A comparison between sire and animal model for lifetime Production traits in Egyptian buffaloes

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ABSTRACT

A total of 1621 lactation records of Egyptian buffaloes, kept at Mehalet Mousa farm, belonging to the Animal production Research Institute, Ministry of Agriculture, were used. Data were analyzed by using sire model (SM) and animal model (AM). For SM, the model includes the fixed effects of year and month of birth and age at first calving as covariate and sire as a random effect. For AM, the model includes the fixed effects of month and year of birth and random effects of animals and errors on lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactation completed (NLC). Means were 10552 kg, 1173 d, 125 mo., and 5.97 for LTMY, TLP, AGDS and NLC, respectively. Estimates of heritability from sire model were 0.45, 0.18, 0.90 and 0.36 for LTMY, TLP, AGDS and NLC, respectively and from AM were 0.27, 0.17, 0.12 and 0.06 for above traits studied, respectively. Estimates of phenotypic correlations among traits studied ranged from 0.55 to 0.73 for SM and for AM 0.40 to 0.80 and genetic correlations among traits studied ranged from 0.19 to 0.96 for SM and from AM ranged from 0.10 to 0.98. Rank correlations among lifetime and longevity traits as estimated from SM were positive and highly significant ($P<0.01$) and ranged from 0.08 to 0.98 as estimated from SM. Rank correlations of sire transmitting ability among lifetime and longevity traits as estimated from AM were positive and significant ($P <0.01$) and ranged from 0.33 to 0.88.

Key words: Sire Model, Animal Model, Egyptian buffaloes

Introduction

Dairy females' longevity is a really important trait in a herd affecting overall profitability in the dairy industry. A high female longevity is desirable because the cost of rearing heifers moreover it allows a greater proportion of culling decisions to be based on production, instead of involuntary culling. Dairy females have been selected intensively for productivity traits whilst longevity within the herd has decreased **(Galeazzi et al. 2010 a).** On other words, stayability is an important economic trait that is analyzed in some programs of breeding. This trait measures the period of permanence of the females in the herds and it is highly correlated to milk production and also to its health **(Galeazzi et al., 2010 b)**.

The aim of the present study are (1) estimates of phenotypic and genetic parameters for lifetime production traits , (2) estimates sire transmitting ability for lifetime production traits by using sire and animal models and (3) comparison between both two models for lifetime production traits in Egyptian buffaloes.

Material and methods

Data

Data of the present study were obtained from lactation records of Egyptian buffaloes kept at Mahalet Mousa Farm, belonging to Animal Production Research Institute Ministry of Agriculture, Cairo, Egypt. Data were collected during the period from 1990 to 2010. The number of sires, cows and total of lactations were 115, 360, and 1621, respectively. Sires with less than 5 daughters were excluded. Abnormal records affected by diseases such as mastitis and udder troubles or disorders such as abortion were excluded. Bulls were assigned to naturally mate the female at random. Artificial insemination (AI) was used starting from 2009 to 2015. Heifers were served for the first time when they reached 24 mo., or 350 kg. Pregnancy was detected by rectal palpation 60 days after the last service. Buffalo bulls were chosen for breeding purposes at 2-3 years of age. They were evaluated for body conformation and for semen characteristics. Each bull was foe breeding for about 3-7 years.

Animals were grazed on Egyptian clover (Berseem) during the period from December to May. During the rest of the year the animals were fed on concentrate mixture alone with rice straw. Cows producing more that that are pregnant in the last two months of pregnancy were supplements with extra concentrate ration. Buffaloes were hand milked twice a day. Lifetime production as estimated by total lifetime milk yield (MT, kg) and total lactation period (TLP, d) and longevity as estimated by age at disposal, mo., (AGDS) and the period from birth to disposal (AGDS) and Number of lactations completed (NLC).Table 1, Show the structure of data used in the analysis.

Analysis

Data were analysis by using sire model (SM) and Animal model (AM). For sire model (SM), data were analyzed using the Mixed Model Least Squares and maximum Likelihood Computer program of **Harvey (1990).** The model include the fixed effects of month and year of birth and parity and age at first calving as covariate and ransom effects of sire and cow within sires. Estimates of sire, cow within sire and residual components of variance and covariance were computed according to method II of **Henderson (1953).** Heritability estimates (h^2) , paternal half – sibs heritability (h^2) estimates were calculated as four times the ratio of $\sigma^2 s$ (sire variance components) to the sum of $\sigma^2 s$, $\sigma^2 c{:}s$ (cow within sire) and $\sigma^2 e$ (remainder variance components) i.e.,

$$h^2 = 4\,\sigma^2 s / (\sigma^2 s + \sigma^2 c{:}s + \sigma^2 e)$$

The standard error (S.E) of heritability was computed by the formula given by **Swiger et al. (1964)**

$$S.E_{(h^2)} = \sqrt[2]{\frac{2(n.-1)(1-t)^2[1+(k_1-1)t]^2}{k_1{}^2(n.-S)(S-1)}}$$

Where : s = total number of sires, n = total number of records and k = harmonic mean of daughters per sire.

Estimates of breeding values are estimated according to program of **Harvey (1990).**

For Animal Model (AM) heritability, genetic correlations and Co-variance components of studied traits were estimated using the MTDFREML program **(Boldman et al. 1995).** The model includes the fixed effects of year and month of birth, age at first calving as covariate, and random effects of animals, permanent environmental and errors.

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

$h2 = \sigma^2 a / (\sigma^2 a + \sigma^2 p_e + \sigma^2 e)$

Where $\sigma^2 a$ is additive genetic variance; $\sigma^2 p_e$ is permanent environmental variance and $\sigma^2 e$ is the random residual effect.

Estimates of breeding values with standard errors and their accuracy are estimated according to **Boldman et al. (1995).**

Results and Discussion

Unadjusted means of lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactations completed (NLC) are presented in Table 2. Mean of LTMY was 10551 kg (Table 2). The present mean was higher than those reported by **Khattab et al. (1992)** (4732 kg) working on another set of Egyptian buffaloes. Also, the present mean was higher than those reported by **Dutt et al. (1966)**(9726kg) on Murrah buffaloes, **Awadesian (1997)**(5395 kg) on Iraq buffaloes, **El- Arian (2001 a)(**6240 kg) on Murrah buffaloes, **Patel and Tripathi (1998)** (5943 kg) on Surit , **Bashir et al. (2007)** (7723 kg) on Nili- Ravi buffaloes and **Thiruvenkadan et al. (2015)**(5442 kg) on Murrah buffaloes. Overall mean of total lactation period (TLP) was 1174 d (Table 2). The present mean was longer than those reported by **Khattab et al. (1992)(**1083 d) on Egyptian buffaloes, **Singh and Yadav (1987)(**1013 d) on Murrah buffaloes, **Awadesian (1997)(**1059 d) on Iraq buffaloes and **Bashir et al. (2007)** (1061 d) on Nili- Ravi buffaloes. Mean of age at disposal (AGDS) was 125 mo., (Table 2). The present mean was longer than those found by **Khattab et al. (1992)(**114 mo.,) on Egyptian buffaloes, **El- Arian and Tripathi (1989)** (95 mo.,) on Murrah buffaloes, and **Thiruvenkadan et al. (2015)(**111 mo,.)on Murrah buffaloes. Mean of number of completed lactations was 5.97 (Table 2). The present mean was longer than those reported by **Khattab et al. (1992), El- Arian (2001 a)** and **Thiruvenkadan et al. (2015)** working on Egyptian buffaloes and Murrah buffaloes, respectively and ranged from 3.0 to 3.88.

Coefficient of variability for lifetime and longevity traits ranged from 45.39 to 73.59 % (Table 2), it is noticeable that CV % was rather high 73.59%. This was mainly due to the fact that the data included records of animals that were culled in various lactations. In addition, such large variation for lifetime and longevity traits may indicate wider scope for genetic important in these traits in the examined herds. Also, higher CV% for lifetime and longevity traits reflects great variation between individual in lifetime and longevity traits.

Non genetic effects

Month of birth had no significant effect on LTMY, TLP, AGDS and NLC (Table 3). Similar results are reported by **Youssef and Asker (1959), Khattab et al. (1992), El- Shafie (1994)** working on another sets of Egyptian buffaloes and **Awadesian (1997)** on Iraq buffaloes, **El- Arian (2001 a)** on Murrah buffaloes, and **Sultan and Khattab (1989)** and **Abou – Bakr (2009)** on Friesian cows. Year of birth had a significant effect on LTMY, TLP, AGDS and NLC (P < 0.01, Table 3). The significant effect of year of birth on lifetime and longevity traits may be due to different nutritional, managerial practices prevalent at different periods and phenotypic trend (Table 3). Similar results are found by different authors working on different breeds of buffaloes. In this respect, In this respect, **Sharaby et al. (1983) and Khattab et al. (1992)** with Egyptian buffaloes, reported that year of birth had a significant effect on age at disposal, herd life and number of lactation completed. **Awadesian (1997)** with Iraq buffaloes, found that year of calving had a significant effect on total lifetime production and total days of lactation, they concluded that the effect of year of calving may be due to annual variation in herd size, feeding system and management practices.

Estimates of phenotypic trends for all lifetime production and longevity traits studied were negative, highly significant and being – 529 kg , -73 d, -5.16 mo., and – 0.34 lact., for LTMY, TLP, AGDS and NLC, respectively (P <0.0001, Table 4). The negative phenotypic trend may be due to limitation of environmental at Mehallet Mousa Farm which did not allow the genetic potential of Egyptian buffaloes to be express fully or may be due to sub- optimal management practices prevailing at the farm and also may be due to different kind of feeding from year to year and different climates and temperature from year to another. Similar results was obtained by **El-Arian (2001 a)** working on Murrah buffaloes, found that the phenotypic trend for LTMY, TLP and NLC were -253 kg, -77 d and – 0.149, respectively.

In Pakistan, **Bashir et al. (2007)** working on Nili – Ravi buffaloes, reported that year of birth had a significant effect on lifetime milk yield, herd life and productive life. The same authors also found that the overall phenotypic trend was negative for lifetime milk yield (-280 kg/d), herd life (-93 d) and productive life (-42 d**). Galeazzi et al. (2010 b)** arrived at the same results on Murrah buffaloes.

Estimates of partial linear and quadratic regression coefficients of LTMY, TLP, AGDS and NLC on age at first calving are presented in (Table 3). Estimates of partial of linear and quadratic regression coefficients of LTMY on age at first calving was not significant and being 78.21±86.13kg/mo., and -8.19±10.48 kg/mo.,^{2}, respectively. Similar results are reported by **El-Shafie (1994)** working on Egyptian buffaloes. Estimates of partial linear and quadratic regression coefficients of TLP on age at first calving were significant ($P < 0.01$, Table 3) and being 13.82±7.25 d/mo., and -1.54±0.88 d/mo.,^{2}, respectively. Similar results are reported by many authors. In this respect, **Khattab et al. (1992)** working on 3400 lactation records of Egyptian buffaloes, found that estimates of partial linear regression coefficients of lifetime milk yield, total lactation period, age at disposal and number of lactation completed were significant and being -73.98±8.85 kg/ mo., and – 16.18±2.06 d/mo., 0.60 mo/mo., and -0.0122 lact/mo., respectively**.** Also, **Katrey et al. (2005)** analysis 953 Friesian cows, reported that age at first calving had a significant effect on productive life, cows with very low age at first calving had lower productive life. This might be because of the cows at a very low age could not attain full growth and thus might have been culled out. Also, the same authors concluded that less number of total calves are produce by those cows which had longer age at first calving as the cows with lower age at first calving had longer productive life.

Estimates of partial linear and quadratic regression coefficients of AGDS and NLC on age at first calving were not significant and being 0.014±0.043 mo/mo., and – 0.085±0.005 mo/mo.,^{2} , respectively for AGDS and 0.042±0.029 lactation/mo., and – 0.008±0.004 lactation/mo., ^{2} , respectively for NLC (Table 3). Similar results are reported by **El-Shafie (1994)** in a study based on 907 Egyptian buffaloes, found that estimates of partial linear regression coefficient of age at disposal and number of lactations completed on age at first calving was not significant.

Genetic parameters

Random effect

Sire of the cow had a significant effect on LTMY, TLP, AGDS and NLC ($P < 0.01$, Table 3). The present results indicated that the genetic improvement of lifetime production and longevity traits were possible by selecting sires to improve the production traits of their progeny. In particular, large magnitude of the sire estimates might indicate a sizable potential for sire in selection programs and or / in change of the herd management to improve yield traits. Similar results are reported by many workers on different breeds of buffaloes. In this respect, **Khattab et al. (1992)** found significant effect of sire on lifetime milk yield and total lactation period. **El- Shaife (1994)** with another herd of Egyptian buffaloes, found that sire of the cow had a significant effect on age at disposal and number of lactation completed.

Heritability estimates for LTMY, TLP, AGDS and NLC as estimated from sire model (SM) and animal model (AM) are presented in Table 5. Estimates of heritability for LTMY, TLP, AGDS and NLC from SM, by using the model including the fixed effects of month and year of birth, age at first calving as a covariate and sire as a random effect, were 0.45±0.18, 0.18±0.10, 0.90±0.80 and 0.36±0.18, respectively (Table 5). The present estimates are higher than those reported by many authors working on different breeds of dairy cattle by using sire model. In this respect, **Kawthar Mourad et al. (1992)** with another set of these data, reported that h^2 estimates for LTMY, TLP, AGDS and NLC are 0.11, 0.16, 0.05 and 0.03, respectively. **El- Arian (2001 a)** with Murrah buffaloes, found that h^2 estimates for LTMY and NLC are 0.308 and 0.342, respectively. Also, higher estimates of h^2 for lifetime and longevity traits are reported by **El Shafie (1994)** stated that h^2 estimates for AGDS and NLC were 0.62 and 0.59, respectively. In addition, **El- Arian (2001 b)** with 3360 normal lactation records of Holstein cows, using sire model, found that heritability estimates for , LTMY, TLP and NLC were 0.344, 0.309 and 0.439, respectively.

Heritability estimates for LTMY, TLP, AGDS and NLC from using multi trait animal model (MTAM), according to MTDFREML program of **Boldman (1995)** which the model including the fixed effects of month and year of calving and age at first calving as covariate and random effects of animals, permanent environmental and errors were 0.27±0.01, 0.17±0.01, 0.12±0.03 and 0.06±0.01, respectively (Table 5). The present estimates are higher than those reported by many authors working on different breeds of buffaloes. In this respect, **Bashir et al. (2007)** working on 1037 Nili – Ravi buffaloes, using Multi Trait Animal Model (MTAM), found that heritability estimates for lifetime milk yield, herd life and productive life were 0.093 ± 0.056, 0.001± 0.055 and 0.144±0.079, respectively. **Galeazzi et al. (2010 a)** analyses 1016 Murrah female buffaloes, reported that h^2 estimates for stayability ranged from 0.11 to 0.23. **Chander et al. (2008)** with Sahiwal cattle, reported that h^2 estimates for lifetime performance traits were found to be higher and ranged from 0.40 (no of days in milk) to 0.90 (lifetime milk yield)**. Khattab et al. (2009)** with 878 Friesian cows, using Multi Trait Animal Model (MTAM), found that heritability estimates for lifetime milk yield, lifetime fat yield, lifetime protein yield and number of lactation completed are 0.24, 0.24, 0.23 and 0.12, respectively. **Kern et al. (2014)** working on Holstein cows in Brazilian, reported that heritability estimates for longevity measures ranged from 0.06 to 0.09 using the linear model and from 0.05 to 0.18 for traits using the threshold model.

According to high and moderate estimates of h^2 for LTMY, TLP (Table 5), it could be concluded that the genetic improvement of milk yield and lactation period could be achieved through sire selection, while the two measurements of longevity (.i.e., age at disposal and number of lactation completed) were low heritability estimates. These results indicated that selection for longevity traits would not be effective due to its low heritability estimates and these traits mainly affected by environmental factors.

The present estimates of h^2 for different traits studied which calculated from Animal Model (AM) are lower than those estimates obtained from Sire Model (SM) (Table 5). This may be attributed to inclusion of some permanent environmental effects in the animal model and consequently a correction for this effect was considered in animal model, which it was not considered in the sire model. In addition, estimate of h^2 from sire model was computed as four times of the covariance between paternal half sibs related to the total phenotypic variance. Similar results are reported by many authors. In this respect, **El- Awady et al. (2014)** with 847 Friesian cows, found that h^2 estimates for 305 day milk yield, 305 day fat yield and 305 day protein yield were 0.245, 0.216 and 0.246, respectively as estimated from SM and were 0.057, 0.046 and 0.048, respectively as estimated from AM.

Phenotypic correlation may be defined as the association between two characters that can be directly observed on the same individuals. Phenotypic correlation between LTMY, TLP, AGDS and NLC are presented in Table 6. Phenotypic correlation between LTMY and each of TLP, AGDS and NLC was positive and highly significant and being 0.80, 0.60 and 0.50, respectively (P <0.01, Table 5), and phenotypic correlation between NLC and each of LTP and AGDS were positive and highly significant 0.40 and 0.70, respectively (P <0.01, Table 5). The present results indicate that high yielding buffalo cows will remain longer in the herd and the low yielder ones leave the herd at early age after they completed their first lactation. Similar results are found by many workers on different breeds of buffaloes. In this respect, **Kawthar Mourad et al. (1992)** with another set of that herd reported that Phenotypic correlation between lifetime production milk yield, total lactation period, age at disposal, productive life and number of lactation completed were positive and ranged from 0.27 to 0.67**. El- Shaife (1994)** with 907 Egyptian buffaloes, found that phenotypic correlation between age at disposal and number of lactation completed was 0.49. **Chauhan et al. (1993)** on Holstein cows, found that phenotypic correlations among lifetime yields of milk, fat and protein, productive life and number of lactations completed were close to one. . **El- Arian (2001 a)** with Murrah buffaloes, reported that phenotypic correlations among lifetime milk yield and longevity traits are positive and high ranging from 0.87 to 0.95.

Estimates of genetic correlations among LTMY, TLP, AGDS and NLC are presented in Table 5. Genetic correlations between LTMY and each of TLP, AGDS and NLC were positive, highly significant and being0.69, 0.63 and 0.63, respectively (P <.0.01, Table 5). Genetic correlations between NLC and each of TLP and NLC were positive, highly significant and being 0.19 and 0.88 (P <0.01, Table 5). Higher genetic correlations between lifetime and longevity traits indicated that the high producing cows are genetically correlated with their longevity. On other words, both the lifetime production traits and longevity traits were likely controlled by the same number of genes so that these traits could be improved simultaneously through selective breeding.

The present estimates are similar to those reported by many workers working on different breeds of buffaloes. In this respect, **Kawthar Mourad et al. (1992)** with another set of that herd, reported that the genetic correlation between lifetime milk yield and total lactation period was 0.75. Genetic correlation between lifetime production milk yield, total lactation period, age at disposal, productive life and number of lactation completed were positive and ranged from 0.41 to 0.63**. El- Arian (2001 a)** with Murrah buffaloes, found that genetic correlations among lifetime milk yield and longevity traits are positive, highly significant ranging from 0.897 to 1.00. These estimates revealed that both the lifetime production traits and longevity traits were likely controlled by the same number of genes. **Bashir et al. (2007)** with Murrah buffaloes, reported that the selection for productive life will increase herd life while lifetime milk yield will also improve. **Thiruvenkadan**

et al. (2015) analysis 664 Murrah buffaloes, found that genetic correlation among longevity and lifetime milk production traits were positive and ranged from 0.68 to 1.00.

Estimates of sire transmitting ability (STA's or BLUP values without A^{-1}) as estimation from the mean for lifetime and longevity traits by using sire model (SM) are presented in Table 6. BLUP values ranged from – 961 to 3414 kg for LTMY, from -243 to 132 d for TLP, from -12.22 to 12.16 mo., for AGDS and from – 0.82 to 0.69 lact., for NLC, with the range being 4375 kg, 375 d, 24.38 mo., and 1.61, respectively (Table 6). The present results show that the large differences between sires in the STA's and gave idea about the genetic variation between sires in lifetime production and longevity traits. Increasing the genetic variations between sires revealed that selection of sires which gave positive BLUP values will be helpful for faster genetic improvement in lifetime and longevity traits. Also, the present results suggested that the importance of evaluating the sires through their daughters and select the top ranking sires with highest positive proofs for future use. Also, the frozen semen of these top ranking sires (to achieve higher selection intensity) for lifetime production and longevity traits as well as their widely and extensively through the field units, this will lead finally to rapid improvement in the genetic potentiality of such important economic traits of Egyptian buffaloes. The present estimates are higher than those reported by **Kawthar Mourad et al. (1992)** working on the same herd and found that the EBV's showed large differences among sires for productive and longevity traits. The EBV's for lifetime milk yield ranged from -962 to 758 kg; for total lactation period ranged from – 568 to 678 d; for age at disposal ranged from -3.97 to 8.82 mo.; for productive life ranged from -4.19 to 4.56 mo. and for number of lactation completed ranged from 0.04 to 0.03. The higher estimates of the present study than those reported by **Kawthar Mourad et al. (1992)** may be due to used proven sires and used artificial insemination (AI) in recent year from the top bulls which kept at Mehalet Mousa farm. Also, the present estimates are higher than those reported by **El- Arian (2001 a)** with Murrah buffaloes, found that ranges of sire transmitting ability were 3070 kg, 820 d and 1.79 for LTMY, TLP and NLC, respectively. The same author suggested that all the elite buffalo cows should be served using the top ranking sires (to achieve higher selection intensity) as well as their sons for the improvement of genetic potential of buffalos for lifetime production and longevity traits.

In addition, **Khattab (1992) and El- Arian (2001 b)** working on Friesian and Holstein cows, respectively, estimated BLUP values from Sire Model (SM). They concluded that the large differences observed among sires in their sire transmitting ability values gave an idea about the genetic variation between sires in these important economic traits. The higher values of genetic variation between sires clarified that selection of sires will be helpful for faster genetic improvement in lifetime production and longevity traits which leads simultaneously to increase the productivity.

Minimum, maximum, range and accuracy of predicted sire transmitting ability (STA's) for different traits studied as estimated from Multi Trait Animal Model are presented in Table 7. Minimum and maximum predicted sire transmitting ability ranged from – 961 to 3414 kg for LTMY, from -243 to 132 d for TLP, from -12.22 to 12.16 mo., for AGDS and from – 0.82 to 0.69

lact., for NLC, with the range being 4375 kg, 375 d, 24.38 mo., and 1.61, respectively (Table 8). The present results show large differences among sires for LTMY, TLP, AGDS and NLC, which indicate the high potential for rapid genetic improvement in lifetime and longevity traits of Egyptian buffaloes. Also, the present estimates were lower than those obtained from SM (Table 7). This may be due to the (1) considering the relationship among sires and (2) considering the genetic covariance among traits and (3).

Rank correlations of STA's among LTMY, TLP, AGDS and NLC as estimated from SM and AM are presented in Tables 8 and 9. Rank correlations among lifetime and longevity traits as estimated from SM were positive and highly significant expect the rank correlation between NLC and LTMY and TLP (P <0.01) and ranged from 0.08 to 0.98 (Table 8). Similar results are reported by **Khattab (1992)** with Friesian cows, found that the product moment correlation between lifetime and longevity traits as estimated from SM, ranged from 0.10 to 0. 0.69.

Rank correlations of sire transmitting ability among lifetime and longevity traits as estimated from AM were positive and highly significant (P <0.01) and ranged from 0.33 to 0.88 (Table 9). The present results suggested that in most cased sires have positive BLUP values for lifetime milk production gives positive BLUP values for total lactation period, productive life and more number of lactations and selection of these sires and collect semen from these sires will increase milk production in next generation. In addition, rank correlation among lifetime and longevity traits as estimated from SM and AM are near similar to genetic correlations (Table 5), while the difference may be due to small number of observations for each sire.

Rank correlations of between sire model and animal model for sire transmitting ability were positive, significant and ranged from 0.20 to 0.62 (Table 10). The present estimates are the same trend obtained from sire model (0.08 to 0.98, Table 8) and animal model (0.33 to 0.88, Table 9). Also, the rank correlation between SM and AM are similar to genetic correlations among lifetime and longevity traits as estimated from sire model (0.10 to 0.98, Table 5) and from animal model (0.19 to 0.69, Table 5). The present results indicated that the both two methods are succeeded in estimating sire transmitting ability, while using sire model is easy in estimation. Similar results are reported by many authors.

In addition, Nowier (2006) in a study based on 2181 Friesian cows, found that the product moment correlations between SM and AM for milk traits were positive, highly significant and ranged from 0.48 to 0.90. Also, the same authors concluded that the product moment correlations between (SM and AM)- AM) were small and ranged from 0.01 to 0.10.

Finally, the present results show that although a little differences between SM and AM and many authors concluded that animal model (AM) are more accurate than sire model (SM). Sire mode are the cheapest in terms of computing costs, while animal model need a higher power of computers and need a starting values to estimate variance components and also suggested that used sire model in small number of observations.

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Table 1. Structure of data used in the analysis.

Observations	
No. of records	1621
No. of cows	360
No. of sires	115
No. of dams	294
Animals in relationship matrix	769
Mixed model equations	5092
No. of iterations	23285

Table 2. Unadjusted means, Standard deviation (SD) and coefficient of variability for Lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactation completed (NLC) for Egyptian buffaloes.

Traits	Mean	SD	CV %
LTMY, kg	10551	7764	73.59
TLP, d	1174	750	63.86
AGDS, Mo	125	57	45.39
NLC	5.97	3.22	53.82

Table 3 Least squares analysis of variance for factors affecting lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactation completed (NLC).

S.O.V.	d.f.	F – Values			
		LTMY	TLP	AGDS	NLC
Between Sires	114	1.46**	1.33**	1.24**	1.36**
Between month of birth	11	0.80	1.20	0.30	1.39
Between Year of birth	20	2.09**	2.57**	2.61**	1.64**
AFC, Linear	1	0.82	3.61**	0.11	0.02
AFC, Quadratic	1	0.61	3.03**	0.09	0.02
Reminder, M.S.	353	42580509	301966	10.39	1792.20

Table 4. Estimates of phenotypic trend (P) for lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactations completed (NLC) for Egyptian buffaloes.

LTMY, kg		TLP, d		AGDS, mo.,		NLC(Lact.)	
P + SE	Pr	P + SE	Pr	P + SE	Pr	P + SE	Pr
-529± 48.71	<0.0001	-73 ±4.09	< 0.0001	-5.16±0.32	< 0.0001	-0.35+0.02	< 0.0001

Table 5. Estimates of heritability (on diagonal) , genetic correlations (below diagonal) and phenotypic correlations (above diagonal) for lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactation completed as estimated from sire model (SM) and Animal model (AM) for Egyptian buffaloes.

Traits	**SM**				**AM**			
	LTMY	**TLP**	**AGDS**	**NLC**	**LTMY**	**TLP**	**AGDS**	**NLC**
LTMY	**0.45±0.18**	**0.73**	**0.55**	**0.13**	**0.27±0.01**	**0.80**	**0.60**	**0.50**
TLP	**0.69±0.18**	**0.18±0.10**	**0.69**	**0.69**	**0.70±0.20**	**0.17±0.01**	**0.70**	**0.40**
AGDS	**0.63± 0.27**	**0.19±0.69**	**0.90±0.80**	**0.72**	**0.66±0.21**	**0.98±0.20**	**0.12±0.03**	**0.70**

NLC 0.63± 0.21 0.88±0.10 0.60±0.48 0.36±0.18 0.30±0.10 0.70±0.20 0.10±0.10 0.06+0.01

Table 6. Estimation of sire transmitting ability (STA) from Sire Model (SM) for lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactation completed (NLC) for Egyptian buffaloes

Traits	BLUP, values											
	LTMY			TLP			AGDS			NLC		
	Min	Max	Range	Min	Max	Range	Min	Max	Range	Min	Max	Range
	-961	3414	4375	-243	132	375	-12.22	12.16	24.38	-0.82	0.69	1.61

Table 7. Estimation of sire transmitting ability (STA) with it is accuracy (rit)from Animal Model (AM) for lifetime milk yield (LTMY), total lactation period (TLP), age at disposal (AGDS) and number of lactation completed (NLC) for Egyptian buffaloes

Traits	BLUP, values															
	LTMY				TLP				AGDS				NLC			
	Min	Max	Range	rit	Min	Max	Range	rit	Min	Max	Range	rit	Min	Max	Range	rit
	-1101	1779	2289	0.30 to 0.35	-106	180	286	0.20 to 0.30	-3.0	2.86	5.87	0.20 to 0.23	-0.57	0.58	1.15	0.30 to 0.40

Table 8. Rank correlation for sire transmitting ability (STA) for different traits by Using Sire Model (SM).

Traits	LTMY	TLP	AGDS
TLP	0.70±0.05		
AGDS	0.46±0.05	0.98±0.06	
NLC	0.08±0.05	0.08±0.06	0.26±0.06

Table 9. Rank correlation for sire transmitting ability (STA) for different traits by using Animal Model (AM).

Traits	LTMY	TLP	AGDS
TLP	0.88±0.01		
AGDS	0.67±0.02	0.68±0.04	
NLC	0.48±0.02	0.55±0.05	0.33±0.04

Table 10. Rank correlation for sire transmitting ability (STA) for different traits by Using animal model (AM) and sire Model (SM)

Variable	LTMY	TLP	AGDS
TLP	0.62±0.10		
AGDS	0.48±0.10	0.37±0.10	
NLC	0.20±0.09	0.28±0.10	0.48±0.10