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Genetic Evaluation of Fertility Traits in US Organic Holstein Cows

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Abstract

Genetic evaluations of cow fertility in the U.S. are primarily based on data from conventional herds. However, how well these evaluations predict fertility in organically certified systems which requires grazing and prohibits reproductive synchronization is unclear. This study aimed to assess fertility traits in organic Holstein cows, including Days Open (DOPN), Pregnancy at First Service (PG1ST), and Number of Inseminations (NSEM). The dataset included 32,572 records from 18,565 cows. A three-trait single-step animal model incorporating 74,817 DNA markers were used, with 1,339 genotyped cows, of which 898 had phenotypic records. Estimated Breeding Values (EBV) with accuracy above 50% were compared with U.S. Genomic Predicted Transmitting Ability (gPTA) for 660 bulls to assess Daughter Pregnancy Rate (DPR), Cow Conception Rate (CCR), and dairy form (DF). Heritability Estimates (± SE) were 0.062 ± 0.008 for DOPN, 0.065 ± 0.012 for PG1ST, and 0.034 ± 0.012 for NSEM. Genetic correlations were -0.508 ± 0.096 between DOPN and PG1ST; 0.717 ± 0.062 between DOPN and NSEM; and -0.775 ± 0.058 between PG1ST and NSEM. EBV for DOPN was negatively correlated with DPR (-0.431), and after adjusting for reliability, the approximate genetic correlation was -0.682. The approximate genetic correlation of gPTA for CCR with PG1ST was 0.588 and with NSEM was -0.652. Higher DF was unfavorably associated with all fertility measures. In conclusion, heritabilities were similar to estimates from conventional herds. While these results suggest that gPTAs from conventional herds can contribute to genetic improvement in organic systems, the observed genetic correlations below one indicates potential differences in trait expression between environments, highlighting the need for further research, including direct estimation of genotype-by-environment interactions to validate these findings.

Key words: Fertility; Holstein; Organic; Heritability; Genomic Predicted Transmitting Ability

Introduction

Cow fertility and reproductive traits significantly influence the efficiency of dairy herds [3,12] and are a critical determinant of profitability and long-term sustainability in dairy production systems. Strong fertility performance leads to shorter calving intervals, enhanced lifetime productivity, and facilitates genetic progress through timely replacement of breeding stock. Since 1960, Holstein dairy cows have experienced a marked decline in fertili

ty as a correlated response to selection for milk production, with unfavorable genetic correlations between production and fertility traits contributing to reduced reproductive performance and serious economic implications for farmers [5,21]. For example, genetic correlations between milk yield and fertility traits such as days open range from 0.33 to 0.38, and calving interval correlations with peak or total milk yield have been reported as high as 0.59 to 0.63 [1]. Consequently, U.S. Holsteins have experienced an increase of

approximately 37 days open between 1960 and 2000, with about 75% of this change attributed to genetics [8,14]. The recent development of genomic selection has helped stabilize fertility traits and, in some cases, reversed this declining trend. Notably, two-thirds of the countries participating in the international genetic evaluation of dairy sires now incorporate national genetic evaluations of female fertility [20].

In the U.S., genomic evaluations primarily focus on three fertility traits, including Daughter Pregnancy Rate (DPR), which indicates the percentage of cows that become pregnant during each 21-day estrus cycle [14]; DPR evaluations were initially derived from days open (DOPN) records with a 1-point increase in DPR corresponding to a 4-day reduction in days open [23]. Later revisions to DPR [36] shifted to an analysis of 21-day windows of confirmed pregnancy which were derived from DOPN, herd insemination and pregnancy confirmation records and which had a correlation of near unity (0.97) with the evaluations derived solely from DOPN. Additional fertility traits include Cow Conception Rate (CCR) and Heifer Conception Rate (HCR), which assess the conception ability of cows and heifers, respectively [26]. Additionally, Dairy Form (DF) or angularity are routinely recorded in national evaluations and are unfavorably correlated with fertility as cows with poor DF have low body condition scores [10,11].

Fertility traits are derived from insemination and calving records and capture various biological processes related to reproductive success, including estrus, ovulation, and embryo survival [7,12]. Despite their critical role, fertility traits generally exhibit low heritability (typically <0.10) and are substantially influenced by management practices, environmental conditions, and overall animal health, thereby posing challenges to genetic improvement [27,29,39].

In the U.S., fertility traits are evaluated genetically through national evaluation systems and are included in selection indices such as the Lifetime Net Merit Index [37,38]. Nevertheless, most of the research and breeding efforts have focused on conventional dairy systems. Organic dairy production, which restricts the use of hormones, antibiotics, and synthetic inputs, presents both unique challenges and opportunities for enhancing fertility [2,30]. Organic herds often employ distinct nutritional, breeding, and health management practices that may influence the expression and recording of fertility traits differently from conventional systems [1,18,19].

Organic production systems typically depend on natural estrus detection and have no access to reproductive technologies such as estrus synchronization or timed artificial insemination. This reliance may contribute to increased phenotypic variation in fertility outcomes and underscores the importance of selecting animals with naturally superior reproductive performance [2,9]. For example, estrus synchronization removes cow-to-cow variation in submission to insemination as cows are bred regardless of expression of estrus behavior; this directly influences DPR as all cows will be inseminated rather than only those detected in estrus. Cows in organic production will not be inseminated if they do not express estrus, so the applicability of DPR derived from conventional data in organic herds could be lessened. As interest in organic dairy production continues to grow in the U.S., there is a pressing need to deepen the understanding of the genetic basis of fertility within these systems and to evaluate whether current fertility trait definitions and evaluation methods accurately reflect the unique conditions and objectives of organic farms.

The objective of this paper is to assess DOPN, Pregnancy at First Insemination (PG1ST) and Number of Inseminations (NSEM) in organic-certified Holstein cows, and to determine the effectiveness of national genomic evaluations based on conventional herd data to predict fertility performance for organic cows.

Material and Methods

Data were collected from 14 USDA certified organic dairy farms on Holsteins fertility traits. These farms were in the Northeastern, Midwestern and Western regions of the US. In total, 18,656 cows were assessed with 32,572 records including lactation number, calving date, birthdate, PG1ST, DOPN, and NSEM. These data were obtained from herd records from Dairy Records Management Systems (Raleigh, NC), AgSource Inc. (Verona, WI) or on-farm software including Dairy Comp 305 (Valley Ag Software, Tulare, CA), PC-DART (Dairy Records Management Systems, Raleigh, NC), and DHI-Plus (Amelicor, Provo, UT). Cows with DOPN of 250 or more were set to 250 DOPN, which is the same procedure used by the Council on Dairy Cattle Breeding for fertility evaluations in the US [8]. Cows with more than 5 inseminations in a lactation were set to a maximum of 5. Data was collected from 2016 through 2019. For variance component estimation and Estimated Breeding Value (EBV) prediction, the following three-trait single-step animal model was applied using the BLUPF90 programs [28]:

$$Y_{ijklmn} = HYSC_i + Lac_j + Age_k + a_l + PE_m + e_{ijklmn}$$

Were, Y represents the vector of records for the studied traits (DOPN, PG1ST, NSEM). The model included vectors of fixed effects for Herd-Year-Season of Calving (HYSC), Lactation Number (Lac), and Age of Calving (Age) as well as random effects for Animal (a), Permanent Environment (PE), and Residual Error (e). Variance components were estimated using GIBBS sampling, incorporating 74,817 DNA markers from 1,339 genotyped cows, of which 898 had phenotypic records and the remainder were dams and siblings without records.

A total of 250,000 iterations with 100,000 burn-ins were performed, and model effect solutions along with variance components were retained every 100 samples to derive the EBV.

Heritabilities (h^2) for DOPN, PG1ST, and NSEM were defined as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_a^2}$$

where σ_a^2 is additive genetic variance, σ_{pe}^2 is permanent environmental variance, and σ_e^2 is residual variance. Reliabilities (rel) for DOPN, PGIST and NSEM were calculated using the equation:

$$rel = 1 - \frac{\sigma_{EBVi}^2}{\sigma_a^2}$$

Where σ_{EBVi}^2 is the variance of the 1500 retained samples for animal i and σ_a^2 is the additive genetic variance.

Genomic PTAs of fertility traits (DPR, CCR, HCR) were extracted from national evaluations [8] and DF gPTA was obtained from national type evaluations (Holstein USA Inc., Brattleboro, VT) for bulls with reliability of DOPN, PG1ST or NSEM ≥0.25 to estimate approximate genetic correlation between nationally recorded fertility related traits and those in this study using the method of [4] as follows:

$$\widehat{rg_{1,2}} = \frac{r_{1,2}}{\sqrt{rel_1} * \sqrt{rel_2}}$$

The approximated genetic correlation between trait 1 and trait 2 is $\widehat{rg_{1,2}}$; the Pearson correlation between the estimated breeding values generated for fertility traits and the genomic (g) PTA of national evaluations is presented as $r_{1,2}$; $\overline{rel_1}$ is the average reliability of the nationally-evaluated gPTA of the sires as provided by CDCB;

and $\overline{rel_2}$ is the average reliability of the respective fertility trait.

Results

Estimates of heritabilities and genetic correlations among reproductive traits are presented in (Table 1). Heritability estimates were low for all traits, with 0.062 ± 0.008 for DOPN, 0.065 ± 0.012 for PG1ST, and 0.034 ± 0.012 for NSEM. Genetic correlations between traits were strong, with DOPN negatively correlated with PG1ST (-0.508 ± 0.096) and positively correlated with NSEM (0.717 ± 0.062); PG1ST and NSEM were negatively correlated (-0.775 ± 0.058). Pearson correlations between fertility traits in organic herds and fertility-related traits from national genomic evaluations for 660 sires are presented in (Table 2) and all were highly significant (p<0.01). Greater DOPN was negatively correlated with DPR (-0.430), CCR (-0.353), and HCR (-0.109), and positively correlated with DF (0.244). Higher PG1ST exhibited positive correlations with DPR (0.353), CCR (0.369), and HCR (0.305), and a negative correlation with DF (-0.166). Higher NSEM was negatively correlated with DPR (-0.381), CCR (-0.409), and HCR (-0.282), and positively correlated with DF (0.193). Approximate genetic correlations between fertility traits in organic herds and fertility-related traits from national genomic evaluations are presented in Table 3. The most direct comparison of our available data and national gPTA are of DOPN and DPR, and of PG1ST and NSEM with CCR. The correlation between DOPN and DPR was -0.682, indicating that selection for DPR from national genomic evaluations is expected to decrease DOPN in organic herds. Selecting for higher CCR is expected to increase PG1ST ($\widehat{rg}$ = 0.588) and decrease NSEM ($\widehat{rg}$ = -0.652), and a negative correlation with DF (-0.267). The approximate genetic correlations of DF with fertility were all unfavorable.

Table 1: Estimates of heritabilities (diagonal) and genetic correlations (below diagonal) among traits[1].

Trait	DOPN	PG1ST	NSEM
DOPN	0.062 ± 0.008		
PG1ST	-0.508 ± 0.096	0.065 ± 0.012	
NSEM	0.717 ± 0.062	-0.775 ± 0.058	0.034 ± 0.012
[1]DOPN = days open; PG1ST = pregnancy at first service; NSEM = number of inseminations.			

Table 2: Pearson correlations between fertility traits in organic herds1 and fertility related traits from national genomic evaluations2 for 660 sires.

	DPR	CCR	HCR	DF
DOPN	-0.430***	-0.353***	-0.109**	0.244***
PG1ST	0.353***	0.369***	0.305***	-0.166***
NSEM	-0.381***	-0.409***	-0.282***	0.193***
[1]DOPN = Days Open; PG1ST = Pregnancy at First Service; NSEM = Number of Inseminations. [2]DPR = Daughter Pregnancy Rate; CCR = Cow Conception Rate; HCR = Heifer Conception Rate; DF = Dairy Form. **P<0.01; **P<0.001.				

Table 3: Approximate genetic correlations between fertility traits in organic herds1 and fertility related traits2 from national genomic evaluations.

	DOPN	PG1ST	NSEM
DPR	-0.682	0.563	-0.608
CCR	-0.562	0.588	-0.652
DF	0.389	-0.267	0.31
[1]DOPN = Days Open; PG1ST = Pregnancy at First Service; NSEM = Number of Inseminations. [2]DPR = Daughter Pregnancy Rate; CCR = Cow Conception Rate; HCR = Heifer Conception Rate; DF = Dairy Form.			

Discussion

The heritability estimates for DOPN, PG1ST, and NSEM are low, aligning with earlier findings that fertility traits in dairy cattle usually show heritability below 0.10. This is largely due to significant environmental and management factors [6,31] (Cole et al., 2021; Pinto et al., 2025). In particular, the heritability estimate for DOPN fits well within the typical range of 0.01 to 0.08 [17,33] (Sun et al., 2010; Haile-Mariam et al., 2023; Fleming et al., 2019), while the estimates for PG1ST and NSEM are in line with other research that also reports low heritability for conception and insemination traits [15]. The genetic correlations found in this study were moderate to high and carry biological significance. The negative correlation between DOPN and PG1ST indicates that cows that tend to have shorter days open are also more likely to conceive on their first service. This is a favorable relationship that has been consistently noted in literature [15,17]. On the other hand, the strong positive correlation between DOPN and NSEM suggests that cows needing more inseminations also tend to stay open longer, a trend observed across various populations and trait definitions [31]. Likewise, the strong negative correlation between PG1ST and NSEM highlights the logical biological connection where better first-service conception leads to fewer total inseminations required [15].

These findings highlight that while fertility traits may not have a strong heritability on their own, they are closely linked genetically, indicating a shared underlying genetic merit for reproductive efficiency [6,31]. From a breeding standpoint, if one focuses on traits such as PG1ST, corresponding improvements in DOPN and NSEM can be expected. However, since the genetic impact on fertility is somewhat limited, we are likely to see better results from a combination of strategies. This means integrating genomic selection with better management practices, such as nutritional support and improved estrus detection [6,31] will improve reproductive efficiency.

The connections between EBV from organic herd fertility traits and national genomic predictions offer insights into the effectiveness of using national gPTA for selecting sires in alternative production systems. The notable negative correlation between DPR and DOPN reinforces the expected biological link, as DPR can be directly inferred from DOPN is genetically tied to shorter intervals from calving to conception [23,35]. Likewise, DPR displayed positive associations with PG1ST and the NSEM, indicating that sires with higher gPTA DPR have daughters in organic herds that conceive more quickly and require fewer inseminations. These results align with recent validation studies that show genomic fertility traits effectively capture variations in reproductive efficiency, even across different herd management practices [34]. On the other hand, HCR showed weaker correlations with cow-based interval traits like DOPN, but stronger links with PG1ST. This difference reflects the physiological and management variations between heifers and cows, a trend noted in other research where correlations between HCR and cow fertility traits were generally modest [22].

While the correlations we observed were statistically significant and aligned with what we expected biologically, they were moderate in strength. This indicates that national genomic predictions account for a considerable, yet incomplete, portion of the fertility variation seen in organic management settings. The gap likely stems from genotype-by-environment interactions, as fertility in organic systems can be affected by specific factors like grazing practices and different reproductive management compared to conventional herds [16,34]. Notably, the correlation between DOPN and DPR that is clearly less than one suggests that genotype by environment interactions is influencing the results [24,32]. National DPR evaluations were originally derived using DOPN records [35] with subsequent modifications that allow earlier use of records from cows without complete records [23] thus, one would anticipate an approximate genetic correlation between DOPN and DPR approaching unity if there was no genotype by environment interaction between organic and conventional production systems. This is consistent with the research by [25] which showed that fertility traits can be genetically re-ranked between herds that use reproductive synchronization programs and those that do not. Given that organic systems limit the use of timed artificial insemination, fertility becomes more dependent on natural estrus detection, which could explain why we see these moderate correlations instead of near-perfect ones with national genomic evaluations.

Selecting for lower dairy form was previously suggested as a trait that grazing herds should consider in selection programs to maintain adequate body condition and to support health and fertility [13]. Our results concur as higher dairy form was unfavorably correlated with DOPN, NSEM and PG1ST, indicating that cows that are bred for more angularity and body refinement have poorer

fertility. Recent research backs this up, revealing that significant weight loss or a focus on angularity reduces levels of fertility [16]. Overall, these findings emphasize the value of genomic fertility traits like DPR and CCR in organic herds, while also pointing out the genotype by environment interactions that could influence the strength of genetic links [25,32]. Therefore, selection programs for organic herds should consider both the reliability of national genomic predictions and the specific management challenges that come with organic farming.

Conclusion

In conclusion, the estimates from this study suggest fertility has low heritability in organic herds, but they align well with what is been reported in traditional herds. The strong and positive genetic correlations among DOPN, PG1ST, and NSEM indicate that if we focus on selecting for shorter days open or higher pregnancy rates at first service, we can also reduce the number of inseminations needed. The correlations between EBV and national gPTA showed a meaningful connection between fertility performance in organic herds and national evaluations. However, the less-than-perfect agreement points to genotype by environment interactions, likely due to management differences such as the lack of reproductive synchronization in organic systems. Overall, these findings highlight the potential of using national gPTAs to boost fertility in organic herds, while also reminding us that we need to take the environmental context into account when crafting our selection strategies.

Acknowledgement

Declaration

The computations for this study were performed using the ICDS-ACI at Penn State University. This study involved only data analysis and did not involve live animals or animal-based experiments. As such, IACUC approval was not required.

Conflict

The authors declare no conflicts of interest.

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