

Quantifying the use of and the genetic progress from advanced mating strategies in US dairy herds

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Abstract

The use of mating technologies, including genomic testing and sexed semen, has recently increased in the breeding programs of commercial dairy herds, along with the use of beef semen. We aimed to quantify the utilization of advanced mating strategies in US dairy herds and the influence of these strategies on genetic merit. Breeding records ($n = 35,124,479$) that resulted in successful pregnancies of cows and heifers by semen type (conventional dairy, sexed dairy, and beef) and records of genomic testing of female dairy cattle were extracted from the National Cooperator Database for the years 2008 to 2023. Herds were categorized within year by semen type used and use of genomic testing of heifers and the genetic merit of heifers born in 2023 ($n = 678,064$) was compared by herd mating strategy. Female dairy cattle in the US are genotyped, on average, at 6 months of age. When the net merit of a genotyped heifer increased by one standard deviation, the odds that she remained in the herd through first lactation increased by 13%. Breeding values of net merit (\$1,203) and most of the traits investigated were most favorable in heifers born in herds that used all mating strategies investigated (genotyping of heifers, and a combination of beef, sexed, and conventional semen). Calves born in herds that used a combination of sexed and conventional semen had the least net merit (\$532) and generally had the least favorable breeding values across production, fertility, and longevity traits. Results confirm that the incorporation of advanced mating strategies has increased rapidly in US dairy herds. Heifers were more likely to enter the milking herd as their genomic merit increased and herds that incorporated all strategies investigated had the greatest genetic progress.

Key words: Genomic testing, sexed semen, beef on dairy

Introduction

Dairy cattle breeders have used artificial insemination for many decades; now newer tools, like genomic testing, allow for more precise breeding strategies. Following the inception of genomic selection, rapid genetic progress has occurred in the US dairy cattle population (Garcia-Ruiz et al., 2016; Guinan et al., 2023). Recent reports support that there has been a rapid increase in genotypes of dairy females (CDCB, 2025) and in dairy cattle being mated to sexed and beef semen (Lauber et al., 2023).

Multiple research groups have simulated the economic and genetic benefits of incorporating

female genomic testing, sexed semen, beef semen, and combinations thereof into mating programs. For example, models suggest that using genomic information to select replacement heifers can reduce genetic lag through increased selection accuracy and selection intensity (Weigel et al., 2012; Calus et al., 2015). Likewise, selection intensity can be increased by mating genetically superior females to sexed semen, ensuring replacement heifers are born to the best cows (Weigel, 2004; De Vries et al., 2008). Combining sexed semen with genomic testing of heifers increased the rate of genetic progress because more heifers in a herd increased room for selection (Calus et al., 2015).

Because of the added value beef x dairy calves have over dairy bull calves, economic models suggest that profitability can be maximized in dairy mating programs when sexed semen and beef semen are selectively used, though not in herds with poor reproductive performance (Pahmeyer and Britz, 2020; Cabrera, 2022). Additionally, as proportions of sexed and beef semen increased, genetic lag was reduced (Hjortø et al., 2015; Clasen et al., 2021). Using genomic testing to inform selective use of sexed and beef semen further reduced genetic lag, though economic gains were similar in models that did not use genomic testing (Hjortø et al., 2015; Clasen et al., 2021).

The combined use of genomic testing, sexed semen, and beef semen in US dairy herds and their influence on genetic progress has yet to be quantified. We aimed to characterize the utilization of advanced breeding strategies in US dairy herds by quantifying genotyping of replacement heifers, and the use of conventional, sexed, and beef semen, and combinations thereof. Further, we sought to test the hypothesis that herds that use combinations of advanced breeding tools produce replacement dairy calves with greater genetic merit than those using exclusively conventional semen.

Materials and Methods

The data used in this study was accessed from the National Cooperator Database, managed by the Council on Dairy Cattle Breeding (CDCB). The phenotypes, genotypes, and pedigree used in the US national dairy cattle genetic evaluation and this study included phenotypes of reproductive events (Format 5), herd test-date records, and genotypes of females born in the US.

Predicted breeding values (PBV) on the lifetime net merit (NM\$ index and PBV of traits evaluated in all dairy breeds from the August 2024 official national genetic evaluation were extracted. All dairy breeds were included in this

study, including crossbred animals. Heifers and cows were classified by the breed base PBV are reported on (Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey, or Milking Shorthorn), when relevant.

Heifer genotypes

Between 2008 and 2023, a total of 5,683,150 individual female dairy cattle born in the United States were genotyped. The earliest instance of genotyping was retained to determine the initial age a farmer intended to genotype a female calf.

Breeding strategies

Breeding events of cows and heifers that were extracted from Format 5 reproductive records submitted by dairy records processing centers. Events that resulted in full-term pregnancies, verified by a calving event that occurred within breed average gestation length $\pm$ 14 days were retained. Data submitted from herds that use less than 80% AI were removed. Miles et al. (2023) recently reported that there are no Format 5 breeding records associated with 97% of calves born via embryo transfer (ET). Due to these data flow and quality issues, we did not attempt to quantify calvings from ET events and animals conceived through ET were removed from the data. Retained AI breeding events that resulted in calvings between the years 2008 and 2023 ($n = 35,124,479$) were used to quantify changes in semen type use over time.

A subset of the genotyped females ($n = 982,536$) was examined to determine the proportion of genotyped heifers that remained in the herd they were born in through their first calving. For inclusion, cattle had to be genotyped as heifers (≤ 24 months of age) to allow for a culling decision to be made prior to their first calving. Likewise, calves were required to be born prior to 2022 to provide adequate opportunity to become cows. To fairly determine that a heifer reached first lactation, only animals born in herds that had at least one DHIA test in 2023 and 2024 were included. Genotyped calves that began their first lactation in the same herd they were born in were denoted

as stay = 1, while those that started their first lactation in a different herd or had no associated lactation records were denoted as stay = 0.

Breedings were classified by 4 semen types: conventional dairy-breed semen, sexed (X-sorted) dairy-breed semen, conventional beef-breed semen, and sexed (Y-sorted) beef-breed semen. Breeding strategies were categorized by herd-year and defined to capture both genomic testing of heifers and types of semen used to conceive the calves born within the herd-year. Herds were binned by semen type within year as follows: conventional (CON), where calves born were exclusively conceived with conventional dairy-breed semen; beef and conventional (BC), where calves born were conceived with conventional dairy-breed semen or with beef-breed semen that could be conventional or sex-sorted; sexed and conventional (SC), where calves born were conceived with sex-sorted or conventional dairy-breed semen; beef, sexed, and conventional (BSC), where calves born were conceived with sex-sorted or conventional dairy-breed semen or beef-breed semen. Additionally, SC and BSC herds that utilized genomic testing (GT) were considered those that genotyped any heifers born in the year observed and were binned separately by semen type as GT-SC, and GT-BSC.

To compare the genetic merit of heifers by herd breeding strategy calving events, dairy heifer calves born in 2023 ($n = 678,064$) were categorized by the breeding strategy of the herd they were born in.

Statistical analyses

The effect of genetic merit on whether a genotyped calf was sold prior to first lactation was evaluated with following binomial generalized linear mixed model:

$$\log \left[\frac{p}{(1-p)} \right] = \mu + \beta_1 NM_i + \beta_2 age_j + herd_k + \varepsilon_{ijkl}$$

where p = the probability of $y_{ijkl} = 1$, where y = heifer stayed in herd through first lactation; μ = model intercept; β_1 = regression coefficient

of stay on NM\$; β_2 = regression coefficient of stay on age genotyped; $herd_k$ = the random effect of the herd the heifer was born in k (herd 1 to herd 2,030); and ε_{ijkl} = residual error.

The odds ratio (OR) of a heifer staying in the herd when NM\$ increased by 1 SD was generated with a 95% CI.

Merit index PBV and PBV of individual traits of heifer calves born in 2023 were compared by herd mating strategy with the following linear mixed model:

$$y_{ijklm} = \mu + MS_i + lact_j + BB_k + S_l + herd_m(MS_i) + \varepsilon_{ijklm}$$

where y = calf PBV; μ = model intercept; MS_i = mating strategy used by the herd the calf was born in i (CON, BC, SC, BSC, GT-SC, GT-BSC); $lact_j$ = dam parity j (1, 2, 3, 4, or ≥ 5); BB_k = the breed base PBV of the heifer calf are reported on k (Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey, or Milking Shorthorn); S_l = the random effect of season calf was born in two-month intervals (1 to 6); $herd_m$ = the random effect of herd m (herd 1 to herd 5613) nested within mating strategy i ; and ε_{ijklm} = residual error.

Differences in least squares means were Tukey-Kramer adjusted for multiple comparisons. Statistical analyses were performed with SAS (9.4). Data visualization was conducted in R (v. 4.4.1) using the ggplot2 package (Wickham, 2016).

Results & Discussion

Heifer genotypes

In 2008, 68% of female dairy cattle genotyped were 24 months or older; average age at genotyping was 42.4 months (Figure 1). By 2009, just less than 1/3 of females were 2 years of age or older when genotyped. The proportion of heifers (≤ 24 mo. old) genotyped increased each year. In 2023, average age at genotyping was lowest at 5.5 months. Over all 15 years of data, average age at genotyping was 6.3 ± 8.5 months.

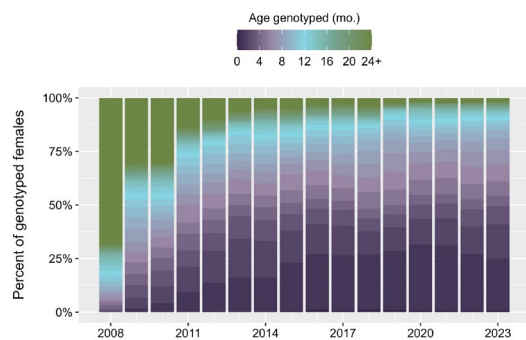


Figure 1. The age US female dairy cattle were genotyped as the percentage of total females genotyped in a year.

Nearly all genotyped females in the US were genotyped as heifers, which aligns with recommendations in the literature to maximize economic return of genomic testing. In simulated data, selecting females for breeding by GEBV resulted in a gain in NM\$, following deduction of the cost of genotyping, over selecting females based on parent average (Weigel et al., 2012). However, the increase in genetic merit was reduced when females were genotyped as cows, thus, authors recommended genotyping calves and heifers for the greatest return on investment (Weigel et al., 2012). By genotyping youngstock, farmers can also leverage genomic information to make mating decisions for an animal in future parities, which Hjortø et al. (2015) demonstrated increases the economic returns of genotyping.

The odds that a genotyped heifer calf stayed through first lactation when NM\$ increased by 1 SD of the mean (\$511) increased by 13.6% (OR = 1.136 [1.131,1.141]). We expected that greater NM\$ would increase the likelihood that a heifer stayed in the herd, but the magnitude is smaller than anticipated. This may indicate that management strategies implemented with genomic results vary across herds. In a scenario where a herd utilizing genomic testing has surplus heifers, culling excess heifers with the least genetic merit is a logical selection strategy. However, some herds may choose to market

their genetically elite heifers as breeding stock while retaining females with lower genetic merit for use as embryo recipients or for mating with beef semen.

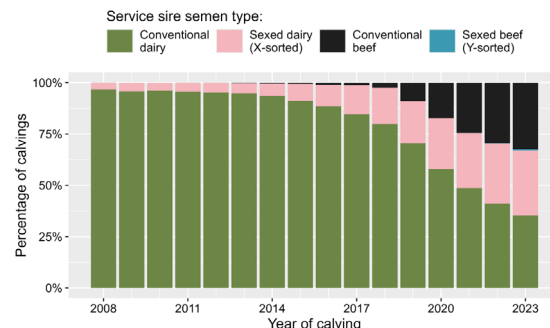


Figure 2. The proportion of annual calvings in US dairy herds by service sire semen type.

Breeding strategies

Over 90% of the calves born from 2008 to 2015 were conceived with conventional semen, with most of the remaining of calves conceived with sexed dairy semen (Figure 2). In 2016, 1% of the calves born were beef-sired and the proportion of calves conceived with sexed semen grew to 10%. By 2019, calvings to beef service sires grew to 9%, and calvings to sexed dairy semen grew to 21%. The proportions of calvings to beef and sexed semen continued to grow through 2023, when the calves born were conceived with nearly equal proportions of beef, sexed, and conventional semen. Additionally, in 2023, about 0.5% of calvings resulted from insemination with sexed (Y-sorted) beef semen to produce terminal beef × dairy steers. Lauber et al. (2023) reported a similar year-over-year increase in proportion of US Holsteins and Jerseys mated to beef and sexed semen from 2019 to 2021.

Calf genetic merit

Calves born in GT-BSC herds had the greatest NM\$ while calves born in SC herds had the least (Table 1). The NM\$ breeding value of calves born in GT-BSC was \$240 greater than calves born in BSC herds. A smaller difference

Table 1. Breeding values of heifers born in 2023 by the mating strategy¹ used by the herd they were born in.

	Herd mating strategy ²						SE
	CON	BC	SC	BSC	GT-SC	GT-BSC	
n heifers (n herds)	25,264 (1,117)	26,684 (786)	32,902 (891)	279,271 (1,810)	17,604 (231)	296,335 (778)	-
PBV							
Net merit, \$	678 ^d	857 ^c	532 ^c	963 ^b	678 ^d	1203 ^a	37
Milk, kg	849 ^c	991 ^b	689 ^d	1,019 ^b	714 ^d	1,091 ^a	34
Fat, kg	30.4 ^d	37.1 ^c	25.1 ^c	42.1 ^b	31.4 ^d	51.6 ^a	1.6
Protein, kg	27.7 ^d	32.7 ^c	23.1 ^c	35.2 ^b	25.9 ^{de}	40.1 ^a	1.1
Somatic cell score	2.90 ^b	2.87 ^c	2.93 ^a	2.86 ^c	2.90 ^b	2.82 ^d	0.01
Productive life, mo.	3.01 ^d	3.80 ^c	2.57 ^c	4.44 ^b	3.53 ^c	6.01 ^a	0.19
Livability, %	-0.13 ^c	0.53 ^b	-1.19 ^d	0.62 ^b	-1.04 ^d	1.26 ^a	0.16
Daughter pregnancy rate, %	-0.97 ^{bc}	-0.85 ^{ab}	-1.21 ^d	-0.81 ^a	-1.23 ^{cd}	-0.71 ^a	0.09
Cow conception rate, %	-0.50 ^d	-0.17 ^c	-0.98 ^e	0.10 ^b	-0.86 ^c	0.60 ^a	0.12
Heifer conception rate, %	1.83 ^d	2.01 ^c	1.78 ^d	2.35 ^b	1.85 ^{cd}	2.82 ^a	0.09
Early first calving, days	8.34 ^d	9.63 ^c	6.97 ^e	10.19 ^b	6.83 ^c	11.36 ^a	0.28
Body weight composite	0.51 ^b	0.29 ^c	0.86 ^a	0.26 ^c	0.87 ^a	0.00 ^d	0.06
Udder composite	0.90 ^d	0.85 ^d	1.39 ^b	1.03 ^c	1.69 ^a	1.11 ^c	0.06
Feet and leg composite	0.54 ^b	0.42 ^c	0.90 ^a	0.48 ^{bc}	1.05 ^a	0.42 ^c	0.05

¹All included model effects, including herd mating strategy, were significant at $P < 0.0001$.

²CON = calves born to conventional semen only; BC = calves born to beef and conventional semen; SC = calves born to sexed and conventional semen; BSC = calves born to beef, sexed, and conventional semen; GT-SC = calves born to sexed and conventional semen and some heifers were genotyped; GT-BSC = calves born to beef, sexed, and conventional semen and some heifers were genotyped.

^{a,b,c,d,e} Values within row with different superscript are different at $P < 0.05$.

(\$106) in heifer calf NM\$ existed between BSC herds and BC herds, while NM\$ of calves born in BC herds was \$179 greater than that of calves born in CON and GT-SC herds.

The PBV of production (milk, fat, protein, and somatic cell score), longevity (productive life and livability), and fertility (daughter pregnancy rate, cow conception rate, heifer conception rate, and early first calving) traits of heifer calves generally ranked in the same order of NM\$ by herd breeding strategy. Across these trait groups, breeding strategies from most to least favorable genetic merit ranked as follows: GT-BSC, BSC, BC, CON, GT-SC, and SC (Table 1). This is expected because these traits are included in the NM\$ index (VanRaden et al., 2021).

An unexpected result was that calves born in CON herds had similar or greater NM\$ and PBV of production, fertility, and longevity traits than heifers born in GT-SC and SC herds. The use of sexed semen in the dairy herd is expected to increase the rate of genetic progress by increasing selection intensity on the dams of

cows selection pathway (Weigel, 2004; De Vries et al., 2008). Increased genetic progress with sexed semen use is clear for GT-BSC and BSC herds but not in GT-SC and SC herds. We theorize that this is due to the breeding goals of SC and GT-SC herd differing substantially from the herds using other breeding strategies investigated.

Among type trait composites, genetic merit of body weight composite (BWC) ranked by herd mating strategy similarly to that of NM\$. Heifers born in GT-BSC herds had the most favorable (least) BWC PBV and those in SC and GT-SC herds had the least favorable (Table 1). Conversely, heifers born in GT-SC herds had the greatest PBV for udder composite and feet and legs composite, followed by calves born in SC herds (Table 1). This may suggest that SC and GT-SC herds are selecting primarily for improvement in type traits, while herds utilizing other breeding strategies select for genetic improvement in many economically relevant traits. In NM\$, increased BWC PBV is not economically favorable because heavier

cows require additional feed for growth and maintenance (VanRaden et al., 2021). However, breed association classification scores do not penalize animal size and, in elite cattle shows, tall, large-framed cows are often favored. Thus, in herds prioritizing selection for conformation, greater BWC may not be considered unfavorable.

Conclusions

Genomic testing of heifer calves and the incorporation of sexed and beef semen in mating programs have increased rapidly in US dairy herds. On average, female dairy cattle in the US are genotyped at 6 months of age. The odds that a genotyped heifer remained in the herd through first lactation increased slightly (by 13%) when her NM\$ PBV increased by \$511, suggesting that knowledge of genetic merit from genotypes may have informed replacement selection. Heifers born in herds that used all mating strategies investigated (genotyping of heifers, and a combination of beef, sexed, and conventional semen) had the greatest genetic merit when measured on the four merit selection indexes and across most PBV investigated. Calves born in SC and GT-SC had the least genetic merit across production, fertility, and longevity traits but had the greatest merit for udder and feet and legs conformation, perhaps due to different breeding objectives. Dairy herds that combine advanced mating strategies generally produce genetically superior replacement heifers.

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