

Genomics and Brown Swiss

By David Kendall, Director of Genetic Research, 3/2011

For the last four years, the single most discussed subject in the US Dairy Genetics industry has been the development and implementation of Genomics. As with all major changes, there have been those who have lauded Genomics as the final, best and only tool needed to breed cows. The extreme believers have promoted the concept that all that will be needed to mate cows in the future are computers aligning the data on chips, you will not have to even look at the animals. On the other hand, there are those who view Genomics with great skepticism. For these people, Genomics has been created to wrest the direction of the future from the hands of those who have raised the foundation upon which Genomics is built, the Purebred breeder.

As with most changes in life, the reality is probably something different from either extreme position. What we hope to convey in this article is that Genomics is a powerful enhancement of “traditional” pedigree information that improves the ability of the Purebred breeder to increase the rate of genetic progress. From this perspective, Genomics is part of the continuum of farmers and geneticists searching for ways to improve cattle populations. While appearing to some to be a paradigm shift, in reality Genomics is a continuation of the building process of breed development constructed on the foundation erected by current and previous breeders and geneticist.

A Little History

Since humanity realized that we liked one Brown cow better than another Brown Cow, we have explored ways to construct the Brown cow we want. The early steps were simple, writing down the sire and dam of each animal. This insight was the crucial cornerstone upon which not only Genomics but also all avenues of genetic improvement have been built.

For many years, breeders would research pedigrees diligently. They would seek patterns and bits of information that would allow them to make breeding decisions propelling their herd upward. The problem was that beyond the names in a pedigree and hearsay what did farmers base their choices on? Early in the development of breeding programs, people would rely on such things as the whorls in the hair above cows’ udder or bulls’ testicles as an indication of both an animal’s ability to produce milk and transmit desirable traits. Next came self-testing, more reliable if the dairy person was honest but open to much manipulation. At the same time, production competitions lasting from one week to a month at shows became popular on all levels, from County Fairs to World Fairs. While less open to tampering, these contests only gave a glimmer of a cow’s yearly output.

Building upon the foundation of the testing competitions, the pioneers of the Dairy Herd Improvement Associations developed on farm milk weighing by an independent supervisor. The creation of the first DHIA was the next vital plank in the construction of genetic improvement. Besides supplying unbiased recording of the production of an animal over her entire lactation, DHIA promoted the widespread adoption of the Babcock butterfat testing procedure to create uniform data in regards to butterfat levels.

The development of DHIA allowed the first sire evaluations. The very first proofs were based on Dam/Daughter comparisons. This was simply the average of the dams’ records compared to the average of the daughters’ records. This process served the industry well. However, over time it was recognized that a dam’s record may have been made in a year with poor production environment due to feed or weather, while the daughter’s records may have been made in a good year for the same reasons. This would make the sire appear to be a better transmitter of production than he truly was. To correct this bias, USDA developed the Herd Mate Comparison. The Herd Mate Comparison looked at animals calving in the same herd not only in the same year but also in the same time of year eliminating some of the bias of good versus bad environment. Not every one liked this change; there was a fair amount of consternation in the industry as some very popular high production bulls suddenly appeared less than sparkling.

As with Dam/Daughter evaluations, the HMC served the industry well during its time. However, further regional differences, the impact of management groups in the herd, and the role that sire selection of herd mates played in the difference between daughter groups was recognized. This last was probably the most crucial realization. These insights lead to the next step in genetic evaluations called the Modified Contemporary Comparison or the MCC.

The MCC was just as controversial if not more so as the previous changes as there was a re-ranking of sires with some winners and some losers; the owners of the loser not being fond of the change.

The most recent major development before Genomics in genetic evaluations was the adoption of the Animal Model. This approach builds on the knowledge gained from Daughter/Dam, HMC and MCC. The Animal Model takes the MCC further by incorporating to a much larger extent pedigree information. The Animal Model looks at many relatives of an animal: sire, dam, daughters, sons, brothers, sisters, aunts, uncles, grandparents, etc., whose production and type information all feed into the system. This provides the industry with higher reliability or knowledge of the genetics of an animal before they or the progeny are in production. In other words, the Animal Model incorporates pedigree information to a much greater extent than any previous system. Amongst other benefits, this has allowed the industry to be more certain of a bull's genetic evaluations with fewer daughters in production. The rate of improvement in production and selected type traits since the introduction of the Animal Model illustrates the inherent value of this approach.

Unfortunately, there was a structural problem with the Animal Model in relation to cows. For the last 20 years, most people in the industry, whether breeder, commercial dairy producer, AI representative or geneticist, have recognized that cows with higher genetic values (from family members) in their pedigree were being overestimated. This has been a major concern as it has a direct impact on the ability to properly sort cows as potential bull mothers. The direct impact was highlighted when bulls received their progeny evaluations. If the Animal Model was perfect the average bull's evaluation should have been the same as his Parent Average. The problem for Brown Swiss was that many young bulls' daughter information was coming in significantly lower than their sire's Parent Averages. We realized as an industry this was a result of having much larger data sets for most sires (with lots of daughters in production making their data more accurate) than dams (with fewer daughters in production and thus less accurate data). Thus, the Brown Swiss Association as well as others knew that the problem was on the dams' side in estimated pedigree values: or knowledge of the actual genes that a cow possesses versus her calculated pedigree information.

What Genomics is in Two Words and a Sign

From the above, we know that the Animal Model for Genetic Evaluation is built on both performance and pedigree information. Genomics does not itself contribute anything new in regards to the measurement of actual performance. What Genomics offers us is the opportunity to increase our knowledge of the genes that an animal has inherited from their parents, grandparents and great grandparents and how those genes relate to their performance.

We know that both human children and cattle full siblings do not inherit the same exact set of genetic information from their parents. If you have a pair of Brown Swiss cows that are full sisters, one can be a heavy milk producer, one a higher fat or protein producer. As heifers, these full sisters would have had the same Parent Average; if there were little difference in type how would you select which one you wanted for your herd?

That is what Genomics offers: to increase our knowledge of the actual inheritance/genes that the animal has from their parents and other ancestors. What Genomics accomplishes is measuring the actual historical information in a pedigree by looking at segments of the chromosomes upon which an animal's performance is built. Thanks to Genomics, we no longer have to use an estimation of what an animal inherited as in the previous Parent Average. We now know with greater accuracy what each individual animal has inherited for production and type potential from their parents, grandparents, etc. Simply put, Genomics allows us to build a more accurate pedigree. Or in two words and a sign: Genomics = Pedigree.

What Genomics Does Not Offer

Some industry leaders feel one of the benefits of Genomics is that there will be no need for progeny testing for production or classification. Others feel that Genomics lowers the number of bulls we need to sample or cows we need to work with to develop young sires. Both of these miss a major point.

Genomics is based on historical data, just as all pedigree information is. While very useful in improving the odds of accurately estimating animals transmitting ability, Genomics is not a guarantee. There will still be a range of results once the daughters are milking for both production and type. Further, while over time Genomics will identify new

mutations or combinations of genes, not every positive or negative contribution will be known from the historical data set.

In practice, this would suggest for Brown Swiss that we continue to select high Genomic/Pedigree value animals as we have selected from high Parent Average animals in the past, with a few others judiciously mixed in. It would also suggest that to maintain a high rate of genetic progress that we do not reduce the number of young sires sampled.

What Genomics has All Ready Accomplished

Above we discussed a problem with the Animal Model, namely over estimation of the production potential of the female side of the pedigree. What has developed over time, due to the differing amounts of progeny/family information between bulls and cows is an upward bias in cow genetic evaluations. The result has been the creation of two scales; one for bulls and one for cows. Previous to the introduction of Genomics there was not a feasible solution to this problem.

With Genomics, an answer for this dilemma has been developed. As noted above, Genomics allows us to look at parts of the actual building blocks of an animal located on their chromosomes. The direct result of this has been a substantial increase in the amount of pedigree (recall Genomics = Pedigree) information that geneticists at USDA-AIPL have to work with. Combined with actual production and type data, this has allowed the geneticists to adjust the overall data for females to create a single scale for bulls and cows. The first practical application of this new knowledge was utilized for Genomically-tested females in the Holstein and Jersey breeds in April, 2010. In the last year, further work by the geneticist at USDA-AIPL has improved the Genomics = Pedigree information to the point that it can be applied to all cows of the Brown Swiss, Holstein or Jersey breeds; Genomically tested or not. The first evaluation incorporating this change will be in April 2011.

As with previous improvements in the history of genetic evaluations, this adjustment will not be without controversy. In the Brown Swiss breed, we will see considerable shifts downward in PPR and NMS values for the top 50% of cows of the breed. We will also see some re-ranking of cows and heifers on the list relating to adjustments in their individual pedigree values. While immediately disruptive, the end result will be significantly improved Genomics = Pedigree information for Brown Swiss. This will allow us to increase our rate of genetic improvement by improving our selection results.

Just the Beginning

Genomics is still early in its development. Built upon the mass of production and type information provided by breeders and geneticist over the last 100 years, Genomics is a continuation of efforts to build the best Brown Swiss cow we can. In future articles, we will discuss the Brown Swiss Cattle Breeders Association's plans in relation to the inclusion of Genomics to construct better and better Brown Swiss. If you have any questions, please feel free to contact the office.