

Genomics ... A Revolutionary Tool

By: Roy Wilson, Associate Vice President Large Herd Business Center, Genex

Genomics. It all started in 2004 when researchers sequenced the cattle genome. They used a Hereford for the project and discovered the bovine is made up of 30 chromosomes and three billion bases or nucleotides... those little letters.

To visualize this, picture a cell. Among other things, a cell contains those 30 chromosomes. The chromosomes consist of deoxyribonucleic acid, which is just a big fancy word for DNA. Looking closely at DNA, you can see it is made up of nucleotides – the As, Ts, Cs and Gs. The sequences of these little letters are what contain the instructions for making proteins. Proteins are the building blocks of life, ultimately determining the phenotype of animals.

In 2007, a company named Illumina Inc. developed a bovine SNP (pronounced snip) BeadChip. This SNP chip allows us to look across all the chromosomes and evaluate the animal for 58,000 markers or those letters called nucleotides. Through extensive research carried out by the USDA, we have found that only 38,000 of these markers are actually useful.

By analyzing these useful markers on a sire, the USDA can determine the sire's genetic ability in certain traits. By genomically proving animals, we can gain substantial reliability in an animal's proof for all traits. Table 1 shows those gains in reliability by three breeds that, to date, have been involved in the project. A quick side note, the American Guernsey Association has initiated some work in genomics.

Table 1. Reliability Gains Across Breeds Due to Genomics.

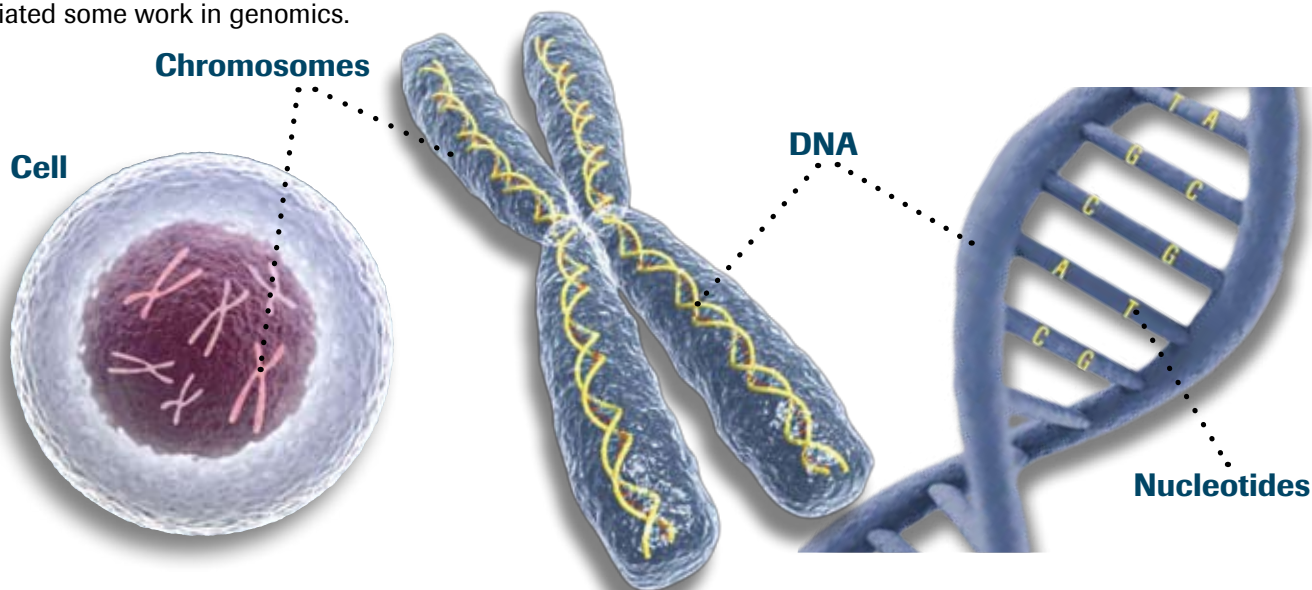
Trait	Gain in Reliability		
	Holstein	Jersey	Brown Swiss
LNM	28%	14%	3%
Milk	30%	6%	-
Fat	30%	10%	5%
Prod. Life	28%	8%	2%
PTA Type	25%	4%	-

Table 2. Holstein Reliability Values: Comparing Traditional to Genomic.

Trait	Traditional PA	Reliability	
		Genomic Realized	Genomic Gain
LNM	37%	65%	28%
Milk	39%	69%	30%
Fat	39%	69%	30%
Prod. Life	32%	60%	28%
DPR	31%	58%	27%
PTA Type	40%	65%	25%

If we look at Table 1, the reliability gains for Holsteins are impressive to say the least. Table 2 shows the gains over parent averages (PA) for Holsteins. Whether you look at the Lifetime Net Merit (LNM) index, yield traits or type traits all the gains are close to 30 percent. This means for a newborn calf, we can accurately predict close to 70 percent reliability (equal to the reliability of a sire with about 50 milking daughters) how superior or inferior that animal will be.

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Now when you evaluate the Jersey and Brown Swiss columns in Table 1, you see their gains are not as impressive. These gains are greatly dependent on the size of the population. However in a short time, maybe as soon as August, Jerseys will have gains substantial enough to implement strategic changes to their genetic programs. While global efforts are underway, it will take more time to see significant reliability increases in Brown Swiss.

Real Life Examples of Genomics

You're an expert when it comes to picking the best genetics, right? Unfortunately even the best have made their share of mistakes when it comes to picking the best flush calf. And, here it is again; the age old question. Looking below at Table 3, these three full brothers have the same sire, same Parent Average (PA) for LNM and the same reliability. Which calf would you choose?

Table 3. Full Sibling Comparison Without Genomic Information.

Name	Sire	PA LNM	PA LNM Reliability
Cash	Ramos	+\$638	35%
Cassino	Ramos	+\$638	35%
Chester	Ramos	+\$638	35%

Now, look at the genomic proof results in Table 4 below. From the table, it is obvious Cassino was the best choice and holds the most potential. Cassino's two brothers were actually predicted below their PA while Cassino was over \$250 higher for LNM than his parent average. This real life example shows just how powerful and exciting genomics really is.

Table 4. Full Sibling Comparison With Genomic Information.

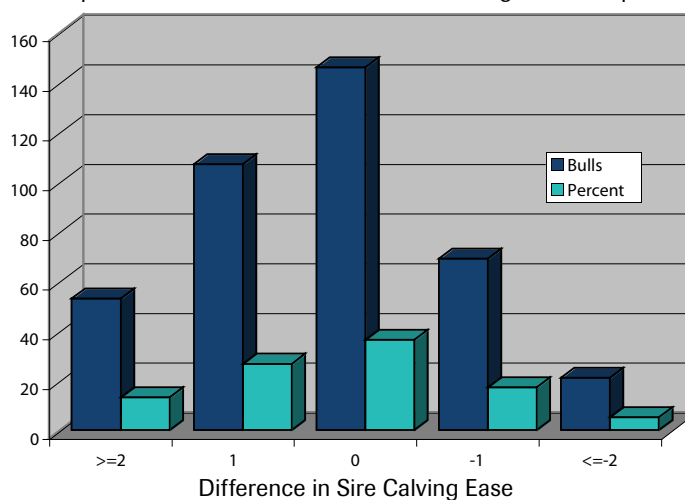
Name	Genomic LNM	Genomic LNM Reliability	LNM Difference
Cash	+\$528	74%	-\$110
Cassino	+\$918	73%	+\$280
Chester	+\$573	73%	-\$65

I am proud to announce that in this example, it was Genex that chose Cassino from this flush. He has a 1H stud code and is producing semen as we speak which will hopefully be made available to our members and customers later in 2009.

I am sure you are wondering if genomics is really as good as it looks. I remember the first time I saw these numbers. I was wondering the same thing. Now after being exposed to it and really thinking about it, I am 100 percent confident in genomics and so is Genex.

Graph 1, below, is one that can build your confidence in genomics in a hurry. The graph includes 401 Genex bulls that were both sampled and genomically tested. Therefore, from sampling they have calving ease observations and a calving ease evaluation. They also have a calving ease evaluation from genomics. To evaluate the differences between the evaluations, we simply subtracted their genomically predicted calving ease from their actual calving ease observations. We found that nearly 75 percent of bulls were $\pm 1\%$ or had exactly the same evaluations. This means if you use 6% genomic calving ease bulls, then three out of four will be a 7%, 6% or 5% for actual calving ease. Impressive!

Graph 1. Genomic and Traditional Sire Calving Ease Comparison



Note: Chart includes 401 bulls with ≥ 100 traditional Sire Calving Ease observations compared to genomic predictions for calving ease. (Genomic calving ease - Traditional calving ease)

The impact of genomics is hard to quantify and hard to summarize. But when you think about the potential impact genomics will have, there is no question this is the greatest discovery since frozen semen touched the genetics world over 50 years ago! Genomics will change how Genex does everything, from genetic programs to how we market bulls.

The Fun Part: Let's See These Bulls

Genex has decided not to brand genomically-proven sires any differently than progeny-proven sires. We look at it this way, all sires are now proven. There is no such thing as a young sire anymore. Sires are proven via daughters or via genomics. Their reliabilities indicate the method of how they were proven.

With this January sire summary, Genex has released 34 sires proven through genomics. These 34 bulls equal genetic power with:

- ✂ 20 different sires including O Man, Shottle, Ramos, Goldwyn and many others.
- ✂ A LNM range of +\$918 to +\$334
- ✂ A group average of +\$615 for LNM.
- ✂ An average +4.9 months of Productive Life
- ✂ An average PTA Type of +2.69
- ✂ An average Udder Composite of +2.63
- ✂ An average Foot & Leg Composite of +2.05

These amazing sires, once not too long ago, were just bulls in-waiting. Now they can be utilized in your breeding programs to maximize your profits.

These genomic giants will not only be available in conventional semen. Nine have been designated for GenChoice™ sexed semen production. The nine GenChoice options include three Shottle and two Boliver sons as well as an O Man, Ramos, Potter and Goldwyn son. As the table below shows, these seven sires are in a league of their own!

Table 5. Average Genomic Merit of New Holstein GenChoice Sires

LNM	Rel.	Milk	Fat	Protein	Prod. Life	DPR	PTAT
+\$617	69%	1272	65	42	+5.1	+0.5	+2.89

USDA/01-09, HA-USA/01-09

The Excitement Continues

The excitement is not even close to over. Genex has identified an additional 20 genomic sires we plan to release throughout 2009 assuming they produce viable semen.

These additional 20 sires raise the bar even higher. They average +\$658 LNM with a range of +\$918 to +\$554. That's right, a second bull at +\$918! They have Productive Life and PTAT to go with it. In this group we see sons of **1H07235 TOYSTORY**, **1H05045 LYNCH**, Billion, Mac and others.

In summary, genomics is a revolutionary tool. Extensive science and research has demonstrated its accuracy and therefore, Genex fully embraces this new technology. It will touch every part of our business. It will continue to improve and increase our abilities to bring you profitable genetics.

Genomics is here to stay. The advancement in genetics is hard to comprehend. Even the proof numbers look overwhelming, but they should. We are removing three years from the generation interval. A lot changes in three years. The progress is and will be amazing.

Genomics **is** a revolutionary tool!

AUTHOR BIO

Roy Wilson has established experience in dairy genetics and reproduction. After undergraduate work at the University of Wisconsin-River Falls, Wilson completed dual master's degrees at the University of Wisconsin-Madison in animal breeding and reproductive physiology. He served as a UW Extension agent before joining Genex.



Common Genomic Terms

Genomics: \jə-'nō-miks\ A broad word for being able to map (read) and interpret the gene sequences in living organisms.

DNA sequencing: Determining the order of the nucleotides in a strand of DNA.

Genes: The nucleotide sequences that give meaning to a cell's function.

Genome: All the genes and genetic material each organism has that predicts how it will act in nature. Each cell in an organism actually has the exact same copy of the genome.

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.

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.

Nucleotide: A group of molecules that, when linked together, form the building blocks of DNA. Includes the bases adenine (A), cytosine (C), guanine (G) and thymine (T).

SNP or Single nucleotide polymorphism: A sequence variation in DNA that occurs when a single nucleotide in the genome sequence is altered.