The Genetic Vision™ You Need to Build the Best Breeding Strategy

Creating the future of your dairy herd is made undeniably easier with the right execution of a breeding strategy powered by genomic testing. Genomic testing allows dairymen to rank animals in their herd according to production, type, and health traits, as well as feed conversion efficiency, and identifies animals with potentially beneficial milk proteins or genetic abnormalities. Successfully utilizing genomic testing as a part of your breeding strategy is based on your understanding of the data that is available and how to use the data to make the right breeding decisions.

Why are genomics so valuable to the **dairy industry?**

Genomics combines pedigree based traditional animal breeding and molecular biology to bring us a tool that allows us to predict future performance on animals that are too young to be progeny tested. There is opportunity to make large improvements in genetic gain by increasing the accuracy of selection with genomic testing. Utilizing genomics in conjunction with other technologies like sexed semen can also rapidly increase genetic gain and therefore profitability in a herd. Since the introduction of genomics into the dairy industry in 2009, there has been a significant reduction in the age at which parents are selected (**Figure 1**) and more genetic progress in the past ten years than in the previous 50 years in the industry, since the introduction of AI (**Figure 2**).

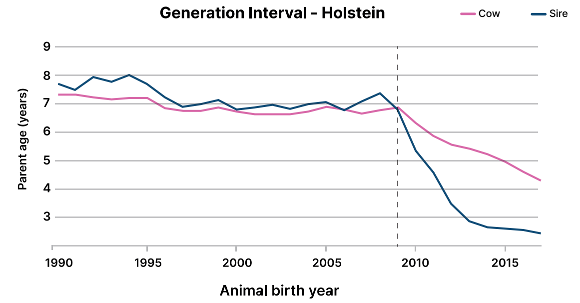


Figure 1 shows the decrease in generation interval, or the average age of parents when their offspring is born, of Holsteins for bull and cow sires since 1990

Modified from: Paul VanRaden, American Dairy Science Association, Cincinnati, OH – June 24, 2019

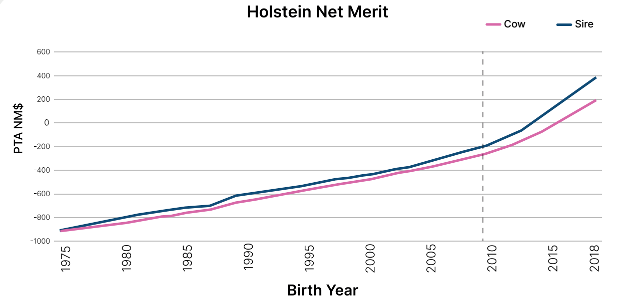


Figure 2 shows the change in Net Merit (NM$) in the US Holstein population for cows and sires from 1975 to 2018. There has been more genetic progress in the dairy industry since the introduction of genomics in 2009 than in the past 50 years in the industry.

Source: CDCB

Why should a commercial dairyman **utilize genomic testing?**

Genomic testing provides commercial dairymen with valuable production, type, and health information that allows them to rank their females based on genetic merit. This allows them to identify their best females to use to make replacements and make other important breeding decisions such as lower genetic value animals being utilized for a beef on dairy breeding strategy to extract more value out of the beef cross calf (**Figure 3**). Genomic testing can also include important information about markers and haplotypes that can help dairymen propagate the markers they want in their herd such as Beta Casein A2 and BB Kappa Casein while avoiding propagating negative haplotypes in their herd that can decrease fertility and therefore profitability.

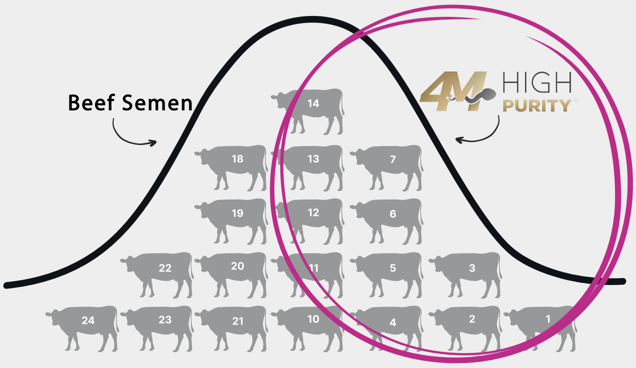


Figure 3 Females with the highest genetic merit can be bred to High Purity 4M™ sexed semen to make replacements, while lesser genetic value animals can be bred to beef semen or sold, depending on the market situation.

What is the advantage of using **genomic evaluations** to make **breeding decisions** instead of **parent averages?**

$$\frac{\text{Accuracy} \times \text{Genetic Variance} \times \text{Selection Intensity}}{\text{Generation Interval}} = \Delta G$$

Accuracy	*√("Reliability") of the animal's breeding value*
Genetic Variance	*Genetic variation in the population*
Selection Intensity	*Function of proportion of selected breeders*
Generation Interval	*Average age of parents when offspring is born*
ΔG	*Genetic gain*

Figure 4 shows the Breeder's Equation which calculates genetic gain per year. Utilizing genomic testing increases accuracy and also reduces generation interval which leads to more genetic gain per year.

In the past, parent averages were used to predict progeny potential. This approach has a low accuracy in identifying the superior animals in a herd. Many farms begin genomic testing and find they have a parent misidentification rate of over 30%. Parent averages are also only about 30% reliable whereas genomic trait predictions are 60-70% reliable. If you utilize parent averages to make breeding decisions, there could be an opportunity cost to making the wrong decision. For instance, if you breed a female to sexed semen believing that she is in the top 1/3 of your herd for NM$ based on parent average information, you have made a long term investment in the genetics of that female if you keep her heifer calf in your milking herd. This particular female could have been genomic tested and found to be in the bottom 1/3 of your herd and actually should have been bred to beef semen. This female should have had a terminal pregnancy instead of a pregnancy propagating her lesser genetics in your herd.

The Breeders Equation shown in **Figure 4** calculates genetic gain per year by multiplying accuracy of selection decisions by selection intensity and genetic variation. This is then divided by the generation interval to give the genetic gain that can be achieved each year. The utilization of sexed semen influences the selection intensity part of this equation. Sexed semen allows you to create more females than conventional semen. If you are able to choose the best females from a larger group of females to use to make replacements, then you increase your selection intensity. The two pieces of this equation that genomics influence are accuracy and generation interval. Genomics increases accuracy and therefore genetic gain. Genomics also influences generation interval. 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 is reliability of genomic evaluations determined?

Reliability in genomic testing is a function of accuracy and quantity of phenotypic information from each trait being evaluated in a training population and heritability of each trait. Production traits have 75% reliability whereas health traits, which don't have a large training population, have an average reliability of 50%. The average reliability of different traits is shown in **Figure 5.**

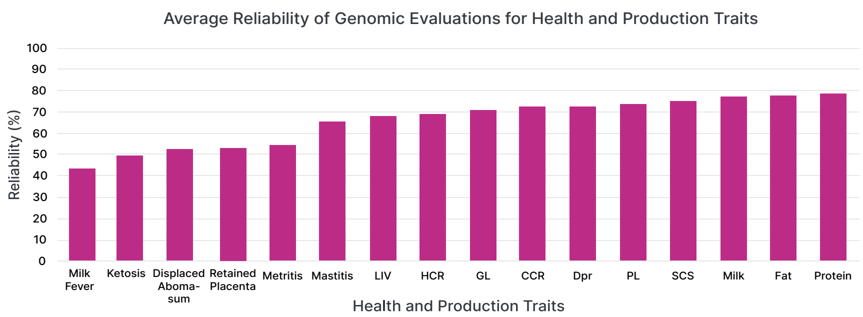


Figure 5 shows the average reliability for genomic evaluations for health and production traits for females born between 2010 and 2015.

What is the difference between **markers** and **haplotypes** and how should that information factor into **breeding decisions**?

Haplotype	Gene	Effect	When
HH1	APAF1	Spontaneous Abortions	All stages of pregnancy
HH2	IFT80	Pregnancy loss	Before day 100
HH3	SMC2	Pregnancy loss	Before day 60
HH4	GART	Impacts production of purines	Early embryonic death
HH5	TFB1M	Pregnancy loss	Before day 60
HH6	SDE2	Pregnancy loss	Before day 35
HCD	APOB	Inability to produce cholesterol	Death typically between 2-6 months of age due to starvation
JH1	CWC15	Pregnancy loss	Before day 60
BH2	TUBD1	Stillborn calf	At birth
AH1	UBE3B	PIRM Syndrome	Developmental impacts at birth; Juvenile mortality

Figure 6 shows the different fertility haplotypes that have been identified with their name, gene location, effect, and when they are expressed.

https://aipl.arsusda.gov/reference/recessive_haplotypes_ARR-G3.html

A haplotype is a stretch of DNA that is inherited together whereas a marker or SNP test is the actual mutation that could be causing the abnormality. A marker or SNP test that is pinpointing the actual causal mutation is more accurate in comparison to a haplotype where the association with the causal mutation might fade over generations.

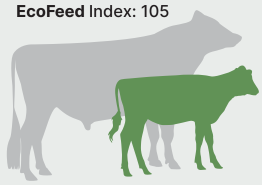
Genetic Visions-ST™ provides the most comprehensive package of markers in the industry, and they are grouped into three categories: key milk protein markers, genetic abnormalities, and other which includes the Dominant Red marker. All of this information is extremely beneficial for dairymen to make the best breeding decisions. Beneficial markers such as certain milk proteins can be identified and used to make breeding decisions such as females that will make replacements. Negative haplotypes can be easily managed in STgenetics® Chromosomal Mating™ program where carriers of the same negative haplotypes will not be mated together, and therefore, the negative effects of the haplotype will not be expressed in the offspring. **Figure 6** shows some of the important haplotypes that affect fertility and survivability of the calf.

What is the **value** of the ecofeed index in a **genomic evaluation?**

The EcoFeed® index allows dairymen to be able to maximize feed conversion efficiency in their herd by adding EcoFeed® to the list of traits they prioritize in their herds. The EcoFeed® index are a feed conversion index based on phenotypic and genomic information of almost 5,000 female progeny tested from many sires. A sire's progeny are evaluated by ranking females based on their ability to efficiently convert feed energy to product. Utilizing their substantial phenotypic and genomic database, STgenetics® is able to make genomic predictions of related animals with high accuracy. EcoFeed® rankings are based on a 100 base system. Every 5 points above 100 are equivalent to 1 pound less feed consumed per heifer per day. EcoFeed® scores are breeding values. This means that a female with an EcoFeed® score of 110 will consume 2 pounds less feed per day (as fed) than her herdmates. To understand what she can transmit to her offspring, you can divide that number by 2. When dairymen select for high EcoFeed® animals in their herd along with other economically important traits, they can expect to save on feed costs in the future. **Figure 7** shows an example of how feed cost can be reduced depending on the EcoFeed® score of a female.

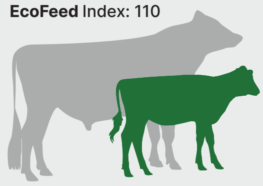
HOW CAN YOU PROFIT
FROM TESTING YOUR FEMALES FOR ecofeed ?

Heifer A
EcoFeed Index: 105



Feed Intake: 1 lb less/per day than herdmates
Feed cost: $0.10/lb
Savings per year: $36.50

Heifer B
EcoFeed Index: 110



Feed Intake: 2 lbs less/per day than herdmates
Feed cost: $0.10/lb
Savings per year: $73.00

IF A 1,000 COW DAIRY HAS REDUCTION IN FEED OF AS LITTLE AS 2 POUNDS PER DAY PER ANIMAL, THIS COULD TRANSLATE INTO

savings of $73,000

Figure 7 shows an example of heifers with a 105 and 110 EcoFeed® score. Heifer A will consume, on average, one pound less feed per day (as fed) than her herdmates which translates to savings of $36.50 per year. Heifer B will consume two pounds less feed per day (as fed) than her herdmates for annual savings of $73.00 per year. If a 1,000 cow dairy has reduction in feed of as little as 2 pounds per day per animal, this could translate into savings of $73,000 (based on feed cost of $0.10/lb of feed as fed).

Is there a **value** in increasing the **chip** or **array density** for genomic **evaluations?**

This is a very complex question that can be answered in two main ways. One answer is from a general point of view, and the second answer is specific to the dairy evaluation in the US. In general, the more markers tested the better, but not all markers are created equal. The impact of number of markers on the reliability of genomic prediction, depends on the heritability of the trait and expected number of genes involved, the population structure, and the array or chip technology. This is why STgenetics® designs their own arrays to take advantage of the most recent information available and why they continue to redesign their array as needed. STgenetics® wants to provide their customers with the most accurate information, so they can make the best decisions for their farm. In a more specific way, the US national dairy genomic evaluations conducted by CDCB are based on a carefully preselected set of markers with about 80k SNPs. Therefore, the most important factor in the success of any genomic testing is how accurately these genotypes can be called. The genomic testing used by Genetic Visions-ST™, Vision+20™ and Vision+75™, have an imputation accuracy to the CDCB panel above 98%, which makes these arrays almost flawless as pertaining to the accuracy of the genomic predictions.

Would it be beneficial to make whole **genome sequencing** available for **commercial dairymen?**

When 99% of the genome is identical between any two individuals, you don't need to report on the full sequence, just on the variants. Theses variants are known as SNPs or single nucleotide polymorphisms (**Figure 8**). A SNP is a variation in a single nucleotide at one location in the genome. The effect of SNPs can be measured by evaluating the phenotype of animals that have the same SNP. New technology, like whole genome sequencing, will allow us to do a better job identifying variants and increase the depth of information reported on each gene and include new genes; however, reporting the whole genome sequence for use in commercial dairies, is unnecessary.

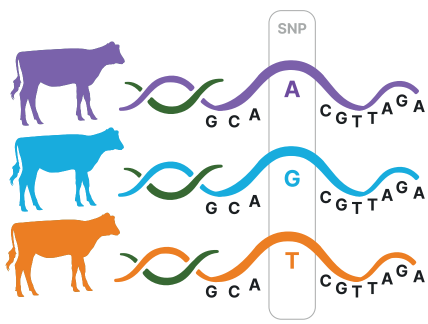


Figure 8 shows three cows, each with the same gene sequence except for one different variant at the same location. This is known as a Single Nucleotide Polymorphism (SNP). SNPs allow us to identify variation that affects different phenotypes or performance.