

How are Genomics Working on the Dairy?

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Dovetailing on Dr. Kent Weigel's presentation, "Future impact of genomics in sire selection and herd management," our panel will include observations by four dairy producers who have been working with genomics in the replacement side of their herds for nearly five years. The panelists include: John Andersen, Double A Dairy in Idaho; Brett Barlass, Yosemite Jersey Dairy in California; Jonathan Lamb, Oakfield Corners & Lamb Farms in New York; and Dan Siemers, Siemers Holsteins in Wisconsin. As panel moderator, I will also weave in some experiences from the Hoard's Dairyman Farm. Together, this group who milks some 25,000-plus cows has perhaps run more genomic tests than any other collective group of herds in the country.

From the dairy producer's perspective, the question is how genomic testing might fit into a herd setting. What are the potential returns to the dairy operation? How might it transform the handling of replacements on a dairy?

Think the cost of incorporating genomics is too high? Then consider all of the dollars spent on seed corn genetics. While valuable, that investment lasts merely one cropping year. Doesn't dairy genetics deserve the same investment? If we raise and calve in our own replacements, these genetics are built upon each generation and we continue to reap rewards each year.

Dairy producer's perspective

As far as genetic progress is concerned, "The whole genetic paradigm has brought us back to generation intervals and pushed us to look at the younger generation," said Dan Siemers, who maintains a 34,000-pound herd average on 2,400 head. "Also, the genomic test profile allows us to correctively mate heifers much better."

"The benefits far outweigh the negatives on genomics," said John Andersen of Jerome, Idaho. "If there is a downside, we are moving quite fast, and there are a number of bulls with two and some with even three generations without actual progeny or production information."

"Inbreeding may be an issue, but you must remember that everyone wants to use the best bulls and

acquire the best genes. That is the main cause of inbreeding in the first place,” said Wisconsin dairyman Dan Siemers.

Genomics also opened a whole new door to evaluating different traits. Traits that could better improve fertility, feed efficiency and perhaps one day even hoof health.

As for future improvements on genetic selection, “The trait I’d like to see an index for and more research on is foot health,” said Jonathan Lamb, Oakfield N.Y. “I think it’s a real black eye for the industry, and we can always do better on our farm,” said the chairman of the Holstein Association USA’s Genetic Advancement Committee. “I don’t think we measure foot health adequately from a phenotypic standpoint right now.”

“Daughter pregnancy rate is a great success story in the Holstein breed,” expressed Lamb. “Just a few years ago, we stopped the longtime decline in fertility. Eight years ago, we had preg rates hovering in the 19 to 20 percent range. Now, we easily reach 25 to 28 percent.”

As for the trait that pays all our bills — production — with an eye to the future, Lamb noted both the present and things yet to come.

“After many discussions over the past year, I am more convinced than ever that protein is more important than fat,” said Lamb. “We need to keep selection pressure on protein production because it’s in demand and it drives our milk checks.”

From an implementation standpoint, Yosemite Jerseys fully employed genomics in 2010.

Herd manager Brett Barlass started using genomics in 2010, testing every heifer calf at one day of age. “Our original goal was to use genomic information primarily to determine which heifers to keep as replacements on the dairy and which ones to sell,” says Barlass.

That strategy changed when the family who owns the herd decided to build a second dairy in Texas. Currently, all of the California herd’s heifers are retained to expand the Texas herd, but Barlass says the genomic results still provide value. Because they use a lot of young sires, “we’re getting a jump on genetic information well in advance of bull proofs,” he says.

The identification of Jersey fertility haplotype 1 (JH1)-carrier females also allows Barlass to avoid breeding them to JH1-carrier bulls, since that particular halotype can negatively affect fertility. And correction of parentage errors helps him prevent inbreeding.

So what might implementing a genomic testing system on your dairy involve?

While Andersen, Barlass, Lamb and Siemers have been working with genomic tests on their

replacements for over five years, the Hoard's Dairyman Farm got started just last year. This real-world experience also could provide the audience questions for the panel or additional insight on how genomics might fit into their operation.

What Hoard's learned from our genomic test results

Do individual cows in high-producing herds have an improved or reduced capacity to express their genetic potential?

“If we have good management on a farm, genetics matter more because a cow's genetic ability has an even greater opportunity to express itself,” Vita Plus' Pat Hoffman explained at a meeting we attended earlier this year.

Such is the case at the Hoard's Dairyman Farm where the Jersey herd is averaging 20,223 M, 984 F and 761 P. As a result, the combination of high production and genetic potential has caused our Jerseys to outperform their genetic predictions.

That's right, by comparing real-world production results with predicted transmitting abilities for milk, we know that, on average, cows from a 1,000-pound-plus milk bull are actually averaging 1,590 pounds more milk than a typical daughter of sires at zero (0) predicted transmitting ability for milk (PTAM).

Put another way, we are getting 50 percent more milk from our genetics than the national average. That was one of the many items the Hoard's Dairyman team learned about our herd's genetics as Cheryl Marti of Zoetis sat down with us to review our genomic test results on the CLARIFIDE platform.

Likewise, the Hoard's team also found our daughter pregnancy rate (DPR) or the likelihood of our cows conceiving expressed itself more dramatically. While it would normally be expected that we'd see four fewer days open for each improvement to a sire's DPR. In our herd, we saw slightly more genetic difference to each positive 1.0 gain in DPR as it yielded five fewer days open.

Besides herd management, accurate sire ID also contributes to individuals outperforming genetic predictions. Thanks to relatively solid pedigree data recorded through registrations and herd records, the reliability of our herd started out at 31 percent for Net Merit. Then, due to the power of studying DNA, that reliability doubled to 62 percent. Milk reliability was even more robust, moving from 34 to 67 percent. Marti, who had held the role of dairy production specialist with Zoetis, noted that the 31 percent was among the highest in commercial herds — either Jersey or Holstein — that she has worked with when studying results.

As we learn more about genetics through genomics, it also spread out the bell-shape curve on our

herd's genetic potential. Prior to the test, the 162 individuals ranged from 12 to 416 NM\$ with an average of 223. After the test results came back, the spread moved from -60 to \$558 NM\$ with a mean of 252 (based on August 2014 genetic evaluations).

We also found out that our Jerseys were slightly less inbred as a whole. Our pedigree-based inbreeding levels were 6.3 percent, but that number fell to 5.6 percent after reviewing the genomic tests. That compares to an industry average of roughly 7.3 percent for pedigree-based inbreeding for the Jersey breed. As far as haplotypes are concerned, the 13.6 percent prevalence of JH1, which reduces fertility, was also lower than the 20 percent level found in the breed. Knowing these results will allow us to make better mating decisions for the next generation.

Some mis-ID'd calves

At first, the entire Hoard's team was alarmed to learn that 8 percent of our calves had misidentified sires. However, after talking to Marti, she pointed out that many herds average rates of 8 to 20 percent with an industry average hovering near 14 percent of misidentified animals. While she assured us our 8 percent figure was good, we wanted to delve deeper into those eight misidentified sires.

Due to good on-farm records and the power of genomics, the Hoard's crew was able to rectify all eight incorrectly identified sires among those tested individuals. All eight originated on ovsynch days when multiple cows were bred on the same day. On ovsynch day, the inseminator was more likely to not double-check the straw after pulling it out of the gun warmer before inseminating the cow. Steps have been taken to correct this issue in the future.

In addition to those errors, the test revealed we did have one misidentified dam. On a very good note, 161 of the 162 maternal grandsires were confirmed to be exact matches due to the genomic tests. The one that could not be verified didn't have a genomic test profile.

Finding a different career

By using the genomic tests, we were able to run some numbers on our heifer crop. In one scenario, culling the bottom 20 percent (all those with NM\$ under 160) could dramatically improve our profitability. In addition, if we had a group of our top individuals in our herd, they would be expected to outperform the worst calves by approximately \$1,200 over their entire lifetime as measured by income over feed costs and other health costs, which are included in \$NM.

While the Hoard's team winced at culling 20 percent of young calves, the idea does have merit. As we looked at each age group on a bar graph, the calves that were the poorest genetic doers were even outranked by cows already in the milking herd. A similar situation would exist in nearly every herd in the nation.

A more plausible scenario might be culling the bottom 5 to 8 percent immediately after getting the genomic results back. To make the best use of this strategy, young calves would have to be tested every 30 days. Even though the largest daily expense is sunk into calves during the first 60 days of life, those heifers still eat a lot of feed before they calve in at an average age of 1 year 11 months, Hoard's Dairyman Farm manager Jason Yurs pointed out. Zoetis has a dashboard tool where we can evaluate economics and different culling levels. It will prove useful in looking further into culling genetically inferior heifers.

The discussion turned to the farm's use of sexed semen. "All our Jersey heifers are serviced to sexed semen on the first service," Yurs reminded those attending the meeting. "We might be better served to breed the top half of the heifer herd to sexed semen twice and the bottom half to conventional semen," Yurs noted as he thought how to implement the strategy easily in the day-to-day operations.

"Can we load the genomic test results into Dairy Comp 305 and mark the genetically superior heifers?" he went on to ask.

"We could easily do that after the meeting," replied Marti.

That just may be one of our first action plans. Of course, there also will be follow-up with some genetically superior heifers that quickly received A.I. interest.

While we have more concepts to follow-up with, we were pleased to learn our herd is on the right track for genetic improvement. We definitely believe the genomic test results can help fine-tune our herd and bottom line.

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