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GENETIC PARAMETERS FOR BUFFALO MILK YIELD AND MILK QUALITY TRAITS USING ANIMAL MODEL

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Abstract

A total of 365 normal first lactation records of Egyptian buffaloes, kept at Mehalet Mousa Farm, belonging to the Animal Production Research Institute, Ministry of Agriculture, Dokki Cairo, Egypt, during the period from 2001 to 2006 were used. Data were analyzed by using Statistical Analysis System (SAS) to study the fixed effects of month and year of calving and random effect of sire on milk yield (MY), lactation period (LP), fat yield (FY), protein yield (PY) and somatic cell count (SCC). In addition, genetic parameters (i.e., heritability, genetic correlation and phenotypic correlation) among different traits studied were analysed by using Multi Trait Animal model (MTAM). Means for MY, LP, FY, PY, and SCC were 1536 kg, 198.84 d, 147.67 kg, 81.21 kg and 156.21, respectively. Month and year of calving of had a significant effect on MY, LP, FY and PY, while month of calving had no significant effect on SCC. Sire of the heifers had a significant effect on all traits studied, expect the effect of sire on SCC. Heritability estimates (±SE) for MY, LP, FY, PY and SCC were 0.40± 0.07, 0.30 ± 0.06, 0.19 ± 0.04, 0.22 ± 0.05 and 0.05± 0.09, respectively. Estimates of genetic correlations ($r_{g)}$ between milk traits (i.e., MY, LP, FY and PY), were positive and highly significant and ranged from 0.18 (0.10) to 0.75 (0.07), while the genetic correlation between SCC and all milk traits were negative and ranged from – 0.18 (0.10) to – 0.40 (0.21). Phenotypic correlations (r_p) among all traits studied are in the same direction of genetic correlations.

Key words: genetic parameters, milk, yield, milk composition, buffaloes

Introduction

A total number of cows and Buffaloes in Egypt are 8,546,957 heads, according to the Annual Statistics, Animal Production Sector, Ministry of Agriculture and Land Reclamation (IFCN, 2011). Number of cows (Native cows, European cows and their crosses) is 4,72872 heads and Egyptian buffaloes is 3,818236 heads which represents 46 % of the total population of dairy animals. Egypt rank 5th in the world and has the largest buffalo herd outside Asia, since it comes to Egypt from Asia centuries ago. Egyptian buffaloes can be considered the main dairy animals in Egypt. They contribute more than 47 % of national milk production. There has not been national selection program for buffaloes. Therefore a high genetic variability among animals would be expected. Selection for multiple traits such as milk yield, lactation period and somatic cell counts would result in improving milk quality compared with single – trait selection for milk yield (*Van Vleck*, 1978).

Somatic cell count (SCC) is a good indicator of milk quality and cow health; high SCC are associated with a reduction in milk yield and an increase in the incidence of subclinical mastitis in cattle (*Castillo- Juarez et al.,* 2002). In addition, *Ceron – Munoz et al.* (2002) reported that high levels of SCC cause reductions in lactose, fat, casein, calcium and potassium in milk and thus reduce the quantity and quality of cheese produced.

The improvement through selection of traits associated with milk quality and milk yield for milking buffaloes is dependent on the availability of reliable genetic parameters estimates is determined by many factors such as the quantity and quality of information (records and pedigree), the statistical model applied, and the method of covatiance estimation. The implementation of a multiple – trait model allows the incorporation of all information available from an animal and hence, increasing the accuracy of genetic parameters estimates (*Asplicueta-Borquis et al.*, 2010).

The objective of the present study was to estimate phenotypic and genetic parameters for milk yield, lactation period, fat yield, protein yield and somatic cell count on a herd of Egyptian buffaloes.

Material and methods

Data in the present study were obtained from first lactation records of Egyptian buffaloes kept at Mehallet Mousa Farm, belonging to Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo, Egypt. They comprised 365 normal first lactation records during the period from 2001 to 2006. All abnormal records without pedigree, breeding dates and cow affected by diseases such as mastitis and under troubles or reproductive disorders were excluded and represented 1.5 % of the total am\animals. Animals were mainly grazed on Egyptian clover (*Trifolium alexandrinum*) berseem during December to May. They were fed on concentrate mixture along with rice straw and limited amount of clover hay when available during the rest of the year. Cows were hand milked twice daily (at 7 am and 4 pm). Bulls were evaluated for semen characteristics. Cows were naturally mated until 2002 and artificially insemination after that. Assignment of sires to cows was at random. Heifers were served for the first time when they reached 24 month or 350 Kg. Genetic analysis include 34 sires which had more than 5 daughter. Traits studied were milk traits total milk yield (MY), lactation period (LP), fat yield (FY), protein yield (PY) and somatic cell count (SCC). Milk yield were recorded daily and both fat and protein percents are estimated weekly in laboratory by using system of Milko–Scan 130 series, type

10900. Maintained at International Livestock Management Training Center (ILMTC) related to Animal Production Research Institute (APRI), this set have special program to estimate milk composition (fat and protein).

Preliminarily analysis of data were made by using Statistical Analysis System (SAS) version 8.2 for Windows were used to study the fixed effects of month and year of calving and sire as a random effect on MY, LP, FY, PY and SCC. In addition, all traits studied analyzed by using multiple trait derivate – Free Restricted Maximum Likelihood (MTDFREML) according to *Boldman et al.* (1995). The model included the fixed effects of month and year of calving and animals and errors are random effects. Estimates of heritability, genetic correlations, phenotypic correlation are estimated from Multi Trait Animal model (MTAM) according to *Boldman et al.* (1995).

Results and discussion

Unadjusted means

Means, standard deviations (SD) and coefficient of variation (CV%) for different traits studied are presented in *Table 1*. Means of MY and LP were 1536 kg and 198.84 d, respectively (*Table 1*). The present mean of MY was higher than those reported by *El-Arian et al.* (2001) (1270±25 kg) and *Khattab et al.* (2010)(1591 kg) working on another sets of Egyptian buffaloes. While, the present mean was lower than those found by *Badran et al.* (2002) (2256 kg) working on another herd of Egyptian buffaloes. The present mean of LP was lower than those found by *El-Arian et al.* (2001) (312 ± 5) and *Badran et al.* (2002)(260.7 - 367.4) for Egyptian buffaloes. While, the present mean of MY was lower than that reported by *Aspilceta- Borquis et al.* (2010) working on Murrah buffaloes in Brazil, found that the average milk yield was 1814 kg. Overall means of fat yield and protein yield were 147.67 kg and 81.21 kg, respectively (*Table 1*). The present means are higher than those reported by *Tonhati et al.* (2011) (90.1 and 56.9 kg, respectively) *Rosati and Van Vlec*k (2002)(197 d). The present mean of somatic cell count (156.21) was lower than that found by *Aspilcuta – Borquis et al.* (2010) (491.3) on Murrah buffaloes in Brazil. Friesian cows in Egypt.

The coefficient of variability (CV %) ranged from 33.40 to 89.94 (*Table 1*). The large CV % for fat yield, protein yield and somatic cell count, reflect the great variation between individuals in important productive traits. The different between the present means and those reported on other studied for buffaloes could be due to, the herds were raised under different climatic and managerial conditions, different herds could possibly be genetic and phenotypic different from other and different methods and models of analysis were used.

***Table 1*: Means, standard deviations (SD) and coefficient of variation (CV%) for milk yield (MY), lactation period (LP), fat yield (FY), protein yield (PY) and somatic cell count (SCC) of Egyptian buffaloes**

Traits	Mean	SD	CV%
Milk yield, (MY) kg	1536	629	40.95
Lactation period, (LP) d	198.64	66.35	33.40
Fat yield, (FY) kg	147.67	72.80	49.30
Protein Yield, (PY) kg	81.21	41.84	51.52
Somatic cell counts (10^{-3})	156.21	140.50	89.94

Non genetic factors

Month of calving had a significant effect on MY, LP, FY and PY, while had no significant effect on SCC (P < 0.05 or 0.01, *Table* 2). The higher MY, FY, PY and LP in winter season may be due to available green fodder and good weather. Similar results are reported by many authors working on different breeds of buffaloes in different countries (*Kawthar Mourad et al*. 1991, and *Khan et al.* 2007).

Year of calving had a significant effect on MY, LP, FY, and PY and SCC (P < 0.01, *Table* 2). These results are agree well with the findings on Egyptian buffaloes are reported by *Kawthar Mourad et al.* (1991), *Badran et al.* (2002) *Khattab et al,* (2003), *Khan et al.* (2007) and *Kawther Mourd and Khattab* (2009)**,** found that year of calving have a significant influence (P < 0.01) on milk traits. The present results show that there is no specific trend for the effect of year of calving on milk traits. The effect of year of calving may be due to changes in production from year to another can be attributed to changes in herd size, age of animals, improved management practices introduced from year to another and phenotypic trend.

Table 2: Least squares analysis of variance for factors affecting milk yield (MY), lactation period (LP), fat yield (FY), protein yield (PY) and somatic cell count (SCC) for Egyptian buffaloes

S.O.V.	**d. f.**	**F- Values**				
		MY	**LP**	**FY**	**PY**	**SSC**
		**	**	**	**	ns
B. Sires	33	4.77	4.78	2.22	2.94	0.67
		**	**	*	*	ns
B. Month	11	2.79	5.88	1.92	2.15	0.92
		**	**	**	**	**
B. Years	5	23.98	33.39	38.94	22.55	4.14
Reminder, M.S	315	367668	3397	66.96	14.53	510985

*P < 0.05 and ** P < 0.01

Random effect

Sire of the heifers had a significant effect on MY, LP, FY and PY, while had no significant effect on SCC (P < 0.01, *Table* 2). The present results are in agreement with those reported by different authors working on different breeds of buffaloes (i.e,. *Kawthar Mourad et al.,* 1991; *Khattab and Mourad*, 1992; *Badran et al*. 2002; *Rosati and Van Vleck,* 2002*; Khattab et al.* 2003; *Kawthar Mourad and Khattab*, 2009 ; *Abdel – Salam et al.* 2010; *Aspilcueta – Borgquis et al*, 2010 and *Fooda et al*., 2010). The present results indicated the possibility of genetic improvement of milk yield and it is composition through selection of sires.

Genetic parameters

Estimates of heritability for MY, LP, FY, PY and SCC by using Multi trait Animal Model (MTAM) are presented in *Table 3*. Heritability estimate for MY was 0.40± 0.07 (*Table 3*). The h^2 value of MY was moderate and in the same time it is similar to that obtained by using animal model, *Khattab et al*. (2003)(0.43) and higher than those reported by *Seno et al* (2010) (0.20) *Tonhati et al*. (2000) (0.22) in Murrah buffaloes.

Heritability estimates for lactation period (LP) was 0.30±0.06 (*Table 3*). The present estimates for LP from multi trait animal model was higher than that found by *Khattab et al.* (2003)(0.14) using multi trait animal model on another set of that herd.

Heritability estimates for FY and PY were 0.19±0.04 and 0.22 ± 0.05, respectively (*Table 3*). Similar results are reported by *Tonhati et al.* (2000) with Murrah buffaloes in Brazil, found that h^2 estimates for FY and PY were 0.21 and 0.26, respectively. *Aspilcueta-Borquis et al.* (2010) estimated genetic parameters for fat (FY305), protein (PY305) by using Bayesian methodology. The posterior means of heritability distributions for FY305 and PY305 were 0.23 and 0.33, respectively. Milk yield and milk components have enough genetic variation for selection purposes. *While, Rosati* and *Van Vleck* (2002) working with Italian buffaloes and applying the REML method, reported lower heritability estimates for FY and PY, with values of 0.11 and 0.14, respectively.

In addition, the present estimate of heritability for MY, FY and PY are higher than those reported by *Manal El- Bramony et al.* (2010) working on other set of Egyptian buffaloes, found heritability estimates for MY, FY and PY were 0.18, 0.16 and 0.13, respectively.

The moderate h^2 estimates for MY, LP, FY and PY suggested that efforts could be made to bring about improvement in those important economic traits through individual selection as well as better management practices. On other words, the genetic improvement in milk production and it is composition can be achieved through selection breeding program**.**

Table 3: Estimates of heritability (h^2) with standard errors (SE), genetic correlations with standard errors (SE) and phenotypic correlations among different traits studied

Traits	**MY**	**LP**	**FY**	**PY**	**SCC**
MY	**0.40±0.07**	0.73	0.64	0.63	-0.01
LP	0.75± 0.07	**0.30±0.06**	0.42	0.32	-0.01
FY	0.18±0.10	0.30±0.10	**0.19±0.04**	0.89	**-0.02**
PY	**0.30±0.17**	**0.27±0.10**	**0.80±0.1**	**0.22±0.05**	-0.12
SCC	-0.27±0.10	-0.18±0.10	-0.20±0.10	-0.40±0.21	**0.05±0.09**

Estimate of heritability for SCC was 0.05±0.09 (*Table 3*). Low heritability estimate for SCC indicate that this trait is affected mainly by environmental factors such as improvement of feeding, management and milking the cow three times per day. The present h^2 estimate of SCC is lower than those reported by several investigators (*Mrode et al.,* 1998; *Koivula et al.*, 2005; *El-Arian and El-Awady*, 2008 and. *Aspilcueta-Borquis et al.*, 2010) which ranged from 0.15 to 0.26.

In general, it is observed that heritability estimates for all milk traits were moderate expect for SCC and this may be allowed to improve them through selection and improving environmental.

Genetic correlation between milk yield (MY) and lactation period (LP) was positive and high (0.75 ± 0.07, *Table 3*). The present results indicating that high yielding buffaloes are also having the longer LP. This correlation suggests that selection for higher yielding cows would cause a correlated increase in their lactation period. *Khattab and Mourad* (1992) and *El – Arian et al*. (2001) arrived at the same conclusion.

Genetic correlation between milk yield (MY) and fat yield and protein yield were positive and being 0.18±0.10 and 0.30±0.17, respectively (*Table 3*). Estimates of genetic correlations between milk yield and milk composition are similar to those that can be found in the literature for dairy cattle. Large estimates for genetic correlations between milk, fat and protein yields are commonly reported for dairy cattle (*Rosati and Van Vleck*, 2002; *Aspilcueta-Borquis et al*. 2010). The present results indicated that milk yield could be used as a good indicator for the genetic values of the other milk traits (FY and PY). Also, the present results indicated that the higher productive cows were lactating for longer time and selection for higher milk yield brings correlated response for lactation period.

Negative genetic correlations between SCC and milk traits which ranged from -0.18 to -0.40 (*Table 3*). Similar results are reported by *El – Awady* (2009) found that genetic correlation between milk yield and SCC was - 0.35. The present results indicated that selection for milk yield and milk composition will decrease somatic cell counts, which indicate the health of udder. Also, *Aspilcueta- Borquis et al.* (2010) with Murrah buffaloes in Brazil, reported that the genetic correlation estimates ranged from -0.13 (between % P and SCS) to 0.94 (between MY305 and PY305). Milk yield, milk components, and milk somatic cells counts have enough genetic variation for selection purposes. The genetic correlation estimates suggest that milk components and milk somatic cell counts would be only slightly affected if increasing milk yield were the selection goal. Selecting to increase FY305 or PY305 will also increase MY305, % P, and % F.

Given the correlation values, there may be an opportunity to include FY or PY as a selection criterion to simultaneously increase milk yield and components, because FY and PY are favorably correlated with MY. Phenotypic correlations among different traits studied are similar to genetic correlation (*Table 3*).

It is observed that selection for high milk yield will be associated with genetic improvement in milk composition and decrease somatic cell counts. On other words, selection program to improve milk yield is expected to result in a favorable response in other milk yield traits without a negative effect on udder health for the Egyptian buffaloes.

References

Abdel – Salam, S. A. M., Abou – Bakr, Ibrahim, M. A. M., Sadek, R. R. and Abdel – Aziz, A. S. (2010): Estimation of breeding values of total milk yield of Egyptian buffalo under different production systems. ICAR Technical Series 13: 167-172.

Aspilcueta-Borquis, R. R.; Araujo Neto, F. R.; Baldi, F.; Bignardi, A. B.; Albuquerque, L. G.; Tonhati, H. (2010): Genetic parameters for buffalo milk yield and milk quality traits using Bayesian .J. Dairy Sci.93:2195-2201.

Badran, A. E.; El-Barbary, A.; Mahdy, A. E.; Assar, G. M. (2002): Genetic and non-genetic factors affecting the lifetime production traits in Egyptian buffaloes. Buffalo Journal. 18: 235-241.

Boldman, K.G., Kriese, L.A., Van Vleck, L.D. and Kachman, S.D. (1995): A manual for use of MTDFREL. Department of Agriculture, Agricultural Research service, Lincoln, PP120.

Castillo- Juarez, H., Oltenacu, P.A. and Cienfuegos- Rivas (2002): Genetic and phenotypic relationships among milk production and composition traits in primiparous Holstein cows in two different herd environments. Livest .Prod. Sci., 78: 223-231.

Ceron – Munoz, M., Tonhati, H., Duarte, J., Oliveira, J., Munoz- Berrocal, M, and Jurado-Gamez, H. (2002): Factors affecting somatic cell counts and their relation with milk and milk constituent yield in buffaloes. J. Dairy Sci., 85:2885-2889.

El-Arian, M. N. and El-Awady, H. G. (2008): Assessment of the Genetic relationships between udder health and milk production traits in relation to selection for improving resistance to clinical mastitis in Friesian cows in Egypt. J. Agric. Sci. Mansoura Univ. 33:181

El- Arian, M.N., kawther, Mourad, A and Khattab, A.S. (2001): A comparison of different selection indices for genetic improvement of some milk traits in a herd of Egyptian buffaloes**.** J. Agric. Sci. Mansoura Univ., 26: 2687-2695.

El – Awady, H. G. (2009): Calculation of the economic values for some udder health traits to estimate the profitability of the selection indices for dairy cows in Egypt. J. Agric. Res. Kaferlsheikh university. 35: 384-401.

Fooda, T., Mourad, K. A. Gebreel, I. A. (2010): Phenotypic and genetic trends for milk production in an experiment stations buffalo herd. Revista Veterinaria, 21 Suppl. (1) 403-407.

IFCN (2011): 12th international Farm Comparison Network Conference, Kiel, Germany, 4-8 June, 2011.

Kawthar Mourad, A., Mohamed, M. M. and Khattab, A. S. (1991): Genetic parameters for milk production traits in a closed herd of Egyptian buffaloes. Egypt. J. Anim. Prod., 28: 11-20.

Khan, M. S.; Faiz-ul-Hassan; Saif-ur-Rehman, M.; Hyder, A. U.; Bajwa, I. R. (2007): Genetic control of milk yield from lactations of different duration in Nili-Ravi buffaloes. Archiv fur Tierzucht. 50: 227-239.

Khattab, A. S, El –Awady, H.G., El Arian ,M. N. and Kawther, A. Mourad (2003): Genetic analysis of some performance traits using an animal model in a herd of Egyptian Buffaloes. Egyptian .J. Anim. Prod.40:15-26.

Khattab, A. S.; Kawther, A. M.; El-Habiab, S.; Awad, S. (2010): Estimation of genetic parameters and breeding values for some productive traits on Egyptian buffaloes. Revista Veterinaria. 2010. 21: Suppl. 1, 1046-1048.

Khattab, A. S and Mourad, K. A (1992): Estimation of genetic parameters and genetic trends for some milk traits in a herd of Egyptian buffaloes. Egypt .J.Anim. Prod.,29: 33-44.

Koivula, M., Mäntysaari, E. A.; Negussie, E. and Serenius, T. (2005): Genetic and phenotypic relationships among milk yield and somatic cell count before and after clinical mastitis. J. Dairy Sci. 88:827.

Manal, M. El- Bramony, Gebreel, I.A., and Set El- Habaeib S. Awad (2010): Genetic analysis of somatic cell count and milk yield traits in Egyptian buffaloes. Egyptian J. Anim. Prod. 47:75-84.

Mrode, A. R., Swanson, G. J. T. and Winter, M. S. (1998): Genetic parameters and evaluations for somatic cell counts and its relationship with production and type traits in some dairy breeds in the United Kingdom. Anim. Sci. 66:569.

Mourad, K. A. M.; Khattab, A. S. (2009): A comparison between different selection indices for some productive traits on Egyptian buffaloes. Archiv Tierzucht. 52: 5, 476-484.

Rosati, A. and Van Vleck, L. D. (2002) Estimation of genetic parameters for milk, fat, protein and mozzarella cheese production for the Italian river buffalo Bubalus bubals population. Livest. Prod. Sci., 74:185-190.

Seno, L. O.; Cardoso, V. L.; El-Faro, L.; Sesana, R. C.; Aspilcueta-Borquis, R. R.; Camargo, G. M. F. de; Tonhati, H. (2010): Genetic parameters for milk yield, age at first calving and interval between first and second calving in milk Murrah buffaloes. Livestock Research for Rural Development. 22: 1-9.

Tonhati, H., Vasconcellors, F.B. Albuquerque, L. G (2000): Genetic aspects of productive and reproductive traits in a Murrah buffaloes herd in Sao Population. J. Anim. Breed Genet.. 117:331-336.

Van Vleck, L. D. (1978): Breeding for increased protein content in milk . J. Dairy Sci., 61:815-824.