

Article

Relationship between Holstein Friesian genetic contribution, milk yield, and disease incidence in F1 and F2 crossbred cattle

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Abstract: Crossbreeding with Holstein Friesian (HF) cattle has become a widely adopted strategy for improving dairy productivity in Bangladesh. However, limited information is available regarding the optimum level of HF genetic contribution that maximizes milk production while maintaining disease resilience in crossbred cattle under smallholder farming conditions. This study evaluated the relationship between HF blood percentage, lactation milk yield, and the incidence of common livestock diseases in F1 and F2 crossbred cattle. It was hypothesized that increasing HF genetic contribution would improve milk yield without significantly affecting the occurrence of major diseases. Data were collected from 1,694 crossbred cattle (847 F1 and 847 F2) maintained by marginal farmers across 27 districts of Bangladesh from May, 2022 to October, 2024. Animals were classified according to HF sire blood percentage. Lactation milk yield and the occurrence of Foot-and-Mouth Disease, Hemorrhagic Septicemia, mastitis, reproductive tract disorders, and dystocia were evaluated. One-way ANOVA, Kruskal–Wallis H test, and Pearson's Chi-square test were used to determine the effects of HF blood percentage on productive performance and disease incidence. HF blood percentage had a highly significant effect on lactation milk yield in both F1 and F2 generations ($P < 0.001$). Crossbred cattle with 93.75% HF blood consistently achieved the highest milk yield in both generations, whereas milk production generally declined with increasing local genetic inheritance. Breed upgradation speed also influenced productive performance, with fast and very fast upgradation producing higher mean lactation yields than normal and moderate upgradation. In contrast, no significant association was observed between HF blood percentage and the incidence of the investigated diseases ($P = 0.614$), indicating that disease occurrence was largely independent of genetic composition. HF genetic contribution improves milk production, whereas disease susceptibility is influenced primarily by non-genetic factors. Strategic crossbreeding and proper management are essential for sustainable dairy production. The findings support sustainable dairy breeding programmes that combine genetic improvement with effective management to enhance milk production while maintaining the adaptability of crossbred cattle.

Keywords: artificial insemination; breed upgradation; dairy production; livestock health; tropical production systems

1. Introduction

In Bangladesh, milk production remains insufficient to meet the increasing demand driven by rapid population growth, urbanization, and changing dietary preferences, resulting in a considerable dependence on imported dairy products (Mahfuza *et al.*, 2024; Yasmin *et al.*, 2026). Improving the genetic potential of dairy cattle has therefore become a national priority for enhancing milk production while ensuring sustainable livestock development (Bell, 2024; Van Eenennaam, 2025). Among the available genetic improvement strategies, crossbreeding indigenous cattle with high-yielding exotic breeds has emerged as one of the most effective approaches for increasing dairy productivity under tropical production systems (Hamid *et al.*, 2017; Pehan *et al.*, 2025).

Holstein Friesian (HF) cattle are widely recognized as one of the highest milk-producing dairy breeds in the world and have consequently become the predominant exotic breed used in crossbreeding programmes across many tropical and subtropical countries (Hridoy *et al.*, 2025). In Bangladesh, the rapid expansion of artificial insemination programmes has facilitated the widespread introduction of HF genetics into indigenous cattle populations, resulting in crossbred animals possessing varying levels of exotic blood across successive generations (Galukande *et al.*, 2013; Azad *et al.*, 2023). The incorporation of HF genetics generally improves milk production because of the superior additive genetic merit of the breed; however, increasing the proportion of exotic blood may also reduce adaptation to tropical climatic conditions, heat tolerance, reproductive efficiency, and resistance to endemic diseases when animals are reared under low-input management systems (Mekonnen *et al.*, 2020; Marchioretto *et al.*, 2023). The performance of crossbred cattle is therefore determined not only by their genetic composition but also by complex interactions among genotype, environment, nutrition, disease pressure, and management practices (Copley *et al.*, 2024; Spoelstra *et al.*, 2026). Furthermore, first-generation (F1) crossbreds frequently exhibit hybrid vigor, whereas subsequent generations may experience recombination losses that alter productive performance and adaptability, emphasizing the importance of evaluating both F1 and F2 generations under practical farming conditions (Chawala *et al.*, 2021; Lijalem *et al.*, 2026).

Sustainable dairy improvement requires breeding strategies that simultaneously enhance productivity and preserve animal health and environmental adaptability (Oduor *et al.*, 2025). Diseases such as Foot-and-Mouth Disease (FMD), mastitis, Hemorrhagic Septicemia (HS), reproductive tract (RT) disorders, and dystocia remain among the major constraints limiting dairy production in Bangladesh because they reduce milk yield, impair reproductive performance, increase veterinary costs, and lower farm profitability (Sobur *et al.*, 2024; Faruk *et al.*, 2025). Although several studies have investigated the effects of crossbreeding on milk production or reproductive traits, relatively few have comprehensively examined the combined influence of different HF blood percentages on both milk production and susceptibility to common livestock diseases across multiple crossbred generations (Galukande *et al.*, 2013; Reyad *et al.*, 2016; Saha *et al.*, 2024; Solarczyk *et al.*, 2024). Moreover, limited information is available regarding the influence of breed upgradation speed on productive performance under smallholder production systems. Addressing these knowledge gaps is essential for identifying the most appropriate proportion of exotic blood capable of maximizing milk yield while maintaining health, resilience, and adaptability. Such evidence will provide valuable scientific guidance for optimizing crossbreeding programmes, improving artificial insemination strategies, and promoting sustainable dairy development in Bangladesh and other tropical production environments (Priyashantha *et al.*, 2025).

Although crossbreeding with HF cattle has become the principal strategy for improving dairy productivity in Bangladesh, the optimum proportion of exotic blood that maximizes milk production without compromising disease resistance and environmental adaptability remains uncertain. Most previous studies have evaluated productive or reproductive traits independently, whereas comprehensive assessments integrating milk yield, disease susceptibility, and breed upgradation speed across different HF blood percentages in both F1 and F2 generations are scarce (Ghazy *et al.*, 2024; Hridoy *et al.*, 2025; Shuvo *et al.*, 2025). Consequently, this study addresses the following research questions: How does HF blood percentage influence milk production in F1 and F2 crossbred dairy cattle? Is HF blood percentage associated with the occurrence of common livestock diseases, including FMD, mastitis, HS, RT disorders, and dystocia? Does breed upgradation speed significantly influence lactation performance? Which proportion of HF blood provides the optimum balance between productivity and disease resilience under smallholder farming conditions in Bangladesh? Based on these questions, the study hypothesized that HF blood percentage significantly influences milk production and is associated with the occurrence of common livestock diseases in crossbred dairy cattle.

Accordingly, the objective of this study was to investigate the relationship between HF exotic blood percentage and its effects on milk production and susceptibility to common livestock diseases in F1 and F2 crossbred dairy cattle in Bangladesh, while also evaluating the influence of breed upgradation speed on productive performance.

The novelty of this research lies in its integrated assessment of productive performance, disease occurrence, genetic composition, and breed upgradation speed using a large field dataset collected from multiple districts across Bangladesh, providing a comprehensive evaluation under practical smallholder farming conditions. The findings are expected to generate evidence-based recommendations for optimizing crossbreeding programmes by identifying an appropriate range of HF blood that enhances milk production without adversely affecting animal health and adaptability.

2. Materials and Methods

2.1. Ethical approval

Ethical approval was not required for this study as no experimental procedures, interventions, or manipulations were performed on live animals.

2.2. Study area and periods

The study was conducted using retrospective farm records collected from dairy farms located across 27 districts of Bangladesh from May, 2022 to October, 2024, representing diverse agroecological and dairy production regions of the country (Figure 1). These farms were primarily smallholder and marginal dairy enterprises where HF crossbred cattle were reared under traditional management systems.



Figure 1. Geographic locations of the dairy farms included in the study across 27 districts of Bangladesh.

2.3. Study population and data collection

The study population comprised a total of 1,694 HF crossbred dairy cows, including 847 F1-generation (50% local $\times$ 50% HF and subsequent crosses) and 847 F2-generation animals. The cattle represented seven genetic groups based on the proportion of HF inheritance: 50% HF (50% local $\times$ 50% HF), 62.5% HF (37.5% local $\times$ 62.5% HF), 75% HF (25% local $\times$ 75% HF), 87.5% HF (12.5% local $\times$ 87.5% HF), 93.75% HF (6.25% local $\times$ 93.75% HF), 100% local (locally born and raised, with imported HF parents), and Pure USA HF. These genetic groups were included to compare productive performance and disease occurrence across different levels of exotic inheritance.

For each animal, information was collected on generation, HF blood percentage, lactation milk yield, and the occurrence of five major diseases, namely FMD, HS, mastitis, RT disorders, and dystocia (Mia *et al.*, 2025). Data were extracted from individual farm records and verified through discussions with the respective farmers whenever clarification was required. Each animal was assigned a unique identification number to ensure traceability and prevent duplicate entries. Before statistical analysis, all records were reviewed for completeness, consistency, and logical accuracy, and observations with incomplete or inconsistent information on breed composition, milk production, or disease history were excluded from the final dataset to maintain data quality.

2.4. Animal management practices

The crossbred dairy cattle included in this study were reared under typical smallholder production systems practiced in Bangladesh, where management practices varied slightly among farms but generally followed similar husbandry protocols. Feeding primarily consisted of locally available feed resources supplemented with commercially formulated concentrate mixtures according to farmers' economic capacity. The concentrate ration commonly comprised rice polish, wheat bran, mustard oil cake, molasses, *Lathyrus sativus* (khesari), common salt, and vitamin–mineral premixes. Roughage was supplied mainly in the form of rice straw and cultivated green fodders, including Napier (*Pennisetum purpureum*), German (*Echinochloa polystachya*), Para (*Brachiaria mutica*), and Jumbo grasses. The quantity and quality of feed provided varied among farms depending on seasonal availability and financial resources.

Routine herd management practices, including housing, feeding, milking, and breeding, were performed according to individual farm management systems. Cows were generally milked twice daily using conventional hand-milking techniques. Breeding was carried out through artificial insemination using commercially available HF semen, which constituted the primary breeding strategy for genetic improvement across the surveyed farms. Preventive and therapeutic veterinary care, including vaccination, deworming, and treatment of clinical diseases, was provided according to farmers' management practices and the availability of local veterinary services. As this investigation was based on retrospective field records collected under existing farm conditions, no modifications were made to the routine management practices during the study period.

2.5 Variable definition and breed upgradation classification

The primary outcome variables considered in this study were lactation milk yield and the occurrence of five common livestock diseases, namely FMD, HS, mastitis, RT disorders, and dystocia. Lactation milk yield was recorded as the total milk produced per lactation and expressed in liters (L). Disease occurrence was treated as a categorical variable and recorded as either present or absent based on farm records and veterinary diagnoses. HF blood percentage was considered the primary explanatory variable and was categorized into seven predefined genetic groups: 50%, 62.5%, 75%, 87.5%, 93.75%, 100% local, and Pure USA HF. Breed upgradation speed was determined by calculating the difference in HF blood percentage between the sires used to produce the F1 and F2 generations. Based on the magnitude of genetic improvement, breed upgradation was classified into four categories. A difference of <13% HF blood was classified as Normal, a difference of $\geq 13\%$ and <26% was classified as Moderate, a difference of $\geq 26\%$ and <38% was classified as Fast, and a difference of $\geq 38\%$ was classified as Very Fast. This classification was used to evaluate the influence of different rates of genetic upgrading on lactation performance. In addition, disease occurrence in both F1 and F2 generations was cross-tabulated according to the HF blood percentage groups to compare disease-free survival and disease incidence across different levels of exotic genetic inheritance.

2.6 Statistical analysis

All data were compiled, coded, and organized using Microsoft Excel (Microsoft Corp., Redmond, WA, USA) prior to statistical analysis. Statistical analyses were performed using IBM SPSS Statistics version 22.0 (IBM Corp., Armonk, NY, USA). Descriptive statistics were calculated to summarize the characteristics of the study population, with continuous variables presented as mean $\pm$ standard error (SE) and categorical variables

expressed as frequencies and percentages. The effect of HF blood percentage on lactation milk yield in the F1 and F2 generations was evaluated using one-way analysis of variance (ANOVA). Since the distribution of milk yield did not fully satisfy the assumptions of parametric analysis for all comparison groups, the non-parametric Kruskal–Wallis H test was also performed to validate differences among genetic groups. Associations between HF blood percentage and the occurrence of FMD, HS, mastitis, RT disorders, and dystocia were assessed using Pearson's Chi-square (χ^2) test. Cross-tabulation analysis was further conducted to compare disease-free survival and disease incidence across different Holstein Friesian blood percentage groups in both F1 and F2 generations. All statistical tests were two-tailed, and differences were considered statistically significant at $P < 0.05$. The study area map was prepared using the QGIS version 3.44 (QGIS development team).

3. Results

3.1. Milk yield across Holstein Friesian blood levels

A significant effect of Holstein Friesian blood percentage on lactation milk yield was observed in both F1 and F2 crossbred cattle ($P < 0.001$). In the F1 generation, both the one-way ANOVA ($F(12, 834) = 112.87$, $P < 0.001$) and the Kruskal–Wallis H test ($\chi^2(11) = 371.82$, $P < 0.001$) demonstrated highly significant differences in milk yield among the genetic groups. Similarly, in the F2 generation, one-way ANOVA ($F(20, 826) = 38.42$, $P < 0.001$) and the Kruskal–Wallis H test ($\chi^2(12) = 381.28$, $P < 0.001$) confirmed a significant influence of HF blood percentage on lactation milk yield. In contrast, no significant association was detected between HF blood percentage and the occurrence of the investigated diseases (Pearson's $\chi^2 = 3.563$, $P = 0.614$) (Table 1).

Table 1. The effects of Holstein Friesian blood percentage on milk yield and disease incidence.

Category	Test	Statistic	df	P-value	Significance
Milk yield (F1)	One-way ANOVA	$F(12,834)=112.87$; $F(12,834)=112.87$	12, 834	<0.001	HS
	Kruskal-Wallis H test	$\chi^2(11)=371.82$; $\chi^2(11)=371.82$	11	<0.001	HS
Milk yield (F2)	One-way ANOVA	$F(20,826)=38.42$; $F(20,826)=38.42$	20, 826	<0.001	HS
	Kruskal-Wallis H test	$\chi^2(12)=381.28$; $\chi^2(12)=381.28$	12	<0.001	HS
Disease association	Pearson Chi- square	$\chi^2=3.563$; $\chi^2=3.563$	5	0.614	NS

HS= highly significant; NS= non-significant

3.2. Effect of Holstein Friesian blood percentage on lactation milk yield

The HF blood percentage had a significant effect on lactation milk yield in both the F1 and F2 generations ($P < 0.01$). Among all genetic groups, cattle with 93.75% HF blood achieved the highest cumulative lactation milk yield in both generations, producing 6,326.67 L (up to the fifth lactation) in the F1 generation and 4,791.54 L (up to the third lactation) in the F2 generation. In the F1 generation, cattle with 62.5% HF blood also exhibited a relatively high milk yield (6,146.31 L), whereas those with 50%, 75%, 87.5%, and 100% local blood produced 3,823.17, 3,854.27, 3,750.00, and 4,681.82 L, respectively. In the F2 generation, milk yield was highest in the 93.75% HF group, followed by the 50% HF (4,147.23 L), Pure USA Holstein Friesian (3,008.52 L), 100% local (2,468.84 L), 87.5% HF (2,353.02 L), 75% HF (2,321.17 L), and 62.5% HF (2,267.25 L) groups (Table 2).

Table 2. Lactation milk yield of F1 and F2 crossbred cattle across different Holstein Friesian blood percentage groups.

Blood percentage	F1 mean yield (L)	F2 mean yield (L)
50	3,823.17	4,147.23
62.5	6,146.31	2,267.25
75	3,854.27	2,321.17
87.5	3,750.00	2,353.02
93.75	6,326.67	4,791.54
100% LOCAL	4,681.82	2,468.84
PURE USA	N/A	3,008.52
Total	4,171.47	2,655.04

The highest mean lactation yields are achieved by the 93.75% sire blood group closely followed by the 62.5% group. Conversely, the lowest yields occur at the 50%, 75%, and 87.5% levels, which remain relatively stagnant, hovering between 750 and 770. The 100% LOCAL baseline group shows a moderate performance, achieving a mean lactation yield of roughly 930 (Figure 2).

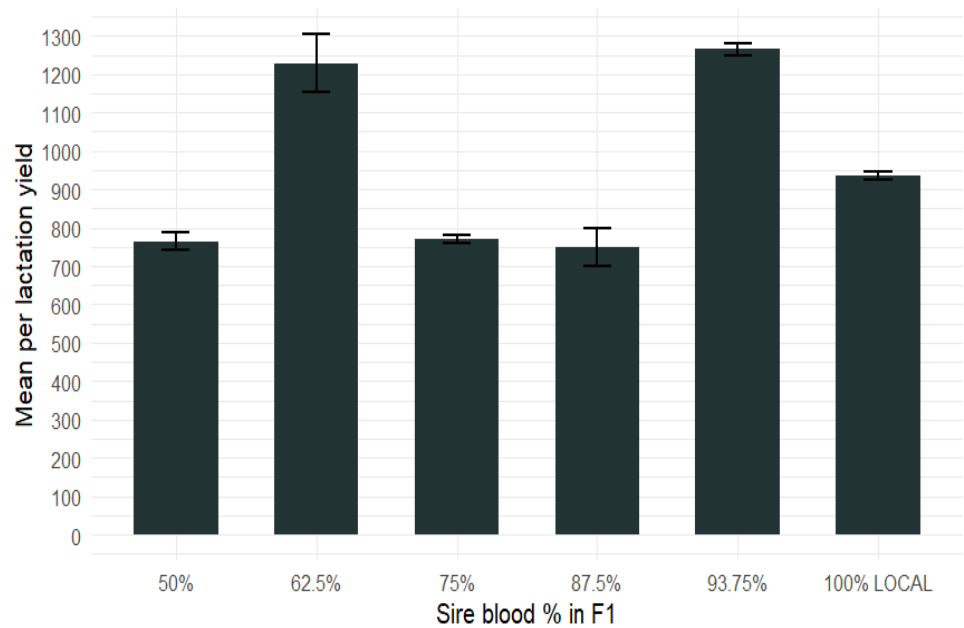


Figure 2. Comparison of mean lactation yields by sire blood percentage in F_1 crosses and local cattle.

The highest mean lactation yield is achieved by the 0.9375 sire blood group in the F_2 generation, reaching approximately 1,600, followed closely by the 0.5 group at roughly 1,400 (though the 0.5 group exhibits highly notable variance/error). In contrast, the lowest yields occur consistently across the 0.625, 0.75, and 0.875 groups, all hovering just below 800, which is slightly lower than the 100% LOCAL baseline (around 830). The PURE USA comparison group sits moderately in between, demonstrating a mean lactation yield of approximately 1,000 (Figure 3).

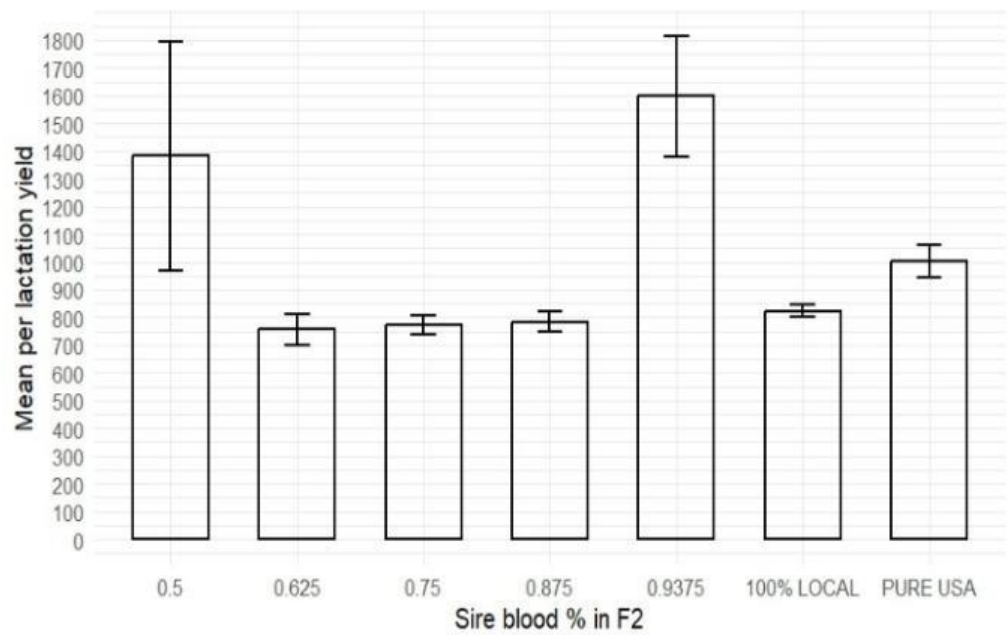


Figure 3. Comparison of mean lactation yields by sire blood percentage in F_2 crosses, local, and pure USA cattle.

3.3. Breed upgradation and milk yield

Breed upgradation speed markedly influenced mean lactation milk yield in both the F₁ and F₂ generations (Figure 4). Cattle classified under the fast and very fast breed upgradation categories exhibited higher mean lactation yields than those in the normal and moderate categories. Among the slower upgradation groups, cattle with normal breed upgradation consistently produced higher mean milk yields than those with Moderate upgradation. A more pronounced difference in mean lactation yield between the F₁ and F₂ generations was observed in the very fast breed upgradation group compared with the other categories. In contrast, cattle belonging to the normal and moderate upgradation groups showed relatively consistent mean lactation yields across both generations.

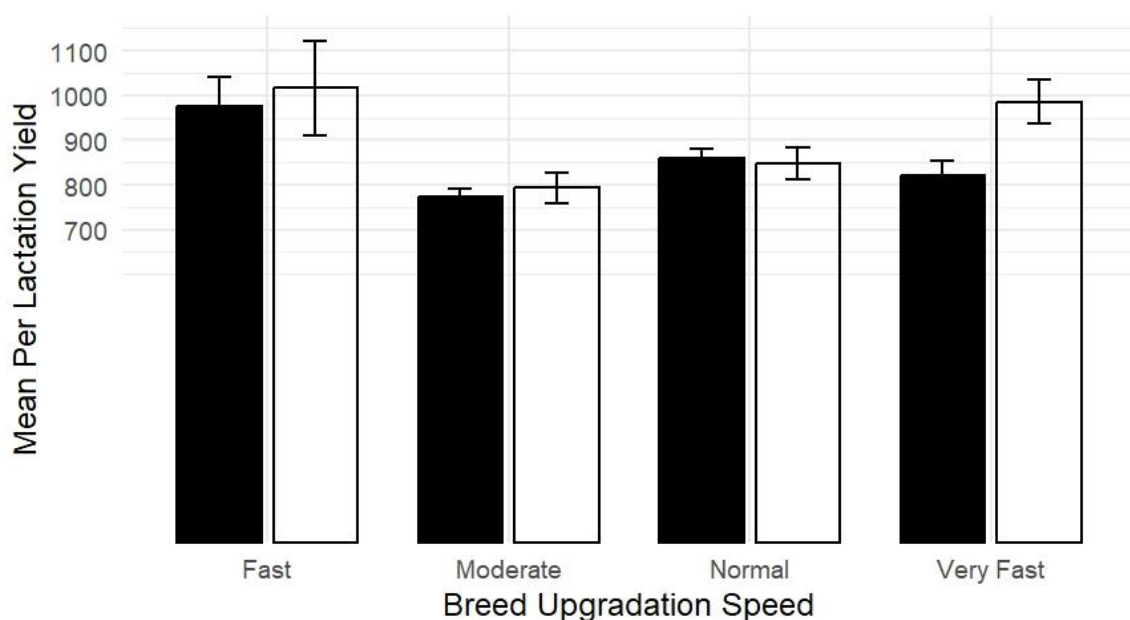


Figure 4. Breed upgradation speed vs mean per lactation yield (F₁ and F₂ generation).

3.4. Holstein Friesian blood level and disease incidence in F₁ cattle

The occurrence of FMD, mastitis, HS, RT disorders, and dystocia was not significantly associated with HF blood percentage in the F₁ generation ($P = 0.614$). Pearson's Chi-square analysis ($\chi^2 = 3.563$) and the likelihood ratio test ($\chi^2 = 3.438$) indicated that variation in HF blood level alone did not significantly influence the incidence of the investigated diseases (Table 3). Nevertheless, descriptive comparisons revealed differences in disease-free survival and disease incidence among the genetic groups. Cattle with intermediate HF blood levels (75–93.75%) generally exhibited a favorable balance between productive performance and health status, whereas cattle with lower exotic inheritance or 100% local background appeared to maintain greater resilience despite their comparatively lower milk production.

3.5. Holstein Friesian blood level and disease incidence in F₂ cattle

The distribution of disease-free animals and disease incidence among different HF blood percentage groups in the F₂ generation is presented in Table 4. Similar to the F₁ generation, no statistically significant association was observed between HF blood percentage and the occurrence of FMD, HS, mastitis, RT disorders, or dystocia ($P = 0.614$). Nevertheless, descriptive analysis revealed variations in disease-free survival and disease occurrence among the different genetic groups. The 100% local group accounted for the largest proportion of both disease-free and diseased animals across most of the investigated diseases, reflecting its greater representation within the study population. In contrast, cattle with intermediate Holstein Friesian blood levels (75–93.75%) generally exhibited comparable proportions of disease-free and diseased animals, while the Pure USA Holstein Friesian and 50% HF groups contributed relatively smaller proportions (Table 4).

Table 3. Distribution of disease-free animals and disease incidence across Holstein Friesian blood percentage groups in F₁ crossbred cattle.

Blood %	FMD-free	FMD-diseased	HS-free	HS-diseased	Mastitis-free	Mastitis-diseased	RT-free	RT-diseased	Dystocia-free	Dystocia-diseased
50	48.1%	50.3%	49.8%	44.2%	50.9%	47.1%	48.8%	50.0%	50.2%	44.7%
62.5	8.7%	7.7%	8.3%	8.7%	7.2%	9.5%	8.4%	7.8%	8.0%	9.7%
75	30.1%	27.2%	28.8%	30.4%	28.5%	29.5%	28.9%	31.3%	27.6%	33.5%
87.5	0.4%	-	0.3%	-	0.5%	-	0.1	1.6%	0.3%	-
93.75	1.5%	2.3%	1.6%	2.9%	1.7%	1.8%	1.7%	3.1%	2.0%	1.0%
100%L	11.3%	12.4%	11.3%	13.8%	11.2%	12.2%	12.1%	6.3%	11.9%	11.2%

FMD=foot-and-mouth disease; HS= hemorrhagic septicemia; RT= reproductive tract

Table 4. Distribution of disease-free animals and disease incidence across Holstein Friesian blood percentage groups in F₂ crossbred cattle.

Blood %	FMD-free	FMD-diseased	HS-free	HS-diseased	Mastitis-free	Mastitis-diseased	RT-free	RT-diseased	Dystocia-free	Dystocia-diseased
50	1.4%	1.8%	1.5%	1.6%	2.2%	1.2%	1.8%	0.5%	1.6%	1.5%
62.5	8.3%	10.2%	9.4%	6.4%	7.5%	9.7%	9.6%	7.1%	9.9%	7.0%
75	20.9%	19.8%	20.8%	19.2%	19.0%	21.2%	21.0%	19.2%	20.8%	19.9%
87.5	10.5%	11.7%	10.7%	12.0%	10.8%	10.9%	10.9%	10.6%	9.7%	13.3%
93.75	7.6%	6.4%	6.9%	8.8%	10.1%	5.9%	6.6%	9.1%	6.6%	8.5%
100% L	40.4%	41.7%	40.0%	45.6%	38.8%	41.8%	40.2%	42.9%	41.5%	39.5%
PURE USA	10.8%	8.5%	10.7%	6.4%	11.6%	9.3%	9.9%	10.6%	9.9%	10.3%

FMD=foot-and-mouth disease; HS= hemorrhagic septicemia; RT= reproductive tract

4. Discussion

The present study demonstrated that HF blood percentage had a highly significant influence on lactation milk yield in both F1 and F2 crossbred cattle ($P < 0.001$), indicating that the level of exotic genetic inheritance is a major determinant of dairy productivity under smallholder farming conditions in Bangladesh. The large F-values obtained for both F1 ($F = 112.87$) and F2 ($F = 38.42$) generations, together with the highly significant Kruskal–Wallis statistics ($\chi^2 = 371.82$ and 381.28 , respectively), suggest substantial variation in milk yield among the different HF blood groups. These findings indicate that genetic composition explained a considerable proportion of the observed variation in lactation performance and that the results were consistent across both parametric and non-parametric statistical analyses, thereby strengthening the reliability of the findings (Liu *et al.*, 2022; Feng *et al.*, 2025).

The significant relationship between HF blood percentage and milk production is consistent with the biological expectation that increasing the proportion of superior dairy genetics enhances the additive genetic merit for milk yield. HF cattle possess greater genetic potential for mammary development, nutrient utilization, and milk synthesis than indigenous cattle, enabling higher productive performance under suitable environmental and nutritional conditions (Ojango and Pollott, 2001; Vance *et al.*, 2013). Consequently, crossbreeding programs that introduce HF genetics into local cattle populations generally result in substantial improvements in milk production compared with indigenous breeds alone (Getahun, 2022). Similar positive associations between increasing HF inheritance and enhanced lactation performance have been reported in Bangladesh, India, Ethiopia, and several other tropical countries, where crossbred cattle consistently outperformed local breeds in milk yield despite differences in production environments (Beneberu, 2023; Islam, 2026).

Although the present results clearly demonstrate the importance of HF genetic contribution, they also suggest that increasing exotic inheritance alone does not fully explain differences in productive performance. The much larger F-value observed in the F1 generation (112.87) compared with the F2 generation (38.42) may indicate that the effect of genetic composition is more pronounced during the first generation of crossbreeding, whereas additional genetic recombination and segregation in subsequent generations may reduce the uniform expression of favorable production traits (Couto *et al.*, 2019). This phenomenon is consistent with the concept of hybrid vigor (heterosis), whereby F1 animals often exhibit superior performance due to favorable combinations of parental alleles, while part of this advantage may diminish in F2 populations because of genetic recombination (Fujimoto *et al.*, 2018; Šimková *et al.*, 2022).

Another important implication of the present findings is that genetic improvement should be accompanied by improvements in management practices. High-producing Holstein Friesian crossbreeds generally have greater nutritional requirements, higher metabolic demands, and increased sensitivity to environmental stress than indigenous cattle (Rahman *et al.*, 2024). Under marginal farming systems, where feed quality, veterinary services, and housing conditions are often suboptimal, animals with high exotic inheritance may fail to express their full genetic potential (Balasubramanian *et al.*, 2025). Therefore, genotype $\times$ environment interactions should be considered when designing breeding programmes, as maximizing milk production depends not only on the proportion of HF blood but also on the production environment in which the animals are maintained (Toro-Ospina *et al.*, 2023; Neto *et al.*, 2024).

Interestingly, despite the highly significant effect of HF blood percentage on milk yield, no significant association was observed between HF blood level and the occurrence of Foot-and-Mouth Disease (FMD), Hemorrhagic Septicemia (HS), mastitis, reproductive tract disorders, or dystocia (Pearson's $\chi^2 = 3.563$, $P = 0.614$). This finding suggests that variation in disease occurrence cannot be explained solely by breed composition. Instead, disease susceptibility under field conditions is likely influenced by multiple interacting factors, including herd management, biosecurity, vaccination status, nutritional management, environmental hygiene, stocking density, and individual immune competence (Barrington *et al.*, 2002). Similar observations have been reported in previous epidemiological studies, where management-related factors contributed more strongly to disease occurrence than breed composition alone (Knap and Doeschl-Wilson, 2020). Consequently, improving farm management and preventive healthcare may have a greater impact on reducing disease incidence than modifying the proportion of exotic blood.

The present study demonstrated that lactation milk yield varied considerably with the proportion of HF blood, indicating that productive performance is influenced by the level of exotic genetic inheritance. Cattle possessing 93.75% HF blood consistently achieved the highest cumulative milk yield in both generations, producing 6,326.67 L in the F1 generation and 4,791.54 L in the F2 generation. This finding suggests that a high proportion of HF genetics can substantially improve milk production under the prevailing production conditions in Bangladesh, provided that the animals receive adequate management and nutritional support (Miah *et al.*, 2021). Similar observations have been reported in previous studies, where crossbreeds with 75–93.75% HF

inheritance exhibited superior lactation performance compared with animals carrying lower proportions of exotic blood (Abera *et al.*, 2016; Azad *et al.*, 2023).

Interestingly, cattle with 62.5% HF blood also showed excellent productive performance in the F1 generation (6,146.31 L), whereas animals with 50%, 75%, and 87.5% HF blood produced comparatively lower yields. This pattern indicates that the relationship between HF blood percentage and milk yield is not strictly linear and may be influenced by heterosis, genetic recombination, and genotype $\times$ environment interactions (Hu *et al.*, 2021). The decline in milk yield observed in several intermediate genetic groups may reflect differences in adaptability, nutritional utilization, or management rather than the direct effect of breed composition alone (Cole *et al.*, 2023). Similar non-linear responses have been reported in tropical dairy production systems, where intermediate levels of exotic inheritance sometimes outperform both lower and higher blood percentages under field conditions (Galukande *et al.*, 2013).

The comparison between generations further revealed that cumulative milk yield was consistently higher in the F1 generation than in the F2 generation. For example, cattle with 93.75% HF blood produced 6,326.67 L in the F1 generation but only 4,791.54 L in the F2 generation. Likewise, the 62.5% HF group showed a marked decline from 6,146.31 L in F1 to 2,267.25 L in F2. This reduction may be attributed to the partial loss of hybrid vigor in subsequent generations resulting from genetic segregation and recombination, a phenomenon that has been widely documented in crossbreeding programmes (Kulmuni *et al.*, 2010).

The graphical presentation of mean lactation yield further supports these observations. In both generations, the 93.75% HF group recorded the highest mean lactation yield, whereas the 75% and 87.5% HF groups consistently showed lower average production. Although the 50% HF group exhibited relatively high milk yield in the F2 generation, the large variation observed within this group suggests considerable heterogeneity among individual animals. Overall, these results indicate that maintaining approximately 75–93.75% HF inheritance may provide an appropriate balance between high milk production and adaptation under tropical smallholder production systems, although further evaluation under different management conditions is warranted (Asfaw *et al.*, 2023).

The present study found no significant association between HF blood percentage and the occurrence of FMD, mastitis, HS, RT disorders, and dystocia in the F1 generation ($P = 0.614$). The low Pearson's Chi-square value ($\chi^2 = 3.563$) and likelihood ratio ($\chi^2 = 3.438$) indicate that variation in HF blood percentage alone was insufficient to explain differences in disease occurrence among the genetic groups. This finding suggests that disease susceptibility in crossbred cattle is likely governed by multiple factors rather than genetic composition alone (Mitra *et al.*, 2024).

Although the statistical association was not significant, descriptive comparisons indicated that cattle carrying 75–93.75% HF blood generally maintained a favorable balance between productive performance and health status. In contrast, animals with 100% local or lower HF inheritance appeared to exhibit greater resilience but produced comparatively lower milk yields. This observation supports the concept that moderate to high levels of exotic inheritance may improve productivity without substantially increasing disease risk when animals are managed appropriately (Lobago *et al.*, 2007). Similar findings have been reported in tropical dairy production systems, where disease occurrence was more strongly associated with nutrition, housing, hygiene, vaccination, and farm management than with breed composition itself (Grout *et al.*, 2020; Mushi *et al.*, 2026).

Similar to the F1 generation, no significant association was observed between HF blood percentage and the incidence of FMD, HS, mastitis, RT disorders, or dystocia in F2 cattle ($P = 0.614$). This finding indicates that increasing or decreasing the proportion of HF inheritance did not significantly alter susceptibility to the investigated diseases. Therefore, disease occurrence in F2 crossbred cattle is likely influenced more by management, nutrition, environmental conditions, and herd health practices than by genetic composition alone (Azad *et al.*, 2023).

Descriptive analysis, however, revealed some variation in disease distribution among the blood groups. The 100% local group represented the largest proportion of both disease-free and diseased animals across most disease categories, which is likely attributable to its larger population size rather than a higher or lower level of disease susceptibility. Meanwhile, cattle with 75–93.75% HF blood exhibited relatively balanced proportions of disease-free and diseased animals, suggesting that intermediate-to-high levels of exotic inheritance did not adversely affect animal health under the prevailing management conditions (Wang *et al.*, 2023). Similar observations have been reported in previous studies, where environmental management and preventive healthcare were identified as the principal determinants of disease incidence in crossbred dairy cattle (Eshete *et al.*, 2023; Hossain *et al.*, 2024; Lijalem *et al.*, 2026).

5. Conclusions

This study demonstrated that Holstein Friesian genetic contribution is an important determinant of lactation milk yield in F1 and F2 crossbred cattle under smallholder production systems in Bangladesh, thereby addressing the study objective of evaluating the relationship between genetic composition, milk production, and disease incidence. Crossbred cattle with relatively higher Holstein Friesian inheritance achieved superior milk production, whereas no significant association was observed between Holstein Friesian blood level and the occurrence of the investigated livestock diseases. These findings indicate that genetic improvement through crossbreeding can enhance dairy productivity, while disease occurrence is more likely influenced by management, environmental conditions, and herd health practices than by breed composition alone. The findings provide evidence to support the development of balanced and location-specific crossbreeding programmes that integrate genetic improvement with appropriate feeding, health care, and management practices to achieve sustainable dairy production. However, the underlying genetic mechanisms responsible for differences in productive performance and the interactions between genotype, environment, and management remain insufficiently understood. Future studies should incorporate longitudinal performance records, genomic analyses, and comprehensive environmental and management variables to determine the optimum breeding strategy for maximizing milk yield while maintaining animal health and adaptability under tropical production systems.

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Data availability

All relevant data are presented within the manuscript.

Conflict of interest

None to declare.

Author's contribution

Md Abu Saif: conceptualization, designed the experiment, data collection and analysis, original draft preparation, review and editing; Md. Roisul Momen: designed the experiment, data collection and analysis, original draft preparation, review and editing; Bikom Chandra Singha: original draft preparation, review and editing; Md. Mahbubur Rahman: data collection and analysis, review and editing; Md. Muin Abdullah: data collection and analysis, review and editing; S.M. Ashraful Islam: designed the experiment, data collection and analysis, review and editing; Md. Hosne Mobarak: supervised and revised the final manuscript, conceptualization, designed the experiment, original draft preparation, review and editing. All authors have read and approved the final manuscript.

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