

Understanding

Genomic
Selection





The Next Great Advancement

Always on the cutting edge of technology, Select Sires has utilized the IGENITY® comprehensive profile for the past three years to know more about the genetic merit of its bulls and allow customers to do the same for their cows and heifers. Information from the IGENITY profile was taken a step further when Select Sires introduced the HealthMark™ category of sires. DNA markers from the profile allow for earlier identification of bulls that excel in health traits. Now, Select Sires continues to lead the industry in utilizing DNA-marker technology by incorporating genomic information from the USDA.

Through advances in bovine DNA mapping and sequencing, USDA researchers have assembled 50,000 carefully selected DNA sequence variations useful in looking for inheritance differences in cattle. These markers have been studied through several generations of highly proven A.I. sires. Key markers have been identified that can be used to more accurately predict the genetic merit of dairy cattle. This comprehensive approach is called genomic selection. The effort improves the effectiveness of DNA testing as a selection tool for performance traits and the USDA is offering it openly to the dairy industry.



This valuable genomic information has many advantages, including that it:

- ◆ Predicts genetic merit of young animals with up to double the accuracy of traditional Parent Averages
- ◆ Has the potential to shorten the generational interval, speeding genetic improvement
- ◆ Enables bull selection from a much wider genetic pool
- ◆ Provides earlier information about genetic differences between siblings
- ◆ Improves the reliability of current progeny testing results for low-heritability or later-expressed traits, including health and fitness traits



How Does it Work?

With genomic technology, scientists can now take a comprehensive look at the actual DNA of dairy cattle. And as long as they know which DNA patterns produce superior results, they can identify the superior animals with no need to wait for progeny performance results – or even for their progeny to be born!

The body is made up of **cells**, and the nucleus of every cell contains the animal's genetic material (generally called **DNA**). DNA is in the form of a strand, or **sequence**, that when uncoiled, would be more than two meters long. Parts of the DNA sequence are coded (called **genes**) and parts are uncoded. The coded parts store the biological information.

The strand of DNA is divided into smaller pieces called **chromosomes**, which are analyzed in small segments, called **profiling**. An individual animal's total hereditary information is called its **DNA profile** or its **genome**.

The goal is to learn what effect the genes in those segments have on economically important traits. These comparisons are made by looking at markers.

A **genetic marker** is the difference in the DNA sequence at the same point in the DNA sequence

between two animals. The markers used in this research have a technical name – single nucleotide polymorphisms, or **SNPs** (referred to as “snips”). SNPs are like snapshots of different places on the DNA sequence which are worthy of notice.

The science of genomic selection involves first identifying which SNPs are linked to important functional traits, using a test sample of proven bulls. The USDA has used DNA samples from thousands of bulls dating back to 1960.

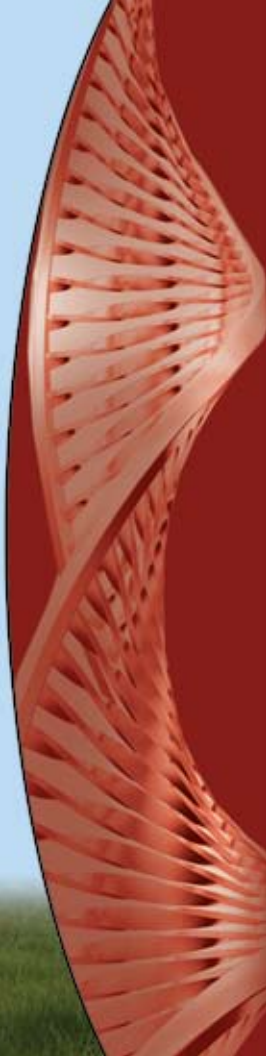
After identifying these key associations, scientists use genomic information to predict, with improved accuracy, which unproven bulls (or cows or heifers) will be successful for certain traits.



Implementing the Technology

The following is an example of full brothers that were tested by Select Sires. It is clear to see the improved accuracy and increased information that the genomic testing provides through Genomic Parent Averages.

Trait	PA	PA Rel.	GenPA Rel.	Calf 1 GenPA	Calf 2 GenPA	Calf 3 GenPA	Calf 4 GenPA	Calf 5 GenPA	Calf 6 GenPA
NM\$	+\$577	37%	66%	+\$602	+\$558	+\$522	+\$475	+\$453	+\$428
Milk	+1,292	39%	70%	+797	+1,136	+435	+963	+1,563	+708
Fat	+70	39%	70%	+58	+62	+60	+25	+31	+73
Protein	+44	39%	70%	+31	+33	+24	+27	+28	+25
SCS	2.93	36%	66%	3.00	2.86	2.91	2.95	2.94	3.01
PL	+4.6	35%	61%	+6.7	+5.7	+5.8	+6.4	+5.3	+3.2
DPR	+0.2	35%	60%	+1.0	+0.6	+0.4	+0.3	-0.1	-0.7
SCE	8%	31%	61%	7%	8%	9%	9%	9%	8%
Type	+2.50	43%	67%	+3.60	+2.20	+2.30	+3.30	+2.80	+2.90
Ft Angle	+1.40	--	--	+1.30	+1.00	-0.10	+1.90	+2.30	+1.30
Udd Dep	+1.60	43%	67%	+4.50	+1.80	+3.50	+3.30	+3.00	+0.80





Glossary

Base: DNA is comprised of smaller molecules called nucleotides. A base is one of the four nucleotides that, according to order and pairing, make up the genetic code. The four bases are adenine (A), cytosine (C), guanine (G) and thymine (T).

Gene mapping: Determining the relative physical locations of genes on a chromosome.

Gene (DNA) sequencing: Determining the exact sequencing of nucleotide bases in a strand of DNA to better understand the behavior of a gene.

Genome: All the genetic material in all the chromosomes of a particular organism.

Genomics: The mapping and sequencing of genetic material in the DNA of a particular organism and the use of that

information to better understand what genes do, how they are controlled, how they work together, and what their physical locations are on the chromosome.

Genomic Selection: The process of combining information from a large set of genetic markers that cover the entire genome with traditional genetic evaluations to select the best animals.

Genotype: The genetic identity of an individual. Genotype often is evident by outward characteristics, but may also be reflected in more subtle ways not visually evident.

Marker: A section of DNA that has a different base sequence and can be used to identify whether or not nearby linked genes are present.

Phenotype: The visible and/or measurable characteristics of an organism (how it appears outwardly).

Single nucleotide polymorphism (SNP): DNA sequence variations that occur when a single nucleotide (A, T, C or G) in the genome sequence is altered. For a variation to be considered a SNP, it must occur in at least 1 percent of the population.



Frequently Asked Questions

Because of genomic selection, will Select's progeny-test system, the Program for Genetic Advancement™ (PGA™), become obsolete?

The PGA will be needed by Select Sires for the foreseeable future. The PGA process of gathering daughter information in real herds throughout the country serves as the basis for genomic selection as well as traditional selection programs. The organized collection of progeny data will always be a priority for Select Sires.

Why should I have confidence in the USDA genomic prediction?

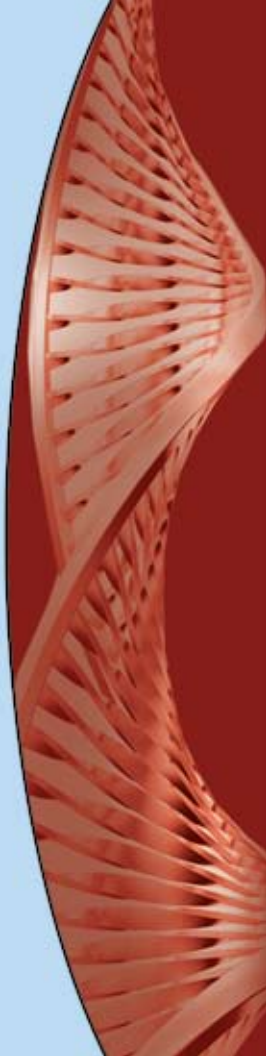
It combines computer-aided statistical analysis with more than four decades' worth of dairy production and type records from the world's most progressive dairy population. The database holds more than 5,000 bulls that date back to 1960, including the great ones like ELEVATION, MARK, BLACKSTAR and BELL. The database will steadily continue to grow as genotyped bulls receive proofs.

Will genomic information replace proofs based on daughter performance?

No. The genomic information will supplement daughter performance data. Genomic PA or genomic PTA values will combine genomic and daughter information. The genomic information will be more heavily weighted for young sires. As bulls gain more daughters in their proofs, the genomic data will receive lower weighting. It is important to remember that although the genomic information improves accuracy, actual daughter performance will always be more significant.

Will the genomic database become more reliable in the future?

While the USDA's method of identifying genomic information is highly accurate, much is being learned about how one DNA marker effects the expression of another. Accuracy and reliability are sure to improve and slightly change as the database grows.





gene
MAX

You can take advantage of this exciting new technology by using Select's new *gene* MAX sires. These young bulls – some offered in conventional semen and others with *gender* SELECTed™ semen – are selected based on their genomic-enhanced Parent Averages, meaning the information is twice as accurate as traditional Parent Averages with higher reliability. Contact your sales representative for a listing of available *gene* MAX sires.



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