

CDCB tools for the improvement of the Jersey breed

21st International Conference of the World Jersey Cattle Bureau

150th Anniversary of the American Jersey Cattle Association

Canton, OH - June 30, 2018

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Outline

- CDCB Overview
- The genomics era
- Dealing with the reality of crossbreds
- Opportunities
- Take home



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CDCB OVERVIEW



COUNCIL ON DAIRY CATTLE BREEDING

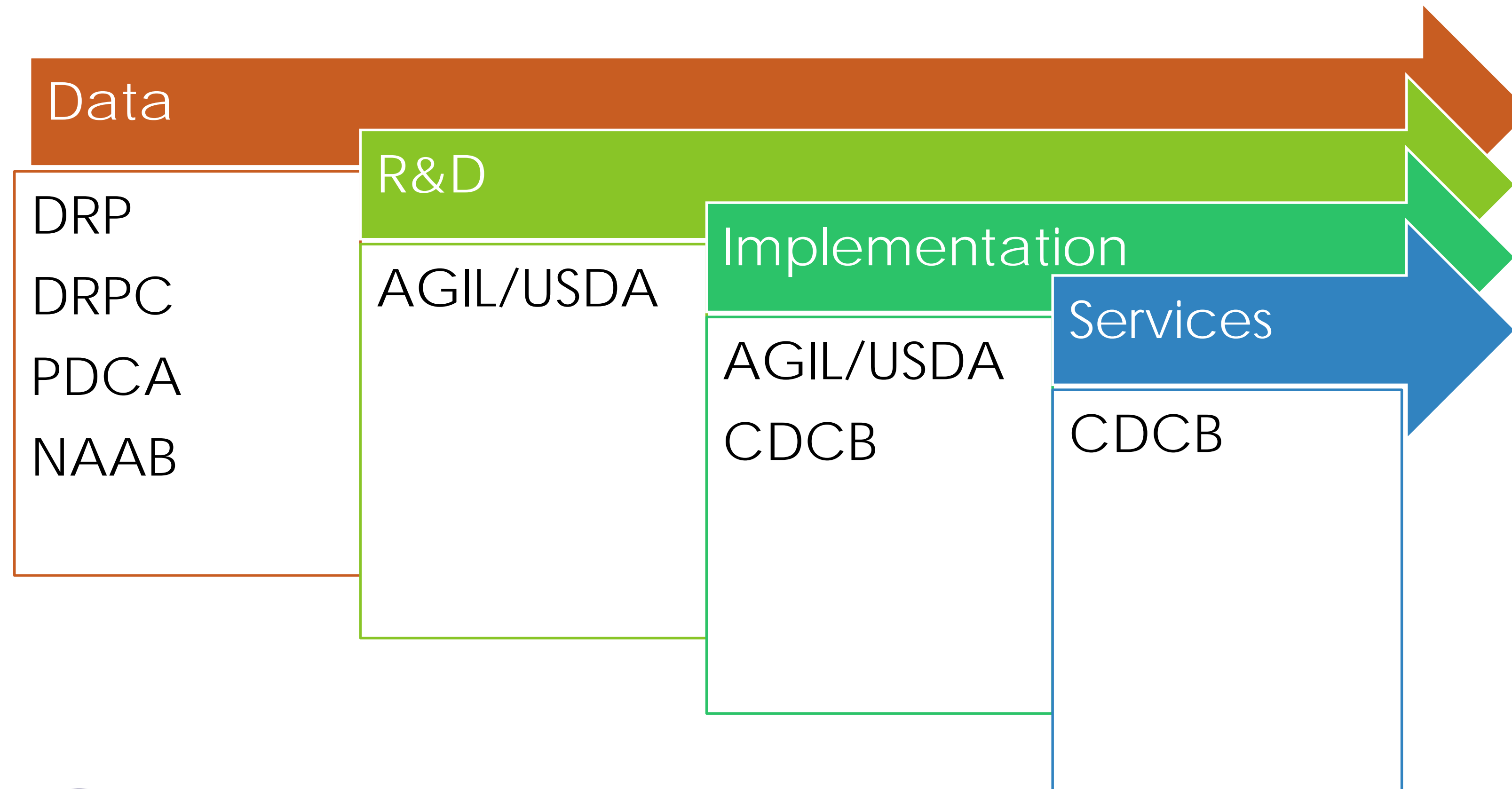
The Council on Dairy Cattle Breeding (CDCCB) is an industry collaboration that benefits the dairy community by promoting dairy cattle improvement and establishing the gold standard of dairy genetics.

Organization



- 12 voting members (3 from each sector)

US Genetic Evaluation Process



U.S. Genetic &
Genomic
Evaluations

AgSource Cooperative Services
Arizona DHIA
Dairy Lab Services
Dairy One Cooperative Inc.
DHI Cooperative Inc.
DHIA West
Gallenberger Dairy Records
Heart of America DHIA
Idaho DHIA
Indiana State Dairy Association
Integrated Dairy Herd Improvement
Jim Sousa Testing
Lancaster DHIA
Mid-South Dairy Records
Minnesota DHIA
Northstar Cooperative DHI Services
Puerto Rico DHIA
Rocky Mountain DHIA
San Joaquin DHIA
Southern DHIA Affiliates
Tennessee DHIA
Texas DHIA
Tulare DHIA
United Federation of DHIA's
Washington State DHIA

Dairy Records Providers (25)

ABS Global. Inc.
Alta Genetics USA
American Jersey Cattle Association
Bio-Genesys Ltd.
Genetic Visions-ST LLC
Genex Cooperative. Inc.
Holstein Association USA. Inc.
Holstein Canada
National Association of Animal Breeders, Inc.
Neogen Corporation dba GeneSeek
New Generation Genetics. Inc.
Select Sires Inc.
Semex Alliance
VHL Genetics
Zoetis Genetics

Genomic Nominators (15)

American Guernsey Association
American Jersey Cattle Association
American Milking Shorthorn Society
Brown Swiss Cattle Breeders' Association
Holstein Association USA. Inc.
Red and White Dairy Cattle Association
U.S. Arshire Breeders' Association

Purebred Dairy Cattle Association (7)

Agriculture and Horticulture Development Board
ANAFI
CDN
Interbull Centre (34)
Intergenomics (8)
Qualitas
Vit

International Partners (7+)

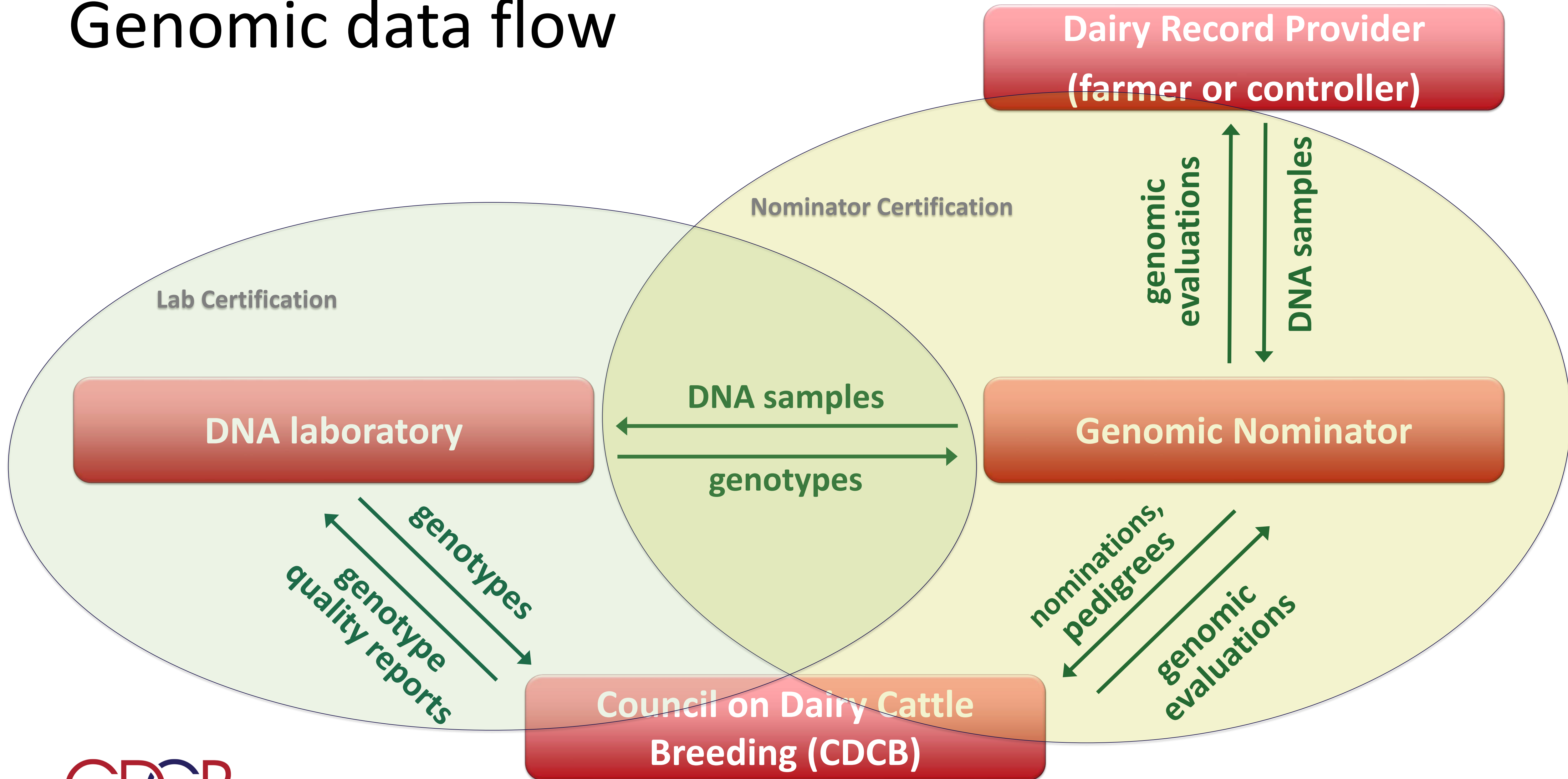
AgriTech Analytics
AgSource Cooperative Services
Amelicor
Dairy Records Management Systems

Dairy Records Processing Centers (4)

Bio-Genesys Ltd.
EuroFins Bio Diagnostics Inc.
Genetic Visions-ST LLC
Neogen Corporation dba GeneSeek
VHL Genetics
Weatherbys Scientific
Zoetis Genetics

Genomic Laboratories (7)

Genomic data flow





Quality Certification Services Inc.



Field Service Providers



Laboratories



Meter Centers

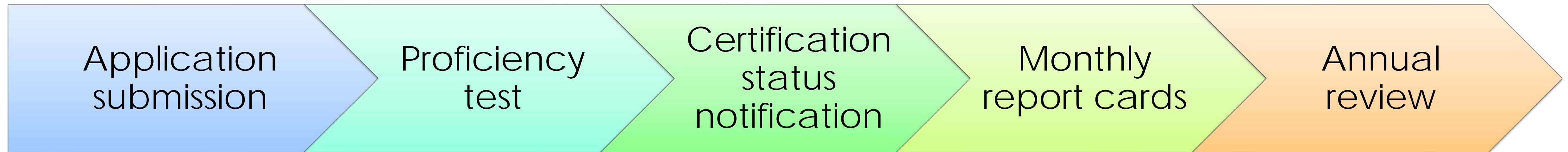


Meter Technicians



Dairy Records Processing Centers

CDCB Genomic Data Certification Process



The CDCB is the result of the U.S. dairy industry working together for the common good, empowering dairy farmers to fulfill their essential role of feeding the world.

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THE GENOMICS ERA

Cows on DHIA per breed

Year	Jersey	%	Holstein	Ayrshire	Brown Swiss	Guernsey
1990	163,085	3.5	4,358,298	16,818	26,431	40,432
2000	157,845	3.8	3,968,052	8,235	16,384	12,846
2005	169,624	4.5	3,594,321	6,643	14,042	8,758
2010	220,419	5.5	3,729,507	4,865	12,086	5,904
2014	273,645	7.0	3,594,321	4,132	11,179	4,340
2015	307,622	7.7	3,668,546	3,891	10,585	3,989
2016	320,400	8.1	3,615,132	3,436	10,291	4,330
2017	321,706	8.2	3,594,876	3,205	10,079	3,948
2018	338,697	8.7	3,545,514	2,600	10,198	3,613
Trend	↑↑		↓	↓↓	↓	↓↓

U.S. domestic semen sales per breed

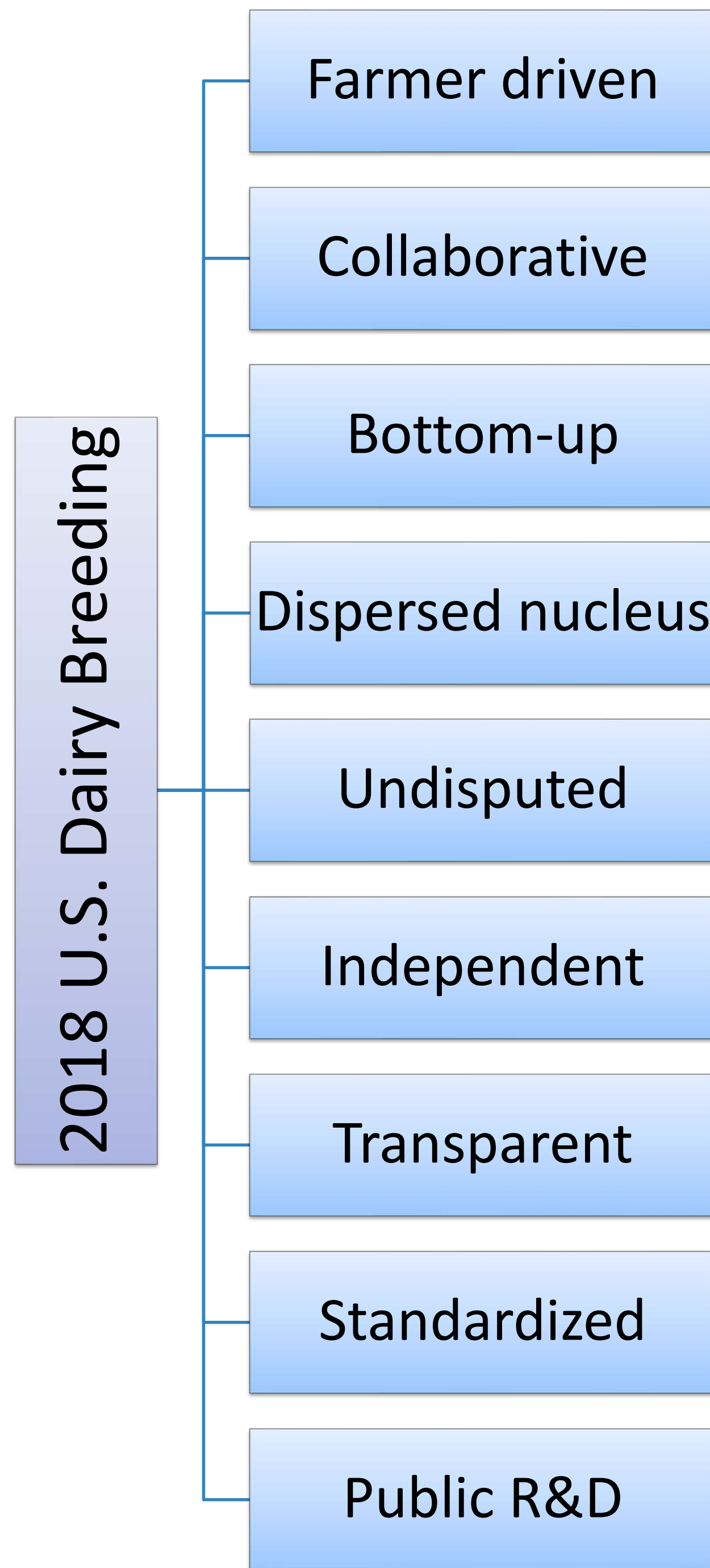
Year	Jersey	%	Holstein	Ayrshire	Brown Swiss	Guernsey
1980	532,746	4.0	12,089,797	75,866	139,104	326,105
1990	610,154	4.6	12,276,057	51,866	251,834	176,525
2000	771,160	5.8	12,271,730	33,955	118,954	55,662
2005	1,362,705	7.5	16,257,394	41,044	165,495	44,101
2010	1,985,997	9.1	19,306,931	54,229	125,162	33,870
2015	3,053,900	12.9	20,230,156	41,257	103,232	30,093
2016	2,947,587	13.1	19,299,126	39,569	109,660	29,326
2017	3,435,468	14.8	19,540,530	32,639	109,562	27,134
Trend	↑↑↑		↑	↓	↓	↓↓↓

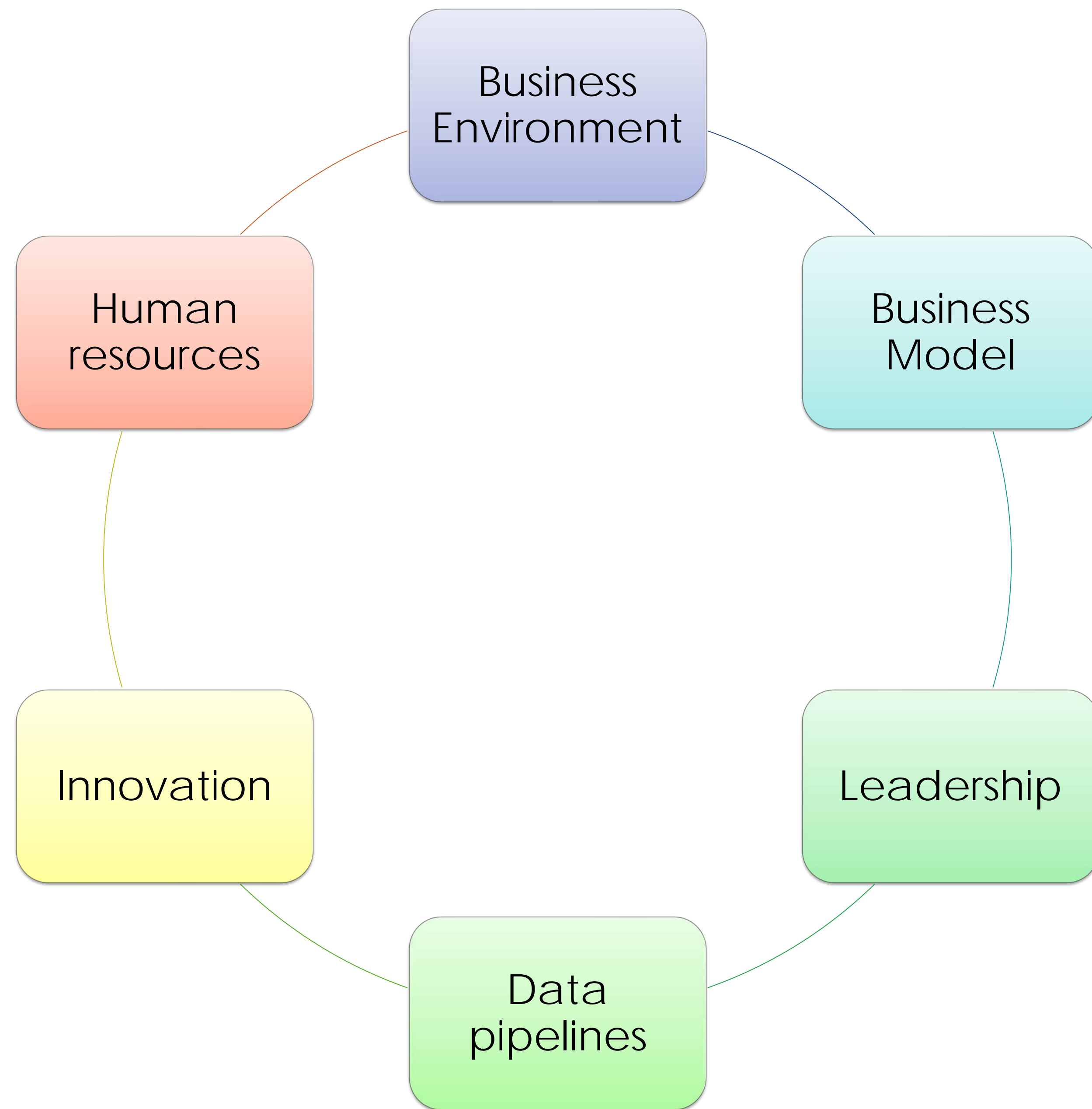
Gain in Standardized Fat + Protein (lbs.)

Difference with Base Year	Jersey	Holstein	Ayrshire	Brown Swiss	Guernsey
2011 vs. 2010	42	24	0	17	-1
2012 vs. 2010	79	58	14	46	17
2013 vs. 2010	123	87	24	51	20
2014 vs. 2010	175	111	60	67	43
2015 vs. 2010	191	129	72	86	62
2016 vs. 2010	231	160	82	89	60

Genotypes in CDCB-Cooperators' Database (7/18)

Breed	Reference		Young		Total
	Male	Female	Male	Female	
Holstein	40,813	480,454	213,658	1,360,433	2,095,358
Jersey	5,937	89,287	23,265	155,872	274,361
Brown Swiss	7,037	2,514	22,071	5,471	37,093
Ayrshire	843	370	1,211	6,193	8,617
Guernsey	490	984	380	2,191	4,045
Total	55,120	573,609	260,585	1,530,160	2,419,474





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
	↓↓	↓↓	↓↓↓	↓↓	↑↑	↓	↑↑↑

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

Animal	AYR	BSW	GUE	HOL	JER	Milking Shorthorn	Other breeds	Cross-breeds
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

Changes in breed composition in the U.S.

- 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.
- A number of herds have used Jersey bulls on cattle of other breeds because of a shortage of Jersey replacements to fill their demands
- The number of crossbreds in US herds have increased by 400% in the last decade

Changes in breed composition in the U.S.

- Production for Jerseys has been increasing at an impressive rate
- Genomics has substantially increased genetic gains and produced new competitive opportunities within the dairy industry
- Breeds can only compete in the genomic era if they have a large reference base

Reality check

- Dairy industry business environment is changing rapidly.
 - Are our business models still relevant in the new environment?
 - How are we securing innovation?
 - Is the future leadership part of the conversation?
 - New players: can we afford NOT to work with (for) them?

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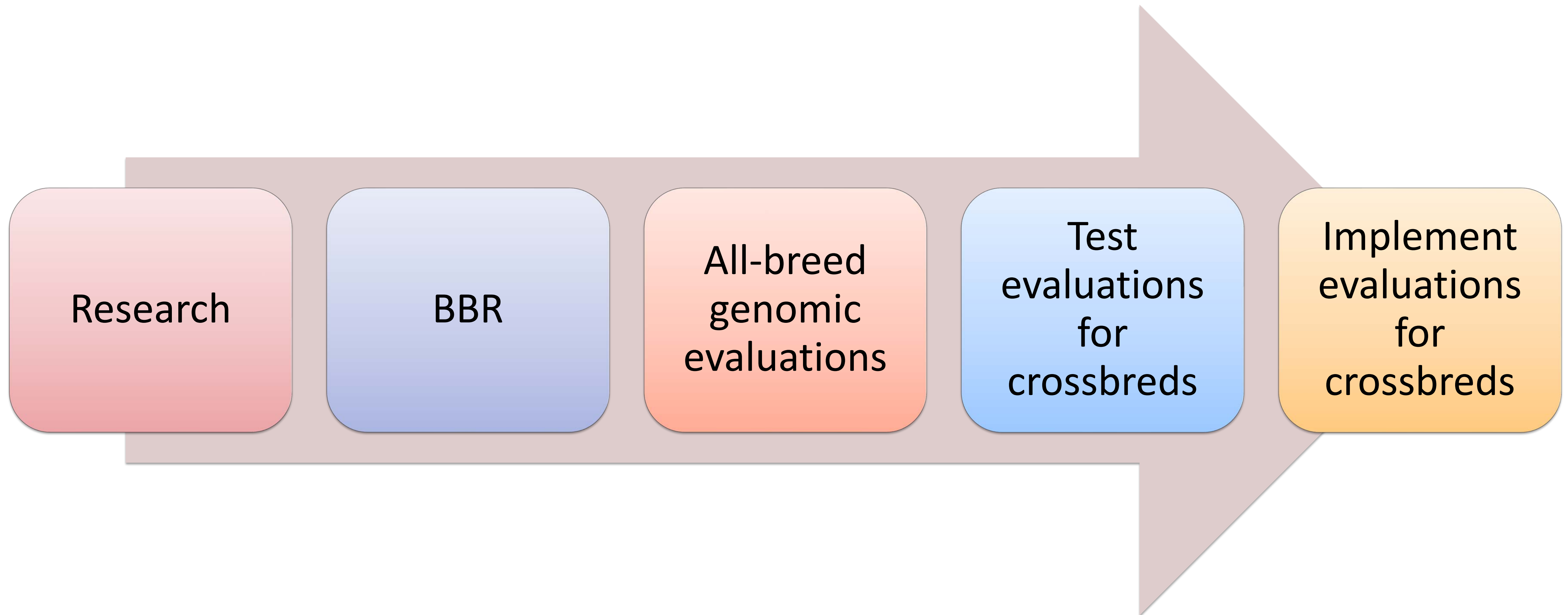
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DEALING WITH THE REALITY OF CROSSBREDS

Handling crossbred genotypes within a purebred framework

- Over 20,000 genotyped animals received no genomic predictions because they don't meet the minimum genomic standards for purebreds
- Genomic predictions in the U.S. rely on separate reference populations for each breed
- Worldwide attempts of calculating genomic predictions for crossbreds using mixed reference populations have delivered inconsistent results so far

The route to estimate genomic PTAs for crossbreds



Two-step Crossbred Genomic Evaluations

(Olson et al., 2012; VanRaden & Cooper, 2015)

- Crossbred phenotypes are extracted and EBV calculated using SNP effects, frequency and inbreeding for each of the 5 genomic breeds
- Marker effects for each breed are blended by BBR to compute evaluations for crossbreds

Main research conclusions (Tooker et al., 2017)

- Accurate GPTAs computed for crossbreds as weighted average of purebred marker effects
- Genomic evaluations of purebreds change little when computed on all-breed scale
- Gains small from multi-trait, multi-breed

Breed Base Representation (BBR)

Breed Discovery through Genotyping

- As DNA can determine who the parents and grandparents are, it can also indicate the breeds of those ancestors
- DNA markers from different dairy breeds can be detected, regardless of whether or not pedigree information is limited or missing

Breed Base Representation (BBR) Defined

- The BBR procedure estimates the similarity of alleles present in 5 purebred reference groups to those of each individual genotyped
- If breeds other than AYR, BSW, GUE, HOL and JER are part of the animal's ancestry then BBR will not be accurate

BBR Interpretation

- BBRs for the primary breed can be lower than 100% because the animal is an outcross to the primary population or because it has one or more other breeds somewhere in the pedigree.
- Even animals whose ancestors have been true purebreds for many generations often obtain a BBR percentage 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 lower usually indicates evidence of crossbreeding.

U. of Minnesota Holstein Selection Project

- The BBRs for an outcross animals will be shown in the next slide. It shows a control bull having “1960s Holstein” genetics from the University of Minnesota’s selection project. This bull has a relatively low relationship to today’s Holstein population because the alleles in the breed have changed over the last half-century.

BBR Outcross Example

- Case: control bull having “1960s Holstein” genetics from the University of Minnesota’s selection project
- This bull has a relatively low relationship to today’s Holstein population because the alleles in the breed have changed over the last half-century
- This bull was tested and had a BBR of 93% Holstein. Other percentages were Ayrshire 3%, Brown Swiss 1%, Guernsey 1%, and Jersey 2%
- Other bulls from the same study were as low as 87%

BBR Presentation

- Reference groups are updated regularly
- BBRs is calculated only once, unless genotyped with a higher density chip
- CDCB Decision: animals that have a BBR derived of greater than or equal to 94 for a breed are considered to have one-breed background and will be expressed as 100% for that breed, and other breeds' percentages will be set to zero

BBR Distribution

- Breed associations receive a file of BBRs for animals if their breed code has the highest percentage
- Nominators receive the BBRs for the animals that they nominated
- Official BBRs are a prerogative of each breed association, so publication should adhere to the official breed policy
- CDCB does not make BBRs public

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

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

All-Breed Genomic Evaluations

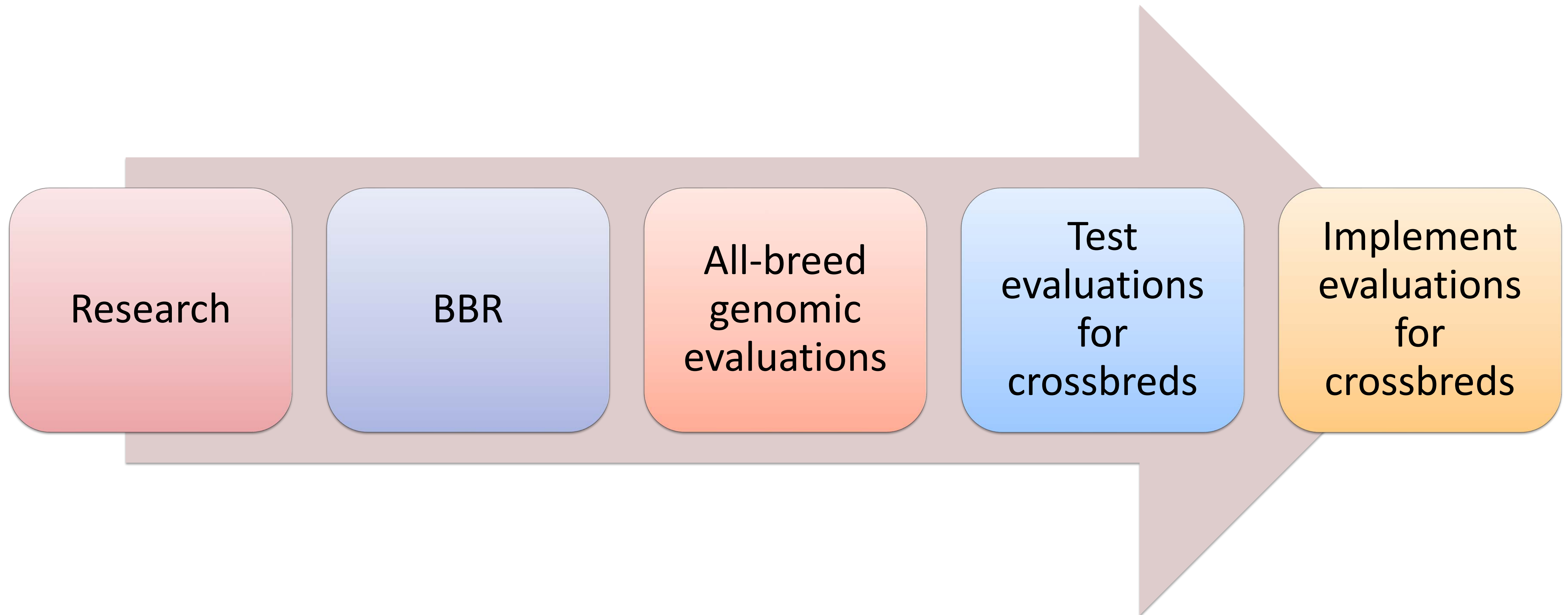
All-breed system extended to genomic evaluations

- **2007**
 - Conventional evaluations combining data for animals of all breeds are calculated on an all-breed genetic base and then converted back to within breed bases before official release
- **April 2018**
 - All-breed system also applied to genomic evaluations
 - Separate marker effects for each breed still computed
 - Parent averages (PA) calculated using the entire pedigree across breeds
 - More accurate evaluations for animals with other breeds in pedigree

Impact of all-breed genomic evaluations

- Most affected:
 - PTAs for those animals with a second breed in their pedigree
 - Jersey and Ayrshire breeds - higher proportion of animals with some percentage of other-breed genetics in their current population
- All animals affected to a certain degree
 - Improved accuracy of the prediction will bring more stability to the evaluations

The route to estimate genomic PTAs for crossbreds



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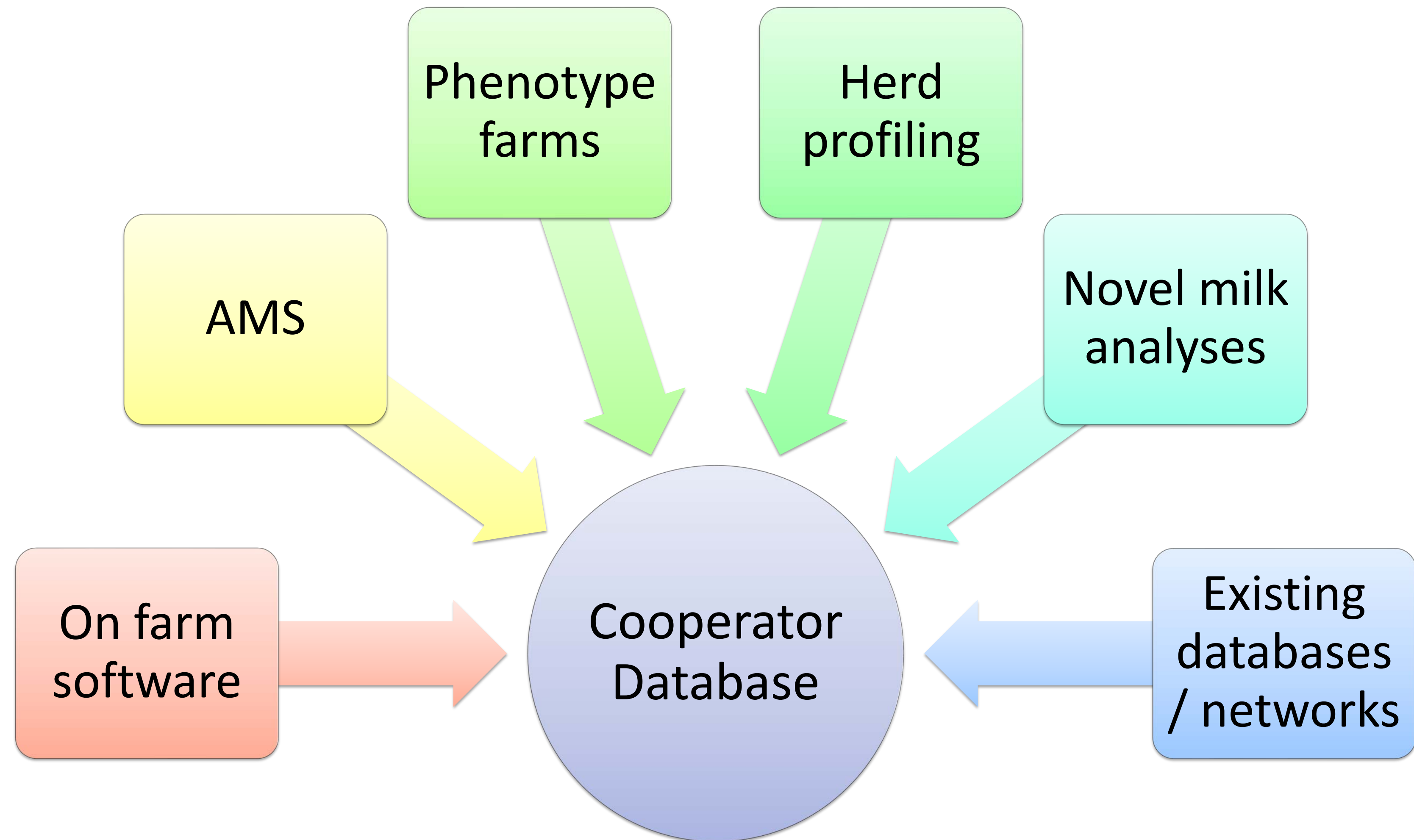
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OPPORTUNITIES

Traits recently added to the CDCB portfolio

- Cow livability
- Gestation length
- Health traits (Holstein)
 - Milk fever, displaced abomasum, ketosis, clinical mastitis, metritis, retained placenta

New data



Expected enhancements to CDCB evaluations

- Include crossbred animals in genomic evaluations
- Develop residual feed intake evaluations
- Update Predictive SNPs (77K)
- Revisit fertility and calving traits evaluations

Research and Development

- CDCB is engaged with the Dairy Innovation Center in developing a sustainable innovation framework for the U.S. dairy industry



Acknowledgments:

- All dairy producers and industry support people who provided data to CDCB's national database
- Paul VanRaden, Katie Olson, Melvin Tooker and Tabatha Cooper who developed BBR
- CDCB staff



Paintings by Thaís Cassel
sites.google.com/view/thaiscasselstudio

Thank you!
www.uscdcb.com