

New Genomic Test Has Industry-Wide Implications

*By Bennet Cassell
Hoard's Dairyman*

There is BIG NEWS in dairy cattle breeding these days, and that's a rare event. How rare? One could argue that there hasn't been any BIG NEWS in my career. No doubt, things have changed, like embryo transfer went from theory to practice, the statistics behind genetic evaluations really are mind-boggling, and two-year-old computers these days make good doorstops. But the basic science behind pedigree selection, progeny testing, and genetic evaluations has been well-known for many years. One possible exception is the development of genetic evaluations for health and fitness traits in recent years - using well-established technology.

The BIG NEWS, as explained in the April 25 issue, page 293, is that an entirely new kind of information has joined the knowledge base about genetic merit of dairy animals. The new information, genome scans, comes from analysis of DNA samples on individual animals. It takes us closer to actually "seeing" genes than we have ever been. My first attempt to describe this process appeared in the October 25, 2007, page 711, issue.

Fourth item added to list . . .

I have taught a number of animal breeding classes through the years. One form of a question that appeared on any number of quizzes was "What are the different sources of information about genetic merit of an animal?" The response, first memorized, later understood more fully, and finally (I may deceive myself here) taught to students in my classes, was "pedigree, performance, and progeny." Today, the list must include one new category - genome scan data.

The three traditional sources of information all originate as performance data. A lactation record is "performance" in the genetic evaluation of the cow that made the record, progeny data for her sire and dam, and pedigree data for her son or daughter. The critical role of performance records won't change because of genome data, as performance remains the ultimate test of genetic merit.

In fact, genome data won't mean anything without performance data. Relationships between genome and performance will be used to predict genetic merit in new animals for which only pedigree and genome scans are available. The handy part is that expected performance predicted from the combination of pedigree and genome data is more accurate than pedigree information alone, but, like pedigree data, genome scans are available when animals are young.

Genome scans come from analysis of DNA in tissue samples. The results are long sequences of nearly 40,000 numbers on each animal. They are incomprehensible nonsense in raw form, but very useful when controlled through computer programming. Each number in the sequence is from a different location on the DNA of the animal. The numbers themselves vary with the source of DNA, but one basic model assigns "0" if a particular nucleic acid - those A and T and C and G symbols - is absent or "1" if it is present at a specific site in the DNA sample.

Locating who got what . . .

The basic idea is to see what piece of DNA an animal inherited from its parent. Only half of each parent's DNA is transmitted to offspring but which half? What do the sequences reveal about own or progeny performance?

Before we ascribe magic properties to genome scans, a little honest biology gets in the way. Almost all the traits in dairy cattle are controlled by at least hundreds, if not thousands, of complex biochemical processes within the cells of the dairy cow. These processes are controlled in most cases by many genes operating in harmony (not to rule out that a single, critical gene mistake can produce total disharmony). Outside of such a disruptive exception, no one gene, or even group of 20 genes, has very much impact on performance for almost all economically important traits. Further, the action of the important genes is usually modified by the action of many other genes at other parts of the genome, often expressed at other times in the life of the animal.

Our most familiar trait, "milk production," is a very complex process, and we simply don't understand much about how individual genes exert control. Maybe we will some day, but, today, nobody knows just what the "best" sequence is from a genome scan for any of our economically important traits. I suspect that there is no one "best" sequence, though there could well be many sequences that don't work very well.

Even if we don't know everything from a genome scan, all that information together tells more than pedigree merit alone. If we ignore sex chromosomes as we do in traditional pedigree evaluation, full brothers or sisters have the same pedigree merit. We expect that 50 percent of their genes are copies of the same genes in the parents; 25 percent from the sire and 25 percent from the dam. The process of germ cell formation called meiosis collects sample halves of each parents' genome to create sperm and egg cells. Each cell may, by chance, contain more or less than 25 percent of genes as copies of the same gene in the parent. As a result, some full sibs will share only 40 percent of their genes in common, while others may share 60 percent.

More extreme differences are possible. In fact, it is possible (but highly, highly improbable) that two full sibs inherited no genes that were copies of the same gene in their parents. They could, with equally low probability, even be identical. Genome scans show which segments of DNA are shared by siblings. Genome relationships are not 50 percent for full sibs or 25 percent for half sibs as we expect them to be from pedigree. That's why genome relationships will be more useful for genetic evaluations than pedigree relationships have been.

A perfect illustration . . .

Cloned bulls make a good point about genome scans. Clones have identical genes, yet progeny test results won't give the same proof to clones. Progeny of each clone will receive a random sample of the sire's genes, and those progeny groups, unless very large, won't be "the same." Environmental complexities certainly don't help any either. At the same time, we certainly don't expect proofs on clones to be very different if the progeny tests are run properly.

Genome relationships, rather than pedigree relationships, tell the genetic evaluation system that two clones are NOT separate individuals. They are a single individual from a genetic view, and progeny data should be merged into a single answer. We could do the same thing in our current system by using a single sire ID, but how could I make a point if we did that?

This is new science. There are struggles ahead before we make the best use of genomic relationships in genetic evaluations. Genome information exists for a limited number of bulls, fortunately, and through foresight, including a number of highly influential sires. Initial research in this country is limited to Holsteins. Still, this is BIG NEWS, whether we see it among the breakthrough science stories that appear constantly on the nightly news or not.

Author Bio: The author is an extension dairy scientist in genetics and management at Virginia Tech, Blacksburg.

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