

Genomics – Information for Enhanced Genetic Evaluations and Sire Selection

By: Jack McAllister, Ph.D.

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The doubling of milk production per cow in the US in the last 50 years did not happen by chance. Research data since the use of AI in dairy herds enrolled in the Dairy Herd Improvement (DHI) program clearly shows that selection for genetic merit for milk yield and the positive environment for feeding and husbandry are about equally responsible for this improvement in milk production.

The dairy industry is now in a position to take another big genetic step forward thanks to new genetic technology which has become available to it in the last 5 years. The technology, called genomics, has allowed researchers to identify differences at about 55,000 sites in the genetic material or DNA of dairy bulls. The DNA of over 13,000 dairy bulls has been characterized to identify which basic subunit of DNA or nucleotide base pair was at these sites.

In the DNA of dairy cattle, each animal has 29 pairs of chromosomes plus a pair of sex chromosomes. One chromosome of each pair is inherited from their dam and the other from their sire. These nucleotide base pairs at each of the sites investigated can be of one of two types. At each of these sites, an animal can have either a pair of one type from both parents, a pair of the other type from both parents or a pair of one type from one parent and the other type from the other parent. The sites, where differences have been identified in the dairy population, are known as single nucleotide polymorphisms (SNP's). Using this information along with data on the traits in the Lifetime Net Merit index (NM\$) and multiple generation pedigrees, researchers have been able to estimate associations of these SNP's with certain traits that are a part of the NM\$ index as well as the NM\$ index itself.

Traditionally, in our genetic evaluations we have used parent and ancestor information along with individual and progeny information to predict the transmitting abilities of bulls and cows. With the new SNP data on bulls, we now have more information to use to make these predictions. Having more information to use in making these genetic predictions will increase their reliability. For young bulls with no progeny, we have only data on their parents and ancestors to predict the young bull's transmitting ability. A recent study by USDA scientists shows that there is a very significant gain in reliability when the genomic data is added to the other data already collected and used in the current genetic evaluations. The data below, from the USDA study, gives the reliability gain for several yield traits and NM\$ for young bulls compared to a reliability of the parent average of about 35%.

Reliability gain for young bulls above parent average reliability of ~ 35% for Holstein, Jersey and Brown Swiss bulls.

Trait	Holstein	Jersey	Brown Swiss
Net Merit (NM\$)	23	9	3
Milk	23	11	0
Fat	33	15	5
Protein	22	4	1
Fat %	43	41	10
Protein %	34	29	5

Source: Paul VanRaden, Genomic History and Genetic Principles. A Centennial Celebration of the Animal Improvement Programs Laboratory. October 28, 2008. Linthicum, MD.

How this information will be used in the new genetic evaluations:

The new genomic evaluations will be published for the first time in January, 2009. Use of the genomics technology and the enhanced genetic evaluations offers potential to radically change dairy cattle selection. Currently, the primary avenues for genetic improvement in an AI bred dairy population are through the selection of the sires and dams of young bulls and the selection of proven sires from among progeny-tested young bulls. The use of genomics data in conjunction with the traditional phenotypic data used in national genetic evaluations could permit more accurate identification of superior young sires and the selection, at a much earlier age, of superior bulls as the sires of the next generation of young sires. The latter choice could dramatically reduce the interval between generations and as a result significantly increase the rate of genetic improvement.