

Breed Base Representation in Dairy Animals

Three weeks after the long-anticipated official release of Breed Base Representation, Dr. H. Duane Norman of the Council on Dairy Cattle Breeding presented a seminar July 2 about its technical aspects and the facts of the U.S. dairy situation underlying its development. It was the concluding program of the 148th Annual Meeting of the American Jersey Cattle Association in San Diego, Calif.

“Fact one,” Dr. Norman said, “the increases in cheese consumption along with changes in milk pricing that pays for the true value of milk have led to growth of the Jersey breed in the U.S.

“Fact two. A number of herds have used Jersey bulls on cattle of other breeds because of a shortage of Jersey replacements to fill their demands. I don’t think there’s any question about that. I call this the Jersey explosion. We’ve gone from a half a million (units) in domestic semen sales in 1980, to 35 years later 5.7 times as much. That’s an increase of 470%.

“Fact three. The number of crossbreds in U.S. herds has increased 400% in the last decade. 400% means there’s five times as many as there were 10 years ago.”

Calling that “an optimistic picture” for Jersey, Dr. Norman presented his last fact, that just like those sitting in the audience, “producers that have lots of crossbreds want PTAs to be calculated. Sometimes they get an index, sometimes they don’t, especially for genotyped animals.”

The problem for geneticists is that ascertaining what breeds are represented in an animal’s genetic makeup, and to what extent, “is a step necessary to give more crossbred cattle genetic indexes.”

And the very thing that created the demand—genomics—contains the solution.

“When identification of the sire, maternal grandsire, or the next generation of the maternal great-grandsire is not reported, their identity can be revealed in over 99%, 97%, and 92% of the cases, respectively,” Dr. Norman stated.

“Isn’t that pretty fantastic? If DNA can determine who the parents and grand-

parents are, it surely can help reveal the breeds of those ancestors.”

And it does. “Often the DNA from different dairy breeds can be detected by genotyping, regardless of whether or not pedigree information is limited or missing.”

BBR Reference Groups

“The BBR procedure estimates—and listen carefully to the rest of this, please—the similarity of alleles present in five purebred reference groups to the alleles of each individual genotyped.

“It says, I’m going to look at the purebred reference population for the Holsteins, the Jerseys, Brown Swiss, Ayrshire and Guernsey, and I’m going to see which one has the closest relationship. Of course, you can’t tell exactly. This isn’t an exact procedure because (breeds) have some of the same alleles.

“Why five breeds? Because that’s all we have in the CDCB genotype database.”

The all-important step in the procedure is deciding which bulls are permitted into the purebred reference groups. “It’s the registered A.I. bulls that have milking daughters. Most of these bulls entered A.I. before there was so much crossbreeding. Most, or all, were confirmed with blood-typing of parents.”

Who was not permitted into the purebred reference groups? It’s all based on the five-generation pedigree. “In a five-generation pedigree you have 30 parents and grandparents. How many of you know

all 30 of your closest ancestors?” The reference groups, he said, do not include “any bull with missing pedigree information. Any bull having another breed in the five-generation pedigree. And females, as they are more likely to have misidentified ancestors than the bulls.”

The number of A.I. bulls in the reference groups were 442 Ayrshires, 5,464 Brown Swiss, 550 Guernseys, 19,209 Holsteins, and 3,147 Jerseys. The average BBR values of the primary breed for the groups ranged from 97.2 to 99.2.

Calculation of BBR

The determination of BBR for one animal is simple: “The more alleles an animal has in common with its recorded breed reference group, the higher its BBR for that primary breed.”

For only Jersey genotypes in the CDCB database, from the U.S. as well as Canada and Denmark, Dr. Norman pointed out, “you can basically see they are all running 98, 99” (Table 1).

The explanation for being less than 100 is that “animals vary” and alleles are shared by the different breeds.

“Even animals whose ancestors have been true purebreds for many generations often obtain a BBR value for their primary breed less than 100. Cases where the principal breed is 90 to 97 can reveal the presence of outcross bloodlines, but if it’s lower than 90, it probably is a pretty good indication in most cases that there’s some crossbreeding.”

Still, “BBR does not dictate whether an animal is a crossbred,” Dr. Norman added. “You have to make a judgment on these things. But one should be careful doing so because the percentages can easily differ by 5%.

“For example, if you crossed a Brown Swiss and an Ayrshire, the first generation should come out with 50%, 50%, right? That’s what you expect. But it could come out with 45 and 55, or 55 and 45 because there are common alleles there.

“The decision that was made by the Council,” he continued, “was that anything 94 and

above is considered to have one-breed background. The BBR will be expressed as 100 for that breed and other breeds will be set to zero. BBRs will be calculated only once, unless the animal is genotyped with a higher density chip. Reference groups will be updated annually.”

Table 1. Count of Jersey genotypes in CDCB database and group averages by country of origin for Breed Base Representation, June 2016.

	U.S.A.	Canada	Denmark	Australia	Great Britain ¹
Males	17,163	1,168	1,408	360	26
Average BBR	98.2	99.0	97.7	99.0	99.0
Females	112,440	3,464	238	281	77
Average BBR	97.8	99.0	97.9	99.0	98.7

¹ Includes animals recorded by Royal Jersey Agricultural & Horticultural Society