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Comparison between different selection indices for some productive traits in Friesian cows

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ABSTRACT

Data pertaining to 3,977 records collected over a period of 29 years for Friesian cows were utilized for the present study. Records were analyzed for actual total milk yield (TMY), 305-day milk yield (305d-MY), lactation period (LP) and days open (DO) by VCE 6.0 software while, selection indices (SI) using one phenotypic standard deviation as REV1 and Lamont method as REV2. Estimates of direct heritability were low and ranged from 0.02 to 0.23 while, maternal heritability were low and ranged from 0.03 to 0.028. The correlation coefficients between all studied traits were highly significant and ranged between 0.82 to 0.93. The results indicated that reducing interval of days open (DO) could be brought about by improving the farm managerial aspects. The selection criteria of different indices proved that the index I_1which incorporated TMY, 305d-MY, LP and DO was the best (RIH = 0.49) and (RE % = 100.00). This index could effectively anticipate in genetic improvement of all the traits of the study; I_1 = 0.144 (TMY) + 0.503 (305day/MY) + 1. 619 (LP) + 1.150 (DO). The application of this index I_1 led to a predictive genetic gain of TMY, 305d-MY, LP and DO by 359.4 kg, 279.5 kg, 15.3 days and 3.2 days, respectively. The correlation coefficient between I_1 and the total economic value was 0.49 while, the heritability estimate of the index was 0.86. Conclusively, such an index can help the investor in the field of dairy cattle to select the best animals in early lactation and in subsequent generation's traits as well; which leads to an increase in economic return.

Keywords: Economic values, Friesian, Genetic parameters, Productive traits, Selection index

In Egypt, cattle play an effective role in meeting the demand of human for milk and meat. Milk yield has been the best selection criterion for Friesian in Egypt due to its great economic importance. Therefore economic returns of dairy farms depends on both milk production and reproductive efficiency. Genetic and phenotypic parameters in quantitative genetics include heritability, genetic and phenotypic correlations, which play a vital role in the formulation of any suitable breeding plan for genetic improvement program (Aynalem 2006).

Berry *et al.* (2003) noted, however, a possibility to select animals for increasing milk production without negatively impacting fertility. Within the selection index are combined, the production levels of two or more characteristics, obtaining a score based on which the selection is made. Such an obtained score is in maximal correlation with the genetic contribution of certain individual (Ivanoviæ *et al.* 2014), since some authors have attempted to use milk yield and some reproductive traits in a combined index (El-Arian 2005, Atil 2006). Estimation of genetic and phenotypic parameters for productive and reproductive traits is an important tool for the definition and evaluation of selection programs.

The selection index (SI) is a method for estimating the breeding value (BV) of a cow combining all information available on the cow and its relatives (Mohammed 2020).

Miglior *et al.* (2005) stated that the most selection indices were based on improving milk yield and outside North America toward increasing fat and protein content. The selection indices were developed for purebred Holstein Friesian cattle reared under climatic conditions of the north of India (Tomar *et al.* 2005). The current study developed an economic selection index (ESI) for cows of the Friesian breed; therefore, the aim of the study was to determine the genetic parameters that may affect milk productivity traits in Friesian cattle. Moreover, an attempt was made to create selection indices including economic traits besides incorporation of its heritability estimates to enable choice of the best selection index to upgrade dairy herd productivity.

MATERIALS AND METHODS

Data used in the present study were collected from the history sheets of Friesian cows maintained at Sakha farm, belonging to Animal Production Research Institute (APRI), Agriculture Research Center (ARC), Egypt. This data were

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used to determine genetic parameters that affect milk production traits of Friesian cattle raised in Egyptian dairy herds. Total 3,977 lactation records, 2,390 animals and dam (2379) of Sakha herd within 29 years were utilized.

Herd management: Animals in the experimental farm were fed concentrate feed mixture in addition to Egyptian clover in winter (November to May) or clover hay during summer. Milking cows were milked twice per day. Heifers were served when reached 18 months and 350 kg. Cows were artificially inseminated. The cows were dried two months before the next calving. Also, veterinary supervision for the prevention of diseases was done.

Statistical analysis: TMY, 305-day MY, LP and DO were considered as examined traits for evaluation of the genetic effects in the current study.

Variance and covariance components (direct additive genetic, permanent environmental, error and phenotypic) and heritability were estimated by restricted maximum likelihood (REML) using the statistical software (VCE 6.0) (Groeneveld *et al.* 2010):

$$y = X_b + Z_a + Z_m + e \quad Cov_{(a,\, m)} = A\, \sigma_{a,m}$$

where Y, observations; b, fixed effects; a, direct additive genetic effects; m, maternal genetic effects and e, residual effect. While X_b, Z_a, and Z_m, are incidence matrices of fixed effects, direct additive genetic effects and maternal genetic effects; A, numerator additive genetic relationship matrix between animals; Cov (a,m), σ_{am} A, where σ_{am} is the covariance between direct and maternal genetic effects; σ^2_a, direct additive genetic variance; σ^2_m, maternal genetic variance, and σ^2_e, variance of residuals. Depending on the model, the log-likelihood function was maximized with concerning direct heritability (h^2_a) and maternal heritability (h^2_m).

Estimation of relative economic value: Derivation of relative economic value were: $REV_1 = 1/\sigma_p$
where σ_p phenotypic standard deviation of trait. It is also estimated by the same method used for research (Safaa 2016).

Also,

$$REV_2 = T / h_i^2,$$

where

$T = h^2$ TMY + $h^2$305d-MY + h^2LP + h^2DO (REV_2).

The index value was calculated as

$$I = b_1P_1 + b_2P_2 + \ldots b_nP_n$$

where I, selection Index (SI); bi, SI weighing factor; pi, phenotypic measure and n, number of traits. In addition

$$b = P{-}1Ga$$

where P–1 is the inverse of the phenotypic (co) variance matrix of the traits in the (SI), G, genetic covariance matrix between traits in the selection goal and the (SI), and a = vector containing the economic values for the goal traits. Also, Standard deviation (SD) of the index (σI) = $\sqrt{b'Pb}$; Standard deviation (SD) of the genotype (σH) = $\sqrt{a'Ga}$ and accuracy (Correlation between the index and genotype) RIH = σI/σH.

Table 1. Estimates of variance components for TMY, 305d-MY, LP and DO of Friesian cows raised in Egypt

Trait	V_a	V_{am}	V_e	V_{ep}
TM	556299.0	83776.0	2323267.0	2786107.0
305	314214.0	42260.0	1174001.0	1381856.0
LP	1199.0	316.0	10482.0	11203.0
DO	54.0	111.0	3513.0	3552.0

V_a, direct additive genetic variance; V_{am}, maternal variance; V_e, residual; V_{ep}, phenotypic variance.

Expected genetic change (EG): The expected genetic change (ΔG) for each trait, after one generation of selection on the index (i = 1) was obtained by Van der Werf and Goddard (2003); $\Delta Gi = (i\ b'Gi)/\sigma_I$; where i, selection differential in SD units, b', transpose of weighting factors as column vector; Gi, i^{th} column of the G matrix and σ_I, standard deviation of the index.

RESULTS AND DISCUSSION

Genetic parameters: Estimates of variance and heritability (h^2) for TMY, 305d-MY, LP and DO are presented in Table 1. The estimates of variance showed increase in TMY and 305d-MY, and decrease in DO. Similar results were obtained by Safaa and Gharib (2017), while it is less than that reported by Hammoud (2013) in Egyptian Friesian.

Heritability (h^2): As shown in Table 1, direct heritability estimates for TMY, 305d-MY, LP and DO range between 0.23 to 0.02 while, maternal heritability ranged between 0.03 to 0.028. These estimates are lower than the range found in the literature (Abd-Elhamid 2018). Differences between study traits in h^2 estimate among the studies for the same traits were due to the number of records used and changing environmental factors. It was observed that h^2_m was lower than the h^2_a. Maybe it is because of small amount of additive maternal genetic effects for the studied traits (Table 1). Conclusively, the additive maternal genetic effects did not show important contributions to the phenotypic variance of milk traits, probably because the environmental influence of the dams on their calves initiates from conception to birth (Safaa and Gharib 2017). In agreement with the current finding, Abd-Elhamid (2018) showed an increase in heritability for TMY, 305d-MY and DO with the increase in lactation number. The direct heritability for DO was 0.02±0.008. The same values were obtained by Belay *et al.* (2016). Heritability estimates were lower for TMY, 305d-MY and LP (0.30, 0.29, and 0.09, respectively) than that reported by Ojango and Pollott (2001). On the contrary, Almaz (2012) found that the h^2 estimates for DO was 0.01±0.03. Although the estimated value of the current study was low, it was within the range values of estimates reported in the literature for dairy cattle under local conditions by Cammack *et al.* (2009).

Genetic and phenotypic correlations between different traits: Genetic and phenotypic correlation coefficients between the different traits are shown in Table 2. The

Table 2. Correlation coefficients between studied traits in Friesian cattle raised in Egypt

Trait	r_a	r_M	r_P
TMY*305	0.932	0.577	0.761
TMY*LP	0.898	0.829	0.687
305*LP	0.824	0.906	0.383
TMY*DO	0.834	0.448	0.146
305*DO	0.885	0.524	0.068
LP*DO	0.767	0.552	0.230

r_a, additive genetic correlation; r_M, maternal genetic correlation and r_P, phenotypic correlation.

additive genetic correlation (r_a) between studied traits was positive and ranged from 0.93 to 0.77. Generally, the additive genetic correlation was higher than the corresponding maternal genetic ones. Whereas those additive genetic correlations between traits studied were higher than the respective maternal genetic correlation (r_m). The genetic correlation between DO and each of TMY, 305d-MY and LP were positive. Also, a strong positive phenotypic correlation was observed between TMY*LP, TMY*DO, 305d-MY*LP, 305d-MY*DO, LP*DO. Hammoud (2013) found that negative (r_a) in Holstein cows (rg= –0.83) between TMY and DO; positive genetic correlation (rg=0.35) between TMY and 305d-MY; between LP and TMY (rg=0.31), 305-dMY (rg=0.29); positive (r_a) DO and 305-dMY (rg=0.89), LP (rg=0.52). Faid-Allah (2015) obtained positive genetic correlation (rg=0.406 and 0.413) between 305/dMY and both of LP and DO; (rg=0.882). Zink *et al.* (2012) found that the estimated genetic correlation between TMY and DO was 0.39. Estimated genetic correlations are important in the process to avoid sensitivity problems in selection indexes (Portes *et al.* 2021).

Selection criteria based on studied milk traits: As shown in Table 3, comparison between all I_1 selection indices when using one phenotypic standard deviation as REV_1 on the basis of relative efficiency of the indices, the following four indices were recommended to maximize the expected gain among traits.

I_1 = 0.0144TMY + 0.503 305d-MY + 1.619 LP + 1.150 DO (RIH=0.490)
I_6 = 0.171 TMY + 0.395 305d-MY (RIH=0.486)
I_5 = 0.138 TMY + 0.328 305d-MY + 0.964 DO (RIH=0.484)
I_2 = 0.151 TMY + 0.598 305d-MY + 2.052 LP (RIH=0.483)

The general index I_1 that included all studied traits had the highest relative efficiency (RE=100%).

It can be observed that the expected genetic changes in the individual traits varied from index to index. In the above mentioned four best indices, as seen from Table 4, the expected change in aggregate genetic worth and heritability values (h^2I) of these indices were also high. The heritability values for indices I_2, I_1, I_9 and I_7 were 0.99, 0.86, 0.83 and 0.75, respectively. The current results showed that the four indices identified as the best (I_1, I_6, I_5 and I_2) can be used effectively by animal breeders for rapid genetic improvement of cows in terms of animal performance. The same trend was observed by Abosaq *et al.* (2016) and Safaa (2016) where the RE value decreased when MY was dropped from general selection indices. So the maximum return can be obtained by using the general index I_1, where improving milk production and minimizing the deterioration trend infertility under economic values are derived by both of the mentioned methods.

Table 3. Selection criteria, weighing factors (b-values) and relative efficiencies of selection (R_{IH})

Index no.	b-values	RIH	RE%
I_1	0.0144 TMY + 0.503 305d/MY + 1.619 LP + 1.150 DO	0.490	100.0
I_2	0.151 TMY + 0.598 305d/MY + 2.052 LP	0.483	98.57
I_3	0.295 305d + 1.360 LP + 0.466 DO	0.473	96.53
I_4	0.291 TMY + 0.461LP + 0.467 DO	0.434	88.57
I_5	0.138 TMY + 0.328 305d/MY + 0.964 DO	0.484	98.78
I_6	0.171 TMY + 0.395 305d/MY	0.486	99.18
I_7	0.356 TMY + 0.499 LP	0.436	88.98
I_8	0.135 TMY + 0.31 DO	0.426	86.94
I_9	0.360 305d/MY + 1.648 LP	0.479	97.76
I_{10}	0.150 305d/MY + 0.325 DO	0.460	93.88
I_{11}	0.077LP + 0.005 DO	0.309	63.06

Economic weight method ($1/\sigma p$) ($I_1 : I_{11}$) to improve TMY, 305, LP and DO in cows. Using one ($1/\sigma p$) as economic relative efficiency (ERV1).

The present results indicated that covariance components for total milk yield and 305-day milk yield were extremely higher than that of days open. Furthermore, the additive

Table 4. Expected genetic change in each trait (ΔG) and the aggregate genetic worth (ΔH) along with the heritability (h^2_I) for indices constructed without restriction in general (I_1 to I_{11})

Index	Δ G				h^2I
No.	TMY (kg)	305d-MY (kg)	LP (day)	DO (day)	
I_1	359.4	279.5	15.30	3.18	0.86
I_2	353.6	271.1	15.06	–	0.99
I_3	–	271.2	15.05	3.09	0.58
I_4	332.4	–	14.07	2.74	0.54
I_5	354.6	271.9	–	3.10	0.36
I_6	352.6	270.1	–	–	0.51
I_7	331.8	–	14.08	–	0.57
I_8	334.3	–	–	2.74	0.10
I_9	–	270.4	15.00	–	0.83
I_{10}	–	270.1	–	3.03	0.11
I_{11}	–	–	11.31	1.28	0.05

maternal genetic effects were limited so that the phenotypic variance of milk traits was not affected by variance maternal. It was suggested that reducing the interval of the trait days open through selection is difficult, but require enhancement of farm managerial conditions. Cow's selection based on selection indices was almost exclusively depended on the direct effects of genetic gain. Therefore, improvement of cow's productivity in the next generation could be possible by using selection indices where total milk yield, 305-day milk yield, lactation period and days open are incorporated leading to more genetic improvement. Conclusively, the four indices identified in the present study were considered as superior in bringing about genetic improvement of Friesian cows in dairy farms for the commercial purpose, the index I_1 (I_1= 0.0144 TMY + 0.503 305d-MY+1.619 LP + 1.150 DO (RIH=0.490)) was obviously the best for genetic improvement. These indexes may aid cow breeders in their selection decisions, increased productivity, genetic progress and profitability of cattle herds.

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