

Genomic testing for genetic gain in a small commercial herd

By Jennifer Heim



In fall 2011, my husband and I purchased a retiree's small herd, which was mostly A.I.-sired. We added them to his family's original herd, which was mostly herd-bull sired. None of the cows were registered, but all were Holstein.

A few months later, after we took over management, we sold the last remaining herd bull and were officially 100 percent A.I. Up to that point, my husband had been breeding using mostly proven sires that were near the middle of the list, for budgetary reasons. However, several of the heifers in the purchased herd were sired by top proven bulls. As we quickly saw the impact good sires had, we committed to using top bulls.

In 2013, we registered and genomic tested three of our cow families.

Early lessons

Right away it was clear, as expected, that the top sires' daughters had higher numbers than the middle-of-the-road sires' daughters, but also as expected, those daughters were not always better cows. Genomics told us things about our animals we couldn't physically

see. We learned our original herd contained haplotypes affecting fertility that were likely widespread due to long-term use of the herd bulls. We also learned our high herd somatic cell count was likely affected, partially, by genetics.

Our approach

To date we still have only registered daughters from those four original cow families. However, in 2014 we began using inventory tags with 840 identification numbers and using Basic ID for all our heifers. This allows us to genomic test any heifer through Holstein USA and to use the Enlight system for managing our genomic and parent average data. We have continued to select a variety of calves for genomic testing from both the registered and basic IDed families.

General benefits

No amount of data, no matter how accurate, is valuable if you don't use it. We have used genomic data for specific matings for special animals and for identifying top genetic females. However, the real value for us has not been the specific, but the general. Based on our earliest tests, we stopped



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using bulls carrying known haplotypes affecting fertility. Since then we have seen improved pregnancy rates and very few haplotypes in recent genomic results. We have also improved both our actual somatic cell count and our genomic somatic cell scores through a combination of breeding, culling and management changes. Genetics are just one piece of the puzzle. ↗

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