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Estimates of Population Parameters of Some Economic Traits in Holstein Friesian Cows by Using Statistical Program

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Abstract: Heritabilities, breeding values, phenoypic and genetic correlations for the various productive and reproductive traits were analyzed by using single-trait animal model analysis. Studied traits were age at first calving (AFC, months), age at calving (AC, months), services per conception (SC, services), calving interval (CI, days), days open (DO, days), dry period (DP, days), days in milk (DIM, days), total milk yield (TMY, kg), 305-days mature equivalent (305-ME, kg) and peak milk yield (PMY, kg). Estimates of heritabilites of AFC, AC, SC, CI, DO, DP, DIM, TMY, 305-ME and PMY were 0.24, 0.51, 0.21, 0.04, 0.10, 0.20, 0.10, 0.29, 0.31and 0.16, respectively. Generally, there were high positive (e.g. DP and CI) and negative (e.g. 305-ME and DP) genetic and phenotypic correlations between most studied traits. The highest range of breeding values for all traits was the range of TMY (9648.7 kg). The wide range of estimated breeding value (EBV) for any trait, suggests the presence of genetic variations between animals and hence the possibility of sire selection for daughter's productive and reproductive traits in the next generation, which would lead to more genetic improvement. In conclusion, this study will help the breeders to select the best dairy animals which will be used for production the future generations based on genetics of milk production and reproduction traits in early lactation.

Key words: Fertility traits · Breeding value · Economic traits · Genetic parameters · MTDFREML program

INTRODUCTION

Genetic improvement of dairy cattle is an important factor for economically important traits, particularly milk yield, which considered an important for overall strategy to improve profitability and sustainability of dairy cattle operations [1]. Knowledge of genetic parameters of some factors affecting milk yield is required for planning efficient breeding programs in animal production [2]. Furthermore, they reported by knowledge of heritability estimate, animal geneticists can judge whether or not a particular trait can be improved by managerial practices and/or by selection.

El-Awady [3] revealed that estimates of genetic and phenotypic correlations are very useful in formulating a plan for genetic improvement and to trace how a particular change in one trait affects other traits associated with it. In livestock populations, estimation of breeding values for selection requires a matrix describing the additive relationship between individuals in the population [4]. Reliable breeding value estimates depend on the statistical model that is capable to recognize the meaningful environment effects and which is solvable without complications due to colinearity [5]. The main objectives of this study are to estimate, genetic and phenotypic parameters and breeding values for some economic traits for Holstein Friesian cattle reared under Egyptian conditions using MTDFREML program.

MATERIALS AND METHODS

Data Source and Herd Management: Data were obtained from lactation records ranged from 1059 to 3464 records relevant to 991 Holstein Friesian cows covering the period between 1994 and 2011. These cows were daughters of 99 sires and of 691 dams, which belong to a commercial dairy herd, situated in Cairo-Alexandria desert

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road and named Alexandria- Copenhagen Company far from Alexandria by about 76 km. All animals were kept in an open system, supplied with a cool spraying system during hot climate. Animals had free access to clean water. The animals allover the year were fed on total mixed ration (TMR). All cows are machine milked, three times with 8 hrs interval between milking. Calves were suckled artificially after calving to weaning excluding first three days of colostrum period. Cows were dried-off about 60 days before expected calving date or abruptly at 210 days of pregnancy.

Statistical Analyses: Estimates of variances and co-variance components were performed using the software of MTDFREML (Multivariate Derivative Free Restricted Likelihood) program according to Boldman *et al.*[6]. Direct and maternal heritability estimates were calculated using single-trait analysis. Best linear unbiased prediction (BLUP) of estimated breeding values were performed by back-solution using MTDFREML software program for all animals in the pedigree according to Shalaby [7]. Phenotype and genetic correlations between all traits were performed using two-trait analyses, which focus for only one random genetic effect (direct genetic effect) in the model according to El Fadilia *et al.* [8]. Starting values for residual variances and additive genetic variances for two trait (bivariate) analyses were estimated from single (univariate) analyses according to Shalaby [7] and El Fadilia *et al.*[8]

General Form of Single-Trait Animal Model: For estimation of parameters and prediction of breeding values, a set of single-trait animal model were used and shown in the following general matrix notation form according to Boldman *et al.* [6] as the following:

$$Y = XB + Z_a a + e$$

Where

Y is a vector of trait measurements.

B is a vector of fixed effects.

a is a vector of random additive genetic effects.

X and Z_a are incidence matrices relating records of fixed effects and additive genetic effects, respectively.

e is a vector of random error (error effects).

The model has the following distributional assumptions:

$$E(Y)= XB \quad E(a) = 0 \quad E(e) = 0$$

The inverse of the numerator relationship matrix (A^{-1}) was considered and the variances and co variances are:

$$Var(a) = A\, ó^2_a \quad var(e) = I\, ó^2_e$$

Where, $ó^2_a$ and $ó^2_e$ are variances due to direct additive genetic effect and random error, respectively. A is the additive genetic relationship matrix and I is the identity matrix. A variance of 10^{-8} of simplex function values were used as the criterion according to El Fadilia *et al.* [8]. Standard errors (SE) of genetic correlations were obtained using the approximate formula as described by Robertson [9] and Falconer and Mackay [10].

RESULTS

Heritability Estimate: Heritability estimates and their standard errors among different studied milk production and fertility traits are summarized in table (1). High heritability estimates were obtained for each of AC and 305-ME. Selection on the basis of individual's own phenotype would be effective. Moderate heritability estimates were detected for each of AFC, SC, DP and TMY. The genetic improvement for moderate heritability is achieved through selection for this trait. Furthermore, low heritability estimates were recorded for each of CI, DO, DIM and PMY. Low heritability tells us that variation due to non-additive gene action is very important.

Phenotypic Correlations: Estimates of phenotypic correlations among different productive and reproductive traits are shown in table (1). There were negative low phenotypic correlations among AFC with each of SC, TMY and 305-ME. The present results indicating that low association between these traits that improving any of them not affected on the other traits. On the other hand, positive low phenotypic correlations obtained between AFC and each of DO, DIM and PMY. Overestimates of either phenotypic and/or genetic correlations obtained between AFC and AC, which may be explained as presence of sampling errors, selection or culling inside the farm, used small number of animals in estimation, structure of analyzed data and/or absence of dam in the model.

Concerning to age at calving, positive phenotypic correlations obtained between AC and each of SC, CI, DO, DP and PMY. On the contrary, negative highly significant phenotypic correlations among AC with each of DIM, TMY and 305-ME. Indicating that older cows at AC had longer lactation length associated by low productivity.

Table 1: Estimates of heritabilities (on diagonal with standard errors between parenthesis), phenotypic (above diagonal) and genetic (below diagonal) correlations among productive and reproductive traits.

Item	AFC	AC	SC	CI	DO	DP	DIM	TMY	305-ME	PMY
AFC	0.24 (0.068)	1.000**	- 0.024	.^{b}	0.128**	.^{b}	0.126**	- 0.006	- 0.001	0.032
AC	1.000	0.51 (0.019)	0.208**	0.651**	0.031	0.450**	-0.106**	- 0.078**	- 0.146**	0.078**
SC	-0.05	-0.70	0.21 (0.019)	0.233**	0.116**	0.225**	0.088**	0.031	- 0.153**	0.006
CI	.^{b}	0.90	0.42	0.04 (0.019)	- 0.034*	0.609**	-0.150**	- 0.026	- 0.092**	0.089**
DO	0.48	0.55	0.34	0.97	0.10 (0.018)	0.062**	0.642**	0.337**	0.073**	0.026
DP	.^{b}	0.60	0.25	0.90	0.82	0.20 (0.024)	-0.171**	- 0.144**	- 0.197**	0.019
DIM	0.03	0.02	0.06	-0.84	0.81	-0.06	0.10 (0.018)	0.616**	0.294**	0.042*
TMY	-0.40	-0.38	0.07	-0.99	0.17	-0.65	0.62	0.29 (0.02)	0.650**	0.161**
305-ME	-0.33	-0.25	-0.20	-0.99	0.03	-0.84	0.55	0.89	0.31 (0.02)	0.113**
PMY	0.24	0.06	0.01	0.69	0.03	0.08	0.26	0.38	0.88	0.16 (0.019)

**.Correlation is significant at the 0.01 level (P<0.01) (2-tailed).

*.Correlation is significant at the 0.05 level (P<0.05) (2-tailed).

b. cannot be computed because at least one of the variables is constant.

Services per conception had low phenotypic associations with each of CI, DO, DP, DIM, TMY and PMY. In contrast, negative low phenotypic relationship of SC with 305-ME. Indicated that superior cows in milk production tend to had longer service period.

Calving interval had low negative phenotypic correlations with each of DO, DIM, TMY and 305-ME. Results indicated an antagonistic relationship between reproductive performance and milk yield. On the contrary, positive highly significant phenotypic correlations were obtained between CI and each of DP and PMY.

Days open had positive significant phenotypic correlations with each of DP, DIM, TMY and 305-ME. Indicating higher yielding cows were associated with longer DO. Indeed, DIM had positive significant to highly significant phenotypic correlations with each of TMY, 305-ME and PMY. Total milk yield had positive significant phenotypic correlations with each of 305-ME and PMY. Also, 305-ME had positive significant phenotypic correlation with PMY.

Genetic Correlations: Estimates of genetic correlations among different productive and reproductive traits are summarized in table (1). Age at first calving had negative low to medium desirable genetic correlations among AFC and each of SC, TMY and 305-ME. Indicated that older heifers at first calving are poorer in milk production. Moreover, negative correlation either genetic or phenotypic were favorable, thus the decrease in AFC would improve milk production traits. Opposite to the above, positive low to high genetic correlations obtained among AFC with DO, DIM and PMY.

Negative medium to high genetic correlations obtained between AC and each of SC, TMY and 305-ME. However, positive high genetic correlations obtained among AC with CI, DO and DP. Moreover, positive low genetic correlations obtained among AC with each of DIM and PMY. Services per conception had positive genetic relationships with each of CI, DO and DP. Moreover, positive low genetic correlations obtained between SC with each of DIM, TMY and PMY. While, negative genetic correlation was obtained between SC and 305-ME. Indicating that increase SC associated by extending each of DO, CI and DP and decrease in milk yield during 305 days. Positive high genetic correlations obtained between CI and each of DO, DP and PMY. However, negative high genetic correlations obtained among CI and each of DIM, TMY and 305-ME. Increasing the length of CI associated by poorer milk yield.

Days open had positive genetic correlations with each of DP and DIM. Indicated that superior cows in milk production associated by longer DO. In addition, positive low genetic correlations obtained between DO and each of TMY, 305-ME and PMY. Dry period had negative genetic correlations with TMY and 305-ME. Indicated that superior cows in milk yield associated with shorter DP. Moreover, negative low genetic correlation obtained between DP and DIM. However, positive genetic correlation obtained between DP and PMY.

Breeding Values: Minimum, maximum, range, standard errors and accuracy of sire breeding values for milk production traits (DP, DIM, TMY, 305-ME, PMY) and fertility traits (AFC, AC, SC, CI, DO) (using data of all

Table 2: Maximum, minimum, standard errors, accuracy and range of estimated breeding values of productive and fertility traits for all animals obtained from single statistical animal model analysis.

Trait	Minimum	S.E.	Accuracy	Maximum	S.E.	Accuracy	Range
AFC	-0.373	0.16	0.65	0.409	0.18	0.54	0.782
AC	-0.955	0.16	0.93	1.704	0.19	0.90	2.659
SC	-1.457	0.55	0.84	8.365	0.71	0.71	9.822
CI	-28.25	1.96	0.40	31.02	1.93	0.44	59.27
DO	-64.03	2.8	0.68	98.09	3.09	0.59	162.12
DP	-30.515	22.28	0.71	178.472	20.72	0.75	208.987
DIM	-76.49	2.47	0.71	75.59	2.96	0.54	152.08
TMY	-4917.4	9.74	0.83	4731.3	11.21	0.77	9648.7
305-ME	-3863.1	7	0.84	3076.4	8.04	0.78	6939.5
PMY	-8.341	3	0.63	11.687	2.61	0.74	20.028

lactations) are shown in table (2). The present results revealed that presence of wide ranges of EBV and SE for different traits. Higher ranges of EBV and standard errors for these traits indicated the existence of more genetic variation among individuals and thus increase the possibility of selection of sire for these traits. Concerning to accuracy of breeding values, the highest accuracy was the value of AC, while the lowest accuracy was the value of CI. High accuracy levels of breeding values help breeders to select for traits in their animals and hence genetic improvement in the health and production of their herds.

DISCUSSION

High heritability estimate for AC is in consistence with the findings of Nawaz *et al.* [11] who calculated heritability estimate of AC to be 0.53 in Holstein Friesian in Balochistan. Moreover, Hammoud [12] and Mariz [13] estimated heritability for 305-ME to be 0.42 and 0.32, respectively. Moawed [14] estimated heritability for TMY and 305-ME to be ranged from 0.29 to 0.91 and 0.43 to 0.89, respectively for all parities. Indicated that heritability estimates of milk yield increased with increasing parity order. As well as he calculated heritability estimate for AFC to be 0.43. Since the heritability of AFC was found to be low, this factor can be improved by providing heifers with good feeding, breeding and managerial programs to increase number of calves per cow during its life time as well as improving the genetic gain per year.

Unlike to the present study, Haile-Mariam *et al.* [15] estimated heritability of SC to be 0.10 on Boran-Friesian crosses. Heritability estimate of DP was slightly lower than reported by Ayied *et al.*[16] who estimated heritability for DP to be ranged from 0.32 to 1.00. But, higher than reported by Mariz [13] (0.12). Furthermore, high estimates of heritability for TMY obtained by Nawaz *et al.*[11] (0.32) and Mariz [13] (0.34). On the other hand, Hammoud [12] reported 0.44 for heritability of TMY and 0.45 for DO.

The present estimate of heritability for DIM is similar to that obtained by Shalaby *et al.* [17] (0.04) and Mariz [13] (0.10). In addition, moderate heritability estimates for DIM were reported by Shalaby *et al.* [18] to be ranged from 0.17 to 0.27. However, Nawaz *et al.* [11] (0.49) and Hammoud [12] (0.48) reported high heritability estimates for DIM. The heritability estimate of PMY was somewhat lower than those reported by Shalaby *et al.*[18] (0.22) and Nawaz *et al.* [11] (0.29).

Negative phenotypic correlations between AFC and each of SC, TMY and 305-ME are in accordance with the findings of Shalaby [7] who measured phenotypic correlations between AFC and each of TMY, 305-ME, DIM and DO to be 0.25, 0.36, -0.20 and -0.19, respectively. Indicating those older heifers at AFC would give higher milk production. Indeed, he reported that higher yielding cows were associated with longer CI. Explained as high milk production affected on the incidence of reproductive disorders and create negative energy balance early after parturition. Furthermore, he calculated phenotypic correlation between CI and DO to be 0.65. Positive significant phenotypic associations between CI and each of DP and DO was recorded by Ahmed *et al.*[19] to be 0.84 and 0.89, respectively.

Animals with low level of milk yield had low positive significant phenotypic correlation between milk yield and CI as reported by Djedović *et al.* [20] who concluded that cows with moderate and high level of production had positive significant phenotypic correlation with CI. Near to the current results Moawed [14] estimated phenotypic relationships between DP and each of TMY and DIM to be negative low for TMY and moderate negative for DIM.

High significant phenotypic correlation between milk yield and PMY is in accordance with the report of Shalaby [7] who also estimated phenotypic correlation between TMY and 305-ME to be 0.85. Phenotypic correlations among 305-ME with fertility traits were low negative except with CI and DO as reported by Moawed [14] he also argued that PMY was moderately correlated with 305-ME, where the correlations were low and fluctuated between positive and negative values.

Unlike the current study, Radwan [21] estimated the genetic correlation between AC and DO to be -0.69. Moreover, Goshu *et al*. [22] observed high genetic correlations between SC and each of DP and CI and between CI and DP. Moawed [14] reported negative favorable genetic correlations for SC with TMY and 305-ME. While, SC showed moderate positive genetic associations with DO, DP and CI. Shalaby [7] calculated the genetic correlations between CI and each of DO (0.83), TMY (0.92), 305-ME (0.77) and DIM (0.97). Moreover, he calculated genetic correlations among DIM with each of TMY and 305-ME to be 0.85 and 0.68, respectively. Similarly, Shalaby *et al*. [18] calculated the genetic correlation between DO and TMY to be 0.46. Opposite to the current findings, Hammoud [12] found that all genetic correlations between productive and reproductive traits were positive and ranged from 0.03 to 0.35 except between DO and TMY was -0.31.

The range of EBV for DP obtained in this study is longer than 8.70 days given by El-Arian *et al*. [23] depending on all available lactation records. Indeed, Rehman and Khan [24] estimated breeding value to be ranged between -78 and 116 for DP. Also, Mariz [13] calculated the range of sire breeding value for DP to be 34.62 days. Range of breeding value for DIM was longer than 6.50 days obtained by El-Arian *et al*. [23] using multi-trait animal model. On the other hand, [7] found that the range of EBV for DIM were 176.04 days and 142.82 days using single-trait analysis depending on all pedigree animals and sire of heifers only, respectively.

Range of breeding value for TMY obtained is larger than the ranges (-442 and 1265 kg), (-3582.2 and 5088.1 kg) given by Rehman and Khan [24] and Hammoud [12], respectively. However, Shalaby *et al*. [18] estimated the range of breeding value for TMY to be 6006 kg and 10280 kg for single-trait and multi-trait analyses, respectively. The range of EBV for 305-ME shown here is higher than 1289 kg obtained by El-Arian *et al*. [23] depending on all available lactation records by multi-trait animal model, Shalaby *et al*. [18] using all pedigree animals for single-trait and multi-trait analyses, respectively and Mariz [13] depending on all available lactation records. However, Rehman and Khan [24] and Hammoud [12] estimated the range of breeding values for 305-ME to be ranged between - 447 and 1254, -2964.8 and 2368.5 kg, respectively.

The range of EBV for SC obtained in this study is lower than 18.30 services given by Radwan [21]. The range of sire breeding values for AFC is smaller than 30 months shown by Abdel-Glil [25] depending on first lactation record. However, Shalaby *et al*. [18] calculated the range of EBV for AFC to be 8.834 months higher than obtained here depending on single-trait analysis for all animals' lactation records. Moreover, Moawed [14] estimated the range of breeding value for AFC using all animals in pedigree to be ranged from -3.478 to 2.687 months. Indicated that the best sire was the one which show the highest negative estimated breeding value. Concerning to calving interval, the range of EBV for CI here is longer than 30.83, 0.95 days given by Kadarmideen *et al*. [26] and Mariz [13], respectively. But, lower than the range (-84 and 107) obtained by Rehman and Khan [24].

Range of breeding value for DO is longer than the range (-27.4 and 16 days) given by Hammoud [12] and shorter than 170.46 days reported by Mariz [13]. In this respect, Shalaby *et al*.[18] estimated the range of breeding value for DO to be 20.9 and 193.9 days depending on single-trait and multi-trait analyses, respectively. On the contrary, Radwan [21] reviewed 852.18 days for range of breeding value for DO. High amount of variation among breeding values of different individuals indicated selection of sire, dam and cow for the next generation would lead to more genetic improvement. The previous results are in consonance with the report of Shalaby [7]. From present study, the EBV showed large deviations among sires for most of milk and fertility traits. Thus, the selection of sires for the future generations would lead to higher and rapid genetic improvement in the herd. The previous findings are in agreement with the findings of Shalaby *et al*. [18].

High standard errors of DO and SC are in accordance to the result of Radwan [21] who estimated standard errors for each of DO and SC to be 2.49, 23.72 and 0.04, 0.39 for maximum and minimum values, respectively. However, Moawed [14] calculated high standard deviations of breeding values for TMY and 305-ME to be ranged from 487.1 to 954 kg and 454.27 to 787.7 kg, respectively for first four parities. Moreover, he estimated standard deviations for DIM to be 27.39, 5.59, 8.73, 22.55 days in first four lactations, respectively.

CONCLUSION

The current study revealed that productive and reproductive status of a dairy herd had a great impact on the profitability and sustainability of a dairy operation. Unfortunately, high yielding cows have a great incidence for reproductive problems due to presence of antagonistic relationship between reproductive and milk production traits. Thus farmers must be select heifers based on a combination of milk production and reproduction traits according to values of heritabilities, genetic and phenotypic correlations and finally the estimates of breeding values. Higher ranges, standard errors and accuracies of estimated breeding values indicated the existence of more genetic variation among individuals and hence increase the possibility sire selection for these traits, which reduce bias from selection and achieve the best accuracy of predictions. In the future this should translate into good herds without productive and reproductive problems which would lead to more and rapid genetic improvement.

REFERENCES

1. Sarakul, M., S. Koonawootrittriron, M.A. Elzo and T. Suwanasopee, 2011. Factors associated with dairy cattle genetic improvement for milk production at farm level in Central Thailand. Journal Animal Science, 24: 1031-1040.
2. Behzadi, B.M.R., A.A. Amini, A.A. Slaminejad and M. Tahmoorespour, 2013. Estimation of genetic parameters for production traits of Iranian Holstein dairy cattle. Livestock Research Rural Development, 25: 9.
3. El-Awady, H.G., 1998. Genetically analysis of reproductive and productive performance of Friesian herds, Ph. D. thesis, Tanta University, Egypt.
4. Hayes, B.J. and M.E. Goddard, 2008. Prediction of breeding values using marker-derived relationship matrices. Journal Animal Science, 86: 2089-2092.
5. Stranden, I., 2009. Test day model in evaluation of dairy cattle. MTT research project database, Agrifood Researsh Finland.
6. Boldman, K.G., L.A. Kriese, L.D. Van Vleck, C.P. Van Tassell and S.D. Kachman, 1995. A manual for use of MTDFREML. A Set of programs to obtain estimates of variances and covariances (Draft). U.S. Department of Agriculture, Agricultural Research Service, Clay Canter NE.
7. Shalaby, N.A., 2005. Genetic evaluation for milk production, reproduction traits and persistency of lactation using single and two-trait animal model analyses for Friesian cows in commercial herds in Egypt. Journal Agriculture Science, Mansoura University, 30: 3637-3653.
8. El Fadilia, M.C., J. Michaux, Detilleux, P.L. and Leroy, 2000. Genetic parameters for growth traits of the Moroccan Timahdit breed of sheep. Small Ruminant Research, 37: 203-208.
9. Robertson, A., 1959. The sampling variance of the genetic correlation coefficient. Biometrics, 15: 469.
10. Falconer, D.S. and T.F.C. Mackay, 1996. Introduction to quantitative genetics. (4th Edition. Longman) London, pp: 464.
11. Nawaz, A., A.H. Nizamani, I.B. Marghazani, Nasrullah and A. Fatih, 2013. Influence of genetic and environmental factors on lactation performance of Holstein-Friesian cattle in Baluchistan. Journal Animal and Plant Science, 23: 17-19.
12. Hammoud, M.H., 2013. Genetic aspects of some first lactation traits of Holstein cows in Egypt. Alexandria Journal Agriculture Research, 58: 295-300.
13. Mariz, O.M.M., 2014. Genetic and environmental factors affecting calving interval in dairy farms, M. S. thesis, Zagazig University, Egypt.
14. Moawed, SH.A.M., 2013. Statistical evaluation of procedures used in estimating population genetic parameters, Ph. D. thesis, Suez Canal University, Egypt.
15. Haile-Mariam, A., B.K. Joshi, W. Ayalew, A. Tegegne and A. Singh, 2009. Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian in Central Ethiopia. Journal Agriculture Science, 147: 81–89.
16. Ayied, A.Y., A. J. Jadoa and A.J. Abdulrada, 2011. Heritabilities and breeding values of production and reproduction traits of Holstein cattle in Iraq. Journal Basrah Research Science, 37: 66-70.
17. Shalaby, N.A., El-Barbary, A.S.A., Oudah, E.Z.M. and M. Helmy, 2012. Genetic parameters and breeding values of some productive and reproductive traits Friesian cattle in Egypt. Proceedings of the 15th AAAP Animal Science Congress 26-30, Thummassat University, Rangift, Thiland.

18. Shalaby, N.A., M.A. Mostafa, M.F. Abdel-Glil and M.A.Z. Alemam, 2009. Genetic evaluation for milk production, reproduction and somatic cell count traits in early lactation for Friesian cattle in Egypt. Journal Agriculture Science, Mansoura University, 34: 9463-9475.
19. Ahmed, M., J.H.J. Van Der Werf and K. Javed, 2001. Genetic and phenotypic correlation for some economic traits in dairy cattle. Pakistan Veterinary Journal, 21: 2.
20. Djedović, R., V. Bogdanović, G. Trifunović, M.D. Petrović, M.M. Petrović and D. Stanojević, 2012. The effect of the level of milk yield on the reproduction traits in Black and White cows. Biotechenology Animal Husbandry, 28: 487-496.
21. Radwan, H.A.A., 2012. Studies on somatic cell count in Holstein–Friesian cows. Ph. D. thesis, Mansoura University, Egypt.
22. Goshu, G., H. Singh, K. Petersson and N. Lundeheim, 2014. Heritability and correlation among first lactation traits in Holstein Friesian cows at Holeta Bull Dam Station, Ethiopia. International Journal Livestock Prodction, 5: 47-53.
23. El-Arian, M.N., H.G. El-Awady and A.S. Khattab, 2003. Genetic analysis for some productive traits of Holstein Friesian cows in Egypt through MTDFREML program. Egypt. Journal Animal Production, 40: 99.
24. Rehman, Z. and M.S. Khan, 2012. Factors affecting performance traits of Sahiwal cattle in Pakistan. Pakistan Veterinary Journal, 32: 329-333.
25. Abdel-Glil, M.F. 1996. Estimation of genetic parameters and genetic trends for some milk traits in a herd of Friesian cows in Egypt. Journal Agriculture Mansoura University, 21: 3479.
26. Kadarmideen, H.N., R. Thompson, M.P. Coffey and M.A. Kossaibati, 2003. Genetic parameters and evaluations from single- and multiple trait analysis of dairy cow fertility and milk production. Livestock Production Science, (81): 183-195.