Documenting Changes in Dairy Breeds in the United States including Genomic Examination using Breed Base Representation

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Possible Reasons for Changing Breeds

- **Shifting demand for different milk products; e.g., more cheese production.**

- **Producer pursuit of functional traits; e.g., reproduction, longevity.**

- **Promotion of non-traditional European breeds; e.g., Scandinavian and French breeds.**

- **Desire to capitalize on heterosis.**

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Change in U.S. Breed Composition

- **Shifts in semen sales across years provides evidence (annual reports from NAAB).**

- **Examining the breed of semen for cows and heifers <u>could</u> be used.**

- **In contrast:**

  - **Documenting breeds within calf inventory means waiting an extra year.**

  - **Documenting breeds within milk cows means waiting 3 extra years.**

Domestic Semen Sales by Breed across Time

Year	Ayrshire	Brown Swiss	Guernsey	Holstein	Jersey	Milking Shorthorn
1996	0.3	0.9	0.6	93.4	4.6	0.1
2006	0.2	0.8	0.2	90.9	7.6	0.1
2016	0.2	0.5	0.1	85.9	13.1	0.1
	↓	↓↓	↓↓↓	↓↓	↑↑↑	

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Objective:

Semen sales only provides a framework for what could have happened. By documenting further, one can determine on which animals the semen was used.

- Review the composition of U.S. animals from producers' recorded breed for the milking herds.

- Review the composition of genotyped animals using a DNA tool called Breed Base Representation.

Categorization of U.S. Herds by Breed:

- **Herds enrolled on the national milk recording program (called DHIA) are each assigned a breed category.**

- **If a producer codes ≥75% of the cows as the same breed, the herd is referred to as a single-breed herd of that breed.**

- **If <75% of cows belong to one breed, the herd is labeled a multiple-breed herd.**

- **This labeling appears in several of the remaining slides.**

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Percentage of Milk Recorded Herds coded by Breed

Year	Ayrshire	Brown Swiss	Guernsey	Holstein	Jersey	Milking Shorthorn	Multiple-Breed Herds
1998	0.6	1.0	0.9	89.4	4.0	0.2	4.0
2008	0.5	1.1	0.7	86.5	4.8	0.2	6.2
2018	0.4	0.9	0.5	81.3	5.3	0.1	11.5
	↓		↓↓	↓↓	↑	↓	↑↑↑

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Percentage of Milk Recorded Cows in Herd by Breed

Year	Ayrshire	Brown Swiss	Guernsey	Holstein	Jersey	Milking Shorthorn	Multiple-Breed Herds
1998	0.2	0.4	0.3	93.4	3.3	0.1	2.4
2008	0.1	0.3	0.2	90.5	4.3	0.1	4.5
2018	0.1	0.2	0.1	80.9	7.7	<0.1	10.9
	↓↓	↓↓	↓↓↓	↓↓	↑↑	↓	↑↑↑

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Breed of Cows Calving (2017) in Single-Breed Herds

Animal	AYR	BSW	GUE	HOL	JER	Milking Shorthorn	Other breeds	Cross-breds
Cows	0.1	0.4	0.1	87.4	10.1	<0.1	0.1	1.7
Sires	0.1	0.5	0.1	87.4	11.6	0.1	0.2	0.0
Dams	0.1	0.4	0.1	87.1	10.5	<0.1	0.1	1.6

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Breed of Cows Calving (2017) in Multiple-Breed Herds

Animal	AYR	BSW	GUE	HOL	JER	Milking Shorthorn	Other breeds	Cross-breds
Cows	0.9	2.2	0.7	42.3	20.8	0.6	1.1	31.5
Sires	1.2	3.3	0.9	52.7	34.8	0.8	6.3	0.1
Dams	0.9	2.4	0.8	51.3	19.9	0.6	1.2	22.7

Genotypes in CDCB-Cooperators' Database (2/18)

Breed	Males	Females	Total
Ayrshire	1,980	6,137	8,117
B. Swiss	27,774	7,175	34,949
Guernsey	786	2,919	3,705
Holstein	240,556	1,631,683	1,872,249
Jersey	27,394	207,397	234,791
Total of 5 breeds	298,490	1,855,311	2,153,811

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Ancestry Discovery through Genotyping

- **Ancestors (often 3 generations) can be verified or uncovered through genotyping, whether reported incorrectly, or not at all.**

- **When the ID of the sire, maternal grandsire, or great-grandsire is not reported, their identity can be revealed (with a 50K chip) in over 99, 97, and 92% of the cases.**

  - **IT WORKS BECAUSE: all AI bulls are genotyped, most tested animals are sired by AI bulls. The same would be possible for cows if all were genotyped.**

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Breed Discovery through Genotyping

- **Because DNA can determine the ancestors, it can reveal the breed composition of those ancestors.**

- **Usually the DNA from different breeds can be detected, regardless of whether pedigree records are missing.**

- **Outcross bloodlines will confuse this picture somewhat.**

The Development of Breed Base Representation

- **A need to have genetic indexes on all animals, specific-ally crossbreds, led Paul VanRaden and his colleagues to develop Breed Base Representation (or BBR).**

- **What is BBR? BBR estimates the degree to which the alleles in each individual animal genotyped are in common with the alleles in the 5 purebred reference groups.**

- **WHY 5 BREEDS? That's the number in CDCB genomic database.**

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BBR Interpretation

- **The more alleles an animal has in common with its recorded breed reference group, the higher its BBR for that primary breed.**

- **The percentages were restricted to be between 0 and 100%. Percentages less than 100 can reveal the presence of outcross bloodlines or crossbreeding, but knowing which is sometimes cloudy.**

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Average BBR Percentage of the Primary Breed (Cows)

Year	Ayrshire	Brown Swiss	Guernsey	Holstein	Jersey	Crossbreds
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

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Average BBR Percentage of the Primary Breed (Bulls)

Year	Ayrshire	Brown Swiss	Guernsey	Holstein	Jersey	Crossbreds
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 HOL/JER

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Conclusion

- **An increasing percentage of U.S. herds have cows and heifers of more than one breed.**

- **Breeds composition has shifted over the last decade with increasing numbers of Jerseys and crossbreds.**

- **The BBR of the primary breed for Ayrshires and Jersey declined below 100%, but any change was less for the other 3 breeds.**

- **Having BBRs takes us a step closer to producing genetic evaluations for crossbreds.**

Acknowledgment

- **All U.S. dairy producers and industry support people who provided data to CDCB's national database.**

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