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A comparison of different selection indexes for milk traits in Friesian cows by using different relative economic values.

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Abstract

The data set contained 2181 normal lactation records of Friesian cows kept at Sakha Experimental Farm, Kafer El- Sheikh Government, belonging to Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo, Egypt were used to construct several selection indexes by using two relative economic values, actual relative economic value (REV_1) and one phenotypic standard deviation (REV_2). Variables studied were 305 day milk yield (305 d MY), 305 day fat yield (305 d FY) and 305 day Protein yield (305 d PY). Data were analysis by using MTDFREMAL Software. The model include the main effects of month and year of calving, parity and days open as covariate and random effects of animals, permanent environmental and errors.

The estimated means and standard deviations for 305 d MY, 305 d FY and 305 d PY were 2806 ±949 kg , 102 ±37 kg and 79 ±28 kg, respectively; and their estimated heritabilities 0.29±0.01, 0.24±0.02 and 0.29±0.02, respectively. Repeatability estimates were 0.37±0.05, 0.44±0.06 and 0.51±0.06 for 305 d MY, 305 d FY and 305 d PY, respectively. Phenotypic, genetic environmental correlations among different variables were positive and significant. Comparison of the two methods for estimating relative economic values explained no changes in any of the two methods for the expected genetic gain per generation for each variable. Our results indicate that, the two methods were succeeded in predicting the genetic progress per generation for the three variables studied. However, the second method (one phenotypic standard deviation) was recommended based on ease of estimation.

Key words: Selection indexes, milk, composition , Friesian cows

1. Introduction

Selection index is the best method of selection for several variables in livestock. It takes heritability of each variable, phenotypic variance of each variable, genetic and phenotypic correlations among variables and relative economic value of each variable **(Hazel and Lush, 1942).**

Relative economic values can estimate by different methods, actual economic value or net profit (**Khattab and Sultan, 1991; Atil et al, 2005; El- Awady, 2009 ; Kassab et al. 2024**), one phenotypic standard deviation (**Falconer and Mackay, 1996; Abosaq et al. 2017; Khattab et al. 2023; Kassab et al. 2024),** Lamont method (**Lamont, 1991; Abosaq et al., 2017 ; Khattab et al. 2023)** and one genetic standard deviation (**El- Awady, 2009 ;Kassab et al. 2024).**

The main objectives of current study were to estimate phenotypic and genetic parameters for 305 day milk yield (305 d MY), 305 day fat yield (305 d FY) and 305 day protein yield (305 d PY) and constructed selection indexes by using two methods of relative economic values for Friesian cows.

2. Material and methods

Data were collected from Sakha experimental farm, belonging to the Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo, Egypt and comprising 2181 cows which completed one or more lactations. Animals were fed on Egyptian clover (*Trifolium alexandrinum*) during winter and spring season and during summer and autumn they were fed on concentrate ration and clover hay. Artificial insemination (AI) was used at random. Heifers were first inseminated at 18 months of age. In subsequent lactations, cows were initially inseminated 60 -70 days postpartum. Milking was performed twice daily at 7am and 4pm during the lactation period. Milk yield were recorded daily and milk components were analyzed weekly by using system of Milko–Scan 130 series, type 10900. Maintained at (ILMTC) related to Animal Production Research Institute (APRI), this have special program to estimate milk composition (fat and protein). Variables studied are milk, fat and protein yield in 10 months (305 d MY, 305 d FY and 305 d PY), respectively. Days open was computed as the interval between parturition and the date of successful mating.

Statistical Analysis:

Data were analysis by using MTDFREML Software Boldman et al. (1995), the statistical models included the fixed effects of month and year of calving and parity and days open as a covariate, and random effects of animal, permanent environmental effect and residual. Heritability (h^2) was estimated by using the following equation ($h^2 = \sigma^2a / \sigma^2a + \sigma^2pe + \sigma^2e$). Repeatability (t) was estimated by using the following equation ($t= \sigma^2a + \sigma^2pe/ \sigma^2a + \sigma^2pe + \sigma^2e$), where, σ^2a = additive genetic variance, σ^2pe= permanent environmental variance and σ^2e= random residual effects.

Selection Index Methodology:
Requires selection on an index or criterion (which correlates best with H):

$I = \sum_{i=1}^{n}(bi\ pi)$

I is selection index, b_i is a selection index weighing factor, p_i is a phenotypic measure and n is number of traits. The optimum set of selection index coefficients are those which maximize the correlation (r_{IH}) or minimize the squared deviation between the selection index and the aggregate genotype. The genetic and phenotypic parameters used for the calculation of the optimal index weights in all index calculations were those observed in the present study, Hazel (1943) proved that maximum r_{HI} is achieved when $Pb = Gv$, then The vector of optimal index weights (b) was calculated for each of the objectives as

$b = P^{-1}Ga$

where:

P^{-1} is the inverse of the phenotypic (co)variance matrix of the traits in the selection index, G is the genetic covariance matrix between traits in the selection goal and the selection index, and a is the vector containing the economic values for the goal traits.

Furthermore, the other different properties of the selection index were calculated as following:
Standard deviation of the index (σ_I) = √b'Pb,
Standard deviation of the aggregate genotype (σ_H) = √a'Ga
Correlation between the index and the aggregate genotype (accuracy)
$R_{IH} = \sigma_I / \sigma_H$

The genetic change per trait from selection ΔG (R_j) was calculated as:

$$R_j = \frac{i^{*}b'^{*}G_j}{\sigma_i}$$

Where R_j = a vector with the genetic change per trait j, i is selection intensity (in the present study this was assumed to equal one), b′ is transpose of the vector containing the index weights, G_j is the jth column of a G matrix containing the genetic covariance between the trait j and the index traits; and σ_i is the standard deviation of the index used. The expected response from selection using the objectives is illustrated in the present study as genetic gain following one cycle of selection with a standardized selection intensity of one.

Estimate of relative economic value (REV):
The economic values were calculated by two methods:
Actual relative economic value: The economic value for each variable was calculates based on the final actual net profit (Khattab and Sultan, 1991; Atil et al., 2005 ; Kassab et al. 2024).
One phenotypic standard deviation: Depending on the phenotypic standard deviation where $V_i = 1 / \sigma_p$. According to (Falconer and Mackay, 1996; Atil et al., 2005; Kassab et al., 2024). The weighted economic values according to the two methods of economic values are shown in Table 1.

Table 1. Relative economic values (REV) for different variables according to actual economic values ($REV_{1)}$ and one phenotypic standard deviation (REV_2).

Variables	REV 1	REV 2
Milk, kg	1	1
Fat, kg	12.60	20
Protein, kg	6.30	25.50

Results and discussion

Means, standard deviation (SD) and coefficient of variability (CV %) for the three variables studied are presented in Table 2. Means of 305 d MY, 305 d FY and 305 d PY were 2806 kg, 102 kg and 79 kg, respectively. The present means of the three variables were lower than those reported by **Kafidi et al. (1992), Atil and Khattab (2000), El- Awady et al. (2002), kadarmideen et al. (2003), Lazarevic et al. (2018), Amina Habib et al. (2020 and 2024) Estrada-León (2024) and Kassab et al. (2024)** worked on Friesian cows in different regions and ranged from 4490 to 9710 kg for 305 d MY , from 200 to 317 to for 305 d FY and from 158 to 296 to for 305 d PY. The variation in estimates of milk variables between our study and previous study may be due to the differences in breed composition, management, climate, feeding system, and models used in the analysis.

The CV % ranged between 33.82 to 35.97 % (Table 2). The estimates between 26.91 to 39.45 % for yield traits were reported **Amina Habib et al. (2020).** The higher CV % values of milk traits cause a great variation between individuals in important productive variables.

Estimates of direct heritability (h^2) for 305 d MY, 305 d FY and 305 d PY were 0.29±0.01, 0.24±0.02 and 0.29±0.02, respectively (Table 3). Our estimates are fall within the range calculated by many workers on different breeds of dairy cows in different regions. In this respect, Ahlborn and Dempfle (1992) with 178 Half-sib groups of 7345 Holstein – Friesian cows, stated that h^2 estimates for milk, fat and protein yield were 0.26, 0.26 and 0.28, respectively. El- Awady et al. (2002) with German Friesian cows, found that h^2 for 305 d MY, 305 d FY and 305 d PY were 0.32, 0.36 and 0.31, respectively. Rahayu et al. (2015) with Baturraden Dairy Cattle in Indonesia found that h^2 for MY, FP and PY were 0.20, 0.30 and 0.17, respectively. Uribe et al. (2017) with 64,029 complete lactation records of dairy cows in Southern Chile, using multi trait animal mode, found that h^2 estimates for milk yield, and fat and protein above 3% yield were 0.16±0.004, 0.44±0.007 and 0.42±0.006, respectively. Lazzrevic et al. (2018) worked on Holstein Friesian and Black and White cows, using mixed model, reported that h^2 estimates for MY, FY and PY were 0.291, 0.319 and 0.273, respectively. Amina Habib et al. (2024) with Holstein Friesian cows using MTAM reported that direct h^2 estimates for 305 d MY, 305 DFY and 305 d PY were 0.36, 0.30 and 0.23, respectively. While the present estimates are higher than those found by many authors. DeGroot et al. (2002) with Holstein cows, found that h^2 estimates for milk, fat and protein yield were 0.13 (0.02), 0.22 (0.08) and 0.09 (0.09) , they concluded that the small sample size could explain the small estimates of h^2 for milk and protein. El-Awady et al. (2002) with another set of that herd, using MTAM, found that direct h^2 estimates for MY, FY and PY were 0.017, 0.046 and 0.048. They concluded that lower estimates of h^2 could be due to higher percentage of permanent and residual environmental factors. Tohidi and Nazari (2023) with Iranian Holstein cattle, found that Heritability estimates using the repeated record animal model for 305 d MY, 305 d FY and 305 d PY were 0.19 ± 0.001, 0.15 ± 0.005, and 0.17 ± 0.006, respectively. Snedddon et al. (2015) worked on New Zealand dairy herds, using bivariate animal model, found that h^2 estimates for MY, FY and PY were 0.23+0.04, 0.15+0.04 and 0.14+0.03 respectively

Table 2. Means, standard deviation (SD) and coefficient of variability (CV%) for milk yield (MY), fat yield (FY) and protein yield (PY) in Friesian cows

	Means	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			

Table 3. Estimates of direct heritability (h^2_d) and repeatability (t) for 305 day milk yield (395 d MY), 305 day fat yield (305 d FY) and 305 day protein yield (305 d PY) for Friesian cows.

Variables	h^2_d	t
305 d MY	0.29±0.01	0.37±0.05
305 d FY	0.24±0.02	0.44±0.06
305d PY	0.29±0.02	0.51±0.06

Table 4. Additive genetic (rg), environmental (re) and phenotypic correlations (rp) for 305 day milk yield (305 d MY), 305 day fat yield (305 d FY) and 305 day protein yield (305 d PY) for Friesian cows.

Variables correlated	r_g	r_{pe}	r_e	r_p
305 d MY X 305 d FY	1.00	0.32	0.35	0.51
305 d MY X 305 d PY	1.00	0.14	0.34	0.52
305 d FY X 305 d PY	1.00	0.80	0.96	0.96

Standard errors ranged from 0.02 to 0.10

Repeatability estimates for 305 d MY, 305 d FY and 305 d PY were 0.37±0.05, 0.44±0.06 and 0.51±0.06, respectively (Table 3) and similar to those values reported by Tohidi and Nazari (2023) , being 0.38 ± 0.002, 0.34 ± 0.002, and 0.36 ± 0.002, for 305 d MY, 305 d FY and 305 PY, respectively.

The moderate h^2 estimates for milk, fat and protein yield, it can be concluded that the genetic improvement in milk yield and it is components can be achieved through selection breeding program, Also, According to moderate repeatability estimates for milk traits, culling of cows based on a single record as commonly practiced by commercial breeders of dairy cattle, would be recommended from a genetic standpoint.

Estimates of genetic correlations among the three variables were unity (Table 4) and were higher than phenotypic correlations which ranged from 0.50 to 0.96 (Table 4). Due to the high genetic correlations among milk yield and it is components, genetic selection for all traits can be achieved through selection for any of them. These results are agreement with previous studied (Ahlborn and Dempfle ,1992; Kafidi et al., 1992; DeGroot et al. 2002; El-Awady, 2002; Amina Habib et al. ,2020 &2024; Tohidi and Nazari (2023) and ranged from 0.68 to 0.995.

Estimates of direct additive genetic variance (σ^2a), permanent environmental variance, error variance (σ^2e) and phenotypic variance (σ^2p) and covariance among different variables which are used in construction selection indexes are presented in Table 5. Four selection indices were made according to REV_1 and REV_2 (Tables 6 and 7). The original index (I_1) included all the three variables (305 d MY, 305 d FY and 305 d PY), to be used for improving the aggregate genotype of the three variables, However, the reduced indexes (I_2, I_3 and I_4) include only two variables to select aggregate genotype.

For method 1 (REV_1) the expected genetic gain per generation in each variable (305 d MY, 305 d FY and 305 d PY) assuming a selection intensity 1 given in Table 6 . The expected genetic change per generation (EG) ranged from 285 to 305 kg for 305 d MY, from 12.22 to 14.0 kg for 305 d FY and from 10.41 to 11.93 kg for 305 d PY. Similarly for method 2 (REV_2) the expected genetic change per generation (EG) ranged from 285 to 305 kg for 305 d MY, from 12.22 to 14.0 kg for 305 d FY and from 10.41 to 11.93 kg for 305 d PY (Table 7).

Table 5. Estimates of (co) variance components for milk yield (MY), fat yield (FY) and protein yield (PY) for Frisian cows.

Estimates	Variables		
	MY	FY	PY
σ^2a	233103 (29%)	492 (23.64%)	358 (29%)
σa with MY		10709	9131
σa with FY			420
σ^2p_e	66527 (8.25%)	144(6.92%)	107(8.66%)
σp_e with MY		991	272
σp_e with FY			72
σ^2e	506780(62.75%)	1445(69.44%)	770(62.34%)
σ^2P	806419	2081	1235
σe with MY		21067	16422
σe with FY			1541

Table 6. Selection indices (I's) for different variables of Friesian cows, expected genetic changes per generation (EG) in each variable, correlation of index with aggregate genotype (R_{IH}) and the efficiency (RE) of different indices relatives to the original index (I_1) by using actual relative economic values (REV_1).

Indices	Variables							
	MY		FY		PY		R_{IH}	RE%
	b	EG	b	EG	b	EG		
I_1	0.3555	305	-9.2833	14.0	20.3613	11.93	0.63	100
I_2	0.3319	285	4.7620	13.1	-----------------------		0.59	94
I_3	0.2368	298	---------------------------		6.0717	11.67	0.62	98
I_4	------------------------------		-3.6176	12.22	10.6254	10.41	0.55	87

Table 7. Selection indices (I's) for different variables of Friesian cows, expected genetic changes per generation (EG) in each variable, correlation of index with aggregate genotype (RIH) and the efficiency (RE) of different indices relatives to the original index (I_1) by using one phenotypic standard deviation (set_1).

Indices	Variables							
	MY		FY		PY		R_{IH}	RE%
	b	EG	b	EG	b	EG		
I_1	0.5680	305	-14.7984	14.0	32.4995	11.93	0.63	100
I_2	0.4033	285	5.78892	13.1	----------------------		0.59	94
I_3	0.3795	298	-----------------------		9.7398	11.67	0.62	98
I_4	-------------------------		-8.3589	12.22	24.6235	10.41	0.55	87

The present estimates are near similar to those reported by El- Awady et al. (2002) with German Friesian cow found that the expected genetic change per generation ranged between 338 kg and 344 kg for 405 d MY from 4.11 kg to10.81 kg for 395 d FY and from 7.55 kg to 7.98 kg for 305 d PY. Amina Habib et al. (2020) with another herd of Holstein Friesian cows reported that the expected genetic gain per generation ranged from 180 to 323 kg for 305 d MY, from 13.79 to 24.95 kg for 305 FY and from 13.79 to 24.95 kg for 305 PY). Ozturk et al. (2021) with Holstein Friesian cows in Turkey, found that the expected genetic gain for 305 d M was 111.5 kg/year. While Rahayu et al. (2015) with Indonesia cows found that the genetic gains of milk yield was 9.76 kg. Tohidi and Nazari

(2023) found that The regression coefficients of breeding values on calving years for 305 d MY, 305 FY and 305 DPY were 17.32 Kg, 0.51 Kg, 0.53 Kg, respectively.

The maximum genetic progress in 305 d MY, 305 d FY and 305 d PY was achieved by the original index (I_1) for both methods. The expected genetic gain in 305 d MY , 305 d FY and 305 d PY increased by 305 kg/generation, 13.0 kg/ generation and 11.93 kg/ generation, respectively (Tables 6 &7).

The index not including 305 d MY (I_4) showed a reduced accuracy (0.87) for both two methods. Therefore including 305 d MY with either 305 d FY or 305 d PY (I_2 and I_3) closed in accuracy to I_1 RIH (tables 6&7). Hence it would be desirable to include 305 d MY in an index incorporating 305 d FY and 305 d PY. Uribe et al. (2017) arrived at the same conclusion.

Compare of selection indices indicated that index I1, which incorporated 305 d MY, 305 d FY and 305 D PY and the third index I_3, which incorporated 305 d MY and 305 d PY are the best for both methods ($R_{IH} = 0.98$, Tables 6 &7).

The comparison of two methods of relative economic values revealed no differences among them for the economic gain (EG) of each trait, the relative importance hierarchy (R_{IH}), and the relative efficiency (RE) compared to the original index (I). Thus, the two 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 one phenotypic standard deviation, as it is simpler to compute.

Conclusion

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

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