

For Tillamook Cheese, our vats are 50,000 pounds. If you fill them with Jersey versus Holstein milk, you end up with 1000 pounds more cheese. When you're processing 28 vats a day, that's 28,000 pounds more cheese at the end of 24 hours for the same amount of time and money. Because they offer a higher yield of the right components, Jersey cows enable us to have a more efficient operation.

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Q: When did you begin using genomic selection tools in your breeding program?

NM: Whenever new technologies come along, I usually get right on them within a short period. It's part my personality, and part surviving in the business world. If you want to stay ahead of the game, you better get on the train quickly.

We did some of the initial genotyping work in late 2007 using some of the first tools, such as microsatellite analysis. Then we took the whole-genome approach and did preliminary testing with the 3K chip. Our first official genomic evaluations for Jerseys were in January 2009 and the first 2 females were genotyped from hair samples in March 2009 using the BovineSNP50 BeadChip. Their first genomic evaluations were produced in April 2009. These 2 cows now have more than 50 combined progeny, 9 sons in AI, and more than 1300 combined grandchildren.

We currently use low-density array systems with content based on the original BovineSNP50 BeadChip. To date, 1991 Jersey males have been genotyped by Martin Dairy, including 85 fourth generation- and 13 fifth generation-bulls. Ninety-four of our bulls have gone to national studs and entered into AI service, with over 10,455 registered Jerseys being sired by a bull originating from our herd.

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Q: How do genomics tools integrate with the new reproductive technologies that you are using to enhance the genetic value of your herd?

NM: We have been using embryo transfer in our cows with the highest genetic value for several years, so we have higher genomic level calves coming through. We genotype all of

our heifers and use a genetic merit measurement called a P-Level to select which will enter our sex-sorted AI breeding. We breed about 60 heifers each month, with those having a P > 7 (on a 0–9 scale) bred with sex-sorted semen. These heifers rank in the top 20% of the Jersey breed. Breeding with sex-sorted semen means that we try to breed more females out of the high-level heifers, creating cows with even higher genetic values. With genotyping, we're now able to identify young sires that have higher genetic levels and use those in our next generation with even more confidence than before.

Q: What traits are you selecting for with genomics tools?

NM: Money is the main trait. I select for cows that will wear well and produce many pounds of liquid cheese that I can ship to the plant. We have many cows that stay around here until they're 8 or 9 years of age and then all of a sudden they get to where they can't compete anymore.

Also, feed efficiency is important to everybody in the dairy business. Feed is our biggest operating cost, and the Jersey breed is the smallest breed. So if you want to look at it as food per pound of cow versus how many pounds of cheese produced, Jerseys are number one in the world.

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Q: Who does the data analysis and how is it integrated with the phenotype information?

NM: The American Jersey Cattle Association, which I'm so proud to be a part of, provides us with all these tools. I'll go through the different AI studs when new bulls come through. I look at their genotypes and pedigrees, make decisions on which ones I want to use, and then I'll send a list of heifers that I'm breeding every month to the Jersey Association and the 15 or 20 bulls that I plan on using. They send me a list back with three different choices, and I make the final decision among the three. Because I run two different groups at a time, I end up with six choices.

It's the genotype that gives me all the information to make breeding decisions and manage inbreeding, which is always an issue. My system gives me all these choices. If I use bull #1, I get this, if I use bull #2 I get that, and if I use bull #3 I get something else entirely, and I make decisions from there. The resulting genetic evaluation uses phenotypic data along with

