Documenting changes in dairy breeds in the United States including genomic examination using breed base representation

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Breed composition of the US dairy population has changed over the last two decades. The changes occurred for various reasons including:

- Shifting demand for milk products.
- Increased interest in different traits.
- Promotion of breeds with little previous presence in the US.
- Desire to capitalize on heterosis.

A few producers are experimenting with rotational crossing schemes, but more are transitioning to another breed by using semen from the targeted breed for multiple generations. Domestic semen sales from Holsteins declined from 93.4% in 1996 to 85.9% in 2016. Jersey sales rose from 4.6 to 13.1% during the same time. For several decades U.S. dairy owners have had a high percentage of their herds made up of a single breed. Herds having $\geq$75% of the milking animals of a single breed were designated as herds of that breed. The remaining herds, coded as multiple-breed herds, were only 4% 20 years ago, but have climbed to 11.5% today, most coming from the Holstein-herd category. Allelic examination is revealing the extent to which breeds are represented in the crossbreds. The procedure is based on assembling *Purebred Reference Groups (PRG)* representing 5 individual breeds (Ayrshire, Brown Swiss, Guernsey, Holsteins, and Jerseys). The procedure, referred to as Breed Base Representation (BBR), estimates for each animal genotyped the percentages of alleles in common with those in the 5 PRGs. The BBR of the primary breed for Ayrshires and Jerseys has declined below 100% over the last decade, but the changes have been smaller for the other 3 breeds.

Key words: breed composition, breed base representation, genomics

Summary

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Introduction

Breed composition of the US dairy population changed across the last two decades. This happened for various reasons including

- Shifting demand for milk products.
- Increased attention to animal longevity and fertility.
- Promotion of a few European breeds.
- Desire to capitalize on heterosis.

A few producers have experimented with 2- or 3-breed rotational crossing schemes. However, more are transitioning to another breed by using semen from the targeted breed for multiple generations. Dairy semen sales provides an indication of these changes. Holstein semen declined from 93.4% of domestic sales in 1996 to 85.9% in 2016. Jersey semen sales rose from 4.6 to 13.1% at the same time (Table 1). Several breed associations now enroll crossbreds, not eligible previously for their traditional herd books.

It has been shown that when the identification of the sire, maternal grandsire, or the maternal great-grandsire are not reported, genomic testing with a 50K chip can reveal these in over 99%, near 97%, and 92% of the cases, respectively (VanRaden and Cooper, 2015). This confirms breeds can be identified among the ancestors, even when on-farm recordkeeping is weak or non-existent. DNA testing, although not entirely random, could reveal changes in the frequency of crossbreeding.

Genomic examination can be used to show the extent to which alleles of various breeds appear to be represented in an animal's genetic makeup (VanRaden *et al.*, 2013). The procedure is based on assembling 5 *Purebred Reference Groups (PRG)*, registered artificial insemination (AI) bulls representing the individual breeds (Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), Holsteins (HO), and Jerseys (JE)). Most are recent bulls, all with milking daughters and having no other breed recorded in their 5-generation pedigree. The procedure, referred to as Breed Base Representation (BBR), estimates the percentages of alleles in common with those in the 5 PRGs for each animal genotyped.

A BBR percentage for the primary breed well below 100% reveals either crossbreeding or an outcross bloodline, but differentiating which has not been the focus of additional investigation. Animals vary and breeds have many common alleles, so assigning contributions from breed sources is not precise, i.e., actual breed contributions which sum to 100% can differ somewhat from the BBR percentages derived. The actual percentage for the primary breed could be off by 5%, or even more, due to limitations of the method.

Material and methods

Summaries were derived that illustrate the changing breed composition of U.S. dairy cattle population. These give the percentage of milking herds and cows by breed 10 and 20 years ago and today. Herds are designated as a single-breed herd if $\geq$75% of the milking cows are of a one breed. Otherwise, they are coded as a multi-breed herd. Summaries were derived also to reveal the percentage of cows that are designated by breed or as crossbreds separately in single- and multiple-breed herds compared to 10 and 20 years ago.

The demand to have genetic estimates for crossbreds has led to requesting more accurate information on breed composition and so BBR has become an integral part of Jersey breed programs. Therefore a detailed summary of the breed composition of

Table 1. Percentage of U.S. domestic semen sales in 1996, 2006, and 2016 by breed[1]

Year	Ayrshire	Brown Swiss	Guernsey	Holstein	Jersey	Milking Shorthorn	Total units of semen
1996	0.3	0.9	0.6	93.4	4.6	0.1	12,677,139
2006	0.2	0.8	0.2	90.9	7.6	0.1	18,709,887
2016	0.2	0.5	0.1	85.9	13.1	0.1	18,930,168

[1]https://www.naab-css.org/file.aspx?id=3a8dab80-6ab1-49eb-8577-dcdae5469717

Table 2. Percentage of milk recorded herds designated by breed on January 1, 1998, 2008 and 2018.

Year	AY	BS	GU	HO	JE	MS	Multiple breeds	Number of herds
1997	0.6	1.0	0.9	89.4	4.0	0.2	4.0	38,920
2007	0.5	1.1	0.7	86.5	4.8	0.2	6.2	23,005
2017	0.4	0.9	0.5	81.3	5.3	0.1	11.5	15,530

Table 3. Percentage of milk recorded cows in herds designated by the herd's breed on January 1, 1998, 2008 and 2018

Year	AY	BS	GU	HO	JE	MS	Multiple breeds	Number of cows
1997	0.2	0.4	0.3	93.4	3.3	0.1	2.4	4,446,460
2007	0.1	0.3	0.2	90.5	4.3	0.1	4.5	4,414,821
2017	0.1	0.2	0.1	80.9	7.7	<0.1	10.9	4,380,995

genotyped cows and AI bulls over recent years was derived by the Council on Dairy Cattle Breeding. One objective of this study is to show some genomic characteristics of the U.S. population over the last 2 decades.

Results and discussion

For several decades U.S. dairy owners have had a high percentage of their herds comprised of a single breed. Herds with 75% or more of their milking animals of one breed were designated as herds of that breed. Herds with no individual breed achieving 75% were coded as multiple-breed herds. Multiple-breed herds have shown considerable growth in the U.S. over the last 2 decades, primarily at the expense of Holstein herds. In 1998, herds designated as multiple-breed herds was 4.0% (Table 2). Today it has increased to 11.5%, most of which came from the Holstein designation. Holstein herds declined by 8.1 percentage points while multiple-breed herds increased by 7.5 percentage points.

Table 3 shows the percentage of cows in the single- and multiple-breed herd designations. Because AY, BS, GU, and MS have smaller herd size, the percentage of cows in these single-breed herds is lower than the percentage of herds shown in Table 2. Single-breed Jerseys represent 5.3% of herds, but have 7.7% of the cows. Four traditional breeds had about half as many cows on test as they had 20 years ago.

Table 4. The percentage of cows[1] by assigned breed in single-breed herds along with the recorded breed of their sires and dams.

Animal	AY	BS	GU	HO	JE	MS	Other breeds	Crossbreds	Number of animals
Cows	0.1	0.4	0.1	87.4	10.1	<0.1	0.1	1.7	3,629,788
Sires	0.1	0.5	0.1	87.4	11.6	0.1	0.2	0.0	3,064,037
Dams	0.1	0.4	0.1	87.1	10.5	<0.1	0.1	1.6	3,119,106

[1]For cows calving from January 1, 2017 to December 31, 2017

Table 5. The percentage of cows[1] by assigned breed in multiple-breed herds along with the recorded breed of their sires and dams.

Animal	AY	BS	GU	HO	JE	MS	Other breeds	Crossbreds	Number of animals
Cows	0.9	2.2	0.7	42.3	20.8	0.6	1.1	31.5	382,042
Sires	1.2	3.3	0.9	52.7	34.8	0.8	6.3	0.1	297,973
Dams	0.9	2.4	0.8	51.3	19.9	0.6	1.2	22.7	314,694

[1]For cows calving from January 1, 2017 to December 31, 2017

Table 6. Breed Base Representation showing the average percentage for the primary breed of genotyped cows with birth dates in 1997, 2007 and 2017 and number genotyped.

Year	AY	BS	GU	HO	JE	Crossbreeds
1997	-	97.9	100.0	98.4	99.1	-
2007	97.6	98.8	97.0	99.0	98.1	66.6 HO
2017	95.9	98.2	97.2	99.0	95.0	78.9 HO

Table 7. Breed Base Representation showing the average percentage for the primary breed of genotyped bulls with birth dates in 1997, 2007 and 2017.

Year	AY	BS	GU	HO	JE	Crossbreeds
1997	99.9	99.8	99.8	99.6	99.5	-
2007	98.0	99.7	99.7	99.6	99.3	-
2017	97.8	99.0	98.3	99.2	97.4	50.0 HO JE

Table 4 provides an examination of the breed designation of animals in the single-breed herds. It shows the breed code assigned to cows calving from July 1, 2016 to June 30, 2017, and the codes assigned to their sires and dams.

Table 5 provides a similar examination of the breed composition in the multiple-breed herds.

Tables 6 and 7 provide evidence of changes in breed composition in cows and bulls, respectively. These results confirm what seems expected from other developments reported in the industry (e.g. semen sales in Table 1). The mean BBR for genotyped Jersey cows declined from 99.1 in 1997 to 95.0 in 2017, apparently as a result of using Jersey (JE) semen on other breed animals. The BBR for Ayrshires was 95.9 in 2017, as a result of more alleles coming from Scandinavian red breeds, although based on limited number of genotyped animals.

There is evidence that BBR is impacted by the chip used for genotyping. Animals with alleles coming from other breeds (e.g., BBR of the primary breed around 87%) often receive a BBR about 4% higher if re-genotyped using a higher density chip. If the BBR is $\geq$97%, common for most animals, there is no consistent change when re-genotyped with a higher density chip.

List of references

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