacements based on genomic data and breeding them to high NM$ bulls utilizing Chromosomal Mating™.

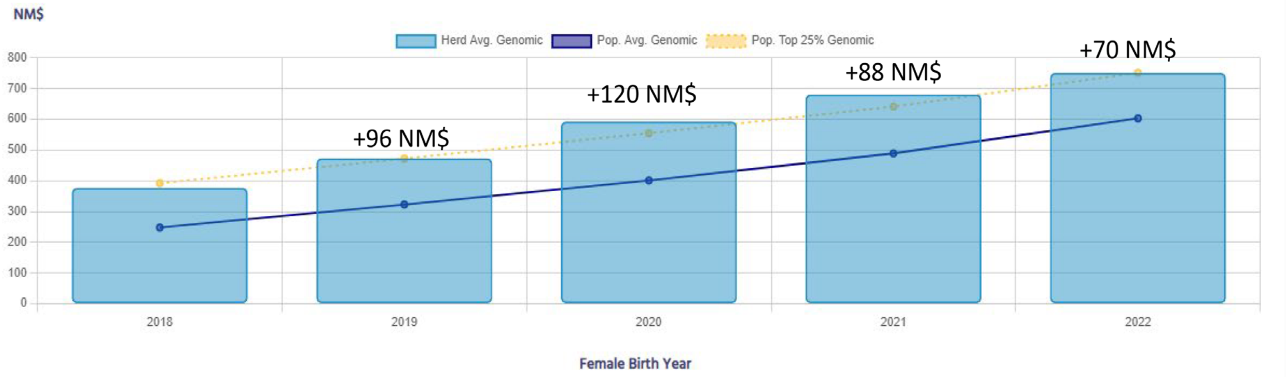


Figure 4

Why is the reliability different for different traits?

If you have received a genomic evaluation for a female in your herd, you may have noticed that the reliability for each trait is slightly different. The reason for the difference in reliability is that reliability is impacted by heritability of the trait, total number of records in the breed for that trait, and the number of records of the trait for the relatives of the animal that is being evaluated. All of these data points are part of the "reference population" for the trait, or the sum total of all data associated with that trait. In simple terms, the larger the reference population the higher the heritability and reliability of a trait. For traits that have high reliability, you can make selection decisions based on this trait with greater confidence. Newer traits that have lower reliability may give some indication of the animals genetic potential for this trait, but there is a greater chance that the trait value will fluctuate, because we are not very certain of the animal's potential for this trait.

Why is it important to screen for haplotypes and markers in your herd?

Genomic testing can also include important information about markers and haplotypes that can help dairymen propagate the markers they want in their herd while avoiding propagating negative haplotypes in their herd that can decrease fertility and therefore profitability. In **Figure 5**, you can see the Marker Frequency Charts that are available in STrategy™ that help you visualize the frequency of different variants of milk markers. In these charts you can see that each of the bars represents the number of females in each birth year that carry each variant. The charts indicate that this herd has been successful in propagating more of the A2A2 variant of Beta Casein A2 and the AB and BB variants of Kappa Casein. For more information about haplotypes and markers, please visit:
https://stgen.com/upload/articles/files/geneSTream_Haplotypes-January%202022.pdf.

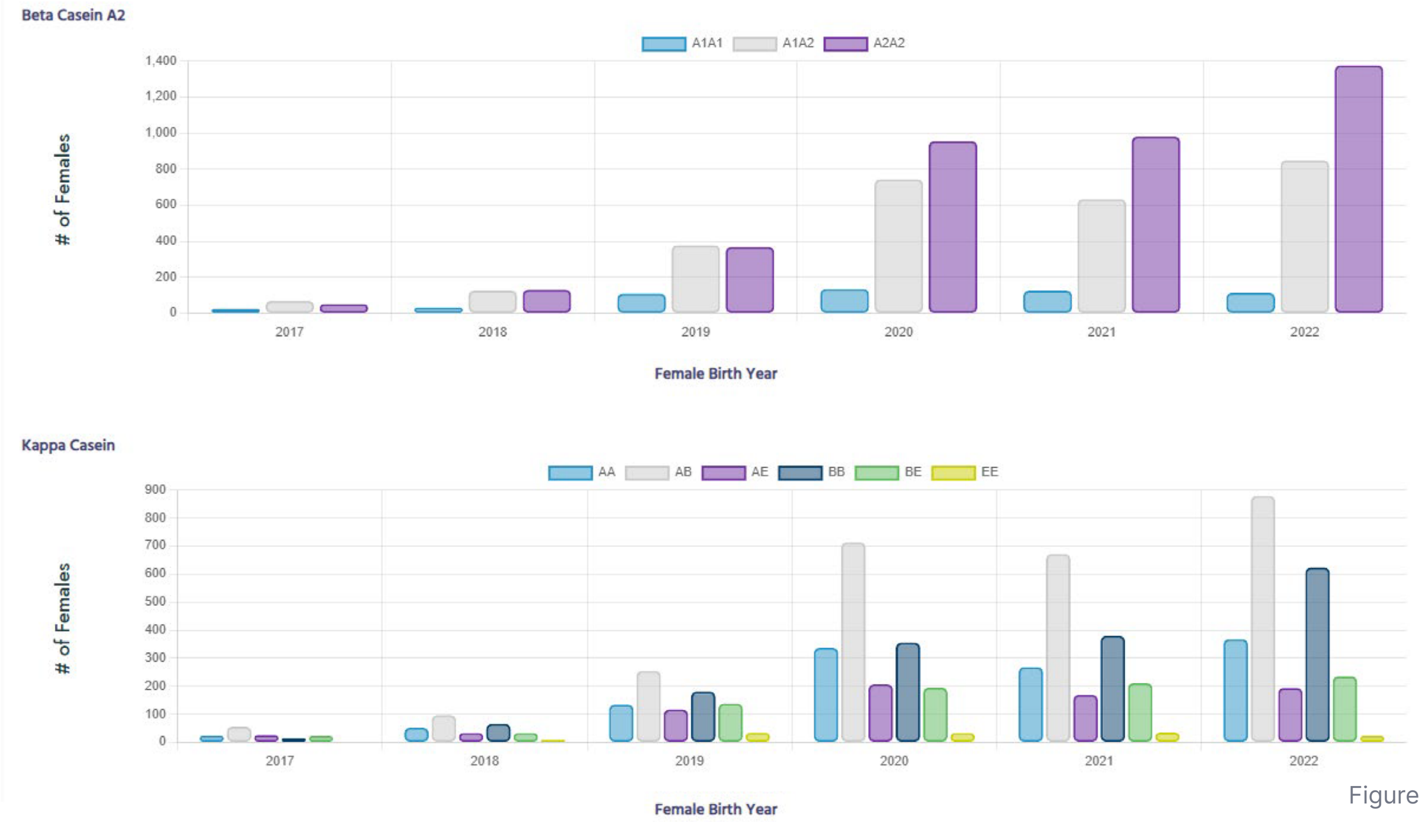


Figure 5

Genomic testing has revolutionized the dairy industry by giving us the power to make better animals, faster. Your herd has genetic potential. You have the ability to identify the best genetics in your herd and make the best management decisions to make the next generation of your herd utilizing genomic data.