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A comparison of different selection indexes for some economic traits in Holstein Friesian cows

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Abstract

The genetic as well as phenotypic parameters for 10-month milk total (10 MMY), lactation length (LL), and age at first calving (AFC) were calculated with data from 1863 first lactation records of Holstein Friesian cows imported from Germany and managed at a private farm in Egypt between 2002 and 2012. Multiple Trait Derivative Free Restricted Maximum Likelihood was used for the data analysis (MTDFREML). Means of 10 MMY, LL and AFC were 9710 kg, 357 days, and 27.17 months, respectively. All the traits examined were significantly impacted by the calving season and year. Heritability estimates for 10 MMY, LL and AFC were 0.37±05, 0.20±0.01 and 0.05±.002, respectively. Four selection indices were calculated by using three different methods of economic values, (1) actual relative economic weight, (2) one phenotypic standard deviation and (3) one genetic standard deviation. Comparison of the three methods for estimating relative economic values revealed no differences in any of the three methods for the expected genetic gain per generation for each trait, the correlation between the total genetic value and the index, or the effectiveness of various indices in comparison to the original index (I_1). Therefore, the three methods were succeeded in predicting the genetic gain per generation for the three traits studied. However, the second method (one phenotypic standard deviation) was recommended based on ease of calculation.

Key words: selection index, genetic gain, economic value, heritability, generation interval

Introduction

To enhance genetic advancement across multiple traits, it is advantageous to consolidate data on said traits into a unified index, such as net merit or total score. Hazel and Lush [1] found that the selection index is the most effective tool for livestock selection. The selection index is used by breeders to simultaneously select for multiple traits. It provides information on the economic importance, genetic and phenotypic diversity, and genetic and phenotypic covariance of these traits.

Multiple methods exist for determining the economic valuation of a trait. Some examples include: The relative economic weight has been studied by Khattab and Sultan [2]; Hussein [3]; El-Arian [4]; Abosaq et al. [5], and Khattab et al. [6]. The phenotypic standard deviation has been studied by Falconer and Mackay [7]; Hussein [3]; El-Arian et al. [8]; Abosaq et al. [5], and El-Sawy [9]. The Lemont Approach is discussed in the works of Abosaq et al. [5] and El-Sawy [9]. The importance of a solitary genetic outlier has been noted in studies conducted by Rogers [10] and El-Awady [11]. The objectives of this study are to investigate the impact of environmental factors on lactation duration, age at first calving, and milk production over a 10-month period. Additionally, we aim to determine the genetic and phenotypic parameters of these traits. Furthermore, we will develop selection indices based on three measures of relative economic value. Finally, we will optimise genetic progress by selecting the most effective combination of two or three traits, considering their accuracy and efficiency.

Materials and methods

A dataset consisting of 1863 first lactation records of Holstein Friesian cows imported from Germany was collected between 2002 and 2012. Animals lacking pedigree information, breeding dates, or affected by disease were excluded from the analyses. Throughout the year, heifers were housed in a spacious open yard with partially enclosed sheds. Throughout the year, the subjects were provided with a diet comprising of a mixture of silage and concentrate ration, supplemented with Berseem (Alfa alfa) as required. Supplements, such as crude protein concentrates, were administered to heifers that exhibited a milk production exceeding 25 kg per day and those within the final two months of pregnancy. The cows underwent machine milking three times daily, at 5 AM, 1 PM, and 10 PM. Cows were typically milked until two months prior to their next calving. The study examined three traits: milk production over a ten-month period (10 MMY), lactation duration (LL), and age at first calving (AYFC).

Mixed-model analysis was conducted on the 10 MMY and LL datasets. To control for potential confounding, we incorporated the calving season and year as fixed effects, the sire as a random effect, and the age at first calving as a covariate in Equation 1. The AFC model incorporated fixed factors such as calving season and year, as well as the random effect of sire (Equation 2).

$Y_{ijkl} = \mu + S_i + Y_j + A_k + b(AGE) + e_{ijkl}$ …………….... Equation 1

$Y_{ijkl} = \mu + S_i + Y_j + A_k + e_{ijkl}$ …………….... Equation 2

Where Y_{ijkl}: the l^{th} observation in the i^{th} season, j^{th} calving year, k^{th} sire. μ: the overall mean; S: fixed effect of i^{th} season (i: 1,....., 4); Y: the fixed effect of j^{th} calving year (j: 1,......11); A: the random effect of the k^{th} sire; b(AGE): the partial regression of Y_{ijk} on age at calving; e_{ijk}: random error assumed to be normally distributed with mean zero and variance σ^2.

Additionally, the heritability, phenotypic, and genetic correlations between the three traits were calculated using the multiple traits animal model [11]. The model is given in Equation 3:

$y = Xb + W_u a + e$…………………. Equation 3

The variables in the model are as follows: y represents a vector of observations for three traits, b represents a vector of fixed effects with an incidence matrix X, a represents a vector of random additive genetic effects with an incidence matrix W_u, and e represents a vector of random residual effects with a mean of zero and a variance of σ_e^2. Vector a was assumed to follow a multivariate normal distribution with mean 0 and covariance matrix $A \otimes G0$. Similarly, vector e was assumed to follow a multivariate normal distribution with mean 0 and covariance matrix $I \otimes R0$. The matrices G0 and R0 represented 3 X 3 variance-covariance matrices for additive genetic and residual effects, respectively. The symbol $\otimes$ represents the Kronecker product of matrices. Matrix A represents the relationship between individuals based on pedigree data, while matrix I represents an identity matrix. The phenotypic variance (σ_p^2) for each trait was calculated as the sum of the additive genetic variance (σ_a^2) and the residual variance (σ_e^2), expressed as $\sigma_p^2 = \sigma_a^2 + \sigma_e^2$. Heritability is commonly expressed as $h^2 = \sigma_a^2 / \sigma_p^2$. The genetic correlation, denoted as r_g, is calculated using the formula $r_g = cov(a_1 a_2)/\surd\, \sigma_{a1}^2 * \sigma_{a2}^2)$. Here, $cov(a_1 a_2)$ represents the covariance between the additive genetic effects on trait 1 and trait 2, σ_{a1}^2 represents the additive genetic effects on trait 1, and σ_{a2}^2 represents the additive genetic effects on trait 2.

Construction of selection indexes

Calculation of economic values

The matrix procedure developed by Cunningham et al. [12] was used to calculate the basic index, which includes the three traits of interest. Initially, three simplified indices were computed by amalgamating the relevant traits.

Relative economic values for all studied traits were derived as:

1. Actual relative economic values (REV1)

Hussein [3] conducted a study on Friesian cows in Egypt, while Khattab and Sultan [2] and Atil et al. [13] conducted separate studies on Holstein Friesian cows in Turkey. These studies aimed to determine the economic value of various traits by approximating the net profit. The economic value for each trait was calculated based on the final actual net profit using a specific methodology. (1) The net profit per kilogramme of milk is calculated by subtracting the cost of producing one kilogramme of milk from its selling price, resulting in a profit of 0.80 Egyptian pounds (LE) per kilogramme (3.70 – 2.90 = 0.80 LE). (2) The linear regression coefficients for the relationship between 10 MMY and LL were estimated to be 12 kilogrammes per day. The economic value for one day in the lactation period is calculated as 9.6LE, based on a multiplication of 12 by 0.8. Additionally, the cost of raising the heifers from birth until the age of first calving is estimated to be 120LE, as determined by the animal husbandry section of the herd.

2. One phenotypic standard deviation (REV2)

Facloner and Mackay [7] used one phenotypic standard deviation as economic value.

3. Actual economic value of the genetic standard deviation (REV3)

The economic values of the traits were determined by multiplying the genetic standard deviation of a specific trait by the treatment costs per unit of that trait, as stated by Rogers [10] and El- Awady [11]. The weighted economic values according to the three methods of economic values are shown in Table 1.

The index value was calculated based on Equation 4:

$$I = b_1P_1 + b_2P_2 + \cdots \ldots \ldots + b_nP_n = \sum_{i=1}^{n} bipi \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{ Equation 4}$$

Where: b_i = partial regression coefficient and, P_i= phenotypic value of traits

Regression coefficients (b) of all selection indices were estimated based on Equation 5:

$Pb = Ga \text{ or } b = P^{-1} \, Ga$ ………………. Equation 5

Where P is the phenotypic variance-covariance matrix,G is the genetic variance-covariance matrix,b is a vector of partial regression coefficients to be used in the index,a is a vector of constants representing economic values of the traits,and P^{-1} is the inverse of phenotypic variance -covariance matrix. Values in vector b and matrix P were used to calculate index variance (Equation 6).

$\sigma^2 I = b'Pb$ … … … … … ……………….. Equation 6

Variance of the total aggregate genotypic ($\sigma^2 H$) was a'Ga. Accuracy of the index (R_{IH}) defined as the correlation between variance of aggregate genotypic value and variance of the index value was

$\frac{\sigma I}{\sigma H} = \frac{\sigma IH}{(\sigma I * \sigma H)}$, since $\sigma IH = \sigma^2 I$……………….. Equation 7

The expected genetic gain (DG) for a trait was calculated using either the formula DG = I*i*BYI. I is the selection intensity assuming that the selection differential equals one unit of standard deviation and BYI is the regression of each trait in the index on the index value, or the formula proposed by Tabler and Touchberry [14], in which I is the selection intensity set to 1.00 for the purpose of comparisons. Where ci is the ith column of the G matrix and BYI = bci / bPb.

Relative efficiency (RE) was computed for each index based on RIH relative to the whole index in order to facilitate comparisons across indices and identify traits that combine most effectively into an index (I1). Different selection indices were built with the help of estimated genetic and phenotypic variances and covariances of traits utilising Henderson's tweaks to Hazel's technique [15].

Results and Discussion

Table 2 displays the means, standard deviation (SD), and coefficient of variation (CV %) for 10-month milk yield (10 MMY), lactation length (LL), and age at first calving (AFC). The high coefficient of variation (CV%) values observed for 10 MMY and LL (35.93% and 35.79% respectively) indicate a significant degree of variation among individuals in terms of their productive traits. This increased variation in these traits is advantageous for the process of improvement through selection. El-Arian et al. [8] found that the coefficient of variation (CV%) for 10 MMY and LL were 27% and 23%, respectively. According to El-Shalmani [16], the coefficient of variation (CV%) for 10-month milk yield (MMY) and lactation period (LP) in British Friesian cows was found to be 27.06% and 20.60%, respectively. Several factors could explain the differences observed between the findings of this study and previous research conducted on Egyptian dairy cattle. Herds may exhibit genetic and phenotypic variations due to several factors: (1) diverse climates and management practices during their upbringing, (2) a mix of imported and locally bred animals, (3) variations in analytical methods and models employed, and (4) the inclusion of different herds in the analysis. Table 3 demonstrates that the calving year significantly influenced all three traits. The influence was primarily determined by the individual animals' conditions, annual climatic variations, heat stress, and phenotypic trends. Khattab and Sultan [2], El-Shalmani [16], Khattab et al. [17], Abosaq et al. [5], Zahed et al. [18], and Khattab et al. [6]. studies on various groups of Friesian or Holstein Friesian cows in Egypt, yielding consistent findings.

The estimates of partial linear and quadratic regression coefficients for the relationship between 10 MMY and AFC were found to be statistically significant. The coefficient for the linear term was estimated to be 110.86 ± 33.61 kg/mo., while the coefficient for the quadratic term was estimated to be -3.20 ± 0.80 kg/mo2, as presented in Table 4. The regression coefficients for the partial linear and quadratic relationship between LL and AFC did not reach statistical significance. Khattab and Sultan [2], El-Shalmani [16], and Khattab et al. [6] obtained similar findings. The current findings indicate a curvilinear relationship between AFC and 10 MMY. Reducing the age at first calving is necessary in order to enhance lifetime production and decrease the generation interval, which are desirable objectives for dairy farmers.

The heritability estimate (h^2) for 10 MMY was 0.37 ± 0.05 (Table 5). The current estimate falls within the range reported in various studies on Friesian cattle raised in different countries using the Animal model. For example, Suzuki and Van Vleck [19] reported a heritability estimate of 0.30 for Friesian cattle in Japan. Several studies have been conducted on different populations of Friesian cattle in various countries. Swalve [20] examined Germany Friesian cattle with a correlation coefficient of 0.28. Mousa et al. [21] investigated Friesian cattle in Egypt, reporting a correlation coefficient of 0.22. Atil et al. [13] studied Holstein Friesian cattle in Turkey, finding a correlation coefficient of 0.26. El-Shalmani [16] focused on British Friesian cows in Egypt, reporting a correlation coefficient of 0.37. Lastly, Khattab et al. [6] conducted a recent study on Friesian cows in Egypt, reporting a correlation coefficient of 0.61.

The heritability of LL was estimated to be 0.20 ± 0.01. These findings suggest that non-genetic factors play a significant role in explaining the variation in LL. Therefore, it is possible to make significant improvements in this attribute by implementing better feeding and management practices. El-Arian et al. [8] and Khattab et al. [6]

also found similar results in Friesian cattle in Egypt using the Animal model. In their study, Atil et al. [13] investigated the heritability (h^2) of LL in Holstein Friesian cows in Turkey. They reported a h^2 value of 0.17 for LL. The study's low heritability estimate for LL indicates that environmental factors play a significant role in determining this characteristic. Improving nutrition, management practices, heat monitoring, and utilising high-quality sperm can potentially lead to an extended calving interval.

The estimated value for AFC was 0.05 with a standard error of 0.002. The current estimate aligns with El-Shalmani's [16] report (0.06). The reported values in this study were lower compared to those reported by Kassab [22] (0.57), El-Gendy [23] (0.41), and Ghonem [24] (0.50). Overall, the h^2 estimate for milk yield was found to be moderate, suggesting that it could be beneficial for selection and improving the environment to enhance milk production. The estimated heritability (h^2) for AFC as a reproductive trait was found to be lower. To enhance this estimate, it is necessary to improve environmental conditions primarily.

The estimated genetic correlation (rg) between 10 MMY and LL was found to be positive and high, with a value of 0.89 ± .01 (Table 5). The findings of this study suggest a correlation between genes related to extended lactation duration and genes that promote high milk production. The current estimate falls within the range reported by previous studies conducted by Khattab and Sultan [2], El-Arian et al. [8], Atil et al. [13], El-Shalmani [16], and Khattab et al. [6], which ranged from 0.39 to 0.94. El-Arian et al. [8] found a strong positive correlation (r = .97) between the age at first calving (305 days) and lifetime milk production in Holstein Friesian cattle in Egypt. The authors proposed that selecting cows with higher milk production or productivity would lead to a corresponding increase in lifetime lactation (LL). The correlation coefficient between MMY and AFC was found to be -0.12 ± 0.02. Khattab and Sultan [2] reported a similar finding. The study found a positive correlation (rg = 0.10 ± 0.04) between LL and AFC, suggesting that selecting for high milk yield will likely lead to genetic enhancements in LL and a decrease in AFC.

The phenotypic correlation (rp) between 10 MMY and LL was found to be positive and highly significant (rp = 0.90 ± 0.02). These findings align with previous studies conducted by Khattab and Sultan [2], El-Arian et al. [8], Atil et al. [13], El-Shalmani [16], and Khattab et al. [6]. Noweir [25] conducted a study on 2181 lactation records of Friesian cows in Egypt. The study found that the estimated genetic correlations (rp) between 10-month milk yield (MMY) and lifetime lactation (LL) were 0.56 and 0.49 using the Sire model and Animal models, respectively. The current findings suggest a positive association between extended lactation duration in highly productive cows and increased 10-month milk yield (10 MMY). The correlation coefficient between LL and AFC (r = .77 ± .008) is consistent with the findings of El-Gendy [23], who reported a correlation coefficient of .09. The findings suggest that cows with higher milk production generally have longer lactation periods, while younger cows tend to produce more milk compared to older cows.

Table 6 presents the phenotypic and genetic variances and covariances among the three traits utilised for estimating various selection indexes. Four selection indices were computed using three distinct approaches for determining economic values: (1) actual relative economic weight (Table 7), (2) one phenotypic standard deviation (Table 8), and (3) one genetic standard deviation (Table 9). The initial index (I1) included all three traits in order to improve the overall genotype of the three traits. However, the reduced indices (I2, I3, and I4) only utilised two traits for selecting the aggregate genotype.

In Method 1 (REV1), the expected genetic change per generation (EG) varied between 47.50 and 83.50 kg for 10 MMY, 8.91 and 17.42 d for LL, and -1.30 and -1.65 mo for AFC (Table 7). The current findings are lower than those documented by Khattab and Sultan [2]. Their study reported that the economic gain (EG) ranged from 88 to 235 kg for 10 months of milking yield (MMY), from 21 to 27 days for lactation length (LL), and from -0.36 to -1.96 for age at first calving (AFC) in a herd of Friesian cows in Egypt. These values were determined using actual relative economic values. El-Awady et al. [26] found that the estimated genetic effect for milk yield in German Friesian cows ranged from 338 to 344 kg. In their study on Holstein Friesian cows in Turkey, Atil et al. [13] observed a range of 363 to 411 kg for 305-day milk yield (MY), 16.78 to 29.92 days for lactation period (LP), and -0.36 to -0.65 months for age at first calving (AFC). El-Awady [11] discovered a range of 110 to 304 kg for the estimated breeding value (EG) in a herd of Friesian cows in Egypt, as determined by various selection indexes. The findings suggest that I1 was associated with the highest genetic improvement in 10 MMY, LL, and AFC. The anticipated genetic improvement in 10-month milk yield (MMY) increased by 83.50 kg per generation, and lifetime milk yield (LL) increased by 17.42 days per generation. Additionally, age at first calving (AFC) decreased by 1.65 months. Therefore, it is recommended to incorporate the Average Fuzzy Consistency (AFC) in an index that includes 10 Modified Moody's Yield (MMY) and Liquidity Level (LL).

The accuracy of the index (I2) that did not incorporate AFC was 45%, indicating a lower level of precision. The accuracy of I3 and I4, when combined with AFC plus 10 MMY or LL, was significantly higher compared to I1. Similar findings have been reported by other researchers, including Khattab and Sultan [2], El-Awady et al. [26], and Atil et al. [13]. The results of the comparison of selection indices indicate that selection index I1 demonstrated the highest performance (RIH = 0.62). The conclusion of the initial lactation period presents an opportune moment for the selection of Holstein Friesian cattle. Khattab and Sultan [2] and Atil et al. [13] found that the selection index I1, comprising of 10 MMY, LL, and AFC traits, was the most straightforward and effective option based on their study with Friesian cows.

Table 8 displays the EG, RIH, and RE values for Method 2 (REV2). The estimated growth (EG) for 10 months of age varied between 46.90 and 83.50 kg. The length of lactation (LL) ranged from 7.05 to 17.40 days, and the age at first calving (AFC) ranged from -1.30 to -1.65 months. I1 achieved the highest genetic improvement in 10 MMY and LL. The anticipated genetic improvement in 10-month milk yield (MMY) increased by 83.50 kg per generation, and lifetime milk yield (LL) increased by 17.40 days per generation. Additionally, age at first calving (AFC) decreased by 1.65 months. The accuracy of the index, excluding AFC (I2), was lower at 0.45. However, when AFC was included with either 10 MMY or LL (I3 and I4), the accuracy approached that of I1. The comparison of selection indexes reveals that index I1, comprising three traits, demonstrated the highest performance (RIH = .62). The outcomes of this are comparable to those of Method 1. El-Arian [4] employed two economic value methodologies, namely Method 1 (real relative economic values) and Method 2, to examine 598 records of the initial lactation of Friesian cows in Egypt, with a focus on one phenotypic standard deviation. Twenty-six selection indices were developed, each corresponding to a different approach for determining relative economic value. The author recommends utilising Method 2 of relative economic values due to its computational simplicity and its inclusion of 10 MMY, 305-day protein yield, calving interval, and age at first calving in the selection index.

Table 9 presents the EG, RE, and RIH as per Method 3.The estimated generation (EG) varied between 46.90 and 83.40 kg for a span of 10 million years (MMY). The longevity (LL) ranged from 7.04 to 17.30 days per generation, while the age at first copulation (AFC) varied between -1.39 and -1.64 months per generation. I1 achieved the highest genetic improvement in 10 MMY, LL, and AFC. The average age at first calving (AFC) decreased by 1.64 months per generation, while the live weight (LL) increased by 17.30 days per generation. Additionally, the estimated genetic gain in 10 years was projected to be 83.40 kg. Excluding AFC, the accuracy index (I2) exhibited a low performance level of .45. The analysis of selection indices reveals that index I1, comprising three traits, demonstrated the highest performance (RIH = .62).

The comparison of three methods of relative economic values revealed no differences among them for the economic gain (EG) of each trait, the relative importance hierarchy (RIH), and the relative efficiency (RE) compared to the original index (I). Thus, all three methods effectively predicted the genetic gain per generation for the three traits under investigation. Therefore, it is recommended to use the second method, which involves calculating one phenotypic standard deviation, as it is simpler to compute. Hussein [3] and El-Arian [4] conducted a study in Egypt on Friesian cows. They found that there was no significant difference between the economic value and one standard deviation of phenotypic variation. Most of the correlation coefficients between the estimated breeding values by the REV1, REV2, REV3 and BLUP for the three traits considered in this study were positive (Table 10). The values fluctuated, with correlation coefficients ranging from -0.068 between BLUP and REV1 to 0.711 between REV2 and REV3 for 10MMY. In LL, correlation coefficients ranging from -0.193 between BLUP and REV2 to 0.886 between REV1 and REV2. In AFC, correlation coefficients ranging from 0.034 between BLUP and REV2 to 0.617 between REV1 and REV3. Correlations between REV1, REV2 and REV3 indicate agreement between these methods. On the other hand, BLUP was quite different from selection index methods, and it was slightly lower.

The major purpose for learning about selection indexes is that they give a straightforward approach to measure selection accuracy before starting a breeding program. This is really handy for comparing different techniques. It also provides a very beneficial framework for trying to enhance many features at the same time by ensuring that all attributes are given the proper relative weighting in the selection criterion. However, with the introduction of genomic selection, genome-wide information enables reliable selection of young animals, as long as phenotypes from a significant number of reference animals are available. This means that genomic breeding values are particularly useful when traditional selection is problematic, for as when phenotypic recording is limited by sex and age. Individual selection using genomic EBV addresses three main animal breeding frontiers: the precision of breeding values for characteristics with low heritability, inbreeding control, and generation interval. The selection index's significance and applicability for current breeding procedures must be reevaluated. As a result, the incorporation of genetic information in cow breeding plans should be regarded in the context of other advancements.

Conclusion

The present work suggested that the three methods of relative economic values predicted the genetic gain per generation for the three traits studied successfully and the second method (one phenotypic standard deviation) was recommended for ease of calculation.

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Table 1. Estimation of relative economic values according to actual relative economic values (REV1), one phenotypic standard deviation (REV2) and one genetic standard deviation (REV3)

Traits	REV1	REV2	REV3
10 month (10MMY)	0.80	3489	13.65
Lactation length (LL)	9.60	128	10.44
Age at first calving (AFC)	-120	2.39	7.81

Table 2. Means, standard deviation (SD) and Coefficient of variation (CV%) for ten month milk yield (10 MMY), lactation length (LL) and age at first calving (AFC) on Holstein Friesian cows in Egypt

Traits	Mean	SD	CV%
10 MMY, Kg	9710	3489	35.93
LL, d	357	128	35.79
AFP, mo.,	27.17	2.39	8.82

Table 3. Least squares analysis of variance for factors affecting 10 month milk yield (10 MMY), lactation length (LL) and age at first calving (AFC) for Holstein Friesian cows

Source of variation	DF	10 MMY (F- values)	LL (F- values)	DF	AFC (F- values)
Sires	73	2.13**	1.82**	73	9.56**
Year of calving	10	5.29**	5.08**	10	2.53**
Regressions					
AFC, Linear	1	17.60**	.671		
AFC, quadratic	1	16.36**	.675		
Error mean squares	1777	182536959.67	102368.64	1777	11.998

** $P < 0.01$

Table 4. Estimates of partial linear and quadratic regression coefficients of age at first parturition (AFP) on ten month of milk yield (10 MMY), and lactation length (LL) of Holstein Friesian cows

Traits	Partial regression AFC, linear	AFC, quadratic
10 MMY, Kg	110.86 ± 33.61**	-3.20 ± 0.80**
LL d	1.54± 01.23	-0.50± 0.90

Table 5. Estimates of heritability on diagonal, genetic correlation below diagonal and phenotypic correlation above diagonal among 10 month milk yield (10 MMY), lactation length (LL) and age at first calving (AFC) on Holstein Friesian cows

Traits	10 MMY	LL	AFP
10 MMY	0.37 ± 0.05	0.90 ± 0.02	-0.09± 0.004
LL	0.98 ± 0.01	0.20 ± 0.01	0.77 ± 0.008
AFP	-0.12 ± 0.02	0.10± 0.04	0.05± 0.002

Table 6. Phenotypic and genetic variances and covariances of 10 month milk yield (10 MMY), lactation length (LL) and age at first calving (AFC)

	Phenotypic			Genetic		
	10 MMY	LL	AFC	10 MMY	LL	AFC
10 MMY	50319			18621		
LL	-8328	53672		-1674	10914	
AFC	9107	-16215	12681	3513	284	969

Table 7. Selection indices (I’s) for different traits of Friesian cows, expected genetic change per generation (EG) in each trait, correlation of index with aggregate genotype (R_{IH}) and the efficiency (RE) of different indices relative to the original index (I), by using actual relative economic weight (REV1)

	10 MMY, kg		LL, d		AFP, mo.,		R_{IH}	RE
	b*	EG	b*	EG	b*	EG		
I_1	9.58	83.50	5.82	17.42	-7.84	-1.65	0.62	100
I_2	0.39	47.50	5.58	16.80			0.45	73
I_3	10.85	80.00			-7.98	-1.40	0.59	95
I_4			6.13	8.91	-15.92	-1.30	0.50	81

Table 8. Selection indices (I's) for different traits of Friesian cows, expected genetic change per generation (EG) in each trait, correlation of index with aggregate genotype (R_{IH}) and the efficiency (RE) of different indices relative to the original index (I) by using one phenotypic standard deviation (REV2).

	10 MMY, kg		LL, d		AFP, mo.,		R_{IH}	RE
	b*	EG	b*	EG	b*	EG		
I_1	10.47	83.50	0.098	17.40	-0.30	-1.65	0.62	100
I_2	0.38	46.90	2.46	16.70			0.45	73
I_3	9.95	81.00			-0.80	-1.40	0.59	95
I_4			1.23	7.054	-9.55	-1.39	0.50	81

Table 9. Selection indices (I's) for different traits of Friesian cows, expected genetic change per generation (EG) in each trait, correlation of index with aggregate genotype (R_{IH}) and the efficiency (RE) of different indices relative to the original index (I), by using one genetic standard deviation (REV3).

	10 MMY, kg		LL, d		AFP, mo.,		R_{IH}	RE
	b*	EG	b*	EG	b*	EG		
I_1	0.22	83.40	0.86	17.30	1.30	-1.64	0.62	100
I_2	0.50	46.90	0.50	16.30			0.45	73
I_3	0.38	80.00			-0.02	-1.40	0.59	95
I_4			0.80	7.024	-1.09	-1.39	0.51	82

Table 10. Person correlation between the estimated breeding values (EBVs) calculated by the actual relative economic weight (REV1), one phenotypic standard deviation (REV2), one genetic standard deviation (REV3) methods and the EBVs obtained by BLUP

	REV1	REV2	REV3
10MMY			
REV2	0.531		
REV3	0.628	0.711	
BLUP	-0.068	0.479	0.347
LL			
REV2	0.695		
REV3	0.886	0.637	
BLUP	-0.629	-0.193	0.014
AFC			
REV2	0.519		
REV3	0.617	0.116	
BLUP	-0.533	-0.034	-0.520