J. Agric. Sci. Mansoura Univ., 31 (11):6999 - 7007, 2006

DIFFERENT METHODS FOR EVALUATION PERFORMANCE TRAITS OF EGYPTIAN BUFFALOES

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ABSTRACT

A total of 1400 records of Egyptian Buffaloes kept at three Farms i.e. Mehallet mousa , Sides and Gimmeza, belonging to Ministry of Agriculture, during the period form 1985 to 2004 were used in this investigation. Genetic and phenotypic parameters of total milk yield (TMY), lactation period (LP) and calving interval (CI) were estimated by two methods i.e. Best linear unbiased prediction (BLUP) and MTDFREML using an animal model. The model included individual , and error terms as random effects, Farm, season and year of calving and parity as fixed effects and ageat first calving and days open as a covariate.

Estimates of heritability were0.16,0.35 and 0.49 for TMY, LP and CI, respectively. Predicted cows breeding values (CBV's) ranged from –214 to 410 kg for TMY, -29 to 29d for LP and –36 to 30 for CI. Also, predicted sires breeding values (SBV'S) ranged between –293 to 173kg,- 63 to 69d and –37 to 40d, for the same traits, respectively estimated by (BLUP). But by animal model were (CBV'S) ranged form –533 to 547kg for TMY,-89 to 96d for LP and -71 to 72d for CI, reflectively, while (SBV'S) ranged between –246 and 261 kg, -44 and 43d and -35 and 36d , for the same previous traits , respectively.

The accuracy of (SBV'S) ranges from 30-46% ,while, (SBV'S) ranges from 25–77% estimates by (BLUP). But, the accuracy of (SBV'S) ranges from 54–87% , while (SBV'S) ranges from 24–87% estimated by animal model.

The results to conclude that using the multiple – trait analysis is recommended to obtain more accurate breeding values for TMY because it make use of all the information about the lactations and the covariances among them as well as relationships between the relatives in the different traits.

INTRODUCTION.

Estimates of genetic parameters for yield traits of dairy cows obtained using sire models are frequent in the literature. Genetic variance might be under estimated if selection intensity is larger for males than females because analysis with sire models accounted only for genetic variance of sires (Khattab *et al.*, 2003). Animal model take into account differential selection of males and females and might provide more accurate estimates of parameters than do sire model.

For dairy cattle improvement, prediction of breeding values with an animal model instead of computation of separate genetic evaluations for cows and bulls is becoming common (Suzuki and Van Vleck, 1994). The animal model is the procedure used to evaluate genetic merit of dairy animals for production . It's calculation starts with the cows as source of production information .

In Egypt few studies have carried out to evaluate breeding values for milk traits in Egyptian buffaloes. Khattab and Mourad (1992) estimated sire transmitting ability for total milk yield and lactation period using BLUP without relationship matriy, while Gebriel (1996) estimated cows and dam transmitting ability for 305– day milk yield and lactation period by using single trait animal model. Khattab et al.,(2003) estimated sire, cow and dam transmitting ability for total milk yield, lactation period and age at first calving by using multi trait animal model .

The main objectives of this investigation are to : (1) estimate the genetic and phenotypic parameters for production and reproduction performance traits of Egyptian buffaloes. (2) evaluate the sires and course on the basis of their transmitting abilities by using best linear unbiased prediction (BLUP) and animal model .

MATERIAL AND METHODS

The data used in the present investigation comprised 1400 records of Egyptian buffaloes maintained at three farms belonging to the Animal Production Research institute, belong to Ministry of Agriculture. The three farms are Mehallet Mousa in the northern part of the Delta. Sides in the upper Egypt and Gimmeza in the middle of the Delta. The records covered the period form 1985 to 2004. Number of sires and cows were 80 and 442, respectively. Cows were mated naturally, while artificial insemination was only practiced when there was a probability of genetical disease infection. Pregnancy was detected by rectal palpation 60days after the last service. Abnormal records affected by disease or by abortion were excluded. Traits studied were total milk yield in kg (TMY), lactation period in day (LP) and calving interval in days (CI) .

Animals were allowed to graze during the period form December to May, while during the rest of the year, they were given pelleted concentrates and rice straw. Cows producing more than 10kg and those that were in the last two months of pregnancy were supplemented with extra concentrate ration. Buffaloes were hand milked twice a day.

Statistical analysis : -

Data were analysed by multiple trait derivative free restricted maximum likelihood (MTDFREML) according to Boldman *et al.* (1995). Using single and multiple trait animal model. Table (1). Shows the structure of data used in the present study. The analysis was stopped (terminated) when it reached the attained with convergence criterion of 5415 rounds of iterations .

Firstly, traits were analysed using single trait animal model using mean literature values as start as estimated by Tonhati et al.(2000). Secondly, variances of genetic and error (residual) effects obtained from the analysis of single trait animal model were used as start values in multi trait animal model, where the genetic and residual covariances were obtained by using Mixed model least squares and Maximum likelihood (LASMLMW) computer program of Harvey (1990).

Table (1) : Structure of data used in the present study :

Observation	No .
No. of records	1400
No. of daughter	1400
No. of cows	442
No. of sires	80
Animal in relationship Matrix, no. A -1	1922
Mixed model equations, No. MME	1916
No. of iterations	5415

The multi trait animal model which are used to analysis TMY, LP and CI included individual and error terms as random effects, farm season and year of calving as fixed effects and age at first calving and days open as a covariate. The mixed model equations are given in detail by Set El– Habaeib Awad and Hoda Zaki (2006).

In matrix notation the animal model used was :

Y= XB + Z g + e

Where:

Y = Observation vector of animals .

B = Fixed effects vector(i.g., farm, season and year of calving and parity) .

g = animal direct genetic effect vector .

e = residual effect vector, X and Z are incidence matrices, and

$$E = \begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

$$V = \begin{bmatrix} a \\ \\ \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2 a1 & A\sigma\, a12 & 0 & 0 & 0 & 0 \\ A\sigma\, a21 & A\sigma^2 a2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma^2 e1 & I\sigma e12 \\ 0 & 0 & 0 & 0 & I\sigma e21 & I\sigma^2 e2 \end{bmatrix}$$

To estimate heritability (h^2) coefficient , the following equation was used:

$H^2 = \sigma^2 a / (\sigma^2 a + \sigma^2 e)$

Where :

$\sigma^2 a$ = additive genetic variance.

$\sigma^2 e$ = temporary environmental variance.

Breeding values were calculated form1400 cows fathered by 80 sires and mothered by 440 dams. The mixed model equation (MME) for the best linear unbiased estimator (BLUE) for estimable function for the best linear unbiased prediction (BLUP) was in matrix notation as follows:

$$\begin{bmatrix} x^- x & x^- z & x^- w \\ z^- x & z^- z + A^{-1} a1 & z^- w \\ w^- x & w^- z & w^- w + Ia_2 \end{bmatrix} \begin{bmatrix} b^- \\ M^- a \\ M^- e \end{bmatrix} = \begin{bmatrix} X^- y \\ Z^- a\, y \\ W^- e\, y \end{bmatrix}$$

where ;

$$X = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix},\ Z = \begin{bmatrix} Z_{a1} & 0 & Z_{E1} & 0 \\ 0 & Z_{a2} & 0 & Z_{E2} \end{bmatrix},\ b^- = \begin{bmatrix} b^-_1 \\ b^-_2 \end{bmatrix}$$

$$\mathbf{M^-} = \begin{bmatrix} M^- a1 \\ M^- a2 \\ M^- 1 \\ M^- e2 \end{bmatrix} \text{ And } Y = \begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix}$$

Accuracy (R^2) :

The accuracy of estimated breeding values was calculated according to the formula of **Robertson (1959)** as follows :

$R^2 = n/n + k$

where :

N = Is the number of daughters per sire.

$k = (4-h^2) / h^2$, for each trait was added to the diagonal of sire effects in the matrix.

H2= Is the heritability estimate .

RESULTS AND DISCUSSION

For multi trait animal model, the structure of data (No. of daughters, No. of sires, No. of cows, mixed model equations (MME) and No. of iterations are presented in Table (1). The average number of equations and iterations recorded were 1916 and 5415, respectively. Results of the present study are higher than those estimated form single trait animal model found by Salem (1998) working on Holstein Friesian cows in Egypt. The author reported that the number of iterations for TMY and LP were 214 and 127, respectively. On the other hand, Khattab *et al.* (2003) and El-Azab (2006) working on Egyptian buffaloes, found that the average number of equations and iterations recorded were highest (7154 & 1983) and (8531 & 7017), respectively. They suggested that the higher number of iterations in the resnits may be due to using three traits in the same analysis and considering also genetic covariancey and errors covariancey among these traits. In general, number of iterations required to reach convergence could be affected by the number of animals, the number of random factors in the model and the traits studied.

The heritability estimates were 0.16, 0.35 and 0.49 for TMY, LP and CI, respectively (Table. 2). These estimates indicate that 35 and 49% of the total variation observed in LP and CI, respectively are due to additive genetic variance. The moderate (h^2) estimates for LP and CI suggested that efforts could be made to bring about improvement in those two important economic traits through individual selection as well as better managerial practices. In the other side, the lower (H^2) estimate for TMY 0.16 indicated that this trait is affected mainly by environmental factors. Therefore, the improvement in this trait could be possible by improving feeding and management system.

The present estimate of TMY was lower than that with animal model by both Khattab *et al.* (2003) on Egyptian buffaloes (0.43) and Tonhati *et al.* (2000) on Murrah buffaloes in Brazil, found that (h^2) estimates for TMY was 0.38. They concluded that the genetic change for this trait is possible by selecting the most productive animals. In the other side, the heritability estimate for LP was 0.01, this mean that the genetic variation among individuals is practically nil. and the individual differences in this trait could be reduced by management and breeding practices.

Lower estimates of heritability for milk yield and lactation period were found by Thevamanoharana (2003) working on 3195 lactation records of 1183 Niliravi buffaloes. The author suggested that most of the observed variation in milk traits collateral relatives and progeny test should be used in selection programs. The improvement of these traits may be achieved by better environmental conditions, i.e. good feeding, better management reduction of heat stress, best control of diseases including vaccination programmes and and wide spread milk recording and testing systems.

In general, Heritability estimates obtained in the present study are higher than those 0.13 and 0.14 reported with sire model by Khattab and Mourad (1992) and Khattab *et al.* (2003) for LP. As well as 0.015 and 0.032 for TMY and LP by Khalil *et al.* (1992) of Egyptian buffaloes and 0.04 for LP by El-Arian (2001) in Indian buffaloes. The estimate of (h^2) for CI was 0.17 reported by Mahdy *et al.* (1999). El-Azab (2006), reported estimate high (h^2) for TMY and LP 0.31 and 0.24, respectively.

Genetic correlations :

The results in table in table (2), show that the genetic correlations between TMY and LP was positive and high (0.61) which was in the desirable direction, indicating that high yielding buffaloes are also having the longer LP. Khattab *et al.* (2003) and El-Azab (2006) arrived to the same conclusion. The genetic correlation between TMY and CI was positive and low (0.11) thus the selection for high yielding buffalo cows might be lead to decrease in their CI. In the same respect, the genetic correlation between LP and CI was positive and high (0.83) and in the dame time quite expected and leads to suggest that selection for higher productivity and reproductively might be lead to longer LP and decrease in CI.

Table(2) : Estimates of variance and covariance components, heritability (h^2), genetic correlation (rg) for total milk yield (TMY), lactation period (LP) and calving interval (CI) .

Estimate	Traits		
	TMY, Kg	LP, days	CI, days
σ^2a	7760	8885	1715
σa TMY with	-	5065	1326
σa LP with	-	-	1021
σ^2e	41044	16355	1804
σe TMY with	-	3616	1148
σe LP with	-	-	846
h^2	0.16	0.35	0.49
rg TMY with	-	0.61	0.11
rg LP with	-	-	0.83

σ^2a = Additive genetic variance. , σa = Genetic covariance.
σ^2e = Residual variance . and σe = Residual covariances .

A reduction in CI. Is a desirable goal of dairymen and will help in minimizing the cost of raising breeding heifers, shortening the generation interval and maximizing the number of lactations per cow. The results was in close agreement with El- Arian *et al.* (2001) and Khattab *et al.* (2003) on Egyptian buffaloes. From the other direction, Mahdy *et al.* (2001) found that the genetic correlation between LP and CI was higher approaching (0.63) and indicated lack of association with productive traits. On the contrary an improvement in LP may lead to improve reproductive traits.

Finally, from the preeding side of view the result revealed that TMY and LP could be considered independently in planning buffalo selection programs.

Predicted Breeding values (PBV 'S) : -

Estimates of minimum, maximum and range of predicted breeding values and their accuracies for TMY, LP and CI calculated for cows (CBV'S) and sires (SBV'S) using the procedure of best linear unbiased prediction (BLUP) are presented in table (3). The results showed that the range of (CBV'S) being 410 Kg, 58 days and 66 days for TMY, LP and CI, respectively, to 28%, 26% and 29% of the herd average, respectively. In the present study showed that the range of (SBV'S) being 466 Kg, 136 days and 77 days for TMY, LP and CI, respectively.

It is clear that the accuracy of sire breeding value (SBV'S) ranges 25-77% which was higher than the accuracy of (CBV'S) ranges 18-46%. The accuracy of sire breeding value was higher than of cow breeding value, which may be due to higher number of daughters for sire.

Ram and Yadav (1990), working on murrah buffalo, found that the estimates of breeding values of sires by BLUP procedures ranged form -201.3 to 263.8 Kg. For milk yield, while, Mahdy *et al*. (1999) working on Egyptian buffaloes, reported that the BLUP estimates for TMY of 66 sires ranged from -428 to 377 Kg and corresponding estimates for 30 SMY and LP were -345 to 227 Kg and -68 to71 days, respectively.

In addition, Khattab and Mourad (1992) using another data set on Egyptian Buffaloes , estimated sire values.

Table (3) : Range of predicted breeding values of cows (CBV'S) and sires (SBV'S) and its accuracy for total milk yield (TMY), lactation period (LP) and calving interval (CI) by best linear unbiased prediction (BLUP).

Traits	CBV'S				SBV'S			
	Min.	Max.	Range	Accuracy	Min.	Max.	Range	Accuracy
TMY	-214	196	410	18-33	-293	173	466	26- 59
LP	-29	29	58	41-46	-63	69	136	62-77
CI	-36	30	66	30-46	-37	40	77	25-54

Table (4) : Range of predicted breeding values of cows (CBV'S) and sires (SBV'S) and its accuracy for total milk yield (TMY), lactation period (LP) and calving interval (CI) by Animal model .

Traits	CBV'S				SBV'S			
	Min.	Max.	Range	Accuracy	Min.	Max.	Range	Accuracy
TMY	-533±150	475±170	1080	83-87	-246±150	261±177	507	40-42
LP	-89±26	96±32	185	70-81	-44±40	43±40	87	24-87
CI	-71±29	72±33	143	54-67	-35±36	36±36	71	27-33

Without A^{-1} for TMY and LP. The authors found that BLUP values as deviation from the mean ranged from 147 to 154 Kg for TMY and from -20 to 31 days for LP.

Estimates of minimum, maximum and range of predicted breeding values and their accuracies for TMY, LP and CI calculated for cows (CBV'S) and sires (SBV'S) using multi trait animal model are presented in table (4). The results showed that the range of CBV'S being 1080 Kg, 185 days and 143 days for TMY, LP and CI, respectively, representing to 75%, 83% and 31% of the herd average, respectively, (Set El-Habaeib, Awad and Hoda Hassan, 2006).

The accuracy of minimum and maximum estimates of sire breeding values and cow breeding values table. 4 were ranged 24-87% and 54-87%, respectively. Khattab *et al.* (2003) found that the accuracy of (SBV'S) and (CBV'S) range 35-90% and 53-82%. The same authors concluded that accuracy of sire evaluation increases as the number of daughters per sire increases .

In addition, the accuracy of minimum and maximum estimates of breeding values of (SBV'S) and (CBV'S) for TMY obtained by multi-trait animal model (Table. 4) are higher than those compared to single–trait animal model obtained by Khattab et al.(2003) ranged from 33 to 51% for (SBV'S) and from 16 to 70% for (CBV'S).

The higher accuracy for multi-trait animal model may be due to consider the covariance among studied traits.

The range of (SBV'S) for the same traits were 507 Kg, 87 days and 71days, respectively with 35%, 39% and 15% from the herd average, respectively. The present results show large differences among breeding values of cows and sires for the different studied traits. Thus The improvement of milk production and calving interval through selection is possible. Genetic progress can be achieved if the farms adopts test for the genetic evaluation of sires and cows. Similarly, Khattab *et al.* (2003) working on Egyptian buffaloes, found that the predicted sire transmitting ability for TMY ranged from -211 to 407Kg. Shalaby, (2005) working on Friesian cows found that the AM estimated for CI being 99.7 days, from -10 to 89 days. But Shahdan (2006), being for LP ranged from –95 to 89 days for the dame trait.

Results of the present study (Table.4) show that the importance of cows, since it gave the higher range of breeding values for TMY, LP and CI than sires breeding values. The selection for cows for the next generation as a maternal line would place emphasis on good genetic maternal effect in addition to good estimates of predicting (184) days, from (-95 to 89) for CI breeding values.

On the other hand, Tonhati *et al.* (2000) on Murrah buffaloes, estimated breeding values of cows, dams and sires by using single trait animal model for milk yield, lactation period and ageat first calving, they concluded that the average breeding values of cows, dams and sires for different studied traits were around zero, which indicated that selection in such cases was not effective. The same authors suggested that there were some difficulties on sires selection for milk yield and that more wide- range tests for genetic evaluations of sires are needed.

This study represent the first attempt for estimating breeding values of milk traits of Egyptian buffaloes kept at there farms (Mehallet Mousa, Sids and Gimmeza), using multi trait animal model, from different sources of pedigree. The stations are of the main sources for providing the farmers by proven sires. Therefore more research work in this respect is needed by seting large data sets and including another milk traits such as fat and protein yields.

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طرق مختلفة لتقييم الأداء الإنتاجى فى الجاموس المصري

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أستخدمت فى هذه الدراسة ١٤٠٠ سجلاً عن الصفات الإنتاجية لقطيع الجاموس المصـرى خـلال الفترة من عام ١٩٨٥ وحتى عام ٢٠٠٤. علماً بأن القطيع ينتمى لثلاثة مزارع وهى محلة موسـى وسـدس والجميزة والتى تتبع معهد بحوث الإنتاج الحيوانى – وزارة الزراعة – جمهورية مصر العربية.

وتم تقدير المعايير الوراثية والمظهرية لإنتاج اللبن ، طول موسم الحليب والفتـرة بـين ولادتـين بواسطة طريقتين هما أفضل إنحدار خطى غير متحيـز (BLUP) ونمـوذج الحيـوان بإسـتخدام برنـامج MTDFREML لـ Boldman *et al.* (1995) وأشتمل نموذج التحليل على المزرعة وموسـم وسـنة الولادة وترتيب الموسم كعوامل ثابتة والعمر عند أول ولادة وفترة الأيام المفتوحة الإنحدار وخطى وكلاً مـن الحيوان والخطأ العشوائي كعوامل عشوائية وكانت النتائج كالتالي :-

- بلغت تقديرات المكافئ الوراثي ٠,١٦، ٠,٣٥، ٠,٤٩ لإنتاج اللبن ، طول موسم الحليـب، الفتـرة بـين ولادتين على التوالي . بإستخدام طريقة الــ (BLUP) تراوحت القيم التربوية للجاموس من -٢١٤ إلـى ٤١٠كجم لإنتاج اللبن ومن -٢٩ إلى ٢٩ يوم لطول موسم الحليب ومن -٣٦ إلى ٣٠ يوم لطول الفتـرة بين ولادتين بينما تراوحت القيم التربوية للأباء من -٢٩٣ إلى ١٧٣كجم ، -٦٣ إلى ٦٩ يوم ، -٣٧ إلى ٤٠ يوم لنفس الصفات السابقة على التوالى. فى حين كانت التقديرات بإستخدام الــ (AM) للقيم التربويـة للجاموس من -٥٣٣ إلى ٥٤٧ كجم لإنتاج اللبن ، -٨٩ إلى ٩٦ يوم لطول موسم الحليـب ، -٧١ إلـى ٧٢يوم للفترة بين ولادتين كما تراوحت القيم التربوية للأباء مـن -٢٤٦ إلـى ٢٦١كجـم ، -٤٤ إلـى ٤٣يوم، -٣٥ إلى ٣٦ يوم لنفس الصفات السابقة الذكر.
- وقد تراوحت نسبة دقة التقديرات للقيم التربوية للجاموس بين ١٨-٤٦% بينما كانت للأباء بين ٢٥-٧٧% عن طريق الــ (BLUP) وكانت نسبة دقة التقديرات للقيم التربويـة للجـاموس بـين ٥٤-٨٧% بينمـا تراوحت هذه الدقة للأباء بين ٢٤-٨٧% بإستخدام (AM) .

وتوصى هذه الدراسة بزيادة دقة تقديرات القيم التربوية لصفة إنتاج اللبن نظراً لإرتباط هذه الصـفة بصورة إيجابية مع بقية الصفات الإنتاجية المختلفة للجاموس المصرى وذلك فى حالة إستخدام برنامج تحليـل عدد كبير من الصفات.