ESTIMATION OF HERITABILITY OF MILK YIELD IN THE PRESENCE OF FARM AND YEAR EFFECTS

By

M. T. Ragab*, A. S. Abdel-Aziz** and S. K. Fahmy

The mean squares among and within sires were calculated by three methods of analysis of variance from milk yield records of paternal half-sibs collected from three farms over a period of 25 years, and where farm and year effects existed.

The mean squares computed from within herd × year cells were the least and were supposed to provide unbiased estimates of the components of variance from which an estimated of heritability of 0.547 was obtained.

Estimating the heritability of milk yield from the ratio of four times the sire component of variance to the total variance among paternal half-sibs, requires that the components of variance be estimated as free as possible form any effects that may influence the intra-class correlation among the daughters of the same sires.

Usually, data for estimating heritability are collected from many farms over a period of time. When the use of certain sires is limited to specific years and farms, the ordinary oneway analysis of variance (yielding among and within sires mean squares) may give based estimates of the components of variances.

The purpose of this study was to find out how would the estimates of heritability of milk yield behave as the method of calculation changes.

Material and Methods

The data used in this study were collected from the records of buffaloes kept in three farms; Sakha, Gimmeza, and Sids. These farms belong to the Ministry of Agriculture, U.A.R. A total of 669 first lactuation milk yield records of daughters of 51 series, collected over a period of 25 years, was used in estimating heritability of milk yield.

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* Chairman, General Organization for Meat and Milk, Cairo, U.A.R.

** Dept. of Animal Production, Faculty of Agric., Univ. of Cairo U.A.R.

The data were first analysed according to a farm-by-year model. The main effects were found to be significant at the 1% level of probability. The farm-by-year interaction was not significant at the 5% level of probability.

The data were then analysed in three different ways : First, the usual one-way analysis of variance yielding among and within sires mean squares, was used for the complete data over all farms and years (method 1). Secondly, the same method of analysis was used for a reduced data comprising only farm-by-year subclasses (cells) that had more than one sire having two or more daughters each (method 2). Third, the reduced data were rearranged in a nested design with sires nested within cells. The mean squares among and within sires were then computed within cells (method 3).

Mean squares were equated to their expectations in the three methods and were solved for the sire components of variance. Estimates of heritability were obtained from the ratio of four times the sire components of variance to their corresponding total variances.

Standard errors of estimates of heritability (SE) were calculated using the equation proposed by Robertson (1959), $SE = (h^2 + (4/n)) \cdot \sqrt{2/S}$, where h^2 the estimate of heritability, n is the number of daughters per sire, and S is the number of sires.

Results and Discussion

In any type of statistical analysis the model which underlies the data should include all effects present. Van Vleck and Henderson (1961) listed the steps to follow : 1) Write the supposed underlying model ; 2) take expectations of the functions of the data used in estimation, considering the effects of any necessary simplifying assumptions ; 3) determine what had been estimated and, if possible, equate these expectations to the calculated values. Then solve for the unknown quantities.

It was assumed that a milk record can be expressed by the following random-effects model :

$$X_{ijkl} = u + s_i + f_{il} + y_{ijk} + e_{ijk}$$

Where X_{ijkl} = the record of the ith cow made in the kth year at the jth farm from the ith sire,

     u   = in effect common to all records,

     s_i = the effect of the ith sire,

     f_{ij} = the effect of the jth farm within the ith sire,

     y_{ijk} = the effect of the kth year at the jth farm within the ith sire, and

     e_{ijkl} = a random effect peculiar to the X_{ijkl} record.

The sire, farm, year, and random effects were assumed to be random with zero means and variances equal to σ^2_s σ^2_f σ^2_y and σ^2_e respectively.

The expectations of the mean squares and the components of variances for the different methods are presented in table 1. It is well to remember that the same analysis was used for the complete data and for the reduced data in methods 1 and 2, respectively

TABLE 1.—EXPECTATIONS OF MEAN SQUARES AND COMPONENTS OF VARIANCE FOR THE DIFFERENT METHODS OF ANALYSING DATA

Source of variance	df*	E (MS)**	Expectations of estimated components
Methods 1 & 2 :			
Sire	S–1	$\sigma^2_e + k_3\,\sigma^2_f + k_4\sigma^2_y + k_5\,\delta^2_s$	$\dfrac{(k_3-k_1)}{k_5}\,\sigma^2_f + \dfrac{(k_4-k_2)}{k_5}\,\sigma^2_y + \sigma^2_s$
Within sire .	N–S	$\sigma_e^2 + k_1\,\sigma^2_f + k_2\,\sigma^2_y$	$\sigma^2_e + k_1\,\sigma^2_f + k_2\,\sigma^2_y$
Method 3 :			
Cell	C–1		
Sire	S–C	$\sigma^2_e + k_6\sigma^2_s$	σ^2_s
Within sire	N–S	σ^2_e	σ^2_e

* S = number of sires, N = total number of progeny, and C = number of cells having more than 1 sire with more than 1 daughter.

** The k values are the harmonic means of subclass numbers.

It could be seen from table 1 that farm and year effects would be included in the within sire components of variance in methods 1 and 2. Solving for the sire components of variance would not result in a complete elimination of farm and year effects. The extreme inequality of the numbers of observations in the subclasses made the solution for thes ire components of variance more difficult. Adjusting the data for farm and year effects might be tedious and not appropriate because many farm-by-year cells were empty. Obviously, method 2 was not expected to improve the accuracy of estimating the component of variance, but was rather used as a "control-method".

A probable solution for this problem might be in calculating the heritability from components of variance computed within farm-by-year cells. The inclusion of only cells having more than one sire with more than one daughter, and the rearranging of the data resulted in an increase in the sire

degrees of freedom. The results obtained from the three methods are shown in table 2.

TABLE 2.—COMPONENTS OF VARIANCES AND ESTIMATES IF HERITABILITY FOR MILK YIELD AND THEIR STANDARD ERRORS FOR THE THREE METHODS OF ANALYSING.

Source of variance	df	MS	Estimated Components	h²	SE
Method 1 :					
Sire	50	2,157,769	103,759	0.467	0.1538
Within sire . .	618	785,027	785,027	—	
Method 2 :					
Sire	50	2,057,852	129,383	0.615	0.1998
Within sire . .	488	712,067	712,067	—	—
Method 3 :					
Cell	39	3,376,377	—	—	—
Sire/cell . . .	99	918,449	90,229	0.547	0.2212
Within sire . .	400	569,441	569,441	—	—

The results presented in table 2 indicated that the mean squares among and within sires tended to decrease as the method of analysis changed. Comparing method 2 with method 1, a reduction of 4.6% and 93% was observed in the mean squares among and within sires, respectively. Method 3 lead to a further reduction of 55.4% and 20% in the mean squares among and within sires, respectively. This might demonstrate the effectiveness of method 3 in removing from the mean squares the fractions of farm and year effects that were included in them in methods 1 and 2.

The sire components of variance did not follow the same trend. Using the reduced data in method 2 resulted in an increase of 24.7% in the sire component of variance over that of method 1. This was mainly due to the fact that the total number of progeny was less in method 2 than in method 1 while the number of sires remained unchanged. Thereby, the number of daughters per sire was reduced. However, the sire component of variance estimated from method 3 was 30% less than that of method 2.

The differences in the rate of change of the components of variance in the three methods were reflected on the estimates of heritability calculated from them. Among the three methods, unbiased estimates of the components of variance could be obtained from method 3. The heritability calculated from these components of variance would, therefor, be considered

the best estimate of heritability. Method 1 underestimated the value of heritability ,while this value was overestimated by method 2. Using the estimates obtained from either method 1 or method 2 might lead to misleading conclusions in predicting the genetic gain expected from a certain scheme of improvement.

The standard error of and estimate of heritability is a function of the magnitude of the estimate, the number of sires, and the number of daughters per sire. The estimates of heritability and the degrees of freedom for sires are given in table 2. The average number of daughters per sire was 13.23, 10.40, and 3.87 for the three methods, respectively.

A lower estimate of heritability along with larger numbers of sires and daughters per sire were expected to give the lowest standard error. This would explain the changes in the standard errors in table 2 when the estimates of heritability, the number of sires, and the number of daughters per sire changed from one method to the other.

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تقدير المعامل الوراثى لناتج اللبن تحت تأثير عاملى المزرعة والزمن

محمد توفيق رجب — احمد سعيد عبد العزيز — سعد كامل فهمى

الملخص

اقترحت طريقة لتحليل التباين عندما تكون السـجلات المسـتعملة
فى تقدير المعامل الوراثى متجمعة من أكثر من محطة خلال فترة طويلة من الزمن .
وقد شملت الدراسة ٦٦٩ سجلا لموسم الحليب الأول لجاموس انصـاف
أشعة ناتجة من ٥١ طلوقة فى ثلاث محطات خلال ٢٥ سنة . وقد كان تأثير
كل من المحطات والسنين معنويا (احتمال لأقل من ١٪) وعلى ذلك فقـد
حسبت مكونات التباين من داخل السنين × المحطات . والمفروض فى هذه
الطريقة المقترحة انها تعطى قيما غير متحيزة لمكونات التباين بين وداخـل
المجاميع الأبوية — ومن هـــــذه القيم قـدر المعـامل الوراثى الذى بلغت
قيمته ٤٧رو٠ .