

Latest Updates to Evaluations

Taylor M. McWhorter, PhD

Wednesday, July 31, 2024

Genomic Nominator and Laboratory Workshop



Overview

- Goal of presentation
- Structure of presentation

To review updates for all 2024 evaluations

Updates to April 2024 run (2404)

Updates to August 2024 run (2408)

Updates in-progress for next run(s) (2412+)

2024 Tri-Annual Evaluation Release Schedule



A graphic with a dark blue background. At the top, three red rounded rectangular boxes contain the dates: "April 2 2024", "August 13 2024", and "December 3 2024". Below these boxes is a white horizontal bar containing the text "Council on Dairy Cattle Breeding" on the left and the CDCB logo on the right. The CDCB logo consists of the letters "CDCB" in a stylized font with "COUNCIL ON DAIRY CATTLE BREEDING" written in smaller text underneath.

Updates to April 2024 Run

1. Health Traits Evaluation Revision
2. Unknown Parent Groups in Multi-Trait Models Revision
3. Brown Swiss Genetic Conditions Exchange at Interbull
4. System-wide Transformation from 8 to 9 Digits for Animal Keys



Updates to August 2024 Run

1. Constructed ID System Update
2. 305-AA (Average Age) Implementation
3. SNP List Update
4. Annual BBR Update
5. HH6 Gene Test SNP Inclusion in Haplotype Estimations
6. JNS Gene Test Result Inclusion in Haplotype Estimations
7. New Brown Swiss Trait: Rear Teat Placement
8. Heifer Livability Updates and Heifer Termination Code Edits
9. IT Updates



Updates in-progress

1. IT: Cybersecurity Certification
2. Milking Speed Evaluation
3. Female Fertility Traits Revision + New Trait
4. Publication and Distribution Internal Rework
5. Inclusion of New Domestic and Foreign Gene Test Results in BS Haplotype Calling
6. Monthly Evaluation Flow Upgrade
7. Multi-trait Reliability for Type Traits Traditional Evaluation
8. New Workflow for Clones



April 2024

Updates to April 2024 Run

- Health Traits Evaluation Revision
- Unknown Parent Groups in Multi-Trait Models Revision
- Brown Swiss Genetic Conditions Exchange at Interbull
- System-wide Transformation from 8 to 9 Digits for Animal Keys



Health Traits Evaluation Revision

BACKGROUND:

- 6 health traits
- First implemented

April 2018 → Holstein

April 2020 → Jersey

August 2022 → Brown Swiss

Resistance to						
	Milk Fever	Displaced Abomasum	Ketosis	Mastitis	Metritis	Retained Placenta

Health Traits Evaluation Revision

BACKGROUND:

- 6 health traits
- First implemented

April 2018 → Holstein

April 2020 → Jersey

August 2022 → Brown Swiss

	Resistance to					
	Milk Fever	Displaced Abomasum	Ketosis	Mastitis	Metritis	Retained Placenta
# Records, Millions (HO) 2018 Estimate	1.2 M	1.9 M	1.4 M	2.4 M	2.0 M	2.2 M
# Records in Database, Millions (HO, JE, BS) Dec 2023	5.8 M	5.8 M	4.3 M	7.7 M	6.3 M	7.6 M
# Records Change from 2018 to 2023	↑ 4.6M	↑ 3.9M	↑ 2.9M	↑ 5.3M	↑ 4.3M	↑ 5.4M



* The number of records are the total number of records in herds that submit health data, not the number of incidences

Health Traits Evaluation Revision

GOAL:

- To enhance national genetic evaluation for health traits by
 - Updating variance component estimates
 - Applying variance-adjusted weight that gives more weight to parities with higher heritability

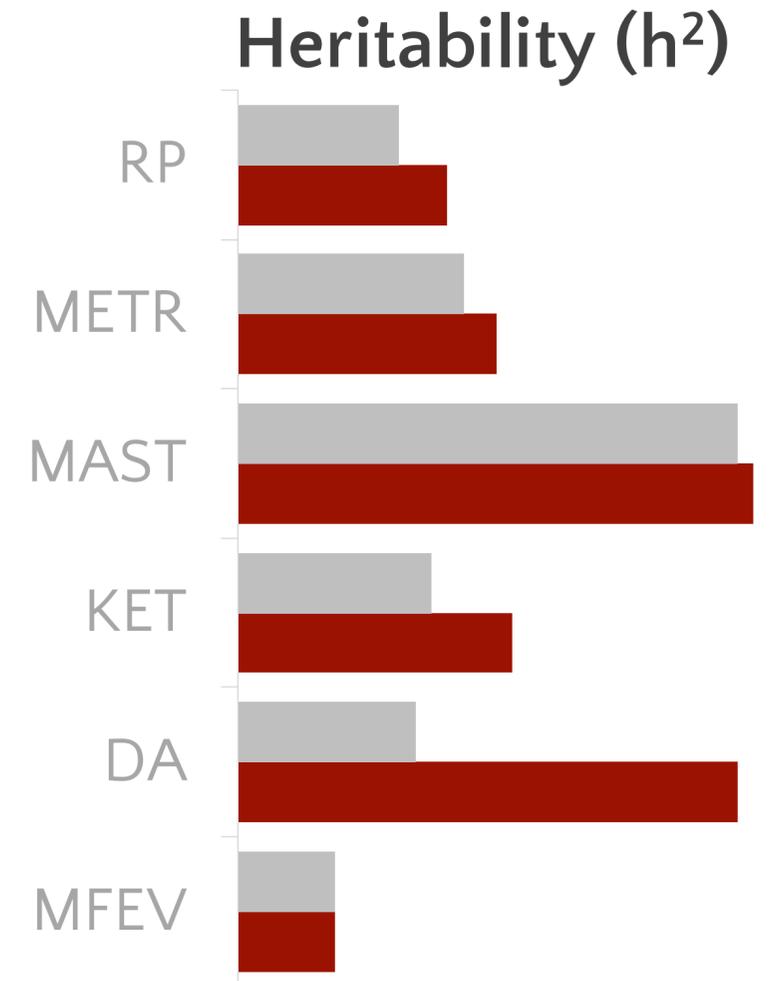
METHOD:

- Adjust phenotype directly → *already implemented*
 - Adjusts and standardizes phenotypic variance of binary trait
- Variance-adjusted weight = ratio of residual variance → *new revision*
- Assumption that the phenotypic adjustment equalizes genetic variance *and* variance of other random effects
 - Therefore, it is assumed only residual variance will differ by lactation

Health Traits Evaluation Revision

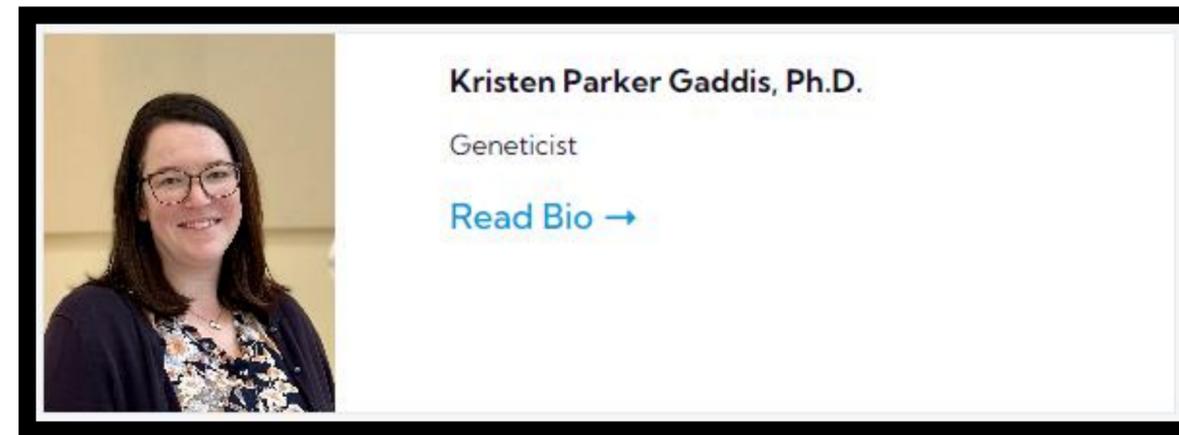
CONCLUSION:

- In August 2023 → *Interbull test run passed*
- Adjusted phenotypes and variance-adjusted weights
 - Account for binary trait
 - Standardize genetic variance across differing parities
- Updates implemented in the April 2024 routine official evaluation
- GEBV correlations were >90% for 5 of the 6 traits
 - DA which had the largest change in h^2
 - >95% HO, but >82% JE, and >81% BS



Health Traits Evaluation Revision

- For more information, stay tuned for Dr. Kristen Gaddis Parker's talk next



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UPG in multi-trait models revision

- **UP** = Unknown Parents
- **UPG** = Unknown Parent Groups

BACKGROUND:

- For animals with missing pedigree info
 - UPG provide average Predicted Transmitting Ability
- Accurate UPG effect estimates require *foreign* UP to have descendants with *domestic* phenotypes
- Genotyping has expanded around the world
 - A high proportion of recently genotyped *foreign* UP do not have descendants with *domestic* phenotypes

OBJECTIVE:

- To merge *domestic* and *foreign* UPG to connect more information to foreign UP

UPG in multi-trait models revision

CONCLUSION:

- In April 2024, all *foreign* UPG effects were merged with *domestic* UPG
- For Holsteins bulls born in last 10 years and reliability >50%:
 - PTA correlations >99.98%
- Across all years:
 - PTA correlations >99.97%
 - Except for Early First Calving, correlation 99.86% (due to 10% faster estimated genetic trend)
- Change had little effect on animal evaluations across the population
 - Some significant effect on specific animals that used the removed UPG

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- System-wide Transformation from 8 to 9 Digits for Animal Keys



Brown Swiss Genetic Conditions Exchange at Interbull

- **BS** = Brown Swiss

BACKGROUND:

- BS data has not exchanged data internationally in most recent years
 - National Cooperator Database contains older data
- In collaboration with Brown Swiss Association, initiative to re-establish international workflow to get more updated information



Brown Swiss Genetic Conditions Exchange at Interbull

- **BS** = Brown Swiss

MOTIVATION:

- To promote national exchange of information

OBJECTIVE:

- To improve genetic factor information flow for BS
 - Allows for improvement of haplotype calls



CONCLUSION:

- Workflow opened for this exchange
 - Foreign data is now received, and domestic data is now sent

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System-wide Transformation from 8 to 9 Digits for Animal Keys

BACKGROUND:

- Previously, system established with 8-digit keys
 - Allowed for max key of 99999999 = 99,999,999 unique animals

MOTIVATION:

- What happens when we try to store the 100 millionth unique animal key?

GOAL:

- To apply system wide change with 9-digit keys

System-wide Transformation from 8 to 9 Digits for Animal Keys

CONCLUSION:

- Work began in 2021 and was completed in 2022
 - Required nearly every team member at CDCB
- The system has max of 9-digit key
 - Maximum of 999999999 = 999,999,999 unique animals
- Would only have to revisit this if we had more than 1 billion animals in National Cooperator Database
- This made room for...



April 24, 2024

The 100 *millionth* unique animal was entered into the National Cooperator Database

HO840F003284867405 was entered as a 3-week-old calf

Thanks to the system-wide change, there was no problem accounting for new animals

August 2024

Updates to August 2024 Run

- **Constructed ID System Update**
- 305-AA (Average Age) Implementation
- SNP List Update
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- HH6 Gene Test SNP Inclusion in Haplotype Estimations
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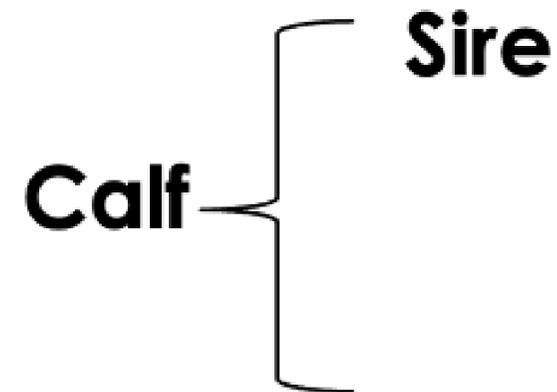


Constructed ID System

BACKGROUND:

- When sire or dam is unknown, animals have gap in their pedigree
 - Paternal ancestry often easily confirmed
 - Most sires are genotyped
 - Maternal ancestors difficult to identify
 - More likely to not be genotyped
 - Can connect to maternal male ancestors
 - Haplotype matching
- BUT U.S. system requires dam identification to link maternal ancestors

- **Constructed Dam ID** → placeholder dam IDs that connects animals to maternal male ancestors



Constructed ID System

GOAL:

- To eliminate “dead ends” in the pedigree
 - More accurate, reliable genetic evaluations for affected animals
 - Thus overall, improving accuracy of U.S. evaluations

CONCLUSIONS:

- First implemented in February 2023 for weekly evaluations (i.e., new, genotyped animals)
- June 2024 the constructed ID system was implemented across the entire US pedigree in preparation for tri-annual
 - This full “sweep” of database allowed for addition of constructed IDs to >3.2 million animals
 - Also impacts other animals directly or indirectly
 - U.S. population is heavily interconnected with pedigrees of animals worldwide



By: P.D. Eastman

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305-AA (Average Age) Implementation

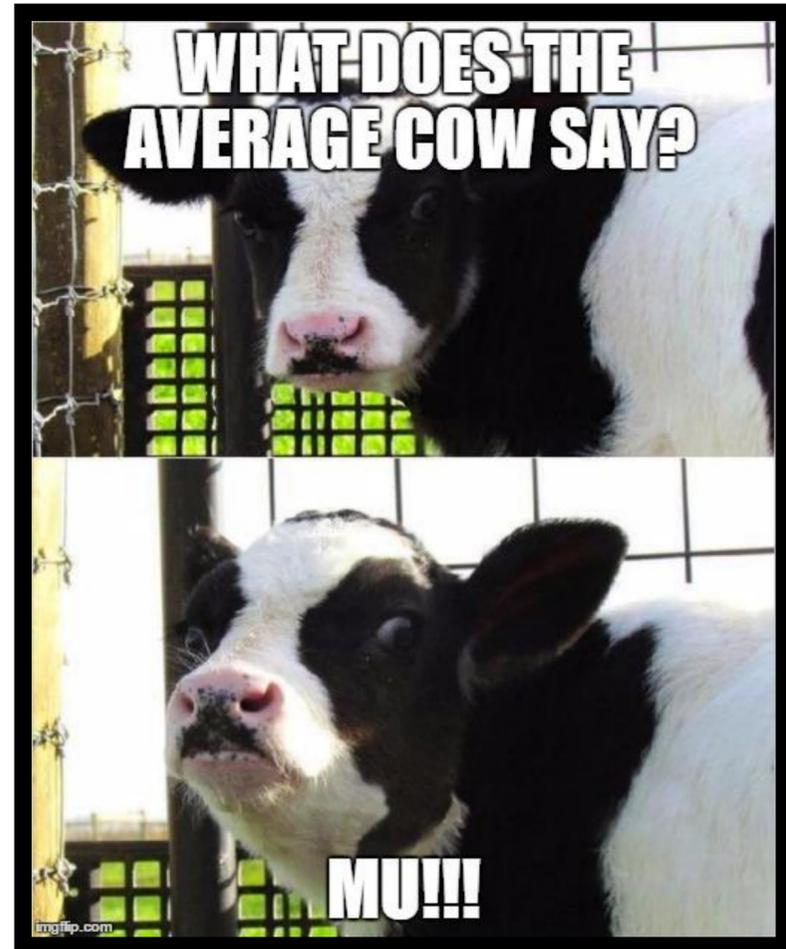
BACKGROUND:

- From 1935 until June 2024
 - Yield records were standardized to **305-ME** (Mature Equivalent)
 - Also referred to as **305d-2X-ME**
 - Last updated in 1994
- Standardization of yields allows for comparisons of cows with different:
 - Ages
 - Seasons of calving
 - Parities
 - Lactation lengths
 - Climates

305-AA (Average Age) Implementation

GOAL:

- To standardize with fairer phenotypic comparisons based on recent analysis in the modern dairy environment
- To implement 305-AA (Average Age) to be new standardized yield estimates for U.S. dairy cows
- Average Age = 36 months
 - Better aligns with today's management practices



305-AA (Average Age) Implementation

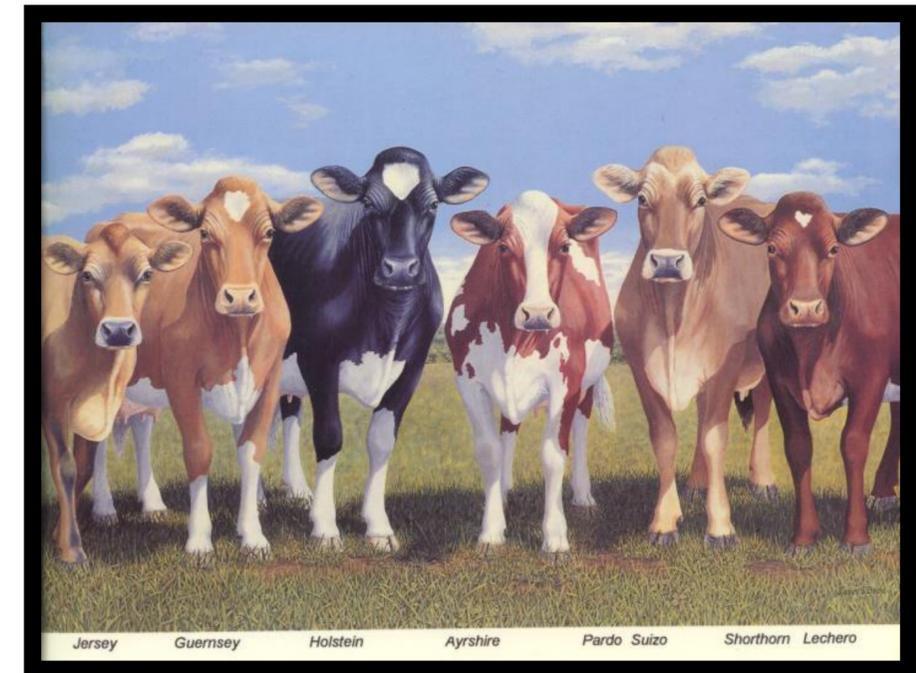
CONCLUSIONS:

- Herd averages from standardized yields closer to actual yield
 - ME records ~10% higher than actual
- Yield traits experience most variation as traits revised directly
 - Potential impact on other traits, but direct impact on Net Merit \$
- 305-AA implementation will have effect similar to a base change
- Impact each breed's PTA differently

305-AA (Average Age) Implementation

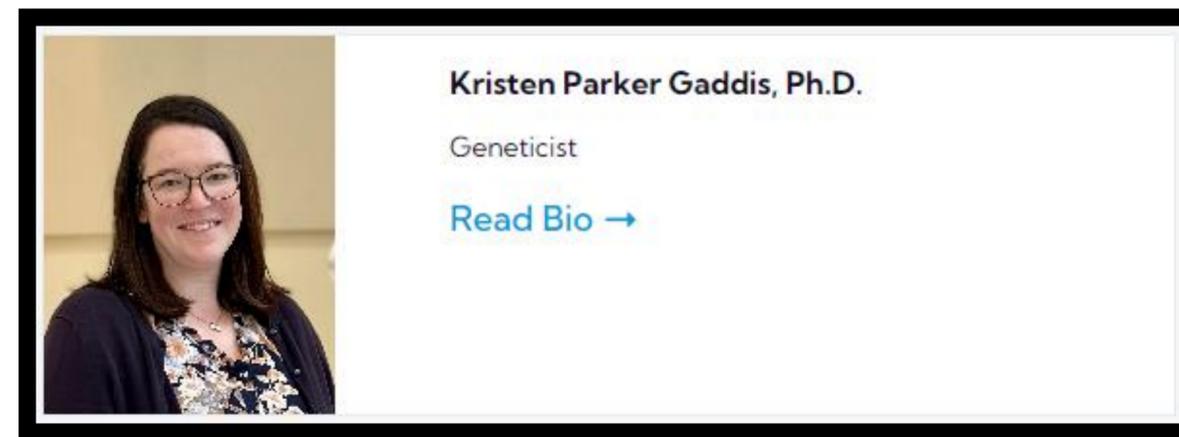
CONCLUSIONS:

- Anticipated impact on yield trait genomic PTA by breed
 - *Ayrshire* Stable, mild increase for younger males
 - *Brown Swiss* Slight increase for younger animals, stable for older animals
 - *Guernsey* Increase for young males, decrease for older males
 - *Holstein* Increase for young males, stable in older animals
 - *Jersey* Noticeable decrease for younger males,
increase for older males



305-AA (Average Age) Implementation

- For more information, stay tuned for Dr. Kristen Gaddis Parker's talk next



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SNP List Update

BACKGROUND:

- Previously, **78,964** genetic markers, gene tests and quantitative trait loci used since August 2021

MOTIVATION:

- **9,769** markers had small **effects on traits**, were **not included on recent chips**, or had **poor genotype quality**
 - 74% of these markers are on the high-density (HD) chip
 - 26% of these markers are on less dense chips (i.e., 50k)

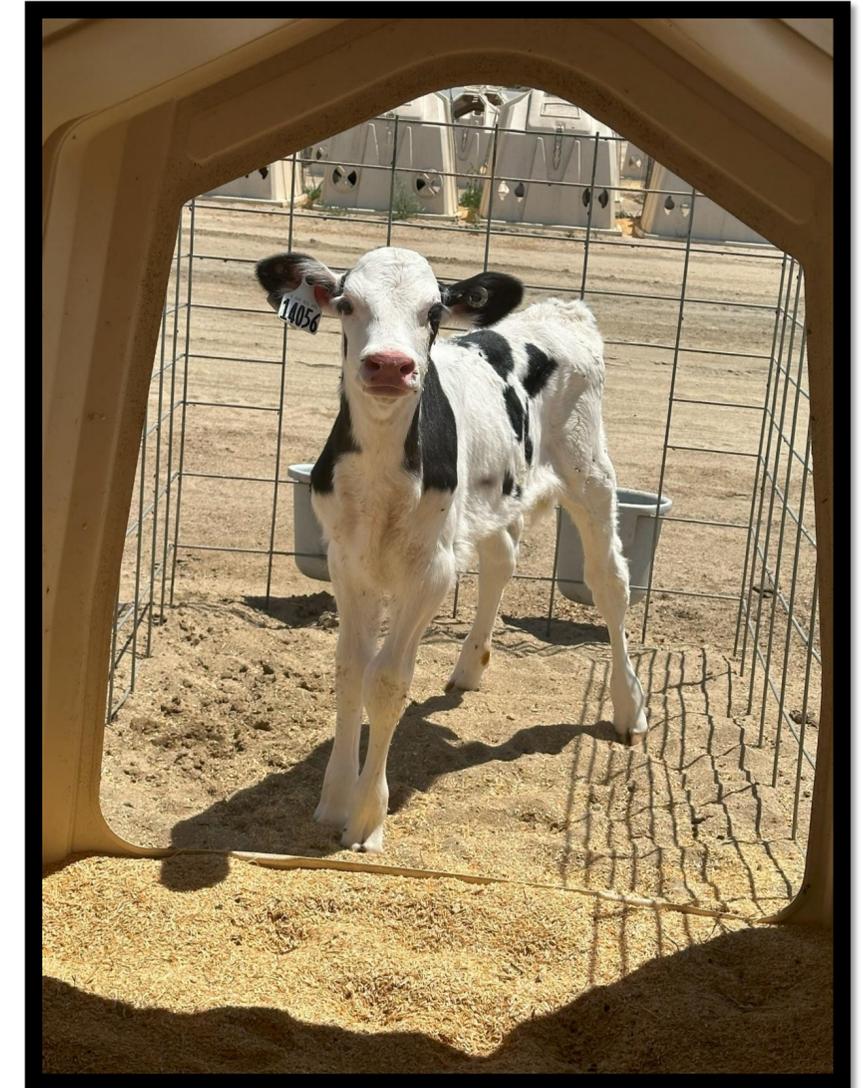
GOAL:

- Update SNP list used in genomic evaluations by removing **9,769** markers and adding new gene tests

SNP List Update

CONCLUSIONS:

- New set of 69,200 genetic markers
 - 12% reduction in processing time
 - Improved processing time very beneficial as evaluations continue to grow
- In February 2024 test run
 - Genomic prediction correlations when using previous versus new SNP list were ~99.6%
- Animals most affected are those with
 - Low density genotypes, incomplete pedigree or loose links to reference population



SNP List Update

- **5 new tests added**
 - At this time, results not published – solely used for monitoring purposes
 - HH7_Rs481920244 → fertility, results in abortion
 - HH7_CENPU → fertility, results in abortion
 - SLICK2 → short hair
 - SLICK3 → short hair
 - FMO3_3 → fish flavored milk

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Annual BBR Update

BBR = Breed Based Representation

BACKGROUND:

- Annual BBR update usually occurs every April tri-annual evaluation
- Given SNP list update in August 2024
 - More beneficial to update BBR in August 2024 too

GOAL:

- Routine annual update of BBR
 - Include usual set of BBR reference animals
 - Uses the new SNP list of 69,200 genetic markers



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HH6 Gene Test SNP Inclusion in Haplotype Estimations

HH6 = Holstein Haplotype 6

BACKGROUND:

- Lethal recessive genetic defect
- Over 1.4 million animals with this gene test SNP already
- Previously, for haplotype calling of HH6, estimation used a section of SNPs that were genotyped or imputed

GOAL:

- To include direct gene test SNP information in haplotype estimation

CONCLUSION:

- HH6 gene test SNP information included directly in imputation and haplotype estimation
- More information is added to estimation to increase accuracy

“The infamous haplotypes: Are they really all that bad?”

Sophie Eaglen, February 24, 2021
Progressive Dairy



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JNS Gene Test Result Inclusion in Haplotype Estimations

JNS = Jersey Neuropathy with Splayed Forelimbs (JNS)

BACKGROUND:

- Previously
 - Received JNS gene test results, but results were not included in haplotype estimation
 - JNS gene effect was likely captured in chunk of SNPs making up JNS haplotype
- Gene test results
 - **JNSC** = Carrier
 - **JNSE** = Free; not a carrier

“The infamous haplotypes: Are they really all that bad?”

Sophie Eaglen, February 24, 2021
Progressive Dairy



JNS Gene Test Result Inclusion in Haplotype Estimations

GOAL:

- To include direct gene test results information into haplotype estimation

CONCLUSION:

- Gene test results for JNS included directly in imputation and used for haplotype estimation

Naming Conventions: Gene tests vs. Haplotype Calls

- Some gene test reports are referred to with haplotype name (i.e., HH1)
- Haplotype calls are also referred to as haplotype name (i.e., HH1)
- However, these are different tests
 - Need a naming convention in place that distinguishes these
- Group working on labeling gene test reports and haplotype calls results
 - To help identify which result is received



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New Brown Swiss Trait: Rear Teat Placement

RTP = rear teat placement

BACKGROUND:

- In January 2024, ~15,000 appraisals used to estimate parameters for this trait
 - ~80% are moderate, between 25 and 35 points, on the 50-point linear scale
 - Intermediate is optimum

CONCLUSIONS:

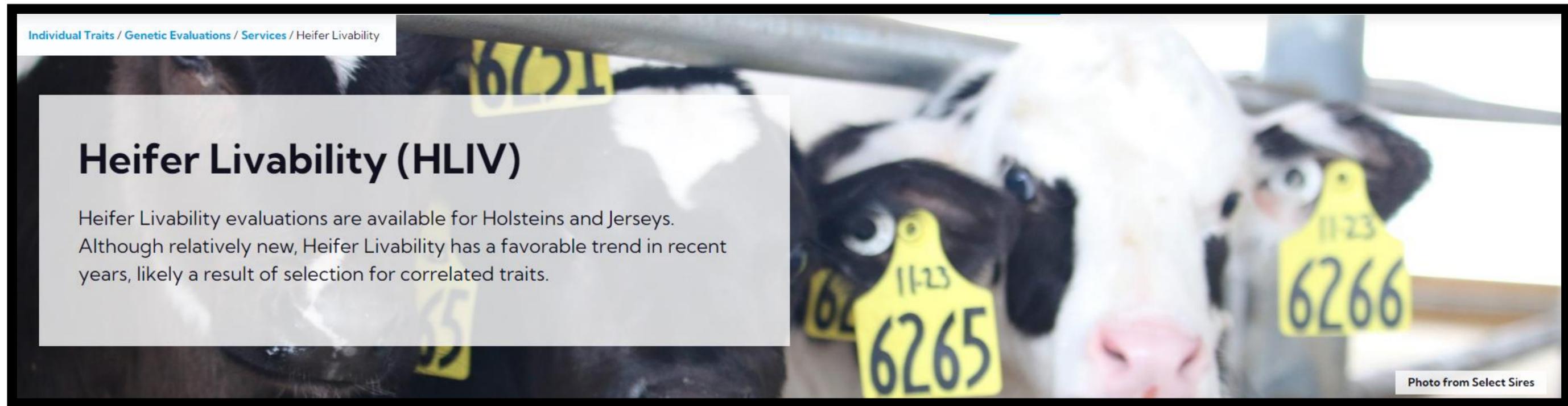
- Heritability (h^2) = 21% → similar to Front Teat Placement h^2 = 22%
- Repeatability = 33%
- Currently uncorrelated with other traits
- Used to provide evaluations for RTP to all ~72,000+ genotyped Brown Swiss Animals

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Heifer Livability Updates and Heifer Termination Code Edits



- Introduced on December 1, 2020
- Expresses expected livability for female offspring from 2 days after birth until 18 months of age
- Heritability 0.72%
- Correlated with Yield Traits (0.34–0.36), Productive Life (0.44), Calving Trait Dollars (0.37) & Early First Calving (0.36)

Heifer Livability Updates and Heifer Termination Code Edits

HLIV = heifer livability

GOAL:

- To improve edits and modeling for HLIV

CONCLUSIONS:

- A revision in storage of cow termination codes in 2019 prevented heifer deaths from being stored in the last two years of included data (2020 and 2021)
 - Corrected revision to store all heifer deaths
- Previously, >1% death loss was required across all years for a herd's HLIV data to be included
 - Now, model requires >1% death loss in *each year* for each herd
 - Within-year edit allows for adaptability to rapid changes in recording

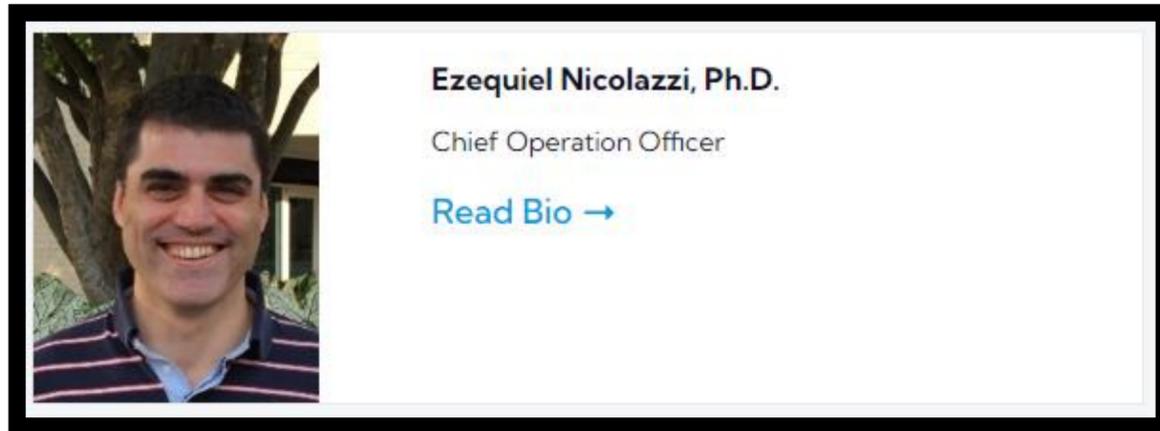
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IT Updates

- Recabling of colocation
- WebConnect Performance Enhancement
 - For more information, stay tuned for Dr. Ezequiel Nicolazzi's talk this afternoon



Updates in progress

Updates in-progress

- IT: Cybersecurity Certification
- Milking Speed Evaluation
- Female Fertility Traits Revision + New Trait
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IT: Cybersecurity Certification

BACKGROUND:

- Unfortunately, the industry is being targeted

GOAL:

- ISO 27001 Certification
- To give assurance and demonstrate our ability to protect the information in our care



IT: Cybersecurity Certification

What is ISO 27001?

- International standard that focuses on information security
 - “ISO/IEC 27001 – Information security, cybersecurity, and privacy protection – Information security management systems – Requirements”
- Global “gold standard” for organization’s ability to protect sensitive data



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Milking Speed Evaluations

BACKGROUND:

- New trait in development: milking speed *collected by in-line sensors in milking equipment*
 - Under investigation to create milking speed evaluation for **Holstein & Jersey**

NOTE:

- This new trait is NOT to be confused with milking speed collected *by appraiser*
 - Used to evaluate milking speed in **Brown Swiss & Milking Shorthorn**

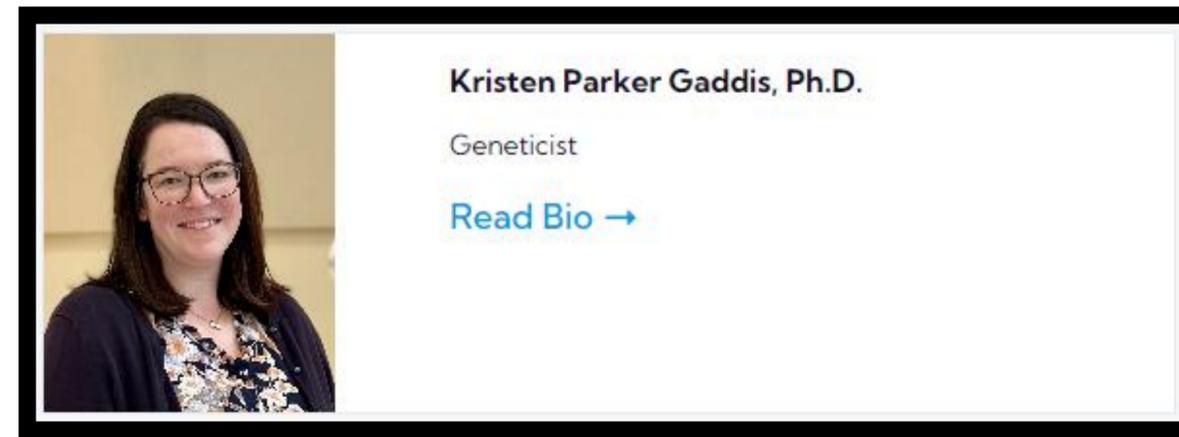
Milking Speed Evaluations

CURRENT STATUS:

- Relationship of milking speed to udder traits is currently under investigation
- Exploring the potential of pre-selection
 - No adverse effect has been observed for selecting fast cows, but investigation for confirmation
- Current design can store up to 2,500 events per cow, calving date, and herd code
 - Up to 100 events per format 8
 - For ex. can accommodate the 915 records from a
 - Cow milking 3x and in milk for ~305 days

Milking Speed Evaluations

- For more information, stay tuned for Dr. Kristen Gaddis Parker's talk next



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Female fertility trait revisions + new female fertility trait

CURRENT STATUS:

- Existing traits
 - DPR = daughter pregnancy rate
 - CCR = cow conception rate
 - HCR = heifer conception rate
 - EFC = early first calving
- Investigation on a potential new trait in collaboration with USDA:
 - “1st insemination to conception”

or

“1st insemination to last insemination”

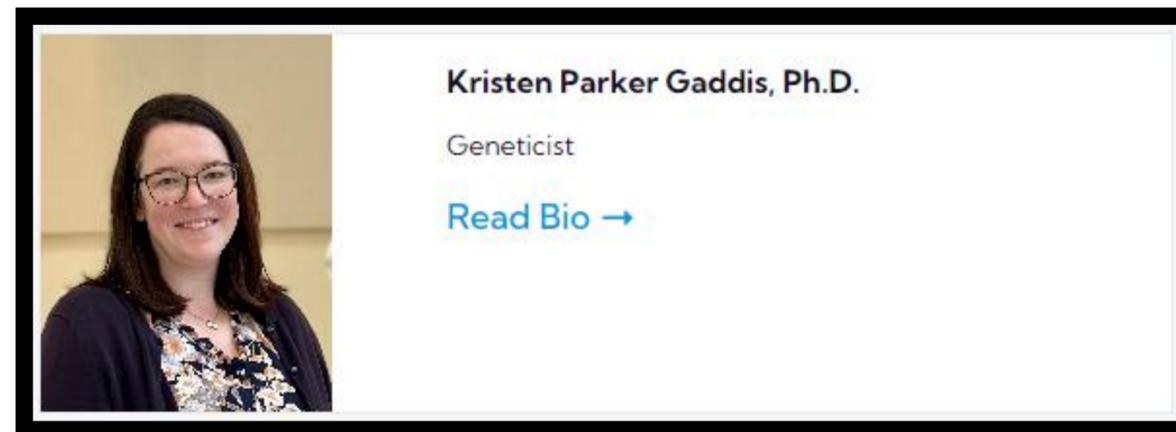
the number of days between the first insemination until the last insemination that results in pregnancy (confirmed with subsequent calving)

the number of days between the first insemination until the last insemination

Female fertility trait revisions + new female fertility trait

GOAL:

- Complete review of the fertility pipeline, and re-assessment of models used
 - To improve stability of fertility evaluations
- For more information, stay tuned for Dr. Kristen Gaddis Parker's talk next



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Publication and Distribution Internal Rework

GOAL:

- A new way of handling data export and delivery of results
- New pipeline to be drastically simplified
- Results distributed in a faster and more efficient way
 - Reduce processing time & more efficient storage

CURRENT STATUS:

- Reworking programs that create output files for genomic results

EXPECTATION:

- Minimal or no impact on results received

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Inclusion of New Domestic and Foreign Gene Test Results in BS Haplotype Calling

BS = Brown Swiss

BACKGROUND:

- Workflow opened for this exchange
 - *Foreign* data for Brown Swiss is now received and *domestic* data is now sent

GOAL:

- Include new flow of *domestic* and Interbull-based Brown Swiss gene tests in haplotype calling

CURRENT STATUS:

- Reworking entire process CDCB stores and manages gene test reported from breed associations

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Monthly Evaluation Flow Upgrade

BACKGROUND:

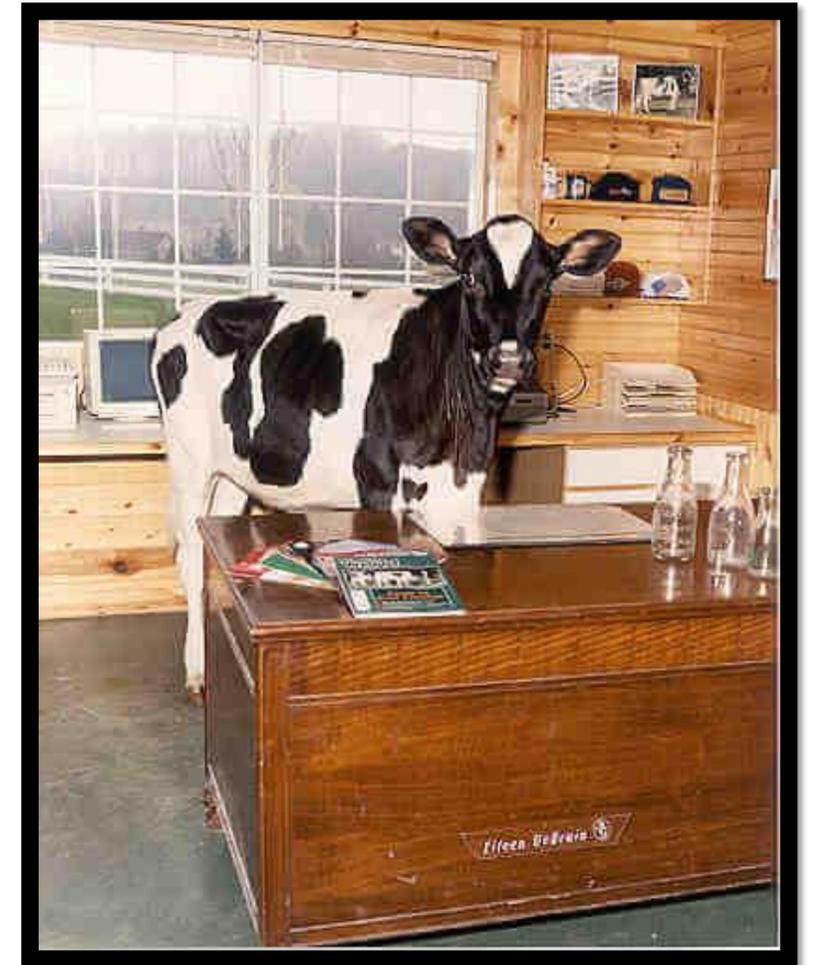
- Current procedure runs on two “engines”
 - One for purebred and one for crossbreds
- Previously, weeklies procedures were blended into one streamline

GOAL:

- To blend monthly procedures into one streamline, like weeklies

EXPECTATION:

- No impact calculations
- Improve efficiency



Updates in-progress

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Multi-trait Reliability for Type Traits Traditional Evaluation

BACKGROUND:

- CDCB is responsible for Ayrshire, Brown Swiss, Guernsey, Jersey, and Milking Shorthorn type trait evaluations

GOAL:

- To enhance reliability estimations for non-Holstein type traits
- To include reliabilities in the multi-trait model as used for PTA calculations

EXPECTATION:

- No affect on PTA
- Potential change in reliabilities (likely increase)

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- **New Workflow for Clones**



New Workflow for Clones

GOAL:

- New handling of clones/identical animals in both traditional and genomic workflows
- To consider all information incoming from clones as coming from the same animal
 - In both traditional and genomic evaluations (BUT accounting for different environments)

CURRENT STATUS:

- In testing for all traits except Holstein type traits
- In-progress
 - Defining policies for international exchanges
 - Reworking workflow when clones are added, removed, or changed for routine evaluations (i.e., weekly, monthly, and tri-annual)
 - Conducting full test run



2013 World Dairy Expo

KHW Regiment Apple-Red-ET, previous 2011 Grand Champion, was beat by her clone, **KHW Regiment Apple-3-Red ETN** 2013 for Grand Champion Red & White Holstein

ACKNOWLEDGMENTS

U.S. dairy producers

Member sectors and collaborators

USDA AGIL

CDCB staff



THANK YOU FOR YOUR ATTENTION

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