USDA AGIL Research Updates:
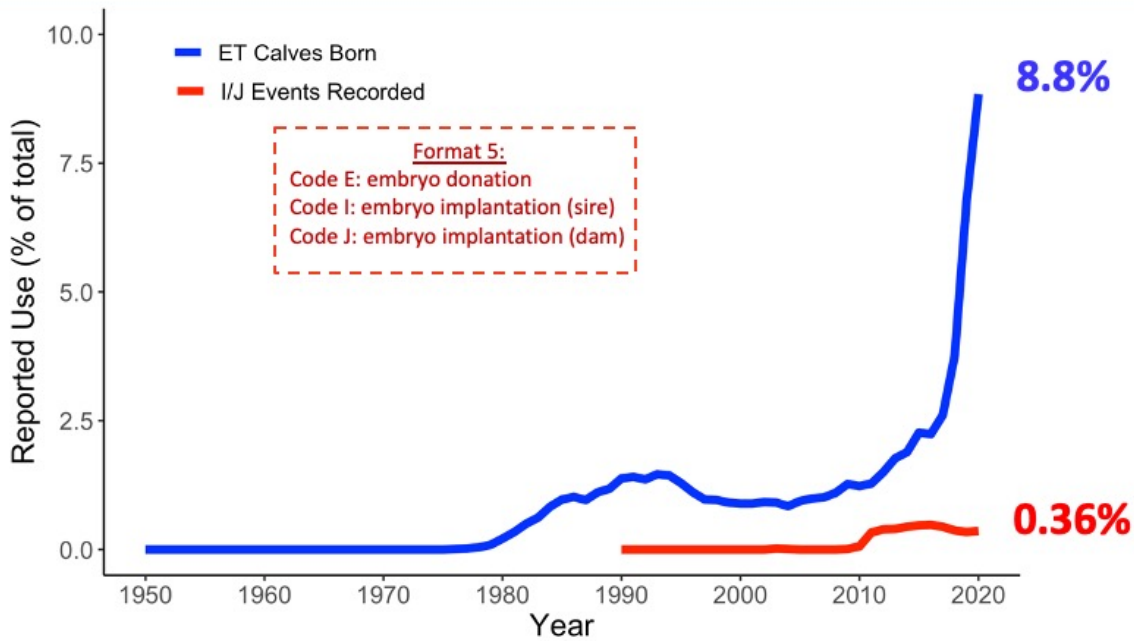
Improving dairy animals by increasing accuracy of genomic prediction, evaluating new traits, and redefining selection goals

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This research is motivated by the exponential increase in calves reportedly born by ET in the last few years. Disappointingly, ET breeding event reporting has not followed the same trend. These come to us through Format 5 codes which have not been available as long as commercial ET use (took off in 1979), but were adopted by the industry in 2002….and yet they still accounted for less than 1% of breeding types in 2020 and are just a fraction of what we would expect given the higher prevalence of ET calves being born.
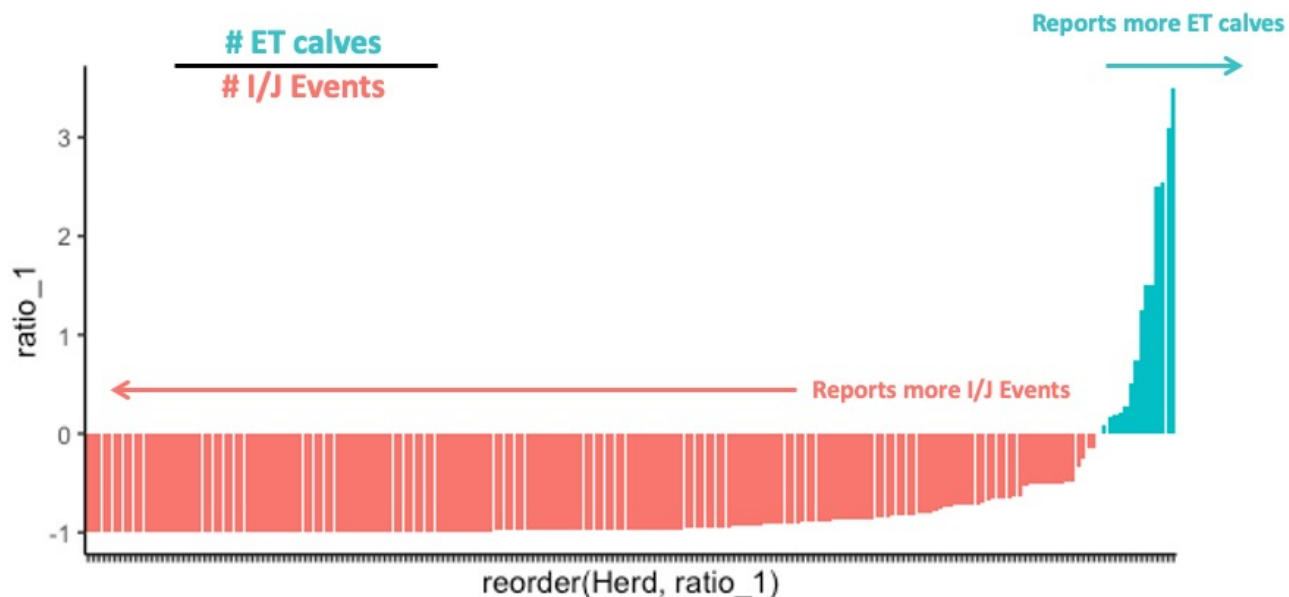
Herds that use a lot of ET are often large and important to the US dairy cattle population so we don't want to remove them entirely, nor should herds responsibly coding ET use be penalized. One possible solution to clean-up this historical data is to censor herds with huge discrepancies in the # of ET calves born compared to the amount of I/J they report. Disappointingly, only 208 herds report both ET and IJ (for context, 964 report ET calves, 1054 report I/J events), but even among herds who report both ET calvings and I/J events, there is little consistency. Here we show a ratio of ET calvings to IJ events, and while overall we are getting many more records of ET calves being born, the majority of farms who are consistently sending us ET data tend to report more I/J events than they do calves born. This could be for any number of reasons, including ET not taking and her next calf being born by a clean-up round of AI or natural service, but that final breeding event not making it into herd management software. We have no way of knowing what the deal is.

Embryo Transfer & Fertility Evaluations

Dr. Asha Miles
Jana Hutchison
Dr. Paul VanRaden

Proposed Edit:

1) **Identify herdyears reporting a substantial amount of ET**
   Defined as > 10% calves born by ET

2) **For those herdyears, remove records if reporting less than half of the I/J events expected given the # of ET calves born**

Determine effect of ET (example):

$$SCR_{DIFF} = \text{Proposed SCR} - \text{Current SCR}$$

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We spent considerable time looking at this historical data and found many anomalies, like 26% of herdyears which reported I/J events, but no calves born at all, ET or otherwise. Curiously, nearly 2% of herdyears reported ET calves evidently born by immaculate conception with no breeding events of any kind. Ultimately we have imposed a 2 step edit which allows us to preserve as much data as possible while removing data most likely to confound our estimates of fertility. Let's take the example of Sire Conception Rate (SCR) and we are evaluating the edit's impact by looking at the difference in SCR estimates with and without ET censoring
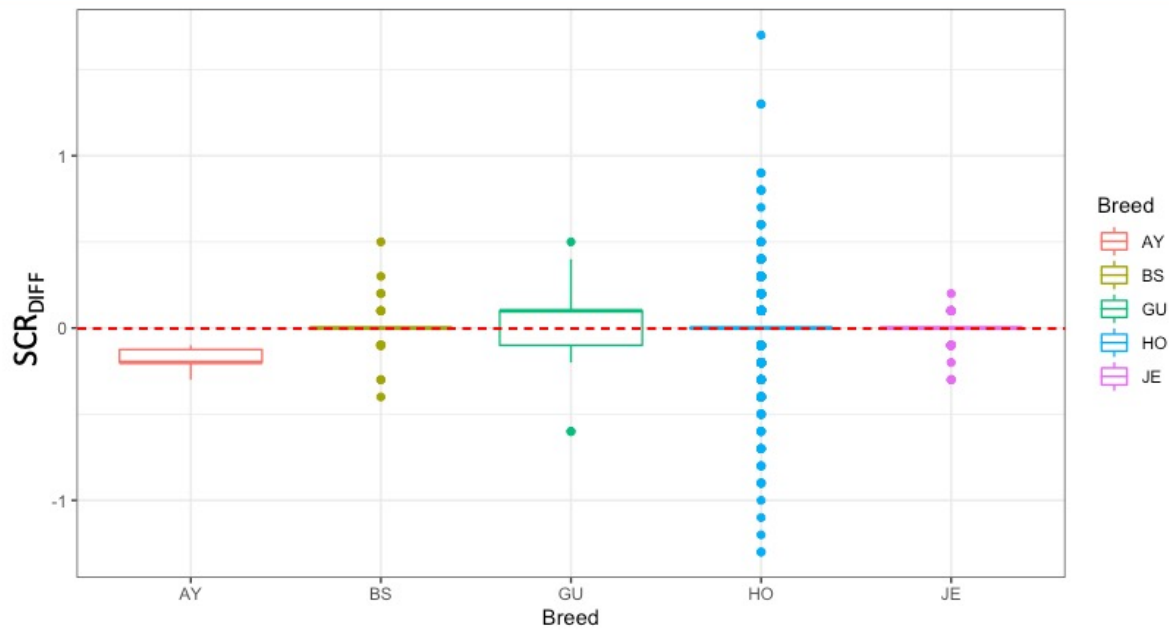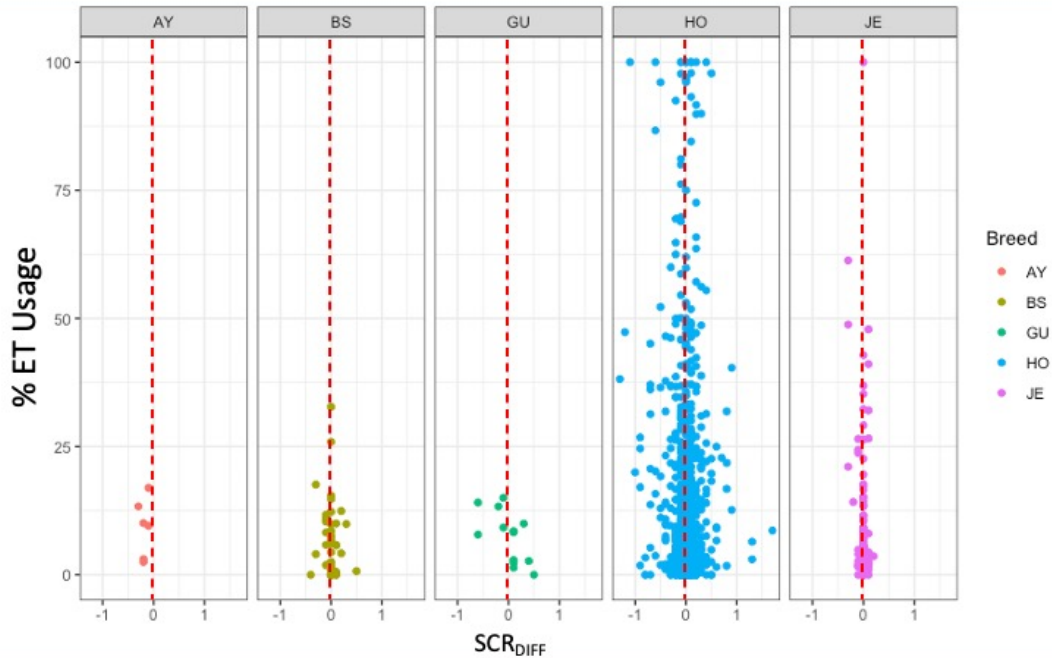
If we look at this difference in SCR by breed, we see nearly all median differences are zero showing the edit is actually having very little effect on evaluations for SCR

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We would expect high correlation of DiffSCR and %ET usage given that records were censored on the basis of ET usage.

If we plot ET useage by SCRdiff for each breed, It seems the service sires with the largest ET % tend to have an SCRdiff of nearly zero – this is most likely a function of total number of matings, with popular, proven bulls being prioritized for ET over young bulls, and their larger number of records making the small proportion of ET errors negligible.
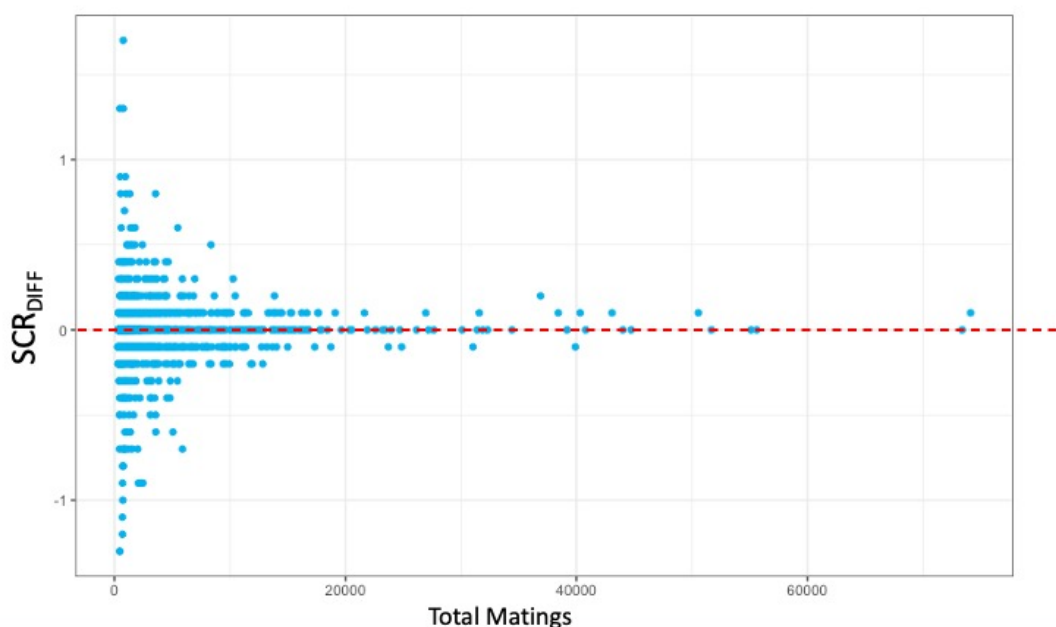
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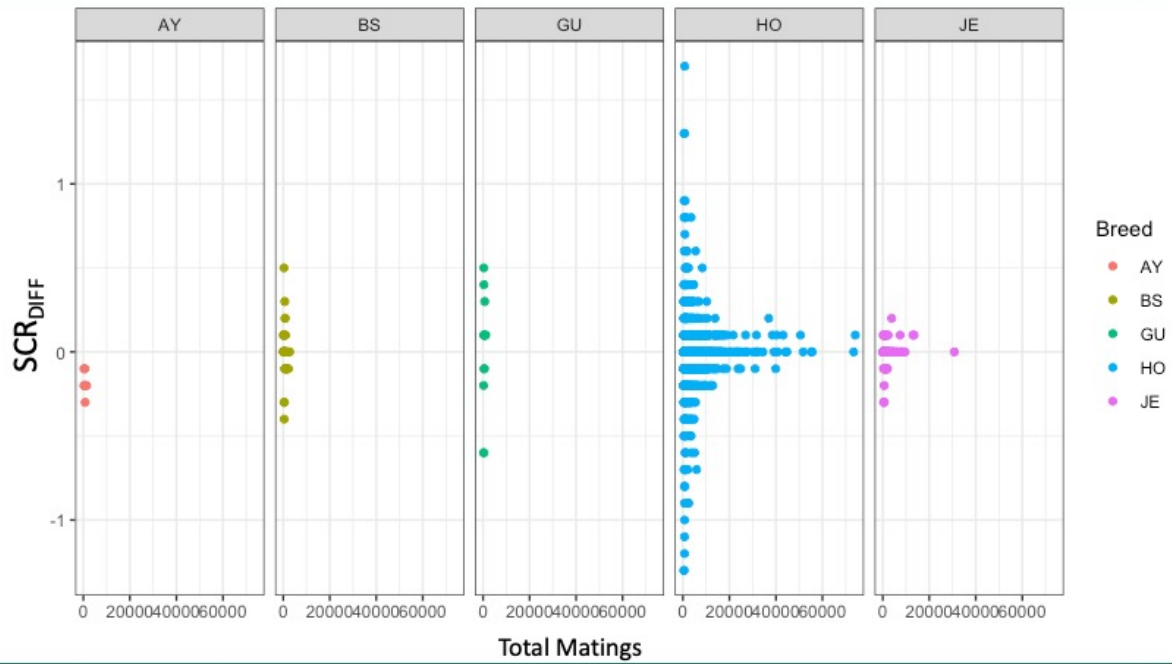
This theory is supported by regressing SCRdiff on Total Matings. The easiest to interpret example are Holstein because there is so much data:

As more mating records are added the diff in SCR converges on zero. This explains anecdotal reports of young bulls whose estimates may change a lot as more records are added. *The good news is, consistent with statistical theory, the more records we add the closer we get to the true value, and the true value of ET influence on SCR for proven bulls appears to be nearly zero.* It's important to note here that even for non-zeros, we are still talking about a difference of +/- 1 percentage point which is going to have very little effect .
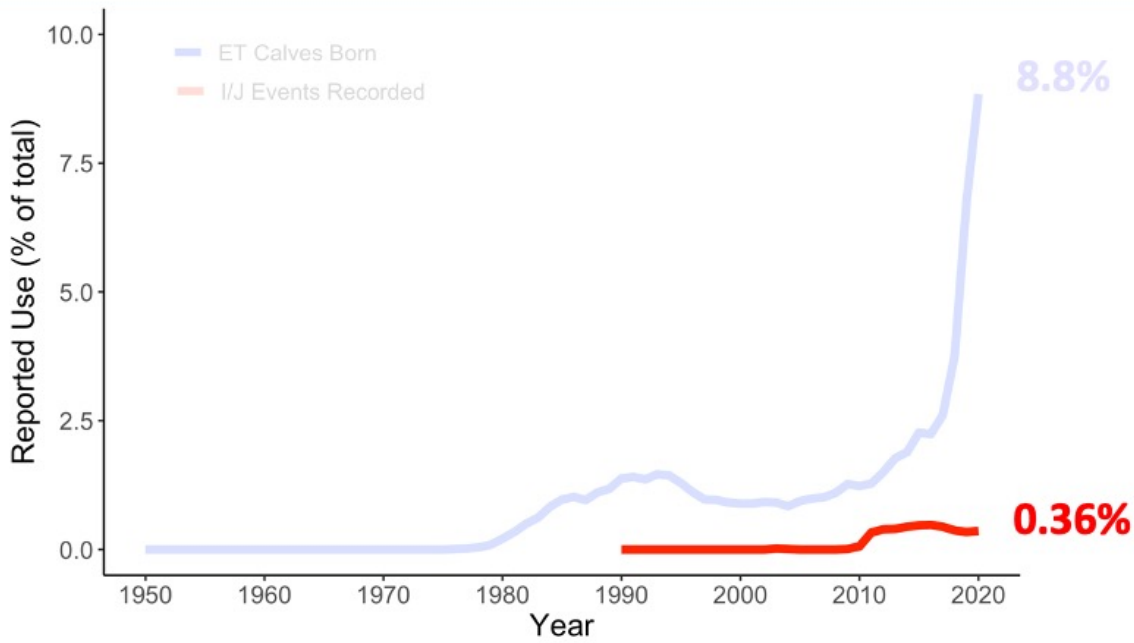
Let's close by revisiting this slide. Given our earlier discovery that some farms are reporting IJ but not ET, it's likely that ET is even more prevalent than we realize
We need strategies to improve data flow before this gets on top of us (right now ET is having very little effect, that is NOT a guarantee if ET calves keep increasing at this rate without a parallel increase in I/J reporting)
It's not obvious in this plot, but if we zoom in on IJ reporting only

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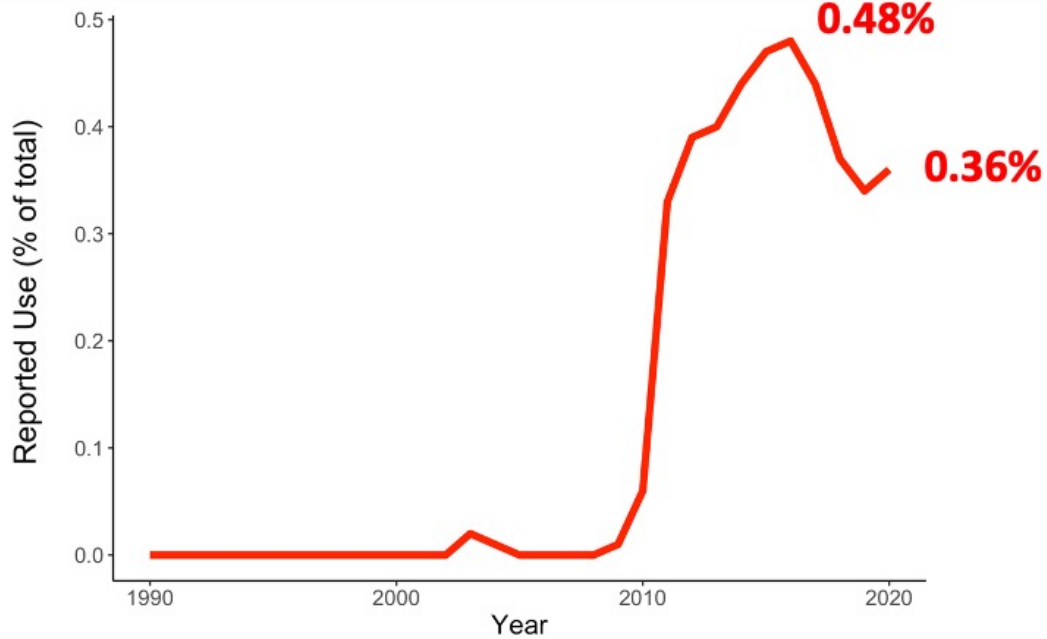
We can see that they peaked in 2016 and then actually experienced a fairly steady decline since then. Which is rather discouraging, and reemphasizes the need to improve reporting. It is not clear where the issue is (barriers to correct use of herd management software, poor reproductive management on farm, roadblocks at DRPC level)

Embryo Transfer & Fertility Evaluations

What do we know?

- ET calves are not being reported as AI
- They are having a low impact even after our edits
- There's not much we can do to clean up historical data
- This means improved data flow is critical
  - Identifying roadblocks

AGIL has completed edits for HCR and CCR
- effects continue to be small overall

## Targeting April 2022 implementation

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The key to improving data flow is to ID roadblocks – the PDQ (Pursing Data Quality team which advises CDCB) identified the primary obstacle to be on-farm recording and a few years ago disseminated resources on correct ET entry into the most common herd management softwares. It seems likely that herd owners and managers who invest so much in running an ET program would have decent management of it, and the problem is that these data aren't reaching us. DRMS believes they are sending all ET records from herds which use PCDART, but we did find inconsistent reporting from those herds so they are investigating. VAS updated DC305 so ET is integrated into their SSF format. In the meantime, AGIL has looked at the effects of ET on SCR/CCR/HCR and aim to implement these edits in national genomic evaluations by April 2022. Down the road we may look at early first calving and DPR to partition genetic effects for conception v. pregnancy but that will depend on many factors related to data quality and availability.

Flexible Testing & Milk-Only Records

Dr. Paul VanRaden
Gary Fok

- Some farms with in-line milk meters do not participate in DHI testing; they record milk weights but not fat and protein

- National genetic evaluations exclude milk-only records; these records are stored but never extracted

- There is not a need for more milk records, but removing the censorship of herds without approved component sampling will allow us to use all of their other traits

These edits have resulted in nearly 1 million additional records that can be used to improve the accuracy of prediction for lower heritability traits
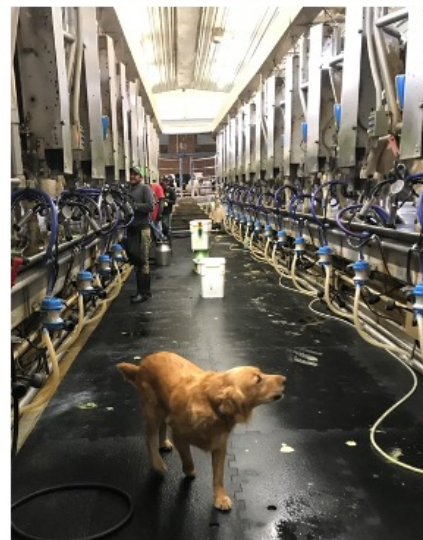
Jack, a Pennsylvania Herd Manager, supervises morning milking

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Members of our group have recently turned attention to the benefits of flexible testing options. Some farms have their own method for getting milk weights, perhaps appx SCC, not participating in DHI monthly testing so no Fat and Protein records. Currently data filtering edits assume fat yield is always recorded and excludes milk-only records, because we don't know that self-measuring farms are meeting quality certifications for meters. So while some milk-only records do reach us, they are stored but never extracted. We don't really need more milk records, BUT, including those herds will allow us to use records for all of their other traits. These edits (which only include data from milk-only herds with certified milk meters) have resulted in nearly 1 million addition records which will improve prediction for lower h2 traits where a larger number of records are required for high accuracy
Programs are finished and CDCB is testing them for April 2022 implementation.

Long term considerations

Our 5-year plan has been submitted

Finished interviewing for new AGIL geneticist

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Every 5 years ARS laboratories submit a plan for future research which goes through a similar review process to grant proposals and is an important step in our funding allocation by Congress. Our plan has been submitted for peer review & we will need to respond and revise based on those comments. This process won't be done until the spring. We finished interviewing candidates for a new geneticist at AGIL yesterday. We should be making an offer in the next week or two. We welcome the addition to the team because primary feedback for 5 year plan thus far is that it is very ambitious given how little staff we have at the moment.

Thank you. Questions?

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As always, I thank you for your time and would like to invite any questions.