Understanding genomic technology and what the future holds

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Over the past few years, dairy producers with access to genomic proven bulls have quickly embraced genomic technology and the opportunity it provides to further improve their herds genetically.

While adapting genomics into a breeding program can be a simple task, understanding the technology behind it may take more effort. To assist, here is a brief explanation of genomics, a genetic comparison and a glimpse into the future of this technology.

Back to the basics

Cells within a bovine's body contain 30 chromosomes. The chromosomes contain strands of DNA. Among other things, DNA consists of pairs of nucleotides (indicated in Fig. 1 by the letters T, A, G and C).

The sequence of nucleotides contains all the instructions used in the development and functioning of the bovine body.

While bovines share many of the same nucleotide sequences, alterations in the sequence are what makes bovines different from each other.

The variation in a DNA sequence that occurs when a single nucleotide is altered is called a SNP. To examine the SNPs within a DNA sequence, a blood, hair, tissue or semen sample is collected.

DNA is extracted from the sample and placed on a special chip that can identify the genetic variants or SNPs that exist between members of a species.

In order to incorporate genomic information into genetic evaluations, the SNPs that impact the genetic traits the industry measures today had to be identified.

To do this, DNA was extracted from semen samples collected from thousands of high reliability progeny proven bulls.

Analysing their SNP variations and comparing those SNPs to their reliable genetic evaluations allowed for the identification of SNPs that impact each genetic trait.

Following the discovery of many significant SNPs, genomic testing has been used to determine the genetic ability of bovines – even of baby calves.

Reliabilities increase significantly for genomic evaluations (Predicted Transmitting Abilities or PTAs) versus Parent Averages. The reliability increases vary depending on the trait evaluated and by breed (Table 1).

In general, most Parent Average reliabilities are about 35%, while reliabilities calculated using Genomics PTAs are near 70%.

Genetic gain

Genomic testing provides several advantages. One advantage is animals can be genotyped at a very young age and their breeding values can be determined with relatively high accuracy.

For instance, artificial insemination (AI) organisations now routinely receive genetic evaluations on calves less than three months of age and u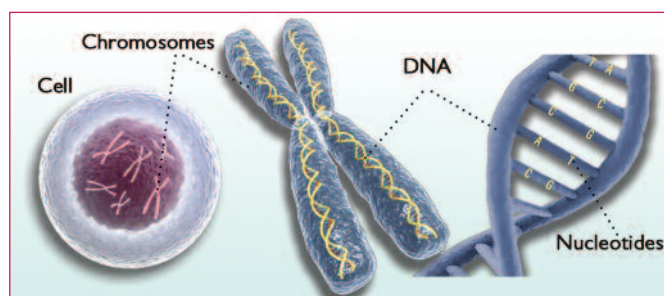tilise that information in making decisions for their breeding program. This allows AI companies to choose, raise and offer to producers only the most elite bulls.

Another advantage is the increase in accuracy or reliability over sires with only parent averages. The higher reliability means individuals can choose animals with more confidence in their true breeding value.

Utilising elite genomic proven animals in breeding programs can increase the profit potential of dairy herds by shortening the generation interval and increasing the rate of genetic progress.

Bulls can now be utilised as sire fathers as soon as they are able to produce semen, and high ranking females can be utilised as sire dams at puberty when they can be flushed.

This shortening of the generation interval is sometimes referred to as the 'speed of genomics.' Dairy producers striving for genetic improvement use bulls of the highest genetic level; many of today's best bulls for a particular trait or index have evaluations based on genomic tests and not on progeny test information.

However, note that a herd's genetic selection standards should be higher for genomic-proven service sires.

Accuracy of evaluations

The next logical question is does all of the science behind genomics work in practice? This has been extensively analysed.

Last year, Cooperative Resources International (CRI) evaluated the correlation of genomic PTAs to the PTAs of the same animals after they had progeny included in their genetic evaluations. The results are shown in Table 2.

This analysis was based on 1,221 bulls born in 2002-2003. It shows the correlations between their genomic PTAs and progeny PTAs range from 0.78 to 0.92 – that indi-

Fig. 1. Cells within a bovine's body contain 30 chromosomes.

Table 1. Genomic reliability gain* over parent average reliability (USDA-AIPL).

Trait	Holstein	Jersey	Brown swiss
Lifetime net merit ($)	23	9	3
Milk	23	11	0
Fat	33	15	5
Protein	22	4	1
Fat (%)	43	41	10
Protein (%)	34	29	5

Parent average reliability is about 35%

Table 2. Correlation of 2004 genomic PTA with 2010 progeny PTA (CRI Analysis of USDA-AIPL data).

Trait	Correlation between genomic PTAs and progeny PTAs	Correlation between parent average and progeny PTAs
LNM ($)	0.78	0.44
Milk	0.86	0.62
Fat	0.82	0.48
Fat (%)	0.92	0.60
Protein	0.83	0.57
Protein (%)	0.89	0.64
Productive life	0.83	0.59
DPR	0.81	0.62
SCS	0.83	0.56
PTA Type	0.83	0.64

cates a high level of confidence in genomic predictions. As a comparison, the correlations between the bulls' traditional Parent Average and progeny PTAs ranged from 0.44 to 0.76. Significant improvement in predicting PTAs has been made with genomics.

The real reason to use sires with genomic PTAs is to increase the genetic level in a producer's herd and make the fastest genetic progress possible. Quite simply, genomic sires are the newest genetics and consistently offer the highest level of genetics. How much better are genomic sires than sires with progeny proofs? Table 3 shows a comparison of the US active AI sire list for Holsteins and Jerseys with the averages for genomic and progeny sires.

In each of the traits evaluated, the genomic sires have an advantage over the progeny tested sires. This is expected and has been known for some time – the best genetics are in the young animals.

The difference today is that genomics does a better job of identifying which young animals have the best genetics.

To be clear, there will be more variance in genomic proofs than in

CRI's 1HO09167 O-Style was released into active AI in January 2009 based on his elite genomic proof. At that time, he was +$767 Lifetime Net Merit and +2112 TPI[SM]. Today, with 108 daughters, he stands at +$776 Lifetime Net Merit and +2239 TPI; his TPI has earned him industry recognition atop the Top 100 TPI list.

bulls with progeny proofs. Bulls will re-rank more. Thus, a producer should use a strategy of using a number of genomic sires rather than relying on one or two individual genomic bulls.

How much risk is there? To help evaluate, CRI looked at the April 2009 USDA active Holstein sire summary list and compared bulls from two groups.

The first group consisted of bulls that had genomic proofs only in 2009 and now have progeny in their evaluation. The second group was bulls with 50 or more daughters in their evaluation in April 2009. The results are shown in Table 4.

The table clearly shows two key points. First, the genomic sires that were available two years ago were genetically superior to the progeny bulls that were available at the same time.

Second, while genomic sires have higher genetic evaluations, they also tend to have more variation.

What the future holds

Genomic testing has revolutionised dairy genetics industry. The selection of bulls for AI has changed significantly. And, inclusion of those genomic sires into a breeding program strategy can be wise for those who want to be in the lead for genetic progress.

In further thinking, widespread female genomic testing may give dairy producers the data needed to determine the optimum type of semen (conventional or sexed) to use on each individual cow or heifer.

There may even be the capability to group cows according to nutritional needs or provide individualised veterinary care based on an animal's genotype.

The genomic era has brought about positive change and still holds great potential! ∎

Table 3. Average PTAs for active AI sires in US by breed (USDA-AIPL).

	Holstein progeny	Holstein genomic	Jersey progeny	Jersey genomic
Number of sires	607	626	137	134
Milk	+634	+925	+404	+764
Fat	+29	+49	+32	+42
Protein	+20	+32	+18	+28
SCS	2.88	2.79	3.00	2.97
Productive life	+1.5	+3.5	+2.2	+3.2
DPR	-0.1	+0.1	0.0	+0.2
LNM ($)	+263	+487	+243	+358

Table 4. Comparison of April 2009 and April 2011 genetic evaluations for genomic sires and progeny sires (CRI Analysis of USDA-AIPL data).

	Progeny sires			Genomic sires		
	April 2009	April 2011	Change	April 2009*	April 2011	Change
Number	812	812	—	139	139	—
No. daughters	2,020	4,323	+2,303	0	117	+117
Average LNM	175	173	-2	388	305	-83
Average TPI	1,589	1,562	-27	1,939	1,765	-174

*Adjusted for 2010 base change.