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### Genetic Components for Milk Production and its Composition Estimated by Using Sire and Animal Models in A Herd of Friesian Cows

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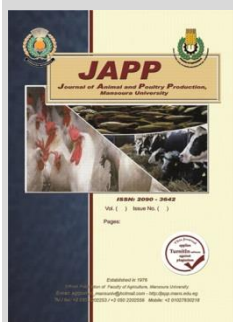


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#### ABSTRACT

A total number of eighty seventy four Friesian cows which, kept at Sakha and El-Karda farms, from 1996 to 2002 are used to estimate heritability ( $h^2$ ), phenotypic ( $r_p$ ) and genetic correlations ( $r_g$ ) among three months and 305 day milk yield traits by using sire model (SM) and animal model (AM). The SM includes the random effects of bull and cows within bulls and main effects of herd year season, and lactation number and days open as a regression. The animal model includes the main effects of herd year season and lactation number and days open as a regression and random effects of animals, permanent and errors. Estimates of  $h^2$  of milk yield traits for sire models are moderate and between from 0.116 to 0.264 as calculated from sire components and from 0.036 to 0.068 from dam components, while the  $h^2$  for milk traits from AM ranged from 0.046 to 0.062. Genetic correlations between milk production traits are positive, high and near similar for SM and AM and between from 0.88 to 0.99. The high estimates of genetic correlation in the present study offer the possibility to select for yield traits as early ages, i.e., at 90 days of lactation. Also, this study indicate that, using of SM is useful when a, small number of observations and little pedigree information is available.

**Keywords:** Friesian cattle - genetic parameters - variance component

#### INTRODUCTION

Estimation of genetic parameters for dairy cattle are estimated by using sire models (Hardie *et al.*, 1978; Ashmawy and Khalil, 1990 and Atil and Khattab, 2000) and animal model (i.e., Ahlborn and Demfple, 1992; Suzuki and Van Vleck, 1994; Mantysaari *et al.*, 2002, Atil and Khattab 2005; Nower, 2005; Salem and Hammoud, 2016). Osman *et al.* (2013) with 3460 lactation records of Holstein Friesian cows, in Egypt, using SM, found that heritability estimates for 305 d MY, fat % and protein % are 0.490, 0.97 and 0.848, respectively, while, El-Arian *et al.* (2003) and Salem and Hammoud (2016) using AM, reported that heritability estimates for 305 d MY are 0.32 and 0.149, respectively. In addition, Nower *et al.* (2005) stated that product moment correlation between expected breeding values for milk traits using SM and AM ranged from 0.66 to 0.99. The same author found that simple correlation between expected breeding values breeding values from animal model and sire model for fertility traits ranged from 0.16 to 0.20. Also, the same author, concluded that the sire model based estimating procedure for genetic parameters could be preferred when a small number of individual and litter pedigree information. The present study aims to compare genetic components for cumulative milk traits by using SM and AM models in a closed herd of Friesian cows in Egypt.

#### MATERIALS AND METHODS

The present experiment are carried out in Sakha and El-karda farms. Data consists of 847 cows which completed one or more lactations calving during 1996 to 2002. Cows were housed free in shaded open yards, grouped according to daily milk yield and fed on Egyptian clover from December to May and after that they were fed on concentrate ration and rice straw. Cows pregnant in the last 60 day are given with extra concentrate. Artificial insemination (AI) was used at random. Heifers are first inseminated at 18 months of age. Cows were initially inseminated 60 to -70 days postpartum. Milk production are recorded daily and both fat and protein percentages were analyzed are estimated weekly in laboratory by using system of Milko-Scan 130 series, type 10900. Maintained at (ILMTC) related to Animal Production Research Institute (APRI), this set have special program to estimate milk composition (fat, protein and lactose). Traits studied are milk, fat and protein yield in the first three months (MY 90, F 90 and PY 90, respectively) and milk, fat and protein yield in 305 day (MY 305, FY 305 and PY 305, respectively). Lactations that began with an abortion or in which milking was interrupted by injury or sickness were excluded. Days open was computed as the interval between date of parturition and conception. Table 1 shows a summary of the analyzed data with means, minimum and maximum of MY 90, FY 90, PY 90, MY 305, FY 305 and PY 305.

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The preliminary analysis of data by using GLM procedure of the SAS Computational program (Statistical Analysis System, 2000) show the significant effect herd-year-season of calving), lactation order and days open as a covariate. Therefore data are analyzed by Pest Program according to Groeneveld et al. (1998) using sire and animal models.

The sire model included the main effects of herd year season, and lactation order, and days open as a regression and the random effects of bulls, cow and dam and random errors. Estimates of sire ( $\sigma_2s$ ), cow ( $\sigma_2c$ ) and dam ( $\sigma_2d$ ) components of variance and covariance are computed according to method III of Henderson (1953). Heritability estimates ( $h^2$ ) were calculated from four times the intraclass correlation among half sibs. Standard errors of  $h^2$  and estimation of genetic correlation were obtained by computing technique described by Pest Program.

The animal model includes the main effects of herd year season, parity and days open as a covariate. Random effects fitted are the animal direct genetic effect and the permanent environmental effects.

For animal model, the model included the fixed effects of HYS, parity and the days open as a covariate, animal direct genetic effect, permanent environmental effect and residual effect. Heritability estimates, phenotypic and genetic correlations are calculated according to Pest Program of Groeneveld et al. (1998).

## RESULTS AND DISCUSSION

Means, minimum and maximum, SD and CV% for milk, fat and protein yields are presented in Table 1. The means for 305-day milk (MY 305), fat (FY 305) and protein (PY 305) are lower than those reported by Hardie et al. (1978), Ashmawy and Khalil (1990), Suzuki and Van Vleck (1994), Mantysaari et al. (2002), Atil and Khatlab (2005) and Salem and Hammoud (2016) in Friesian cows in different countries and ranged between 4227 to 11571 kg for MY 305, from 162 to 419 kg for FY 305 and from 138 to 361 kg for PY 305. The coefficient of variability are between 32 to 41 % (Table 1). The estimates between 22 to 23 % for yield traits were reported by Ashmawy and Khalil (1990). The CV% of fat yields are slightly high compared with those of milk and protein yield. Similar results were obtained by Ashmawy and Khalil (1990). The higher coefficients of variability of milk traits reflect a great variation between individuals in important productive traits.

**Table 2. Heritability estimates from sire and dam component on diagonal and genetic correlations below diagonal among different traits studied by using multi-traits sire model.**

	Sire Component						Dam component					
	MY 305	FY 305	PY 305	MY 90	FY 90	PY 90	MY 305	FY 305	PY 305	MY 90	FY 90	PY90
1	0.245						0.068					
2	0.996	0.216					0.975	0.050				
3	0.999	0.999	0.264				0.972	1.000	0.036			
4	0.996	0.985	0.991	0.164			0.961	0.876	0.868	0.060		
5	0.996	0.991	0.998	0.990	0.116		0.986	0.999	0.998	0.900	0.040	
6	0.996	0.991	0.998	0.990	0.990	0.115	0.986	0.999	0.998	0.900	0.050	

According to the medium values of  $h^2$  for MY 305, FY 305 and PY 305, as calculated from sire model, concluded that the genetic progress of milk production, fat and protein production could achieved through selection, of bulls and cows as well as better management. In

**Table 1. Structure of data used in analysis, unadjusted means, minimum, maximum, standard deviation (SD) and CV % for different traits studied in a herd of Friesian cows in Egypt.**

Trait (kg)*	Mean	Minimum	Maximum	SD	CV %
MY3	1222	288	2888	393	32
FY3	42.48	10.20	115.10	15.43	36
PY3	32.50	7.80	76.20	10.98	34
MY10	3050	751	7077	979	32
FY10	105.54	25.10	237.90	43.74	41
PY10	81.61	20.40	184.80	26.29	32

Observations

No. of records	1992
No. of cows	847
No. of sires	77
No. of dams	483
No. of Animals in relationship ( $A^{-1}$ )	2144
No. of parity	9
No. of HYS	57
Average of days open, day	142

\*MY3, FY3 and PY3 are milk yield, fat yield and protein yield in the first three months, respectively. MY10, FY10 and PY10 are milk yield, fat yield and protein yield in the ten months, respectively.

Estimates of heritability ( $h^2$ ) of milk production and its components traits as estimated by SM and AM are given in Table 2. Estimates of  $h^2$  were moderate from sire components, and ranged from 0.116 to 0.264 and from AM ranged from 0.046 to 0.057. The present estimates of  $h^2$  for MY 305, FY 305 and PY 305 as estimated from SM are similar to those reported by Ashmawy and Khalil (1990) with British Friesian cows, found that  $h^2$  estimates from sire components for milk, fat and protein yields were 0.25, 0.24 and 0.23, respectively. However, the present estimates were lower than those obtained by different workers on Friesian cows on different countries by using sire models (i.e., Gacula et al., 1968; El-Awady et al., 2002) and ranged between 0.20 to 0.48 for MY 305, from 0.24 to 0.30 for FY 305 and from 0.23 to 0.29 for PY 305. Also, Hardie et al. (1978) analysis data on Holstein cows in Madison, using SM, found that  $h^2$  estimates for milk yield and fat yield are 0.27 and 0.38, respectively. In addition, Osman et al. (2013) with Holstein Friesian cows in Egypt, found that  $h^2$  estimates for 305 d MY, F % and P % by using sire model are 0.209, 0.90 and 0.951, respectively. While, heritability estimates from dam components ranged from 0.036 to 0.068 (Table 2).

addition, low genetic effect from dam components may be due to small number of daughters per dam.

Estimates of  $h^2$  for milk traits from multiple trait animal models are presented in Table 3 and from 0.046 to 0.062. The present estimates are lower than estimates from

sire model and also are lower than those estimated by many authors on different countries, using animal model (Ahlborn and Dempfle, 1992; Suzuki and Van Vleck, 1994; Mantysaari *et al.*, 2002 ; Kadarmideen *et al.*, 2003; Atil and Khattab., 2005 ; Salem and Hammoud, 2016 ; Abosaq *et al.*, 2017) and from 0.10 to 0.33. Nower (2005) with another set of that herd concluded that Multiple –trait analysis improve accuracy of estimated breeding value (EBV) for each trait evolved by reducing variances of prediction error (PEV) of (EBV).

Unexpected lower estimates of  $h^2$  for milk traits (Table 3) by using animal models, could be due to higher percentage of permanent and residual environmental factors. Also, the present result is the first attempt for calculated fat and protein percentages in government farms in Egypt, and the sample of cows which used in this study were taken from different parities in a short period (seven years) and also small number of observations.

**Table 3. Heritability estimates on diagonal and genetic correlations ( $r_g$ ) below diagonal, permanent correlation ( $r_{pe}$ ) above diagonal and residual correlations between practices among different traits studied by using multi-traits animal model.**

Traits	MY 305	FY 305	PY 305	MY 90	FY 90	PY 90
MY 305	0.057	0.999(0.929)	1.000(0.962)	0.998 (0.696)	0.998 (0.560)	0.997(0.550)
FY 305	0.980	0.046	1.000(0.948)	0.994(0.631)	1.000(0.660)	0.993 (0.600)
PY 305	0.986	0.999	0.048	0.996(0.652)	0.999(0.580)	0.992(0.560)
MY 90	0.958	0.882	0.989	0.062	0.992(0.848)	0.990(0.600)
FY 90	0.999	0.985	0.990	0.949	0.052	0.992(0.600)
PY 90	0.999	0.982	0.990	0.939	0.990	0.050

Genetic correlations between milk yield traits (Tables 2 and 3) are positive, highly significant for both two models (SM and AM) and from 0.882 to 0.999. Estimates of genetic correlation between MY 305, FY 305 and PY 305 are higher than those reported by Hardie *et al.* (1978), Ashmawy and Khalil (1990), Ahlborn and Dempfle (1992) , Kadarmideen *et al.* (2003), Atil and Khattab (2005) and Abosaq *et al.* (2017) and from 0.68 to 0.89. Our results concluded that selection of cows with higher milk yield, would cause a correlated increase in fat and protein yields. In addition, the first three months of milk traits can be good indicators of production in 305 day milk, fat and protein yield. Most of the estimates in the literature (e.g. Ashmawy and Khalil , 1990) showed that the genetic correlations between initial yield traits and 305 day yield traits were positive and high ( $< 0.85$ ). Estimates of permanent correlations among milk traits are positive and high and from 0.992 to 1.00 and residual correlations among different traits (Table 3). These results suggested that it is important to improve the environmental.

**CONCLUSION**

Finally, from the moderate estimate of  $h^2$  for milk yield and it is composition in a closed herd of Egyptian Friesian cows by using sire models, reported herein, it can be concluded that genetic progress of milk yield traits can be achieved through selective breeding. High estimates of genetic correlation in the present study offer the possibility to select for yield traits at early ages, i.e., at 90 days of lactation. The using of sire model is useful when only a small number of records and little pedigree information is available.

In this respect, Silvestre *et al.*(2005) with Holstein Friesian cows, found that heritability estimates for milk yield, fat yield and protein yield are 0.22, 0.14 and 0.19, respectively.

Gutierrez *et al.* (1994) compared sire and animal models, concluded that sire models may be preferred when a small number of individuals, little pedigree information and highly dis-equilibrated distribution of effects characterize the data. In addition, Abdel Salam *et al.* (2001) analysis 2245 lactation records of Holstein, using animal model, found that  $h^2$  estimates for 305 day milk yield was 0.05 and concluded that the low  $h^2$  estimates may be due to size of the data and natural editing of the data. Besides, several other factors must be considered for reliable estimation of genetic parameters (Suzuki and Van Vleck, 1994).

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**المكونات الوراثية للإنتاج اللبن ومكوناته المقدرة من نموذج الأب ونموذج الحيوان في قطع من أبقار الفريزيان**  
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استخدم في هذه الدراسة ٨٤٧ سجل إنتاج لبن لأبقار الفريزيان في مصر وذلك في مزرعتي سخا والقرضا لتقدير التباين والتغاير الوراثي والمظهري بين صفات إنتاج اللبن في ٣٠٥ يوم وإنتاج اللبن في ثلاثة شهور وذلك باستخدام نموذجي الاب والحيوان. إحتوى نموذج الاب على التأثيرات الثابتة لـ HYS اي القطيع والسنة والموسم، وعدد مواسم الحليب وفترة الأيام المفتوحة كمتباين مشترك واستخدمت التأثيرات العشوائية للاب والام والأثر المتبقي. اشتمل نموذج الحيوان على نفس التأثيرات الثابتة الموجودة في نموذج الاب بالإضافة الى التأثير الوراثي المباشر للحيوان والتأثير البيئي الدائم كتأثيرات عشوائية. تراوحت تقديرات المكافئ الوراثي لصفات اللبن في نموذج الاب بين ٠,١١٦ الى ٠,٢٦٤ و من مكونات تباين الام ما بين ٠,٠٣٦ الى ٠,٠٦٨ بينما تراوحت قيم المكافئ الوراثي لصفات اللبن في نموذج الحيوان بين ٠,٠٤٦ الى ٠,٠٦٢. كانت قيم معامل الارتباط الوراثي بين صفات اللبن ايجابية وعالية وشبه متماثلة لكل من نموذجي الاب والحيوان .