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SELECTION INDICES FOR IMPROVING SOME BEEF CHARACTERISTICS IN FRIESIAN CATTLE IN EGYPT

Ghoneim, E. M.; M. A. El-Saied; F. H. Abdou and E. Faid-Allah
Dept. of Animal Production, Fac. of Agric., Minufiya University, Egypt

ABSTRACT

The main purpose of this paper is to construct different selection indices (general index, reduced indices, and sub-indices) to improve some beef characteristics in Frisian bull calves by using collected data during 10 years (1995-2004) for body weights at 12 (w12), 15 (w15), 18 (w18) months of age and four years (2001-2004) for slaughter weight (SLW) at the experimental farm of Faculty of Agriculture, Minufiya University. The secondary objective is to evaluate and predict genetic parameter estimates of body weights at 12, 15, 18 months of age and SLW. Overall means for the previous body weights were 291.97, 358.74, 418, 17 and 540.35 kg respectively. Heritability estimates for the previous traits were 0.59, 0.74, 0.71 and 0.46, respectively. All estimates of genetic (r_G) and phenotypic (r_P) correlations among different body weights were positive. Fifteen selection indices were constructed, indices (I_2), (I_5) and (I_9) gave high (R_{IH}) and (RE) values compare with general index (I_1). Therefore, it could be suggested that to use (I_2), (I_5) and (I_9) to improve beef traits in Friesian bull calves under the large scale.

Keywords: Body weight, Genetic parameters, Selection indices

INTRODUCTION

Several investigators have shown that live weight preceding slaughter is the most important variable for predicting carcass weight. Henningsson et al. (1986) reported that live weight was the most important explanatory factor for weight of carcass and muscle for beef bull. Beef production traits used in genetic evaluation in dairy sires varies widely between countries. Lately some European countries have started to use the routinely collected data from slaughter houses on progeny carcass in the genetic evaluation of dairy bulls (Liinamo and Van Arendonk 1999). Growth in dairy cattle has not been studied extensively, particularly the genetic component of growth (Coffey *et al*., 2006).

In Egypt beef production from dairy cattle is obtained mainly from bull calves that passed the veal stage in addition to young and old cows or bulls culled from the breeding stocks of dairy cattle herds after being fattened (Farrag et al., 2001). Friesian cattle are the most reputed dairy cattle in Egypt and they are potential dual-purpose animals (Abdel-Glil and Elbanna, 2001).

Selection for many traits simultaneously saves time and effort. Selection index was developed by Hazel and Lush (1942) and Hazel (1943) as a method of selection for more than one trait at the same time. This method helps breeders to rank and evaluate the individuals on their total breeding values by condensing and summarizing the breeding values of the different economic traits in one total score for each one.

Multiple trait selection requires the definition of a breeding goal including individual traits weighted according to their relative contribution to efficiency of production as expressed by economic values (Hazel, 1943).The number of traits used to construct a selection index depends mainly on the ultimate breeder's goal.

The main objective of this study is to improve beef characteristics by using different selection indices (i.e. General, reduced, and sub-indices).

MATERIALS AND METHODS

Data used for this study obtained through the period of 1995 to 2004 for body weights at 12, 15, 18 months of age and for four years (2001-2004) for slaughter weight (SLW) around 24 months of age in Friesian bull calves. Data collected from Experimental and Researches Unit of Animal Production in Tokh Tanbisha, in the middle Nile Delta, Egypt, which belong to Faculty of Agriculture, Minufiya University. Calves were produced mainly by artificial insemination (imported frozen semen of Friesian sires) rather than by natural service mating. Data consisted of 1342, 1291, 1066 and 538 records of body weights at 12, 15, 18 months of age and SLW respectively of Friesian bull calves.

After weaning, male calves were separated from females and were housed in open corrals. Calves were vaccinated against brucellosis and other contagious diseases. The feeding program was essentially that applied in the experimental farm under consideration. Feeding allowances were calculated as described by NRC (1988) for Friesian calves. Calves were housed in adjacent pens in a fattening calf barn and were bedded on straw, where and all calves had free access to water.

Data were analyzed to evaluate traits included body weights at 12, 15, 18 months of age and SLW during the fattening period. The genetic parameters were estimated by derivative free REML with a simplex algorithm using the Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) programs of Boldman et al. (1995).

The animal model in matrix notation was:

$$Y = Xb + Za + e$$

Where: Y= the vector of observations (body weights at 12, 15, 18, Slw)

b= the vector of fixed effect (Year)

a= the vector of random additive genetic direct effects;

X and Z=Known incidence matrices relating observations to the respective

e= fixed and random effects with Z augmented with columns of zeros for animals without records; and the vector of residual effects.

Selection Index Program (Wagenaar, et al., 1995) and Matlab program (Matlab, 2002) were used to set up and construct the selection indices. The four traits studied were used in different combinations to construct fifteen selection indices.

$$I = b_1P_1 + b_2P_2 + \cdots b_nP_n = \sum_{i=1}^{n} biPi$$

Where: I = selection index, bi = index weights for each trait in the index

Pi= phenotypic measurement for each trait in the index.

The general index **(I_g)** was obtained in terms of heritability, phenotypic and genetic correlations among the studied traits by solving the following equations given in matrix expression according to Cunningham (1969):

$$Pb = GV \qquad \text{to give} \qquad b = P^{-1}\,GV$$

Where: P = Phenotypic variances and covariances matrix.
G = Genetic variances and covariances matrix.
V = Economic weights column vector.
b = Weighting factors column vector, which is going to be solved.

Furthermore, according to Cunningham (1969) the other different properties of the selection index were calculated as following:

The standard deviation of the index = $\sigma I = \sqrt{b'Pb}$

The standard deviation of aggregate genotype = $\sigma T = \sqrt{V'GV}$

The correlation between the index and the aggregate genotype = $R_{IH} = \sigma I/\sigma T$

The expected genetic change (ΔG) for each trait, after one generation of selection on the index (i = 1) was obtained by solving either of the following equations (Van der Werf, 2003):

$$\Delta G_i = (i\ b'\ G_i)/\square I.$$

Where: i = Selection differential in standard deviation units.
σI = Standard deviation of the index.
Gi = the i^{th} column of the G matrix.

The reduce selection index can be developed by omitting one or more traits from the original index. In relation to the original index the efficiency of the new index, the reduced index, is expected to decrease depending on the value of the omitted trait in the original index. The breeder can decide whether such traits can be included or not in selection index to save time, cost and effort depending on the relative importance of the omitted trait in the original index and the value of including such that trait in the index.

The relative efficiency or enhancing of each trait in the general index can be calculated by dropping this trait from the general index. The efficiency of the new reduced index can be compared with that of the general index by using the following formula:

$$\Delta_{TI}/\Delta_T = \sqrt{(\ B'SB/\ b'Pb)}$$

Where: B'SB is the reduced index variance after dropping some sources of information with new weighting factors (B) produced from reduced matrix of phenotypic covariances (S). Omitting one variant means that the reduced index has no phenotypic information about this trait and the variance of the aggregate genotype is the same as for the general index (v`Gv) before omitting due to including of all variants in the aggregate genotype.

The relative economic values (**V**) of the traits under study were calculated by estimating the expected change in the slaughter weight (SLW= 1.00) per kg as a marketing weight that determine the profit depends on the change one unit per kg in the trait (w12= 0.2010, w15=0.3160 and w18= 0.5080) by using the regression method.

RESULTS AND DISCUSSIONS

Table 1 show the overall means, standard deviation and coefficient of variation (C.V) of W12, W15, W18 and SLW. The yearling body weight obtained for Friesian bull calves in the present study was 292 kg. However, yearling body weight in this study is much lower than the estimates reported by Nigm et al. (1984) for Friesian (315 kg) and much lower than the mean (376 kg) reported by Nigm et al. (1995) for Charolais X Friesian in Egypt. The same trend can be seen when body weight at 15 and 18 months of age were examined. The differences getting larger between the present estimates and corresponding estimates reviewed for the same breed or for Holstein X Friesian in temperate areas. These differences could be due to the straight dairy breeding of Holstein and the feeding practices followed for fattening bulls in those commercial dairy farms. The overall means of body weights at slaughter of 538 bulls was 540.35 kg which seems to be higher value than of Arnold et al. (1991) who reported from Hereford steers was 492.3 ± 27.3.

Table 1: The overall means, standard deviations and C.V % for body weights at 12, 15, 18 of age and SLW for Friesian bull calves.

Trait	№ of animal	Mean (kg)	±	S.D (kg)	C.V (%)
w12	1342	291.967	±	34.784	11.91
w15	1291	358.739	±	43.119	12.02
w18	1066	418.171	±	51.062	12.21
SLW	538	540.348	±	70.393	13.03

Estimates of heritability (h^2) as well as genetic (r_G) and phenotypic (r_P) correlations among different body weight traits are presented in table (2). Heritability estimates for body weights at 12 and 15 months of age were 0.59 and 0.74, respectively. The heritability estimates, which reported in literature for both traits were similar to those obtained in the present study when compared with that reported by Al-Amin (1979) 0.72 and 0.83 for heritability estimates of body weight at the similar ages, respectively. Meanwhile, Abdel-Moez (1996) reported 0.30 and 0.31, respectively in Holstein.

In the present study, an estimate of heritability for body weight at 18 months is 0.71. Preston and Willis (1974) cited estimates of heritability ranged from 0.12 to 1.00 for body weight at 18 months for various breeds, while the value of heritability was 0.70 for body weight at 18 months as shown by Abdel-Moez, (1996).

Table 2: Heritabilities, genetic and phenotypic correlations for body weights at 12, 15, 18 of age and SLW for Friesian bull calves.

Trait	w12	w15	w18	SLW
W12	**0.59**	0.86**	0.83**	0.104*
W15	0.97	**0.74**	0.88**	0.205**
W18	0.95	0.99	**0.71**	0.388**
SLW	0.67	0.76	0.80	**0.46**

Heritabilities are on the diagonal, Genetic Correlations (r_g) below; Phenotypic Correlations (r_p) are above the diagonal.

In the present study, an estimate of heritability for slaughter weight was 0.46. This is in agreement with that reported by Veseth et al. (1993) (0.42 ± 0.18), Reynolds, et al. (1991) (0.49) from Hereford bull calves, Northcutt and Wilson (1993) from Angus bull calves (0.48 ± 0.10). These moderate to high heritability estimates in this study indicate the possibility of improving growth performance of Friesian calves through effective selection program.

Table (2) also presents phenotypic (above diagonal) and genetic (below diagonal) correlation coefficients among body weights of Friesian bull calves**.**

All phenotypic correlations among body weights were positive and significant. The highest coefficient was found among body weights at ages of 15 and 18, (0.88, table 2). Genetic correlations among body weight traits were positive and near to or equal one. These results are of practical significance in managing beef production projects

General (I_g) and Reduced (RD) selection indices are shown in table (3). The general index (I_g) is considered as the main index due to its properties, whereas this index is assumed to contain all traits under selection program without any reducing or restrictions. Furthermore, the general index is used as a standard efficient index to determine the relative efficiencies of the other types of selection indices.

Fifteen selection indices were constructed (Table 3). The original selection index (I_1) which included the four traits (body weights at 12, 15, 18 of age and SLW) was suggested to be used for improving the aggregate genotype of four traits, while the reduced indices (I_2 to I_5) included three traits, (I_6 to I_9) included two traits, while the sub-indices (I_{12} to I_{15}) included only one traits. The expected genetic change per generation (EG) in each trait (body weights at 12, 15, 18 of age and SLW) assuming the selection intensity of 1.00 is given in Table 3. The expected genetic change per generation (EG) ranged between 18.921 to 22.395 kg for w12, 34.332 to 35.723 kg for w15, 40.129 to 42.419 kg for w18 and 34.834 to 40.884 kg for SLW. The maximum genetic improvement in body weights were achieved by using the selection indices (I_1, I_2, I_5 and I_9)

The comparisons of the various selection indices indicate that the selection (I_2) which incorporated w12, w15 and w18 was the most efficient (RE=100).

The least accuracy (R_{IH} =0.68 (I_{15}), 0.76 (I_8), and 0.77 (I_{12}) would result from any index ignoring W15, W18 or both of them. On the other hand, including w15 and w18 in (I_2), (I_5) and (I_9) increased the accuracy (R_{IH}) being 0.87, 0.86, and 0.87 respectively, and came to the efficiency of 100.16, 99.17, and 100 respectively. relatively from the original index (I_1). Shemeis *et al.* (2006) working on Holstein cattle concluded that the selection indices which incorporated yearling body weight were high in R_{IH} (0.53 to 0.54).

Furthermore, the selection indices (I_2), (I_5) and (I_9) gave high (R_{IH}) and (RE) values compared with general index (I_1). Therefore, it could be suggested that to use (I_2), (I_5) and (I_9) to improve beef traits in Friesian bull calves under the large scale.

The expected genetic gain after one generation through the general index (I_1) will be (1) increase in W12 by 21.556 kg, (2) increase in W15 by 35.284 kg, (3) increase in W18 by 42.283 kg (4) increase in SLW by 40.474 kg. This index is very simple and easy to construct, therefore, its use is recommended for selection of beef characteristics in Friesian bull calves

Table (3): Selection indices for W12, W15, W18 and SLW for Friesian bull calves.

Selection index	Trait									
	W12		W15		W18		SLW		R_{IH}	RE
	b1	EG	b2	EG	b3	EG	b4	EG		
I_1	-0.3354	21.556	1.1362	35.284	0.2612	42.282	0.4075	40.474	0.87	100
I_2	-0.1190	22.314	0.5224	35.723	0.2926	42.419			0.87	١٠٠,٠٠
I_3	-0.2040	21.045	0.9212	34.519			0.3715	40.884	0.85	٩٧,٧٠
I_4	0.1307	20.533			0.7218	40.425	0.3591	39.329	0.83	٩٥,٤٠
I_5			0.9342	35.216	0.1607	42.098	0.4172	40.365	0.86	٩٨,٨٥
I_6	0.0346	22.395	0.3044	35.177					0.86	٩٨,٨٥
I_7	0.0884	21.629			0.3907	41.040			0.84	٩٦,٥٥
I_8	0.5978	18.921					0.4000	38.329	0.76	٨٧,٣٦
I_9			0.4039	35.691	0.2464	42.288			0.87	١٠٠,٠٠
I_{10}			0.7027	34.332			0.3653	40.812	0.83	٩٥,٤٠
I_{11}					0.7230	40.129	0.3461	39.487	0.82	٩٤,٢٥
I_{12}	0.1193	20.639							0.77	٨٨,٥١
I_{13}			0.2325	35.192					0.86	٩٨,٨٥
I_{14}					0.3614	41.041			0.84	٩٦,٥٥
I_{15}							0.4559	34.834	0.68	٧٨,١٦
V	0.201		0.316		0.508		1.00			

Index weights for each trait in the index (bi), Expected genetic change per generation in each trait (EG), correlation of index with aggregate genotype (R_{IH}) and the efficiency (RE) of different indices relative to original index (I_1), Economic weights column vector (V).

Conclusion

Results show that it is possible to improve beef traits of Friesian cattle during fattening period in Egypt. The beef traits are high heritable and the genetic correlations of body weights at 12, 15, 18, and SLW are also generally favorable. Fifteen selection indices were constructed, indices (I_2), (I_5) and (I_9) gave high (R_{IH}) and (RE) values compare with general index (I_1). Therefore, it could be suggested that to use (I_2), (I_5) and (I_9) to improve beef traits in Friesian bull calves under the large scale.

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تحسين بعض صفات اللحم فى ماشية الفريزيان فى مصر باستخدام أدلة انتخابية مختلفة

الهام محمدغنيم ، مختار عبد اللطيف السيد ، فاروق حسن عبده و اسلام فيض الله
قسم الانتاج الحيوانى -كلية الزراعة- جامعة المنوفية

الهدف الرئيسى من هذا البحث هو بناء ادلة انتخابية مختلفة (دليل عام – ادله مختزله من الدليل العام) و استخدامها فى تحسين صفات اللحم فى ذكور الفريزيان و ذلك بالاستعانه ببيانات مجمعه على مدار ١٠ سنوات من سنه ١٩٩٥ الى ٢٠٠٤ لصفات وزن الجسم عندعمر ١٢و١٥و١٨ شهر و لمدة ٤ سنوات من ٢٠٠١ الى ٢٠٠٤ لصفة وزن الجسم عند الذبح و ذلك بالمزرعة البحثية لكلية الزراعة بجامعة المنوفية. الهدف الاخر كان للتقييم و التنبؤ بالمعايير الوراثية لصفات وزن الجسم عندعمر ١٢و١٥و١٨ شهر و لصفة وزن الجسم عند الذبح. متوسطات اوزان الجسم السابقة كانت ٢٩١,٩٧ و ٣٥٨,٧٤ و ٤١٨,١٧ و ٥٤٠,٣٥ كجم على التوالى. و قيم المكافىء الوراثى لنفس الاوزان كانت ٠,٥٩ و ٠,٧٤ و ٠,٧١ و ٠,٤٦ على التوالى. وقد وجد ان كل الارتباطات الوراثية و المظهرية بين هذه الاوزان كانت موجبة و معنوية. وقد تم بناء خمسة عشر دليل انتخابى منها ادله(I_2)و (I_5) و (I_9) و التى اعطت اعلى قيمه لدقة الدليل (R_{IH}) و الكفاءة النسبية للدليل با لنسبة للدليل العام (RE) وذلك مقارنة بالدليل العام (I_1) و بالتالى فاننا نقترح استخدام هذه الالة الانتخابية الثلاث لتحسين صفات اللحم فى ذكور الفريزيان على نطاق واسع.