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GENETIC AND PHENOTYPIC TRENDS FOR TEST DAY MILK, FAT AND PROTIN YIELDS APPLYING RANDOM REGRESSION MODEL IN EGYPTIAN BUFFALOES

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SUMMARY

The aim of this study was to detect genetic and phenotypic trends for test day milk, fat and protein yields in Egyptian buffalo applying the random regression model (RRM) and determining the genetic and phenotypic trend. Data of 4971 test days (TD) milk yield traits were recorded for 691 Egyptian buffalo cows, daughters of 120 sires and 532 dams from four herds belonging to the Animal Production Research Institute, Egypt. Ten-month classes of lactation days were considered for the test-day yields. The model included the random effects of direct additive genetic, permanent environment and error, while the fixed effects were herd-test day, year and season of calving and parity as well as days in milk as a covariable, which was modeled by orthogonal Legendre polynomials. The additive genetic variance estimates at first test day for milk, fat and protein yields were respectively 0.035kg, 2.26g, 0.80g, increased until the fourth (0.807kg, 30.52g, 12.52g), decreased thereafter, reaching the lowest value at the ninth test day for milk and protein yields (0.238kg, 0.97g) and at the tenth test day for fat yield (7.28g).Heritability estimated at first test day was 0.05, increased until the fourth test day (0.30), and decreased thereafter and reached the lowest value at the tenth test day (0.06). The highest heritabilities were found to be 0.29 and 0.31 for fourth test day in fat and protein yields, respectively. The range in phenotypic values change decreased from 7.99 to 5.66kg, 53.37 to 35.07g and 30.86 to 21.54g, while the respective genetic values change increased from -0.22 to 0.17kg, -1.41 to 1.36g and -0.82 to 0.70g for milk, fat and protein yields, respectively. The genetic trends were slightly positive for all traits indicating that the selection program performs correctly. For all traits, the phenotypic trends showing deteriorating trends indicating the presence of some environmental inadequacies especially for nutritional level.

Keywords: Egyptian buffalo, test day milk, fat and protein yields, random regression model, genetic and phenotypic trends

INTRODUCTION

Milk yield in the day of record is defined as the sum of milk yield of a buffalo cow during 24 hours. Test day models allow for better modeling because it is possible to take into account effects specific to the day at recording (test day). With this method, the environmental effects are better modeled (Ptak and Schaeffer, 1993), and the genetic parameter estimates are expected to be more accurate (Swalve, 2000). These methods have been used in the genetic evaluation for milk yield in many countries (INTERBULL, 2009). By using the test day milk yield (TDMY) parameter, there is no need to extend the lactation period for animals to reach 305 lactation days, by means of adjusting factors. Different methods have been proposed to estimate the (co) variance structure among TD. Meyer (1998) clarified that the best method of dealing with longitudinal traits measured over a trajectory is to fit a set of random coefficients to describe the covariance structure along this trajectory. Kirkpatrick *et al*. (1990) added that random regression models (RRMs) facilitate more accurate modeling of the variance-covariance structure over a given trajectory. In Murrah buffalo, Aspilcueta-Borquis *et al.* (2012) estimated the additive genetic and permanent environment variances for milk, fat, and protein yields, using single trait RRM.

It is imperative to follow the results of an animal breeding program to assess its development as well as to make effective adjustments. One way of evaluating an animal breeding plan is to determine the phenotypic and genetic trends. Thus, the study of genetic trend in a population is a significant element in monitoring of the selection, since it corresponds to the observed changes in the average breeding values of animals studied for a specific trait during the selection work (Potocnik *et al.*, 2007).

The objectives of the present study were: (1) to investigate improvement possibilities through the application of RRM for TD milk, fat and protein yields in Egyptian buffalo and (2) detect genetic and phenotypic trends.

MATERIAL AND METHODS

Dataset:

Data used in this study were collected at monthly intervals over the period from 1999 through 2009 from four buffalo experimental herds (El-Nattafe El-Gadid, El-Nattafe El-Kadim, MahaletMousa and El-Gemmiza) belonging to the Animal Production Research Institute (APRI), Ministry of Agriculture and Land Reclamation, Egypt. Test day (TD) records for milk, fat and protein yields were measured following an alternative am-pm monthly recording scheme. Milking was practiced twice a day at 7 am and 4 pm throughout the lactation period. Fat and protein yields were measured by the automated method of infrared absorption spectrophotometry (Milk-o-Scan; Foss Electric, Hillerφd, Denmark) at the Dairy Services Unit, Animal Production Research Institute, Sakha, Kafr El-Sheikh Governorate. Buffalo cows with less than four TD records per lactation were excluded from the data set, while the maximum number of test day records per lactation was 10 records.Moreover, upnormal phenotypic values of daily milk yield, fat and protein yield were removed from the dataset. The data are normally distributed and all known relationships among the individuals were considered in the animal model.The structure of the data analyzed is shown in Table (1).

Table 1. Structure of test day (TD) data analyzed in Egyptian buffaloes

Item	Data
No. of sires	120
No. of dams	532
No. of cows with records	691
No. of base animals	469
No of non-base animals	684
Total number of animals	1153
Total number of lactation records	4971

Statistical analysis:

The model of the analysis included the fixed effects of herd test day (40 levels), year (10 years) and season of calving (two seasons) and parity (five parities) as well as days in milk as a covariable. Variance-covariance components were estimated by REML using the computer package VCE6 (Groeneveld, *et al.*, 2010).The animal model was:

$$Y_{ijkl} = HTD_i + \sum_{m=1}^{4} \beta_{km} Z_{jlm} + \sum_{m=1}^{4} \alpha_{jm} Z_{jlm} + P_j + e_{ijkl}$$

where: Y_{ijkl} is the record 1on trait within lactation made on HTD subclass i for the j^{th} buffalo cow belonging to k^{th} subclass (k ranged from 1 to 10 starting with k=1 and increased by 1 every 30 days thereafter along the trajectory from 4 to 304-d); HTD_i is the fixed effect of herd test day, P_j = random effect of permanent environment associated with all TD yields of the j^{th} buffalo; β_{km} and α_{jm} = fixed and random regression coefficient, and e_{ijkl}= random residual effect associated with Y_{ijkl}.

The VCE6 program applying the Random Regression Model (RRM) was used to analyze the data using the Legendre polynomials method (Kirkpatrick *et al.*, 1990).The general RRM can be represented in matrix notation as:

$$Y = Xb + Za + Wp + e,$$

Where, Y = vector of observations on animal; b= vector of the fixed effects; a= vector of solutions for additive genetic random coefficients; p= vector of solutions for permanent environmental random coefficients; e= vector of N different residuals; X, Z, and W = incidence matrices for fixed and random genetic and permanent environmental random effects, respectively. The assumptions with respect to the components of the model were (Jamrozik and Schaeffer, 1997; Schaeffer, 2004):

$$\begin{pmatrix} a \\ p \\ e \end{pmatrix} \square\, N\left(0, V\right) \;\; where, \quad V = Var \begin{pmatrix} a \\ p \\ e \end{pmatrix} = \begin{pmatrix} G \otimes A & 0 & 0 \\ 0 & I\sigma_p^2 & 0 \\ 0 & 0 & R \end{pmatrix}$$

where G and P are (co)variance matrix of additive genetic and permanent environment random regression coefficients, respectively; A is an additive genetic relationship matrix among the buffaloes; $\otimes$ is a Kronecker product function; I is identity matrix and R is the diagonal matrix of temporary environmental variances. The mixed model equations for this model would be:

$$V = \begin{pmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + G^{-1} \otimes A^{-1} & Z'W \\ W'X & W'Z & W'W + I \otimes P^{-1} \end{pmatrix} \begin{pmatrix} b \\ a \\ p \end{pmatrix} = \begin{pmatrix} X'Y \\ Z'Y \\ W'Y \end{pmatrix}$$

$$E\begin{bmatrix} y \\ a \\ p \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix}; \text{ and } \begin{matrix} V(a) = K_a \otimes A; \\ V(p) = K_p \otimes I; \\ V(e) = R, \end{matrix}$$

Where k_a and k_p are the genetic and permanent environmental covariance matrices between random regression coefficients, respectively. A is the additive genetic relationship matrix; I is an identity matrix, and R represents a diagonal matrix containing the residual variances.

Orthogonal polynomials of standardized units of time have been recommended as covariables (Kirkpatrick et al., 1990). Orthogonal polynomials have computational advantages. The primary general advantage is the reduced correlations among the estimated coefficients. A standardized unit of time, *t*, ranges from -1 to +1, and is derived as

$$t^* = \frac{2(t - t_{\min})}{t_{\max} - t_{\min}} - 1$$

Where "t" is "t_{min}" is the lowest age and "t_{max}" is the highest age.

The genetic (G) and permanent environmental (P) covariances between test-days were estimated using:

$$G = (1 \;\; ti \;\; ti^2 \;\; ...)Ka \begin{bmatrix} 1 \\ tj \\ tj^2 \\ ...... \end{bmatrix} \quad and \quad P = (1 \;\; ti \;\; ti^2 \;\; ...)Kp \begin{bmatrix} 1 \\ tj \\ tj^2 \\ ...... \end{bmatrix}$$

When the structure of residual variance was fitted by variance function, the variances were estimated by:

$$V_{e_i}^2 = V_{e_0}^2 \left(1 + \sum_{r=1}^{q} \beta_r t_{ij}^r\right),$$

Heritabilities (h^2) are computed using the SAS IML matrix package as (Groeneveld *et al.*, 2010):

$$h^2 = \frac{\sigma^2_{gi}}{\sigma^2_{gi} + \sigma^2_{pi} + \sigma^2_{ei}}$$

Where:σ^2_{gi} is the additive genetic variance of the ith TD; σ^2_{pi} is the permanent environmental variance and σ^2_{ei} is the residual variance.

Predicted breeding values:

Buffaloes predicted breeding values (PBVs), predicted error variance (PEV) (i.e. standard errors, SE) and accuracies of predictions ($r_{a\hat{a}}$) were estimated by REML using the computer package PEST (Groeneveld *et al.*, 2001) for test day milk, fat and protein yields according to the following model:

$$y = Xb + Za\, a + Zc\, c + e$$

where: y = Vector of observations, X = Incidence matrix relating fixed effects to y, b = Vector of an overall mean and fixed effects (herd-test day, season of calving, parity and days in milk as a covariable), Za = Incidence matrix relating direct additive genetic effects to y, a = Vector of random effect (direct additive genetic associated with the incidence matrix Za, Zc = Incidence matrix for permanent environmental effect, c = Vector of permanent environmental effect associated with the incidence matrix Zc and e = Vector of random residual effects N (0, $I\sigma^2_e$); I is an identity matrix.

Solutions for equations of animals were computed from the pedigree file, one animal at a time for animals with records and animals without records (sires and dams). A diagonal element (d_t) and an adjusted right-hand side (${}^{y^*}{}_{t}$) were accumulated with each pedigree file record for the tth animal. For animal with and without records, the formula used to estimate the PBV was (Kennedy, 1989):

$$PBV = [{}^{y}{}_{t}/d_t]$$

The predicted error variance (PEV) of predicted breeding values (PBV_p) were estimated for each individual as: $PEV_p = d_j\sigma^2_e$(Korsgaard*et al.,* 2002); where d_j and σ^2_e were defined before.The accuracy of PBV for each individual was estimated according to Henderson (1975) as:

$$r_{A\hat{A}} = \sqrt{1 + F_j - d_j\alpha_a}$$

where $r_{A\hat{A}}$ = the accuracy of prediction of the ith animal's breeding value; F_j=inbreeding coefficient of animals (assumed equal to be zero); d_j=the jth diagonal element of inverse of the appropriate block coefficient matrix; and $\alpha_a = \sigma^2_e/\sigma^2_a$.

Genetic and Phenotypic trends:

The phenotypic trend was measured as the regression of least squares means on year-test-day. As stated before animal with records and without records breeding values were estimated using the theory of PEST (Groeneveld *et al*., 2001). Accordingly the genetic trend was measured by regressing the breeding values on year-test-day.

RESULTS AND DISCUSSION

Means:

The observed means, the standard deviations and the coefficients of variation for TD milk,fat and protein yieldsare shown in Table (2). The means for TDMY showed a lactation curve initializing with 5.19*kg*, followed by an increase in milk yield until the peak of the lactation, occurred in the third test-day (8.47*kg*), and a decrease until the end of lactation with a production of 5.14*kg* in the tenth test-day lactation. The means observed for fat and protein yields were showing the same trend as that for TDMY. The means for fat and protein yields are 33.45 and 20.42*g*, *respectively*, on the first test day, followed by an increase until the peak of lactation (54.21 and 32.29*g*) and decrease at the end of lactation (35.12 and 20.22*g*).Tonhati *et al*. (2008) for Murrah buffalo and Madad *et al*. (2013) for Iranian buffaloes reported similar results of milk means unlike the first test day. Aspilcueta-Borquis *et al*. (2010) in Murrah buffalo reported higher means of milk in the first test day and the milk yield decreased at the end of lactation. The authors reported the same result regarding fat and protein.

Variances:

Estimates of additive genetic, permanent environmental and phenotypic variances are presented in Figures (1), (2) and (3) for milk, fat and protein yields. The additive genetic variance estimates at first test day were 0.035*kg*, 2.26*g* and 0.80*g*,increased until the fourth test (0.807*kg*, 30.52*g* and 12.52*g*) and decreased thereafter, reaching the lowest value at the ninth test day for milk and protein yields (0.238*kg* and 0.97*g*) and at the tenth test day for fat yield (7.28*g*). Similar results have been reported by Silvestre *et al*. (2005) and Sesana *et al*. (2010) who working with dairy buffaloes.

Table 2. Number of observations, means, standard deviations (SD) and coefficients of variation (CV) for test day (TD) milk, fat and protein yields

TD	Number of observation	Test day milk yield			Test day fat yield			Test day protein yield		
		Mean (*kg*)	SD (*kg*)	CV (%)	Mean (*g*)	SD (*g*)	CV (%)	Mean (*g*)	SD (*g*)	CV (%)
1	693	5.19	1.02	19.6	33.45	7.99	23.9	20.42	4.32	21.2
2	693	7.51	2.20	29.4	47.19	15.66	33.2	28.75	8.87	30.8
3	693	8.47	2.42	28.5	54.21	17.22	31.8	32.29	9.39	29.1
4	693	8.23	2.39	29.1	54.05	17.95	33.2	31.36	9.63	30.7
5	664	7.51	2.33	31.1	49.67	16.92	34.1	28.69	9.09	31.7
6	595	6.71	2.10	31.3	44.17	14.75	33.4	25.70	8.06	31.4
7	454	6.10	1.89	31.0	40.78	13.73	33.7	23.26	6.92	29.7
8	302	5.61	1.75	31.1	37.58	12.33	32.8	21.89	6.65	30.4
9	141	5.42	1.63	30.0	36.48	11.29	30.9	21.32	6.69	31.4
10	55	5.14	1.42	27.6	35.12	10.62	30.2	20.22	5.16	25.5

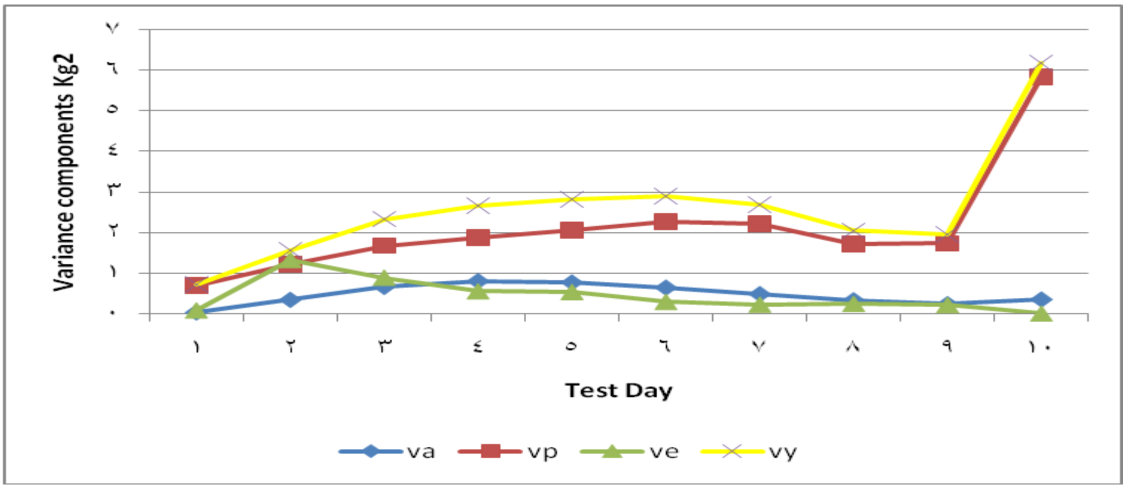

Fig. 1. Estimates of additive genetic (va), permanent environmental (vp), residual variances (ve) and phenotypic variances (vy) for test day milk yield (*kg*) in Egyptian buffaloes

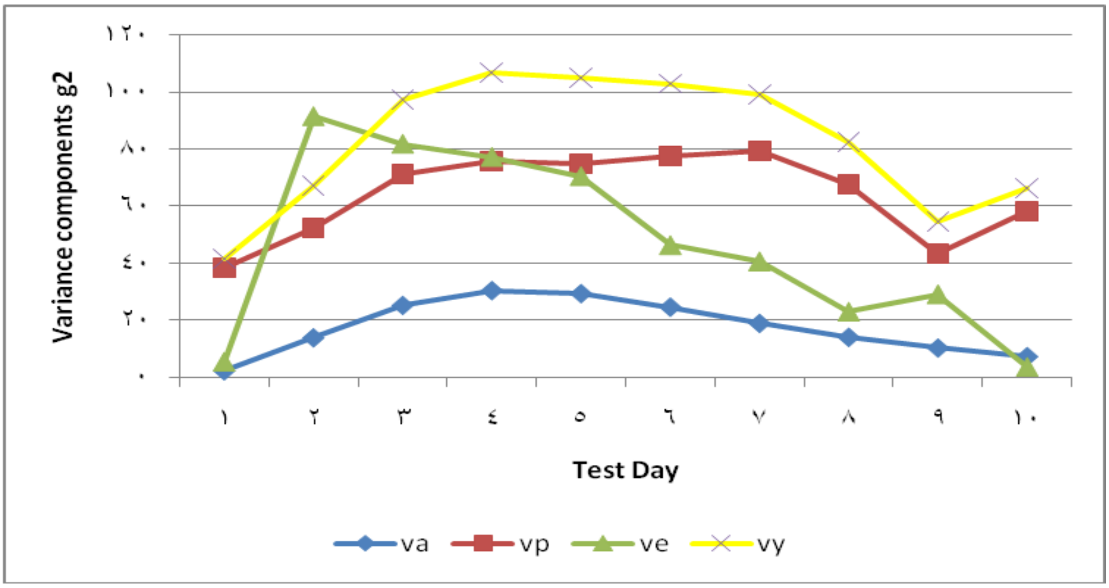

Fig. 2. Estimates of additive genetic (va), permanent environmental (vp), residual variances (ve) and phenotypic variances (vy) for test day fat yield (*g*) in Egyptian buffaloes

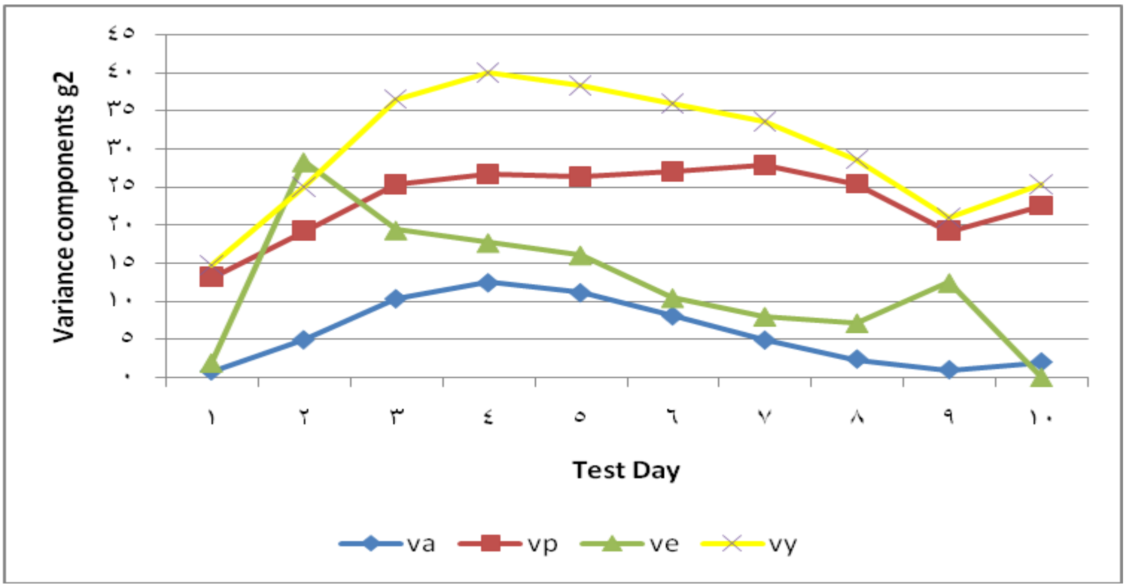

Fig. 3. Estimates of additive genetic (va), permanent environmental (vp), residual variances (ve) and phenotypic variances (vy) for test day protein yield (*g*) in Egyptian buffaloes

The additive genetic variance estimates showed the same trend, as the permanent environmental and phenotypic variance estimates for milk, fat and protein yields in our studies. The estimates were relatively low at early lactation; increased gradually and then decreased except at the end where the estimates increased again suddenly and the increase was very clear in the curve of permanent environmental and phenotypic variances. This trend is compatible with that obtained fort he heritability. These results are in agreement with the results reported by El-Bramony *et al*. (2004) for buffalo. While, Aspilcueta-Borquis *et al*. (2010) reported higher estimates of additive genetic in all test day of lactation as well Tonhati *et al.* (2008) for Murrah buffalo. Madad *et al.* (2013) for Iranian buffalo reported a lower additive genetic. Aspilcueta-Borquis *et al*. (2007, 2010) reported lower additive genetic variance at all test days for fat and protein yield in Murrah buffalo. Additive genetic variances for all traits are high. High variance could be due to the availability of most pedigree information. Genetic variance estimates for milk yield indicate that selection program for this trait would be effective.

Residual variance for TDMY tended to be low at both edges. Similar trends were also reported by Jamrozik and Schaeffer (1997) and Jensen *et al*. (2001) for cattle. However Aspilcueta-Borquis *et al*. (2007) for buffalo reported higher estimates in the first three months and lower estimates at the end of lactation.

Hertabilities:

Heritability estimates for TDMY at selected TD are shown graphically in Figure (4). Estimates were low at the beginning of the test day (0.049), and gradually increased, reaching the highest value at the fourth test day (0.302). Estimates decreased gradually until reached the lowest value at the tenth test day of lactation (0.057). The heritability estimates for fat and protein yields showed the same trend as for milk yield estimates. On the first day, estimates were (0.054, 0.057) and reached at the fourth test day (0.28, 0.31), and finally decreased at the tenth test day (0.10, 0.08). Similar trends were reported for milking buffaloes by Rosati and Van Vleck (2002), and El-Bramony *et al*. (2004).These results differ from those of Aspilcueta-Borquis *et al*. (2007, 2010) in buffalo for all traits.

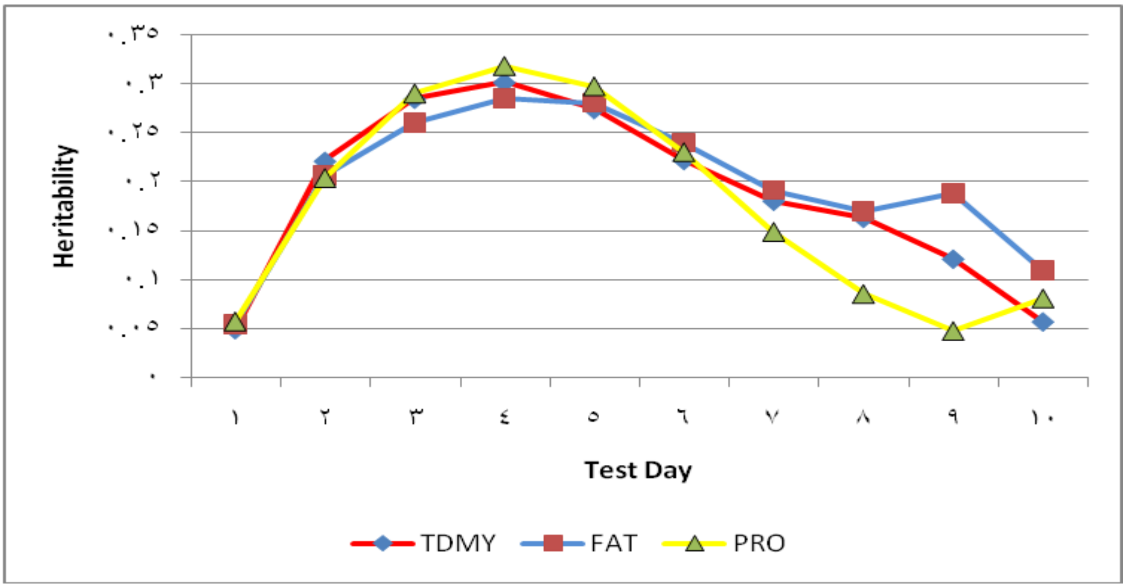

Fig. 4. Estimates of heritability at test days for daily milk, fat and protein yield in Egyptian buffaloes

In general, heritability estimates for traits had wide ranges and tended to increase toward the edges of the defined lactation trajectory. Most heritability estimates obtained by RRM were high at the edges (Jamrozik and Schaeffer, 1997) for dairy cows. Difficulties in the model in getting acceptable variances at the extremes of the lactation can be explained, in part, by the biological processes that occur at the beginning of lactation and the smaller number of records at the end Jamrozik and Schaeffer (1997), and El-Saied (2004) pointed out that these parametric functions tend to overestimate the genetic variances and underestimate the genetic correlations between milk yield at the beginning and the end of lactations. Probably this is also valid for Legendre polynomials.

Predicted breeding value (PBV):

Estimates of minimum and maximum predicted breeding values (PBV) and their accuracies for milk, fat and protein yields are given in Table (3). The PBV for test day milk, fat and protein yields ranged from -1.7 to 1.8*kg*, -11.2 to 11.3*g* and -6.1 to 7.1*g*, respectively. Using TD animal model methodology in cattle, Zutere (2008) found that the estimated breeding values for milk, fat and protein ranged from -1013.9 to 1965.7*kg*, from 40.75 to 93.59 *kg* and from -37.33 to 59.86 *kg*, respectively. Ahmed *et al*. (2008) showed that the estimated breeding value for milk yield ranged from -323.40 to 345.12*kg* in a buffalo. Abdel-Salam *et al*. (2009) showed that the maximum and minimum estimates of breeding values of total milk yield for commercial, experimental, flying and small holder production systems in buffalo were -377 to 368, -302 to 297, -290 to 190 and -76 to 96, respectively.

The accuracies ($r_{a\hat{a}}$) of minimum and maximum estimates of PBV were high in all traits (Table 3). This may be due to that estimate of heritability were highly associated with more available pedigree information for all individuals (Korhonen, 1996; Korsgaard *et al.*, 2002).

Table 3. Minimum, maximum and ranges of predicted breeding values (PBV), predicted error variance (PEV) and accuracy of prediction ($r_{A\hat{A}}$) for TD milk, fat and protein yields in Egyptian buffaloes

Trait	Minimum			Maximum			Range in PBV
	PBV	PEV	$r_{A\hat{A}}$	PBV	PEV	$r_{A\hat{A}}$	
TDMY, kg	-1.7	0.22	0.95	1.8	0.47	0.98	3.5
Fat yield, g	-11.2	0.22	0.99	11.3	0.47	0.995	22.5
Protein yield, g	-6.1	0.22	0.97	7.1	0.47	0.99	13.2

Genetic and Phenotypic trends:

Phenotypic and genetic trends for test day milk, fat and protein yields are shown in Figures from (5) to (10). The range in phenotypic values of year-test day milk, fat and protein yields decreased from 7.99 to 5.66*kg*, 53.37 to 35.07*g* and 30.86 to 21.54*g*,respectively, while the respective genetic values increased from -0.22 to 0.17*kg*, -1.41 to 1.36*g* and -0.82 to 0.70*g*.These results explain the correct methodology of elimination and replacement activities. The positive genetic trends for all milk traits were a result of the good selection program. The decrease in phenotypic trend in all traits may be attributed to low nutritional level applied and management practices in different herds. Yaeghoobi *et al.* (2011) and Katok and Yanar (2012) found the same trend in test day milk yield in cattle. On the other hand, opposite trends showing an increase in genetic and phenotypic trends were reported by Muller and Botha (2003) for TDMY, while Khan (1998) in buffalo reported a decrease genetic and phenotypic trends in cattle. Katok and Yanar (2012), Hallowell *et al*. (1998) found that the genetic and phenotypic trends were increasing in milk, fat and protein yields in cattle. In the Egyptian buffalo, contrary to the present results, Khattab and Mourad (1992) reported that the phenotypic trend was increased, while, the genetic trend was decreased for total milk yield from the year of 1966 to 1987. Fooda *et al.* (2010) reported that the phenotypic and genetic trends for total milk yield were increased in all farms of (APRI) through the period from 1990 to 2008.

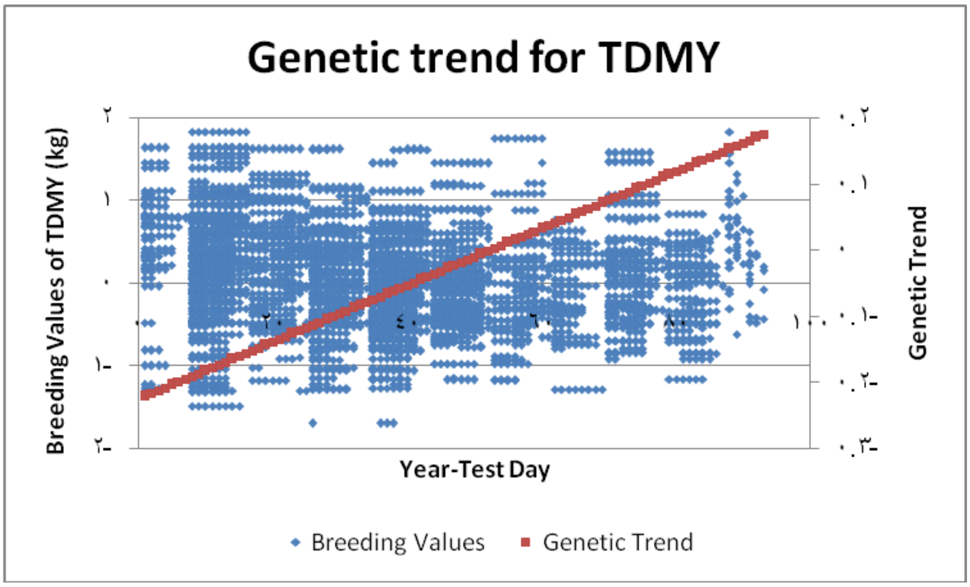

Fig. 5.Genetictrend for test day milk yield in Egyptian buffaloes

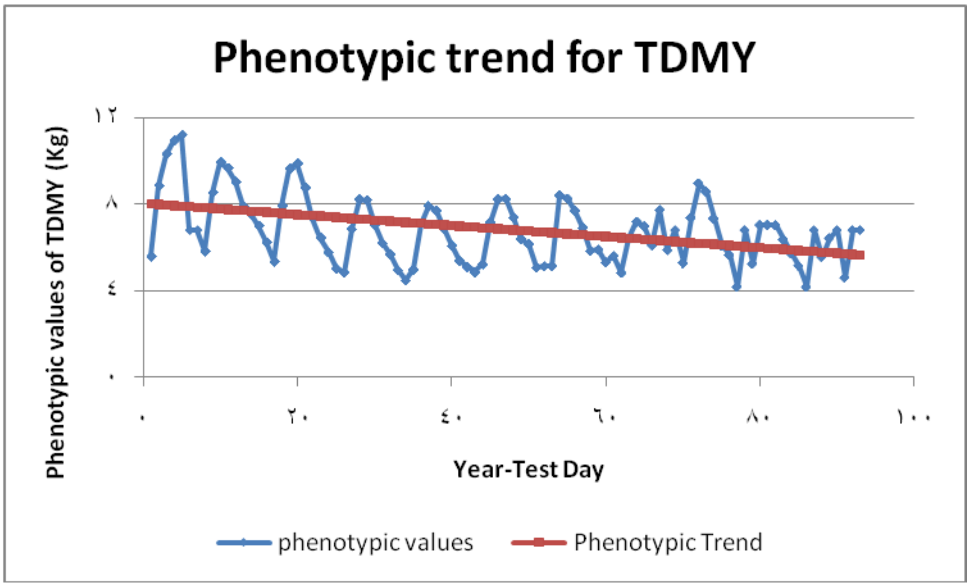

Fig. 6. Phenotypic trend for test day milk yield in Egyptian buffaloes

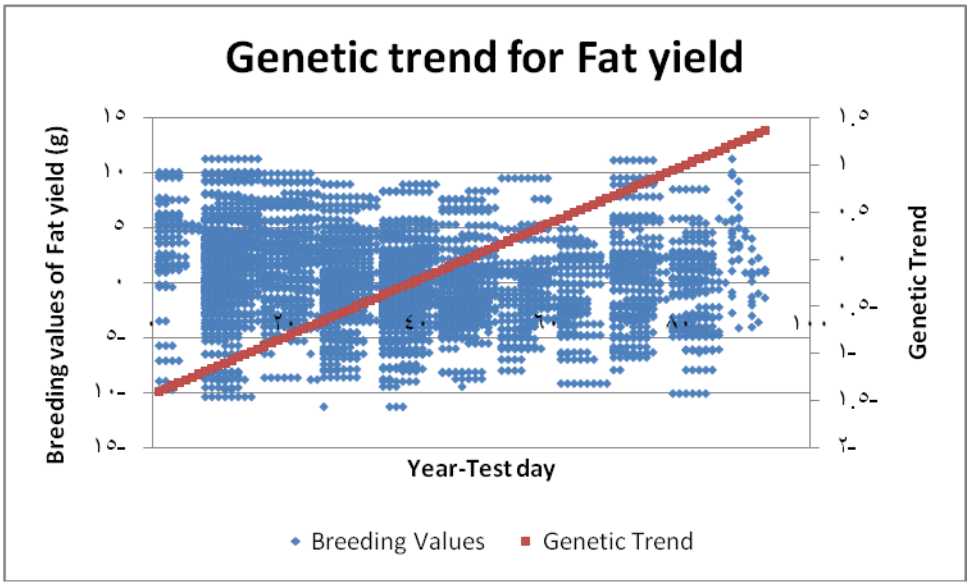

Fig. 7. Genetictrend for test day fat yield in Egyptian buffaloes

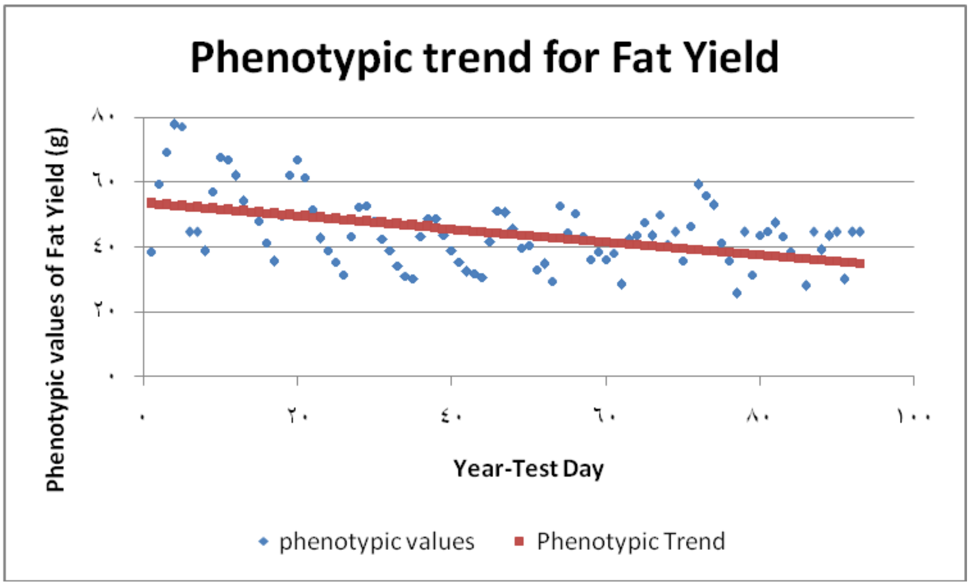

Fig. 8. Phenotypic trend for test day fat yield in Egyptian buffaloes

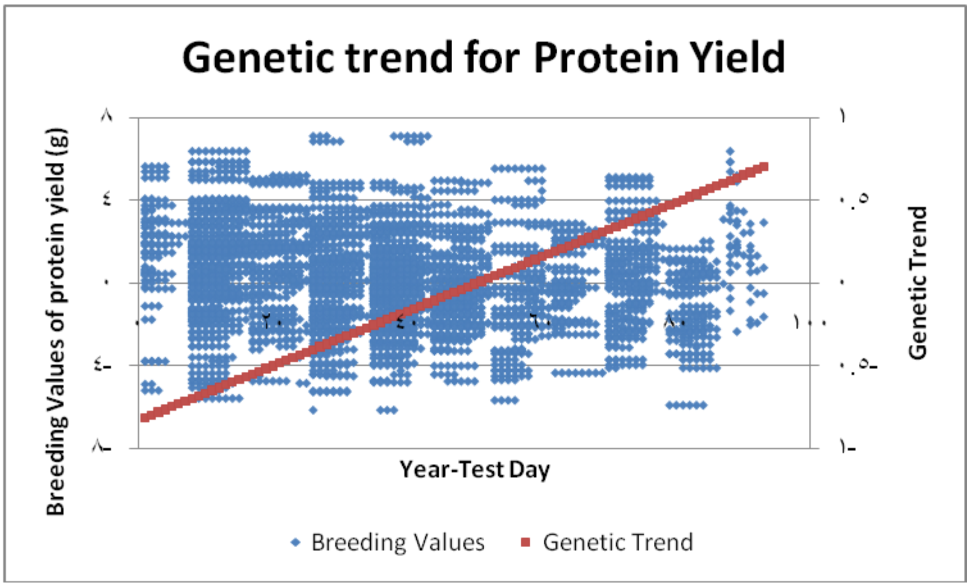

Fig. 9.Genetictrend for test day protein yield in Egyptian buffaloes

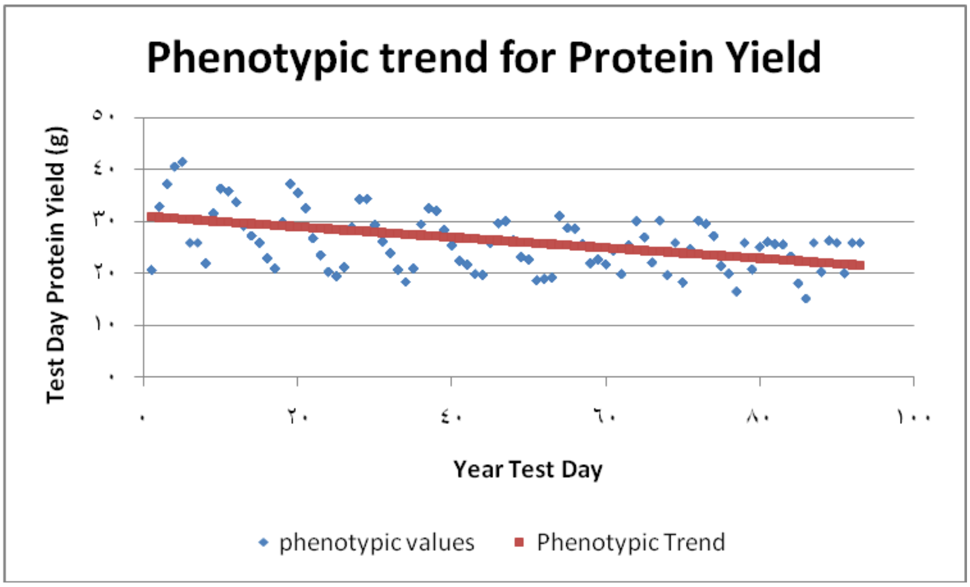

Fig.10.Phenotypic trend for test day protein yield in Egyptian buffaloes

CONCLUSIONS

1) The test-day milk yield during the first three to five months of lactation could be adopted as an early selection criterion to increase milk yield.
2) Random regression model (RRM)was considered to be efficient in detecting the fluctuations in genetic variance along the lactation period. It would permit better modeling for repeated records throughout the lactation period and could be chosen as an accurate method for predicting breeding values.
3) Improving the animal environment, particularly the nutrition and using the selection indexes could improve milk yield traits in Egyptian buffaloes.

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الإتجاهات الوراثية والمظهرية لمحصول يوم الاختبارمن اللبن والدهن والبروتين بتطبيق نموذج الانحدار العشوائي في الجاموس المصري

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استهدفت هذه الدراسة الكشف عن الاتجاهات الوراثية والمظهرية لمحصول اللبن والدهن والبروتين باستخدام بيانات يوم الاختبار في الجاموس المصري مع تطبيق نموذج الانحدار العشوائي (RRM)Random Regression Model. تم استخدام بيانات ٤٩٧١ يوم اختبار (Test Day(TDلعدد ٦٩١ جاموسه مصريةمولوده من ١٢٠ أب و ٥٣٢ أمتمثل أربعة قطعان تابعة لمعهد بحوث الإنتاج الحيواني، مصر. تم استخدام بيانات الشهور العشر الأولى من موسم الحليب. تضمن النموذج التأثيراتالعشوائية للعوامل الوراثية التجمعية المباشرة والبيئة الدائمة والخطأ، في حين اشتملت التأثيرات الثابتة على يوم الاختبار والقطيع والسنة وموسم الولادة وفصل السنة وكذلك أيام الحلب كتغاير covariable. وكان التباين الوراثي التجمعيليوم الاختبار الأول لمحصول اللبن، والدهن والبروتين على التوالي هو ٠.٠٣٥ كجم، ٢.٢٦ جرام، ٠.٨٠ جرام، وأستمر فى زيادة حتى اليوم الرابع ليصل الى 0.807 كجم، ٣٠.٥٢ جرام، ١٢.٥٢ جرام، وانخفضت بعد ذلك القيم لتصل إلى أدنى قيمة لها في اليوم التاسع لمحصولالبن والبروتين (٠.٢٣٨ كجم، ٠.٩٧ جرام) وفي يوم الاختبار العاشر لمحصول الدهن (٧.٢٨ جرام). كانالمكافئ الوراثيلأول يوم اختبار هو ٠.٠٥، وارتفع حتى يوم الاختبار الرابع ليصل الى ٠.٣٠، وانخفض بعد ذلك حتي وصل إلى أدنى قيمة في يوم الاختبار العاشر (٠.٠٦). كان أعلى مكافئ وراثيلمحصول الدهن والبروتين على التوالي هو٠.٢٩ ، ٠.٣١ في يوم الاختبارالرابع. انخفضت القيم المظهرية لإنتاج اللبن من ٧.٩٩ إلى ٥،٦٦ كجم والدهن من ٥٣.٣٧ إلى ٣٥.٠٧جرام والبروتين من ٣٠.٨٦ إلى ٢١.٥٤جرام ، في حين ارتفعت القيم الوراثية للبنمن ٠.٢٢- إلى ٠.١٧ كجم والدهن من ١.٤١- إلى ١.٣٦ جرام والبروتين من ٠.٨٢- إلى ٠.٧٠ جرام. وكانت الاتجاهات الوراثية Genetic trends تميل الى الايجابيه لجميع الصفات مما يدل على أن برنامج التحسين الوراثي في القطعان ينفذ بشكل صحيح. بينما أظهرت الاتجاهات المظهرية لجميع الصفات تدهوراًممايشير إلى وجود بعض أوجه القصور البيئية في القطعان وخاصة بالنسبة لمستوى التغذية.