*Egyptian J. Anim. Prod. (2025) 62(1): 1-17*

# RANDOM REGRESSION MODEL AND BLUPF90 ANALYSES TO EVALUATE THE GENETIC AND PHENOTYPIC TRENDS FOR LACTATION AND REPRODUCTIVE TRAITS IN THE EGYPTIAN BUFFALO

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***Article History: Received:9/12/2024; Accepted:1/1/2025; Published: 16/2/2025***

***DOI: 10.21608/ejap.2025.343178.1094***

## *SUMMARY*

*The aims of this study were to estimate the variance components and heritability estimates for some lactation and reproduction traits of Egyptian buffaloes using a repeatability animal model and Random Regression Model (RRM) and plot the genetic and phenotypic trends. A total number of 7345 test-day records (TD) of milk yield (TDMY), fat yield (TDFY), protein yield (TDPY) and somatic cell score (TDSCS) were gathered monthly from 686 buffaloes. Also, a total number of 7279 reproduction records were collected from 1951 buffaloes. All herds belong to the Animal Production Research Institute (APRI), Ministry of Agriculture and Land Reclamation (MALR), Egypt. The genetic trends for lactation traits favorably increased from -4.63 kg to be 1.61 kg for TDMY, -5.0 g to be 495 g for TDFY and -26 g to be 280 g for TDPY, associated with favorably decreasing trend from 1.19 to be 1.37 for TDSCS as year of TD of milk advanced. On the contrary, the phenotypic trends decreased from 7.49 to 5.69 kg for TDMY, 510 to 360 g for TDFY and 284 to 223 g for TDPY, while that of TDSCS increased to be from 1.62 to 2.43. The genetic trends for reproduction traits slightly decreased from 0.24 mo to be -0.14 mo for AFC, 5.5 d to be 2.9 d for DO and 6.9 d to be 3.6 d for CI, while the phenotypic trends favorably decreased from 36.57 to 36.52 mo for AFC, 127 to 71 d for DO and 416 to 354 d for CI.*

***Keywords: Egyptian buffalo, Genetic and phenotypic trends, Lactation traits, Reproduction traits, Random regression model.***

## INTRODUCTION

In the dairy buffalo, test-day milk (TD) has been used in the genetic evaluation of animals for milk, fat and protein yields in several countries particularly in Egypt (El-Bramony *et al*., 2004, 2017; El-Bramony 2014 and Amin *et al*., 2015), in Italy (Costa *et al.*, 2020), in India (Sahoo *et al*., 2014; Singh *et al*., 2015 and 2016), in Brazil (Tonhati *et al*., 2008; Aspilcueta-Borquis *et al*., 2012), in Colombia (Hurtado-Lugo *et al*., 2009) and in Iran (Madad *et al*., 2013). Using TD milk yield parameters, ruled out the need to extend the lactation period to the standard 305 days length. The TD model allows better modeling for genetic and phenotypic trends because it considers the specific effects of TD, *i.e.* the environmental effects are accurately modeled (Ptak and Schaeffer, 1993) and the genetic parameter estimates are expected to be more accurate (Swalve, 1995). Precise methodology has been proposed to estimate the (co) variance structure among TD records using the Random Regression Model (RRM; Meyer, 1998), *i.e.* RRM can be used for TD milk traits which are expressed repeatedly. In addition to the significance of TD recording, the substantial assessment of the estimated breeding values is an essential step in genetic improvement programs (Meyer, 2004). Accordingly, the package of BLUPF90 software (Misztal *et al.*, 2018; http://nee.ads.uga.edu//wiku///doku.php) has become the worldwide remarkable standard methodology for predicting the breeding values (PBV) for TD lactation traits and reproduction performance using the repeatability animal model.

Pursing the stereotypical behavior and patterns of genetic trends in buffalo populations over years is a significant element in monitoring the selection programs, since this genetic trend corresponds to the observed changes in the breeding values of the animals for specific lactation and reproduction traits during selection. Studies of genetic and phenotypic trends for milk, fat, and protein yields in Egyptian and non-Egyptian buffalo have shown irregular routes. In Egyptian buffalo studies, favorable increases in both genetic and phenotypic trends for milk, fat and protein yields were reported (El-Arian *at al.*, 2012; Ahmad *et al.*, 2017; Abo-Gamil *et al.*, 2017 and EL-Hedainy *et al.*, 2020), while Amin *et al.* (2015) has shown an increase in the genetic trend accompanied by a decrease in the phenotypic trend. Also, most of the non-Egyptian buffalo studies have shown that the genetic and phenotypic trends for milk, fat and protein yields were increasing together (Pawar *et al*., 2018 and Kour and Narang, 2021), while some other studies revealed increases or decreases in the genetic trend (Seno *et al.*, 2010; Aspilcueta-Borquis *et al.*, 2015 and Nazari *et al*., 2021). Regarding the reproduction traits in buffalo, the genetic and phenotypic trends exhibited favorable decreasing trends in AFC, DO and CI of Egyptian buffalo (Shalaby *et al*., 2016 and Amin *et al.*, 2021) or non-favorable increasing trends in AFC and CI as reported by Gupta *et al.* (2015) and Kour and Narang (2021) for the Murrah buffalo.

The genetic evaluation of the breeding animals of the Egyptian buffalo requires accurate estimation of the genetic parameters (*i.e.* heritability and predicted breeding values) for lactation and reproduction traits. These estimates are essential for plotting the genetic and phenotypic trends to be used in evaluating the breeding programs and assessing the selection process. Therefore, the main objectives of the present study were: 1) evaluate genetically some lactation and reproduction traits in Egyptian buffalo through estimating the variance components and heritability using Bayesian Gibbs Sampling Algorithm, and 2) predict the breeding values and plot the genetic and phenotypic trends for these traits.

## MATERIALS AND METHODS

### *The studied Buffalo herds:*

Six experimental buffalo herds, nominated as El-Nattafe El-Gadid (NG), El-Nattafe El-Kadim (NK), El-Nubariya (EN), El-Serw (ES), El-Gimmeza (EG) and Sids (S), belong to the Animal Production Research Institute (APRI), Agricultural Research Center (ARC), Ministry of Agricultural and Land Reclamation (MALR), Egypt were used in this study. The herds NG and NK are located in Kafr El-Sheikh Governorate, while EN herd is located in Behira Governorate, EG herd in Gharbia Governorate, ES herd in Damietta Governorate and S herd in Beni Suef Governorate. All the herds are located in the Nile Delta region, lower Egypt except Sids herd is in Upper Egypt.

### *Management and feeding:*

Buffaloes were kept under semi-open sheds; heifers were joined for the first service when reaching 24 months of age or 330 kg body weight. Buffaloes were naturally mated in a group-mating system and in few cases the buffaloes were artificially inseminated. Rectal palpation was applied to check pregnancy at 60 days post-mating. Milking was practiced twice a day at seven AM and four PM throughout the lactation period. Buffaloes were fed Egyptian Berseem (*Trifolium alexandrinum*) along with varying amounts of integrated concentrate feed mixture (48% decorticated cotton seed cake, 21% wheat bran, 20 % maize, 5 % rice polish, 3 % molasses, 2 % limestone, and 1 % sodium chloride) according to APRI feeding routine. The diet contains 16 % protein for breeding buffaloes and heifers and 17 % protein for suckling calves during the period from 2 to 6 months of age. Feed is offered manually starting with the roughage (silage - rice straw - alfalfa – alfalfa hay), followed by the concentrate feed. Feeding takes place twice a day at six AM and then at five PM and clean water is available all the time. The amount of feed required for each animal was calculated depending on the animal weight and quantity of daily milk produced. The calves were weighed immediately after birth and then weighed monthly. Buffaloes were dried off two months before the expected day of calving. The abnormal lactations or reproduction records affected by diseases or having missing birth dates, dry off dates or yields were excluded.

Fat and protein percentages as well as the somatic cell count 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, Egypt. The somatic cell count (SCC) is recorded monthly in thousands per *ml* and transformed to somatic cell score (SCS) using $\log^{10}$ scale to achieve an approximate normal distribution (EL-Bramony *et al.*, 2004). Buffaloes were regularly vaccinated against foot and mouth disease at four months interval and yearly against Clostridia, Pasteurelloses and three-day fever.

### *Data structure of lactation traits:*

A total number of 7345 TD records of milk, fat and protein yields and somatic cell scores were gathered monthly from 686 buffaloes, daughters of 83 sires and 423 dams for a period of 21 years starting from 2003 up to 2023 in three experimental buffalo herds of NG, NK and EG. Records of TD milk were collected following an alternate AM: PM monthly recording scheme. The buffaloes having abnormal phenotypic values for daily milk yield or less than four TD records per lactation were excluded from the milk data set. The maximum number of TD milk records per lactation per buffalo was 9. All available relationships among animals were considered in the statistical analyses. The pedigree file comprised a total of 10802 relationship records. The number of buffalo animals and records belonging to the three studied herds used in data analyses for lactation traits are shown in Table 1.

Data of TD lactation yields of milk (TDMY), fat (TDFY) and protein (TDPY) and somatic cell score (TDSCS) were used in the present study. TD records between 5 and 270 days in milk (DIM) were considered in the statistical analysis. The first TD included test days between 4 and 15 days in milk (DIM) and all the subsequent tests were classified as 30-d interval up to 270 DIM and therefore the buffaloes used in the analyses had at least four TD records per lactation. TD data after 270 days was discarded from the data file because it had few numbers of observations. TD records per lactation were classified into nine test-days (TD1 to TD9) according to days in milk.

**Table 1. Summary of the data available for lactation traits used in data analysis of the three studied Egyptian buffalo herds**

| Item | Herd | | | |
|---|---|---|---|---|
| | **NG** | **NK** | **EG** | **All herds** |
| **Number of buffaloes with records** | 212 | 440 | 34 | 686 |
| **Number of sires with records** | 22 | 59 | 2 | 83 |
| **Number of dams with records** | 140 | 268 | 15 | 423 |
| **Total number of animals (buffalo, sires and dams)** | 374 | 767 | 51 | 1192 |
| **Total number of test-day milk records** | 2201 | 4713 | 431 | 7345 |

NG= El-Nattafe El-Gadid herd, NK= El-Nattafe El-Kadim herd and EG= El-Gimmeza herd.

### *Data structure of reproduction traits:*

Records of age at first calving (AFC), days open (DO) and calving interval (CI) were collected from the database file of the six studied APRI herds. A total number of 7279 reproduction records collected for a period of 22 years (2002 to 2023) from 1951 buffaloes, daughters of 155 sires and 1179 dams were used in this study. Also, all available relationships among animals were considered in analyses of reproduction traits.

The number of buffalo animals and records belonging to the six herds were used in data analyses of reproduction traits (Table 2). The differences among the numbers of animals and records for lactation traits relative to those for reproduction traits are attributed to the fact that the data related to the reproduction traits are easy to record each parturition to track any fertility disorders, while the data related to milk composition traits are lesser due to the cost of measuring milk composition.

**Table 2. Summary of the data available for reproduction traits used in data analysis of the six studied Egyptian buffalo herds**

| Item | Herd | | | | | | |
|---|---|---|---|---|---|---|---|
| | **NG** | **NK** | **EN** | **S** | **EG** | **ES** | **All herds** |
| **Number of buffaloes with records** | 805 | 285 | 42 | 253 | 526 | 40 | 1951 |
| **Number of sires with records** | 75 | 30 | 8 | 13 | 25 | 4 | 155 |
| **Number of dams with records** | 479 | 187 | 27 | 159 | 309 | 18 | 1179 |
| **Total number of animals (buffalo, sires and dams)** | 1359 | 502 | 77 | 425 | 860 | 62 | 3285 |
| **Total number of reproduction records** | 3104 | 1278 | 103 | 861 | 1885 | 48 | 7279 |

NG= El-Nattafe El-Gadid, NK= El-Nattafe El-Kadim, EN= El-Nubaria, S= Sids, EG= El-Gimmeza and ES= El-Serw.

### *Animal Model and Random Regression Model used for analyzing lactation traits:*

The variance-covariance components of the random effects were estimated for TD milk, fat and protein yields and somatic cell score using TM software of Bayesian Gibbs Sampling Algorithm (Legarra *et al.*, 2008). The estimates obtained by Gibbs Sampling were used to solve the corresponding mixed model equations, using the PEST software to obtain the generalized least-squares means (GLM) for TD lactation traits (Groeneveld, 2006). Therefore, the following single-trait repeatability animal model was used (Model 1):

$y = Xb + Z_a u_a + Z_p u_p + e$ (Model 1, Repeatability Single-trait animal model)

where: Y = the recorded lactation trait; b = vector of the fixed effects of herd-year test-day (271 levels), parity (5 levels), season of calving (4 levels) and covariable of days in milk (DIM); $u_a$ = the vector of random additive genetic effects of buffaloes; up = the vector of random non-additive permanent environmental effects of buffaloes; X, $Z_a$ and $Z_p$ = incidence matrices for fixed effects, random additive genetic effects and random permanent environmental effects, respectively; e = vector of random error. The variance-covariance components of the random effects were estimated using the following matrices:

$$Var\begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I_p\sigma_P^2 & 0 \\ 0 & 0 & I_n\sigma_e^2 \end{bmatrix}$$

where: A = Numerator relationship matrix, $I_p$ and $I_n$ = identity matrix with order equal to number of animals and number of records, respectively, $\sigma^2{}_a$, $\sigma^2{}_P$ and $\sigma^2{}_e$ = the variances due to direct additive genetic effects, permanent environmental effects and random error, respectively. A single-trait repeatability animal model was used in analysis of lactation traits, considering the relationship coefficient matrix ($A^{-1}$) among the animals (Korhonen, 1996). The occurrence of local maxima was checked by repeatedly restarting the analyses until the log-likelihood did not change beyond the first decimal. Heritabilities ($h^2$) for TD lactation traits were computed using the TM software of Bayesian Gibbs Sampling Algorithm (Legarra *et al.*, 2008): $h^2 = \frac{\sigma^2{}_a}{\sigma^2{}_a+\sigma^2{}_p+\sigma^2{}_e}$, where $\sigma^2{}_a$, $\sigma^2{}_P$ and $\sigma^2{}_e$ as defined before.

For random regression model analysis (RRM), the VCE6 program was employed to analyze the data of TD lactation traits using the Legendre polynomials method. The variance-covariance components were estimated using the computer package VCE6 (Groeneveld *et al*., 2010) as (Model 2, RRM):

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

where: Yijk*l* = the test-day observation of yields of milk (TDMY), fat (TDFY) and protein (TDPY) or test-day somatic cell score (TDSCS) within l$^{th}$ lactation made on i$^{th}$ herd test-date (HTD$_i$) of the j$^{th}$ buffalo cow belonging to k$^{th}$ subclass TD (k ranged from 1 to 9 starting with k=1 equal 4 to 15 DIM and all the subsequent classes were classified as 30-d interval up to 270 DIM); HTD$_i$ = the fixed effect of i$^{th}$ herd test-day (114 levels), DIM = days in milk as linear and quadratic covariables; $\beta_{km}$ = the fixed regression coefficients for m$^{th}$ TDMY or TDFY or TDPY or TDSCS on DIM of the k$^{th}$ TD (year-season of calving, 80 levels and parity, 5 levels), $\alpha_{jm}$ = the random regression coefficients of additive genetic effects for m$^{th}$ TDMY, TDFY, TDPY or TDSCC on DIM for j$^{th}$ buffalo cow, $\chi_{jm}$ = the random regression coefficients of permanent environment effects for m$^{th}$ TDMY, TDFY, TDPY or TDSCS on DIM of the j$^{th}$ buffalo cow; m= the number of traits (4 traits); Z$_{ilm}$ = the random genetic effect of TD lactation trait associated with all TD yields of the j$^{th}$ buffalo cow and e$_{ijkl}$ = random residual effect associated with Y$_{ijkl}$.

### *Animal model for analyzing reproduction traits:*

The systematic environmental effects on DO and CI traits were evaluated using linear model fitting the fixed effects to avoid over-parameterization in the model. The variance components of random effects and heritabilities were estimated by TM software based on Bayesian Gibbs Sampling Algorithm (Legarra *et al.*, 2008). The estimates obtained from Gibbs Sampling were used to solve the corresponding mixed model equations, obtaining the solutions for DO and CI traits using the PEST software (Groeneveld, 2006). Therefore, the following single-trait repeatability animal model was used for analyzing DO and CI (Model 3):

$y = X_b + Z_a u_a + Z_p u_p + e$ (Model 3, Repeatability Single-trait animal model)

where y = the vector of observed DO and CI trait for the buffalo cow; b = the vector of fixed effects of herd year-season of calving (380 levels), and parity (four levels); u$_a$ = the vector of random additive genetic effects of the buffalo cow; up = the vector of random non-additive permanent effects of the buffalo cow; X, Z$_a$ and Z$_p$ = the incidence matrices relating records to the fixed effects, random additive genetic effects and permanent environment effects, respectively; e = the vector of random residual effects. Data of AFC was analyzed using the same Model 3 after excluding the fixed effect of parity and the random non-additive permanent effects. Heritabilities (h$^2$) for reproduction traits were computed using TM software of Bayesian Gibbs Sampling Algorithm (Legarra *et al.*, 2008) as; $h^2 = \frac{\sigma^2{}_a}{\sigma^2{}_a + \sigma^2{}_P + \sigma^2{}_e}$ for DO and CI traits, while $h^2 = \frac{\sigma^2{}_a}{\sigma^2{}_a + \sigma^2{}_e}$ for AFC trait, where $\sigma^2{}_a$, $\sigma^2{}_P$ and $\sigma^2{}_e$ are as defined before.

### *Predicting breeding values (PBVs) using BLUPF90 program:*

The predicted breeding values (PBVs), predicted error variance (PEV *i.e.* standard errors, SE) and accuracies of predictions (rA) for lactation and reproduction traits were estimated using the computer package of BLUPF90 software (Misztal *et al*., 2018; http://nee.ads.uga.edu//wiku///doku.php). The values of PBV were estimated for 1192 buffaloes for lactation traits of TDMY, TDFY, TDPY and TDSCS using the repeatability animal model mentioned before (Model 1), while the values of PBV for reproduction traits were estimated from 3285 buffaloes (Model 3). The solutions for the equations of animals were computed from the pedigree file for buffaloes with records and sires and dams without records. The accuracy for PBV (rA) was defined as the correlation between the true and predicted breeding values and is calculated as described by Meyer (2004) as: r$_A$ $= \sqrt{1 - (PEV/\sigma^2 a)}$

Where PEV = the prediction error variance estimated using the elements from the mixed model equations as PEV = (SEP)$^2$; SEP = the standard error of prediction and σ²a = the additive genetic variance of the trait.

### *Plotting the genetic and phenotypic trends:*

The phenotypic trend for each lactation trait was measured by regressing the phenotypic values of a lactation trait for 7345 lactation records of TDMY, TDFY, TDPY and TDSCS on herd-year-TD (271 levels). The breeding values of 1192 buffaloes with records and without records estimated by BLUPF90 software were used for plotting the genetic trends (Misztal *et al*., 2018). Accordingly, the breeding values for 1192 animals with 7345 lactation records were used to plot the genetic trends by regressing the breeding values for TDMY, TDFY, TDPY and TDSCS on herd-year test day (271 levels).

For reproduction traits, the phenotypic trends were measured as the regression of the phenotypic values for DO, CI and AFC traits on herd-year-season of calving (380 levels). The breeding values estimated by BLUPF90 software (Misztal *et al*., 2018) for 7279 reproduction records were used in plotting the genetic trends by regressing the breeding values for AFC, DO and CI on herd-year-season of calving (380 levels).

## RESULTS AND DISCUSSION

### *Descriptive statistics for lactation and reproduction traits:*

The generalized least square means (GLM), standard errors (SE), minimum and maximum values and coefficients of variation (CV %) for lactation and reproduction traits are shown in Table (3). The GLM for lactation traits were 5.76, 7.49, 7.79, 7.34, 6.72, 5.98, 5.28, 4.65 and 4.41 kg for TDMY, 0.36, 0.49, 0.51, 0.49, 0.45, 0.40, 0.35, 0.32 and 0.31 kg for TDFY, 0.23, 0.29, 0.30, 0.28, 0.26, 0.23, 0.21, 0.19 and 0.18 kg for TDPY and 2.01, 2.01, 2.02, 2.01, 2.02, 2.05, 2.10, 2.05 and 1.92 for TDSCS of the consecutive monthly TD traits solutions throughout lactation, respectively. These TD estimates were in accordance with those obtained by El-Bramony *et al.* (2004, 2017) and Amin *et al*. (2015) on Egyptian buffalo, while were greater than those obtained by Aspilcueta-Borquis *et al*. (2012) on Murrah buffalo, by Sahoo *et al*. (2014) on Indian buffalo and by Madad *et al*. (2013) on Iranian buffalo.

Wide ranges between minimum and maximum values for TD lactation traits were detected, ranging from 1.5 to 20 kg for TDMY, 0.1 to 1.7 kg for TDFY and 0.1 to 0.8 kg for TDPY and 1.0 to 3.6 for TDSCS (Table 3). In Egyptian buffalo, Amin *et al*. (2015) and El-Bramony *et al*. (2017) reported that the ranges between minimum and maximum values for TDMY were 5.14 to 8.51 kg. The coefficients of variation (CV%) values for lactation traits were mostly moderate or high but decreased with the advancement of TD (Table 3) and ranged from 31 to 52 % for TDMY, TDFY and TDPY, while they were 22% to 24% for TDSCS. The large coefficients of variation for lactation traits present good opportunities for selection and possible genetic improvement for these traits. Similarly, coefficients of variation for lactation traits of Egyptian buffaloes were mostly moderate or high, ranging from 19.6 to 41.57% for TDMY, 23.9 to 39.85% for TDFY and 21.2 to 40.87% for TDPY as reported by Amin *et al.* (2015) on Egyptian buffalo, Tonhati *et al*. (2008) and Aspilcueta-Borquis *et al*. (2012) on Murrah buffalo and Madad *et al.* (2013) on Iranian buffalo.

The GLM for reproduction traits were 36.55 *mo*, 99.4 *d* and 385.6 *d* for AFC, DO and CI, respectively (Table 3). In the Egyptian buffalo studies, the means were 484 *d* for CI and 184 *d* for DO (Mostafa *et al*., 2017). Wide ranges between minimum and maximum values for reproduction traits in Egyptian buffaloes were observed, being 24.8 to 49.7 *mo* in AFC, 39 to 300 *d* in DO and 300 to 600 *d* in CI (Table 3). Furthermore, the coefficients of variation for reproduction traits were mostly moderate or high, 15% for AFC, 76% for DO and 22% for CI. Other studies on Egyptian buffaloes indicated that the coefficients of variation for reproduction traits were mostly moderate (Aziz *et al.*, 2001), being 27% for CI and 68.1% for DO and by Mostafa *et al*. (2017) to be 70.46% for DO and by Helmy and Somida (2021) to be 15.13%, 19.67% and 57.67% for AFC, CI and DO, respectively.

**Table 3. The generalized least square means (GLM), standard errors (SE), minimum and maximum values and coefficients of variation (CV%) for test-day (TD) lactation and reproduction traits in the Egyptian buffaloes**

| **Trait** | **GLM** | **SE** | **Minimum value** | **Maximum value** | **CV%** |
|---|---|---|---|---|---|
| **Lactation traits (N= 7345 records):** | | | | | |
| TD1 at 4 days in milk (N= 941records): | | | | | |
| TDMY (*kg*) | 5.76 | 0.086 | 1.5 | 18.0 | 46 |
| TDFY (kg) | 0.362 | 0.006 | 0.1 | 1.7 | 52 |
| TDPY (kg) | 0.229 | 0.003 | 0.1 | 0.7 | 46 |
| TDSCS | 2.01 | 0.016 | 1.0 | 3.4 | 24 |
| **TD2 at 30 days in milk (N= 1055 records):** | | | | | |
| TDMY (kg) | 7.49 | 0.092 | 2.0 | 20.0 | 40 |
| TDFY (kg) | 0.485 | 0.007 | 0.1 | 1.4 | 46 |
| TDPY (kg) | 0.288 | 0.004 | 0.1 | 0.8 | 41 |
| TDSCS | 2.01 | 0.015 | 1.0 | 3.3 | 24 |
| **TD3 at 60 days in milk (N= 1094 records):** | | | | | |
| TDMY (kg) | 7.79 | 0.083 | 2.0 | 18.0 | 35 |
| TDFY (kg) | 0.512 | 0.006 | 0.1 | 1.4 | 41 |
| TDPY (kg) | 0.301 | 0.003 | 0.1 | 0.8 | 37 |
| TDSCS | 2.02 | 0.015 | 1.0 | 3.2 | 24 |
| **TD4 at 90 days in milk (N= 1120 records):** | | | | | |
| TDMY (kg) | 7.34 | 0.082 | 2.0 | 18.0 | 37 |
| TDFY (kg) | 0.485 | 0.006 | 0.1 | 1.4 | 41 |
| TDPY (kg) | 0.282 | 0.003 | 0.1 | 0.8 | 40 |
| TDSCS | 2.01 | 0.014 | 1.0 | 3.6 | 24 |
| **TD5 at 120 days in milk (N= 1051 records):** | | | | | |
| TDMY (kg) | 6.72 | 0.077 | 2.0 | 17.0 | 37 |
| TDFY (kg) | 0.449 | 0.006 | 0.1 | 1.3 | 41 |
| TDPY (kg) | 0.261 | 0.003 | 0.1 | 0.7 | 39 |
| TDSCS | 2.02 | 0.015 | 1.0 | 3.3 | 24 |

**Table 3. Cont.**

| Trait | GLM | SE | Minimum value | Maximum value | CV% |
|---|---|---|---|---|---|
| **TD6 at 150 days in milk (N= 922 records):** | | | | | |
| TDMY (kg) | 5.98 | 0.069 | 1.5 | 15.0 | 35 |
| TDFY (kg) | 0.402 | 0.005 | 0.1 | 1.1 | 41 |
| TDPY (kg) | 0.233 | 0.003 | 0.1 | 0.6 | 36 |
| TDSCS | 2.05 | 0.015 | 1.0 | 3.4 | 22 |
| **TD7 at 180 days in milk (N = 652 records):** | | | | | |
| TDMY (kg) | 5.28 | 0.072 | 1.5 | 15.0 | 35 |
| TDFY (kg) | 0.354 | 0.006 | 0.1 | 1.3 | 42 |
| TDPY (kg) | 0.210 | 0.003 | 0.1 | 0.6 | 36 |
| TDSCS | 2.10 | 0.018 | 1.0 | 3.2 | 22 |
| **TD8 at 210 days in milk (N= 354 records):** | | | | | |
| TDMY (kg) | 4.65 | 0.077 | 2.0 | 12.5 | 31 |
| TDFY (kg) | 0.316 | 0.007 | 0.1 | 0.9 | 41 |
| TDPY (kg) | 0.185 | 0.003 | 0.1 | 0.5 | 33 |
| TDSCS | 2.05 | 0.024 | 1.1 | 2.9 | 22 |
| **TD9 at 240 days in milk (N= 156 records):** | | | | | |
| TDMY (kg) | 4.41 | 0.114 | 2.0 | 8.5 | 32 |
| TDFY (kg) | 0.313 | 0.010 | 0.1 | 0.6 | 38 |
| TDPY (kg) | 0.177 | 0.005 | 0.1 | 0.4 | 36 |
| TDSCS | 1.92 | 0.034 | 1.1 | 3.4 | 22 |
| **Reproduction traits:** | | | | | |
| AFC, month (N= 1951 records) | 36.55 | 0.120 | 24.8 | 49.7 | 15 |
| DO, day (N= 7279 records) | 99.4 | 0.883 | 39 | 300 | 76 |
| CI, day (N= 7279 records) | 385.6 | 0.983 | 300 | 600 | 22 |

TDMY= Test-day milk yield, TDFY= Test-day fat yield, TDPY= Test-day protein yield and TDSCS ($\log^2$) = Test-day somatic cell score; AFC= Age at first calving; DO= Days open; CI= Calving interval.

### *Heritability estimates and permanent environmental effects:*

Heritability values estimated by repeatability single-trait animal model for lactation traits were mostly moderate ranging from 0.05 to 0.40 for TDMY, 0.05 to 0.45 for TDFY, 0.06 to 0.44 for TDPY and 0.03 to 0.39 for TDSCS (Table 4). Thus, selection for lactation traits in Egyptian buffalo could be performed efficiently. These estimates were within the range of those heritability values estimated by animal model in other studies on Egyptian buffalo (Ibrahim *et al*., 2012 and El-Bramony *et al*., 2017), Brazilian Murrah buffalo (Tonhati *et al*., 2008 and de Camargo *et al*., 2015) and Indian Murrah buffalo (Sahoo *et al*., 2014 and Singh *et al*., 2016).

The proportions of permanent environmental effects ($p^2$) estimated by animal model for lactation traits were moderate, ranging from 0.10 to 0.31 for TDMY, 0.06 to 0.29 for TDFY, 0.09 to 0.25 for TDPY and from 0.07 to 0.22 for TDSCS (Table 4). During the lactation period, the lactation traits of buffalo become sensitive to the environmental and management changes. El-Bramony *et al.* (2017) reported that the $p^2$ estimated by animal model for lactation traits were high and ranged from 0.56 to 0.74 for TDMY, 0.53 to 0.69 for TDFY and 0.51 to 0.70 for TDPY.

Heritability values estimated by RRM for lactation traits were mostly low at the beginning of lactation, increased gradually to reach the highest value then decreased gradually to reach the lowest value towards the end of lactation, these estimates ranged from 0.04 to 0.25 for TDMY, 0.05 to 0.18 for TDFY, 0.03 to 0.23 for TDPY and 0.07 to 0.57 for TDSCS (Table 4). Similarly, Amin *et al.* (2015) reported definite trend for heritability values estimated by RRM for milk yield in Egyptian buffalo to be low at the beginning of the TD process (0.049 to 0.057) and gradually increased to reach the highest value at the fourth TD (0.28 and 0.31), then the estimates decreased gradually until reaching the lowest value at the tenth TD (0.06 to 0.10). Aspilcueta-Borquis *et al.* (2012) found that heritability estimates of Brazilian Murrah buffalo estimated by RRM were 0.16 to 0.29, 0.20 to 0.30 and 0.18 to 0.27 for TDMY, TDFY and TDPY, respectively.

The proportions of $p^2$ estimated by RRM for milk, fat and protein yields were mostly low or moderate, ranging from 0.05 to 0.09, 0.17 to 0.21, 0.26 to 0.28, 0.28 to 0.31, 0.27 to 0.31, 0.23 to 0.27, 0.18 to 0.21, 0.09 to 0.16 and 0.02 to 0.12 for the consecutive TD number between 1 and 9 (Table 4). However, *p2* for TDSCS were mostly high, ranging from 0.18 to 0.59. El-Bramony *et al.* (2017) reported that $p^2$ estimated by RRM ranged from 0.09 to 0.31 for TDMY, 0.02 to 0.31 for TDFY, 0.05 to 0.28 for TDPY and 0.18 to 0.59 for TDSCS. Aspilcueta-Borquis *et al.* (2012) reported that in Murrah buffalo the $p^2$ estimated by RRM were moderate or high, ranging from 0.35 to 0.45 for TDMY, 0.30 to 0.52 for TDFY and 0.40 to 0.45 for TDPY. Recently, Ranjan *et al*. (2023) in Murrah buffaloes showed that the $p^2$ estimated by

RRM for TDMY were high and ranged from 0.21 to 0.85.

The heritability estimated by single-trait animal model for reproduction traits were low, being 0.10 for AFC, 0.02 for DO and 0.02 for CI (Table 4). The proportions of permanent environmental effects ($p^2$) were also low for DO and CI, being 0.02 and 0.01, respectively (Table 4). In several Egyptian buffalo studies, the heritability estimates of reproduction traits were mostly low or rarely moderate, being 0.12 to 0.35 for AFC, 0.002 to 0.19 for CI and 0.0001 to 0.18 for DO (El-Bramony., 2014; Mostafa *et al.*, 2017; ShafiK *et al.*, 2017; El-Bramony *et al.*, 2017; Amin *et al.*, 2021; Helmy and Somida, 2021 and Easa *et al.*, 2022).

**Table 4. Heritability estimates ($h^2$) and proportions of permanent environmental effects ($p^2$) and random error effects ($e^2$) for test-day (TD) lactation traits and reproduction performance in the Egyptian buffaloes**

| **Trait** | **Animal Model** | | | **Random Regression Model** | | |
|---|---|---|---|---|---|---|
| | **$h^2$±SE** | **$p^2$±SE** | **$e^2$±SE** | **$h^2$** | **$p^2$** | **$e^2$** |
| **Lactation traits (N= 7345 record):** | | | | | | |
| **TD1 at 4 days in milk (N= 941 record):** | | | | | | |
| TDMY (*kg*) | 0.07 (0.06) | 0.24 (0.06) | 0.68 (0.05) | 0.22 | 0.09 | 0.69 |
| TDFY (kg) | 0.07 (0.05) | 0.21 (0.06) | 0.72 (0.05) | 0.16 | 0.09 | 0.75 |
| TDPY (kg) | 0.08 (0.06) | 0.21 (0.07) | 0.70 (0.05) | 0.23 | 0.05 | 0.72 |
| TDSCS | 0.07 (0.05) | 0.07 (0.04) | 0.85 (0.04) | 0.07 | 0.58 | 0.35 |
| **TD2 at 30 days in milk (N= 1055 record):** | | | | | | |
| TDMY (kg) | 0.09 (0.06) | 0.17 (0.06) | 0.74 (0.05) | 0.25 | 0.21 | 0.54 |
| TDFY (kg) | 0.05 (0.04) | 0.10 (0.05) | 0.84 (0.04) | 0.17 | 0.21 | 0.62 |
| TDPY (kg) | 0.08 (0.06) | 0.11 (0.05) | 0.80 (0.05) | 0.22 | 0.17 | 0.60 |
| TDSCS | 0.06 (0.05) | 0.18 (0.05) | 0.76 (0.05) | 0.24 | 0.51 | 0.25 |
| **TD3 at 60 days in milk (N= 1094 record):** | | | | | | |
| TDMY (kg) | 0.20 (0.09) | 0.24 (0.08) | 0.56 (0.04) | 0.24 | 0.28 | 0.48 |
| TDFY (kg) | 0.10 (0.07) | 0.18 (0.07) | 0.71 (0.05) | 0.15 | 0.28 | 0.57 |
| TDPY (kg) | 0.14 (0.08) | 0.15 (0.07) | 0.71 (0.05) | 0.19 | 0.26 | 0.55 |
| TDSCS | 0.06 (0.04) | 0.16 (0.05) | 0.79 (0.04) | 0.23 | 0.55 | 0.21 |
| **TD4 at 90 days in milk (N= 1120 record):** | | | | | | |
| TDMY (kg) | 0.05 (0.05) | 0.31 (0.06) | 0.63 (0.04) | 0.20 | 0.31 | 0.48 |
| TDFY (kg) | 0.05 (0.05) | 0.24 (0.06) | 0.71 (0.05) | 0.12 | 0.31 | 0.57 |
| TDPY (kg) | 0.06 (0.06) | 0.25 (0.06) | 0.68 (0.05) | 0.16 | 0.28 | 0.55 |
| TDSCS | 0.10 (0.08) | 0.18 (0.06) | 0.71 (0.05) | 0.25 | 0.54 | 0.21 |
| **TD5 at 120 days in milk (N= 1051 record):** | | | | | | |
| TDMY (kg) | 0.09 (0.06) | 0.30 (0.06) | 0.61 (0.04) | 0.16 | 0.31 | 0.53 |
| TDFY (kg) | 0.10 (0.07) | 0.20 (0.06) | 0.69 (0.05) | 0.08 | 0.30 | 0.62 |
| TDPY (kg) | 0.11 (0.08) | 0.19 (0.07) | 0.69 (0.04) | 0.13 | 0.27 | 0.60 |
| TDSCS | 0.10 (0.06) | 0.13 (0.06) | 0.77 (0.05) | 0.18 | 0.59 | 0.23 |
| **TD6 at 150 days in milk (N= 922 record):** | | | | | | |
| TDMY (kg) | 0.08 (0.06) | 0.14 (0.06) | 0.78 (0.05) | 0.11 | 0.27 | 0.62 |
| TDFY (kg) | 0.05 (0.04) | 0.09 (0.05) | 0.86 (0.05) | 0.05 | 0.26 | 0.69 |
| TDPY (kg) | 0.08 (0.06) | 0.11 (0.06) | 0.80 (0.05) | 0.09 | 0.23 | 0.68 |
| TDSCS | 0.03 (0.03) | 0.14 (0.05) | 0.82 (0.05) | 0.25 | 0.49 | 0.26 |
| **TD7 at 180 days in milk (N = 652 record):** | | | | | | |
| TDMY (kg) | 0.09 (0.06) | 0.10 (0.06) | 0.82 (0.07) | 0.06 | 0.21 | 0.72 |
| TDFY (kg) | 0.06 (0.05) | 0.06 (0.04) | 0.88 (0.05) | 0.05 | 0.18 | 0.77 |
| TDPY (kg) | 0.08 (0.06) | 0.09 (0.06) | 0.83 (0.07) | 0.06 | 0.18 | 0.76 |
| TDSCS | 0.11 (0.08) | 0.21 (0.09) | 0.68 (0.07) | 0.25 | 0.46 | 0.29 |
| **TD8 at 210 days in milk (N= 354 record):** | | | | | | |
| TDMY (kg) | 0.18 (0.13) | 0.20 (0.11) | 0.62 (0.09) | 0.04 | 0.16 | 0.80 |
| TDFY (kg) | 0.15 (0.11) | 0.13 (0.09) | 0.72 (0.11) | 0.09 | 0.09 | 0.82 |
| TDPY (kg) | 0.19 (0.13) | 0.21 (0.11) | 0.60 (0.09) | 0.03 | 0.15 | 0.82 |
| TDSCS | 0.13 (0.11) | 0.13 (0.11) | 0.71 (0.12) | 0.40 | 0.31 | 0.29 |
| **TD9 at 240 days in milk (N= 156 record):** | | | | | | |
| TDMY (kg) | 0.40 (0.23) | 0.24 (0.19) | 0.35 (0.20) | 0.04 | 0.12 | 0.84 |
| TDFY (kg) | 0.45 (0.25) | 0.29 (0.22) | 0.24 (0.19) | 0.18 | 0.02 | 0.80 |
| TDPY (kg) | 0.44 (0.24) | 0.25 (0.20) | 0.30 (0.20) | 0.03 | 0.11 | 0.85 |
| TDSCS | 0.39 (0.24) | 0.22 (0.19) | 0.38 (0.22) | 0.57 | 0.18 | 0.24 |

**Table 4. Cont.**

| Trait | Animal Model | | | Random Regression Model | | |
|---|---|---|---|---|---|---|
| | $h^2$±SE | $p^2$±SE | $e^2$±SE | $h^2$ | $p^2$ | $e^2$ |
| **Reproduction traits:** | | | | | | |
| AFC, month (N= 1951 record) | 0.10 (0.043) | --- | 0.92 (0.04) | | | |
| DO, day (N= 7279 record) | 0.02 (0.01) | 0.02 (0.01) | 0.96 (0.01) | | | |
| CI, day (N= 7279 record) | 0.02 (0.01) | 0.01 (0.01) | 0.97 (0.01) | | | |

SE=Stander error; TDMY= Test-day milk yield, TDFY= Test-day fat yield, TDPY= Test-day protein yield and TDSCS = Test-day somatic cell score; AFC= Age at first calving; DO= Days open; CI= Calving interval.

### *Predicted breeding values (PBV):*

Estimates of minimum and maximum PBVs and their accuracy of predictions ($r_A$) and ranges for TDMY, TDFY, TDPY, TDSCS, AFC, DO and CI are given in Table (5). The ranges of PBVs were moderate or high, being -2.01 to 3.4 *kg* for TDMY, -0.358 to 0.521 *kg* for TDFY, -0.053 to 0.095 *kg* for TDPY, -0.183 to 0.313 $log^2$ for TDSCS, -8.24 to 10.84 *mo* for AFC, -124.7 to 123.9 *d* for DO and -141.8 to 132.5 *d* for CI. The ranges of PBVs decreased up to TD4 and then increased till end of lactation TD9. These estimates were in agreement with those previously reported on Egyptian buffaloes, where the reviewed estimates of PBVs were moderate or high, ranging from -1548 to 2954 kg for total milk yield, -85 to 93 kg for total fat yield, -47 to 44 kg for total protein yield and -1.16 to 8.03 ($log^2$) for somatic cell count (Khattab *et al*., 2003; El-Arian *et al*., 2012; Shalaby *et al*., 2016; Ahmad *et al*., 2017; Abo-Gamil *et al*., 2017 and EL-Hedainy *et al*., 2020). For reproduction traits of Egyptian buffalo, the ranges in PBVs were high, ranging from -15.8 to 143 *d* for AFC and -43.1 to 97.9 *d* for DO (Shalaby *et al*., 2016; ShafiK *et al*., 2017; Abo-Gamil *et al*., 2017 and Amin *et al*., 2021). Therefore, using the breeding values for AFC and lactation traits (milk, fat, protein and somatic cell score) in selection program will reduce the generation interval and increase the productive period in the Egyptian buffalo, while using the breeding values for CI or DO in selection could attain limited improvement in these reproduction traits.

The percentages of experimental animals (buffaloes, sires and dams) having positive PBVs for TDMY, TDFY, TDPY and TDSCS were more than 50 % and ranged from 52 to 74 % for TDMY, 52 to 74 % for TDFY, 50 to 77 % for TDPY, 55 to 74 % for TDSCS and 53 to 64 % for reproduction traits (Table 5). The high positive PBVs for such lactation traits reveal a good opportunity for the genetic improvement of the total merit of buffaloes when including these traits in a selection scheme. However, for the reproduction traits, the negative PBVs are desired for selection purposes, the percentages of the experimental animals having negative PBVs for AFC, DO and CI were 47, 37 and 36 %, respectively.

The accuracies ($r_A$) of minimum and maximum estimates of PBVs were moderate or high in most TD milk yields and compositions and reproduction traits, ranging from 0.315 to 0.986 for lactation traits and 0.791 to 0.999 for reproduction traits (Table 5). These high accuracies may be because heritability estimates were highly associated with more available pedigree information for all animals (Korhonen, 1996). Such high accuracies in PBVs obtained in the present study suggest that selection plans to be used in future generations would lead to sustainable genetic improvement for lactation traits of the Egyptian buffalo.

### *Genetic and phenotypic trends for lactation traits:*

The genetic trends plotted for TDMY, TDFY, TDPY and TDSCS across the years from 2003 to 2023 are shown in Figure 1. The regression line of PBVs on TD lactation traits of 1192 animals (buffaloes with records and sires and dams without records) indicated favorable increase in genetic trend line of milk, fat and protein yields associated with favorable decrease in the genetic trend line for TDSCS as year of TD advanced. The ranges of genetic trends for TD lactation traits were favorably increased from -4.63 to 1.61 kg for TDMY, -5.0 to 495 g for TDFY and -26 to 280 g for TDPY, along with favorable decrease of 1.37 to 1.19 in the genetic trend of TDSCS over time of lactation. Such wide ranges of genetic trends reflect an appropriate culling and replacement practices performed in these herds. Also, the positive genetic trends for all lactation traits were resulting from the selection program applied for these traits in the experimental herds studied. The slight increase in genetic trend registered over 20 years of recording activity in the present study could be explained depending on the following facts: 1) progeny testing of selection could not practice in the proper direction for lactation traits and it was not performed on a large scale due to the difficulties to use artificial insemination in the buffalo herds efficiently, 2) selection was not much effective to be in the desired changes over 20 years due to natural insemination was applied and low management practices for the improvements in lactation performance, 3) the size of the lactating buffaloes in the herds was small, 4) inbreeding was practiced in few cases, 5) sometimes there are problems in recording milk production quantities and components, and 6) In recent years, the breeding strategy relied on only few proven sires due to challenging of economic conditions and a lack of funding, which led to the exclusion of many proven sires.

**Table 5 Minimum and maximum predicted breeding values (PBVs), standard errors (SE) and accuracy of predictions ($r_A$) for test-day (TD) lactation traits and reproduction performance in the Egyptian buffaloes**

| **Trait** | **Minimum PBV** | | | **Maximum PBV** | | | **Range in PBV** | **Positive PBV (%)** |
|---|---|---|---|---|---|---|---|---|
| | **PBV** | **SE** | **$r_A$** | **PBV** | **SE** | **$r_A$** | | |
| **Lactation traits (N= 1192 animal with 7345 records):** | | | | | | | | |
| **TD1 at 4 days in milk (N= 1031 animals):** | | | | | | | | |
| TDMY (*kg*) | -0.765 | 0.427 | 0.501 | 1.301 | 0.428 | 0.498 | 2.06 | 52 |
| TDFY (kg) | -0.058 | 0.034 | 0.489 | 0.088 | 0.034 | 0.471 | 0.147 | 53 |
| TDPY (kg) | -0.032 | 0.019 | 0.494 | 0.041 | 0.019 | 0.504 | 0.073 | 50 |
| TDSCS | -0.087 | 0.086 | 0.408 | 0.110 | 0.083 | 0.467 | 0.197 | 63 |
| **TD2 at 30 days in milk (N= 1096 animals):** | | | | | | | | |
| TDMY (kg) | -1.156 | 0.532 | 0.587 | 1.815 | 0.512 | 0.627 | 2.97 | 53 |
| TDFY (kg) | -0.059 | 0.036 | 0.574 | 0.085 | 0.038 | 0.514 | 0.145 | 52 |
| TDPY (kg) | -0.026 | 0.022 | 0.406 | 0.049 | 0.024 | 0.548 | 0.075 | 56 |
| TDSCS | -0.129 | 0.066 | 0.659 | 0.145 | 0.078 | 0.469 | 0.275 | 55 |
| **TD3 at 60 days in milk (N= 1109 animals):** | | | | | | | | |
| TDMY (kg) | -2.005 | 0.713 | 0.669 | 3.419 | 0.671 | 0.715 | 5.42 | 53 |
| TDFY (kg) | -0.358 | 0.055 | 0.315 | 0.521 | 0.054 | 0.376 | 0.878 | 57 |
| TDPY (kg) | -0.052 | 0.027 | 0.599 | 0.095 | 0.027 | 0.605 | 0.147 | 52 |
| TDSCS | -0.091 | 0.077 | 0.422 | 0.147 | 0.081 | 0.333 | 0.235 | 57 |
| **TD4 at 90 days in milk (N= 1121 animals):** | | | | | | | | |
| TDMY (kg) | -1.024 | 0.426 | 0.562 | 1.638 | 0.450 | 0.488 | 2.66 | 54 |
| TDFY (kg) | -0.058 | 0.033 | 0.535 | 0.064 | 0.036 | 0.434 | 0.123 | 57 |
| TDPY (kg) | -0.040 | 0.019 | 0.569 | 0.051 | 0.020 | 0.477 | 0.091 | 53 |
| TDSCS | -0.151 | 0.103 | 0.475 | 0.212 | 0.089 | 0.644 | 0.363 | 65 |
| **TD5 at 120 days in milk (N= 1090 animals):** | | | | | | | | |
| TDMY (kg) | -0.952 | 0.515 | 0.717 | 1.928 | 0.502 | 0.709 | 2.88 | 58 |
| TDFY (kg) | -0.072 | 0.045 | 0.557 | 0.126 | 0.043 | 0.618 | 0.199 | 59 |
| TDPY (kg) | -0.044 | 0.024 | 0.567 | 0.089 | 0.024 | 0.057 | 0.132 | 60 |
| TDSCS | -0.123 | 0.098 | 0.529 | 0.185 | 0.094 | 0.454 | 0.308 | 60 |
| **TD6 at 150 days in milk (N= 997 animals):** | | | | | | | | |
| TDMY (kg) | -0.505 | 0.434 | 0.507 | 0.712 | 0.406 | 0.589 | 1.22 | 60 |
| TDFY (kg) | -0.019 | 0.031 | 0.429 | 0.037 | 0.029 | 0.506 | 0.056 | 60 |
| TDPY (kg) | -0.022 | 0.019 | 0.522 | 0.042 | 0.017 | 0.607 | 0.064 | 64 |
| TDSCS | -0.048 | 0.052 | 0.435 | 0.056 | 0.053 | 0.369 | 0.104 | 58 |
| **TD7 at 180 days in milk (N = 836 animals):** | | | | | | | | |
| TDMY (kg) | -0.338 | 0.417 | 0.402 | 1.249 | 0.368 | 0.590 | 1.587 | 72 |
| TDFY (kg) | -0.021 | 0.031 | 0.984 | 0.081 | 0.028 | 0.986 | 0.102 | 73 |
| TDPY (kg) | -0.012 | 0.017 | 0.493 | 0.043 | 0.016 | 0.575 | 0.055 | 74 |
| TDSCS | -0.144 | 0.088 | 0.496 | 0.162 | 0.089 | 0.483 | 0.306 | 66 |
| **TD8 at 210 days in milk (N= 562 animals):** | | | | | | | | |
| TDMY (kg) | -0.541 | 0.478 | 0.520 | 0.992 | 0.449 | 0.596 | 1.533 | 73 |
| TDFY (kg) | -0.046 | 0.039 | 0.535 | 0.044 | 0.041 | 0.513 | 0.089 | 74 |
| TDPY (kg) | -0.025 | 0.021 | 0.534 | 0.041 | 0.021 | 0.556 | 0.066 | 77 |
| TDSCS | -0.137 | 0.101 | 0.524 | 0.114 | 0.108 | 0.392 | 0.251 | 74 |
| **TD9 at 240 days in milk (N= 241 animals):** | | | | | | | | |
| TDMY (kg) | -0.934 | 0.656 | 0.727 | 1.415 | 0.645 | 0.738 | 2.35 | 74 |
| TDFY (kg) | -0.063 | 0.039 | 0.887 | 0.163 | 0.049 | 0.809 | 0.226 | 74 |
| TDPY (kg) | -0.053 | 0.027 | 0.778 | 0.057 | 0.027 | 0.778 | 0.109 | 77 |
| TDSCS | -0.183 | 0.173 | 0.724 | 0.313 | 0.173 | 0.723 | 0.497 | 68 |
| **Reproduction traits (N= 3285 animals with 7279 records):** | | | | | | | | |
| AFC (month) | -8.24 | 0.393 | 0.950 | 10.84 | 0.321 | 0.791 | 19.08 | 53 |
| DO (day) | -124.7 | 0.735 | 0.996 | 123.9 | 0.409 | 0.998 | 248.7 | 63 |
| CI (day) | -141.8 | 0.735 | 0.997 | 132.5 | 0.409 | 0.999 | 274.3 | 64 |

SE=Stander error; TDMY= Test-day milk yield, TDFY= Test-day fat yield, TDPY= Test-day protein yield and TDSCS= Test-day somatic cell score; AFC= Age at first calving; DO= Days open; CI= Calving interval.

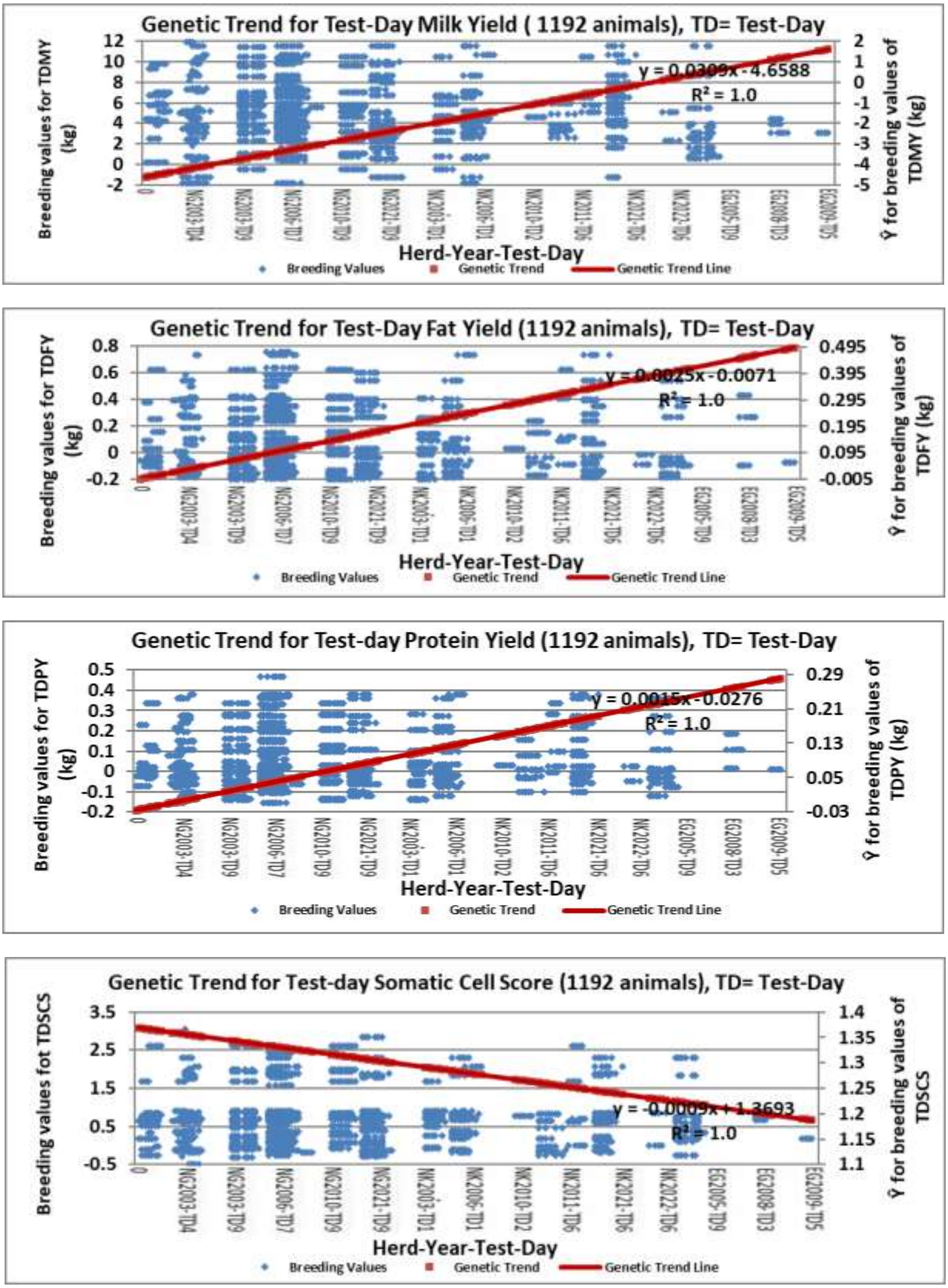

**Figure 1. Genetic trends for test-day milk yield (TDMY), fat yield (TDFY), protein yield (TDPY) and somatic cell score (TDSCS) plotted by regressing the breeding values estimated by BLUPF90 software for TD lactation traits on herd-year-test-day of lactation in the Egyptian buffaloes.**

The phenotypic trends plotted for TDMY, TDFY, TDPY and TDSCS throughout the experimental period of 21 years (2003 to 2023) showed an apparent deteriorating trend (Figure 2), indicating that the change in environmental situations along with inefficient management strategy during the last 20 years in these herds play large role in determining the performance of lactation traits. The regression line of the phenotypic values of 7345 TD lactation records on Herd-Year-Test-Day showed a decrease in the phenotypic trend line as year of TD advanced. Sometimes, ineffective management decisions regarding the culling schemes in the herds were not implemented in the recommended breeding strategy for the studied herds. Moreover, high milk yielding animals had to be disposed during some outbreaks of highly contagious diseases, like brucellosis and tuberculosis … *etc*. However, the ranges in the values of phenotypic trend of lactation traits decreased unfavorably from 7.49 *kg* to be 5.69 *kg* for TDMY, 510 *g* to be 360 *g* for TDFY and 284 *g* to be 223 *g* for TDPY, associated with unfavorable increase in the phenotypic trends of TDSCS from 1.62 to be 2.43 (Figure 2). The decrease in phenotypic trends of all lactation traits over time was suggested to be attributed to low nutritional and feeding levels used and the management practices applied in different herds (Amin *et al*, 2015, 2021). Therefore, it is necessary to improve the husbandry/management schemes in herds of the present study.

As shown in Figures 1 and 2, the genetic and phenotypic trends for lactation traits were irregular, as stated previously in Egyptian buffalo (El-Bramony, 2014 and Amin *et al*., 2015 and 2021). In non-Egyptian buffalo studies, the genetic and phenotypic trends obtained for milk yield and components revealed not only decreasing trends (Chakraborty and Dhaka, 2012 and Pawar *et al*., 2018), but also, other studies reported increasing trends (Seno *et al*., 2010; Aspilcueta-Borquis *et al*., 2015 and Nazari *et al*., 2021).

### ***Genetic and phenotypic trends for reproduction traits:***

Across the years from 2002 to 2023 in the experimental herds of the present study, the genetic trends plotted for reproduction traits are shown in Figure 3. The regression line of breeding values for reproduction traits of 3285 animals (buffaloes with record and sires and dams without records) showed favorable decrease in the genetic trend line over time of calving. Also, the ranges of the genetic trends for AFC, DO and CI were favorably decreased from 0.24 *mo* to be -0.14 *mo*, 5.5 *d* to be 2.9 *d* and 6.9 *d* to be 3.6 *d*, respectively. The positive genetic and phenotypic trends obtained for all reproduction traits resulted from selection applied in these experimental herds.

The present results and previous Egyptian reports (El-Bramony, 2014 and Amin *et al*., 2015 and 2021) gave evidence that genetic improvement in buffalo herds is limited despite of the frequent attempts made to improve lactation and reproduction traits. This is due to the following reasons: 1) insufficient or lack of recording induced difficulty to keep track of genealogical aspects, 2) natural insemination was applied and practiced in APRI research herds and consequently the planned progeny test could not be performed accurately because the technology of artificial insemination is not widespread at the field levels. The above-mentioned reasons are of considerable contribution to slow-down the Egyptian buffalo genetic improvement for reproduction traits. In fact, buffalo estrus is not detectable easily and inseminations were often offered at the wrong time, causing low pregnancy rates and seasonal anestrus and therefore the buffalo producers are afraid of missing detection of heat period.

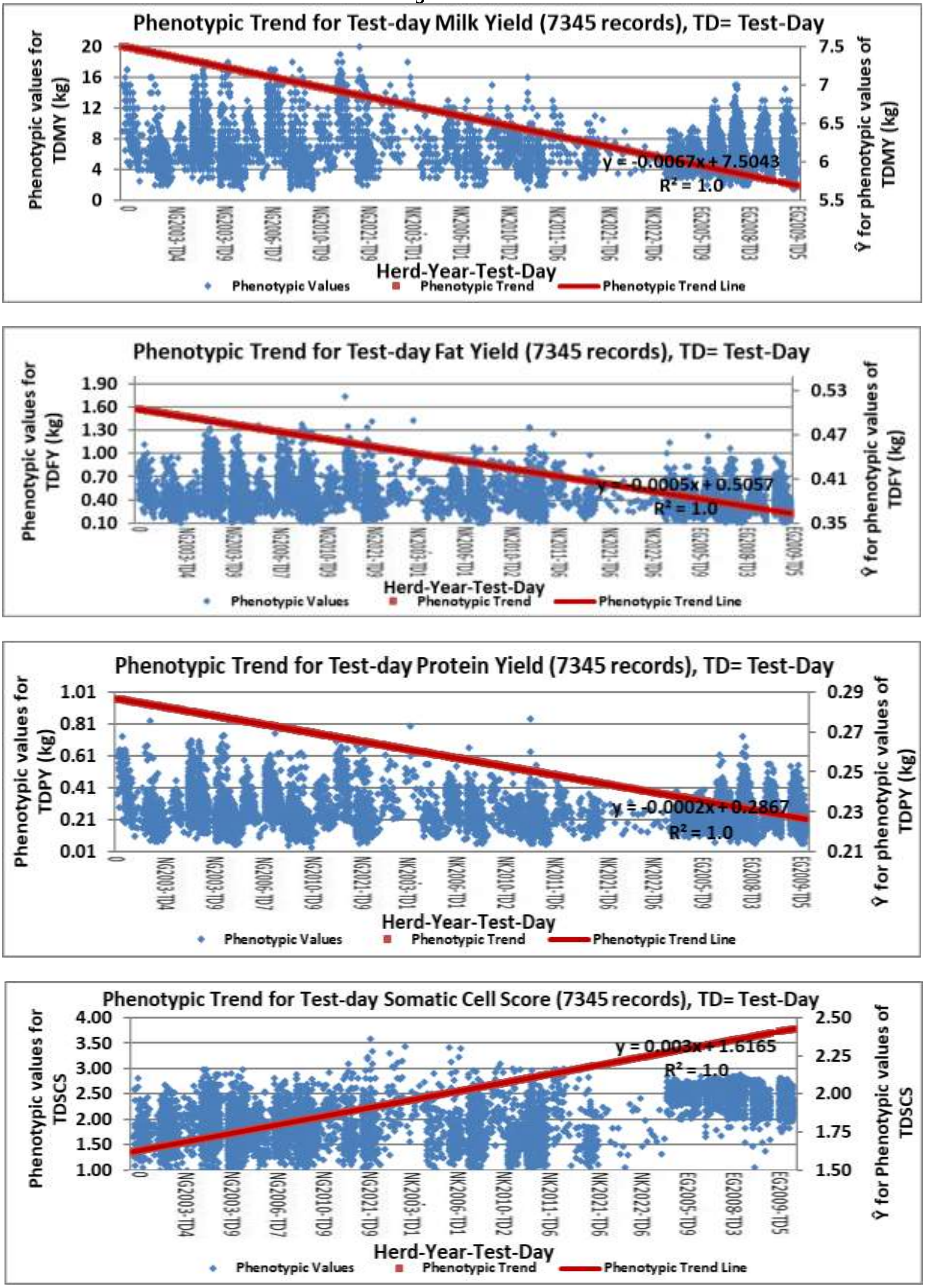

**Figure 2. Phenotypic trends for test-day milk yield (TDMY), fat yield (TDFY), protein yield (TDPY) and somatic cell score (TDSCS) plotted by regressing the phenotypic values of TD lactation traits on herd-year-test-day of lactation in the Egyptian buffaloes.**

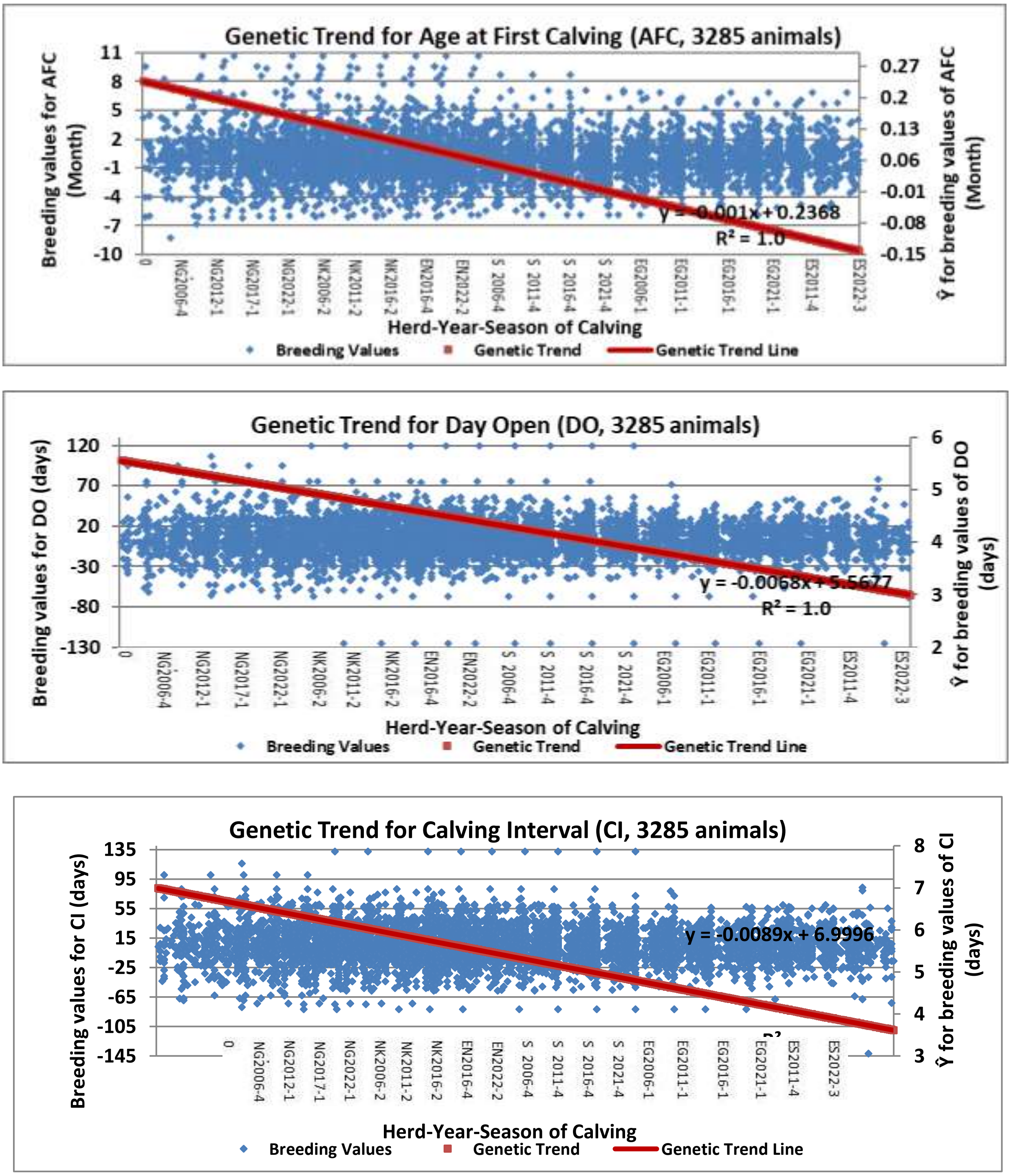

**Figure 3. Genetic trends for reproduction trait plotted by regressing the breeding values estimated by BLUPF90 software for age at first calving (AFC), day open (DO) and calving interval (CI) on herd-year season of calving in the Egyptian buffaloes.**

The regression line of phenotypic values on 1951 records for AFC or on 7279 records for DO and CI revealed favorable decreasing in phenotypic trend over time (Figure 4). Wide ranges in the phenotypic values of reproduction traits in herd-year-season of calving subclasses were observed, being 36.57 *mo* to be 36.52 *mo* for AFC, 127 *d* to be 71 *d* for DO and 416 *d* to be 354 *d* for CI.

The genetic and phenotypic trends for AFC and CI were increasing together as cited by Kour and Narang (2021) in Murrah buffalo, while reversible trends were observed by Amin *et al.* (2021) in Egyptian buffalo where the genetic trend was increasing, and the phenotypic trend was decreasing or *vice versa*. Bashir *et al*. (2009) in Nili-Ravi buffalo in Pakistan showed favorable decreasing in genetic trend for AFC, while Gupta *et al*. (2015) reported unfavorable increase in genetic trend for AFC in Indian Murrah buffalo. In Egyptian buffalo, Shalaby *et al*. (2016) reported that the genetic and phenotypic trends for DO and CI decreased favorably, while the results of Amin *et al*. (2021) indicated unfavorable increase in the genetic trends for these traits.

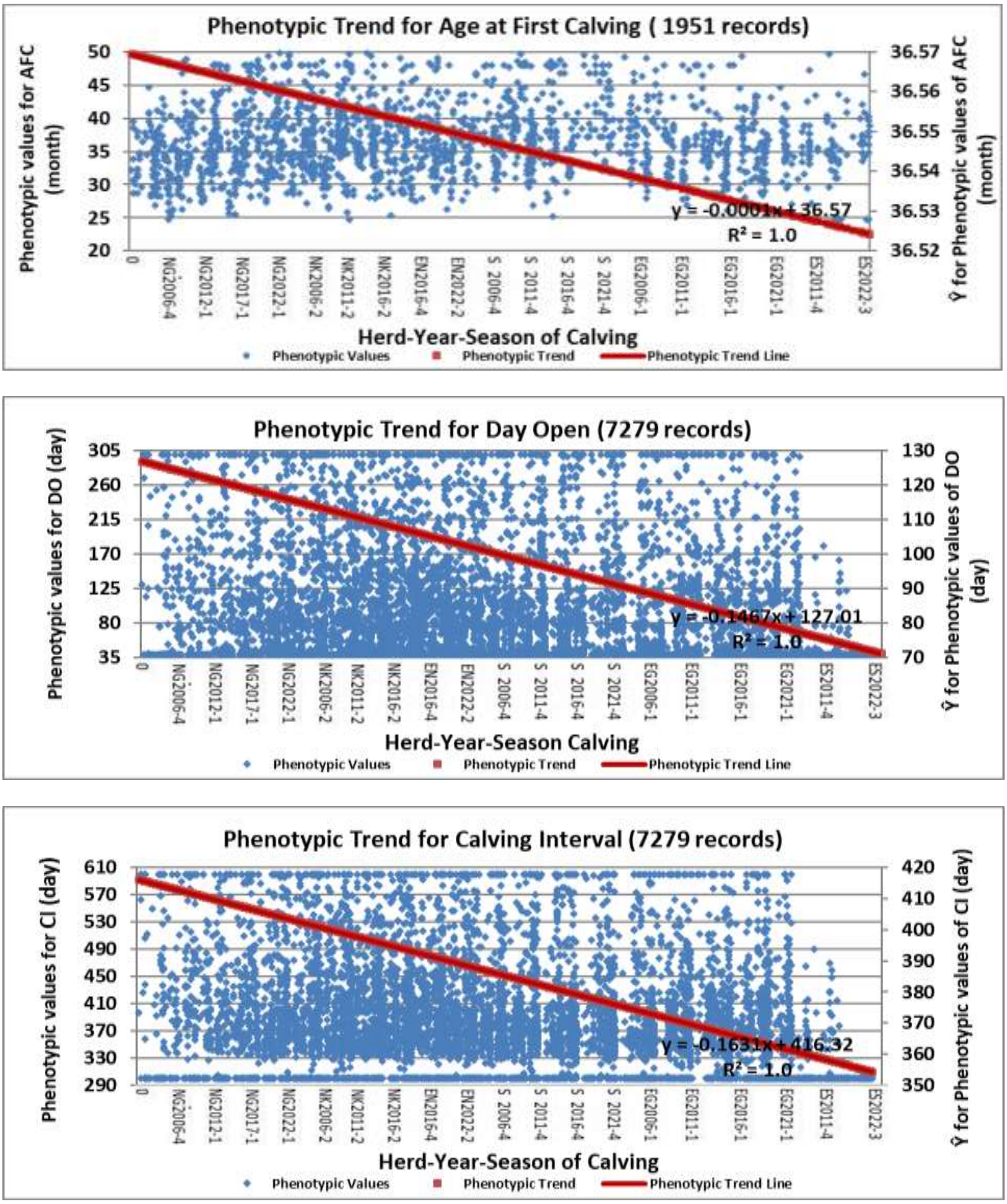

**Figure 4. Phenotypic trends for reproduction trait plotted by regressing the phenotypic values for age at first calving (AFC), day open (DO) and calving interval (CI) on herd-year season of calving in the Egyptian buffaloes.**

## CONCLUSIONS

The test-day (TD) lactation trait during the first three to five months of lactation could be adopted as an early selection criterion to increase milk yield and its components in buffaloes. The favorable genetic and phenotypic trends for lactation and reproduction traits obtained here could be dedicated to the fact that it is necessary to improve the management and feeding scheme and to use accurate estimates of predicted breeding values in the genetic improvement programs of Egyptian buffalo. In practice, TD milk records, RRM parameters estimated by VCE6 program, PBV and genetic and phenotypic trends estimated by BLUPF90 could be safely used in the genetic improvement programs in Egyptian buffalo of APRI herds. However, subsequent work is needed to evaluate the applicability of such analyses under the conditions of some private farms scattered in the Egyptian countryside.

## FUNDING

This work was funded by the project No. 33531, entitled "A genomic Approach to Improve Production and Reproduction Traits in Egyptian Buffalo" from the Science, Technology & Innovation Funding Authority (STDF), Ministry of Scientific Research, Egypt.

## ETHICS STATEMENT

All experimental procedures involving animals handling and treatment were approved by the Research Ethics Committee of the Faculty of Agriculture, Benha University, Egypt (Approval No. REC-FOABU. 3/00022).

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# نموذج الإنحدار العشوائي وتحليل BLUPF90 لتقييم الإتجاهات الوراثية والمظهرية لصفات الإدرار والتناسل في الجاموس المصري

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إستهدفت هذه الدراسة التقييم الوراثي لبعض صفات الإدرار والتناسل في الجاموس المصري وذلك عن طريق تقدير مكونات التباين والمكافئ الوراثي بإستخدام نموذج الحيوان Animal Model (AM) معتمداً على أسلوب Bayesian Gibbs Sampling Algorithm وكذلك نموذج الإنحدار العشوائي Random Regression Model (RRM) للتنبؤ بالقيم التربوية للحيوانات (PBVs) ورسم خطوط الإتجاهات الوراثية والمظهرية لمحصول اللبن والدهن والبروتين وعدد الخلايا الجسمية باللبن بإستخدام بيانات يوم الإختبارالشهري Test day (TD) وكذلك للصفات التناسلية. إستخدم لذلك عدد ٧٣٤٥ سجلا لبيانات يوم الإختبار لكل شهر من الإدرار (TD) لصفات محصول اللبن والدهن والبروتين وعدد الخلايا الجسمية باللبن لعدد ٦٨٦ جاموسة الناتجة من ٨٣ أب ، ٤٢٣ أم في ثلاث قطعان للجاموس المصري (النطاف الجديد، النطاف القديم والجميزة)، بينما تم إستخدام عدد ٧٢٧٩ سجلاً لصفات التناسل لعدد ١٩٥١ جاموسة الناتجة من ١٥٥ طلوقة ، ١١٧٩ أماً في ستة قطعان (النطاف الجديد، النطاف القديم، النوبارية، السرو، الجميزة وسدس) من الجاموس المصري التابعة لمعهد بحوث الإنتاج الحيواني، مركز البحوث الزراعية، وزارة الزراعة، مصر. كانت قيم المكافئ الوراثي المحسوبة من نموذج الحيوان Animal Model منخفضة وأحياناً متوسطة وتراوحت بين ٠,٠٥ الي ٠,٤٠ لمحصول اللبن عند يوم الإختبار ، ٠,٠٥ إلى ٠,٤٥ لمحصول الدهن عند يوم الإختبار ، ٠,٠٦ إلى ٠,٤٤ لمحصول البروتين عند يوم الإختبار ، ٠,٠٣ إلى ٠,٣٩ لعدد الخلايا الجسمية باللبن بينما تراوحت قيم المكافئ الوراثي المقدرة بإستخدام نموذج الإنحدار العشوائي بين ٠,٠٤ إلى ٠,٢٥ لمحصول اللبن عند يوم الإختبار ،٠,٠٥ إلى ٠,١٨ لمحصول الدهن عند يوم الإختبار ، ٠,٠٣ إلى ٠,٢٣ لمحصول البروتين عند يوم الإختبار، ٠,٠٣ إلى ٠,٥٧ لعدد الخلايا الجسمية باللبن عند يوم الإختبار. قدرت قيم المكافئ الوراثي للصفات التناسلية لإناث الجاموس بإستجدام نموذج الحيوان وهي صفة العمر عند أول ولادة وصفة عدد الأيام المفتوحة وصفة الفتره بين الولاتين وكانت القيم منخفضة وهي ٠,١٠، ٠,٠٢، ٠,٠٢ على الترتيب. كانت القيم التربوية المتنبأ بها متوسطة وأحياناً عالية وتراوحت بين -٢,٠١ إلى ٣,٤ كجم لصفة محصول اللبن عند يوم الإختبار، -٠,٣٥٨ إلى ٠,٥٢١ كجم لصفة محصول الدهن عند يوم الإختبار، -٠,٠٥٣ إلى ٠,٠٩٥ كجم لمحصول البروتين عند يوم الاختبار، -٠,١٨٣ إلى ٠,٣١٣ $log^2$ لصفة عدد الخلايا الجسمية في اللبن عند يوم الإختبار، -٨,٢ الي ١٠,٨ شهراً لصفة العمر عند أول ولادة، -١٢٤,٧ إلى ١٢٣,٩ يوماً لصفة عدد الأيام المفتوحة، -١٤١,٨ إلى ١٣٢,٥ يوماً لصفة الفترة بين ولادتين. في حين إرتفعت قيم الإتجاهات الوراثية إرتفاعا ملحوظاً من -٤,٦٣ ليصبح ١,٦١ كجم لصفة محصول اللبن عند يوم الإختبار ومن -٥ ليصبح ٤٩٥ جراماً لصفة محصول الدهن عند يوم الإختبار ومن -٢٦ ليصبح ٢٨٠ جراماً لصفة محصول البروتين عند يوم الإختبار ومصحوباً بإنخفاضاً مرغوباً في قيم الاتجاهات الوراثية لصفة عدد الخلايا الجسمية في اللبن عند يوم الإختبار من ١,٣٧ ليصبح ١,١٩ $log^2$ مع تقدم سنة الإدرار. بينما أظهرت الاتجاهات المظهرية تدهوراً تراوحت قيمته من ٧,٤٩ ليصبح ٥,٦٩ كجم لصفة محصول اللبن عند يوم الإختبار ومن ٥١٠ ليصبح ٣٦٠ جراماً لصفة محصول الدهن عند يوم الإختبار ومن ٢٨٤ ليصبح ٢٢٣ جراماً لصفة محصول البروتين عند يوم الإختبار ومصحوباً بزيادة غير مرغوبة في صفة عدد الخلايا الجسمية في اللبن عند يوم الإختبار بمقدار من ١,٦٢ لتصبح ٢,٤٣ $log^2$ مع تقدم سنة الإدرار. أظهرت قيم الإتجاهات الوراثية إنخفاضاً طفيفاً من ٠,٢٤ ليصبح -٠,١٤ شهراً لصفة العمر عند أول ولادة ومن ٥,٥ ليصبح ٢,٩ يوما لصفة عدد الأيام المفتوحة ومن ٦,٩ ليصبح ٣,٦ يوماً لصفة الفترة بين ولادتين ومصحوباً بإنخفاصا مرغوباً في الإتجاهات المظهرية من ٣٦,٥٧ ليصبح ٣٦,٥٢ شهراً لصفة العمر عند أول ولادة ومن ١٢٧ ليصبح ٧١ يوماً لصفة عدد الأيام المفتوحة ومن ٤١٦ ليصبح ٣٥٤ يوماً لصفة الفترة بين ولادتين مع تقدم سنة الولادة. من خلال النتائج السابق ذكرها يمكن التوصية بإستخدام سجلات اللبن ليوم الإختبار Test day (TD) والمقاييس الوراثية المقدرة بإستخدام نموذج الإنحدار العشوائي (RRM) وكذلك القيم التربوية المتنبأ بها للحيوانات (PBVs) وكذا الإتجاهات الوراثية والمظهرية المقدرة بواسطة برنامج BLUPF90 في برامج التحسين الوراثي للجاموس المصري في قطعان معهد بحوث الإنتاج الحيواني بمركز البحوث الزراعية بوزارة الزراعة وإستصلاح الأراضي، مصر.