

AGIL REPORT 2023

Milking Speed, Cloning, Age-Season-Parity Factors,
& Planned Research

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MILKING SPEED:

Data Trends, Udder Health, & Preliminary PTAs

**Asha Miles, Robert Fourdraine, Kristen Parker Gaddis,
Steven Sievert, Jeffrey Bewley, Sophie Eaglen, Jay Weiker,
Jana Hutchison, and Joao Dürr**



Agricultural Research Service
U.S. DEPARTMENT OF AGRICULTURE



PROPOSED RESEARCH

- OBJ. 1:** Assemble a high-resolution dataset pertinent to MS representing different dairy breeds, equipment manufacturers, parlor types, and milking management strategies
- OBJ. 2:** Characterize MS for herds grouped by equipment manufacturer and parlor type and assess the impact of additional system effects on the phenotype
- OBJ. 3:** Characterize any biological effects that impact MS, especially concerning udder health
- OBJ. 4:** Standardize MS trait definition and estimate heritability to determine its suitability for selection

AVAILABLE DATA



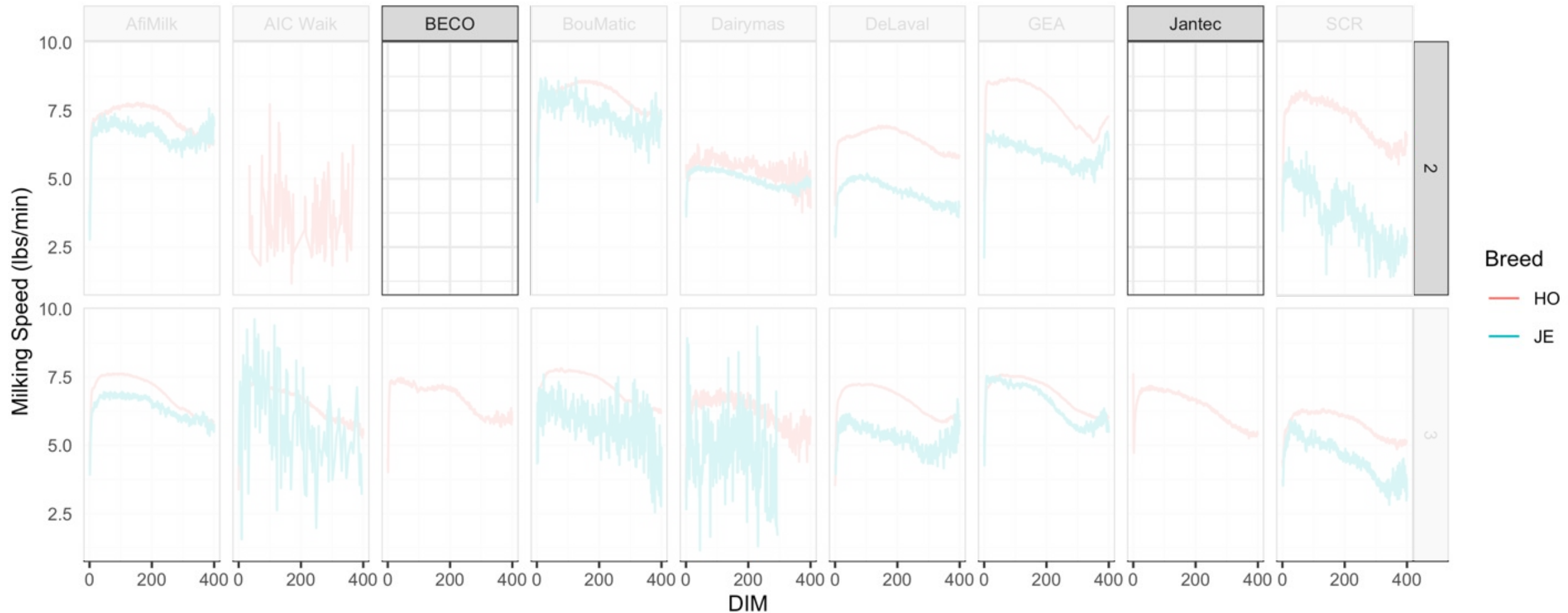
Demographics

~300 herds
>230,000 cows
>300,000 lactations
>40 million observations

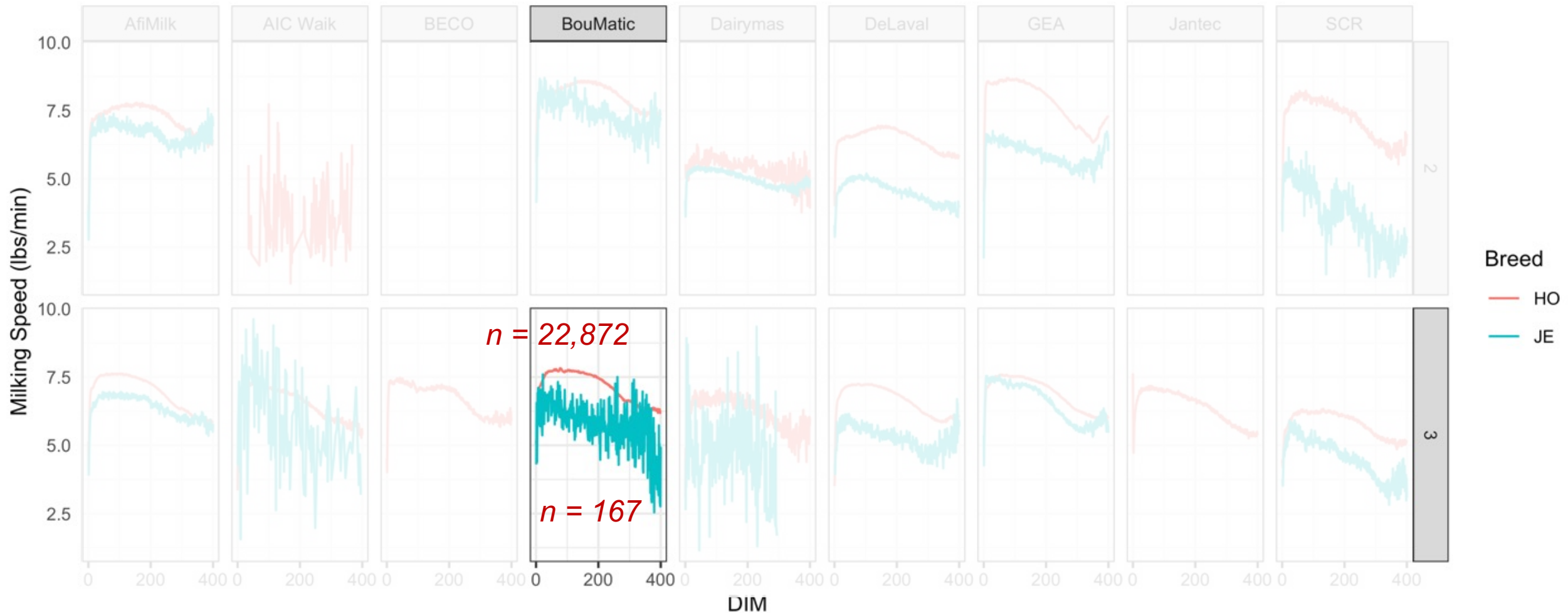
31 States
6+ Breeds
11 OEMs

DeLaval	80
GEA	75
Lely	47
Boumatic	46
AfiMilk	45
SCR	13
DairyMaster	10
AIC Waikato	5
AMS Galaxy	3
Jantec	2
Universal	2

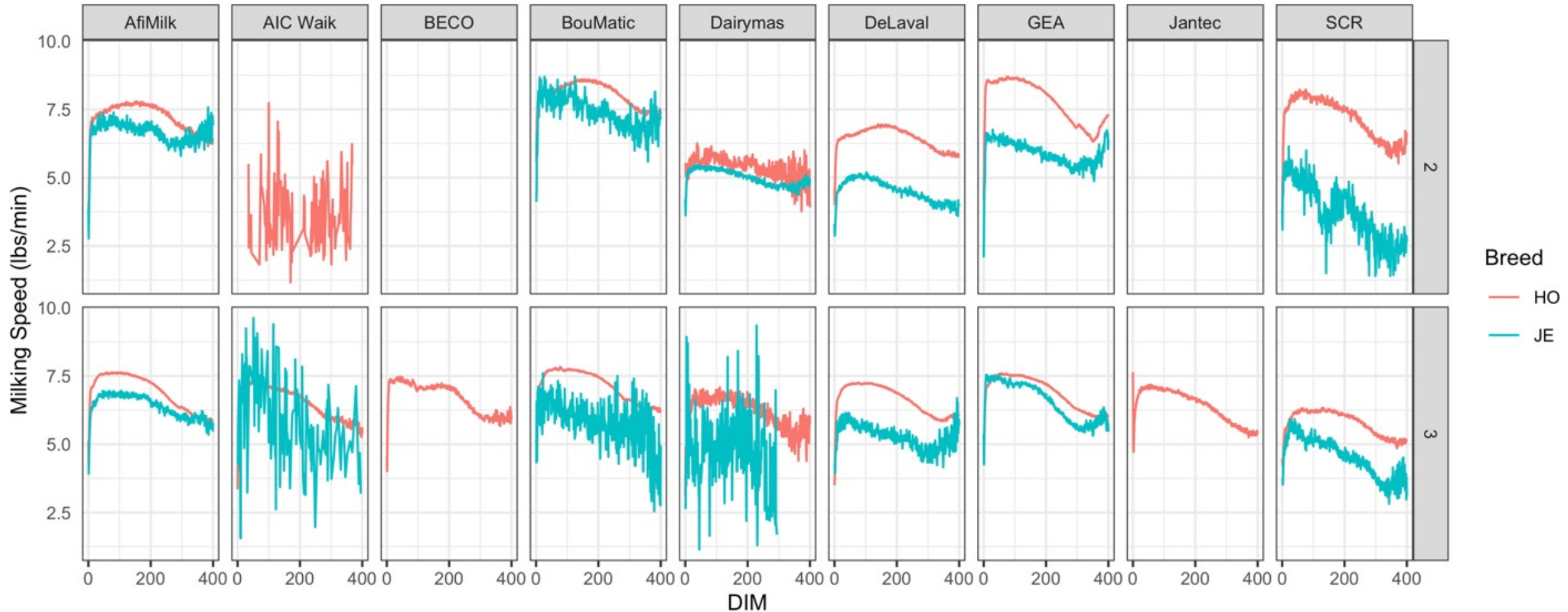
OEM, FREQUENCY, & DIM EFFECTS



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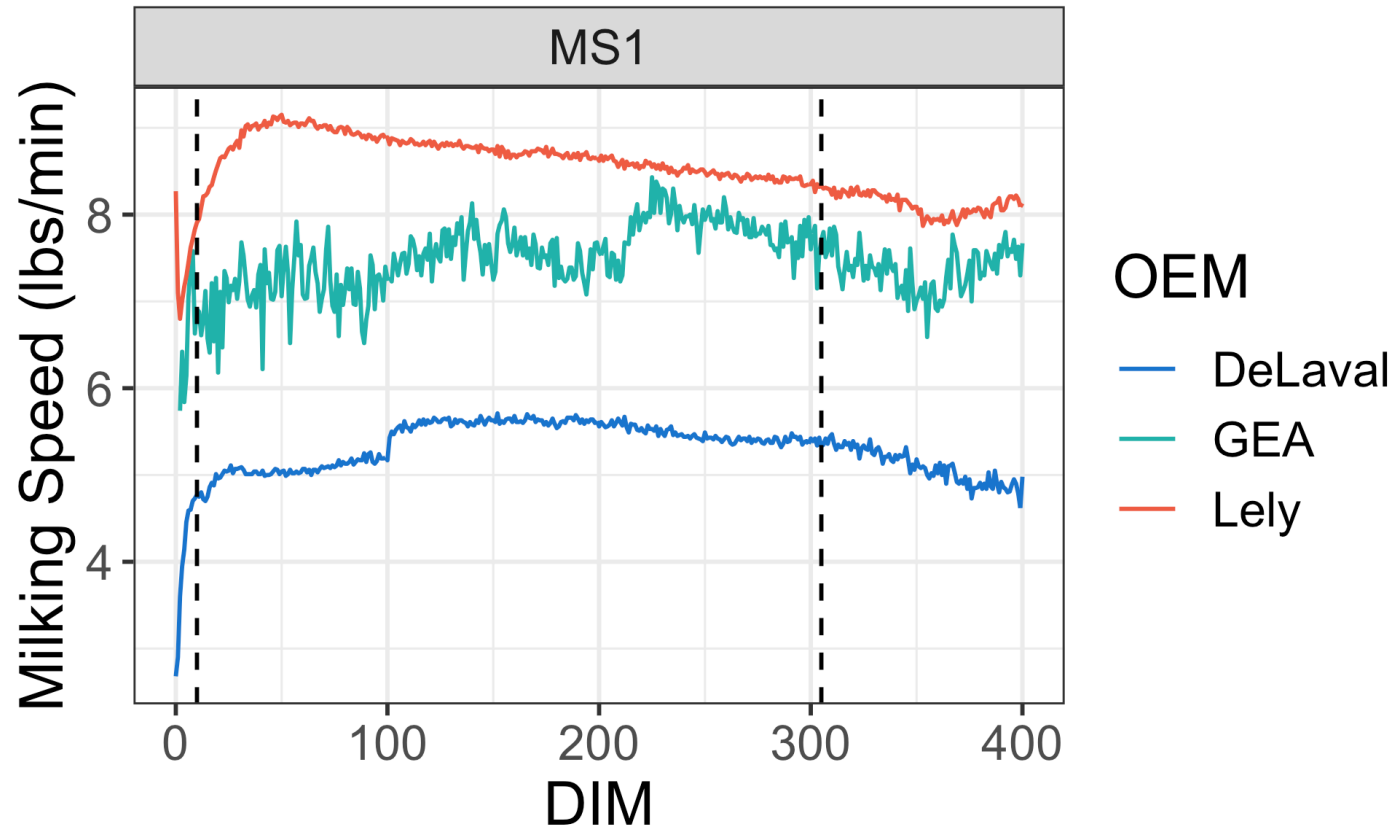


OEM, FREQUENCY, & DIM EFFECTS



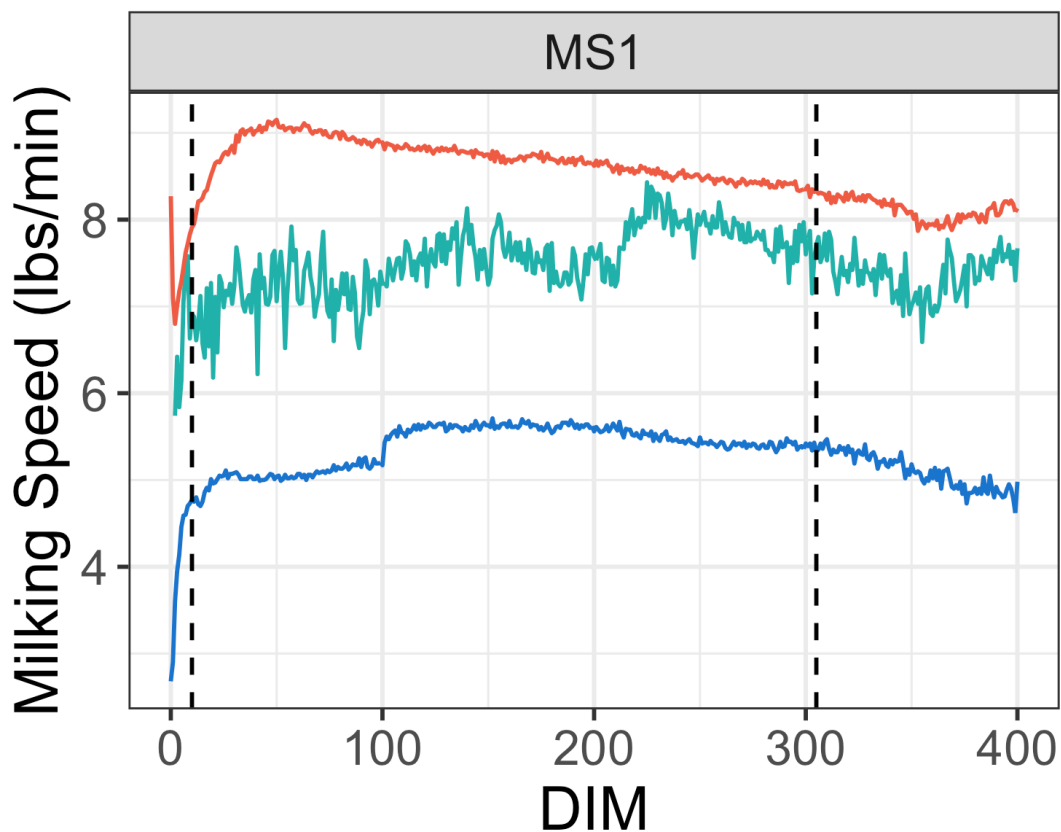
AMS & OEM EFFECTS

Holstein Only



AMS & OEM EFFECTS

Holstein Only



OEM
— DeLaval
— GEA
— Lely

**THIS DOES NOT SUGGEST
COWS MILK MORE SLOWLY
ON A DELAVAL SYSTEM**

It is an artifact of how each OEM
measures milking duration

UDDER HEALTH; MILK COMPONENTS

HOLSTEIN

	SCS	FAT %	PROTEIN %
2X	-0.02*	0.10***	0.13***
3X	-0.04***	0.04***	0.06***
AMS	-0.18***	-0.27***	-0.29***

JERSEY

	SCS	FAT %	PROTEIN %
2X	-0.13***	-0.07 ^t	-0.24***
3X	-0.13***	-0.14***	-0.27***
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- Average MS for all milkings on a test day
- Correlated with SCS, Fat, and Protein on respective test day
- No statistically significant association with clinical mastitis
- **Linear correlations may mask trends for extremes (very slow, very fast)**

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WHAT'S NEXT?

PTAs/HERITABILITIES

1. **Average MS (lbs/min) over all available data**
 - a) *Fixed effects: breed, parity, lactation length, OEM*
 - b) *n = 20,000 cows with complete lactations (1 year)*



PRELIMINARY RESULTS

$$h^2 = 0.37$$

Genetic Correlations

SCS	0.39
Milk Yield	0.14
NM\$	0.08

Mean REL **0.67**

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 - a) *Fixed effects: breed, parity, lactation length, OEM*
 - b) *n = 20,000 cows with complete lactations (1 year)*
2. Average MS (lbs/min) from test-days only
3. Primiparous cows only



PRELIMINARY RESULTS

$$h^2 = 0.37$$

Genetic Correlations

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Milk Yield **0.14**

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Mean REL **0.67**

Modeling identical animals and clones in genetic evaluations

For December 2023 Implementation

Paul VanRaden, Gary Fok, Sajjad Toghiani, and Ezequiel Nicolazzi



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HOW ARE CLONES REPORTED?

- **Multiple birth codes:**
 - 4,762 pairs of natural identical twins (code 2 and verified by genotype)
 - 1,776 split embryos (code 4)
 - 530 nuclear transfer clones from embryos, calves, or adults (code 5)
- **Clones make up ~0.1% of genotyped animals (~7 million)**

Code	Birth description
1	Single
2	Multiple birth (not from embryo transfer)
3	Birth from embryo transfer
4	Split embryo (artificially)
5	Clone from nuclear transfer
6	Embryo pedigree (implantation date stored as birth date)

CLONES MULTIPLY THEIR CONTRIBUTION

Apple – 2011 World Dairy Expo



Photo by Nina Linton
Apple had 361 progeny.

Apple-3 – 2013 World Dairy Expo



Malcolm, D. 2019. [KHW Regiment Apple-Red-ET – Everything and more.](#)
Photo by The Bullvine. **Apple's 9 clones added 325 more progeny.**

CHANGES IN HOW WE MODEL CLONES

- Previously, pedigree matrix treated clones as full sibs
- New model stores a “source animal” for each identical group, then switches dam/sire ID to source ID
- Keeps separate permanent environment effect for each clone

Example results:

- Calf born in 2020
(HO840003218920809)
 - Maternal great grandsire was a clone of the paternal 2nd great grandsire (ManOMan and ManOMan2)
 - Pedigree inbreeding of 9.8% corrected to 10.6%
 - Genomic inbreeding was 13.5%

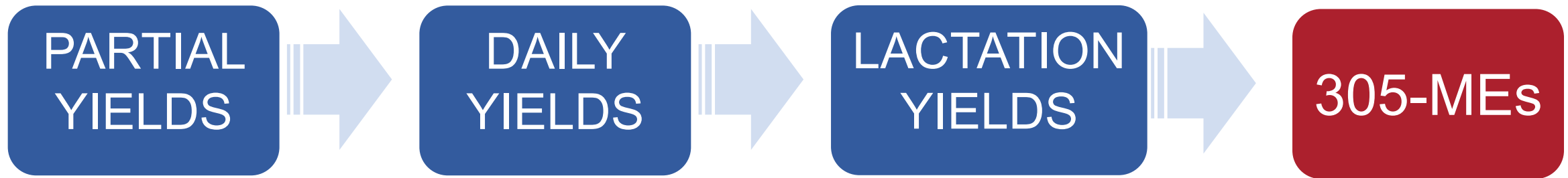
STANDARDIZING LACTATION YIELDS

Age-parity-season-region corrections for fair comparisons
across individual cows & environments

For December 2023 Implementation

**Asha Miles, Paul VanRaden, Jana Hutchison, Gary Fok, Mike
Schutz**

HOW DO WE COMPARE YIELDS?



- **Genetic selection changes maturity patterns** (Norman et al 1995)
- **Mature Equivalent factors last estimated in 1994**
 - **Corrected for parity, age, season of freshening, previous days open, geographical region, and 2X milking**

ESTIMATING NEW FACTORS

DATA

Lactation Records

Milk: 101.5 million

Fat: 100.5 million

Protein: 81.2 million

UNCHANGED

2X Milking Frequency
Previous Days Open

IMPROVED

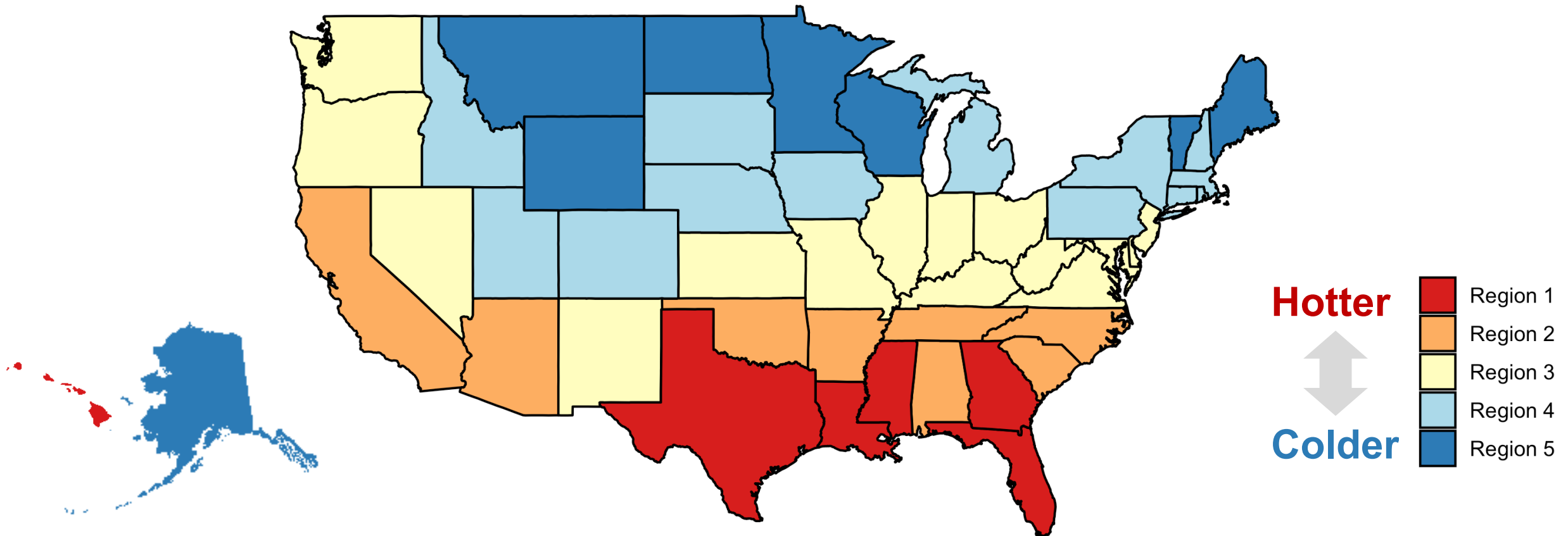
SEASON-REGION

~~3 Geographical Regions~~ → **5 Climate Regions**
~~Within Breed~~ → **Across Breed**

AGE-PARITY

~~Age Groups~~ → **Age in Months**
~~Mature Age~~ → **Average Age (36mo)**

NEW CLIMATE-BASED REGIONS

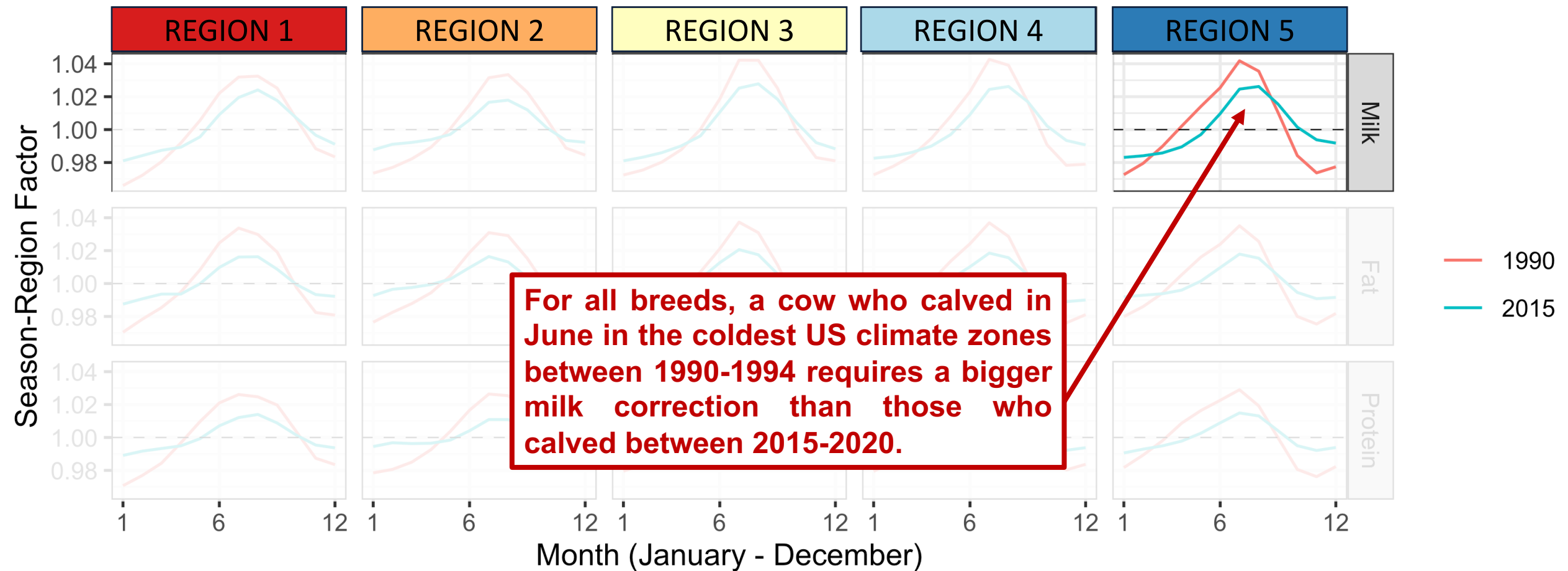


International Energy Conservation Code (IECC). 2021.

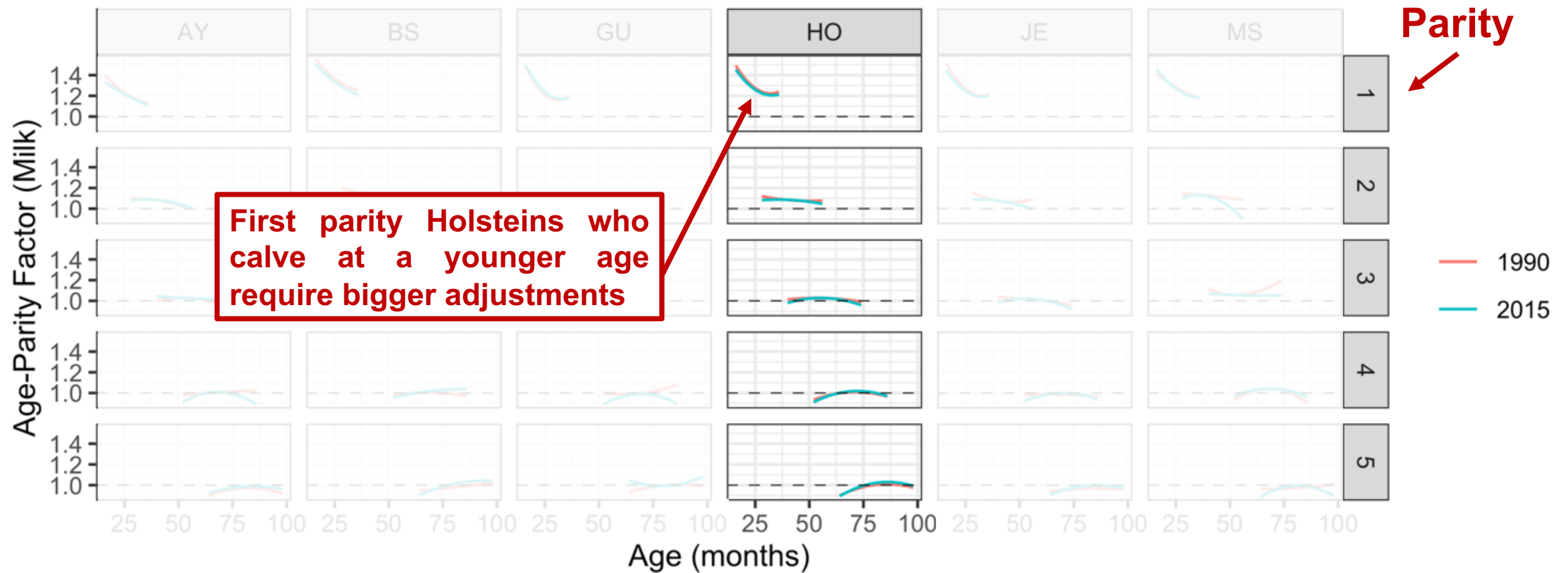
<https://codes.iccsafe.org/content/IECC2021P2/chapter-3-ce-general-requirements>

Miles et al., in prep

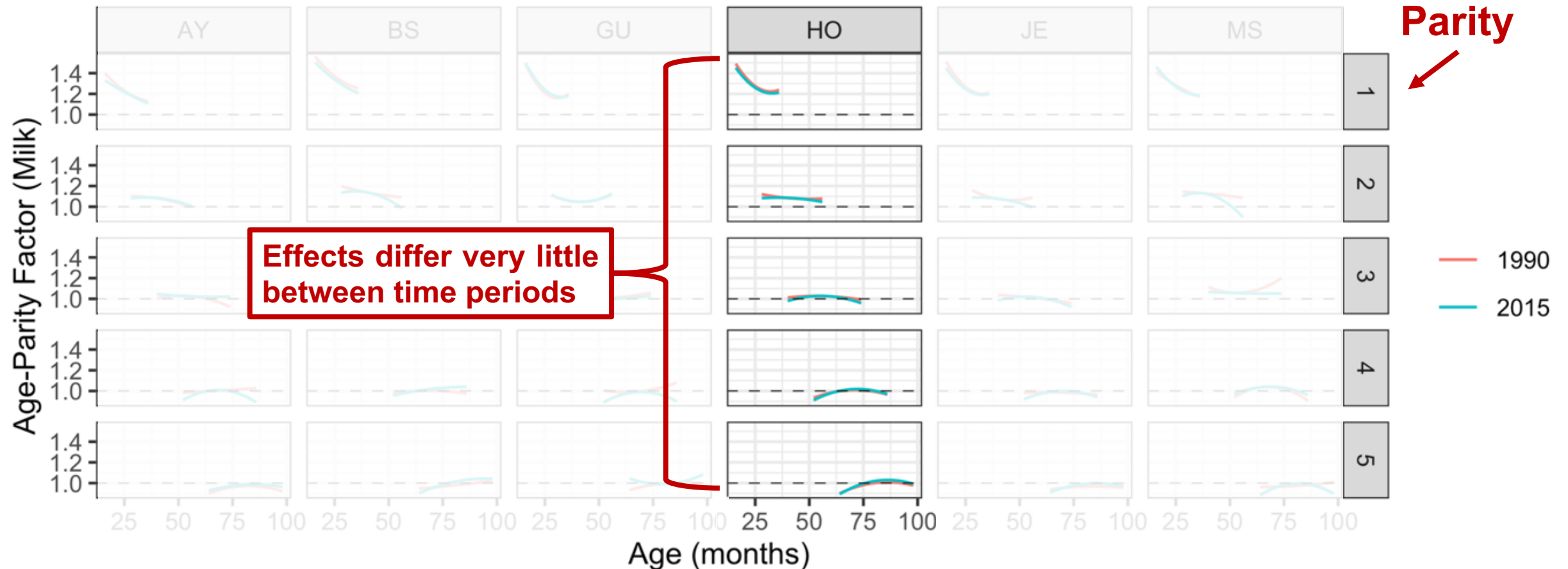
NEW SEASON-REGION FACTORS



NEW AGE-PARITY FACTORS



NEW AGE-PARITY FACTORS



NEW SOFTWARE IS AVAILABLE

Animal Genomics and Improvement Laboratory: Beltsville, MD

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At this Location

Programs and Projects

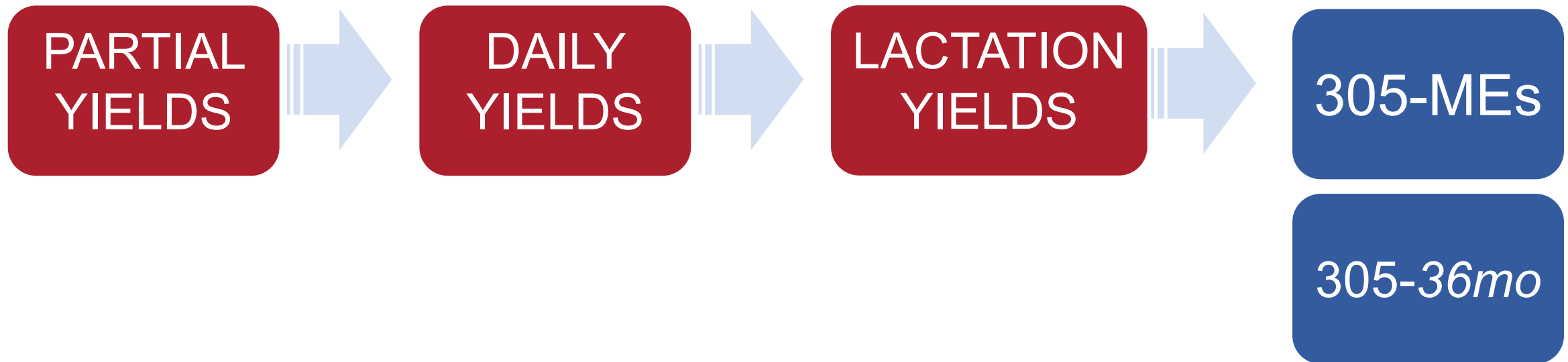
newfactors.f90 Apply new factors for age, parity, season, and previous days open to compare cows more fairly within herds

DOWNLOAD [Programs, example files, and executable](#)

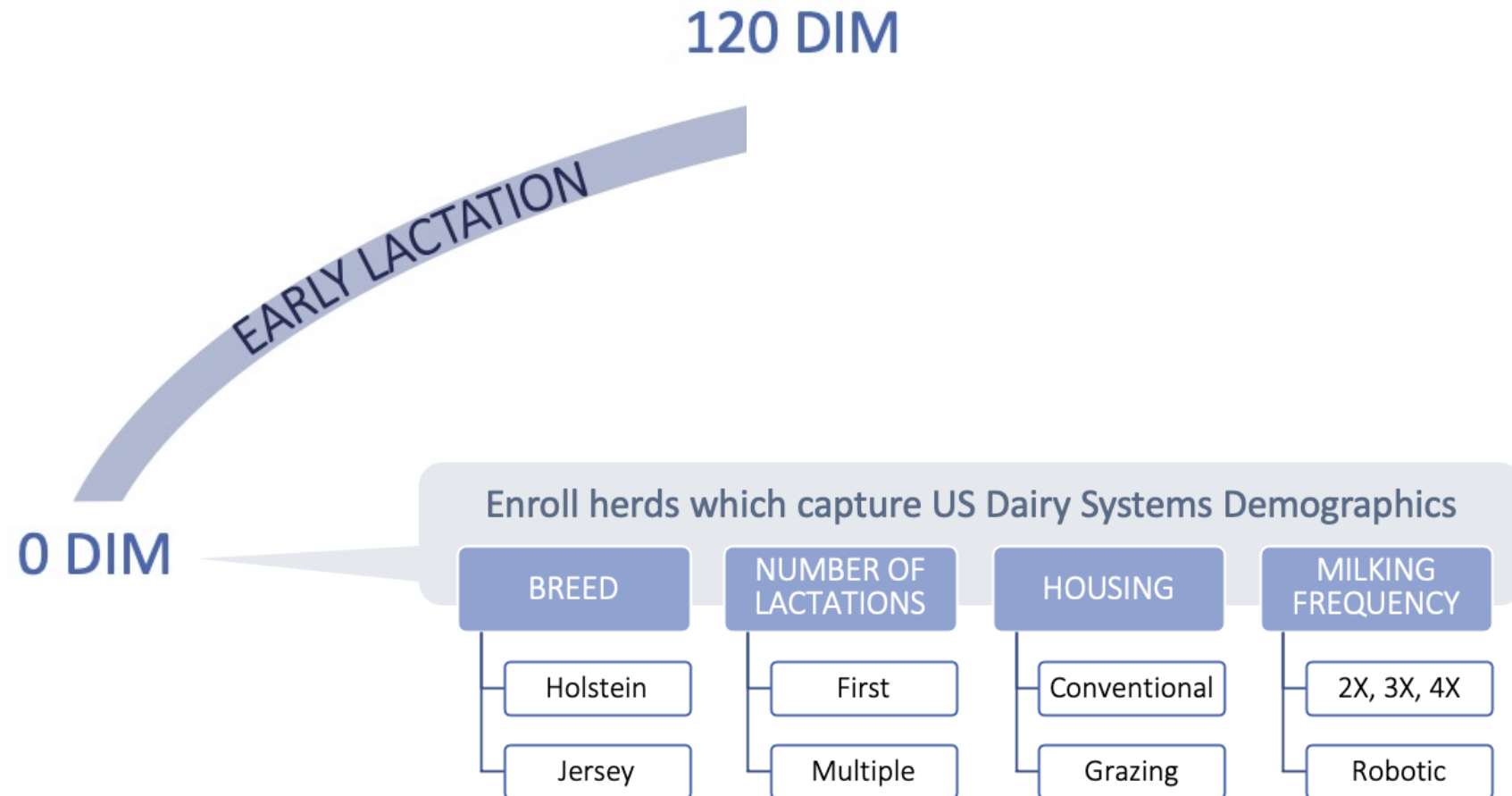
INPUT	ageparityfactors1	from Jana Hutchison's ageparityfactors.sas as input for aiplage2.c
	SeasonFactors2023.txt	from Paul VanRaden's agefactor.sas as input for aiplage2.c
	PrevDOfactorsHO	from Paul VanRaden's maindcr.f90 as input for aiplage2.c
	ClimateRegions	defined by Asha Miles as input for aiplage2.c

<https://tinyurl.com/new-factors>

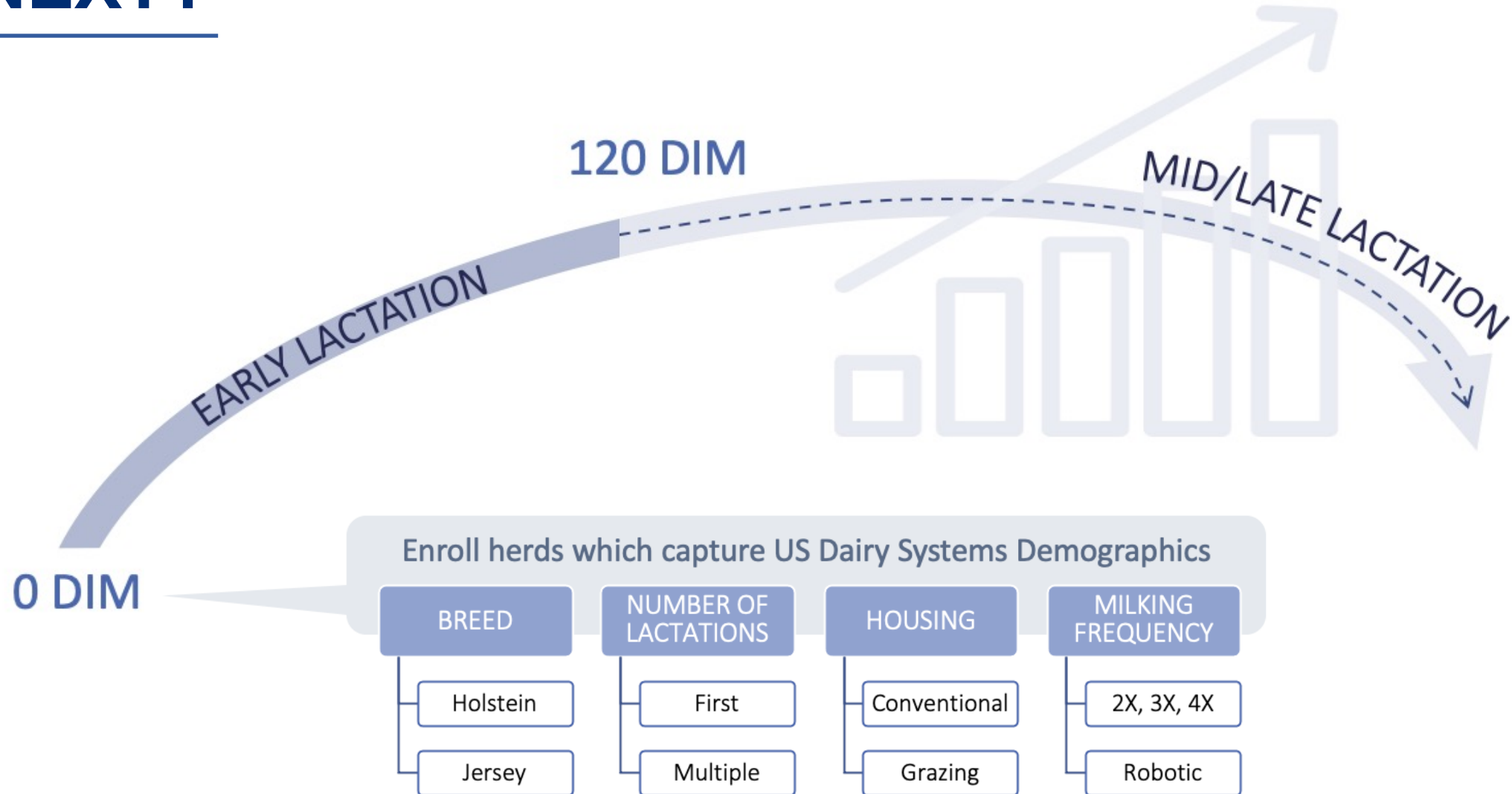
WHAT'S NEXT?



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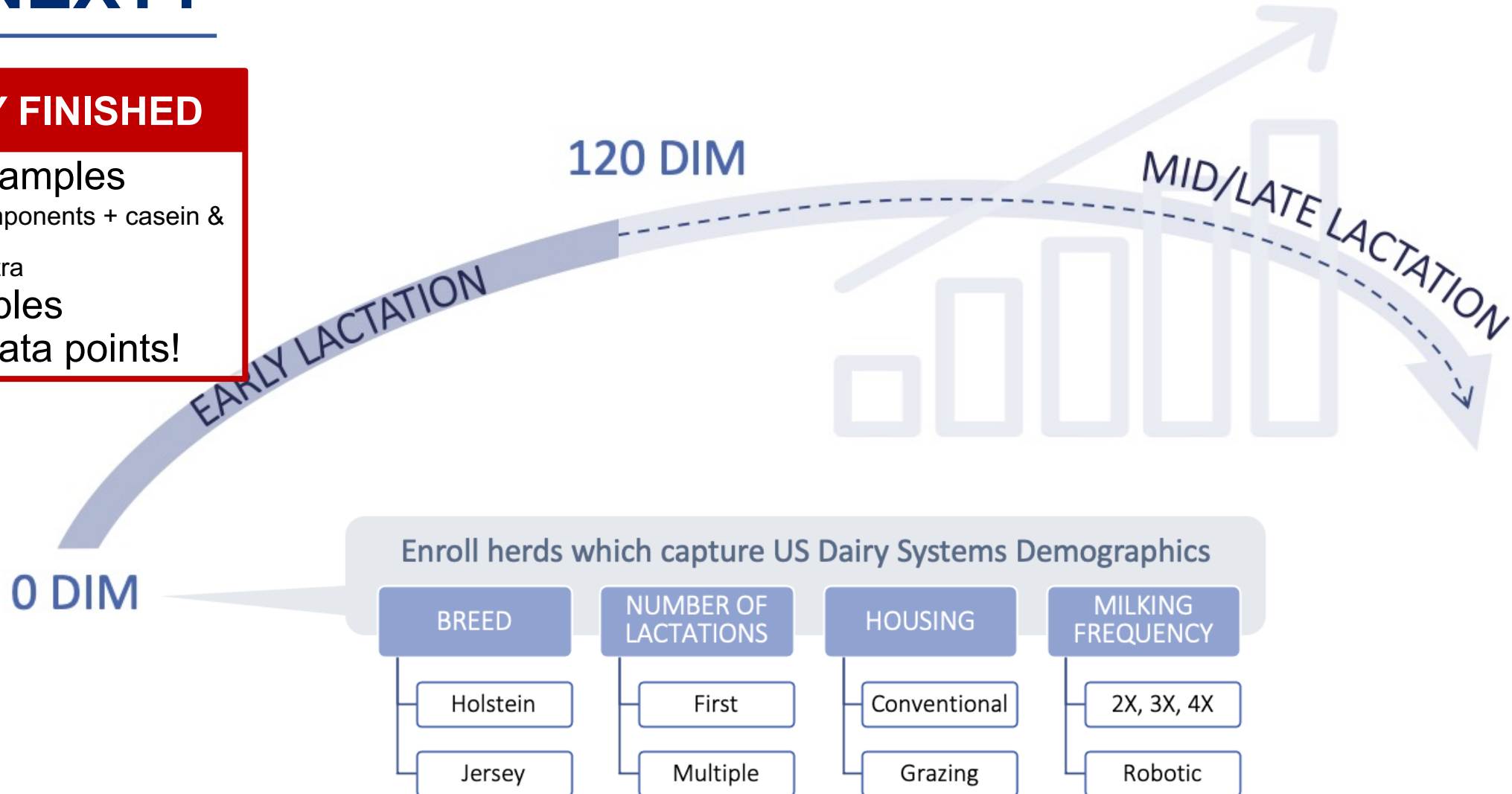
WHAT'S NEXT?



WHAT'S NEXT?

FARM 1 WEEKLY FINISHED

- 63,562 milk samples
 - traditional components + casein & fatty acids
 - raw MIR spectra
- 54 TMR samples
- 68.3 million data points!



OTHER ONGOING RESEARCH



 Beef x Dairy

 GPTA Validation for Cows



 Heat-Stress GxE

 Hoof Health & Lameness



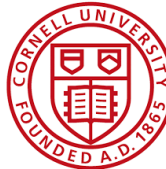
 Methane Emissions

 Inbreeding & Diversity



 Heat Stress & Microbiome

 Energy Efficiency & Metabolism



 Colostrum Microbiome

 Single-Step GBLUP



 Johnes Disease

 F_{ST} SNP Selection for Faster Computation



THANK YOU

Data were available to the authors from CDCB under USDA Agricultural Research Service Material Transfer Research Agreement #58-8042-8-007. While CDCB offers data stewardship, sole ownership and rights pertaining thereto remain with the producer and we thank U.S. dairy producers for sharing their data for research use.

This work was supported by USDA-ARS project 8042-31000-113-000D, “Improving Dairy Animals by Increasing Accuracy of Genomic Prediction, Evaluating New Traits, and Redefining Selection Goals”.

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