

I Have a Question about Genomics

By: Roy Wilson, AVP-Large Herd Business Center, Genex

Genomics has not lacked press in recent months. Although the tone of each article has been slightly different, each author has attempted to explain the technology's background and potential impact. But have we really answered the farm owner's questions? I have had the privilege to speak to thousands of dairy producers on this subject; some in one-on-one conversations and some on grand stages such as the Professional Dairy Producers of Wisconsin annual conference, the National DHIA annual meeting and the CRI annual meeting. Here are the top 10 questions farm owners have asked.

#10 How does genomics impact crossbreeding? Several who considered or tried crossbreeding did so for immediate impact on some "challenging" traits for the Holstein breed. For example, many producers were frustrated with the lack of progress in Daughter Pregnancy Rate (DPR). This trait is relatively new in dairy genetics time (first reported in 2003) so procurement staff have not had ample time to procure sires specifically for it. DPR has also "lagged" due to low heritability and low reliability. Therefore, in some instances crossbreeding has been used as a quick fix.

Now, with genomics, procurement staff can realize the true effect of traits like DPR sooner. When selecting a mating sire or dam of future sons, genomic tests on those animals reveal an accurate description of their DPR at a much higher reliability. Holstein procurement staff that select intensely for these kinds of traits can utilize genomic evaluations to produce faster genetic improvement. So does genomics erase crossbreeding? Most likely not, but it does allow the Holstein breed to address a few troublesome traits that prompted some to start crossbreeding in the first place.

#9 Do we make faster progress on low heritable traits now?

The simple answer is yes. The increased reliability gained from genomics dramatically increases the rate of genetic progress for low heritable traits. This is another huge benefit to utilizing genomics.

Let me explain further. After sire summaries, the sire procurement staff decides which sires to use as sires of sons. These are generally new releases with 80 to 120 daughters and reliability ranges from the high 70s to mid 80s. Few 99 percent reliability sires are used because by

the time they reach this high reliability level, their genetics are considered "old." (When talking about an 80 percent reliability sire, the reliability refers to his production PTA reliability. In actuality, his reliability for a low heritable trait such as DPR is about 60 percent.)

Adding genomic information results in a higher reliability; bringing it to a more comfortable level for procurement staff. Then adding daughter information brings it to an even more acceptable level.

#8 Why do the numbers look so big? +4.75 PTA Type and +8.5 Productive Life are large numbers, but it makes sense. Right now, genomics identifies the superior bulls that would typically have received daughter proofs in 2011, 2012 and 2013.

It is also important to remember that every five years the USDA-AIPL performs a base change. In simple terms, this re-adjusts the proof numbers for genetic progress. It keeps the numbers in a "normal" range or prevents PTAs (Predicted Transmitting Ability) from getting too large. Therefore, genomically-proven sires should have large PTA numbers as they represent genetic progress. Next January's base change will lower these PTAs to some degree.

#7 Can there really be this many bulls in the 90th percentile?

There appears to be an unbelievable number of sires in the 90th percentile for Lifetime Net Merit (LNM). The USDA-AIPL calculates the percentiles from the previous sire summary's list of active sires with daughter information. For instance, in January 2009 the USDA-AIPL used the August 2008 list of active sires to determine the percentiles. For the April sire summaries and into the near future, the USDA will continue to base percentile breaks on traditional methods, meaning genomic sires will not be included.

#6 How soon will we have new traits like feed efficiency or resistance to Johnes?

The ability to investigate non-traditional traits is an exciting benefit of genomics. DNA analysis allows for discovery of such traits. These "new" traits will not be discovered overnight as 10,000 to 25,000 observations are needed. But compared to traditional methodology this is a vast improvement.

Together with other organizations, Genex is aggressively pursuing the discovery of several new traits. Other large corporations have also expressed interest in this research. While it may take a few years, we are confident this technology will lead to several new selection traits.

#5 Will reliabilities stay the same or go up? As reported in April, most reliabilities range from 68 to 74 percent for genomically-proven sires. With that in mind, you may wonder why the reliabilities differ. The answer is some bulls come from more “popular” families. If more of the sire’s family members have been genomically tested, the reliability of the sire is higher. If pedigree information was not recorded and no direct family members were genomically tested, his reliability is lower.

The reliabilities of genomically-proven sires continue to increase based on the number of animals in the breed that have been genomically tested. However, the increase in overall reliability is now smaller due to diminishing returns. For instance, the 1,000th animal tested increased the overall reliability for genomic evaluations more than the 31,000th. Without improvements to the calculation methodology and/or larger marker panels, I do not foresee the average reliability increasing much over 75 percent.

#4 How does the system work, from sample to result?

A sample containing DNA must be submitted to one of the three approved labs. The samples consist of a clump of hair, blood or semen. Upon receiving the sample, the lab extracts DNA and submits the marker sequence to the USDA-AIPL. Approximately every 45 days the USDA-AIPL calculates genomic proofs. Then the owner of the animal receives a one-page report with the animal’s PTA and corresponding reliabilities for all the traits.

Anyone can test female animals through kits provided by the Holstein and Jersey associations. The cost is approximately \$250. Until May 2013, only a NAAB member can have a bull genomically tested.

#3 How can genomics just all of a sudden be here? Genomics, although new to the A.I. marketplace, has been a work in progress for several years. The USDA-AIPL and eight A.I. companies have supported research on genomics since 2004. A.I. companies have been saving semen (DNA) samples on every bull sampled for the past 15 years thinking this technology would one day be possible.

#2 How quickly will this technology improve? It is hard to say how fast this technology will progress. Although it is a new technology for the dairy

industry, the poultry and swine industries successfully implemented this technology long ago.

The next step in the dairy industry is the development of a “low-density” chip. This is scheduled for release in early 2010 and will allow for large application on the female side. For approximately \$30, dairy producers will be able to receive evaluations with reliabilities averaging in the 50s. This should allow incorporating female genomic evaluations into breeding program scenarios to become more affordable.

After that, the next step is identification of 100,000 or 300,000 markers (compared to the 58,000 markers currently identified) followed by over a million markers and/or entire genome scanning. Some predict this will happen in less than 10 years.

#1 What confidence should I have in 70% reliability?

There are a few things to consider when deciding how to use 70 percent reliability sires in your breeding program.

Keep in mind the reliability advantage of genomic information. Before genomics, young sire evaluations were based only on parent averages with about 35 percent reliability. New active sires with daughters averaged about 80 percent reliability. Now, genomically-proven sires average about 70 percent reliability.

Secondly, think about the projected change in performance for a 70 percent reliable genomically-proven sire as he adds daughters and goes to 95 percent reliable. According to calculations, the change for a trait such as LNM is $\pm\$147$. Said another way, if the genomically-proven bull is $+\$700$ LNM at 70 percent reliability, then at 95 percent reliability he is expected to be between $+\$847$ and $+\$553$ LNM. Take that range into consideration when selecting 70 percent reliable sires. If your current genetic requirement for a sire is 90th percentile (or $+\$490$) to maintain that level use genomically-proven sires above $+\$637$ LNM. I tell producers to get greedy with genomics. Raise your genetic requirements if considering genomic sires.

AUTHOR BIO

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

