

# Genomic Selection: A Practical Explanation

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Since December 2007, roughly 15,000 North American dairy bulls have been genotyped using a technology developed in a partnership between Illumina Inc., the USDA Agricultural Research Service, the National Association of Animal Breeders, Merial, and researchers at several universities and institutes.

## Major Breakthroughs

The major breakthrough delivered by this technology is the ability to carry out more than 54,000 DNA marker tests simultaneously at a modest expense. These single nucleotide polymorphism (SNP) markers, which represent single base changes (A, T, C or G) within the DNA sequence, can be genotyped much more efficiently than the labor-intensive (one at a time) microsatellite markers that had been used in the past.

The second breakthrough that makes genomic selection possible is the recent finding that, once a large number of more or less evenly spaced genetic markers (e.g., at least 30,000) are available for an individual animal, it is possible to estimate the breeding value of that animal based on associations between these marker genotypes and milk yield, Somatic Cell Score, Productive Life, Daughter Pregnancy Rate, and other key traits. These associations are estimated using data from the animal's ancestors, in particular the progeny tested bulls represented in the animal's pedigree.

The key animals in this process have been the dairy bulls represented in the Cooperative Dairy DNA Repository (CDDR), which was formed nearly 15 years ago, when artificial insemination (A.I.) companies began storing semen samples from every young bull entering their progeny testing programs for the purpose of future research.

## A Simple Explanation

Although it sounds mysterious, genomic selection is actually rather simple. In the past, all we knew about a young animal's genetic potential was its parent average (PA), which was simply the average of the predicted transmitting abilities (PTA) of its parents. We had no way to determine whether this young animal got a better than average or poorer than average sample of genes from its parents. We also had no choice but to wait two years

until we could measure its own performance, in the case of females, or wait five years until we could measure the performance of its progeny, in the case of males.

Now, because the relationships between SNP markers and important functional genes that we observe in an animal's ancestors are maintained for several generations (before recombination breaks down these genetic links), we can finally glimpse into the crystal ball and see what the future holds for a particular young animal.

Recent research shows that, for a young Holstein bull or heifer, we can combine the animal's PA with genomic information to get a "genomic PTA" with a reliability of 60 to 70 percent. This is vastly better than the reliability of merely its PA, which is typically only 30 to 40 percent.

For a heifer calf, reliability of its genomic PTA is equivalent to that from measuring several lactation records on the animal and her daughters. For a young cow, information can be combined with its lactation records to obtain a significantly more accurate estimate of its genetic merit. For a bull calf, reliability of its genomic PTA is equivalent to that obtained by measuring performance on a couple dozen daughters. However, once this bull completes progeny testing and has performance data from 80 to 100 daughters, genomic information has somewhat less value.

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### What Can the Industry Expect?

What does this mean for the dairy industry? On the male side, nearly every young bull entering a North American A.I. center is now tested and many potential bull dams are tested as well. This will yield a much higher success rate from progeny testing in the future, as we know prior to entry into the A.I. center that each young bull has received a good sample of genes from its parents.

A.I. centers will begin to market semen from individual young bulls or “teams” of young bulls that have genomic PTAs but no daughters of their own. These “genome tested” bulls will tend to replace older, proven bulls that were at the lower end of the sire lineup, and some young bulls with really outstanding genomic PTAs will be used in contract matings.

In the long run, as A.I. centers and producers become more comfortable with this technology, we may see a decline in progeny testing, because its purpose is basically the same as that of the BeadChip – to see which young bulls received the best samples of genes from their parents. On the female side, DNA testing of potential bull dams is already becoming the norm, and testing of potentially valuable calves or heifers in consignment sales may soon be common as well. In the case of embryo transfer, whether it’s used to produce a bull calf for A.I. or a heifer calf for consignment sale or export, first choice of the flush just became a lot more valuable.

### Industry Applications

As one would expect, these developments have led to an explosion in dairy genomics research. Many new and useful tools, some of which cannot yet be imagined, will be developed in the next decade based on genome-related technologies. A topic of keen interest is development of low-cost systems that can be used for widespread genotyping of animals (e.g., replacement heifers) on commercial farms. Such a product could also be used for screening “outcross” families to find elite males or females that can make unique genetic contributions to the breed.

Another topic of interest is the development of mating programs that are based on the results of DNA testing, rather than pedigree or conformation data. Lastly, it should be emphasized that at this point results for breeds other than Holstein have not been as promising. Gains in reliability for Jerseys have been about half as large as the gains observed in Holsteins. Gains in reliability for Brown Swiss have been negligible. However, this poor performance is largely due to smaller population size (i.e., not as many progeny tested bulls available for estimating the associations between SNP markers and important traits), and efforts are already underway to combine information from North American sires with that of key populations internationally.

### AUTHOR BIO

*Dr. Kent Weigel joined the Department of Dairy Science at the University of Wisconsin-Madison as assistant professor and extension specialist in dairy cattle breeding and genetics in 2001. As state extension specialist for dairy cattle genetics, Weigel educates dairy producers, A.I. organizations and other dairy industry participants with interests in animal breeding. He also serves as genetics program administrator for the National Association of Animal Breeders.*

