

Genetic parameters of milk yield and reproductive performance traits in Holstein-Friesian dairy cattle

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ABSTRACT

Understanding the genetic structure of economically important traits in dairy cattle is a fundamental requirement before designing any effective breeding program. This study was conducted to estimate genetic parameters, including heritability and genetic and phenotypic correlations, for 305-day Milk Production (P305), Calving Interval (CI), Dry Period (DP), Peak Yield (PY), and Days to Peak Yield (DPY) in Holstein-Friesian dairy cattle in Indonesia. The data were collected from 2017 to 2024 and analyzed using the restricted maximum likelihood (REML) procedure. The overall least-squares means were $8,178.04 \pm 23.08$ kg for P305, 395.37 ± 1.21 days for CI, 66.60 ± 0.53 days for DP, 40.60 ± 0.12 kg for PY, and 78.00 ± 0.58 days for DPY. Heritability estimates were moderate to high for P305 (0.40 ± 0.02) and PY (0.48 ± 0.02), low for CI (0.18 ± 0.02) and DP (0.10 ± 0.02), and very low for DPY (0.03 ± 0.01). A strong positive genetic correlation was found between P305 and PY (0.99). These results provide useful baseline information for developing a National Dairy Cattle Improvement Program in Indonesia's tropical management conditions.

Keywords: Genetic parameters, Holstein-Friesian, Milk production, Reproductive traits.

INTRODUCTION

Improving dairy cattle through selective breeding is a cost-effective and sustainable way to increase productivity. Among dairy breeds worldwide, Holstein-Friesian (HF) is the most widely distributed and intensively selected dairy breed under temperate or tropical conditions. Adaptability, combined with genetic selection, has made HF the main breed in commercial dairy operations. In recent years, recognition has grown that single-trait selection focused on milk production has compromised reproductive efficiency and fitness. Studies in different environments show that intensive selection for high milk

yield can be linked with delayed first service, extended calving intervals, reduced conception rates, and longer dry periods (Pangmao *et al.*, 2022; Abdel-Hamid *et al.*, 2019). These unfavorable relationships between production and fertility have economic consequences that reduce benefits from genetic improvement, especially where resources are limited (Boonkum *et al.*, 2024).

Genetic parameters, such as heritability and genetic correlations, are essential for breeding programs. Heritability shows the proportion of phenotypic variance from additive genetic effects, indicating the expected response to selection. Genetic correlations describe the degree to which traits share genetic factors, important for

predicting indirect selection responses and building multi-trait selection indices (Hussein *et al.*, 2025). Without reliable estimates, breeding decisions risk becoming inefficient.

HF cattle have been the subject of many genetic studies in developed countries with large national recording systems. However, published estimates vary across environments, management, and genetic backgrounds, reflecting genotype-by-environment interactions (Ducrocq *et al.*, 2022). In tropical and subtropical regions, where feed quality, heat stress, disease, and management differ from temperate conditions, estimates from European or North American populations may not be directly applicable (Santana *et al.*, 2016). Furthermore, environmental conditions in the tropics may influence the expression of economically important traits, including reproductive performance and semen quality, highlighting the importance of developing locally relevant genetic evaluation systems. Similar observations have been reported in tropical cattle populations, where significant differences in fresh semen quality were observed among *Bos taurus*, *Bos indicus*, and *Bos sondaicus* bulls under tropical environmental conditions (Wijaya *et al.*, 2023). This shows the importance of generating locally relevant estimates.

The 305-day standardized milk yield (P305) is the main selection criterion because it provides a standardized and comparable measure of lactation performance. Traits such as peak yield (PY) and days to peak yield (DPY) provide information about the lactation curve, with implications for nutritional management and selection (Pangmao *et al.*, 2022). Reproductive traits, including calving interval (CI) and dry period (DP), are indicators of reproductive efficiency and herd health (Dominguez-Castaño *et al.*, 2021). Despite the importance of these traits, comprehensive genetic studies covering both simultaneously evaluating production and fertility traits under tropical management are relatively rare. Some studies reported estimates for individual traits, but multi-trait analyses within a single analytical framework are not common (Hussein *et al.*, 2025; Pangmao *et al.*, 2022; Ayalew *et al.*, 2017). Such analyses account for genetic relationships and provide more comprehensive information for designing effective selection strategies.

The approach in this study is based on restricted maximum likelihood (REML) within the animal model framework, the widely used for estimating genetic parameters (Awady *et al.*, 2016). The animal model accounts for genetic relationships among animals through pedigree information bias in estimating breeding values and variance components (El-Naser *et al.*, 2020). Applied to multi-trait data, this approach estimates genetic and phenotypic (co)variances, giving a picture of the population's genetic relationships among traits.

The objectives of this study were: (1) to describe the performance of Holstein-Friesian cattle for P305, CI, DP, PY, and DPY across lactations; (2) to estimate heritability for each trait; and (3) to estimate genetic and phenotypic correlations among all pairs of traits. Results are expected to contribute to designing locally adapted, multi-trait selection programs and provide benchmark estimates for tropical and subtropical environments.

MATERIALS AND METHODS

Animals, Farm, and Data Collection

The dataset used in this study was collected from Holstein-Friesian dairy cows maintained at a commercial dairy farm in West Java, Indonesia. The herd was operated under an intensive management system, with animals housed in free-stall barns that had automated milking facilities, computer-based feeding management, and climate control systems including evaporative cooling and ventilation. Animals received a total mixed ration (TMR) that was formulated to meet the nutritional requirements of high-producing dairy cows according to the National Academies of Sciences, Engineering, and Medicine (NASEM, 2021), with ration composition adjusted periodically based on body condition scores and stage of lactation.

Records were collected over multiple production seasons from 2017 to 2024 to ensure that the dataset captured sufficient genetic and environmental variation for reliable parameter estimation. Only complete lactation records were retained. Records from cows with incomplete pedigree information, unknown parents, were treated as unrelated founder animals in the relationship matrix. Those affected by major health

disorders that were documented to have meaningfully altered milk production or reproductive performance, or those with values that were biologically implausible, were all excluded from the analysis. The cleaned dataset comprised 1,248 cows from 98 sires and 997 dams, yielding a total of 2,428 to 2,858 records per trait for 8 lactation period, from a commercial dairy farm in West Java, Indonesia. In addition, the cows were mated by artificial insemination (AI) using semen from proven bulls with published estimated breeding values (EBVs). Milk yield was recorded at each individual milking and then combined to calculate total lactation yield. Where necessary, lactation records were extended to 305 days using standard projection algorithms as recommended by the International Committee for Animal Recording (ICAR, 2020). Reproductive events, including calving dates, dry-off dates, and service records, were maintained in a farm management information system and extracted directly from there for the calculation of the reproductive traits evaluated in this study.

Trait Definitions

Five traits were analyzed in this study.

305-day standardized milk yield (P305): Defined as total milk production accumulated over a standardized 305-day lactation period, expressed in kilograms.

Calving interval (CI): Calculated as the number of days between two consecutive calving dates.

Dry period (DP): Defined as the number of days from the last milking in a given lactation to the next calving.

Peak yield (PY): Defined as the highest daily milk yield recorded a lactation, expressed in kg / day.

Days to peak yield (DPY): Defined as the number of days from calving to the day when peak yield was recorded.

Statistical Model for Fixed Effects

Prior to the genetic analysis, the effect of lactation number on each trait was examined using a General Linear Model within SAS 9.0. The effects included in the analyses were parity (from first to fourth) as the primary fixed effect, and year-season of calving was included to account for environmental variation associated with different production periods. Pairwise com-

parisons among parity groups were conducted using Tukey's Honest Significant Difference (HSD) test, with significance declared at $P < 0.05$. All least-squares means are reported together with their respective standard errors. The statistical model was as follows:

$$Y_{ij} = \mu + L_i + YS_j + \varepsilon_{ij}$$

Where Y_{ij} is the observed value of traits (P305, CI, DP, PY, and DPY), μ is the mean population, L_i is the lactation or parity effect, YS_j is the Year-Season effect, and ε_{ij} is the error.

Genetic Parameter Estimation

Heritability estimates and genetic and phenotypic correlations were obtained using the restricted maximum likelihood (REML) method, implemented through a multi-trait animal model. The animal model used in this study incorporated all pedigree relationships available in the dataset, including sire and dam information. The general form of the multi-trait animal model used for variance component estimation was:

$$y = Xb + Za + e$$

where y is the vector of observations; b is the vector of fixed effects (lactation/parity and year-season of calving); a is the vector of random additive genetic effects; e is the vector of random residual effects; X and Z are incidence matrices relating the respective effects to observations. The random effects were assumed to follow multivariate normal distributions:

$$a \sim MVN(0, A \otimes G) \quad \text{and} \quad e \sim MVN(0, I \otimes R)$$

where A is the numerator relationship matrix derived from pedigree, G is the genetic (co) variance matrix, R is the residual (co)variance matrix, and I is an identity matrix.

Heritability (h^2) for each trait was calculated as the ratio of additive genetic variance to total phenotypic variance:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

Genetic correlations (rg) and phenotypic correlations (rp) between pairs of traits were calculated from the corresponding (co)variance components estimated from the multi-trait analysis. All variance component estimations were performed using REML procedures available in VCE 6.0 software package (Groeneveld *et al.*, 2010), which

employs an average information algorithm for efficient convergence in large datasets. Convergence was assessed by monitoring the change in the log-likelihood function between iterations, with a criterion of less than 10^{-8} used as the stopping threshold.

RESULTS

Data Description

The descriptive statistics for all five traits analyzed in this study are presented in Table 1. The number of observations varied across the studied traits because some animals had incomplete records. Across all parities combined, the overall mean for 305-day yield (P305) was $8,178.04 \pm 23.08$ kg. This reflects a productive herd that falls within the range reported for Holstein-Friesian cattle managed under well-supervised tropical and subtropical conditions. The calving interval (CI) averaged 395.37 ± 1.21 days. Although this slightly exceeds the industry target of 365 days, it is consistent with values commonly observed in herds that do not employ intensive hormonal synchronization protocols.

The dry period (DP) averaged 66.60 ± 0.53 days. The mean peak yield (PY) was 40.60 ± 0.12 kg/day, with cows reaching peak production at an average of 78.00 ± 0.58 days. Coefficients of variation (CV) ranged from 14.68% for P305 to 42.12% for DP, indicating that reproductive traits (CI and DP) had considerably higher phenotypic variability compared to production yield traits.

Effect of Lactation on Performance Traits

The least-squares means for all five traits across the four parity groups are summarized in Table 2. Lactation or parity had a statistically significant effect ($P < 0.05$) on all traits included

in the analysis, which is broadly consistent with the well-established understanding that parity has a profound influence on both productive and reproductive performance of dairy cows.

A progressive increase was observed from first to third lactation, with means of $7,505.64 \pm 33.25$ kg (1st), $8,127.98 \pm 37.80$ kg (2nd), and $8,654.14 \pm 44.91$ kg (3rd) for P305. The fourth lactation showed a slightly lower mean of $8,609.98 \pm 63.24$ kg, which was not significantly different from the third ($P > 0.05$), suggesting that milk yield reaches a plateau after third parity. A similar trend was observed for peak yield (PY), which increased from 34.21 ± 0.13 kg in first to 43.61 ± 0.19 kg and 43.69 ± 0.28 kg in the third and fourth parities, respectively.

The calving interval (CI) was shortest in first-parity (382.09 ± 2.07 days) and it progressively increased through subsequent parities, reaching 403.87 ± 2.55 days by the third lactation. This pattern is consistent with the well-documented negative association between advancing parity and reproductive efficiency in high-producing dairy cattle. The dry period (DP) showed a similar trend, increasing from 53.68 ± 0.55 days in first-parity cows to over 71 days in cows of second parity and beyond. Notably, days to peak yield (DPY) showed an inverse relationship with parity, declining from 89.68 ± 1.17 days in first-parity to 71.61 ± 0.92 days in second-parity, then it remained stable thereafter. This suggests that older cows reach their peak production more quickly after calving compared to first-parity heifers.

Heritability Estimates

Heritability estimates obtained from the multi-trait animal model REML analysis are presented in Table 3. The heritability of P305 was 0.40 ± 0.02 , indicating that a substantial propor-

Table 1. Descriptive statistics for the traits

	n	Mean $\pm$ SE	STD	Min	Max	CV
P305	2,705	$8,178.04 \pm 23.08$	1,200.33	6,000.57	13,527.18	14.68
CI	2,858	395.37 ± 1.21	64.71	300.00	789.00	16.37
DP	2,842	66.60 ± 0.53	28.05	35.00	212.00	42.12
PY	2,610	40.60 ± 0.12	6.11	30.00	80.60	15.06
DPY	2,428	78.00 ± 0.58	28.50	40.00	210.00	36.53

P305 = 305-day milk yield (kg); CI = calving interval (days); DP = dry period (days); PY = peak yield (kg); DPY = days to peak yield (days); n = number of records; SE = standard error; STD = standard deviation; CV = coefficient of variation; Min = Minimum; Max = Maximum

Table 2. Least-squares means ($\pm$ SE) for milk production and reproductive performance traits by lactation number

Lactation	P305	CI	DP	PY
1 st	7,505.64 $\pm$ 33.25 ^a	382.09 $\pm$ 2.07 ^a	53.68 $\pm$ 0.55 ^a	34.21 $\pm$ 0.13 ^a
2 nd	8,127.98 $\pm$ 37.80 ^b	398.59 $\pm$ 2.12 ^b	71.24 $\pm$ 1.02 ^b	40.81 $\pm$ 0.18 ^b
3 rd	8,654.14 $\pm$ 44.91 ^c	403.87 $\pm$ 2.55 ^b	71.65 $\pm$ 1.10 ^b	43.61 $\pm$ 0.19 ^c
4 th	8,609.98 $\pm$ 63.24 ^c	398.40 $\pm$ 3.20 ^b	72.16 $\pm$ 1.47 ^b	43.69 $\pm$ 0.28 ^c
Average	8,178.04 $\pm$ 23.08	395.37 $\pm$ 1.21	66.60 $\pm$ 0.53	40.60 $\pm$ 0.12

Different superscripts within the same column indicate significant differences ($P < 0.05$). P305 = 305-day milk yield (kg); CI = calving interval (days); DP = dry period (days); PY = peak yield (kg); DPY = days to peak yield (days).

Table 3. Heritability estimates for production and reproductive traits in Holstein-Friesian cows

Traits	σ_a^2	σ_e^2	σ_p^2	$h^2 \pm se$
P305	560,400	853,574	1,413,974	0.40 $\pm$ 0.02
CI	775	3,491	4,266	0.18 $\pm$ 0.02
DP	75	655	730	0.10 $\pm$ 0.02
PY	14	15	28	0.48 $\pm$ 0.02
DPY	23	719	742	0.03 $\pm$ 0.01

σ_a^2 = additive genetic variance; σ_e^2 = residual variance; σ_p^2 = phenotypic variance; h^2 = heritability; se = standard error.

tion of phenotypic variation in 305-day milk yield is attributable to additive genetic effects and that meaningful genetic progress through selection would be expected. The heritability of PY was even higher at 0.48 ± 0.02 , suggesting that PY is strongly governed by additive genetic effects.

In contrast, reproductive traits showed considerably lower heritability estimates. The calving interval (CI) had a moderate heritability of 0.18 ± 0.02 , while the dry period (DP) showed a low heritability of 0.10 ± 0.02 . The days to peak yield (DPY) had the lowest estimate at 0.03 ± 0.01 , suggesting that this trait is largely determined by environmental and management factors rather than additive genetic effects, and that direct selection for DPY would give only minimal genetic improvement.

Phenotypic and Genetic Correlations

The matrix of genetic (below the diagonal) and phenotypic correlations (above the diagonal) is presented in Table 4. Among the most noteworthy findings was the near-unity genetic correlation between P305 and PY ($rg = 0.99 \pm 0.01$), indicating that these two traits are controlled by essentially the same set of genes. Breeders who select for higher 305-day milk yield can therefore expect a correspondingly large increase in peak daily yield, and the same applies in reverse.

The genetic correlation between P305 and CI was positive and moderate ($rg = 0.52 \pm 0.08$), while that between CI and PY was also notably positive ($rg = 0.53 \pm 0.07$), which indicates that cows with higher milk production potential are also more likely to have longer calving intervals, which has important implications for selection against reproductive delay. The genetic correlation between DP and P305 was negative and moderate in magnitude ($rg = -0.36 \pm 0.08$), suggesting that cows with high genetic merit for milk production tend to have shorter dry periods, possibly reflecting the difficulties in drying off high-producing cows at a conventional time.

Phenotypic correlations, which reflect both genetic and environmental covariances, were generally of smaller magnitude than genetic correlations and were not always in the same direction. The phenotypic correlation between P305 and CI was -0.16 ± 0.02 , indicating that at the phenotypic level, higher-producing cows did not necessarily have longer calving intervals, possibly because management interventions such as hormonal treatments can partially separate the phenotypic expression of these traits from their genetic association. Similarly, the phenotypic correlation between P305 and DP was -0.16 ± 0.02 , suggesting a modest negative phenotypic relationship between milk yield and dry period length.

Table 4. Phenotypic (upper diagonal) and genetic (lower diagonal) correlations among traits in Holstein-Friesian cows

	P305	CI	DP	PY	DPY
P305		-0.16 ± 0.02	-0.16 ± 0.02	0.56 ± 0.02	-0.06 ± 0.02
CI	0.52 ± 0.08		0.53 ± 0.02	0.14 ± 0.02	-0.06 ± 0.02
DP	-0.36 ± 0.08	-0.16 ± 0.15		0.09 ± 0.02	-0.14 ± 0.02
PY	0.99 ± 0.01	0.53 ± 0.07	-0.22 ± 0.09		-0.13 ± 0.02
DPY	0.28 ± 0.12	0.32 ± 0.18	-0.14 ± 0.25	0.20 ± 0.11	

P305 = 305-day milk yield; CI = calving interval; DP = dry period; PY = peak yield; DPY = days to peak yield, standard errors are shown with ± symbol

DISCUSSION

Performance and Effect of Lactation Number

The mean P305 (8,178.04 kg) in this study compares with yields from Holstein-Friesian herds under similar tropical and subtropical management. Ayalew *et al.* (2017) reported yields ranging from 3,500 to 7,500 kg in Ethiopian herds. In well-managed South and Southeast Asian herds, Abdel-Hamid *et al.* (2019) reported P305 values of 7,600 to 8,500 kg, placing the present estimate within range for high-input tropical production systems.

Progressive increase in milk yield from first to third lactation followed by a plateau in the fourth parity is a biological phenomenon explained by mammary development during early reproductive life (Abdel-Hamid *et al.*, 2019). Cows in first lactation have not reached full body size and metabolic capacity, and their mammary gland is still growing. By the third and fourth lactations, approach their mature production potential, after which yields start to decline due to aging and reproductive stress (Ayalew *et al.*, 2017). This parity-related pattern has been documented across Holstein-Friesian populations, including those studied by Junior *et al.* (2021) and Huang *et al.* (2012).

The mean calving interval (395.37 days) is consistent with comparable production environments. Wahinya *et al.* (2020) reported average CI of 402 to 425 days, emphasizing challenges of reproductive efficiency in the tropics. Abdel-Hamid *et al.* (2019) documented CI means of 398.2 days in Egyptian herds. The ideal 365-day CI was not achieved, which is common in intensive systems where high milk yields can suppress estrous expression and impair uterine involution (Worku *et al.*, 2021).

The mean DP of 66.60 days falls above the recommended 45- to 60-day range, although research suggests short dry periods (15 to 30 days) may be advantageous under certain conditions (Fathoni *et al.*, 2022). The CV for DP (42.12%) indicates variation in this management parameter, reflecting differences in individual production levels at dry-off and variability in protocols across farm units (Wahinya *et al.*, 2020).

Estimates of Heritability

The heritability of P305 (0.40 ± 0.02) is consistent with ranges in international literature. Studies from Europe and North America placed h^2 for milk yield between 0.25 and 0.55, with variation attributable to management, pedigree depth, and statistical models. Miglior *et al.* (2017) reported estimates for milk yield ranging from 0.22 to 0.52, including the estimate in this study.

In tropical environments, heritability for milk yield in Holstein-Friesian cattle tends toward the lower to moderate range, reflecting larger environmental variance from climatic and nutritional variation. Anang *et al.* (2019) reported heritabilities between 0.18 and 0.22. Pangmao *et al.* (2022) estimated h^2 at 0.19 to 0.45 in Thai herds, while Abdel-Hamid *et al.* (2019) and Hussein *et al.* (2025) documented heritabilities between 0.22 and 0.28. The higher estimate of 0.40 in this study may reflect controlled management conditions, reducing environmental variance and increasing the heritability estimate (Hassan *et al.*, 2018). This value indicates a proportion of phenotypic variation in P305 is genetically determined, justifying selection programs.

The high heritability of PY (0.48 ± 0.02) has practical implications. Peak yield is a determinant of lactation yield and linked to the lacta-

tion curve. Dominguez-Castaño *et al.* (2021) noted its high genetic correlation with total lactation yield, supported by the near-unity correlation (0.99) in this study. The high h^2 of PY suggests that selection for PY as an indirect criterion could be an efficient strategy for improving total lactation output when full records are unavailable.

Low to moderate heritability for CI (0.18), DP (0.10), and DPY (0.03) is consistent with the understanding that fertility traits are influenced by numerous genes and sensitive to environmental conditions. Berry *et al.* (2014) reported CI heritability between 0.02 and 0.10 in temperate herds, though tropical estimates reached 0.06 to 0.11 (Wahinya *et al.*, 2020). The estimate of 0.18 for CI may reflect a uniform management system reducing environmental heterogeneity. Similar findings have been reported by Setiaji and Oikawa (2019), who observed generally low heritability estimates for reproductive traits in Japanese Black cattle, emphasizing the substantial influence of management and environmental conditions on fertility-related phenotypes. Genetic selection for CI is possible, though progress will be slower than traits with higher heritability, and improvement through management and nutrition may give more immediate impact (Pryce *et al.*, 2022).

The very low heritability of DPY ($h^2 = 0.03 \pm 0.01$) indicates it is responsive to nutritional management in early lactation, with energy balance and body condition score having substantial influences (Habimana *et al.*, 2023). Genetic improvement in DPY through direct selection would be practically impossible, and management-level interventions represent a more practical approach to optimizing this trait.

Genetic and Phenotypic Correlations

The near-unity genetic correlation between P305 and PY ($rg = 0.99 \pm 0.01$) is a striking finding with implications for breeding program design. This strong association indicates that the same genes drive higher total lactation yield and peak daily yield. As the peak point of the lactation curve reflects an animal's maximum secretory capacity, it shares a strong genetic correlation with total 305-day yield ($r = 0.86$; Pangmao *et al.*, 2022), allowing its early use as a reliable predictor of genetic merit for total lactation yield

(Dominguez-Castaño *et al.*, 2021). Positive genetic correlations between P305 and CI, and PY and CI (0.52 and 0.53) confirm an unfavorable genetic antagonism between milk production and reproductive efficiency in Holstein-Friesian. High-yielding cows enter negative energy balance after calving, as energy demands exceed dry matter intake (Habimana *et al.*, 2023; Pryce *et al.*, 2022). Prolonged negative energy balance delays ovarian activity, impairs signaling, reduces oocyte quality, and extends the interval from calving to ovulation and conception (Fathoni *et al.*, 2022; Worku *et al.*, 2021). Houlahan *et al.* (2021) and Miglior *et al.* (2017) emphasized the need for breeding programs to account for these correlations by incorporating reproductive traits into multi-trait selection indices, where pressure for milk yield is counterbalanced by selection against unfavorable reproductive genotypes. Economic weights in indices should reflect the impact of unit improvements, considering genetic correlations.

The negative genetic correlation between DP and P305 (-0.36 ± 0.08) indicates cows with higher genetic potential for milk production tend to have shorter dry periods, reflecting management decisions to dry off high-producing cows later or difficulty in suppressing milk secretion (Worku *et al.*, 2021). Genetic improvement for higher milk yield may shorten dry periods to suboptimal lengths, potentially compromising mammary regeneration and metabolic preparation for the next lactation (Fathoni *et al.*, 2022; Pryce *et al.*, 2022). This effect should be considered when evaluating selection index design.

Phenotypic correlations were smaller than genetic correlations, and some were in the opposite direction. Negative phenotypic correlations of P305 with CI (-0.16) and DP (-0.16) contrast with positive genetic correlations, illustrating that genetic and phenotypic correlations can differ when environmental factors exert differential effects (Worku *et al.*, 2021). These negative phenotypic correlations likely reflect management practices that keep high-producing cows in lactation longer and rebreed them earlier, partially offsetting the genetic predisposition toward longer intervals (Fathoni *et al.*, 2022; Wahinya *et al.*, 2020).

Implications for Breeding Program Design

The genetic parameter estimates in this study are relevant to Holstein-Friesian breeding programs in tropical environments. The moderate to high heritability of P305 and PY confirms that selection is expected to result in meaningful annual genetic gains (Wahinya *et al.*, 2022).

Unfavorable genetic correlations between production and fertility support the use of a multi-trait total merit index rather than single-trait selection (Fathoni *et al.*, 2022; Worku *et al.*, 2021). Integrating CI into the selection index would curb the deterioration of reproductive efficiency, rather than focusing selection pressure solely on P305 (Wahinya *et al.*, 2022). Genomic selection offers tools for more precise management of these trade-offs, particularly with reference populations of sufficient size (Cheruiyot *et al.*, 2022; Pryce *et al.*, 2022). Establishing a national genomic reference population including production and fertility phenotypes would enhance the accuracy of genomic estimated breeding values (GEBVs) and accelerate progress (Ducrocq *et al.*, 2022).

The very low heritability of DPY indicates this trait is not an efficient target for direct selection, but could be improved through nutritional management of transition cows and optimization of calving protocols (Pryce *et al.*, 2022). Farms achieving a shorter time to peak yield by ensuring high dry matter intake in early lactation are likely to observe improvements in total yield and reproductive performance, given the associations between earlier peak yield and lactation performance (Habimana *et al.*, 2023).

CONCLUSION

This study provides genetic parameter estimates for five traits in Holstein-Friesian dairy cattle under Indonesia's tropical conditions. Findings confirm that 305-day milk yield and peak yield are moderately to highly heritable and share a near-perfect genetic correlation, which supports selection for improving lactation performance. Reproductive traits showed low heritability, but genetic correlations with production traits underline the importance of fertility in selection programs. Positive genetic correlations between production traits and calving interval emphasize the need for multi-trait selection indices that balance production with reproductive performance.

These findings serve as a reference for breeding strategies in tropical regions.

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CONFLICT OF INTEREST

The authors certify that there is no conflict of interest with any financial, personal, or other relationships with individuals or organizations related to the material presented in this manuscript.

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