



Photo: Cybill Fisher

Genomics — an early report card

An evaluation of 238 bulls that graduated from genomic only to progeny test plus genomic status confirmed genomics is for real. For best results, use a group of high-end genomic bulls, not an elite few.

by Kent Weigel

GENOMICS has taken the dairy cattle breeding world by storm over the past 18 months. Since the commercial release of the BovineSNP50 BeadChip in December 2007, more than 30,000 North American dairy cattle have been genotyped. Research by scientists at the USDA-ARS Animal Improvement Programs Laboratory in Beltsville, Md., indicates that genomic testing can boost reliability about 30 percent for a young Holstein that has no production records or offspring of its own.

Because preliminary results looked so promising, genomic information was incorporated into routine genetic evaluations for U.S. dairy cattle in January 2009 . . . just 13 months after the genomic test was released. That also begs the question, "How well are genomic evaluations working in practice?"

That is the focus of this article. We will look at the first batch of bulls that had genomic data in January 2009 and at least 50 milking daughters in the August 2009 sire evaluations.

In this year's genetic evaluations, genomic data have been combined with pedigree data to compute official predicted transmitting abilities (PTAs). That means genomic information still has a considerable impact on official PTAs . . . even after that animal has records or progeny of its own. So, to complete a true comparison, we used unofficial or "traditional" August 2009 progeny test genetic evaluations that did not contain any genomic information. In fact, we actually used daughter yield deviations (DYDs) so that we also could escape the influence of pedigree information.

Looked at 238 bulls . . .

As shown in Table 1, a total of 238 Holstein bulls had official PTAs in January 2009 and then, based solely on genomic information, had daughter yield deviations this August on at least 50

milking daughters. Note that only 60 of these 238 bulls had at least 50 daughters in their genetic evaluations for daughter pregnancy rate (DPR), and because none of these bulls had productive life data from at least 50 daughters in August, that trait could not be considered in our study. The reliabilities for the groups were:

- Average January 2009 reliability (REL) based on parent average (PA) information was 42 percent for yield traits, 39 percent for somatic cell score (SCS), and 26 percent for DPR.
- That compares to reliabilities for genomic predicted transmitting abilities (GPTAs) which include both pedigree and genomic information

which averaged 72 percent, 67 percent, and 62 percent, respectively.

- Data from an average of 71 daughters per bull (62 for DPR) provided an average REL of 84 percent for yield traits, 67 percent for SCS, and 62 percent for DPR in August 2009.

It is interesting to note that the average REL of January 2009 GPTAs for SCS was equivalent to that of August 2009 evaluations based on 71 milking daughters, whereas average REL of the August 2009 evaluations for DPR was still considerably lower than REL of the corresponding GPTAs in January. This illustrates the challenge in improving lowly heritable health and fertility traits through genetic selection. It is also very important to note that August 2009 DYDs of the bulls in this study are somewhat preliminary, as significant changes can occur when more records from first- and second-crop daughters become available.

The correlations between August 2009 DYDs resulting from progeny testing and January 2009 PAs and GPTAs for each trait are also shown in Table 1. In all cases, correlations were much higher with the inclusion of genomic information. Bias, the average difference between the January 2009 PA or GPTA and the corresponding August 2009 DYD for each trait, is significantly less for the yield traits when genomic information is incorporated. This is not surprising because it is well known that preferential treatment of some elite females for yield traits leads to inflated PAs for their offspring.

Scatter plots of the January 2009 GPTAs for protein yield and SCS are shown in Figures 1 and 2, along with the corresponding August 2009 DYDs for these traits. As you can see, there is generally good agreement between genomic predictions and progeny test results, as we would expect by correlations of 0.632 for protein and 0.531 for SCS. Bulls that lie above the line in Figure 1 were underpredicted in January 2009, such that their August 2009 DYDs were better than expected, and bulls that lie below the line were overpredicted. The opposite is true for SCS in Figure 2 because lower values are desirable for this trait.

Better, but not perfect . . .

For both SCS and protein yield, a large proportion of the bulls have evaluations within a few pounds or units of their genomic predictions, but some wide misses occur, as well. This phenomenon is not unique to genomic evaluations,

Table 1. Genomic bulls compared to actual daughter yield deviations

	Milk Fat	Protein	SCS	DPR	
No. bulls	238	238	238	237	60
Reliability (Jan. 2009 PA)	42%	42%	42%	39%	36%
Reliability (Jan. 2009 GPTA)	72%	72%	72%	67%	62%
No. daughters (Aug. 2009 DYD)	71	71	71	71	62
Reliability (Aug. 2009 DYD)	84%	84%	84%	67%	52%
Correlation (Jan. 2009 PA, Aug. 2009 DYD)	0.444	0.540	0.476	0.376	0.213
Correlation (Jan. 2009 GPTA, Aug. 2009 DYD)	0.624	0.695	0.632	0.531	0.341
Bias (Jan. 2009 PA) +259		+7.7	+7.9	+0.012	-0.232
Bias (Jan. 2009 GPTA)	+194	+4.4	+4.4	+0.016	-0.012

Table 2. Average genetic merit of top groups of bulls

	Milk	Fat Protein	SCS	DPR
Top 10 bulls based on Jan. 2009 GPTA	1,825	87.55	2.72	1.5
Top 10 bulls based on Jan. 2009 PA	1,123	71	2.75	0.8
Difference	+702	+16	-0.03	+0.7
Top 25 bulls based on Jan. 2009 GPTA	1,564.71	50	2.73	1.2
Top 25 bulls based on Jan. 2009 PA	1,224	63	2.77	1.1
Difference	+340	+8	-0.04	+0.1
Top 50 bulls based on Jan. 2009 GPTA	1,404	62	2.75	0.6
Top 50 bulls based on Jan. 2009 PA	1,314	57	2.81	0.5
Difference	+90	+5	-0.06	+0.1


The author is an assistant professor, extension genetics specialist, University of Wisconsin programs administrator, and a National Association of Animal Breeders geneticist.

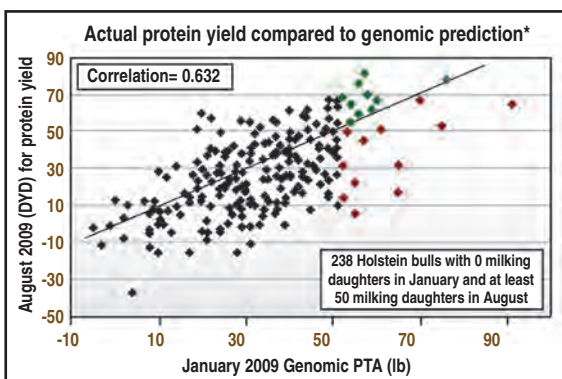
as genetic predictions based on limited information have occasionally missed the mark for decades, regardless of the method or approach.

The important thing to recognize is the fact that, although the GPTA for a young animal will usually be much more accurate than its traditional PA, it will generally be less accurate than information that comes later via progeny testing. Therefore, breeders should limit the amount of semen that is used from an individual bull with high-ranking GPTA, and instead they should focus on choosing a larger group of bulls (perhaps three or four times as many as they've chosen in the past) to control the risks associated with lower REL bulls.

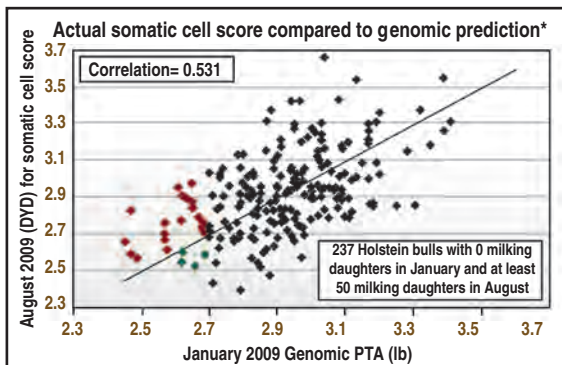
Many producers put a strong emphasis on REL in sire selection, and, for this reason, some pedigree breeders and commercial producers have chosen to avoid genome-tested bulls entirely. This strategy also comes at a cost because many outstanding bulls will be missed, including some bulls whose semen is marketed at a very reasonable price.

mation, in contrast to 697 proven Holstein with data from 10 or more milking daughters. However, when we focus on bulls with PTA for Lifetime Net Merit of \$450 or greater, the list is dominated by genome-tested bulls. . . a total of 306 "G status" (genomic) bulls exceed \$450 for Net Merit, whereas only 138 "A status" (active) bulls meet this criterion.

Even though using young, genome-tested bulls comes with increased risk, ignoring these bulls comes with a heavy opportunity cost, as well. As with most good things, moderation is the key, and producers who supplement their traditional sire selections with a group of outstanding genome-tested bulls will achieve the greatest genetic progress in their herds. 



*Figure 1. Scatter plot of January 2009 genomic predicted transmitting ability (GPTA) versus August 2009 (DYD) for protein yield. The top 25 bulls based on January 2009 GPTA are shown in color (green = underpredicted; red = overpredicted).



*Figure 2. Scatter plot of January 2009 genomic predicted transmitting ability (GPTA) versus August 2009 (DYD) for somatic cell score. The top 25 bulls based on January 2009 GPTA are shown in color (green = underpredicted; red = overpredicted).

Table 2 shows the average August 2009 DYD for milk, fat, protein, SCS, and DPR when bulls were chosen based on January 2009 PA or GPTA. For example, the top 10 Holstein bulls based on GPTA for milk yield were 702 pounds per lactation superior to the top 10 bulls based on PA, and corresponding advantages were 16 pounds for fat and 8 pounds for protein. It is interesting to note the bulls with the highest PAs for milk yield did not have the highest DYDs. In other words, average of the top 25 or top 50 was better than that of the top 10. This occurred because of a few very wide misses among bulls with extreme (and most likely, biased) PAs for milk yield.

It is clear that genomic information enhances the accuracy of genetic evaluations for yield traits and, to a lesser extent, for health and fertility traits. As of August 2009, North American breeding companies were marketing 365 young Holstein bulls based solely on their genomic infor-