

RESPONSE TO SELECTION FOR MILK YIELD TRAITS IN EGYPTIAN BUFFALO

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SUMMARY

The aim of the present study was to estimate the genetic response to improve milk yield traits (milk, fat and protein) in Egyptian buffalo. Seven selection indices were constructed from data of 699 lactations of 478 buffalo daughter of 82 sires and 383 dams. The first index (I1) which included all milk yield traits was assumed to be the base of comparison while the rest indices are defined as reduced ones. Genetic parameters were estimated by a multiple-trait repeatability animal model using restricted maximum likelihood (REML) procedure. The model included herd year-season of calving and age nested within lactation for the first three lactations as fixed effects and additive genetic and permanent environment as random effects. Results indicated that selection to improve milk yield traits might be achieved through multiple-trait selection. Therefore, a selection index including MY (I1, I2, I3 or I5) was recommended as the best criterion from both the economic and the practical points of view to improve milk yield traits of Egyptian buffaloes. Using I5 which includes only milk yield, as a criterion of selection results in an increase of the expected genetic response for MY, FY and PY. For local breeders, I5 could be considered as the best criterion from the practical point of view and easy to apply.

Keywords: *Genetic parameters, multiple-trait repeatability animal model, multiple-trait selection*

INTRODUCTION

In Egypt, buffaloes are considered as the main dairy animal. They contribute more than 50% of national milk production (FAOSTAT, 2007). There has not been national selection program for buffaloes; therefore a high genetic variability among animals would be expected. Selection for milk yield traits (milk, fat and protein) would result in improving milk quality compared with single-trait selection for milk yield (Van Vleck, 1978).

Hazel and Lush (1943) and Hazel *et al.* (1994) concluded that when improvement is desired for several traits, multiple-trait index selection which gives proper weight to each is more effective than selection for single-trait at a time or several traits with an independent culling level for each trait. Investigating improvement possibility using selection indices is an important step in the evolution of the dairy industry in developing countries (Wilmink, 1988 and Harris, 1998). The main aim of the present study was to estimate selection responses for milk yield traits (milk, fat, and protein),

using multiple-trait index selection in breeding program to improve milk production of Egyptian buffaloes.

MATERIALS AND METHODS

Animals and Management:

Buffalo cows were kept under semi-open sheds. Amounts of rations given to the animals were determined according to animal body weight and level of milk production. The ration was offered twice daily and clean water was available all the time. Buffalo cows were naturally mated in a group-mating system. Rectal palpation was performed to check pregnancy. As a rule, buffalo heifers were to be first mated at 24 mo of age or 330 kg of weight, and milking buffalo cows were to be dried 2 mo before their expected calving dates and allowed to be re-mated 2 mo postpartum.

Data:

Data used in this study were recorded over the period from 1999 through 2008 from four experimental herds belonging to the Animal Production Research Institute (APRI), Ministry of Agriculture and Land Reclamation.

A total of 699 lactation records of milk yield traits for 478 buffalo cows, daughter of 82 sires and 383 dams were used in the study. Data were classified according to the month of calving into two seasons: hot (April through September) and mild for the rest of months. All known relationships among individuals were considered in the animal model.

Statistical analysis:

Genetic parameters were estimated by the Restricted Maximum Likelihood (REML) procedure, using the software VCE 4.0 (Groeneveld and García Cortés, 1998), fitting a multiple-trait repeatability animal model and incorporating all available pedigree information. The following multiple-trait animal model was employed to analyze milk yield traits.

$$Y_{ijklmn} = \mu + A_i + Pe_j + HYS_k + P_l + AWP_m + e_{ijklmn}$$

where: Y_{ijklmn} is the record of (305-d milk yield, 305-d fat yield, 305-d protein yield); μ is the overall mean; A_i is the additive genetic random effect of buffalo assumed to be NID (0, σ_a^2); Pe_j is the permanent environment random effect on the buffalo assumed to be NID (0, σ_{pe}^2); HYS_k is the fixed effect of herd-year season of calving; P_l is the fixed effect of parity number; AWP_m is the fixed effect of age at calving within parity as a coverable and e_{ijklmn} is the residual random error term assumed to be NID (0, σ_e^2). Phenotypic parameters were estimated by the GLM procedure of SAS (SAS, 2000).

Traits:

The present study included milk yield traits in kilogram: 305-d milk yield (MY), 305-d fat (FY) and 305-d protein (PY) yields for the first three lactations.

Index equations:

The breeding objective is a particular combination of weighting factors (economic weights/values) and genetic information (EBV's) of all the traits to be improved (Falconer and Mackay, 1996 and Bourdon, 1997).

Hazel (1943) permits a selection index toward a breeding objective:

$$\mathbf{I} = \sum_i^n b_i x_{ij} \quad i=1, 2 \text{ and/or } 3$$

Where; \mathbf{I} = selection index, \mathbf{b} = weighting factor, and \mathbf{X}_i = a phenotypic measure. The optimum set of selection index coefficients are those which maximises the correlation (r_{HI}) between the selection index and the aggregate genotype according to breeding objectives. This can be achieved when $\mathbf{Pb} = \mathbf{Gv}$, Selection index weights (partial regression coefficients) are then calculated as:

$\mathbf{b} = \mathbf{P}^{-1}\mathbf{Gv}$, Where; \mathbf{P}^{-1} : is an inverse of "n x n" phenotypic (co)variances matrix of correlated indicator traits between sources of information; \mathbf{G} : is a "n x m" genetic (co)variances matrix for m traits (MY, FY and PY) and n correlated indicator traits and incorporates the additive genetic relationships between sources of information and \mathbf{v} : is a "nx1" vector of weights for MY, FY and PY which were assumed to be 1: 14: 20. An equal change in standard deviation units was considered for each trait. The weights assigned were therefore the reciprocals of the phenotypic standard deviations (Falconer, 1989). Several authors have concluded that the efficiency of a selection index is not very sensitive to changes in the weights (Smith, 1983).

The index (σ_I^2) and the aggregate genotype (σ_H^2) variances were obtained as follows: $\sigma_I^2 = \mathbf{b}'\mathbf{Pb}$ and $\sigma_H^2 = \mathbf{v}'\mathbf{Cv}$, Where, \mathbf{P} is a phenotypic (co)variances matrix and \mathbf{b}' is a transpose of \mathbf{b} vector, \mathbf{v}' is a transpose of \mathbf{v} vector and \mathbf{C} is a matrix of genetic (co)variances of traits in total aggregate genotypic.

The correlation of a particular index with total aggregate genotypic value (r_{HI}) was estimated as: $r_{HI} = \mathbf{b}'\mathbf{Gv} / \sqrt{\mathbf{v}'\mathbf{Cv}}$.

The expected genetic response in each trait (ΔG) is constructed as the standard deviation of the index (σ_I) and selection intensity (i), assuming, for comparison only, it was equal to one and regression of the trait on the index (b_{YI}), as: $\Delta G = (\sigma_I) (i) (b_{YI})$ where; σ_I : is the standard deviation of the index; i : is the selection intensity and b_{YI} : is the regression of the trait on the index.

Relative selection efficiency of the index (RSE) was expressed as follows: $RSE = r_{HI}^* / r_{HI}$ where r_{HI} is the correlation between the total aggregate genotypic value and the index which included all studied traits, r_{HI}^* is the correlation of index I_i which included one or more trait with the aggregate genotypic value.

Seven selection indices were constructed (including all combinations of studied traits) using Inverse Matrix Linear procedure (IML) (SAS, 2000) with alternative selection criteria. The first index (I1) which included all milk yield traits was assumed to be the base of comparison while the rest indices were defined as reduced ones.

RESULTS AND DISCUSSION

Estimates of means, phenotypic standard deviation (σ_p) and heritability for MY, FY and PY (kg) are presented in Table 1. The means of yields for (milk, fat and protein) are smaller than the corresponding estimates reviewed by Mourad *et al.* (1990 and 1991), Rosati and Van Vleck (2002) and Ahmad *et al.* (2009) working on different populations of buffalo. The wide range of phenotypic estimates of all traits may be due to no selection was performed for this population.

Table 1. Means, phenotypic standard deviations (σ_p), heritability (bold on the diagonal), phenotypic correlation coefficients (above the diagonal) and genetic correlations (below the diagonal) of milk yield traits.

Trait*(kg)	Mean	σ_p	MY	FY	PY
MY	1402	606	0.18(0.04)	0.94	0.89
FY	92	43	0.98	0.16(0.03)	0.85
PY	59	30	0.99	0.99	0.13(0.01)

*MY: 305-d milk yield; FY: 305-d fat yield; PY: 305-d protein yield; standard errors of heritability estimates are in parenthesis and standard errors of genetic correlation ranged from 0.16 to 0.40 for studied traits.

Heritability estimates for MY, FY and PY were 0.18, 0.16 and 0.13, respectively (Table 1). The corresponding estimates by Rosati and Van Vleck (2002) were 0.14, 0.11 and 0.14, respectively for Italian buffalo.

In general, estimates of heritability obtained in the current study are low despite the fact that the Egyptian buffalo has not gone through intense genetic selection that could result in eroding the additive genetic variance. Table 1 presents the phenotypic and genetic correlations between milk yield traits considered in construction of selection indexes. The estimates obtained for genetic correlations were positive and higher than their corresponding phenotypic correlations. This means that a genetic program to select any of them would result in a favorable genetic response to improve the others. Similar estimates for genetic correlations were previously reported by Rosati and Van Vleck (2002) for Italian buffalo and Duarte (2002) for buffalo in Brazil.

Selection indices:

Index coefficients. Index coefficients for MY, FY, PY, standard deviations of indexes and accuracy of selection estimated from each index and relative selection efficiency are presented in Table 2. The results are in agreement with reported by Seno *et al.* (2006) for buffalo and Ashmawy and Khalil (1990) for dairy cattle.

According to the correlation between the indices and total aggregate genotypic value (r_{HI}), the most accurate and highest index standard deviation were obtained when selection was based on an index including MY from I1, I2, I3 and I5 (Table 2). The least accuracy ($r_{HI} = 0.36$ to 0.40) would result from ignoring MY from I4, I6 and I7. de Jager and Kennedy (1987) indicated that including protein in the index

increased the accuracy of sire breeding value. When two traits are included in a selection index, the expected genetic response in yields will be reduced as compared to including the three traits (Gjedrem, 1972).

Expected genetic response. The expected genetic response (ΔG) through the use of selection indexes assuming intensity of selection to equal the one are given in Table 3. All indices provided an increase in yields of MY, FY and PY. The genetic response ranged between 92 and 110 kg, for MY, between 6.1 and 7.2 kg for FY, and between 3.9 and 4.5 kg for PY. Moreover, (ΔG) in milk yield traits were high when incorporated MY with both FY and PY (I1), MY and FY or PY (I2 & I3) and MY only (I5). I5 had genetic response as compared with the index including MY with both FY and PY (I1), MY and FY or PY (I2 & I3). Thus, using I5, as a criterion of selection result in an increase of the expected genetic response for MY, FY and PY. Therefore, genetic response for selection for milk yield traits can be achieved through a selection scheme.

de Jager and Kennedy (1987) and Mbah and Hargrove (1982) reported that selection indices based on milk and fat yields are nearly as effective as selection indices that include protein yield or milk and protein yields.

Table 2. Index coefficients (b's), standard deviations of indexes (σ_I) and accuracy of selection estimated from each index (r_{IH}) and relative selection efficiency (RSE)

Index	Index coefficients *			σ_I	r_{IH}	RSE**
	MY	FY	PY			
I1	0.55	0.30	-1.87	299.70	0.42	100.00
I2	0.48	0.16	-----	298.65	0.42	99.60
I3	0.57	-----	-1.84	299.67	0.42	99.90
I4	-----	5.48	1.85	282.97	0.40	94.40
I5	0.49	-----	-----	298.64	0.42	99.60
I6	-----	6.56	-----	281.49	0.40	93.9
I7	-----	-----	8.60	254.45	0.36	84.9

*See abbreviations in table 1, **RSE: relative selection efficiency to I1.

Table 3. Expected genetic response (ΔG) of milk yield traits (kg)

Index	Trait*	Expected genetic response in:		
		MY	FY	PY
I1	MY, FY, PY	109.64	7.16	4.49
I2	MY, FY	109.08	7.14	4.48
I3	MY, PY	109.71	7.15	4.49
I4	FY, PY	101.49	6.88	4.25
I5	MY	109.12	7.13	4.48
I6	FY	100.85	6.87	4.23
I7	PY	91.79	6.12	3.85

* See abbreviations in Table1.

Ashmawy and Khalil (1990) recommended that, selection to improve milk yield traits might be achieved through multiple-trait selection based on index including milk yield with either fat yield or protein yield for Holstein-Friesian cows. Selection for milk yield traits (milk, fat and protein) would result in improving milk quality compared with single-trait selection for milk yield (Van Vleck, 1978 and Wilmink, 1988). Large losses in efficiency of an index occur when important traits are omitted (Smith, 1983). The efficiency of selection was predicted using a selection index for sires in a breeding plan for dairy cattle (Nielsen *et al.*, 2004).

Relative selection efficiency. In all indices, the relative efficiency of selection (**RES**) ranged from 84.9 to 99.9 relative to the first index (I1). Therefore, a selection index including MY (I1, I2, I3 or I5) was recommended as the best criterion from both the economic and the practical points of view to improve milk yield traits of Egyptian buffalo. For local breeder, I5 could be considered as the best criterion from the practical point of view and easy to apply.

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إستجابة الإلتخاب لصفات إنتاج اللبن في الجاموس المصري

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استهدفت الدراسة بحث مقدار التحسين الوراثي في إنتاج اللبن والدهن والبروتين في الجاموس المصري. استخرجت سبعة أدلة للإنتخاب من بيانات مأخوذة على ٦٩٩ موسم حليب من سجلات لعدد ٤٧٨ جاموسة نسل ٨٢ طلوقة و٣٨٣ أم. استخدم الدليل الأول (I1) الذي اشتمل على كل صفات انتاج اللبن كدليل انتخابي للمقارنة بين الأدلة المستخرجة الأخرى. قدرت المعايير الوراثية للصفات تحت الدراسة لغرض بناء أدلة انتخابية باستخدام النموذج المتكرر للحيوان-المتعدد الصفات بطريقة (REML). اشتمل النموذج الإحصائي على التأثيرات الثابتة "القطيع-موسم-سنة الولادة" والعمر عند الولادة داخل كل موسم للثلاثة مواسم الأولى بينما استخدم التأثير الوراثي التجمعي والبيئي الدائم كتأثيرين عشوائيين. تشير النتائج الي إمكانية تحسين صفات إنتاج اللبن من خلال الإلتخاب المتعدد الصفات. ولذلك يوصى باستخدام الدليل الإلتخابي المشتمل على إنتاج اللبن (I1, I2, I3 or I5) كأفضل مقياس اقتصادياً وعملياً لتحسين صفات انتاج اللبن للجاموس المصري. استخدام الدليل I5 والذي يحتوي علي إنتاج اللبن فقط - كمقياس للإنتخاب يتوقع أن يؤدي ذلك زيادة مقدار التحسين المتوقع لكل من انتاج اللبن والدهن والبروتين. وللمربين يفضل استخدام الدليل I5 بإعتباره أفضل مقياس عملياً وأسهل في التطبيق.