

Genetic Analysis of Performance Traits Across Different Exotic Blood Levels of Holstein Friesian Crossbred Cattle in Pakistan

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ABSTRACT

Enhancing dairy productivity in Pakistan relies heavily on crossbreeding indigenous cattle with exotic breeds like Holstein Friesian (HF). This study comprehensively evaluates the performance, genetic parameters, and effects of exotic inheritance level and sire selection on key economic traits in HF crossbred cattle to inform sustainable breeding strategies. Data on 1,123 lactation records were analyzed to estimate descriptive statistics, variance components, heritability, and genetic correlations for milk production (Daily Milk Yield-DMY, 305-day Standard Yield-SMY, Lactation Yield-LY), reproduction (Age at First Service-AFS, Age at First Calving-AFC, Calving Interval-CI, Dry Period-DP), and lactation length (LL). Results indicated a mean SMY of 3569 ± 729 L, AFC of 1161 ± 107 days, and CI of 423 ± 24 days. A significant linear trade-off was observed: increasing HF blood level from 50% to >75% raised SMY from 2919 to 4077 L but worsened AFC (1126 to 1191 days). Both blood level and sire group had highly significant ($p < 0.001$) effects on milk yield and AFC. Crucially, the sire group had no significant effect on CI or DP. Heritability was high for milk yield traits ($h^2 = 0.38-0.40$), moderate for AFC ($h^2 = 0.188$), and low for CI and DP ($h^2 = 0.14$). Genetic correlations were near-perfect among milk traits ($r > 0.91$) and between CI and DP ($r = 0.87$), but negligible between SMY and AFC ($r = -0.07$). The study concludes that an intermediate exotic inheritance level (62.5% HF) optimizes the yield-adaptation balance. The absence of genetic antagonism between yield and AFC, coupled with significant sire variance, enables simultaneous genetic improvement of both traits through the selection of proven sires. However, the low heritability of postpartum fertility traits necessitates management-driven interventions for optimal calving intervals. A successful dairy improvement strategy must therefore integrate balanced crossbreeding, strategic sire selection for yield and early maturity, and intensified nutritional and herd health management to unlock the full genetic and economic potential of HF crossbreds in Pakistan.

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Authors' Contribution

KU, SMS, and RK conceptualized the research, analyzed the data, and used software. KU and RK developed the methodology, and under the supervision of SMS analysis, data curation was done. FA and AR helped in editing and conducted the investigation. All authors approved the manuscript.

Key words

Crossbreeding, Heritability, Genetic Correlation, Milk Yield, Age at First Calving, Calving Interval, Sire Selection, Pakistan

INTRODUCTION

Livestock remains the most dynamic and resilient sub-sector of Pakistan's agriculture, contributing 63.6 percent to agriculture's value addition and 14.97 percent to the country's GDP (Economic Survey, 2025). The global dairy industry increasingly relies on genetic improvement strategies to meet rising milk demand. Cattle in Pakistan

have historically been raised for the purpose of producing draught animals, except for Sahiwal and Red Sindhi, which are milch breeds (Khan *et al.*, 2008). Crossbreeding is regarded as a rapid method for enhancing the performance of low-yielding tropical breeds. For the last four decades, crossbreeding of indigenous cattle with exotics such as Holstein Friesian (HF) has been practiced in Pakistan (Hassan and Khan, 2013) and has emerged as a cornerstone of dairy sector modernization due to its exceptional milk production capabilities. Through systematic crossbreeding with indigenous breeds, particularly the heat-tolerant Sahiwal, dairy farmers aim to combine high productivity with adaptation to local environmental conditions.

However, the performance of crossbred cattle can vary significantly based on their genetic composition, particularly the proportion of Holstein blood they possess. The estimation of genetic and phenotypic parameters for performance traits serves as a crucial tool for assessing

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the overall genetic gain from such selection programs and may also assist in revising or amending breeding policies. The assessment of genetic parameters aids in identifying the selection method to forecast direct and correlated responses to selection, selecting a breeding system for future enhancement, and estimating genetic response. Assessments of genetic parameters, such as the heritability of various production and reproduction traits and the genetic correlations among them, are essential for creating effective breeding plans and calculating breeding values. Currently, animal models are used to estimate the breeding values of animals (Kelm *et al.* 2000). Exotic genes are frequently introduced, although often without prior consideration of the implications for the relevant farming systems (Marshall, 2014; Wollny, 2003). It is frequently carried out in an unorganized manner, jeopardizing the survival of locally adapted native breeds (Martyniuk *et al.*, 2010). This has become a concern for breeders and researchers.

The integration of Holstein genetics into Pakistan's cattle populations aims to address critical challenges in dairy farming: low milk yields, extended calving intervals, and limited reproductive efficiency (Rehman *et al.*, 2024). However, crossbreeding outcomes vary substantially based on genetic composition, specifically the proportion of Holstein inheritance (commonly termed "blood level"). Understanding how different Holstein blood fractions ranging from 50% to over 75% influence productive and reproductive performance is essential for developing evidence-based breeding strategies. This study undertakes a comprehensive investigation of performance traits across different blood levels of Holstein Friesian (HF) crossbred Pakistani cattle by examining the influence of HF blood level on different productive and reproductive traits.

MATERIALS AND METHODS

Source of data

The study was conducted at a State Dairy Farm located in the Punjab province of Pakistan. Production and reproduction records of HF crossbred cows from 2000 to 2024 have been utilized. Traits, including standard 305-day milk yield (SMY), lactation length (LL), age at first service (AFS), age at first calving (AFC), calving interval (CI), and dry period (DP) were calculated from data.

Statistical model and experimental design

Data organized in an MS Excel sheet were analyzed in a statistical analysis system (SAS, V 9.1.3) (Rodenhuse *et al.*, 2004). A general linear model was utilized for variance analysis employing a CRD design. Means were compared using Duncan's multiple range test. The effect of different

class variables on performance traits was modeled as:

$$Y_{ijk} = \mu + \alpha_i + \beta_j + \epsilon_{ijk}$$

Where; Y_{ijk} is represents the k-th observed value of the dependent variables for the i-th level of HF blood level in the cow (HFBL) and j-th group of sires at different locations. μ is population constant. α_i is the i-th effect of HFBL (HF blood level i-e 50%, 62.5%, 75% and above 75%), $i = 1, 2, \dots, 4$. β_j is the j-th effect of group of sires (SG) at different locations, $j = 1, 2, \dots, 13$, and ϵ_{ijk} is represents the random residual error.

$$\text{Heritability calculation: } h^2 = \frac{4 \times \text{Var}_s}{\text{Var}_s + \text{Var}_w}$$

Where h^2 is heritability. Var_s is the variance between sires and Var_w is the variance within sires.

Correlation analysis

Correlation among different variables in the current research was estimated utilizing Pearson's correlation coefficient. $r_{xy} = \frac{\delta xy}{\sqrt{\delta^2 x \cdot \delta^2 y}}$

Where r is coefficient of correlation. $\sigma^2 x$ is variance of trait x , $\sigma^2 y$ is Variance of trait y and σ_{xy} is Covariance of traits x and y .

$$\text{Genetic correlation: } r_g = \frac{\text{Cov}_s}{\sqrt{\text{Var}_s(x) \times \text{Var}_s(y)}}$$

Where r_g is the genetic correlation between two traits; Cov_s is covariance between sires; $\text{Var}_s(x)$ is between sire variance of trait x and $\text{Var}_s(y)$ is between sire variance of trait y .

RESULTS

Daily milk yield (DMY)

The overall mean for DMY was 11.70 ± 2.39 L, ranging from 7.48 to 20.03 L. HF blood level (HFBL) and sire group both had highly significant ($p < 0.01$) effects on DMY (Table I). DMY increased progressively with increasing exotic inheritance (Fig. 1): 9.57 L (50% HF), 10.81 L (62.5% HF), 12.02 L (75% HF), and 13.37 L (>75% HF). Progeny of sire group 2 produced the highest DMY (13.38 L (Fig. 2). Both phenotypic ($r = 1.00$, $p < 0.0001$) and genetic correlation ($r = 1.00$ and 0.912) for DMY with SMY were strong and positive. The heritability estimate for DMY was 0.339 (Table I), which is moderately high.

Standard 305-day milk yield (SMY) and lactation yield (LY)

Mean SMY was 3569 ± 729 L (range: 2283-6108 L) and mean LY was 3583 ± 655 L (range: 2158-5390 L). Both traits were significantly influenced by HFBL and sire group ($p < 0.01$, Table I). SMY increased from 2919 L (50% HF) to 4077 L (>75% HF). SMY was perfectly correlated with DMY ($r = 1.00$) and strongly with LY ($r = 0.819$ phenotypically, 0.912 genetically). LY also showed positive phenotypic correlation with LL ($r = 0.115$, $p < 0.001$).

Table I. Descriptive statistics, ANOVA P-value and heritability estimate of various traits of performance of HF crossbred cattle in Pakistan.

Traits	Mean $\pm$ SD	Range		ANOVA P-Value		h ²
		Min	Max	HFBL	SG	
DMY (L)	11.70 $\pm$ 2.39	7.48	20.03	< 0.0001	0.0003	0.399
SMY (L)	3569 $\pm$ 728.95	2283	6108	< 0.0001	0.0003	0.395
LY (L)	3583 $\pm$ 655.03	2158	5390	< 0.0001	0.0021	0.381
LL (Days)	308.50 $\pm$ 29.68	219.00	369.00	0.0274	0.2464	0.135
AFS (Days)	879.57 $\pm$ 106.52	643.00	1098.00	< 0.0001	0.0001	0.186
GP (Days)	281.78 $\pm$ 4.15	270.00	289.00	0.0916	0.6813	0.015
AFC (Days)	1161 $\pm$ 106.69	921.00	1378.00	< 0.0001	0.0001	0.188
CI (Days)	422.72 $\pm$ 24.04	369.00	496.00	< 0.0001	0.5330	0.138
DP (Days)	115.97 $\pm$ 32.21	65.00	227.00	< 0.0001	0.0688	0.145

DMY, daily milk yield; SMY, standard 305-day milk yield; LY, lactation yield; LL, lactation length; AFS, age at first service; GP, gestation period; AFC, age at first calving; CI, calving interval; DP, dry period; HFBL, HF blood level; SG, sire group and h², narrow sense heritability.

The heritability estimates for both SMY and LY (0.395 and 0.381, respectively) were moderately high (Table I).

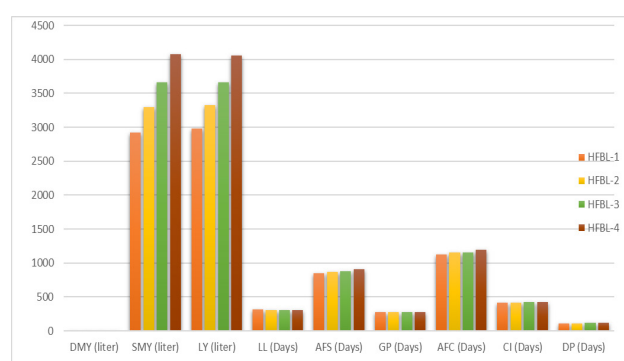


Fig. 1. Mean comparison of performance traits of HF crossbred cattle in Pakistan in response to HF Blood levels. HFBL-1: 50 % HF blood level, HFBL-2: 62.5 % HF blood level, HFBL-3: 75 % HF blood level, and HFBL-4: Above 75 % HF blood level. For other abbreviation, see Table I.

Lactation length (LL)

The average LL was 308.50 $\pm$ 29.68 days, ranging from 219 to 369 days. HFBL had a significant effect ($p < 0.0274$, Table I) with 50 % HF blood group having the longest LL (312.73 days) and >75 % HF blood group the shortest (306.15 days, Fig. 1). LL had a positive phenotypic correlation with the CI ($r = 0.258$, $p < 0.0001$) and a moderate negative correlation with production traits ($r = 0.451$, $p < 0.0001$). Genetic correlation of LL to milk yield traits was also negative ($r = -0.348$). The heritability estimate for LL was low (0.135, Table I).

Reproductive traits

Age at first service (AFS) and age at first calving (AFC)

The mean AFS and AFC were 879.57 $\pm$ 106.52 days and 1161.00 $\pm$ 106.69 days, respectively. AFS ranged from 643 days to 1098 days, whereas AFC ranged from 921 to 1378 days. Both traits were significantly influenced by HFBL and sire group ($p < 0.0001$, Table I). The 50% HF blood group had the lowest AFS (~845 days), and AFC (~1126 days), followed by HFBL-2, HFBL-3 in increasing linear trend. HFBL-4 (above 75 % HF blood) cows had the highest AFS (~909 days) and AFC (~1191 days) (Fig. 1). Genetic correlations of AFS and AFC for milk yield were very weak. Both AFS and AFC exhibited low to moderate heritability estimates (0.183 and 0.188, Table I).

Gestation Period (GP)

Mean GP was 281.78 $\pm$ 4.15 days, with no significant effects from HFBL or Sire group.

Calving interval (CI) and dry period (DP)

Mean CI was 422.72 $\pm$ 24.04 days, and mean DP was 115.97 $\pm$ 32.21 days. HFBL had high significant effect on both traits ($p < 0.0001$), while sire group was non-significant (Table I). CI increased from 417 days (50% HF blood group) to 428 days (>75% HF group, Fig. 1). The phenotypic correlation between CI and DP was very strong and positive ($r = 0.767$, $p < 0.0001$). The genetic correlation was even stronger ($r = 0.869$). Pearson's correlation analysis revealed a weak but highly significant association between SMY and CI ($r = 0.169$; $p < 0.0001$). Similarly, genetic correlation analysis also demonstrated a positive relationship between SMY and CI ($r = 0.189$), indicating

that increased milk production tended to be associated with prolonged CI (Fig. 3). Both traits had low heritability estimates (CI: 0.138, DP: 0.145).

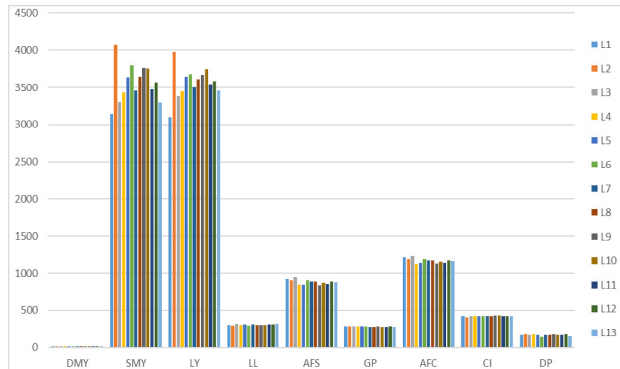


Fig. 2. Mean comparison of Performance traits of HF crossbred cattle in Pakistan in response to Sire Group at location L1, L2, L3 L13. For other abbreviation, see Table I.

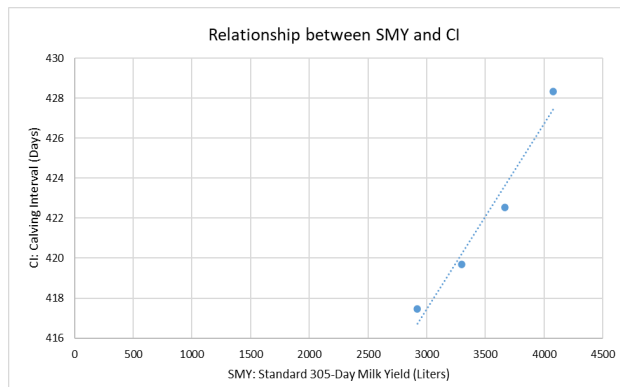


Fig. 3. The relationship between Standard 305-day milk yield (SMY) and calving interval (CI) across different HF blood level groups in HF crossbred cattle of Pakistan.

DISCUSSION

Milk production traits

The mean DMY of 11.70 ± 2.39 L represents a substantial improvement over earlier reports from Pakistan (Hassan and Khan, 2013; Qureshi *et al.*, 2008), indicating genetic progress through systematic crossbreeding and improved management practices (Rehman *et al.*, 2025). The linear increase in milk yield with increasing HF blood level aligns with (Bhadauria and Katpatal, 2003) and (Hassan and Khan, 2013), consistent with the principle of hybrid vigor and introgression of high-production alleles from the Holstein breed (Madalena *et al.*, 2012).

The highly significant sire group effect ($p < 0.0003$)

confirms substantial genetic variability among bulls, providing a strong basis for selective breeding programs. The near-perfect genetic correlations among milk yield traits ($r = 0.912-1.00$) validate the use of SMY as a robust selection criterion (Jamrozik and Schaeffer, 2012). Heritability estimates for milk yield traits (0.38-0.40) fall within the typical range for crossbred cattle populations (Rath *et al.*, 2026), confirming that direct selection for these traits would be effective.

Reproductive traits

The mean AFC of 1161 days (~38 months) is economically suboptimal, delaying the onset of revenue-generating life. The finding that higher HF blood levels are associated with delayed AFC (1126 days at 50% HF vs. 1191 days at > 75% HF) supports the assumption that higher exotic inheritance delays maturity. However, (Shonka-Martin *et al.*, 2019) demonstrated that Holstein heifers raised under intensive nutritional management can achieve puberty at younger ages, suggesting that management can unlock genetic potential for early maturity.

The positive association between milk yield and calving interval suggests a potential antagonistic relationship between production and fertility traits in HF crossbred cattle. Since the gestation period remains relatively constant, prolonged CI in high-producing cows may primarily reflect delayed conception associated with metabolic stress and negative energy balance during lactation. Increased lactational demand in high-yielding animals can adversely affect reproductive hormonal regulation and delay resumption of ovarian cyclicity after calving, consequently prolonging CI and AFC. Similar findings were reported by Ullah *et al.* (2020) and (Qureshi *et al.*, 2016), who observed prolonged calving intervals in animals with the higher exotic blood levels, possibly due to reduced resistance to thermal stress. Although direct endocrine or metabolic indicators were not evaluated in the present study, the observed production fertility relationship indirectly supports this possibility.

CONCLUSION

This study provides a comprehensive evaluation of performance traits and genetic parameters in HD crossbred cattle in Pakistan, yielding clear, actionable conclusions for breeding strategy and farm management.

Crossbreeding has successfully elevated milk production potential, with average yield surpassing earlier national reports. However, a pronounced trade-off exists; increasing exotic inheritance beyond 62.5% linearly boosts milk yield but simultaneously delays age at first calving and prolongs postpartum intervals. An intermediate

exotic inheritance level (approximately 50 to 62.5% HF) represents the most sustainable genetic structure for the prevailing production environment.

Critically, the genetic architecture is favorable for selection. Milk yield traits exhibit high heritability (~0.39) and are strongly correlated, making them highly suitable for genetic selection. While calving interval shows very low heritability, confirming it is primarily management driven, age at first calving possesses moderate heritability (0.188). Most importantly, there is no significant negative genetic correlation between milk yield and age at first calving, proving that simultaneous genetic improvement of both is feasible.

The significant variation due to sire group for both production and AFC underscore the paramount importance of within-breed sire selection. Proven sires exist that can propagate high yield alongside early maturity, offering a direct tool to enhance herd profitability.

A dual-pronged approach is required for optimizing HF crossbred performance by adapting a strategic breeding program focusing on high 305-day milk yield and early age at first calving, utilizing progeny tested sires and precision management, prioritizing excellent nutrition and health management for heifers to realize genetic potential for early calving, and intensifying postpartum care for high-producing cows to mitigate extended calving intervals.

By integrating targeted genetics with intensified management, the productivity, efficiency, and sustainability of Pakistan's dairy crossbreeding enterprise can be significantly enhanced.

DECLARATIONS

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Data availability statement

Data is not publicly available due to confidentiality agreements with State Dairy Farm. Reasonable requests may be directed to the corresponding author.

IRB approval

This manuscript is part of the Ph.D. research study. The synopsis was duly approved at the BOS meeting of the Department of Livestock Management, Breeding and Genetics, University of Agriculture Peshawar.

Ethical statement

The experimental animals were handled as per approved guidelines of the ethical committee of the Faculty of Animal Husbandry and Veterinary Sciences, The University of Agriculture Peshawar, notified vide notification No./11/PS/UAP dated 11-03-2025.

Generative AI and AI assisted technology statement

The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Statement of conflict of interest

The authors have declared no conflict of interest.

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