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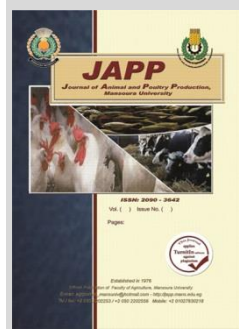
Genetic Evaluation for some Economically Importance Variables in Friesian Cows

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ABSTRACT

A total of 1018 standard lactating of Friesian cows, progeny of 54 sires and 432 dams kept at Sakka Experimental farm, during 2012 to 2017 are used to calculate phenotypic and genetic effects for milk production in tenth months (MP), lactation length (LL) and fat percent (F%). Four selection indexes are calculated using relative economic weights (REW), method 1: standard deviation (REW₁) and method 2: Lamont method (REW₂). The overall means of MP, LL and Fat % are 3879 kg, 301 d and 3.69%, respectively. Month, year of parturition and lactation order had significant (P<0.01) effects on all studied traits, except month of parturition and lactation order effects (P>0.05) on F%. Bulls and cow within bulls had significant (P<0.01) effects on all traits studied. Heritability estimates are 0.32, 0.10 and 0.55 for MP, LL and Fat %, respectively. Genetic correlations among three variables are significant and ranged from 0.21 to 1.00. The basic index (Index₁), which includes the three variables MY, LL and Fat % was the best (had the highest accuracy (R_{IH}) and relative efficiency values (R_{IE} was 0.87 and 0.88 for REW₁ and REW₂, respectively).

Keywords: economic traits - Friesian cows - genetic parameters – selection indexes

INTRODUCTION

The selection index includes pooling information on the individual traits being considered into a single value called an index. The aim of the index is to give the best prediction of the animals overall merit by pooling information in the best possible way. Total score was the best method for selection for several variables (Hazel and Lush, 1942). Also, total score is used when the breeder simultaneously selects for several traits and need information about economic value for each trait, phenotypic and genetic (co)variances among different traits in the index (Becker, 1984).

There are different methods to calculate the economic value: (1) actual economic weight (Khattab and Sultan, 1991; El- Arian *et al.*, 2004; Abosaq *et al.*, 2017), (2) phenotypic standard deviation (Falconer and Mackay, 1996; El-Arian *et al.*, 2004; Abosaq *et al.*, 2017; El-Saway, 2019) and (3) Lamont method (Abosaq *et al.*, 2017; El- Saway, 2019).

El-Arian *et al.* (2004) analysis 2181 lactating Friesian cows, studied five traits (milk yield, fat yield, protein yield, age at first calving and days open). Twenty six of selection indices were calculated using all combinations among five traits. Using two methods of economic weights, one phenotypic standard deviation and actual economic weight, found that there is no different between the two methods.

The present study aimed to investigate some environmental factors affecting MP, LL and Fat %, calculate heritability, genetic and phenotypic correlations among different traits studied and estimates four total

scores using two economic values (standard deviation and Lamont method) to select the best combination of two and three traits on the basis of their accuracy and their relative efficiency, which maximize the genetic progress in a closed herd of Friesian cows in Egypt.

MATERIALS AND MEHTODS

Data records were 1018 lactating Friesian cow daughters of 54 sire and 473 dam covering the period from 2012 to 2017 kept in Sakha Farm, are used in the present experimental. The records without pedigree, breeding dates and cows affected by diseases and aborted cows are excluded. Traits studied are milk production in the first tenth months (MP), lactation length (LL) and fat % (Fat %). The management of that herd, breeding plans and feeding system are explains by Shehab El- Din (2020).

All traits are analysis by using mixed model, the model includes the main effects of month and year of parturition and lactation order and random effects of bulls and cows within bulls (according to SAS, 2000). In addition, genetic parameters are estimated according to program of Boldman *et al.* (1995). The model includes month and year of parturition, lactation order as main effects and animals, permanent environmental and errors as random effects.

Relative economic weight

Prior to computing the complete index, the economic weight (v) were calculated by two methods, (1) standard deviation (REW): the economic weight are calculated depending on the phenotypic standard deviation as described by Falconer and Mackay (1996) and (2) Lamont method (REW₂): according to Lamont (1991) the

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method depending on heritability estimates of the all traits as follows:

$$REW_2 = T / h_i^2$$

$$T = h^2MY + h^2LL + h^2F\%$$

Where REW₂ = relative economic weight;

H_i² = heritability of the i th trait;

T= total heritability of the three traits (MY, LL and F %).

The index value was calculated as

$$I = \sum_{i=1}^n (b_i p_i)$$

I is selection index, b_i is a selection index weighing factor, p_i is a phenotypic measure and n is number of traits. Hazel (1943) proved that maximum r_{IH} is achieved when Pb = Gv, then The vector of optimal index weights (b) was calculated for each of the objectives as b=P⁻¹Ga 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} = σ_I / σ_H . The basic index including the three traits was calculated using the matrix technique as described by Cunningham (1970). In addition, to the complete index, three reduced indices were computed using all combination of traits.

RESULTS AND DISCUSSION

The overall means (unadjusted means) and their standard deviations and coefficients of variability of milk production in tenth months (MP), lactation length (LL) and fat % (Fat %) are showed in Table 1. The present estimate of actual mean of MP in across all lactations of the study (3879 kg) is higher than those stated by Khattab and Sultan (1991)(2254 kg), Khattab and Atil (1999)(3252 kg) ; Shehab El- Din (2020)(2939 kg) , while the present mean of MP are lower than reported by Salem and Hammoud (2016) (8315 kg) and Abosaq *et al.* (2017)(4227 kg) working on commercial herds of Friesian cows in Egypt. The overall unadjusted mean of lactation length (301 d), it was similar to that estimated by Shehab El- Din (2020)(310 d) and it was lower that reported by Khattab and Atil (1999)9 367 d) using Friesian cows. The overall unadjusted mean of Fat % (3.69) which was quite similar to those values reported by Cue *et al.* (1987) and Gabr (2013) ranged from 3.52 to 4.0%.

Table 1. Means, standard deviation (S) and coefficient of variation (CV%) for milk production (MP), lactation length (LL) and fat percent (Fat %) of Friesian cows.

Variables	Means	S	CV%
MP	3879	1757	45.29
LL	301	111	36.73
Fat %	3.69	1.84	68.81
No. records		1018	

The coefficient of variability for MP, LL and Fat % (45.29 %, 36.73 % and 68.81 %, Table 1) are similar to reported by than those reported by Ageeb and Hayes (2000) with Holstein Friesian in Canada, reported that the

average CV% for 305MY and LP were 39% and 37.1%, respectively. While, the present CV % for Fat % are higher than that found by De Jager and Kennedy (1987) with Holstein cows in Canada stated that the average CV % for F% was 10.2%. The higher estimates of coefficient of variability in the present study indicated that there are great differences between cows in an economic traits and it is possible to improve these traits by selection the best cows.

The least squares analysis of variances for data of all available lactations (Table 2) gave evidence that bulls and dams within bulls are significant source of variation (P <0.0001) in the studied traits. Our results indicated the possibility of genetic improvement in milk traits through sire and dam selection. This agrees well with findings of Mostafa *et al.* (1999), Khattab and Sultan (1991), El- Arian *et al.* (2004), Abosaq *et al.* (2017) and Shehab El-Din (2020). Also Mostafa *et al.* (1999) reported that sire variance accounted 5.56%, 5.48% and 1.37% for MP, LL and fat %, respectively.

Least squares analysis of variance in (Table 2) indicated that month of parturition, year of parturition and lactation order are considered the major factors affecting MP, LL and Fat %, expect month of parturition had no significant (P>0.05) effect on Fat %. The same trend obtained by (Kassab *et al.*, 1987; Khattab and Ashmawy, 1988; El- Arian *et al.*, 2004; El- Shalmani, 2011; Abosaq *et al.* 2017; Shehab El- Dain, 2020). The effect of month and year of parturition depended mainly on the conditions of individual animals, feeding, management practices and year to year climatic changes. In addition, the effect of lactation order may be due to increased body size of animals and increased udder secretion tissue. This lead to conclude that adjusting of lactating records for these factors are very important for estimating genetic parameters which are used in constructed selection indexes.

Table 2. F – Values¹ for factors affecting milk production (MP), lactation length (LL) and fat percent (Fat %) of Friesian cows.

S.O.V.	d.f.	F-Values		
		MP	LL	Fat %
Bulls	53	5.11**	2.33**	1.39**
Cows : Bulls	432	2.38**	1.87**	2.04**
Month of parturition	11	3.14**	4.04**	0.46ns
Year of parturition	5	18.85**	17.12**	7.75**
Lactation order	6	6.16**	1.46**	0.83ns
Error M.S.	510	1339110	7230**	2.26

1: ns = not significant p<0.05, ** P,0.01

Estimate of direct heritability (h²) for MP, LL and Fat % are 0.32 ± 0.02, 0.10±0.03 and 0.55 ±0.02, respectively (Table 3). The medium values of h² for MP and Fat % would indicate moderate contribution of additive genetic variance, while, low h² estimates for LL concluded that improvement of LL could be through improving environmental condition. On other words, low estimate of h² for LL indicated that the influence of herd management and other environmental factors were greater than the genetic background. Our results are agree with Khattab and Atil (1999), Mostafa *et al.* (1999), Abosaq *et al.* (2017) and Shehab El- Din (2020) found that h² estimates for MP are 0.30, 0.33, 0.33 and 0.35, respectively. Also, Khattab and Atil (1999), Ghonem (2002) and Abosaq *et al.* (2017) working on Friesian cows

in Egypt, stated that h^2 for LL are 0.10, 0.09, 0.09 and 0.07, respectively. The present estimate of h^2 for Fat % are lower than those reported by Mostafa *et al.* (1999)(0.799) and Osman *et al.* (2013)(0.090).

Table 3. Heritability estimates (h^2) on diagonal, genetic correlation (r_g) below and phenotypic correlation (r_p) above diagonal for milk production (MP), lactation length (LL) and fat percent (Fat %) of Friesian cows.

Variables	MP	LL	Fat %
MP	0.32±0.02	0.98	0.20
LL	1.00	0.10±0.03	0.67
F%	0.10	0.21	0.55±0.02

In respect of estimates of genetic and phenotypic correlations among the studied traits are present in (Table 3) all correlations are positive ranged between 0.10 and 1.00 for (r_g) and from 0.20 to 0.98 for (r_p). Our results agree with Khattab and Sultan (1991), Mostafa *et al.* (1999), El- Shalmani (2011), Abosaq *et al.* (2017) and Sheab El- Din (2020) and ranged from 0.60 to 1.0. Also, Carabano *et al.* (1990), found that r_g between milk yield and F% was 0.99, while the present estimate of genetic correlation between 305MY and LP were higher than (0.209) found by Osman *et al.*(2013). Negative genetic correlation (-0.285) between milk yield and F% was reported by Cue *et al.* (1987). Very low magnitude of phenotypic correlation (0.025) between MP and LL was reported by Shehab El-Din (2020). On the other hand, negative phenotypic correlations (-0.33 and -0.388) between milk yield and F% were reported (De Jager *et al.*, 1987 and Van Der Werf *et al.*,1989, respectively). Our results indicated that selection cows with high lactating milk production will be associated with genetic progress in both LL and Fat %.

Tables 4 and 5 show the ranking of selection indices on the basis of their accuracy (R_{IH}), weighting coefficients (bs), relative efficiency (RE) and expected genetic change (DG) per generation of various traits studied and using two phenotypic standard deviation and Lamont methods.

Comparison between all the four selection indices when using phenotypic standard deviation as REV_1 and Lamont method as REW_2 , showed that, the maximum genetic progress per generation as estimated by using phenotypic standard deviation ranged from 37.23 to 95 kg for MP, from 5.1 to 7.5 d for LL and from 0.35 to 0.56 % for Fat %, while it was ranged from 41.50 to 95 kg for MP, from 4.39 to 7.40 d for LL and from 0.33 to 0.50 % for Fat % as estimated by Lamont method. Similar results are obtained by Abosaq *et al.* (2017) stated that genetic gain per generation ranged from 389.5 to 462 kg for MP and from 0.13 to 13.6 d for LL as estimated by using one phenotypic standard deviation and ranged from 389.5 to 464.2 kg for MP and from 8.1 to 13.6 d for LL by using Lemont method.

The basic index (I_1), which includes MP, LL and Fat % was the best ($R_{IH} = 0.87$ and 0.88) as estimated by phenotypic standard deviation and Lemont method, respectively (Tables 4 and 5). Therefore, high similar results are obtained by the two methods.

Index (I_4) showed a reduced accuracy (0.51, Tables 4 & 5), while including MP with Fat % (I_3) will increase the accuracy. Therefore, including milk production and /or fat % in the index will increase the accuracy. El- Arian *et al.* (2004) and Gabr (2013) working on another sets of that herd arrived at the same results.

Table 4. Selection criteria , weighting factor (b-values) , expected genetic gain (DG), accuracy of the index (R_{IH}) and relative efficiencies of selection (RE) by using phenotypic standard deviation method to improve MP, LL and Fat %.

Selection Index	Variables						R_{IH}	RE
	MP, kg		LL, d		Fat %			
	b	DG	b	DG	b	DG		
I_1	-14.63	95.0	-0.25	7.5	7.44	0.56	0.87	100
I_2	0.27	37.2			1.03	0.35	0.72	0.86
I_3	-11.69	80.1	-0.34	6.7			0.66	0.76
I_4			0.29	5.1	0.47	0.35	0.51	0.59

Table 5. Selection criteria , weighting factor (b-values) , expected genetic gain (DG), accuracy of the index (R_{IH}) and relative efficiencies of selection (RE) by using Lamont method to improve MP, LL and Fat %.

Selection Index	Variables						R_{IH}	RE
	MP, kg		LL, d		Fat %			
	b	DG	b	DG	b	DG		
I_1	-9.66	95.0	-0.06	7.4	5.79	0.50	0.88	100
I_2	1.59	41.5			4.03	0.38	0.72	0.85
I_3	-7.86	80.9	-0.70	6.9			0.64	0.73
I_4			0.52	4.4	0.67	0.33	0.51	0.58

The present results indicated quite high similarity of genetic gains under the two different groups of economic weights. It might be reliable to $aREV_1$ and REW_2 due to its simplicity and high applicability. In addition, relative efficiency and accuracy of index indicated the same results.

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التقييم الوراثي لبعض الصفات الاقتصادية الهامة في أبقار الفريزيان

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تم استخدام 1018 سجل حلب لأبقار الفريزيان والتي تمثل بنات لـ 54 أب و 432 أم والمرباه في المحطة البحثية بسخا - معهد بحوث الإنتاج الحيواني - وزارة الزراعة - مصر، خلال الفترة من عامي 2012 وحتى 2017، وذلك لتقدير المقاييس المظهرية والوراثية لصفات كمية اللبن في 10 أشهر (MY) وطول موسم الحليب (LL) و نسبة الدهن في اللبن (F%). تم بناء أربعة أدلة إنتخابية باستخدام طريقتين لتقدير القيمة الاقتصادية النسبية حيث تتمثل الطريقة الأولى في استخدام مقدار الوحدة الواحدة من الخطأ القياسي (REV₁)، بينما تتمثل الطريقة الثانية في طريقة ليمونت (REV₂). كانت قيم المتوسطات لصفات MY، LL و F% هي 3879 كجم، 301 يوم و 3.69% على التوالي. كان لشهر وسنة الولادة وكذلك عدد مواسم الحليب تأثير معنوي (P<0.01) على جميع الصفات بينما لم يظهر شهر الولادة وعدد مواسم الحليب أى تأثير معنوي (P>0.05) على نسبة الدهن. كان لكل من الأب والبقرة داخل الأب تأثير معنوي (P<0.01) على جميع صفات اللبن التي تم دراستها. كانت قيم الماكافى الوراثي 0.32، 0.10 و 0.55 لصفات MY، LL و F% على التوالي. كانت قيم معامل الارتباط الوراثي بين صفات اللبن موجبة وتتراوح بين 0.21 إلى 1.00. تم بناء أربعة أدلة إنتخابية لكل طريقة من طرق حساب القيمة الاقتصادية النسبية. كان أفضل دليل إنتخابي هو الذي يحتوى على الثلاث صفات مجتمعة (I₁) حيث كانت قيمة الارتباط بين الدليل والقيمة الوراثية المجمعة هي 0.87 في الطريقة الأولى (REV₁) و 0.88 في الطريقة الثانية (REV₂)، على التوالي.