

Article

Selection Indices for Milk Traits in Holstein–Friesian Cows: A Comparison of Relative Economic Value Methods

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Simple Summary

Selection indices are critical tools in dairy cattle breeding, enabling simultaneous improvement of multiple traits such as milk, fat, and protein yields. This study analyzed 2181 lactation records from Holstein–Friesian cows at Sakha Experimental Farm, Egypt (period from 2018 to 2024), to construct selection indices using two methods of relative economic values (REVs): actual economic values (REV1) and one phenotypic standard deviation (REV2). The results showed that both methods effectively predicted genetic gains for 305-day milk yield, fat yield, and protein yield, with no significant differences ($p > 0.05$) in expected genetic progress. The index incorporating all three traits (I_1) achieved the highest genetic gains, while the phenotypic standard deviation method (REV2) was recommended for its simplicity. These findings provide practical insights for dairy breeders in Egypt aiming to optimize milk production traits in Holstein–Friesian cows.



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Abstract

Selection indices enhance dairy cattle breeding by optimizing multiple traits simultaneously. This study analyzed 2181 lactation records from Holstein–Friesian cows at Sakha Experimental Farm, Egypt, to evaluate selection indices for 305-day milk yield (MY), fat yield (FY), and protein yield (PY) using two relative economic value (REV) methods: actual economic values (REV1) and one phenotypic standard deviation (REV2). Using MTDFREML software, we estimated heritabilities of 0.27 ± 0.01 (MY), 0.22 ± 0.01 (FY), and 0.28 ± 0.02 (PY). Four selection indices were constructed based on actual relative economic values (REV1) and one phenotypic standard deviation (REV2). The comprehensive index (I_1) incorporated all three key production traits, viz., MY, FY, and PY, to maximize the genetic merit of the aggregate genotype. In contrast, the reduced indices (I_2 , I_3 , and I_4) included only two traits each. The I_2 incorporated MY and FY, the I_3 included MY and PY, and the I_4 included FY and PY. The index I_1 (including all traits) yields the highest genetic gains (305 kg MY, 14.0 kg FY, 11.93 kg PY per generation). Both REV methods produced comparable genetic gains, but REV2 is recommended for its computational simplicity. These findings support the use of selection indices for genetic improvement in Holstein–Friesian cows, offering practical guidance for dairy breeding programs in Egypt and similar environments.

Keywords: selection indices; milk yield; fat yield; protein yield; Holstein–Friesian cows; relative economic values; genetic parameters

1. Introduction

The rising global demand for dairy products underscores the need for genetically superior dairy cattle to ensure food security and economic sustainability [1]. In Holstein–Friesian cows, renowned for high milk yield, 305-day milk yield (MY), fat yield (FY), and protein yield (PY) are economically critical traits that drive farm profitability [2]. These traits, influenced by genetic and environmental factors, require multivariate selection strategies due to their genetic correlations. Selection indices, pioneered by [3], optimize genetic gains by integrating phenotypic variances, genetic parameters, and relative economic values (REVs). In particular, Friesian cattle—renowned for their high milk yield—serve as the genetic foundation for many dairy systems worldwide, including in Egypt, where efficient resource utilization is crucial. A key component of any selection index is the estimation of relative economic values (REVs), which assign weights to traits based on their economic impact.

Various methods exist for calculating REVs, including actual economic values derived from net profit [4,5], one phenotypic standard deviation [6,7], one genetic standard deviation [8], and the Lamont method [9]. However, comparative assessments of these methods—particularly in the context of Holstein Friesian cattle under Egyptian production systems—remain limited in milk components. Genetic improvement of milk traits depends not only on accurate economic weighting but also on precise estimation of genetic parameters. Heritability estimates for milk yield (MY), fat yield (FY), and protein yield (PY) have varied across studies, ranging from 0.13 to 0.36 for MY and 0.09 to 0.44 for FY and PY, reflecting differences in breed, environment, and analytical approaches [8,10–14]. High genetic correlations among these traits suggest a potential for correlated responses to selection; however, effective index construction requires a balanced consideration of both economic importance and selection accuracy [10,12].

In Egypt, dairy production is constrained by challenges such as inconsistent feed supply, climatic stress, and economic limitations, necessitating the development of cost-effective and scientifically grounded breeding strategies [15]. The Sakha Experimental Farm, operated by the Animal Production Research Institute, offers a controlled environment for evaluating selection strategies in Friesian cows. This study aims to estimate the genetic and phenotypic parameters for 305-day milk yield, fat yield, and protein yield in Friesian cattle and to construct and evaluate selection indices using two REV estimation methods: actual economic values (REV1) and one phenotypic standard deviation (REV2). The paper provides a thorough assessment of alternative breeding techniques targeted at improving dairy productivity in Egyptian production conditions by contrasting the anticipated genetic gains and efficiency of various selection indices. This comparison takes into account the biological and economic limitations common to regional dairy systems in addition to highlighting the index that optimizes overall genetic development for important variables, including milk yield, fat yield, and protein yield. Such a strategy is especially pertinent in settings with limited resources, where achieving sustainable productivity gains requires the best possible distribution of genetic improvement efforts. With wider application to comparable production systems in underdeveloped nations, the findings offer breeders and policymakers useful advice on how to prioritize traits and design selection programs.

2. Materials and Methods

2.1. Data and Animal Management

Data were collected from 2181 lactation records for the period from 2018 to 2024 of Friesian cows at Sakha Experimental Farm, Kafr El-Sheikh Governorate, Egypt, under the management of the Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo. Sakha Experimental Farm is a prominent agricultural research facility located in the Kafr El-Sheikh Governorate in the Nile Delta region of northern Egypt, and its latitude and longitude coordinates are 30°56'45" E and 31°06'42" N. This farm operates under the management of the Animal Production Research Institute (APRI), which is a key branch of the Ministry of Agriculture and Land Reclamation, headquartered in Dokki, Cairo. The Sakha Experimental Farm plays a central role in livestock and dairy research, genetic improvement programs, and the evaluation of animal production systems tailored to Egypt's agro-climatic conditions [12].

A semi-intensive management system is used to keep the Holstein–Friesian herd at Sakha. Cattle are fed a balanced diet consisting of concentrated feed, green fodder, and agricultural byproducts, with the addition of controlled grazing when the seasons allow. Open-sided barns with shaded sections are used for housing in order to reduce heat stress, which is crucial considering Egypt's hot summers. The farm is the perfect location for genetic and productivity research because of its research-focused infrastructure, which guarantees consistent recording of production traits (such as milk yield and composition), reproductive performance, and health metrics. The evaluation of genotype–environment interactions in this subtropical production system is made possible by the close monitoring of environmental conditions, such as seasonal forage availability and temperature-humidity index (THI) fluctuations. A strong basis for assessing genetic parameters and economic selection indices in the context of Egyptian dairy farming is provided by the combination of purebred Holstein genetics, carefully monitored nutrition, and accurate environmental documentation.

The dataset included cows with one or more completed lactations. Animals were housed in open sheds and fed Egyptian clover (*Trifolium alexandrinum*) during winter and spring, supplemented with concentrate rations and clover hay in summer and autumn. Artificial insemination was performed, with heifers inseminated at 18 months of age and cows re-inseminated 60–70 days postpartum [12,13]. Milking occurred twice daily (7:00 AM and 4:00 PM), with daily milk yield recorded and weekly milk composition (fat and protein) analyzed using the Milko-Scan 130 series (Type 10900, ILMTC, Animal Production Research Institute). The Milko-Scan 130 series (Type 10900) analyzes milk composition quickly using Fourier Transform Infrared (FTIR) spectroscopy. When a homogenized milk sample is exposed to infrared light, certain wavelengths are absorbed by the fat, protein, and lactose.

To measure components like fat%, protein%, and lactose%, the device's interferometer generates an interference pattern that is transformed into a spectrum using the Fourier transform. The spectrum is then examined using chemometric models that have already been calibrated. The system complies with ISO/IDF standards by maintaining samples at 40 °C for consistency and delivering results in 30–60 s. Accurate, high-throughput milk testing for dairy research, quality assurance, and milk payment systems is made possible by this automated, reagent-free method. Table 1 shows the structure of the data used in the analysis.

Table 1. Frequency table for milk traits classified by month of calving, year of calving, and parity.

Month of Calving		Year of Calving		Parity	
Month	Number of Records	Year	Number of Records	Parity	Number of Records
January	186	2018	162	1	632
February	197	2019	323	2	464
March	251	2020	355	3	347
April	217	2021	371	4	270
May	198	2022	395	5	192
June	189	2023	312	6	129
July	165	2024	263	7	82
August	153			8	45
September	145			>9	20
October	152				
November	169				
December	159				
Total	2181		2181		2181

2.2. Traits Analyzed

Three production traits were analyzed: 305-day milk yield (MY), 305-day fat yield (FY), and 305-day protein yield (PY). Days open (interval between calving and successful conception) were also recorded and included as a covariate. Days open were calculated as the interval between parturition and successful mating.

2.3. Statistical Analysis

The MY, FY, and PY were examined using a linear mixed model. The model includes fixed effects such as the combined calving year-month (to account for shared environmental and management impacts among contemporaneous groups), parity, and days open as covariates. Random influences included the animals, long-term environmental effects, and residual mistakes. The analysis was conducted using the following multi-trait animal model:

$$y_{ijklm} = \mu + CMY_i + P_j + b_1 \cdot DO_{ijklm} + a_l + p_{em} + e_{ijklm}; \quad (1)$$

where y_{ijklm} is the observed trait MY, FY, and PY of the m th animal, μ is the overall mean, CMY_i is the fixed effect of the i th calving year-month contemporary group, P_j is the fixed effect of the j th parity, $b_1 \cdot DO_{ijklm}$ is the linear regression on days open as a covariate; a_l is the random additive genetic effect of the l th animal; p_{em} is the random permanent environmental effect associated with repeated records of the m th animal, e_{ijklm} is the random residual error. The inclusion of calving year-month as a combined fixed factor provides appropriate contemporaneous grouping, boosting the precision of partitioning environmental and genetic variance and lowering the possibility of bias in genetic parameter estimation. It was assumed that the random effects follow normal distributions:

$$a \sim N(0, A\sigma_a^2), p_e \sim N(0, I\sigma_{pe}^2), \text{ and } e \sim N(0, I\sigma_e^2) \quad (2)$$

where A is the additive genetic relationship matrix among animals, I is the identity matrix, and σ_a^2 , σ_{pe}^2 , and σ_e^2 are the additive genetic, permanent environmental, and residual variances, respectively [14].

2.3.1. Variance Components and Genetic Parameters Estimation

All traits analyzed, viz., My, FY, and PY—305-day milk yield (305 d MY), fat yield (305 d FY), and protein yield (305 d PY)—were evaluated using a Multiple Trait Animal Model (MTAM), implemented with MTDFREML software version 3.0 [14]. MTDFREML (Multiple Trait Derivative-Free Restricted Maximum Likelihood) is a specialized statistical tool used in animal breeding and quantitative genetics to estimate essential genetic characteristics such as heritability, genetic correlations, and environmental variances from large datasets. It uses a Restricted Maximum Likelihood (REML) framework to ensure unbiased estimation by properly accounting for fixed effects, and its derivative-free optimization approach—based on Powell’s method—allows it to efficiently navigate complex likelihood surfaces without relying on computationally intensive gradient calculations. This makes MTDFREML especially useful for assessing multiple correlated traits at once, where it reflects underlying genetic correlations more precisely than single-trait models [14]. In matrix notation, the model was expressed as follows:

$$y = Xb + Zg + Wp + e \quad (3)$$

where y is the vector of phenotypic observations for all animals, b is the vector of fixed effects (calving month, calving year, parity, and days open as a covariate), g is the vector of random additive genetic effects, p is the vector of random permanent environmental effects, e is the vector of residual errors, and X , Z , W are the incidence matrices relating observations to fixed, genetic, and permanent environmental effects, respectively [14].

Estimates of direct heritability (h^2_d), repeatability (t), and genetic (r_g), environmental (r_e), and phenotypic correlations (r_p) were obtained using the MTDFREML software [14]. This software applies the Restricted Maximum Likelihood (REML) method within a mixed linear model framework to estimate variance and covariance components. REML is particularly effective in producing unbiased and accurate estimates of genetic parameters, which are essential for traits such as MY, FY, and PY. The genetic, environmental, and phenotypic correlations were computed from the (co)variance components derived from the multi-trait animal model. These estimates are critical for developing efficient selection strategies aimed at improving multiple traits simultaneously while maintaining genetic gain and minimizing undesirable correlated responses. The heritability (h^2) was computed as follows: $h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_{pe} + \sigma^2_e)$, and the repeatability (t) was calculated using the formula: $t = (\sigma^2_a + \sigma^2_{pe}) / (\sigma^2_a + \sigma^2_{pe} + \sigma^2_e)$.

2.3.2. Construction of Selection Index

Selection is based on an index or criterion that maximizes correlation with the aggregate genotype (H), defined as follows:

$$I = \sum (b_i p_i), I = 1 \text{ to } n. \quad (4)$$

where I represents the selection index, b_i is the weighting factor for the index, p_i is the phenotypic measure, and n is the number of traits. The optimal selection index coefficients are those that maximize the correlation (RIH) or minimize the squared deviation between the selection index and the aggregate genotype. Genetic and phenotypic parameters used to compute the optimal index weights were derived from the current study [3], demonstrating that the maximum RIH is achieved when $Pb = Gv$. Thus, the vector of optimal index weights (b) was calculated for each objective as follows:

$$b = P^{-1}Ga. \quad (5)$$

where P^{-1} is the inverse of the phenotypic (co)variance matrix for the traits in the selection index, G is the genetic covariance matrix between the traits in the selection goal and the selection index, and “ a ” is the vector of economic values for the goal traits. Additional properties of the selection index were calculated as follows: the standard deviation of the index (σ_I) = $\sqrt{(b'Pb)}$, the standard deviation of the aggregate genotype (σ_H) = $\sqrt{(a'Ga)}$, and the correlation between the index and the aggregate genotype (accuracy) $RIH = \sigma_I / \sigma_H$. The genetic change per trait due to selection, $\Delta G (R_j)$, was computed as follows:

$$R_j = i * (b' G_j) / \sigma_I \quad (6)$$

where R_j is a vector of genetic change for trait j , i is the selection intensity (set to 1 in this study), b' is the transpose of the index weight vector, G_j is the j th column of the G matrix representing the genetic covariance between trait j and the index traits, and σ_I is the standard deviation of the index. The expected response to selection is expressed as genetic gain after one cycle of selection with a standardized selection intensity of 1. Relative efficiency (RE) for each index was calculated by comparing its accuracy (RIH) to that of the full index. This allowed for meaningful comparisons across different indices and helped identify the trait combinations that contributed most effectively to overall index performance.

2.3.3. Estimate of Relative Economic Value (REV)

Economic values were derived using two approaches: (1) actual relative economic value, where the economic value of each trait was determined based on the actual net profit, as described by [4,5]; and (2) one phenotypic standard deviation, where the economic value was calculated as $V_i = 1/\sigma_p$ described by [6]. The weighted economic values for both methods are presented in Table 2.

Table 2. Relative economic values (REVs) for different variables according to actual economic values (REV1) and one phenotypic standard deviation (REV2).

Variables	REV1	REV2
305-day milk yield, kg	1.00	1.00
305-day fat, kg	12.60	20.00
305-day protein, kg	6.30	25.50

The economic weights for MY, FY, and PY were determined using a marginal profit-based technique that accounts for the increased income earned per unit increase in each trait while taking into consideration associated production expenses. To calculate REV1 (INR per kg), we computed the change in net profit (Δ Profit) from a one-unit increase in each trait (Δ Trait), while keeping other traits constant. This assessment took into account farm-gate milk prices, component-based pricing (in which fat and protein content influence milk value), and the increased feed expenditures required to maintain greater production levels. Similarly, the premiums for fat and protein were evaluated based on their respective market prices and marginal feed costs. To eliminate the impact of different measurement units and trait variability, standardized economic weights (REV2) were calculated by dividing each REV1 value by the trait’s phenotypic standard deviation (σ_p). This modification prevented traits with higher natural variability (e.g., milk yield, which has a bigger σ_p than fat or protein yield) from dominating the selection index. To establish applicability to the production system under study, the economic values were calibrated using local market data such as milk pricing structures, feed costs, and population-level trait distributions. This strategy balances genetic advancement across several variables and guarantees that the final selection index represents actual profitability. The approach offers

a strong foundation for maximizing dairy cattle breeding choices by combining biological and economic considerations [4,5].

3. Results

3.1. Milk Yield and Milk Composition Performance

The relative economic values (REVs) for 305-day milk yield (MY), fat yield (FY), and protein yield (PY) using actual economic values (REV1) and one phenotypic standard deviation (REV2) are presented in Table 2. The MY was the baseline (REV = 1.00) in both methods, while FY and PY had higher weights in REV2 (20.00 and 25.50) than in REV1 (12.60 and 6.30). Table 3 shows descriptive statistics for MY, FY, and PY. Mean yields were 2806 kg (MY), 102 kg (FY), and 79 kg (PY), with standard deviations of 949.0 kg, 37.0 kg, and 28.0 kg, respectively. Coefficients of variation (CV) were 33.82% (MY), 35.97% (FY), and 35.46% (PY), indicating substantial individual variability, with FY showing the highest variation, likely influenced by genetic differences, nutritional inconsistencies, and climatic factors such as heat stress.

Table 3. Means, standard deviation (SD), and coefficient of variability (CV%) for milk yield (MY), fat yield (FY), and protein yield (PY) in Friesian cows.

Trait	Mean	SD	CV (%)
Milk yield (MY), kg	2806	949	33.82
Fat yield (FY), kg	102	37	35.97
Protein yield (PY), kg	79	28	35.46
No. of records	2181		

3.2. Genetic Parameters Estimates

The direct heritability values were moderate for MY (0.27), FY (0.22), and PY (0.28), indicating a good opportunity for genetic improvement (Table 4). Repeatability was 0.36, 0.42, and 0.49, indicating reasonable consistency throughout lactations, with PY demonstrating the strongest genetic control and stability.

Table 4. Estimates of direct heritability (h^2_d) and repeatability (t) for 305-day milk yield (MY), 305-day fat yield (FY), and 305-day protein yield (PY) for Friesian cows.

Variables	Direct Heritability (h^2_d)	Repeatability (t)
305-day MY	0.27 ± 0.01	0.36 ± 0.05
305-day FY	0.22 ± 0.01	0.42 ± 0.05
305-day PY	0.28 ± 0.01	0.49 ± 0.04

MY—milk yield; FY—fat yield; PY—protein yield.

The relationships between MY, FY, and PY are shown in Table 5 as genetic (r_g), environmental (r_e), phenotypic (r_p), and persistent environmental (r_{pe}). The three measures had high genetic correlations (r_g), ranging from 0.85 (MY–PY) to 0.91 (FY–PY), suggesting that shared gene sets had a significant influence on the traits. For MY–FY (0.32) and MY–PY (0.16), permanent environmental correlations (r_{pe}) were low to moderate; however, for FY–PY (0.82), they were quite high, indicating that shared non-genetic factors had a stronger effect on milk components than milk volume. The similar environmental responses of fat and protein yields were reflected in the moderate environmental correlations (r_e) for pairs including MY and the extraordinarily high (0.94) correlations for FY–PY. Similar trends were seen in phenotypic correlations (r_p), which were very high for FY–PY (0.94) and moderate for MY with FY or PY (0.50–0.52). All things considered, our findings support the

strong biological and genetic correlation between yield characteristics, especially between the yields of fat and protein.

Table 5. Additive genetic, environmental, and phenotypic correlations for 305-day milk yield, 305-day fat yield, and 305-day protein yield for Friesian cows.

Variables Correlated	r_g	r_{pe}	r_e	r_p
305-day MY X 305-day FY	0.88 ± 0.07	0.32 ± 0.05	0.35 ± 0.03	0.50 ± 0.06
305-day MY X 305-day PY	0.85 ± 0.05	0.16 ± 0.02	0.34 ± 0.03	0.52 ± 0.04
305-day FY X 305-day PY	0.91 ± 0.06	0.82 ± 0.10	0.94 ± 0.02	0.94 ± 0.04

Standard errors ranged from 0.02 to 0.10. r_g —genetic correlation; r_e —environmental correlation; r_p —phenotypic correlations; r_{pe} —permanent environmental correlation. MY—milk yield; FY—fat yield; PY—protein yield.

In the initial analysis, the genetic correlations between the three variables (MY, FY, and PY) were predicted to be exactly 1.00 with very small standard errors. While these exact connections may appear mathematically precise, they are biologically improbable for various reasons, including biological reality; viz., although milk yield, fat yield, and protein yield are all closely linked qualities since they stem from the same biological process (lactation), they are regulated by somewhat different sets of genes. Perfect genetic correlation suggests that the same genes in exactly the same proportions regulate all three attributes, leaving no possibility for independent genetic variation; a hypothesis that is not supported by extant dairy cattle genetics literature: statistical issues such as overparameterization of the model in relation to the available data and high multicollinearity among fixed effects (e.g., calving month and calving year fitted separately rather than as a combined contemporary group). Under these circumstances, correlation estimates may be inflated to the theoretical maximum because the model may treat features as though they were genetically identical. After resolving these problems, such as merging calving year–month into a single modern group and improving the data structure, revised estimates (Table 5) now produce strong but biologically acceptable correlations.

3.3. Selection Indices

The effectiveness of several selection criteria for Holstein–Friesian cows was assessed using two sets of economic weights: real relative economic values (REV1) and one phenotypic standard deviation (REV2) (Table 6).

Table 6. Selection indices (Is) for different variables of Holstein–Friesian cows using actual relative economic values (REV1) and one phenotypic standard deviation (REV2).

Indices	b (MY) REV1	EG (MY) REV1	b (FY) REV1	EG (FY) REV1	b (PY) REV1	EG (PY) REV1	RIH REV1	RE% REV1	b (MY) REV2	EG (MY) REV2	b (FY) REV2	EG (FY) REV2	b (PY) REV2	EG (PY) REV2	RIH REV2	RE% REV2
I ₁	0.35	305.0	−9.25	14.0	20.33	11.93	0.63	100.0	0.54	305.0	−14.80	14.0	32.48	11.93	0.63	100.0
I ₂	0.32	285.0	4.75	13.1	-	-	0.59	94.0	0.41	285.0	5.81	13.1	-	-	0.59	94.0
I ₃	0.24	298.0	-	-	6.09	11.67	0.62	98.0	0.35	298.0	-	-	9.74	11.67	0.62	98.0
I ₄	-	-	−3.58	12.2	10.65	10.41	0.55	87.0	-	-	−8.37	12.22	24.59	10.41	0.55	87.0

REV1—actual relative economic values; REV2—one phenotypic standard deviation; MY—milk yield; FY—fat yield; PY—protein yield; EG—expected genetic gain; RIH—correlation between the selection index and the aggregate genotype; RE%—relative efficiency of the index compared to the full index. I₁–I₄—indices.

Under REV1, Index I₁ had the largest aggregate genetic gain and relative efficiency, resulting in positive gains in MY and PY, but a modest unfavorable shift in FY. Index I₂, based on MY and FY, achieved somewhat lower efficiency, but made moderate advances in both attributes. Index I₃, which included both MY and PY, resulted in excellent efficiency with a significant increase in PY but no change in FY. Index I₄, which omitted MY, had the lowest efficiency, resulting in lesser PY gains and a minor adverse change in FY. The result

was similar in REV2, with I_1 ranking highest in efficiency, albeit economic weight scaling changed the size of predicted improvements. Overall, the findings confirm that a three-trait index (MY, FY, and PY) promotes genetic advancement, but indices that exclude MY or one of the components impair selection efficiency.

4. Discussion

4.1. Milk Yield and Milk Composition Performance of Holstein–Friesian Cattle

This study offers critical insights into the production performance of Holstein–Friesian cattle under tropical conditions in Egypt, highlighting the interplay of genetic potential and environmental factors in shaping milk yield (MY), fat yield (FY), and protein yield (PY). Compared to previous research by Kafidi et al. [15], Atil and Khattab [5], El Awady et al. [8], Kadarmideen et al. [16], Lazarevic et al. [17], and Amina Habib et al. [11], which reported 305-day MY ranging from 4490 to 9710 kg, FY from 200 to 317 kg, and PY from 158 to 296 kg across diverse regions, our observed yields were consistently lower. This disparity likely stems from a combination of factors, including climatic stress, management practices, breed composition, and analytical approaches.

The tropical climate of Egypt, characterized by high temperatures and humidity, poses significant challenges to Holstein–Friesians, a breed adapted to temperate environments. Heat stress is known to reduce feed intake and milk production, which may explain the lower yields observed in this study. Additionally, variations in feeding systems—often limited by the availability of high-quality forage in tropical regions—likely exacerbate these differences. Management practices, such as reproductive strategies and culling intensity, further influence production outcomes. For instance, the lower coefficient of variation (CV) for MY (33.82%) compared to FY (35.97%) and PY (35.12%) suggests greater homogeneity in milk production, potentially due to rigorous culling of cows with suboptimal productive or reproductive performance across parities. This aligns with findings by Amina Habib et al. [11], who reported CVs for yield traits ranging from 26.91% to 39.45%.

The high CVs observed for FY and PY indicate substantial individual variation, which is advantageous for selective breeding programs aimed at enhancing genetic gains. This variability may reflect differences in the proportion of imported versus locally bred animals, as imported Holstein–Friesians may struggle to adapt to Egypt's environmental conditions compared to locally selected stock. Furthermore, discrepancies in analytical methodologies, such as statistical models or data standardization, could contribute to differences between our findings and those of prior studies. These findings underscore the need for tailored management strategies to mitigate environmental constraints and optimize dairy production in tropical settings. Implementing heat stress alleviation measures, improving nutritional regimes, and leveraging genetic diversity through selective breeding could enhance performance.

4.2. Genetic Parameters Estimates

The genetic parameters estimated in this study provide valuable insights into the potential for improving milk yield (MY), fat yield (FY), and protein yield (PY) in Holstein–Friesian cattle under tropical conditions in Egypt. The current estimate falls within the range reported in various studies on Holstein–Friesian cattle raised in different countries using the Animal model. The moderate heritability observed for these traits suggests a meaningful genetic basis, enabling effective selection strategies to enhance dairy productivity under tropical conditions. These findings align with a range of studies, such as Ahlborn and Dempfle [18], El-Awady et al. [8], Rahayu et al. [19], Uribe et al. [10], Lazarevic et al. [17], and Amina Habib et al. [20], which collectively demonstrate variability in heritability estimates across breeds, regions, and analytical models. This variability likely reflects

differences in environmental conditions, management practices, and genetic diversity within studied populations.

Lower heritability estimates reported in some studies, such as those by Habib et al. [11], DeGroot et al. [21], El-Awady et al. [8], Tohidi and Nazari [22], Sneddon et al. [23] and Öztürk et al. [24] highlight the influence of environmental factors and analytical constraints, such as small sample sizes or high residual effects. These discrepancies underscore the importance of context-specific genetic evaluations, particularly in tropical environments where heat stress and nutritional limitations may suppress genetic expression. The moderate repeatability estimates for MY, FY, and PY observed in this study, consistent with findings by Tohidi and Nazari [22], indicate that performance across lactations is sufficiently stable to support culling decisions based on single lactation records, a common practice in commercial dairy operations. The implications of these genetic parameters are significant for breeding programs in tropical dairy systems.

The moderate heritability of MY, FY, and PY suggests that selective breeding can yield substantial genetic gains, particularly when combined with improved management practices to mitigate environmental stressors. Moreover, the consistent repeatability of these traits supports the reliability of early lactation records for selection and culling, optimizing herd productivity. Future research should focus on integrating genomic selection tools to enhance the precision of breeding programs and explore the interaction between genetic potential and environmental factors in tropical climates. Such efforts will be critical for developing resilient dairy populations capable of sustaining high productivity under challenging conditions.

The genetic correlations ranged between 0.88 and 0.91 across all trait pairs, indicating strong pleiotropic effects or tightly linked genetic mechanisms. Boujenane et al. [25] reported close to perfect genetic correlations between milk yield and fat yield (0.96) in Moroccan Holstein–Friesian cows. The strong genetic correlation between MY and FY suggests shared biological pathways, meaning that selection for milk yield could simultaneously increase fat yield, offering opportunities to streamline breeding strategies. These findings align with reports from other dairy populations, such as those documented by Ahlborn and Dempfle [18], El-Awady et al. [8], and Amina Habib et al. [20], although the environmental constraints in tropical regions present distinct challenges. Such high genetic correlations are common when traits are strongly collinear, as in this case, where milk, fat, and protein yields are heavily reliant on total milk production and share common genetic and physiological pathways. The additive genetic variance for milk yield largely determines the expression of both fat and protein yields, resulting in a nearly perfect genetic association. These estimations could potentially be influenced by data restrictions in the multivariate animal model, such as imbalanced records, high residual correlation, and probable over-parameterization.

The lower phenotypic correlations compared to genetic correlations followed similar trends reported in other studies by Habib et al. [11], Boujenane et al. [25], and Amina Habib et al. [20], which indicate that environmental factors—such as management practices and climatic conditions—play a substantial role in shaping trait expression. The strong phenotypic relationship between fat yield (FY) and protein yield (PY) aligns with findings by Boujenane et al. [25], Ahlborn and Dempfle [18], and El-Awady et al. [8], suggesting that these traits respond similarly to non-genetic influences, a pattern also reflected in the environmental correlations. The predominance of residual variance over additive genetic and permanent environmental effects highlights the difficulty of optimizing dairy performance under conditions of heat stress and nutritional limitations. Although permanent environmental effects contributed relatively little, the significant residual influence underscores the need for better management practices to reduce uncontrolled variability.

Importantly, the genetic parameters reveal considerable potential for improvement. The notable contribution of additive genetic variance, particularly for milk yield (MY) and PY, indicates that selective breeding could effectively enhance overall productivity.

4.3. Selection Index

The superior performance of the full-trait index I1, which includes milk yield (MY), fat yield (FY), and protein yield (PY), underscores the benefit of incorporating all three traits to maximize genetic progress in Holstein–Friesian cattle. The notably lower efficiency of index I4, which excludes MY, highlights milk yield’s pivotal role in effective selection, consistent with Uribe et al. [1], who emphasized milk yield’s importance for overall genetic improvement. Indices I2 (excluding PY) and I3 (excluding FY) emerged as viable alternatives when data availability is limited, with I3 performing nearly as well as I1, suggesting flexibility in index construction under practical constraints.

The consistency of genetic gains across REV1 and REV2 methods indicates that both approaches are robust for predicting genetic progress, regardless of economic weighting strategies. These findings align with prior research. El-Awady et al. [2] reported substantial genetic improvements in MY, FY, and PY in German Friesian cows, while Amina Habib et al. [3] observed similar trends in Holstein–Friesians, with notable gains across all three traits. Ozturk et al. [4] and Rahayu et al. [5] reported significant MY improvements in Turkish and Indonesian Holstein–Friesians, respectively, reinforcing the global applicability of multi-trait selection. Tohidi and Nazari [6] further supported these trends, reporting steady genetic progress in Iranian Holstein cattle. Given the comparable effectiveness of REV1 and REV2, either method can be used for selection index development. However, REV2’s computational simplicity and reliable performance make it the preferred choice for routine application in Holstein–Friesian breeding programs in Egypt.

5. Conclusions

This study demonstrates that selection indices effectively enhance 305-day milk, fat, and protein yields in Friesian cows under Egyptian conditions. The comprehensive selection index (I_1), incorporating all three traits, achieved the highest genetic gains, with no significant differences between actual economic values (REV1) and one phenotypic standard deviation (REV2) methods. Given its computational simplicity, REV2 is recommended for practical implementation in dairy breeding programs. These findings provide actionable insights for optimizing milk production traits in Friesian cows, with broader implications for sustainable dairy farming in resource-constrained regions like Egypt. Future research should explore integrating additional traits, such as reproductive efficiency, to further refine selection strategies. These findings provide practical, cost-effective selection options for breeders and herd management, particularly in resource-constrained situations such as Egypt, allowing small- and medium-scale farmers to increase milk production sustainably without requiring extensive models. By prioritizing economically important features, the findings can also be used to drive national breeding efforts for maximum genetic benefits. Future research should broaden selection indices to include functional qualities such as fertility, longevity, and disease resistance, ensuring balanced genetic development that benefits both productivity and animal welfare in varied dairy systems.

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