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AGIL UPDATE 2022

Research happenings in the last year

Asha M. Miles, PhD | Research Geneticist

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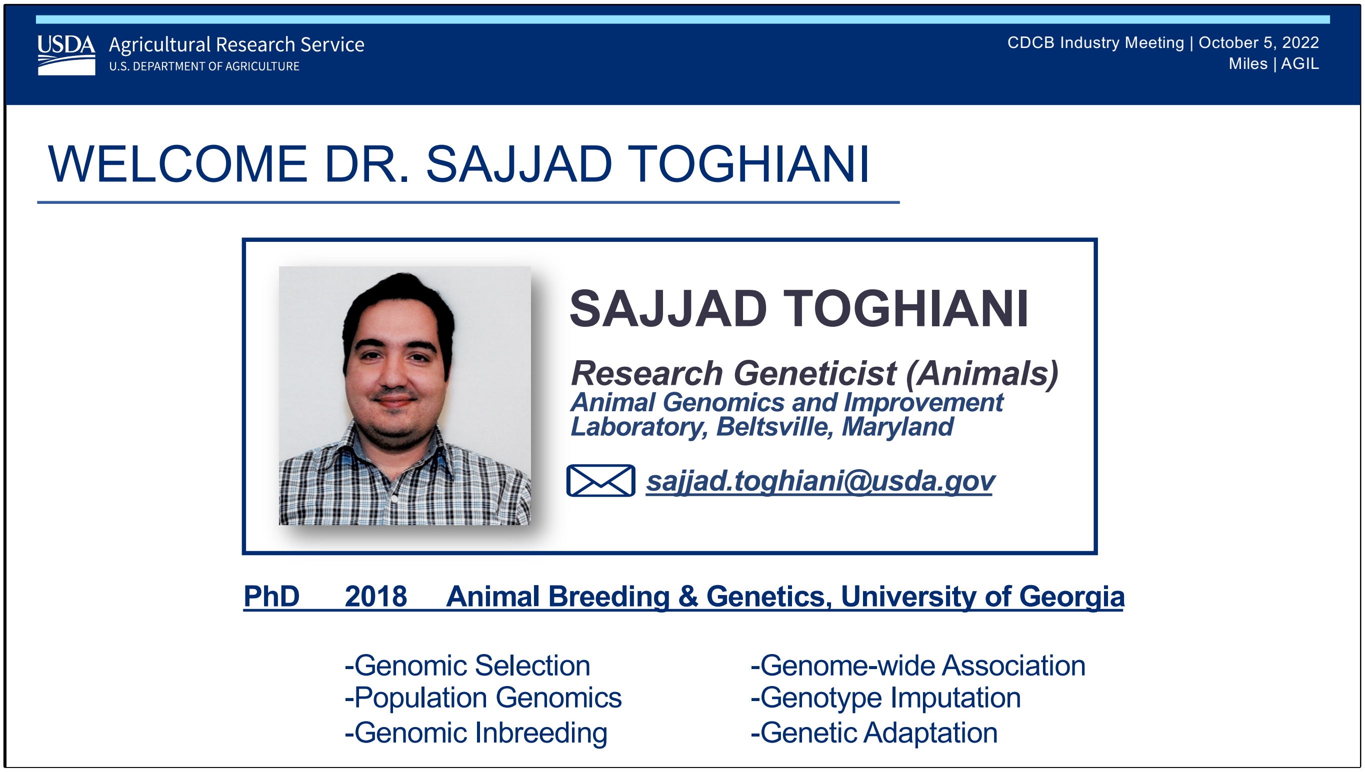
A year in review



WELCOME DR. SAJJAD TOGHIANI

SAJJAD TOGHIANI

Research Geneticist (Animals)
Animal Genomics and Improvement Laboratory, Beltsville, Maryland

✉ ***sajjad.toghiani@usda.gov***

PhD 2018 Animal Breeding & Genetics, University of Georgia

-Genomic Selection
-Population Genomics
-Genomic Inbreeding
-Genome-wide Association
-Genotype Imputation
-Genetic Adaptation

Welcome to Dr. Sajjad Toghiani who accepted a permanent position on our team of scientists earlier this year. He completed is PhD in Animal Breeding and Genetics @ U of Georgia and has been with USDA for 4 years, the last 2 of which he worked for AGIL as a support scientist. We are very excited about his enthusiasm and expertise and look forward to sharing his work with you in the future.

WE'RE HIRING!

2 positions available:

- **Closes 10/12/2022**
- Permanent, Full-Time
- Beltsville, MD
- Technical support to scientists involved in deriving, computing, and delivering genetic evaluations to the US dairy industry

USAJOBS

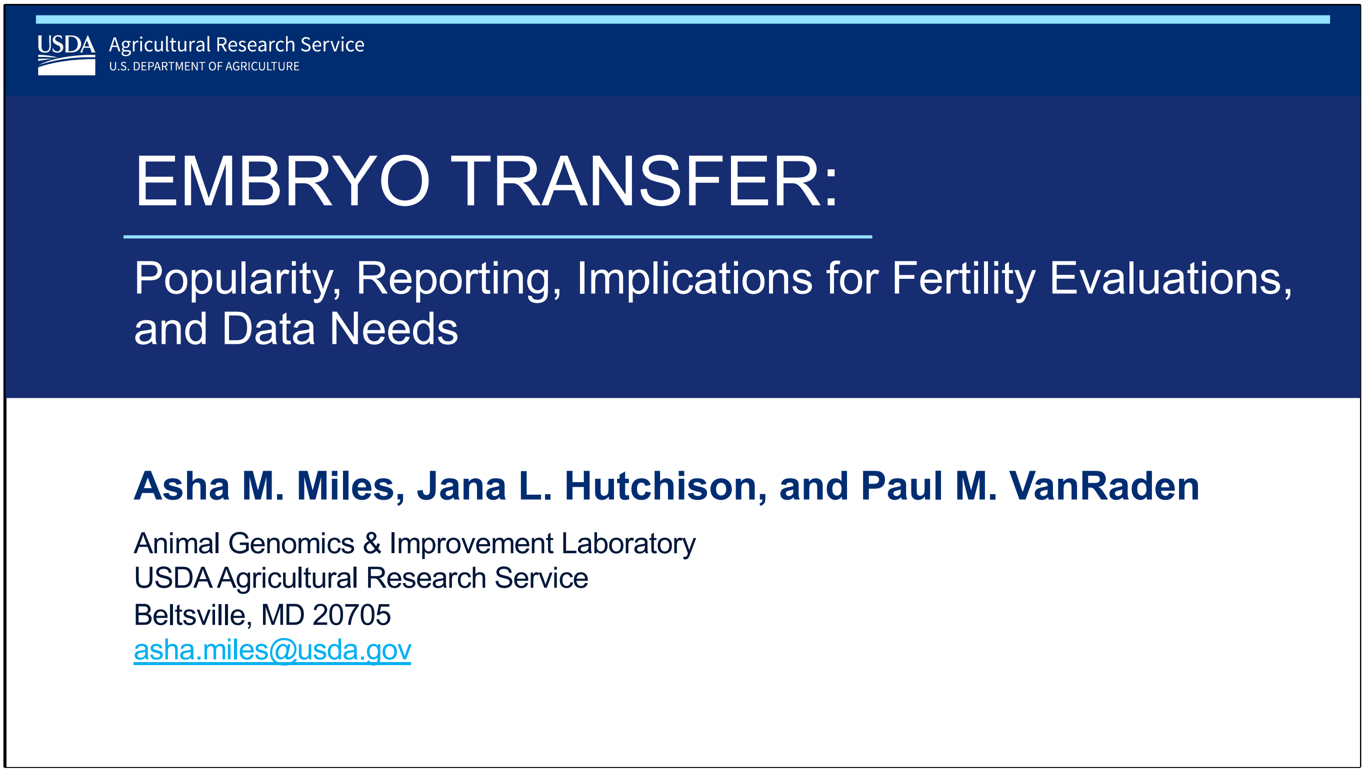
Animal Scientist

DEPARTMENT OF AGRICULTURE - AGENCY WIDE

Agricultural Research Service

https://www.usajobs.gov/job/680444900

We are hiring for 2 support scientist positions. None of the research you will see in this presentation was possible without the efforts of our support staff and we are excited to welcome some talented people to our team.



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EMBRYO TRANSFER:

Popularity, Reporting, Implications for Fertility Evaluations, and Data Needs

Asha M. Miles, Jana L. Hutchison, and Paul M. VanRaden

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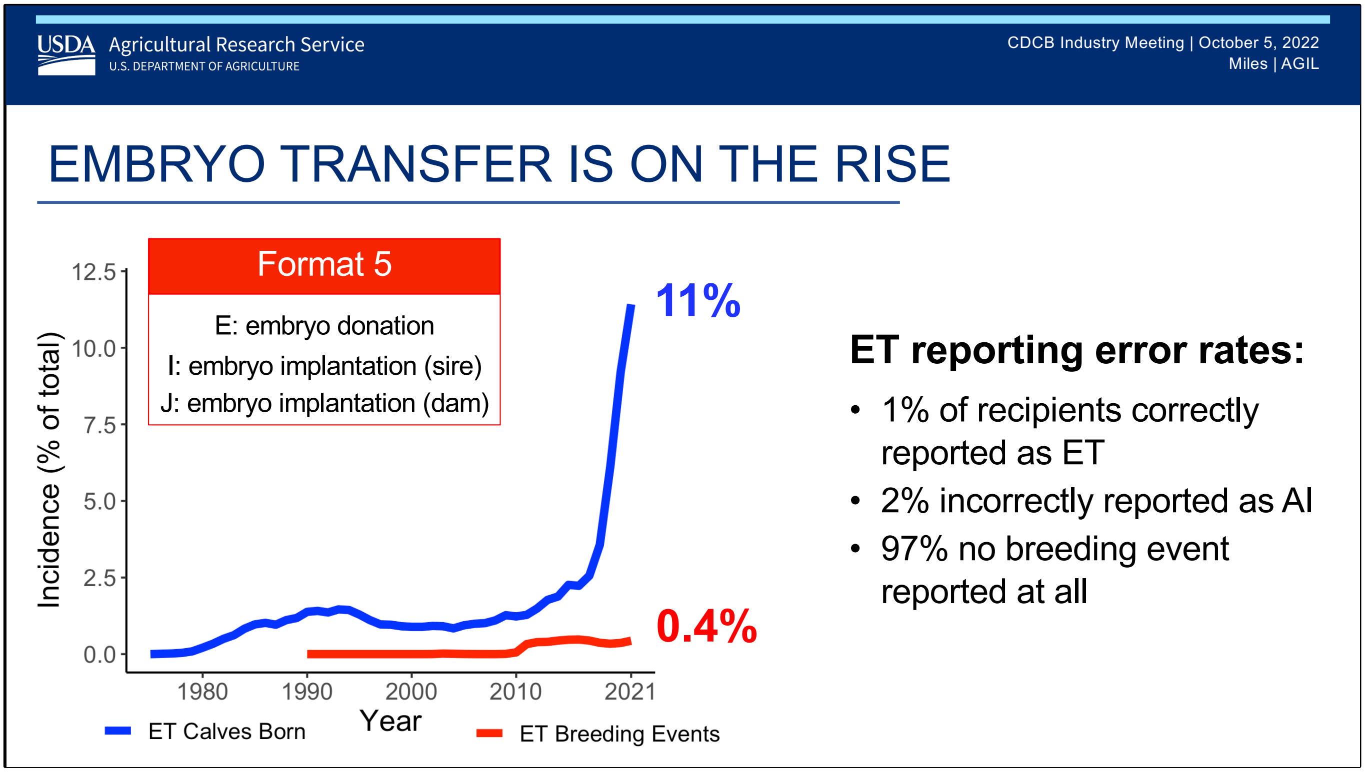
Last year this research was just beginning & today we can report significant progress.



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EMBRYO TRANSFER IS ON THE RISE

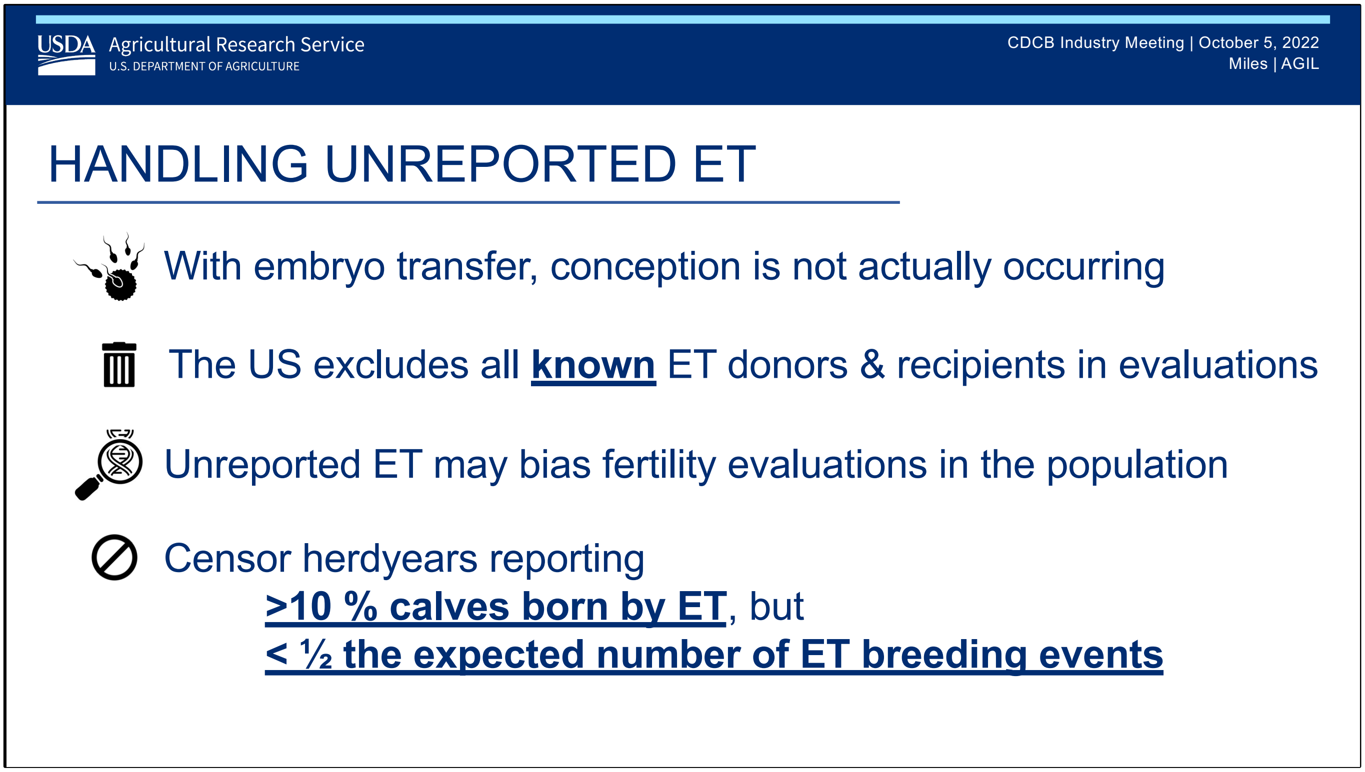
Format 5

E: embryo donation
I: embryo implantation (sire)
J: embryo implantation (dam)

ET reporting error rates:

- 1% of recipients correctly reported as ET
- 2% incorrectly reported as AI
- 97% no breeding event reported at all

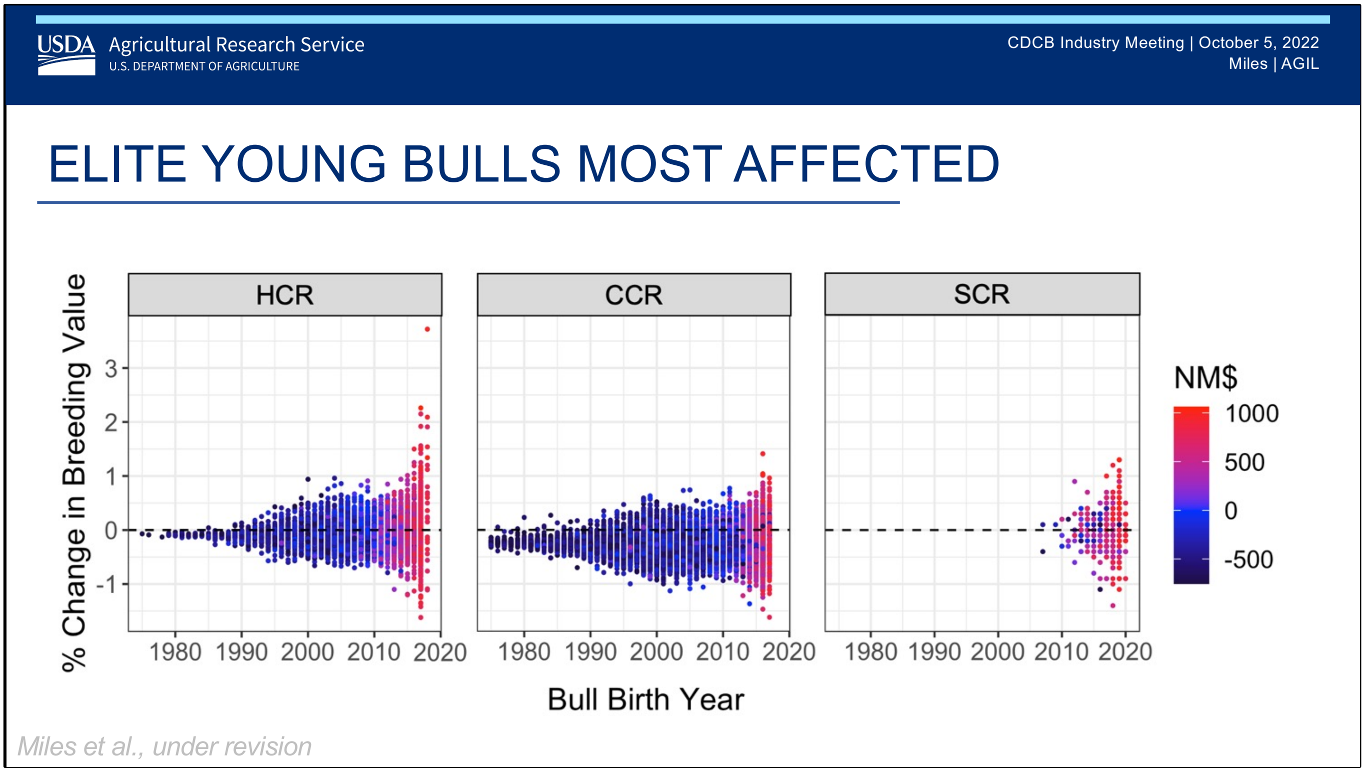
This research was initiated when we noticed an exponential increase in the # of ET calves born in the last 2 years. Unfortunately, ET breeding event reporting is not matching its popularity. While 11% of calves born in the US last year were attributable to ET, only a fraction of the expected breeding events were reported. These breeding events flow into the National Cooperator Database via Format 5 records reporting either embryo donation or implantation.



HANDLING UNREPORTED ET

- With embryo transfer, conception is not actually occurring
- The US excludes all **known** ET donors & recipients in evaluations
- Unreported ET may bias fertility evaluations in the population
- Censor herdyears reporting
  - **>10 % calves born by ET**, but
  - **< ½ the expected number of ET breeding events**

So how do we handle unreported ET? The problem is that with embryo transfer there is no conception event, pregnancy occurs with the successful implantation of a high-quality embryo. Unreported ET may be muddying our phenotyping and biasing fertility evaluations. Historically the US has excluded any ET-related records, but this isn't a reliable strategy if we don't have accurate reporting of ET and we wouldn't want to completely remove herds using ET because these are representing our most elite animals and becoming a larger and larger portion of the dairy cattle population, A new edit was implemented in April 2022 evals that excludes herdyears with > 10% of their calves born by ET but less than half of the expected ET breeding events given the number of ET calves born. This edit maximizes data preservation while removing the records most likely to introduce confounding bias.



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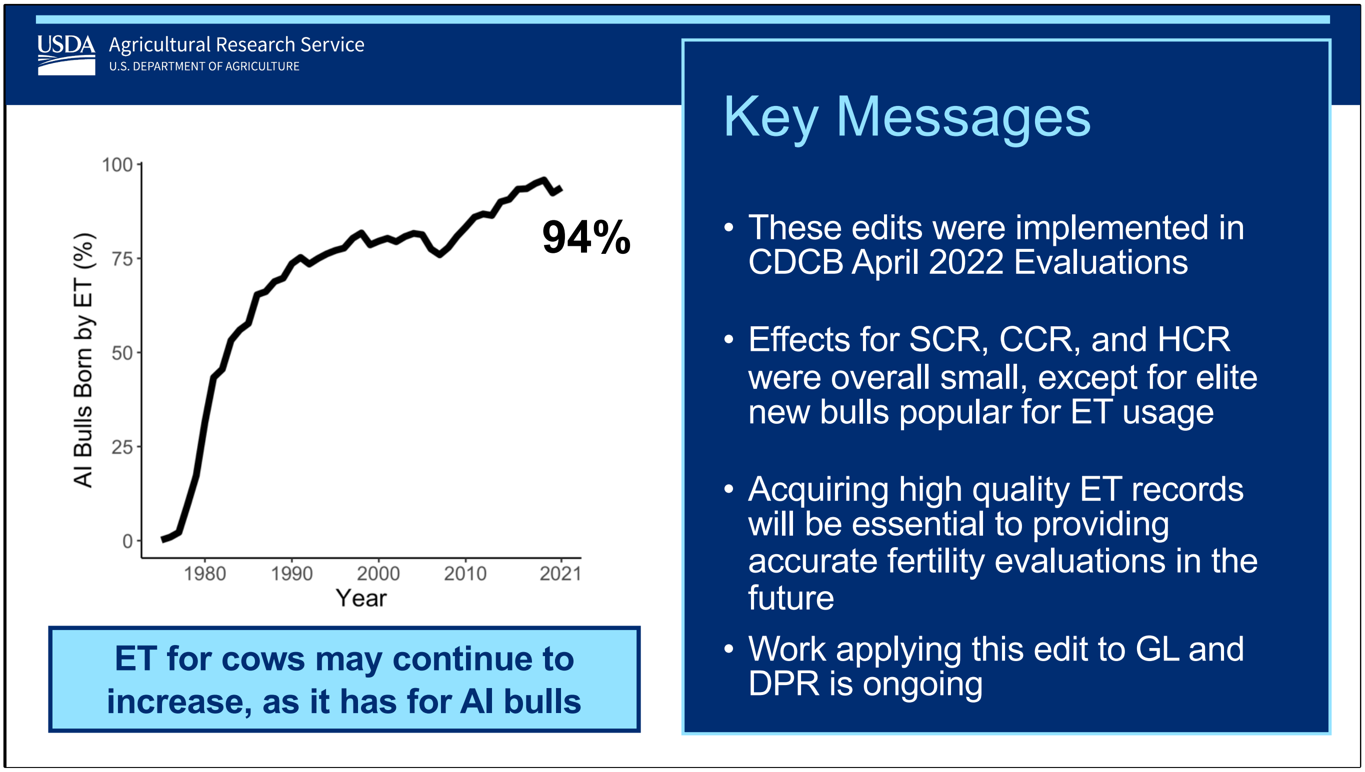
ELITE YOUNG BULLS MOST AFFECTED

Miles et al., under revision

This edit was applied to heifer, cow, and sire conception rates. On the y axis we have the change in breeding value between the original evals and the ones recalculated with newly edited data. Here we see that younger bulls have greater differences and higher Net Merit (red dots). It's important to remember that these differences are still on the scale of 1 or 2 percentage points with a rare exceptions, so the effects are overall small. Correlations between old and new breeding values were all high (on the order of >0.99) and the edit only removed 1-2% of data used in these computations, but this may be a large proportion of data for young bulls with fewer daughter records explaining some of the bigger changes observed in elite young bulls.



ET for cows may continue to increase, as it has for AI bulls

Key Messages

- These edits were implemented in CDCB April 2022 Evaluations
- Effects for SCR, CCR, and HCR were overall small, except for elite new bulls popular for ET usage
- Acquiring high quality ET records will be essential to providing accurate fertility evaluations in the future
- Work applying this edit to GL and DPR is ongoing

Currently, unstandardized ET reporting is having minimal effect, but that is not a guarantee if the ET calf birth rate continues to rise without a parallel increase in accurate ET breeding event reporting. And it’s possible we will see ET for cows follow a similar trend as it has for ET bulls, where 94% of bulls born last year were resulting from ET, in which case accurate ET reporting and updated models will become much more critical. This edit may also be needed for other fertility traits like gestation length and daughter pregnancy rate, and this work is ongoing.

MILKING SPEED:

Summary of Knowledge, Key Questions, & Proposed Research

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

The CDCB Board of Directors has appointed a task force to investigate the feasibility of milking speed evaluations in the US. We meet regularly to move this research forward with the end goal of providing an implementation plan to the CDCB board.

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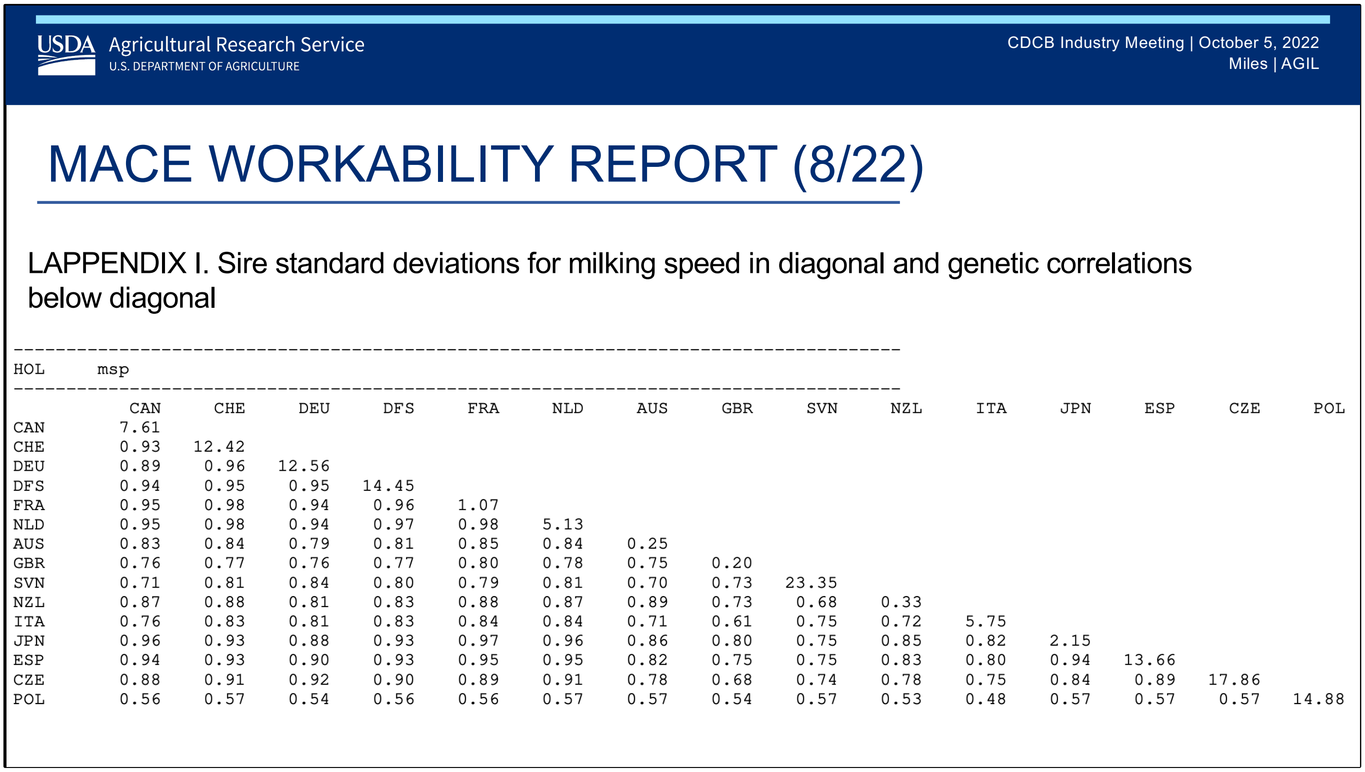
EVALUATIONS FOR MILKING SPEED

- Interbull-participating countries (N = 14) include milking speed in their “workability” evaluations
  - Australia, Canada, Denmark/Sweden/Finland, France, Germany/Austria/Luxembourg, Great Britain, Italy, Japan, the Netherlands, New Zealand, Norway, Poland, Slovenia, and Switzerland
- Nearly all phenotypes collected during first parity only and sometimes from a single classification
- If milk flow rates were available, classification data were discarded

There are 14 Interbull-participating countries currently reporting milking speed, phenotyping usually involved a trained classifier traveling to the farm and working with the farmer to assign subjective scores to their animals. If quantitative data is available they use it, but this is not common. A classification system is unlikely to be practical in the US with larger average herd sizes and the task force agrees that eliminating the human factor is ideal for both reducing labor costs and the biases of subjective scoring.

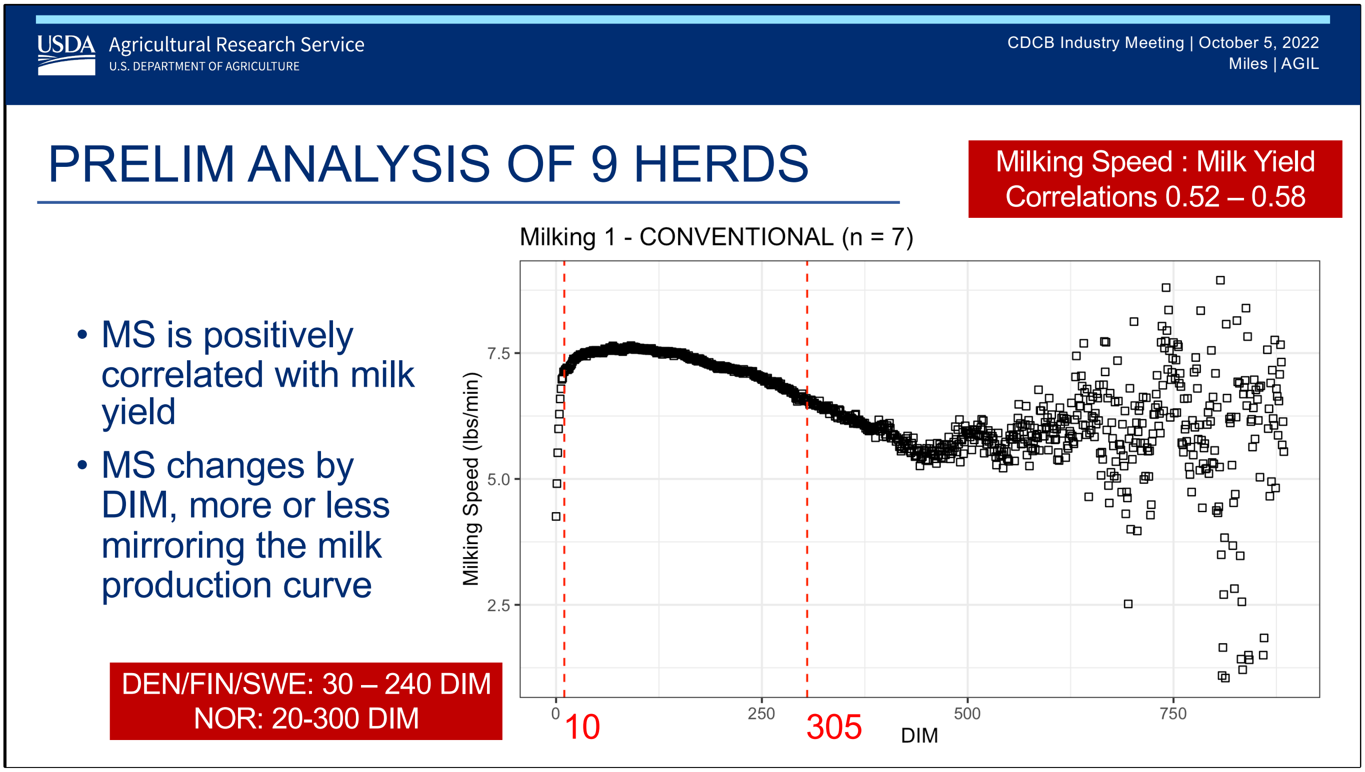


MACE WORKABILITY REPORT (8/22)

LAPPENDIX I. Sire standard deviations for milking speed in diagonal and genetic correlations below diagonal

```
------------------------------------------------------------------------------------
HOL     msp
------------------------------------------------------------------------------------
           CAN      CHE      DEU      DFS      FRA      NLD      AUS      GBR      SVN      NZL      ITA      JPN      ESP      CZE      POL
CAN       7.61
CHE       0.93    12.42
DEU       0.89     0.96    12.56
DFS       0.94     0.95     0.95    14.45
FRA       0.95     0.98     0.94     0.96     1.07
NLD       0.95     0.98     0.94     0.97     0.98     5.13
AUS       0.83     0.84     0.79     0.81     0.85     0.84     0.25
GBR       0.76     0.77     0.76     0.77     0.80     0.78     0.75     0.20
SVN       0.71     0.81     0.84     0.80     0.79     0.81     0.70     0.73    23.35
NZL       0.87     0.88     0.81     0.83     0.88     0.87     0.89     0.73     0.68     0.33
ITA       0.76     0.83     0.81     0.83     0.84     0.84     0.71     0.61     0.75     0.72     5.75
JPN       0.96     0.93     0.88     0.93     0.97     0.96     0.86     0.80     0.75     0.85     0.82     2.15
ESP       0.94     0.93     0.90     0.93     0.95     0.95     0.82     0.75     0.75     0.83     0.80     0.94    13.66
CZE       0.88     0.91     0.92     0.90     0.89     0.91     0.78     0.68     0.74     0.78     0.75     0.84     0.89    17.86
POL       0.56     0.57     0.54     0.56     0.56     0.57     0.57     0.54     0.57     0.53     0.48     0.57     0.57     0.57    14.88
```

That said, looking at the genetic correlations for MS across participating countries for Holstein we see they are quite high. This is encouraging because if this much uniformity can be achieved using subjective scores, we should be able to do pretty well with quantitative ones even across different milking systems.



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PRELIM ANALYSIS OF 9 HERDS

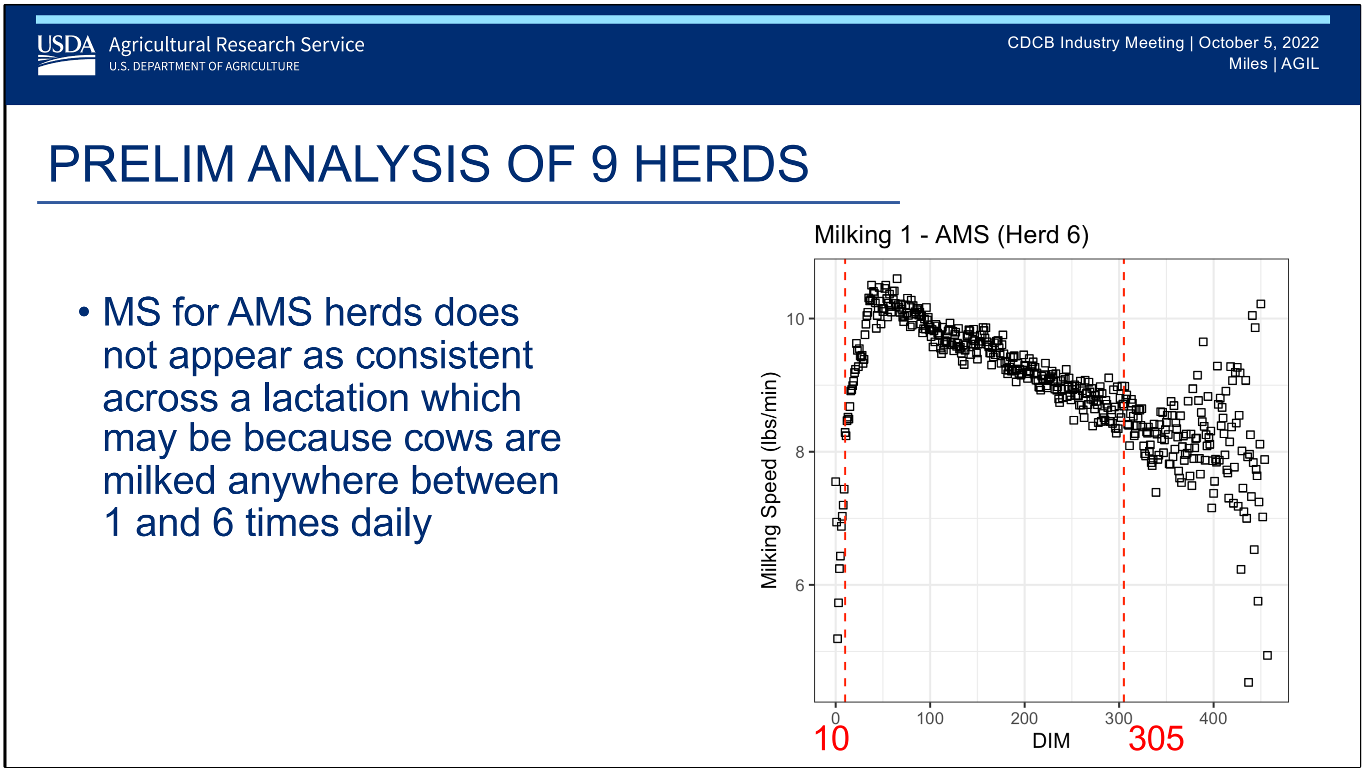
Milking Speed : Milk Yield
Correlations 0.52 – 0.58

- MS is positively correlated with milk yield
- MS changes by DIM, more or less mirroring the milk production curve

DEN/FIN/SWE: 30 – 240 DIM
NOR: 20-300 DIM

Milking 1 - CONVENTIONAL (n = 7)

DRMS provided some archival data from 9 herds, 7 of which were conventional and 2 AMS. Our prelim analysis showed that MS is positively correlated with milk yield and that MS changes by DIM, more or less mirroring the milk production curve. Restrictions to observations within a certain window of DIM are advisable; MS is confounded by inflammation following parturition and the clearance of colostrum during early lactation and changing management (e.g., milking frequency) in the case of extremely persistent lactation. This is already practiced by some other countries using more conservative windows than those shown here.



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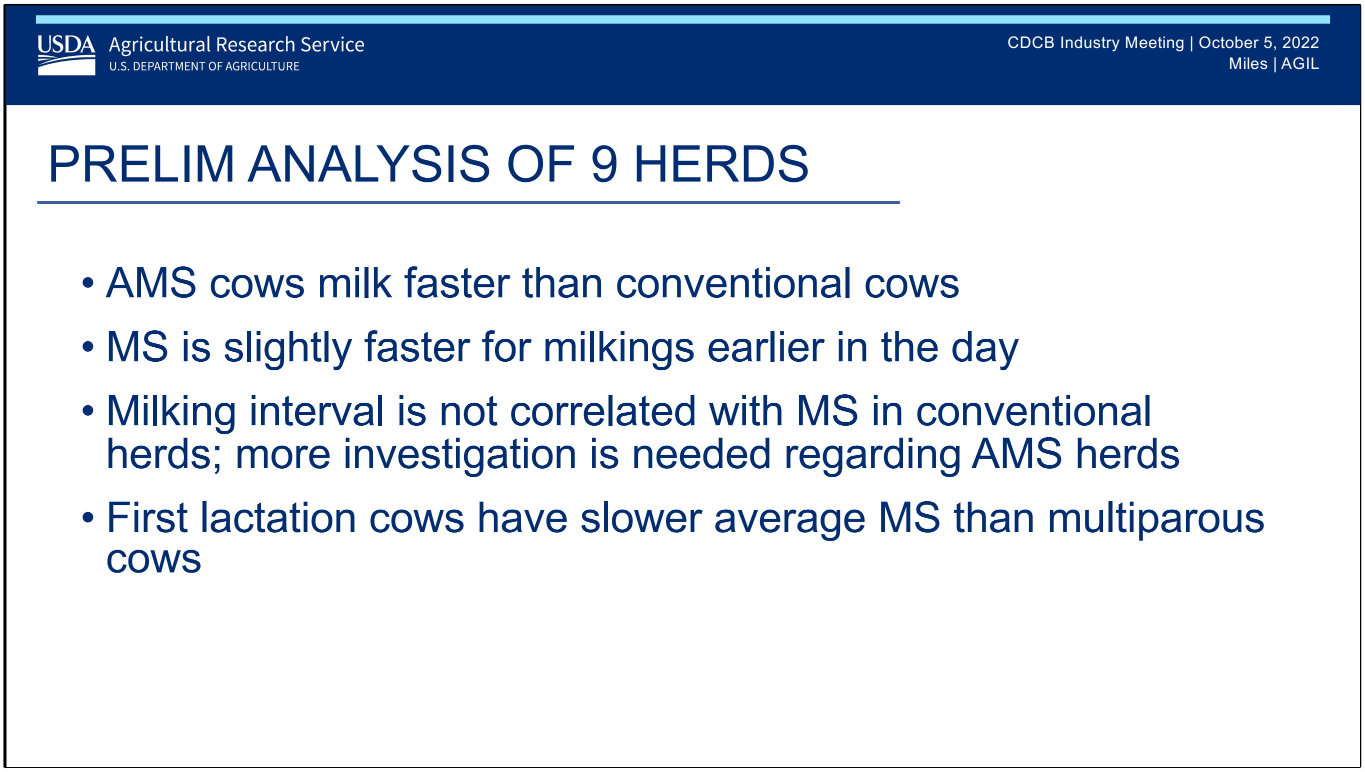
PRELIM ANALYSIS OF 9 HERDS

- MS for AMS herds does not appear as consistent across a lactation which may be because cows are milked anywhere between 1 and 6 times daily

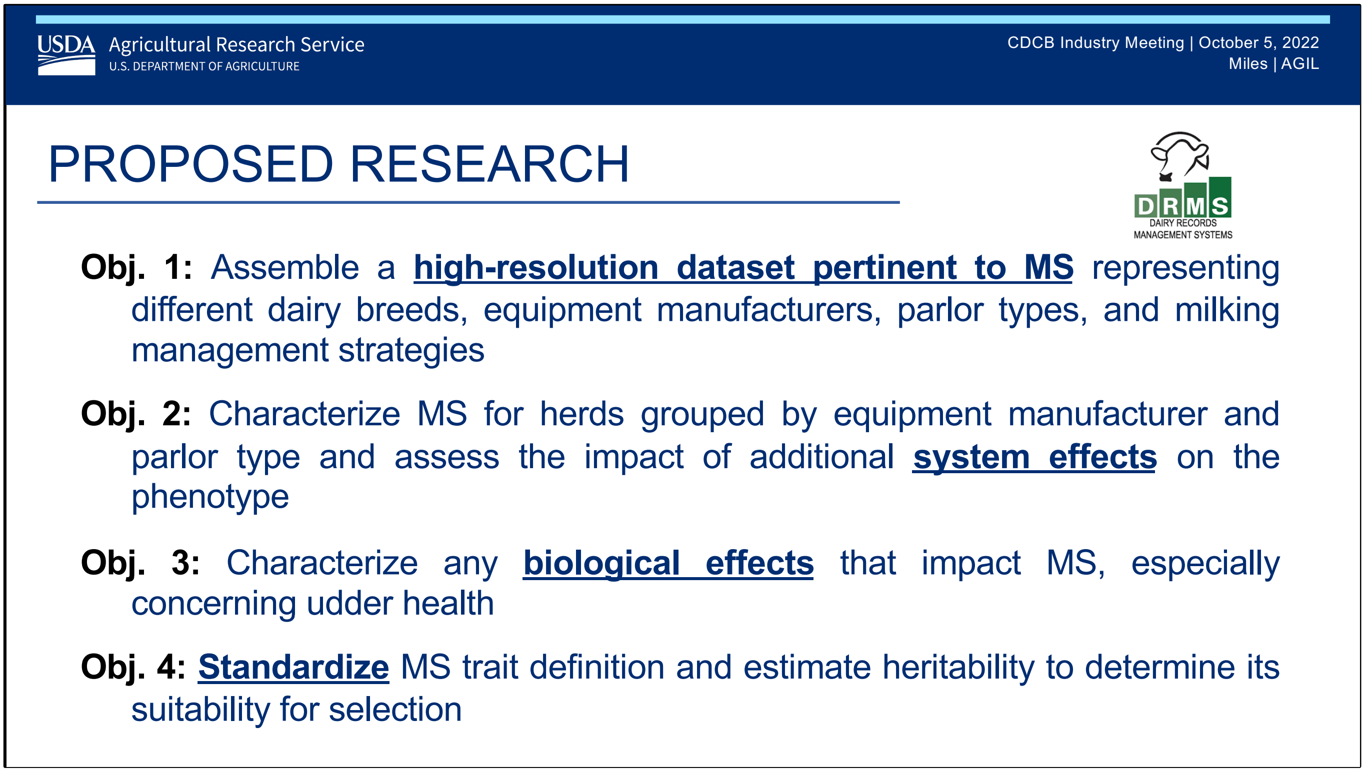
These trends are less clear when we look at the AMS herds that report up to 6 milkings a day per cow, but an individual cow may not have been milked the same number of times each day. One day she may milk 2 times, then 4, then 3, etc. The times of day she milked may also not be consistent. Sophisticated programming will be required to tease out what's happening here, but the bottom line is we need more data before we can draw any conclusions about AMS herds.



PRELIM ANALYSIS OF 9 HERDS

- AMS cows milk faster than conventional cows
- MS is slightly faster for milkings earlier in the day
- Milking interval is not correlated with MS in conventional herds; more investigation is needed regarding AMS herds
- First lactation cows have slower average MS than multiparous cows

What else did we learn? AMS cows tend to milk faster by 1-2 lbs/min than conventional cows, and AMS herds may have been selecting for MS for some time on their own. MS tends to be a little higher for the first milking of the day. MS does not appear to be related to milking interval in conventional herds, but preliminary analysis of the one AMS herd we have data for suggests it may have a bigger impact in those systems. First lactation cows have slower average MS than multiparous cows. This is probably partially explained by culling bias with hard milkers being removed from the herd but could also be related to biological phenomena like the teat sphincter relaxing with increasing age. Many questions could not be answered by this initial dataset. A full investigation of system and biological effects on MS, and the validation and interpretation of these observations, will require the assembly of an extensive, high-quality dataset relating to milking speed.



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PROPOSED RESEARCH

DRMS
DAIRY RECORDS MANAGEMENT SYSTEMS

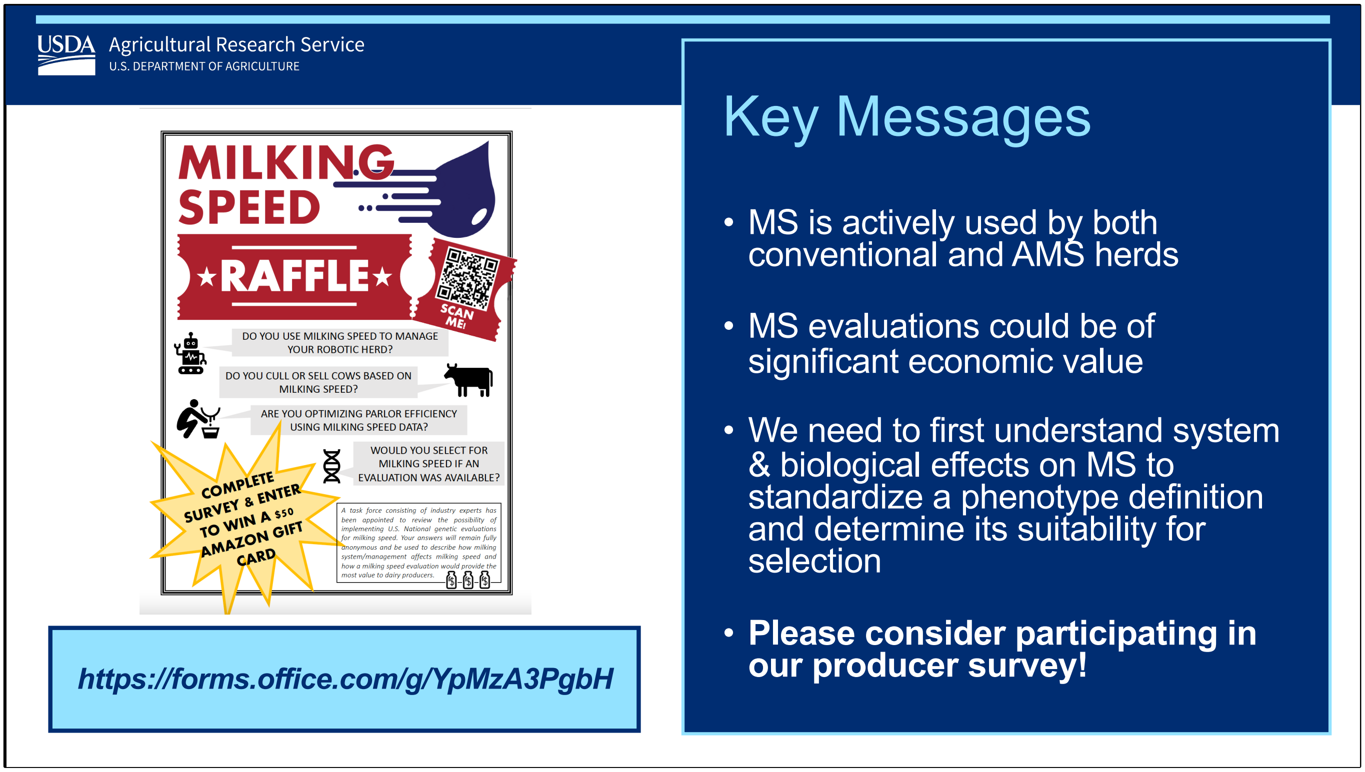
Obj. 1: Assemble a **high-resolution dataset pertinent to MS** representing different dairy breeds, equipment manufacturers, parlor types, and milking management strategies

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

A research agreement is being developed between DRMS and AGIL. Our intentions fall under 4 research objectives: 1) assemble a dataset that can answer these unknowns, 2) characterizing MS by what we are calling different milking systems (a combination of OEM, parlor type, and milking management factors), 2) characterizing MS by biological effects like breed and udder health parameters, and finally 4) using the outcomes from Obj 2 and 3 to develop a method for standardizing MS and assessing its suitability for genetic evaluation



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MILKING SPEED

★RAFFLE★

SCAN ME!

DO YOU USE MILKING SPEED TO MANAGE YOUR ROBOTIC HERD?

DO YOU CULL OR SELL COWS BASED ON MILKING SPEED?

ARE YOU OPTIMIZING PARLOR EFFICIENCY USING MILKING SPEED DATA?

WOULD YOU SELECT FOR MILKING SPEED IF AN EVALUATION WAS AVAILABLE?

COMPLETE SURVEY & ENTER TO WIN A $50 AMAZON GIFT CARD

A task force consisting of industry experts has been appointed to review the possibility of implementing U.S. National genetic evaluations for milking speed. Your answers will remain fully anonymous and be used to describe how milking system/management affects milking speed and how a milking speed evaluation would provide the most value to dairy producers.

https://forms.office.com/g/YpMzA3PgbH

Key Messages

- MS is actively used by both conventional and AMS herds
- MS evaluations could be of significant economic value
- We need to first understand system & biological effects on MS to standardize a phenotype definition and determine its suitability for selection
- **Please consider participating in our producer survey!**

Evaluations for MS may be of significant economic value. If you are a producer who uses MS (or is interested in doing so!) please consider completing our survey (closes Nov 1). We want to hear from you.

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GETTING YIELDS RIGHT:

Evaluating projection factors, updating yield predictions, revisiting daily & lactation yield standardization

Asha Miles, Nick Wu, Paul VanRaden, Curt Van Tassell, Ransom Baldwin, Steven Sievert, Javier Burchard, Jay Mattison, and Joao Durr

NATIONAL DHIA
CDCB COUNCIL ON DAIRY CATTLE BREEDING
USDA Agricultural Research Service
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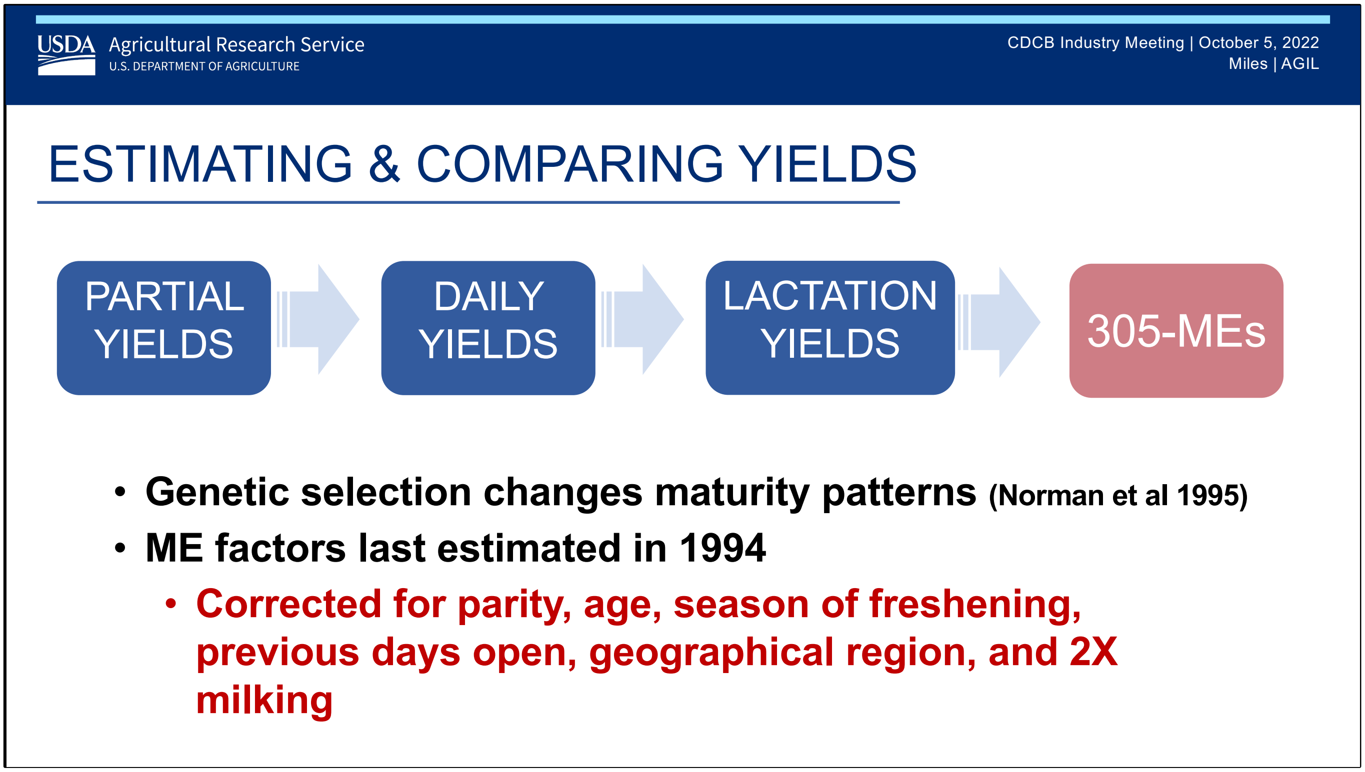
A large research effort is being made to update our estimations of milk, fat, and protein yields in collaboration with NDHIA, CDCB, and AGIL.



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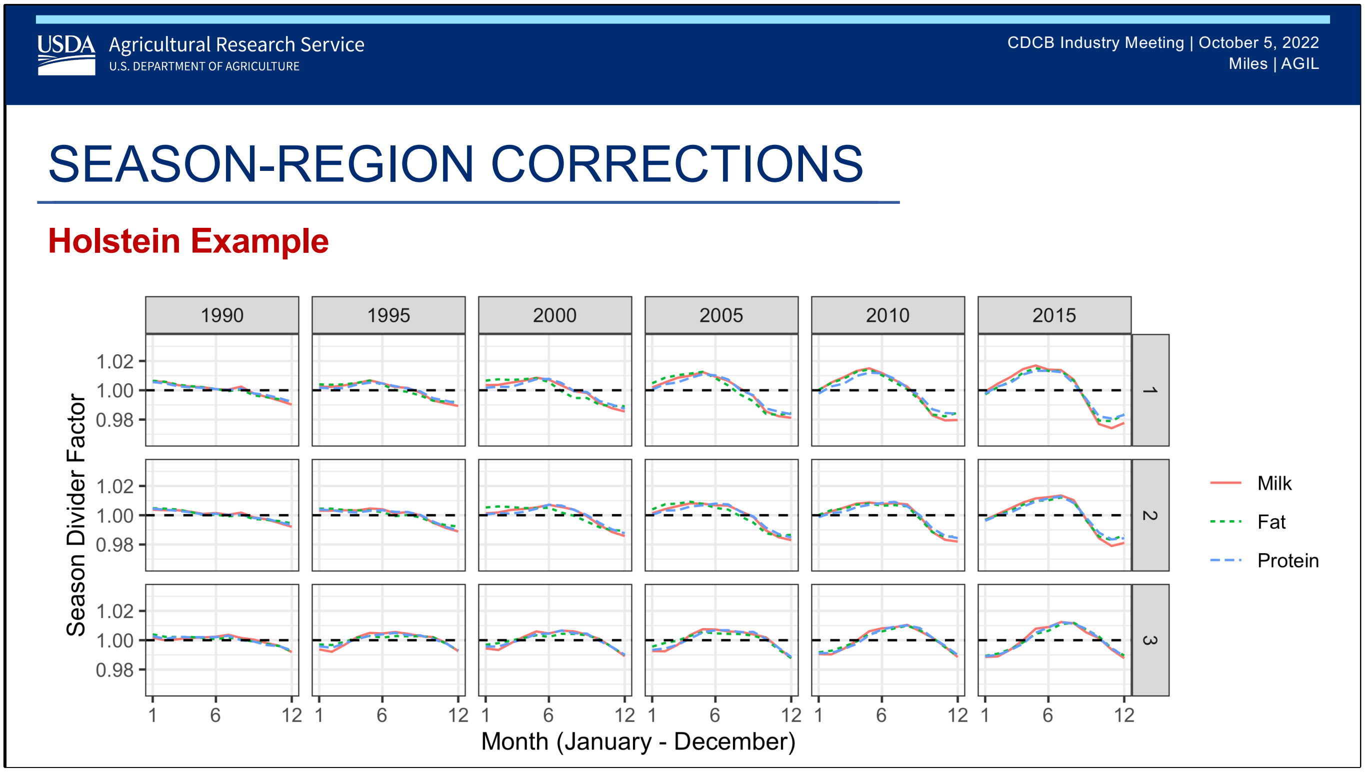
ESTIMATING & COMPARING YIELDS

PARTIAL YIELDS → DAILY YIELDS → LACTATION YIELDS → 305-MEs

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

How do we estimate yields? Herds who want to know their yields participate in DHI testing, where a trained technician travels to the farm and samples a single milking in a day. This only measures part of a cow's yield, and from that her total daily yields are estimated, and these total daily yields from her monthly tests are in turn used to estimate her total lactation yields. These total lactation yields are then standardized to a 305 day lactation length and the "mature equivalent" for her breed. This allows fair comparisons of cows across different environments which is useful for management and key to accurate genetic evaluation. But we know that genetic selection changes maturity patterns, and these correction factors were last estimated in 1994. It is time to revisit them after nearly 30 years.



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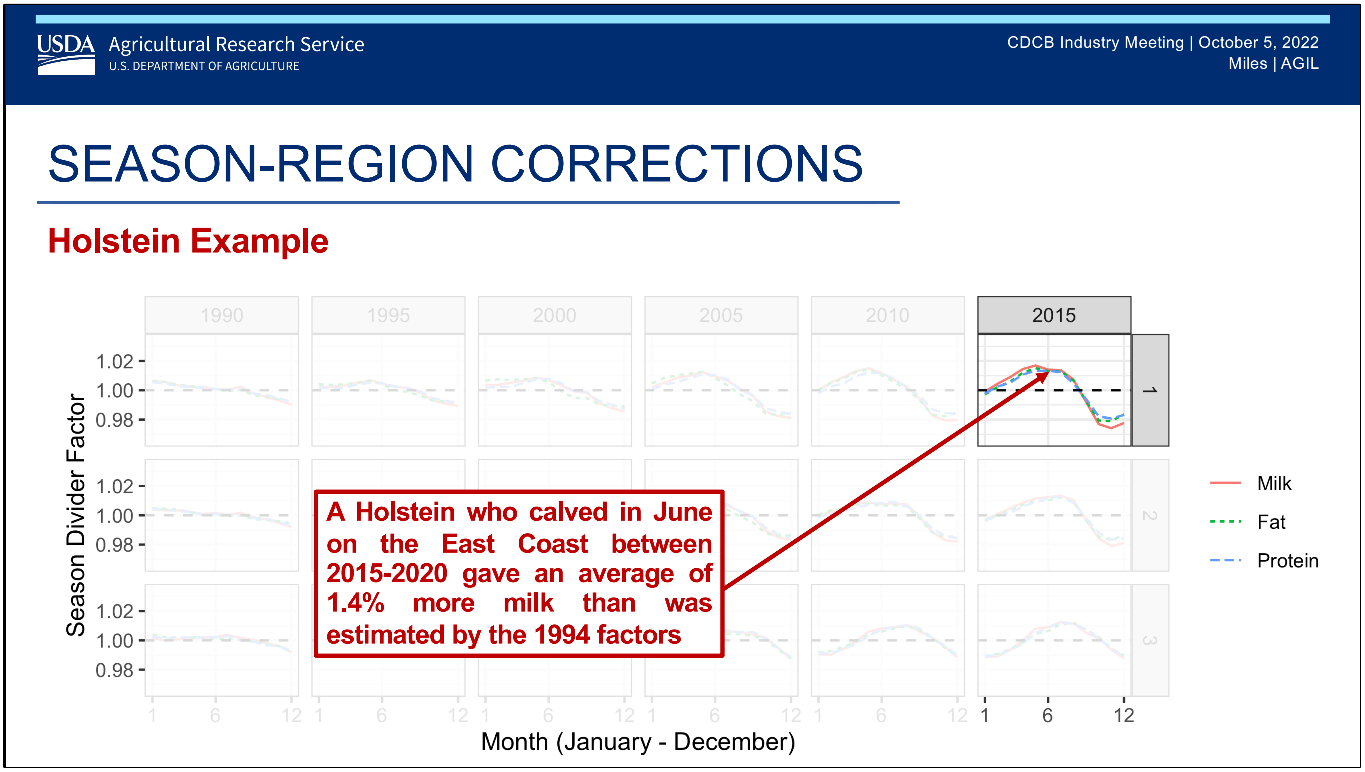
SEASON-REGION CORRECTIONS

Holstein Example

Here is an example of a Season-Region correction shown for Holstein. Lactation records are grouped in 5yr increments for these computations as shown in the column headers. The 3 geographical regions of northeast (1), Midwest + South (2), and West (3) are shown here on the right. Across the X axis for each grid we have month of calving, and the values on the Y are the differences between the seasonal effects observed now & the ones estimated in 1994, normalized to the 1994 factors. The baseline we are comparing to is the dotted line at 1.0 (this is the null value, multiply anything by 1 and it stays the same). If the 1994 factors were perfectly capturing season-region effects we would expect the milk/fat/protein lines to be totally flat alone the dotted line. As we can see that is not happening, seasonal effects are becoming larger over time.



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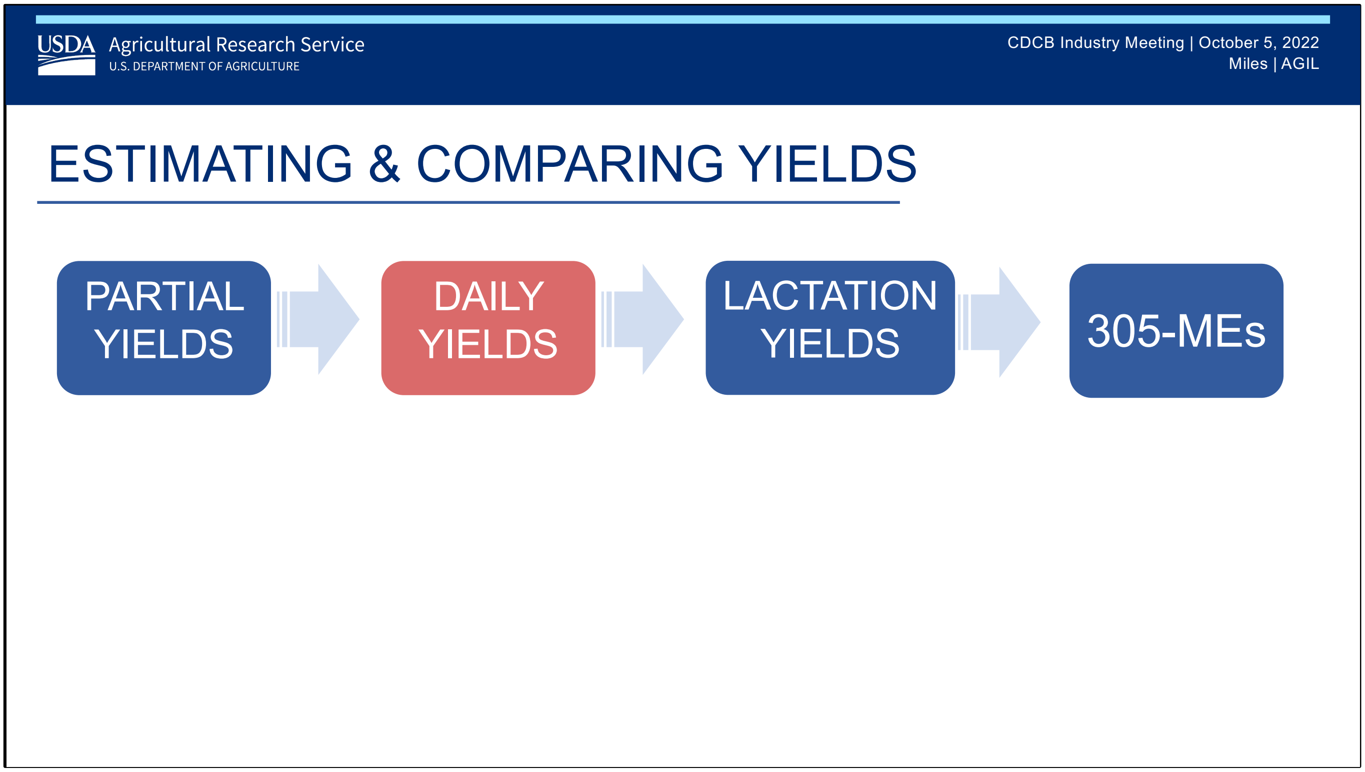
SEASON-REGION CORRECTIONS

Holstein Example

A Holstein who calved in June on the East Coast between 2015-2020 gave an average of 1.4% more milk than was estimated by the 1994 factors

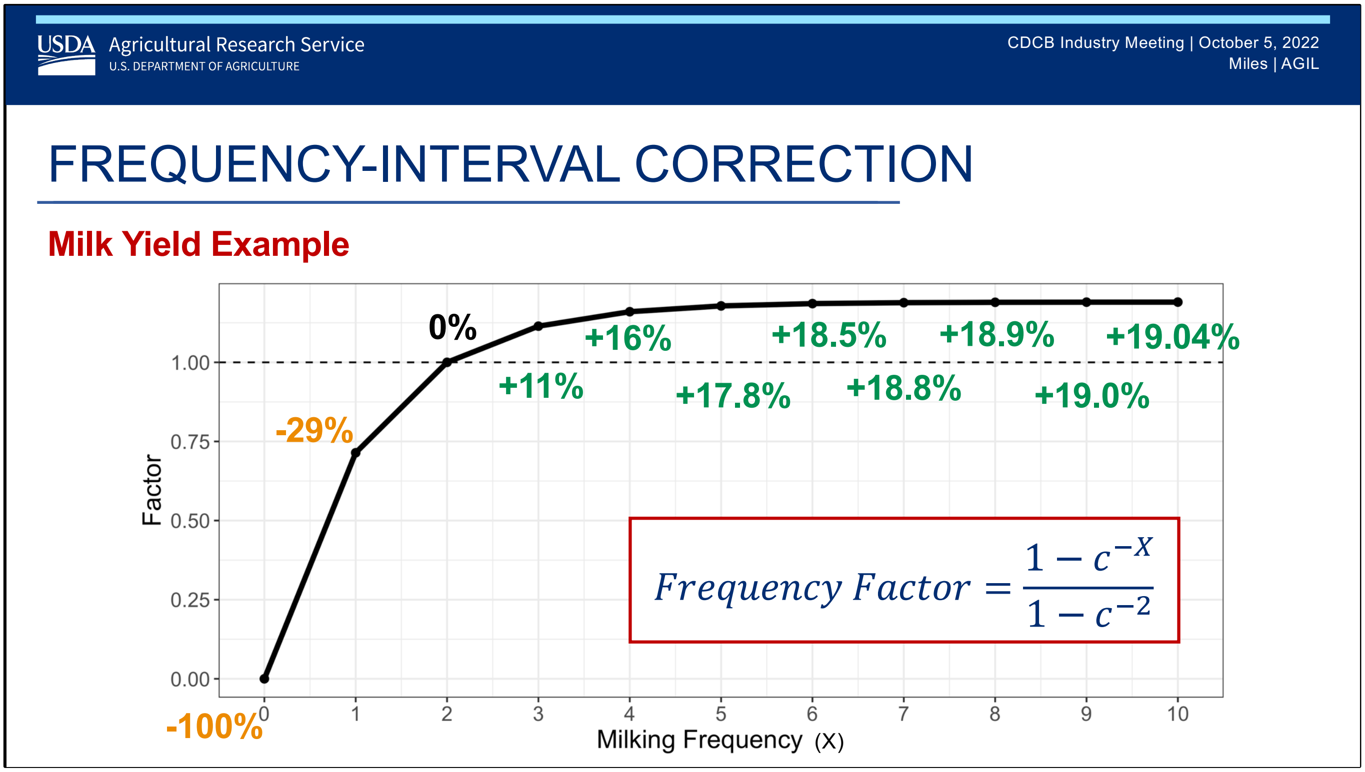
Example interpretation of these factors: A Holstein to who calved in June on the East Coast between 2015-2020 gave an average of 1.4% more milk than was estimated by the 1994 factors. This is good news because it appears Holstein are performing better in hotter months than we predicted they would 30 years ago, and this is likely reflective of the huge strides in heat stress management and suggests we are doing a better job of controlling a cow's environment.



ESTIMATING & COMPARING YIELDS

PARTIAL YIELDS → DAILY YIELDS → LACTATION YIELDS → 305-MEs

We have covered an example of lactation yield standardization but this is also needed for daily yield estimations



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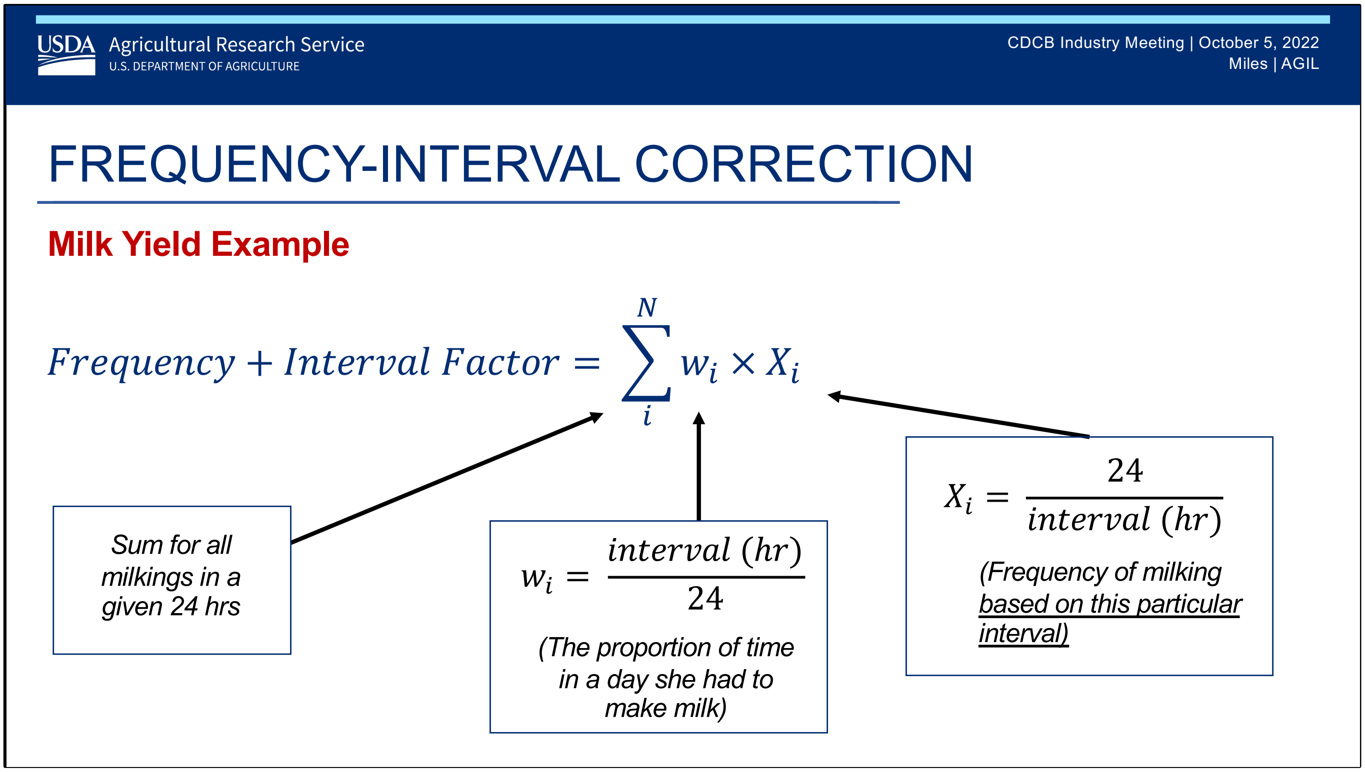
FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

$$Frequency\ Factor = \frac{1 - c^{-X}}{1 - c^{-2}}$$

Currently, all records are adjusted to 2X milking. Our group has developed a new method of adjustment that fits milk yield to a smooth function shown here where "X" represents milking frequency and these factors are adjusted to 2X. A smooth function means this equation is solvable for an infinite # of milkings, so if we plot it out for a hypothetical 10X milking frequency we can get an estimate of the gains in yield achieved by milking more frequently. Again, everything is standardized to 2X so we have a 0% increase in MY shown for the 2X frequency. If you only milked your cows 1X per day you would lose 29% of the production you would have with 2X milking, If you forgot to milk them altogether, you would have a 100% loss in milk yield. Now when we go to 3X we see an 11% increase in MY given compared to 2X, 16% with 4X, and so on until eventually we reach a point of diminishing returns.



FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

$$Frequency + Interval\ Factor = \sum_{i}^{N} w_i \times X_i$$

Sum for all milkings in a given 24 hrs

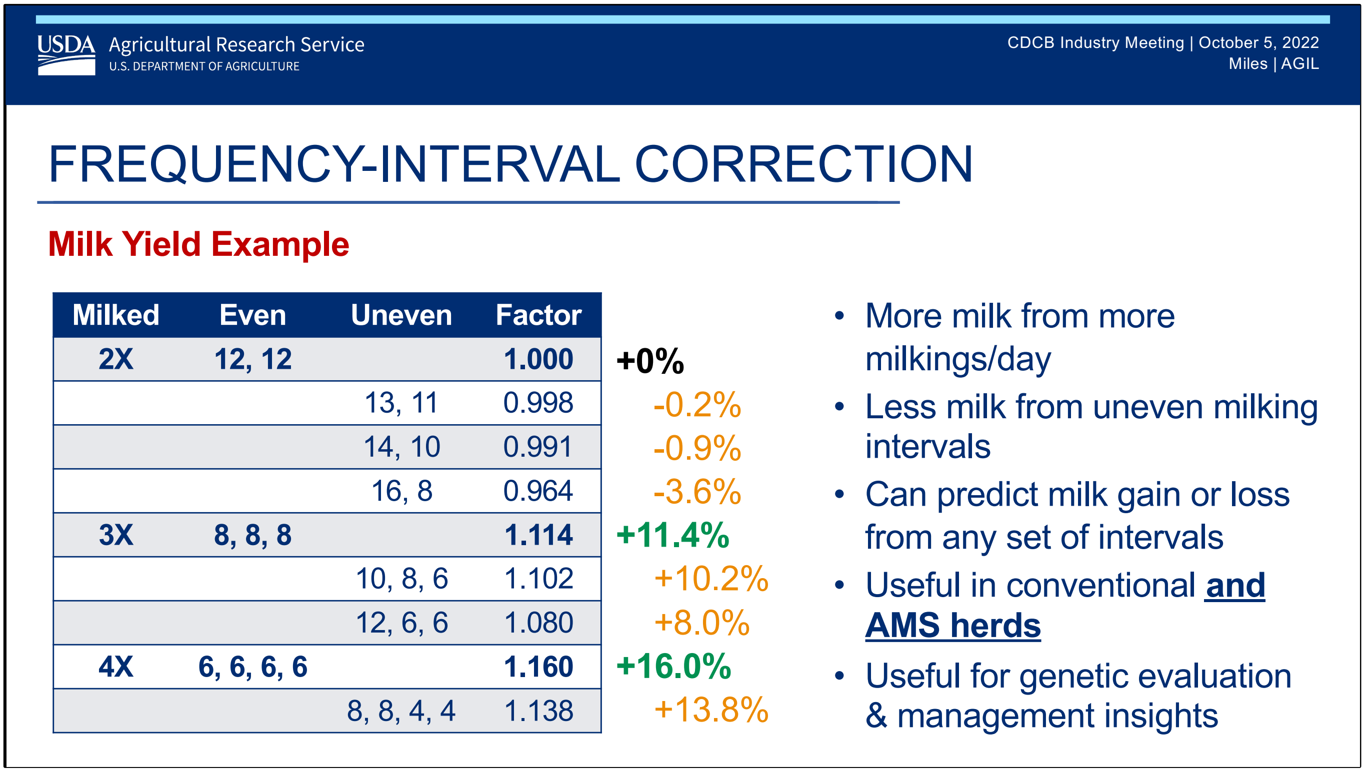
$$w_i = \frac{interval\ (hr)}{24}$$

(The proportion of time in a day she had to make milk)

$$X_i = \frac{24}{interval\ (hr)}$$

(Frequency of milking based on this particular interval)

Now the model shown assumes equal milking intervals which is rarely true and has a known effect on milk yield. We can adjust this using this new equation, where Wi is the proportion of time a cow had to make milk since her last milking, and Xi is the milking frequency BASED ON THE OBSERVED INTERVAL. This is critical because mathematically we can define a fixed # of milkings in a 24 hr period but the cow’s biology does not know that. We might know she is a 3X cow with intervals 6, 6, 12, but if she is milked after 6 hours, she may think she is a 4X cow with intervals 6:6:6:6 and that will be reflected in the amount of milk she gives in her subsequent milking. So this new equation accounts for the impacts of milking interval, and is then summed for all milkings in a given 24 hr period.



FREQUENCY-INTERVAL CORRECTION

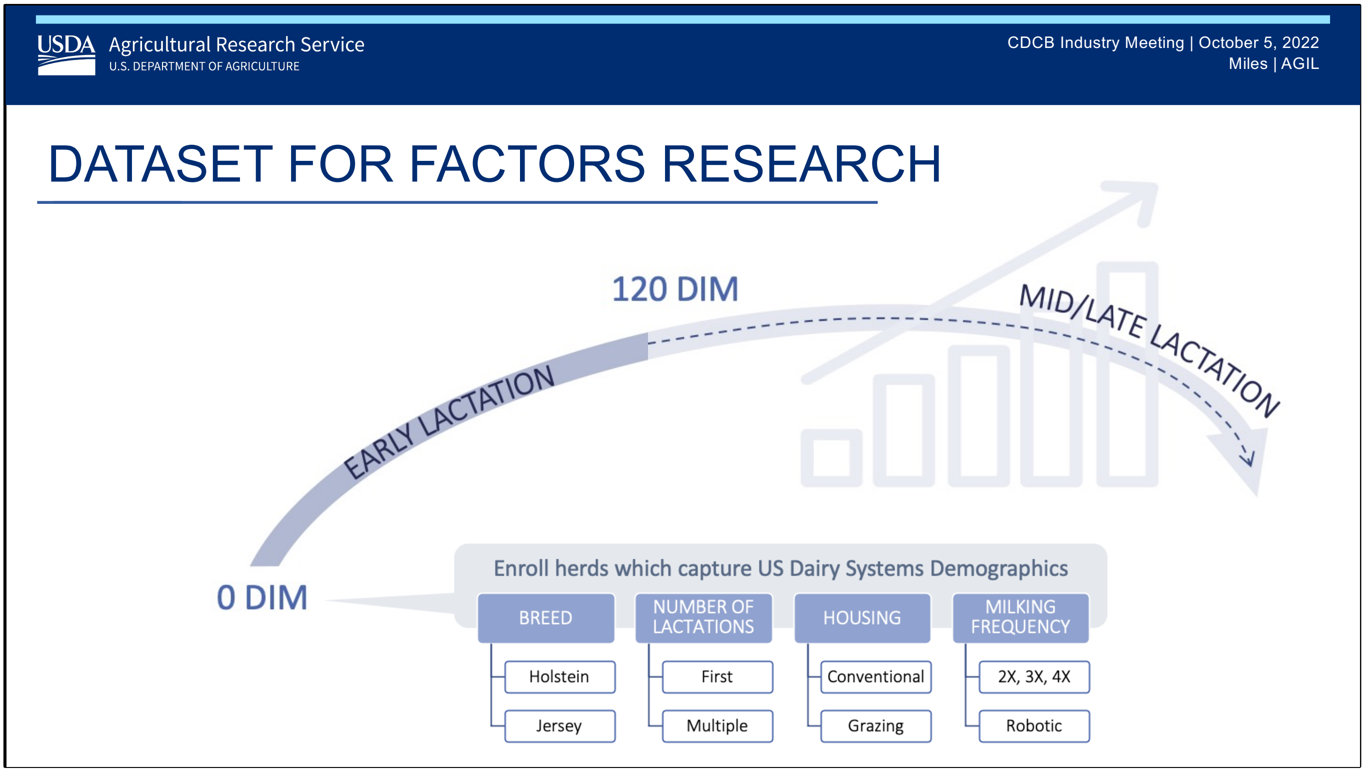
Milk Yield Example

Milked	Even	Uneven	Factor	
2X	**12, 12**		**1.000**	**+0%**
		13, 11	0.998	-0.2%
		14, 10	0.991	-0.9%
		16, 8	0.964	-3.6%
3X	**8, 8, 8**		**1.114**	**+11.4%**
		10, 8, 6	1.102	+10.2%
		12, 6, 6	1.080	+8.0%
4X	**6, 6, 6, 6**		**1.160**	**+16.0%**
		8, 8, 4, 4	1.138	+13.8%

- More milk from more milkings/day
- Less milk from uneven milking intervals
- Can predict milk gain or loss from any set of intervals
- Useful in conventional **and AMS herds**
- Useful for genetic evaluation & management insights

What does this tell us? This table shows the frequencies & gains in yield we saw on the graph earlier, assuming equal intervals. But we can see that if a 2X cow was milked offset by 1 hr, there is a 0.2% reduction in her yield. If she is off by 2 hrs we see a nearly 1% reduction in her yield. But if her intervals are even more significantly imbalanced, then we see a 3.6% reduction in her yield which may be a sufficient pain point to restructure the milking schedule.

We see these same trends repeated for 3X and 4X cows where with unequal milking intervals, they give less milk than if they were milked on even intervals, but STILL they give more milk than if they were only milked twice a day. With this method we can predict milk gains or losses for an infinite set of intervals and frequencies. This will be especially useful as we see more herds utilizing robots, where cows may have highly varied milking frequency and intervals within and across days and so the hope is that this can be a tool useful for genetic evaluation but also management insights. This research was performed using simulation data. Nick Wu (CDCB) has done some preliminary testing with a small yields dataset and reports that this method fits the data quite well, but we need a very comprehensive dataset to do more testing and be confident in all yield estimations.



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CDCB Industry Meeting | October 5, 2022
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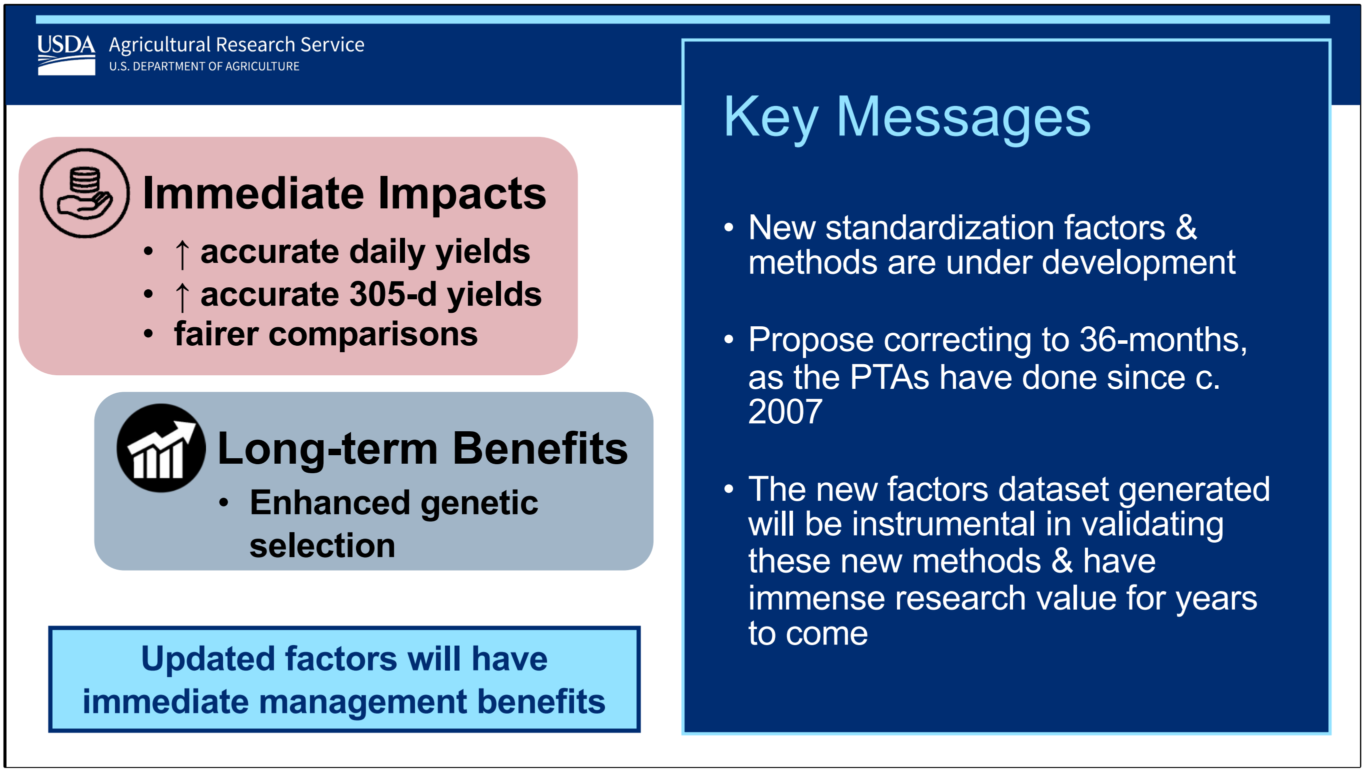
DATASET FOR FACTORS RESEARCH

Enroll herds which capture US Dairy Systems Demographics

BREED	NUMBER OF LACTATIONS	HOUSING	MILKING FREQUENCY
Holstein	First	Conventional	2X, 3X, 4X
Jersey	Multiple	Grazing	Robotic

An effort to assemble this type of dataset is underway, spearheaded by NDHIA and CDCB. This project involves enrolling dairy herds across the US, considering factors like most common breeds, number of lactations, and management styles to capture US dairy systems demographics. This graphic details our initial approach and later phases will expand to include other breeds. A subset of cows will be chosen from each herd and sampled weekly, capturing milk & component yields & milking interval. Intensive sampling has been designed for the first 120 DIM when key economic decisions are being made and we want as much resolution as is realistic to understand yield trends, then this subset of cows will be sampled according to their regular DHIA schedule along with the rest of the herd. This approach will give us a curated, high-quality dataset which has not existed before and will allow us to both characterize the modern cow and explore different methodologies to identify the best approach to accurately predicting yields.



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Immediate Impacts

- ↑ accurate daily yields
- ↑ accurate 305-d yields
- fairer comparisons

Long-term Benefits

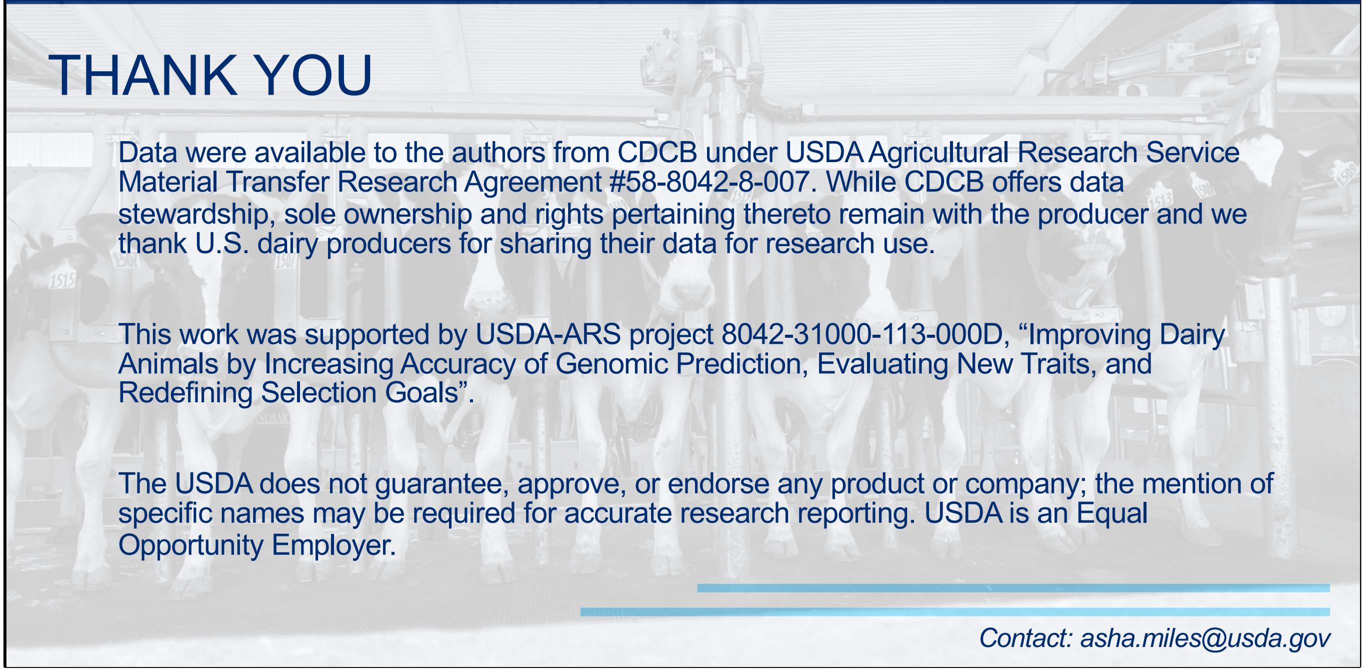
- Enhanced genetic selection

Updated factors will have immediate management benefits

Key Messages

- New standardization factors & methods are under development
- Propose correcting to 36-months, as the PTAs have done since c. 2007
- The new factors dataset generated will be instrumental in validating these new methods & have immense research value for years to come

This research will have immediate management benefits but also be key to continuing to deliver accurate genetic and genomic evaluations to the industry. Not detailed earlier due to time is the recommendation that 305d standardization factors be corrected to average age (36 mo) rather than “mature equivalent”. Few cows reach mature age and correcting to average age also allows fairer comparisons across breeds. This strategy has been used for standardizing traditional PTAs since ~2007 when we moved to the all-breed model.



THANK YOU

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