USDA AGIL Station Report

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One of our highest priority projects is looking the use of embryo transfer and its impact on evaluations of fertility. This was motivated by the exponential increase in calves reportedly born by ET (blue line) in the last few years. Disappointingly, ET breeding event reporting (red line) 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.

Code	Mating Type	ET Births	All Other Calvings		_	
А	AI	35,100	11,060,000	0.32%	The rate at which ET is incorrectly recorded	
G	AI (sexed semen)	14,833	1,175,795	1.25%		
Ν	Natural Service	2,035	584,971	0.35%		
E	Embryo Donation	0	13	0.00%	The rate at which FT is	
I/J	Embryo Implantation	372	1.25%	correctly		
	This suggest	ts ET is not l	peing reported at a	ıll,		
	rather tr	iali Deilig ie				

Is this discrepancy because ET is incorrectly being coded as AI?

This discrepancy led us to wonder if ET is being incorrectly coded as AI. Using a subset of data from the last 5 years, we matched reported mating types with the recorded birth types, under the assumption that ET calving is more likely to be recorded correctly than breeding events. We can interpret the first line of this table to say that 35,100 AI breedings correspond to calves who were later reported born by ET, suggesting ~.3% of AI matings are likely incorrectly reported. We extrapolated this to other breeding events and see the error rates are consistently low. This appeared to be good news, but if you note the green % in the lower right you'll see that ET is also being reported correctly at a very low rate.

While this is a start to understanding the problem, it's not fool-proof. For example, this approach does not distinguish instances when the genetic and maternal dams are the same but the calf is coded ET, and that conflict would seem to indicate that the calf is not really ET, it is AI! Or it could indicate that the calf is ET but the owner forgot and reported the maternal dam instead of the genetic dam, in which case it is a pedigree error.

Embryo Transfer & Fertility Evaluations

Dr. Asha Miles Jana Hutchison Dr. Paul VanRaden



Now 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.



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 born, but absolutely no breeding events ET or otherwise. Ultimately we have imposed a 2 step edit (see slide). This allows us to preserve as much data as possible while removing data most likely to confound our estimates of fertility. We have begin testing with SCR, and we are evaluating its impact by looking at the difference in SCR estimates with and without ET censoring.



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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 SCRdiff and %ET usage given that records were censored on the basis of ET usage. It seems the service sires with the largest ET % tend to have an SCRdiff of nearly zero – this is almost certainly 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.



This theory is supported by regressing SCRdiff on Total Matings. The easiest to interpret example are Holstein because there are so much data:

Embryo Transfer & Fertility Evaluations



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 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 .



I want to close by revisiting this slide. Given our earlier discovery that some farms are reporting IJ events but not ET births, 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 usage keeps increasing at this rate).



It's not obvious in the earlier plot because of the scale, but if we zoom in and look only at I/J event reporting we can see that they peaked in 2016 and then actually experienced a fairly steady decline since then, which is rather discouraging

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

Next, AGIL will look at HCR and CCR

 effects may be larger than what we are observing for SCR (e.g., in cases where daughters were ET recipients)

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 like that herd owners and managers who invest so much in running an ET program would have decent management of it, the problem is that these data aren't reaching us. In the meantime, AGIL will continue looking at the effects of ET on SCR, HCR, and CCR, and aim to implement these edits in national genomic evaluations by April 2022.

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Flexible Testing & Milk-Only Records

Dr. Paul VanRaden Gary Fok

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- 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, but are not participating in DHI monthly testing so don't have 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, 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. Will be implemented once we finish testing.

Top bull lists obtained using Multitrait Across-Country Evaluations (MACE) on each country's scale

Table 1. Actual percentages of foreign sire use and expected use based on the top 100 or top 1000proven Holstein sires in each country's ranking

Foreign%	AUS	CAN	CHE	DEU	DFS	ESP	FRA	GBR	IRL	ISR	ITA	JPN	NLD	NZL	USA
Actual ¹	60	56	38	51	15	73	13	73	15	5	52	39	18	2	8
Expected ²		83	100	94	90	100		100	81	91	100	98	87	24	
Expected ³	98	88	100	91	90	99	95	99	86	95	98	96	92	54	23

¹ Percentages of milk-recorded cows with foreign sires born since 2008.

² Percentages of top 100 proven sires born 2005-2013 that are foreign.

³ Percentages of top 1000 proven sires born 2005-2013 that are foreign.

Most countries should increase their use of foreign sires

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At the April Interbull meeting Dr. Sajjad Toghiani of AGIL compared national indexes and their Rankings. Using MACE evaluation method, he assembled lists of top bulls for each country according to their respective scale. He found Foreign bulls were >80% of the top bulls in nearly all countries but often sired <50% of domestic cows. For example, take Japan where only 2-4% Japanese bulls were among the top ranked sires, and: Only 39% of their milk recorded cows had foreign sires. Reasons might include health restrictions, higher prices, lack of information/technician service, or protectionism. Most countries should use foreign sires much more, and this is good news for us because USA sires dominate the top bull lists

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Projection Factors for Yield Traits



We are collaborating on a CDCB and National DHIA project to update Milk, Fat, and Protein predictions. The current factors used were last estimated in 1994, and anecdotal reports suggest predictions for milk can be off by as much as a thousand Ibs. This is potentially a big problem for herds making culling and management decisions in the crucial first 120 DIM

Projection Factors for Yield Traits



We are addressing this with an intensive cohort study. We will enroll a robust cross section of dairy herds across the US, with Holstein & Jersey cows representing the majority. Later study phases will include other breeds and management systems. Number of lactations, housing/feeding regimen, and milking frequency are other important factors influencing yield traits and will be accounted for in our sampling scheme. A subset of cows will be chosen from each herd. During the critical first 120 DIM, this "Study Group" of cows will be sampled weekly, and we will measure milk yield, milk components, and milking interval. For the remainder of the lactation, the Study Group will be sampled according to their regular DHIA schedule along with the rest of the herd. The goals are 2-fold: update predictions & expand use of MIR spectral data currently used for milk components to other traits

Develop Hoof Health Data Pipeline

• Consortium: CDCB, CattleEYE, U of Minnesota, den Dulk Dairy Farms



Dr. Asha Miles

CattleEye has developed a lameness detection system using a video analytics platform. A 2D camera mounted above the exit to the milking parlor collects measurements and scores cows for lameness on a quantitative scale of 1-100, their analytics can speak to herd management software and then flag a cow for lameness and have her sorted for treatment. A validation study was conducted at U of Liverpool and found this method to be highly accurate, this research is just beginning.

Planning for the future:

USDA is writing our 5-year plan for submission this November

"Improving Dairy Cattle by Increasing Accuracy of Genomic Prediction, Evaluating New Traits, and Redefining Selection Goals"

Principal Investigators: Paul VanRaden (Lead Scientist), Asha Miles, Curt Van Tassell (0.25), Ben Rosen (0.25), and Vacant

ARS Project No. 8042-31000-002-00-D (https://www.ars.usda.gov/research/project/?accnNo=433412)

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5-Year Plan Overview

Our Plan is due at the end of November and goes through a similar review process to a grant

Evaluation by 2 external reviewers is required before submission

(Feedback needed by November 22, any volunteers may identify themselves in the chat ⁽²⁾)

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Thank you. Questions?



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