

PARAMETER ESTIMATES FOR DIRECT AND MATERNAL GENETIC EFFECTS FOR MILK YIELD TRAITS IN A FRIESIAN CATTLE HERD IN EGYPT

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ABSTRACT

Data on 2181 normal lactation records of Friesian cattle raised at an experimental station during the period from 1996 to 2002 were used. Number of sires and dams were 92 and 878, respectively. Data were analyzed using MTDFREML program. Two animal models were fitted. Model 1 considered the animal (additive direct genetic effects) and the permanent environmental effects as a random effect. Model 2, the maternal genetic effects was added to Model 1, which allowed for the estimation of the genetic covariance between the direct and maternal genetic effects. In the two models fitted, the fixed effects were month and year of calving and parity. Age of cow at calving was included as a covariate. Direct and maternal genetic effects and genetic parameters for 305 day milk yield (MY), 305 day fat yield (FY) and 305 day protein yield (PY) were estimated. Estimate of direct heritability of the mentioned traits was 0.28, 0.24, and 0.26, respectively using Model 1, and 0.31, 0.34, and 0.40, respectively using Model 2. Maternal heritability estimate was 0.01, 0.06 and 0.13, respectively. Permanent environmental variance as a proportion of phenotypic variance was 0.03, 0.11 and 0.11, respectively (Model 1) and 0.12, 0.12 and 0.10, respectively (Model 2). Estimates of genetic correlations between direct and maternal genetic effects for all milk yield traits studied were negative and ranging from -0.36 to -0.18. Direct genetic correlation between these traits was positive and high, ranging from 0.95 to 1.00 for Model 1 and from 0.85 to 0.96 for Model 2. Results of the present study, indicated that the inclusion of maternal genetic effects in the model of analyses for milk yield traits, is recommended, as, it leads to higher estimates for genetic parameters.

Keywords: Genetic parameters, direct and maternal genetic effects, direct heritability, maternal heritability, genetic correlation, milk yield traits, Friesian cattle

INTRODUCTION

In the usual mixed linear model for maternally influenced traits, the phenotype is partitioned into, additive genetic effects from the sire and the dam (direct genetic effects), additive genetic ability of the dam to provide a suitable environment (indirect or maternal genetic effect), permanent environmental effects (permanent environmental influences on the dam's mothering ability and maternal non-additive genetic effects of the dam) and random environmental effects (residual effects), (Mrode, 1996).

Genetic evaluation often ignores permanent environment effects (Wall *et al.*, 2005). However, as breeding goals become more complex there may be a need to review this position.

Animal models used to analyze maternally influenced traits typically include direct, maternal effects, covariance between them and a permanent environmental effect of the dam (Waldrøe *et al.*, 1993, Robinson, 1996).

Published researches on direct and maternal genetic effects and permanent environmental effects of milk yield traits are very few. Analla *et al.*

(1999) concluded that when the association between direct and maternal effects to final performance is not negligible i.e., when the additive correlation between them is strong, inclusion of them in genetic evaluation is unavoidable.

It is unclear whether additive maternal effects influence yield traits in dairy cattle. Maternal genetic effects are present in beef cattle, for which genetic mothering ability influence preweaning growth of calves. In contrast, dairy dams generally do not nurse their calves, so additive maternal effects would be caused by intrauterine environment.

The objectives of this study were to estimate the genetic parameters for milk yield traits using two animal models (with and without maternal genetic effects), to quantify the contribution of additive direct and maternal genetic effects to phenotypic variance and to choose the most appropriate statistical model for estimating the genetic parameters for milk yield traits.

MATERIALS AND METHODS

Data

Data on 2181 normal lactation records of Friesian cattle raised at Sakha Experimental Station, Animal Production Research Institute, Ministry of Agriculture, Egypt. Records spread over the period from 1996 to 2002. Number of sires and dams were 92 and 878, respectively. Abnormal records affected by disease such as mastitis and udder troubles or by disorders such as abortion were excluded. Lactation records with less than 150 days lactation period were also discarded. Traits studied were 305 days milk yield (MY), 305 days fat yield (FY) and 305 days protein yield (PY) in kilograms.

Data were analyzed by Multiple Traits Derivative Free Restricted Maximum Likelihood (MTDFREML) program according Boldman *et al.* (1995), using repeatability multiple trait animal model. Two animal models were used to estimate variance and covariance components. Model 1 included the fixed effects of month and year of calving and parity and the random effects of animal (additive direct genetic effects), permanent environmental effects and residual effects. Age of cow at calving was included as a covariate. In matrix notation the model 1 used was:

$$Y = Xb + Zd + Wp_e + e$$

where, Y = vector of observation, b = vector of fixed effects, d = vector of direct genetic effects, p_e = vector of permanent environmental effects contributed by dams to the records of their progeny, W is the incidence matrix relating records to permanent environmental effect and e = vector of random residual effects. X and Z are incidence matrices relating records to fixed and direct genetic effects, respectively.

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Model 2 included the maternal genetic effect which allowed for estimation of the genetic covariance between direct and maternal genetic effects as follow:

$$Y = Xb + Zd + Mm + Wp_e + e$$

where, M = vector of maternal genetic effects, M is the incidence matrix relating records to maternal genetic effect. The variance and covariance structure for model 2 was as follows:

$$V \begin{bmatrix} d \\ m \\ p_e \\ e \end{bmatrix} = \begin{bmatrix} A \sigma_d^2 & A \sigma_{dm} & 0 & 0 \\ A \sigma_{dm} & A \sigma_m^2 & 0 & 0 \\ 0 & 0 & I_n \sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & I_N \sigma_e^2 \end{bmatrix} \quad E(y) = Xb \text{ and}$$

where, n , is the number of dam s and N is the number of records, A is the numerator relationship matrix among animals, σ_d^2 is the additive direct genetic variance, σ_m^2 is the maternal genetic variance, σ_{dm} is the direct and maternal genetic covariance, σ_{pe}^2 is the maternal permanent environmental variance, I_n , I_N are Identity matrix of appropriate order, the number of dam and number of animals with records respectively and σ_e^2 is the random residual effect associated with each observation.

To estimate heritability (h^2) from model 1, the following equation was used:

$$h^2_d = \sigma_d^2 / (\sigma_d^2 + \sigma_{pe}^2 + \sigma_e^2)$$

From model 2 estimates of additive direct (h^2_d) and maternal (h^2_m) heritabilities were calculated as ratio of estimates of additive direct (σ_d^2) and maternal genetic (σ_m^2) variances, respectively to the phenotypic variance σ_p^2 . The direct maternal correlation was computed as the ratio of the estimates of direct maternal covariances (σ_{dm}) to the product of the square roots of estimates of σ_d^2 and σ_m^2 , and c^2 is the fraction of total phenotypic variance σ_p^2 due to the permanent environmental variance (σ_{pe}^2) and t^2 is the fraction of total phenotypic variance σ_p^2 due to residual effects (σ_e^2).

Estimation of covariance components was carried out by restricted maximum likelihood employing a simplex algorithm to search for variance components to minimize $-2 \log$ likelihood (L) (Boldman *et al.*, 1995), convergence was assumed when the variance of the function values ($-2 \log L$) of the simplex was less than 10^{-9} . After the convergence, a restart was performed to verify that it was not a local minimum. Restarts were performed for all analyses, using the final results of the previous analysis, in order to locate the global maximum for the log likelihood. Starting values for variance components for multi-trait analyses were obtained from single-trait and two traits analyses.

RESULTS AND DISCUSSION

Overall Mean

Unadjusted means and their standard deviation (SD) and coefficients of variability (CV) for 305 day milk yield (MY), 305 day fat yield (FY) and 305 day protein yield (PY) are presented in Table 1.

Table (1): Unadjusted means (x), standard deviation (SD) and coefficient of variability (CV%) for 305 day milk yield (MY), 305 day fat yield (FY) and 305 day protein yield (PY).

Trait	Mean, kg	SD, kg	CV%
MY, kg	2806	948.9	33.8
FY, kg	102	36.8	36.0
PY, kg	79	28.0	35.5
No. of records 2181			

Genetic parameters

Estimates of variance and covariance components, heritability estimates and proportion of variance due to the genetic variance of direct effects, genetic variance of maternal effects, permanent environmental variance and residual variance effects as a fraction of phenotypic variance are shown in Table 2, while in the Table 3 are those for other genetic parameters.

Table 2 : Estimates of variance components and genetic parameters of milk yield traits using two animal models (1 and 2).

parameters	Model 1			Model 2		
	MY	FY	PY	MY	FY	PY
σ_d^2	1855.4	250.3	165.2	1801.6	232.5	171.4
σ_m^2	-	-	-	82.1	44.0	54.5
σ_{dm}^2	-	-	-	-159.3	-36.4	-35.6
σ_{pe}^2	168.4	111.8	71.4	714	85.2	42.9
σ_p^2	6664.9	1052.2	644.5	5787.3	686.1	429.6
σ_e^2	4641.1	690.1	407.9	3348.7	360.8	196.5
h_d^2	0.28	0.24	0.26	0.31	0.34	0.40
h_m^2	-	-	-	0.01	0.06	0.13
c^2	0.03	0.11	0.11	0.12	0.12	0.10
t^2	0.70	0.66	0.63	0.58	0.53	0.46

The term σ_d^2 is the direct genetic variance, σ_m^2 is the maternal genetic variance, σ_{dm}^2 is the genetic covariance between direct and maternal effects, σ_{pe}^2 is the permanent environmental variance, σ_p^2 is the total phenotypic variance, σ_e^2 is the residual variance, h_d^2 is the direct heritability, h_m^2 is the maternal heritability, c^2 is the fraction of total variance due to the permanent environmental variance and t^2 is the fraction of total variance due to residual variance.

Estimates of direct heritability for MY, FY and PY were 0.28, 0.24 and 0.26, respectively, using model 1, and 0.31, 0.34 and 0.40, respectively using model 2 which including the maternal genetic effects. These estimates were close to the often reported range of 0.25 to 0.35 recorded for yield traits by Boettcher and Gibson (1997) using Canadian Holsteins, but smaller than that reported for MY (0.38) by Van der Werf and De Boer (1989) for Dutch Holsteins.

The results of this study showed that Model 1, which ignored maternal genetic effects, resulted in smaller estimates compared with those obtained by Model 2. Removal of maternal genetic effects from Model 2 increased the fraction of direct genetic variance (σ_d^2) by 0.03(11%) for MY, 0.10 (42%) for FY and 0.14 (54%) for PY than those of Model 1. In this respect, Waldron *et al.* (1993) stated that animal model ignoring maternal effects tended to overvalue direct heritability.

The current fractions are higher than those reported by Albuquerque *et al.* (1996) for milk and fat yield (0.014 and 0.021, respectively) using New York Holstein and that of MY (0.01) reported by Khattab *et al.* (2005) using Friesian cattle. The higher estimates of direct heritability (h_d^2) with model 2, suggests that including maternal genetic effects should not be ignored from the model of analyses for estimating the genetic parameters of milk yield traits.

The maternal heritability (h_m^2) estimates were 0.01 for MY, 0.06 for FY and 0.13 for PY (Table 2), which represented 4%, 25% and 50%, respectively

of direct heritability. Similarly, Khattab *et al.* (2005) recorded 0.01 for MY. While, smaller estimate of 0.001 for MY reported by Albuquerque *et al.* (1996) and higher estimate of 0.026 was declared by Schutz *et al.* (1992) for MY using Holstein cattle.

Estimates of variances due to residual effects (t^2) as a fraction of phenotypic variance were 0.58 for MY, 0.53 for FY and 0.46 for PY in Model 2. These values were smaller than those recorded for the same traits in Model 1 (0.70, 0.66 and 0.63, respectively), this amount of decrease accounted for the maternal genetic effects (Table 2).

The variance estimates due to permanent environmental effects (c^2) as a proportion of total phenotypic variance were 0.12, 0.12 and 0.10, respectively in Model 2 and 0.03, 0.11 and 0.12, respectively in Model 1, for the same mentioned traits.

Although, maternal genetic effects and covariance between maternal and direct genetic effects do not seem to make important contribution to the phenotypic variance of MY, FY and PY (1%, 6% and 13%, respectively), probably because the only environmental influence of the dams on their calves is from conception to birth, its addition in the Model 2, leads to noticeable increase in the heritability estimates of direct genetic effects. In general, estimates of direct heritability were inflated with Model 2 compared with Model 1. This increase in h^2_d is most likely due to maternal effects which inflates the estimates of direct heritability. This suggests that maternal effects should not be ignored when analyzing for estimating the genetic parameters for selection programs of milk yield traits.

Similarly, Analla *et al.* (1999) concluded that the inclusion of maternal breeding values in the selection criteria is unavoidable. They also added that the maternal genetic effects should be used in order to get a correct ranking of a candidate to selection and higher increase in final performance values.

Table 3: Direct and maternal genetic correlations and direct maternal genetic correlations between various traits studied.

Covariance parameters	MY with FY	MY with PY	FY with PY
Model 1			
r_d	0.96	1.00	0.95
Model 2			
r_d	0.96	0.85	0.86
r_m	0.20	0.13	0.21
r_{dm}	-0.18	-0.36	-0.24

r_d is the correlation between direct genetic effects, r_m is the correlation between maternal genetic effects, r_{dm} is the correlation between direct and maternal genetic effects.

All estimates of direct genetic correlations between milk yield traits were positive and high, ranging from 0.95 to 1.00 for Model 2 and from 0.85 to 0.96 for Model 1. The estimates of correlations between direct and maternal genetic effects of milk yield traits studied were negative ranging from -0.36 to -0.18 (Table 3). This result is similar, to that recorded by Khattab *et al.* (2005) using Friesian cattle. Some confounding between direct and maternal genetic effects should be expected because the dam that contributes the

maternal genetic effect also transmits half of her genetic value for direct effects to her daughter. These negative correlations may be due to that the pedigree structure not being adequate for obtaining clear estimates. Therefore, more research work in this respect is needed by using a larger number of records.

Conclusion

The results of this study, showed the importance of inclusion of maternal genetic effects to the model of analyses, since its inclusion leads to higher estimates for genetic parameters, better chance for genetic improvement and higher accuracy of selection for milk yield traits than models without maternal genetic effects.

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المعايير الوراثية للتأثيرات الوراثية المباشرة والأمية لصفات ناتج اللبن في قطيع
للماشية الفريزيان في مصر
محمد نجيب العريان
قسم الإنتاج الحيواني - كلية الزراعة - جامعة المنصورة

أخذت بيانات ٢١٨١ سجل إنتاج لبن لأبقار فريزيان مرباة بمحطة تجارب سخا أثناء الفترة
من عام ١٩٩٦ إلى ٢٠٠٢ م. كان عدد الطلائق والأميات ٩٢ و ٨٧٨ على التوالي. حللت البيانات
باستخدام برنامج الـ MTDFREML

استخدم موديلان لنموذج الحيوان . الموديل ١ اشتمل على التأثير الوراثي التجمعي للحيوان
والتأثير البيئي الدائم كتأثير عشوائي . والموديل ٢ أضيف فيه التأثيرات الوراثية الأمية بالإضافة
لمحتويات الموديل ١، بما يسمح بتقدير الارتباطات الوراثية المباشرة والأمية . فسي الموديلان
المستخدمان كانت التأثيرات الثابتة هي شهر وسنه الولادة وترتيب موسم الحليب ولخذ عمر البقرة
عند الولادة كإحدار . قدرت التأثيرات الوراثية المباشرة والأمية والمعايير الوراثية لصفات ٣٠٥
يوم ناتج لبن ، ٣٠٥ يوم ناتج دهن ، ٣٠٥ يوم ناتج بروتين .

كانت قيم المكافآت الوراثية للتأثيرات المباشرة للصفات المذكورة ٠,٢٨ ، ٠,٢٤ ، ٠,٢٦ ،
على التوالي باستخدام الموديل ١ وكانت تلك القيم ٠,٣١ ، ٠,٣٤ ، ٠,٤٠ على التوالي باستخدام
الموديل ٢ . وقيم المكافآت الوراثية للتأثيرات الأمية ٠,٠١ ، ٠,٠٦ ، ٠,١٣ على التوالي . قدرت
قيم التباين البيئي الدائم كنسبة من التباين الظاهري فكانت ٠,٠٣ ، ٠,١١ ، ٠,١١ على التوالي
(موديل ١) وكانت ٠,١٢ ، ٠,١٢ ، ٠,١٠ على التوالي (موديل ٢) . قدرت الارتباطات
الوراثية بين التأثيرات الوراثية المباشرة والأمية بين جميع صفات ناتج اللبن المدروسة فكانت
سالبة وتراوحت قيمها من - ٠,٣٦ إلى - ٠,١٨ . وكانت الارتباطات الوراثية للتأثيرات الوراثية
المباشرة بين كل الصفات موجبة وعالية وتراوحت قيمها من ٠,٩٥ إلى ١,٠٠ في موديل ١ ومن
٠,٨٥ إلى ٠,٩٦ في موديل ٢ .

أوضحت نتائج هذه الدراسة انه ينصح بإضافة التأثيرات الوراثية الأمية إلى الموديل
المستخدم في التحليل لصفات إنتاج اللبن ، حيث أن إضافتها قد أدى إلى زيادة تقديرات المعالم
الوراثية .