# OPTIMUM NUMBER OF DAUGHTERS TO EVALUATE THE SIRES IN A SMALL HERD OF DAIRY CATTLE IN EGYPT

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## ABSTRACT

A total of 2143 normal lactation records of 473 Friesian cows sired by 89 bulls kept at Sakha farm of the Animal Production Research Institute Ministry of Agriculture, Egypt, collected between 1981 and 2000 were used to estimate the genetic parameters and the breeding values of sires for 305 days milk yield (305dMY) using single trait animal model applied on groups of different number of daughters per sire. The statistical model included the fixed effects of month and year of calving and parity, days open and days dry as a covariates and the individual, permanent environment and residual as random effects.

Estimates of heritability for 305dMY were 0.14, 0.13, 0.14, 0.12 and 0.13 when number of daughters per sires were $\geq 5$, $\geq 10$, $\geq 20$, $\geq 30$ and $\geq 40$, respectively. Ranges of sire breeding values were 867, 793, 844, 863 and 908 kg, for the same groups of daughters, respectively. Although the reliability of sire breeding values estimates for 305dMY were from 0.19 to 0.85 and increased as number of daughters per sire increased. Little difference in accuracy between the first three groups of daughters per sire were found. So, five daughters per sire might be the least sufficient number to be used in estimating the genetic parameters for 305dMY in small herd of dairy cattle.

**Key words:** *Optimum, number of daughters per sire, Friesian Egypt*

## INTRODUCTION

Prediction of the genetic merit of sires for milk traits necessitates the utilization of female records of either ancestors or progeny. Sire evaluation on the basis of progeny records proved

much greater accuracy than pedigree evaluation (Van Vleck, 1979). Zollinger (1993) concluded that the accuracy of the expected progeny difference (EPD) of bulls increases as the number of progeny records increase, so will the reliability of the estimates. In this respect, Khattab et al., (1987) in a study based on 2005 normal lactation records of Friesian cattle in Egypt, reported high efficiency in estimating sire transmitting ability for 305 day milk yield when number of daughters per sires was 20. Elsaid et al., (2005) simulated data for continuous and binary traits using $h^2$ levels of 0, 0.1, and 0.5 and number of daughters per sire of 5, 10, 15 and 20. analysis was executed once with sire model and another with animal model using MTDFREML and Gibbs sampling (GS) algorithms. The animal model should better efficiency in describing the variance components of the continuous trait when using both algorithms with all levels of $h^2$ and the sire model was better in case of the binary trait when using GS at $h^2$ level of 0.1 and number of daughters per sire above 5. When using higher levels of $h^2$ and 20 daughter per sire both models had equivalent efficiency and at all levels of $h^2$ using 20 daughters per sire caused reduction in mean squares errors.

The objectives of the present study were to estimate heritability and predict sires breeding values for 305 days milk yield of Friesian cattle in Egypt using a single trait animal model for several groups of different numbers of daughters per sire.

## MATERIALS AND METHODS

A total of 2143 normal lactation milk records from the Friesian cattle herd stationed at Sakha farm, Animal Production Research Institute, Ministry of Agriculture, Egypt collected between 1981 and 2000 were used in this study. Abnormal records affected by diseases, abortion or udder troubles were excluded. Management regimes practiced on this herd were detailed thoroughly by El-Awady, (1998); Hussein, (2004) and Khattab et al., (2005). Table (1) show the structure of the considered in the analysis.]

**Table (1) The structure of the data used in the analysis classified according to number of daughters per sire**

| Items | No. of daughters/sire | | | | |
|---|---|---|---|---|---|
| | ≥5 | ≥10 | ≥ 20 | ≥30 | ≥40 |
| No. of records | 2143 | 1982 | 1714 | 1443 | 1263 |
| No. of cows | 473 | 444 | 396 | 344 | 303 |
| No. of sires | 89 | 62 | 40 | 25 | 18 |
| Animals in relationship matrix ($A^{-1}$) | 1249 | 1144 | 987 | 834 | 727 |
| Mixed model equations (MME) | 1978 | 1823 | 1578 | 1339 | 1173 |
| No. of iterations | 20 | 20 | 19 | 25 | 21 |

Sires which had 5 daughters or more were included in the genetic analysis and were divided to five groups according to number of daughters per sire ($\geq 5$, $\geq 10$, $\geq 20$, $\geq 30$, and $\geq 40$ daughters per sire). Cows were artificially inseminated randomly to ensure that no specific sires were bred to certain good or poor dams.

Milk production records in 305 days milk yield (305dMY) were analyzed using Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) according to Boldman et al., (1995) with Single Trait Animal Model (STAM). The model included the fixed effects of month of calving from January to December, year of calving between 1981 and 2000 and parity from 1 to 6. Days dry and days open were treated as covariates and individual (animal effect), permanent environment (maternal permanent environmental effect) and residual (temporary environment) as random effects. Estimates of genetic, permanent environmental and temporary environmental variances ($\sigma^2 a$, $\sigma^2 pe$ and $\sigma^2 e$, respectively), heritability ($h^2$) and sire breeding values were calculated according to Boldman et al., (1995). More information about estimates of genetic parameters, mixed model equations, best linear unbiased estimator (BLUE) and best linear unbiased prediction (BLUP) are described by El–Arian et al., (2003).

## RESULTS AND DISCUSSION

Unadjusted mean of 305dMY, standard deviation (SD) and coefficient of variability (CV %) were 2543 kg, 1015 kg and 39.40 %. The high CV% value, reflect considerable amount of variation between cows for 305dMY trait.

The numbers of Mixed Model Equations (MME) and number of iterations for groups of different number of daughters per sire are presented in Table (1). Number of iterations were lower than those reported by Salem (1998) who executed 153 rounds of iteration used STAM to obtain sire solutions for another herd of Friesian cattle in Egypt. Also, Swalve and Van Vleck (1987) realized only 18 rounds of iteration while using records of 4000 cows in animal model to estimate genetic parameters for milk yield of first, second and third lactations. In general, number of iterations required to reach convergence could be affected by number of animals, number of random effects in the model and number of traits studied.

Estimates of variance components and genetic parameters of 305dMY for groups of different numbers of daughters per sire are presented in Table (2). Estimates of direct genetic variances and $h^2$ for the five groups of daughters numbers per sire which ranged from 0.12 to 0.14 seem to be low. Similar results were reported by Khattab et al., (2005) in Egypt when using Animal Model. In this respect, Abdel-Salam et al., (2001) reported a heritability value of 0.5 for 305dMY of Holstein Friesian and referred this to either the analytical model or to the percent of records having adequate relationships. Khattab et al., (2005) using Multi Trait Animal Model, obtained $h^2$ estimates of 0.17 for 305dMY. In addition, Abou-Bakr et al., (2006) estimated $h^2$ for 305dMY was 0.13.

However, high heritability estimates were reported by Khattab et al., (1987) and Atil et al., (2001). Mousa et al., (2002) using similar analytical procedures with two different animal models, reported $h^2$ values of 0.22 and 0.38 for 305dMY. El-Arian et al., (2003) estimates for the same traits was 0.32. Similarly high heritability estimates of 0.35 were reported by Konig et al., (2005) for 305dMY of Holstein Friesian cattle in Thailand, when using at least 20 daughters per sires, and in Turkey Atil and Khattab (2005) obtained $h^2$ estimates of 0.26 for the same trait of Friesian cattle.

The percent of unknown parents in this study was 17%. Dong et al., (1988) reported that if 20 % of the cows have

unknown parents, the components of the additive variance would be under estimate and reduced the bias in these estimations when included the unknown parents in the model. Rosati and Van Vleck (2002) concluded that misleading paternity identification would result in assigning part of the genetic variability to environmental effects and would reduce the estimate of heritability for direct genetic effects. Also, Short et al., (1990) found differences in the heritability estimates due to the level of production of the herds.

**Table (2). Estimates of genetic ($\sigma^2a$), permanent environmental ($\sigma^2p_e$), temporary environmental ($\sigma^2e$) variance components and heritability ($h^2$) of 305dMY for groups of different number of daughters per sire.**

| Variance components | $\geq5$ | $\geq10$ | $\geq20$ | $\geq30$ | $\geq40$ |
|---|---|---|---|---|---|
| $\sigma^2a$ | 1059 | 969 | 1037 | 869 | 1020 |
| $\sigma^2p_e$ | 1806 | 1920 | 1820 | 1882 | 1750 |
| $\sigma^2e$ | 4486 | 4482 | 4433 | 4391 | 4356 |
| $p_e\%$ | 0.25 | 0.26 | 0.25 | 0.26 | 0.25 |
| $e\%$ | 0.60 | 0.61 | 0.61 | 0.61 | 0.61 |
| $h^2$ | 0.14 | 0.13 | 0.14 | 0.12 | 0.14 |

The present low estimates of heritability of 305dMY for groups of different numbers of daughters per sire obtained from STAM indicated relatively high permanent and temporary environmental variability. The permanent portion of the environmental of variance presented about one quarter, while the temporary environmental portion of variance centered around the figure of 60 %. This illustrates the necessity of improving the environmental components in order to achieve improvement in such an important economic trait. On other words more efforts could be made to bring about improvement 305dMY through selection as well as through better management practices. Results obtained by Khattab et al., (2005) using another herd of Friesian cattle in Egypt, indicated that the temporary environmental fraction of variance for 305dMY was 66%. Rosati and Van Vleck (2002) suggested that the variation in production can be assigned mainly to environmental effects causing low heritability estimates.

The ranges of sire breeding values for 305dMY of groups of different number of daughters per sire presented in Table (3) indicated large differences among breeding values of sires, with reliabilities increasing as the number of daughters per sire

increased. Similar large sire differences recorded ranges of 1239 and 388 were reported by El-Arian et al., (2003) and Atil and Khattab (2005) when evaluated Friesian sires for milk yield in Egypt and Turkey, respectively. In addition, Abdel-Salam et al., (2001) working on another herd of Holstein Friesian cattle in Egypt, reported large sire breeding values for 305dMY ranging from -396 to 259 kg of milk yield. VanRaden et al., (1990) analysis for 14 linear type traits on Holstein Friesian cattle, indicated that the reliabilities of prediction the sire breeding values increased by increasing number of daughters per sire and approached 99% when using 1000 daughters per sire.

**Table (3) Ranges of predicted breeding values of sires (kg) and the accuracy of predictions (Rti) for 305dMY for groups of different number of daughters per sire.**

| No. of daughters | Predicted breeding values | | | | Range | Accuracy (Rti) |
| | Min. | | Max. | | | |
| | Mean | S.E | Mean | S.E | | |
|---|---|---|---|---|---|---|
| ≥5 | -503 | 20 | 364 | 19 | 867 | 0.19 - 0.82 |
| ≥10 | -480 | 20 | 313 | 19 | 793 | 0.18 - 0.81 |
| ≥20 | -509 | 20 | 335 | 19 | 844 | 0.19 - 0.82 |
| ≥30 | -504 | 22 | 359 | 17 | 863 | 0.45 - 0.82 |
| ≥40 | -571 | 19 | 337 | 17 | 908 | 0.55 - 0.85 |

The present results showed the little differences in the accuracy of sires breeding values in the first three groups of numbers of daughters per sire, (≥5, ≥ 10 and ≥ 20) and the increased accuracy by increasing number of daughters per sire. The same results reported by Willis (1998), who obtained accuracy evaluating from 46 to 95% when the number of daughters per sire increased from 5 to 120 at $h^2$ value of 0.2, and those by Khattab et al., (1987), they reported that the greatest sire evaluations were obtained when the bull had 20 daughters made it reliable to conclude that the accuracy of sire evaluation increase as the number of daughters per sire increases but that may vary from one trait to another and depends on the structure of the data sets used. These results and those reported by Elsaid et al., (2005) illustrated that for continuous traits, the animal model describes the data best when using MTDFREML or GS at all levels of $h^2$ with any number of progeny per sire.

## CONCLUSION

The present estimates of $h^2$ of 305dMY for groups of different numbers of daughters per sire are near similar (0.12 to 0.14), which suggests that the minimum number of five daughters per sire is quite sufficient for estimation of genetic parameters in a small herd of dairy cattle in Egypt. In this respect, Willis (1998) stated that the least sufficient number of progeny per sire to be evaluate may be as low as ten for some traits and may grow big as 300 daughters per sire for other traits, like dystocia.

The high range of sire breeding values for 305dMY of groups of different numbers of daughters per sire, indicated a high potential for rapid genetic improvement through selection in milk production of Friesian cattle raised in Egypt. Genetic progress can be achieved if the small farms common in Egypt adopts simple system for testing the genetic value of sires, consequently, selection of top sires will increase milk production of the future generations of cows and this is a main objective of the dairymen.

Finally, the genetic improvement in dairy cattle depends mainly on the success of AI organizations in operating success full progeny test programs with sufficient size of progeny groups. Under the situations of small herds of dairy cattle, progeny testing may perform considerably better accuracy than pedigree testing especially with traits having low heritability even when using only five daughters per sire chosen randomly and might be comparable to performance data.

## ACKNOWLEDGEMENT

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# الملخص العربي

## العدد الأمثل للبنات المستخدم فى تقييم الآباء فى قطيع صغير من ماشية اللبن فى مصر

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استخدم ٢٤١٣ سجل حليب لعدد ٤٧٣ بقرة فريزيان تزاوجت مع ٨٩ طلوقة بمزرعة سخا التابعة لبحوث الإنتاج الحيوانى – وزارة الزراعة – مصر خلال الفترة من ١٩٨١ إلى ٢٠٠٠ وذلك لتقدير المكافئ الوراثى والقيم التربوية للطلائق لصفة إنتاج اللبن فى ٣٠٥ يوم من موسم الحليب باستخدام معادلات نموذج الحيوان على أعداد مختلفة من البنات لكل أب.

اشتمل نمـوذج التحليل الإحصائى على شهـر وسنـة الولادة ورقم موسم الحليب كعوامل ثابتة. بينما استخدمت الفـترة مـن الـولادة حتى الإخـصاب وأيام الجفـاف كعوامل مستمرة أما العـوامل العشـوائية فكانت الحيـوان، التأثير البيئى الـدائم والتأثيـر المـؤقت (المتبقى).

بلغـت تقديرات المكافئ الـوراثى لكميـة اللـبن فى ٣٠٥ يـوم ٠،١٤، ٠،١٣، ٠،١٤، ٠،١٢ و ٠،١٣ عند استخدام أعداد ≤ ٥، ≤ ١٠ ، ≤ ٢٠ ، ≤ ٣٠، ≤ ٤٠ بنت لكل أب على التـوالى. بينـما كان مـدى القيم التربوية للآبـاء لمحصـول اللـبن فى ٣٠٥ يـوم ٨٦٧، ٧٩٣، ٨٤٤، ٨٦٣ و ٩٠٨ كيلـوجرامات لمجـاميع الأعـداد المختلفـة مـن البنـات لكل أب.

تراوحت قيمة دقة الاختبار لإنتاج اللبن فى ٣٠٥ يـوم بين ٠،١٩ و ٠،٨٥ وقد زادت هـذه الدقـة بزيادة عـدد البنات لكل أب. كان حجم الاختلاف فى الدقة قليل بـين المجـاميع الثلاثة الأولى لأعـداد البنات لكل أب. لـذا فإنه يمكن الإكتفاء باستخـدام خمسة بنات لكل أب كأقل عدد لتقدير المعايير الوراثية فى القطعان الصغيرة لحيوانات اللبن.