

Asian Journal of Animal and Veterinary Advances



www.academicjournals.com

Published: January 15, 2017

ISSN 1683-9919 DOI: 10.3923/ajava.2017.80.87



Research Article Different Single-trait Animal Models for Estimating **Direct-maternal Covariance Components in Holstein Cows**

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Abstract

Objective: This study aimed to detect the effect of inclusion of maternal genetic effect on variance, covariance components and genetic parameters of some productive traits in Holstein cows. Methodology: First milk production data set and pedigree information were collected from 991 Holstein dairy cows during the period from 1994-2011. Records were pre-adjusted to mature equivalent yields (ME-2X-305d). Three different animal models were fitted, which were differentiated by including or excluding maternal genetic effect. Results: Direct and maternal genetic variances and heritabilities were high in model 2 which account for maternal effect with $cov (a,m) = A\sigma_{am}$. The highest direct and maternal genetic variances were 39846.9 and 4583.2 kg for LMY and 305 ME, respectively. In the same line, the highest direct and maternal heritability estimates were ranged from 0.233 for DO to 0.438 for DIM, however, the maternal heritability ranged from 0.021 for DO to 0.104 for 305 ME. Additive genetic values were estimated and used to characterize genetic trend across the time period investigated. Ranges of breeding values were high in model 3 which account for maternal component with cov (a,m) = 0. Conclusion: In summary, the first lactation milk yield traits can be used as selection criteria for development an efficient selecting and breeding programs and maternal genetic effect should include during constructing breeding plans in order to select future generation improved genetically.

Key words: Additive genetic value, maternal heritability, additive maternal genetic covariance, lactation milk yield, DO

Received: October 09, 2016

Accepted: December 01, 2016

Citation: Hend A. Radwan, Eman A. ABO Elfadl and Khairy M. El-Bayoumi, 2017. Different single-trait animal models for estimating direct-maternal covariance components in Holstein cows. Asian J. Anim. Vet. Adv., 12: 80-87.

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Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

The performance of a dairy animal is determined by yield traits affected milk production, most of yield traits affected by many genes which known by quantitative traits. They controlled by small additive effects¹. Quantitative traits influenced by two genetic components, animal genotype (direct genetic effect) and dam genotype (maternal genetic effect) as reported by Edriss *et al.*².

Different studies have demonstrated the existence of maternal effect on yield and reproduction of dairy cattle that may indicative to cytoplasmic inheritance³. Because mitochondria are transmitted only from female parents to ensuing offspring⁴, mitochondrial DNA is a source of cytoplasmic inheritance⁵. They postulated, cytoplasmic origin was a significant source of variation in yield traits of dairy cattle. Gudex *et al.*^{6,7} stated any maternal effect occurred at prenatal stage, that prenatal effects include maternal additive genetic effect which mean genetic ability of the dam to provide an appropriate conditions to embryo plus maternal permanent environmental effect which include both maternal non additive genetic effect of the dam and the dam's mothering capacity as reported by Gudex *et al.*⁷.

Maternal effect in the form of maternal permanent environmental effect is essential to be included in designing agreeable breeding program to get accurate estimates of genetic parameters in Arabi sheep⁸.

Diop et al.9 deduced maternal genetic effects are consequential, even at 18 months of age. Thereby, models for the genetic evaluation growth traits in Gobra cattle should include additive and maternal genetic effects with covariance between them but grandmother effects could safely ignored. Furthermore, Koyuncu and Duru¹⁰ studied on birth weight of Karacabey Merino lambs then reported maternal effects which included to maternal additive genetic and maternal permanent environmental effects should be considered in any breeding program. Indeed, ABO Elfadl and Radwan¹¹ concluded maternal additive genetic should be considered in any selecting program especially if the variation among dairy animals is high. Presence of adequate genetic variation in Libyan Holstein herds assists to make large genetic gain in milk through conventional selection method as stated by Ward¹².

First lactation order is considered as test lactation in order to the cow's body is still burgeons that first lactation milk production increases the value as an indicator for a long-term tendency toward shortening the length of production life in dairy cows¹³. In addition, selection interval is reduced using first lactation information as reported by Sahin *et al.*¹⁴. Estimation of breeding values and genetic parameters are essential in formulating breeding policy and managerial decisions¹⁵. They also stated that selection based on first lactation order could be used satisfactory to improve milk production traits. Additive genetic value has an essential role in genetic improvement of production traits as reviwed by Sahin *et al.*¹⁴.

Genetic evaluations of dairy cows for some economic traits have been shown to depend on estimation of variance, covariance, heritability, genetic and phenotypic correlations essential for predicting correlated and direct response to selection¹⁶. Estimation genetic and phenotypic variance components among animals has an important role in evaluation direct additive geneic effect of milk yield traits in Simmental cows population as mentioned by Pantelic *et al.*¹⁷.

Supplying good conditions for expression animal's genetic potential is essential that improvement of animal's genetic potential should be achieved through subsequent generation parents selected from current animals which have the highest genetic merit¹⁸.

Therefore, the main objectives of the current study were to determine the extent of a maternal effect which is indicative to cytoplasmic inheritance on milk yield traits in a herd of dairy cattle through comparison among three single trait animal models based on inclusion or exclusion of maternal effect and test the possibility of using first lactation milk yield traits as selection criteria to improve milk yield in the subsequent lactations.

MATERIALS AND METHODS

Data in this study were the accumulated records of Holstein-Friesian cows over the years 1994-2011 obtained from Alexandria-Copenhagen Company, situated in Cairo-Alexandria desert road, Egypt. Production records of 1059-3464 that were progeny of 99 sires and of 691 dams were used to estimate genetic parameters. The studied population has a typical hierarchical structure within each generation.

All animals were stanchioned in roofed open barns. Animals were allowed to drink water *ad libitum*. The animals around the year were fed on Total Mixed Ration (TMR). The ingredient composition of rations were formulated according to National Research Council (NRC)¹⁹ and the TMR composition was 30% corn silage, 28.6% alfalfa, 18-19% crude protein, 14.7% corn, 7% glutein, 6.4% linseed meal, 4.6% soybeans meal, 3% cotton seed meal, 1.3% wheat bran, 1.2% hay, 0.4% calcium carbonate, 0.3% sodium bicarbonate and 0.3% sodium chloride. Mineral mixture bricks were offered *ad libitum* as lick salt in front of the animals. Robotic milking was done three times a day with regular intervals between milking. Daily milk yield per cow was weighed and recorded. Calves were suckled artificially after calving to weaning excluding first 3 days of colostrums period. Cows were dried-off about 2 months before expected calving date. Animals were regularly vaccinated against infectious diseases (foot and mouth disease etc).

Studied traits were Days Open (DO, days), days in milk (DIM, days), Lactation Milk Yield (LMY, kg), 305-day mature equivalent (305 ME, kg), fat yield (FatY, kg) and protein yield (ProY, kg). The genetic correlation (r_{am}) between direct and maternal genetic effects, direct maternal genetic covariance (σ_{am}), direct (h_a^2) and maternal (h_m^2) heritability coefficients and direct additive genetic (σ_a^2), maternal additive genetic (σ_a^2), residual (σ_e^2), phenotypic variances (σ_p^2) were calculated from the covariance components at convergence by applying REML package of VCE for single trait animal model according to Groeneveld *et al.*²⁰. Three models were formulated to estimate covariance components and corresponding genetic parameters of the studied traits as followed:

Model 1: $Y = XB+Z_1a+e$ Model 2: $Y = XB+Z_1a+Z_2m+e$ with cov (a,m) = $A\sigma_{am}$ Model 3: $Y = XB+Z_1a+Z_2m+e$ with cov (a,m) = 0

where, Y is a vector of records for studied traits, B, a, m and e are vectors of fixed, direct genetic, maternal genetic effects and the residual effects, respectively.

X, Z_1 and Z_2 are corresponding design matrices associating the fixed, direct genetic, maternal genetic effects to vector of Y. With assumption of direct additive genetic, maternal additive genetic and residual effects are normally.

The model had the following distributional assumptions:

E(Y) = XB E(a) = 0 E(m) = 0 E(e) = 0

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

Var (a) =
$$A\sigma_a^2$$
 Var (m) = $A\sigma_m^2$ Var (e) = $I\sigma_e^2$

where, σ_a^2 , σ_m^2 and σ_e^2 are variances due to direct additive genetic, maternal 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 calculated as the criterion according to El Fadili *et al.*²¹. Standard errors of genetic correlations were obtained using the approximate formula as described by Robertson²² and Falconer and Mackay²³.

RESULTS

Descriptive statistics of data used and pedigree information for each trait of first lactation order are summarized in Table 1. The means of yield traits are ranged from 185.9 days for DO to 8950 kg for LMY. Coefficients of variations were in the range 25.96 for 305 ME to 70.84% for days open.

For all traits direct and maternal variances were higher in model 2 than those for both model 1 and model 3 for the studied traits. Residual variances were higher in model 3 than their corresponding values in both model 1 and 2. However, phenotypic variances were higher in full animal model than their corresponding values were obtained either in model accounted for maternal effect with cov (a,m) = $A\sigma_{am}$ or with cov (am) = 0 among animals.

Referring to heritability, direct and maternal heritabilities were higher in model 2 than those obtained from model 1 and model 3 for all studied traits. Direct maternal genetic correlations and covariances were negative for all traits as given in Table 2. Estimates of additive genetic values for the traits under study in first lactation are presented in Table 3.

High ranges of estimated additive genetic values were mostly obtained in model 3 than those corresponding values in model 1 and 2. Moreover, standard deviations were higher in model 3 for all studied traits except for 305 ME was in model 1.

Spearman's correlation coefficients of breeding values among different models for the studied traits were positive highly significant ($p \le 0.01$) and ranged from 0.928-1.000 as presented in Table 4.

Table 1: Least squares means, Standard Errors (SE) and coefficients of variation	on (CV %) for six milk production traits in first lactation order of Holstein cows
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Trait	Mean±SE	CV (%)
Days Open (DO, days)	185.9±131.7	70.84
Days in Milk (DIM, days)	398.9±126.6	31.73
Lactation Milk Yield (LMY, kg)	8950±3480.9	38.89
305-day mature equivalent (305 ME, kg)	8801±2261	25.69
Fat yield (FatY, kg)	268.0±100.8	37.61
Protein yield (ProY, kg)	219.0±83.28	38.03

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Trait/estimates	Models	σ_a^2	$\sigma_{\rm m}^2$	σ_{am}	σ_{e}^{2}	σ_p^2	$h_a^2 \pm SE$	$h_m^2 \pm SE$	$r_{am} \pm SE$
DO	1	2376.78			12599	14975.7	0.186±0.06		
	2	3275.48	292.11	-978.16	12412.8	14024.1	0.233 ± 0.08	0.021±0.031	-1.0 ± 0.0003
	3	2226.61	0.86×10 ⁻⁷		12729.3	14955.9	0.149±0.08	$0.58 \times 10^{11} \pm 0.47 \times 10^{-6}$	
DIM	1	3728.45			11129.5	14857.9	0.251±0.08		
	2	5471.58	1063.36	-2412.1	10779.3	12490	0.438±0.12	0.085±0.075	1.0 ± 0.0001
	3	3565.69	0.42×10 ⁻⁷		11265.5	14831.2	0.240 ± 0.08	$0.29 \times 0^{11} \pm 0.36 \times 10^{-6}$	
LMY	1	29827.8			82322.2	112150	0.265 ± 0.07		
	2	39846.9	2582.5	-1014.1	80318	102459	0.389 ± 0.10	0.025±0.028	$-1.0\pm0.26 imes10^{-7}$
	3	28679.3	0.13×10 ⁻⁴		83265.2	111944	0.256±0.08	$0.12 \times 10^{9} \pm 0.25 \times 10^{-5}$	
305 ME	1	17010.6			32383.8	49394.4	0.344±0.06		
	2	18988.9	4583.2	-5271.9	31049.8	44077.9	0.431 ± 0.08	0.104±0.081	-0.56512±0.21
	3	16819.8	36.496		32497.9	49354.2	0.341 ± 0.07	$0.74 \times 0^{-3} \pm 0.045$	
FatY	1	2071.8			7252.89	9324.69	0.222 ± 0.06		
	2	3093.09	753.19	-1526.3	7002.89	7796.51	0.397±0.19	0.097±0.116	-1.0 ± 0.00000
	3	1991.62	0.92×10 ⁻⁹		7322.69	9314.31	0.214±0.06	$0.99 \times 10^{13} \pm 0.59 \times 10^{-7}$	
ProY	1	1259.14			4934.64	6193.78	0.203 ± 0.06		
	2	1687.22	218.36	-606.97	4897.26	5588.9	0.302 ± 0.08	0.039 ± 0.047	-1.0 ± 0.00083
	3	1202.36	0.70×10 ⁻⁷		4982.55	6184.91	0.194±0.06	$0.11 \times 10^{10} \pm 0.65 \times 10^{-6}$	

Table 2: Variance components of the productive traits for all animals obtained from single statistical animal model analysis in first lactation order of Holstein cows

DO: Days open, DIM: Days in milk, LMY: Lactation milk yield, 305 ME: 305-day mature equivalent, FatY: Fat yield, ProY: Protein yield, σ_a^2 . Direct additive genetic variance, σ_m^2 : Maternal additive genetic variance, σ_a^2 : Direct maternal genetic covariance, σ_e^2 : Residual variance, σ_p^2 : Phenotypic variance, h_a^2 : Direct heritability, SE: Standard error, h_a^2 : Maternal heritability, r_{am}: Direct maternal genetic correlation

Table 3: Maximum, minimum, standard deviations and ranges of breeding value of the productive traits for all animals obtained from single statistical animal model analysis for first lactation order of Holstein cows

		First lactation						
Variables	Models	SD	Minimum	Maximum	Range			
DO	1	21.27	-65.45	123.16	188.604			
	2	20.21	-62.65	116.12	178.77			
	3	24.00	-74.80	146.06	220.852			
DIM	1	30.78	-95.68	143.10	238.775			
	2	29.73	-91.98	138.32	230.29			
	3	33.57	-123.29	179.46	302.75			
LMY	1	90.53	-289.08	475.06	764.14			
	2	87.84	-280.10	459.31	739.41			
	3	99.84	-315.62	555.08	870.7			
305 ME	1	77.46	-321.26	283.68	604.94			
	2	76.84	-319.05	282.12	601.17			
	3	72.92	-330.44	299.85	630.29			
FatY	1	23.46	-73.74	95.84	169.576			
	2	22.77	-71.65	93.62	165.275			
	3	25.97	-81.33	119.00	200.328			
ProY	1	17.44	-55.59	57.47	113.054			
	2	16.86	-54.57	55.28	109.846			
	3	18.58	-60.81	62.11	122.911			

DO: Days open, DIM: Days in milk, LMY: Lactation milk yield, 305 MY: 305-day mature equivalent, FatY: Fat yield, ProY: Protein yield, SD: Standard deviation

Traits	DO DI		DIM	DIM		LMY		305 ME		FatY		ProY	
Models	Model 1	Model 2											
Model 2	0.999**	-	0.999**	-	0.999**	-	1.000**	-	0.999**	-	0.999**	-	
Model 3	0.983**	0.983**	0.949**	0.947**	0.989**	0.988**	0.980**	0.980**	0.929**	0.928**	0.971**	0.970**	

DISCUSSION

The aim of this study was to elucidate the importance of a maternal effect through comparison among three single trait

animal models based on inclusion or exclusion of maternal effect of first lactation Holstein cows. Regarding descriptive statistics of data, Mashhadi *et al.*²⁴ worked on first lactation records of Iranian Holstein cows using single trait animal

model then make descriptive analysis to data and found that means and SD were lower than current study to be 6947±1229, 225±41.8 and 216±35 kg for milk, fat and protein yields, respectively. High values of standard deviations indicated more variation among animals which is the raw material with which the breeder should work and thereby possibility for improvement a trait. In addition, they estimated variance components and genetic parameters for milk, fat and protein yields to be 534658, 582.70 and 397.8 kg, respectively for additive genetic variance and residual variances being 976402, 1167.32 and 852 kg, respectively however, phenotypic variances were 1511060, 1750 and 1249.8 kg, respectively, which higher than those in the current study in case of milk yield and lower than those in the present study for both fat and protein yields. Differences did exist between results of literatures may attributed to different genetic models; genetic sources used in analyses, number of records and data sets. They also estimated heritability coefficients and their standard errors for milk, fat and protein yields to be 0.35 ± 0.02 , 0.33 ± 0.02 and 0.31 ± 0.017 , respectively, which higher than their corresponding values in the current study except model 2 for both milk and fat yields due to the effect of maternal component with cov $(a,m) = A\sigma_{am}$. Inclusion of maternal effect in the model lead to increase variances, covariances and genetic parameters calculated from this model. This result is in consonance with the result of current study and the reports of ABO Elfadl and Radwan¹¹ in first and third lactations order in Holstein cows.

Conflicting opinion was published by El-Awady²⁵ who used single trait analysis to estimate variance, covariance components and reported model which ignored both maternal genetic and permanent environment effects had the largest estimates for direct additive variance and direct heritability. However, the addition of maternal genetic effect and maternal permanent environmental effect reduced both of them as well as model which accounts for direct maternal genetic effect would reduce the values of direct genetic variance and direct heritability than previous model. This result supported by Hassen *et al.*²⁶ in pure and crossbred sheep in Ethiopia.

According to the findings of ABO Elfadl and Radwan¹¹ they compared among three multi-trait animal models based on inclusion or exclusion of the maternal additive genetic effect. They concluded inclusion of maternal additive genetic effect with cov (a,m) = $A\sigma_{am}$ would increase maternal heritability and additive maternal variance of first and third lactation in dairy cows.

Unlike the current study, Edriss *et al.*² applied six animal models to evaluate the importance of direct genetic, maternal

genetic and maternal permanent environmental effect for milk and fat yield traits using single trait animal model in Iranian Holstein cows as well as to compare between different models according to include or exclude maternal genetic effect that these models are full animal model, full animal models with and without covariances between direct and maternal effect. respectively other three models were accounted for maternal permanent environmental effect with or without covariances between animals. Comparison between the previous first three models with the current study, the highest additive genetic variance for milk and fat yields were 401941 and 283.13 kg, respectively obtained from full animal model and the highest maternal genetic variances for milk and fat yields were 137947 and 34.4 kg obtained from full animal model with cov(a,m) = 0. Ignoring the maternal genetic effect overestimated direct additive genetic effect as stated by Koyuncu and Duru¹⁰.

Conversely, Edriss *et al.*² calculated positive direct maternal covariances and correlations being 51684 and 0.029 kg for milk yield and 35.17 and 0.029 kg for fat yield, respectively. Both r_{am} and σ_{am} were higher in full animal model with cov (a,m) = $A\sigma_{am}$. In contrast to the present study, the highest phenotypic variances for milk and fat yields were 1780876 and 1197.15 kg obtained in models with cov (a,m) = $A\sigma_{am}$ and cov (a,m) = 0, respectively.

On the other hand, the same authors estimated some of genetic parameters that the highest direct heritability estimates for milk and fat yields being 0.229 ± 0.028 and 0.242 ± 0.026 , respectively were obtained in full animal model. However, the highest maternal heritability estimates for milk and fat yields being 0.077 ± 0.019 and 0.029 ± 0.018 , respectively were obtained in full animal model with cov (a,m) = 0. They concluded genetic parameters in model ignoring maternal effect were higher than those values obtained in model which include maternal effect but with cov (a,m) = 0, which contradicted current findings.

Konig *et al.*²⁷ calculated means and SD for 305 ME and DO to be 3867 kg and 129.5 days on 2764 and 1623 Northern Thai dairy cattle, respectively using REML applying the package of VCE for single and multi-trait animal models to define the optimal breeding strategies which were lower than those in the current study. High milk yield could indicate good managerial and feeding program. They calculated additive genetic variance (67.97 days) and residual variance (2124.64 days) for DO being lower than their corresponding values in the present study in all models. In contrast, additive genetic and residual variances for 305 ME (250518.83 kg) (461186.83 kg) were higher than those obtained in this research in the three models, respectively.

Furthermore, Roman *et al.*²⁸ studied on first parity in a herd of Jersey cattle used univariate analysis to estimate additive genetic variance, direct heritability, permanent and temporary environmental variances using animal model and DFREML program that additive genetic variances of milk, fat and protein yields were 71500.14, 182.50 and 61.30 kg, respectively which higher than those obtained in the present study in case of milk yield and lower than their corresponding values in the current study in case of fat and protein. Direct heritability estimates of milk, fat and protein yields were 0.26 ± 0.11 , 0.31 ± 0.10 and 0.17 ± 0.09 , respectively which within the same range for lactation milk yield in the current study except in model 2, higher than those in the current study for fat yield except model 2 and lower than their corresponding values in the present study for protein yield.

Albuquerque et al.29 estimated maternal heritability for both milk and fat yields to be 0.008 and 0.006, respectively. Also, they stated that an increasing of direct heritability from 0.014-0.021 obtained by ignoring maternal genetic and direct maternal covariances effect in milk and fat yields. Furthermore, Sahin et al.¹⁴ estimated direct heritability for milk production traits such as lactation length, LMY and 305ME to be 0.10, 0.26 and 0.25, respectively in first parity in Brown Swiss cattle. Estimates of heritability for milk yield were lower than those in the current study except model 1 and model 3 have nearly the same value for lactation milk yield. High estimates of heritability for milk yield were accompanied by high direct additive genetic variances. Selection and designing breeding programs for improving the production and keeping the genetic potential should be based on the results obtained from the genetic parameters estimates as mentioned by Tesfa and Garikipati³⁰.

Hammoud and Salem³¹ evaluated some of first lactation traits of Holstein cows in Egypt, then calculated heritability estimates of total milk yield, 305-day mature equivalent, lactation period and days open to be 0.05, 0.11, 0.05 and 0.18, respectively, which lower than their corresponding values in all models except model 1 (within the same range) and model 3 for days open being high. Maternal additive genetic variances were higher than those of direct additive genetic variances which agree with the current study. They added ignoring maternal genetic effect may lead to overestimate heritability coefficient, thus it should be included during long term selection program.

Concerning days in milk, the range of breeding values for DIM in the current study was longer than 17 days obtained by Afifi *et al.*³² using single trait genetic analysis for all available lactation records. They also calculated the range of breeding values for 305 ME to be higher than those in the current study

(1404 kg) depending on entire lactation records by single trait model in Egypt. Higher ranges of additive genetic values for cows and sires indicate higher genetic variation and higher opportunity for selection of the top sires and cows in additive genetic value which would result in rapid genetic gain in future generations^{33,34}. Contradicted to the above results, Zahed *et al.*³⁵ calculated range of breeding value for the same trait to be lower (127 kg) than their corresponding values in the current study depending on first lactation record by univariate animal model. Presence of negative and positive breeding values in the current paper may attribute to using sires of unknown breeding values which agreed with Sahin *et al.*¹⁴.

In the same connection with the current study, Mashhadi and Kashan²⁴ calculated means, maximum and minimum estimates of breeding values in Iranian Holstein cattle using single trait animal model for milk, fat and protein yields to be 180.20 ± 270.8 , 03.70 ± 1.26 and 02.30 ± 1.06 kg for means, 1287, 27.30 and 26.90 kg for maximum values and -265, -27.50 and -29 kg for minimum values. Furthermore, Ben Gara *et al.*³⁶ estimated breeding value using BLUP method, they found that breeding value is lower than their corresponding values were obtained by most of literatures which may be due to loss of information from data set or limited levels of production. Maternal effect should be included during breeding value estimation that ignoring maternal effect lead to incompetence additive genetic value estimation El-Awady *et al.*³⁷.

Moreover, Ulutas and Sezer³⁸ applied univariate animal model to calculate covariance components of 305 ME such as additive genetic variance (85513 kg), residual variance (370135 kg) and phenotypic variance (559306 kg) to be higher than their corresponding values in three models in the present research. Higher standard deviation for any trait means there are more genetic differences among animals and increase the chance of selection of sire for this trait. The previous results are in consonance with the reports of Shalaby *et al.*³⁹, Ward¹² and Radwan *et al.*³⁴.

Unlike to current study, Deb *et al.*⁴⁰ estimated direct heritability for LMY (0.404 \pm 0.087) to be higher than those in the current study. However, direct heritability for lactation length (0.333 \pm 0.059) was higher than their corresponding values in the present study except in model 2. Indicated that continuous selection of high producing animals would associate by high milk yield and increase length of lactation in the next generations in Bangladesh cattle. In addition, they reported moderate to high heritability estimates with high genetic correlations among most of milk production traits useful in planning future selective breeding program for further genetic improvement. Differences in variance, covariance components and genetic parameters among different studies are associated by inter-herd differences (housing, milking, feeding), different statistical models, data sets and variation in genetic potential of milk production traits Mosharraf *et al.*⁴¹. Positive highly significant Spearman's correlation coefficient of breeding values among different models denoted the same rank of animals in different models for the studied productive traits.

CONCLUSION

Deductively, inclusion of the maternal genetic effect with cov (a,m) = $A\sigma_{am}$ leads to elevation of the additive, maternal variances and direct heritability estimates than if maternal effect present but not considered (cov (a,m) = 0). Variances and genetic parameters obtained from full model were higher than if maternal effect present with cov (a,m) = 0, except for residual variances and maternal heritability estimates. In a brief, maternal effect on first lactation milk yield traits of Holstein cows were significant and should include in any breeding program implemented for this breed.

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