

EFFECT OF DIFFERENT LEVELS OF PEDIGREE INFORMATION AND HERITABILITY MAGNITUDE ON THE QUALITY OF ESTIMATES OF GENETIC PARAMETERS

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SUMMARY

Milk production of the first (Milk1) and second (Milk2) parities was simulated according to the genetic and environmental variance-covariance structure of the two traits. Genetic and environmental variances and covariances between the two traits were 202956, 275398, 216091 and 468931, 692353, 183786, respectively. The simulated heritability (h^2) estimates for the two traits were 0.3 and 0.28 and simulated genetic correlation (gc) 0.91. Four levels of missing-sire pedigree information (m) were considered (complete, 10%, 30% and 50% missing-sire pedigree). Two types of analyses (t) were performed, for the first trait Milk1, single and multiple traits analysis. In the case of single trait analysis, the real variance components of this trait were modified to simulate three levels of (h^2) (0.1, 0.3 and 0.5). Twenty samples were simulated for each of 12 h^2 -m combinations. The effect of different levels of m on the estimates of h^2 and gc was also considered. Twenty samples were simulated in the case of multiple traits analysis (Milk1 and Milk2) for each level of m. The simulated heritabilities and gc were 0.3, 0.28 and 0.91 (the real values), respectively. MTDFREML program was used to estimate h^2 and gc in different cases. Mean squared error (MSE) and bias were used as criteria to evaluate the accuracy of different studied cases.

In the case of single trait analysis the smallest values of MSE (0.0221, 0.0441) were observed at $h^2=0.1$ and at $m=10\%$, respectively. As h^2 increased both bias and MSE significantly increased. The effect of m levels was not significant on bias but significant ($P<0.05$) on MSE estimates where it generally increased with m. Considering the gc, the least estimate of MSE was obtained at the 10% level of m and the least accurate one was at the highest level of m. The effect of m was not significant ($p>0.05$) on the estimates of h^2 , bias and mean squared error estimates, whereas the effect of t was significant ($p<0.05$) on both of h^2 and bias estimates. Results of single trait analysis for Milk1 showed that the trait with low heritability (0.1) and low amount of m yielded the most accurate estimate of h^2 , whereas the results of multiple traits analyses indicated that as the amount of m increases, the estimates of h^2 and genetic correlation become far from the true values. Type of analysis only affected significantly the estimates of h^2 and bias estimates but did not affect the estimates of MSE under the circumstances of this study.

Keywords: Simulation, missing pedigree, heritability, genetic correlation

INTRODUCTION

Measurement of genetic variability involves in one way or another pedigree information and most of estimates of genetic parameters are sensitive to the degree of completeness of this information (Baumung and Silkner, 2002). The lack of proper pedigree that makes the record unusable for genetic estimates results in many cows not being genetically evaluated (Tomaszewski, 1985). The same author also reported that the most common pedigree deficiency is missing sire identification. Pedigree information determines the numerator relationship matrix, which in turn affects the animal model estimators of variance components (Reverter and Kaiser, 1997). Pedigree structure also affects the accuracy of the estimates of variance components estimates, so that population should be designed to yield optimal information on genetic parameters (Reverter and Kaiser, 1997). Also, complete pedigrees allow mating programs to estimate inbreeding more precisely and result in more reliable predicted transmitting abilities (Kuhn and Van Raden, 2003)

Considerable interest exists among animal breeders and geneticists in the estimation of heritability and genetic correlation for the prediction of possible genetic improvement and changes in traits under consideration (Roman and Wilcox, 2000). Estimation of these parameters can be affected by many factors among which the magnitude of the parameters and the algorithm for the estimation.

As collecting field data is the most expensive component of most sire evaluation programs, a balance between the amount data collected and the extra relevant information is a desired feature for such programs. Thus, objectives of this study were to evaluate the effect of different levels of missing pedigree information and of heritability magnitude on the quality of heritability estimates of a simulated continuous trait (milk production) in a single trait analysis, and to evaluate the effect of varying levels of missing pedigree information on estimating the heritability and genetic correlation in a multiple traits analysis. The final objective was to evaluate the effect of type of analysis (single and multiple traits analyses) on estimating the heritability of the milk production in the first lactation with different pedigree information levels.

MATERIALS AND METHODS

Simulation of the Single Trait

Data sets with a random pedigree structure were simulated with 100 sires (s), each mated to 100 dams (d) to produce 10000 cows with 10000 records of milk production. Pedigree file contained individual, sire and dam.

Total phenotypic variance of σ_p^2 was assumed to be 671887 kg² according to estimates from Dkova and Olf (2001). Additive genetic variance was assumed 202956 and residual variance 468931 for h^2 of 0.3. These real variance components were modified to simulate three levels of h^2 (0.1, 0.3 and 0.5). Four levels of randomly missing sire pedigree information were considered (complete pedigree, 10%, 30% and 50% missing sire pedigree). Twenty replicates were generated for each of 12 combinations (20*12) of h^2 levels (3 levels) * m levels (4 levels). The levels of missing sire pedigree were simulated by omitting (at random) 10%, 30% and 50% of sires from each complete pedigree sample.

The formula of Analla *et al.* (1995) was used to generate the records:

$$Cg_i = 0.5(g_s + g_d) + r * \sqrt{(0.5h^2\sigma_p^2)}$$

where,

Cg_i : is the additive genetic value of a cow i a daughter of sire g_s and dam g_d ;
 r : is a random number taken from normal distribution with 0 mean and variance 1;
 h^2 : is the heritability level ; and
 σ_p^2 : is the phenotypic variance.
 Mean Squared Error (MSE) is the criteria used to judge between different studied cases.

$$MSE = \sigma^2(b^R) + [E(b^R) - \beta]^2 ; \quad (\text{Neter } et \text{ al.}, 1985)$$

where

b^R is the observed value of the estimate; β is the true value of the parameter; and σ^2 is the variance of the estimate values.

The model was used to estimate heritability in different studied cases using MTDFREML program of Boldman *et al.* (1993), was

$$y = X\beta + Zu + e$$

where,

y : is an $n*1$ vector of observations of milk yield;
 β : is $k*1$ vector of overall mean;
 μ : is $r*1$ vector of random effects; and
 e : is a vector of random residual;

X and Z are appropriately dimensioned incidence matrices.

Single Trait Analysis:

The fixed model used to test significant differences, and to estimate means and corresponding standard errors (SE) of the different heritability and missing pedigree information levels was

$$Y_{ijk} = u + h_i^2 + m_j + (h^2 * m)_{ij} + e_{ijk}$$

where,

Y_{ijk} : is the estimate bias of k^{th} record in the i^{th} heritability level and j^{th} missing pedigree information level;
 μ : is the overall mean of bias estimates;
 h_i^2 : is the effect of heritability level ($i=1,2$ and 3);
 m_j : is the effect of missing pedigree information level ($j=1,2,3$ and 4);
 $(h^2*m)_{ij}$: is the effect of the interaction between i^{th} heritability level and j^{th} missing pedigree information level; and
 e_{ijk} : is the effect of random error.

The same model was used for MSE but with interaction omitted for the y here pertains to a whole replicate, i.e. there is no individual readings and the interaction term is actually used as error. Data of mean squared error was transformed to their square root equivalent to be suitable for testing hypothesis. SAS program (1998) was used to perform the statistical analysis.

Simulation of the Multiple Traits:

Observations were generated according to the genetic (G) and environmental (E) variance and covariance structure for two traits (milk production of the first (Milk1) and second (Milk2) lactations) from the study of Dkova and Olf (2001) as follows:

$$G = \begin{matrix} & \begin{matrix} \text{Milk1} & \text{Milk2} \end{matrix} \\ \begin{matrix} \text{Milk1} \\ \text{Milk2} \end{matrix} & \begin{pmatrix} 202956 & 216091 \\ 216091 & 275398 \end{pmatrix} \end{matrix} \quad \text{and} \quad E = \begin{matrix} & \begin{matrix} \text{Milk1} & \text{Milk2} \end{matrix} \\ \begin{matrix} \text{Milk1} \\ \text{Milk2} \end{matrix} & \begin{pmatrix} 468931 & 183786 \\ 183786 & 692353 \end{pmatrix} \end{matrix}$$

where G and E are the genetic and environmental variances covariances matrices, respectively.

Twenty samples, each of 100 vectors of the order 2, representing sires, were sampled from the genetic structure assumed. Each sire produced 100 daughters (d) according to the following equation:

$$G_{di} = 0.5G_{si} + 0.5r_i\sigma_{ai} + r_i'\sqrt{0.5\sigma_{ai}^2} \quad (\text{Elsayed, 1997}),$$

where,

r_i and r_j are random numbers from normal distribution with 0 mean and variance equal to 1, and

σ_{ai}^2 is animal genetic variance of trait (i).

From the previous environmental variance covariance matrix another 10000 vectors were simulated. The phenotypic values of each daughter for the two simulated traits were the sum of their genetic and environmental values. Each sample of the twenty samples contained cow, sire and dam identification and the two traits of interest Milk1 and Milk2. Only, one level of heritability was simulated for each trait, which was the real heritability (0.3 for Milk1 and 0.28 for Milk2). Also, one level of genetic correlation was studied (0.91, the real genetic correlation between the two traits). Four levels of m were simulated for each sample of the twentieth (complete, 10%, 30% and 50% missing sire pedigree).

Multiple Traits Aanalysis

Multiple traits animal model program (MTDFREML) proposed by Boldman *et al.* (1993) was used to estimate the heritability for Milk1 and Milk2 and to estimate the genetic correlation between the two traits. Each sample was analyzed four times each with one level of missing sire pedigree information.

The following model was used in the analysis:

$$y = c + z_a a + e$$

where,

y: is the vector of observations of Milk1 and Milk2,

c: is the vector of overall mean,

z_a : is the incidence matrix for random effects,

a: is the vector of direct genetic effects of cow and

e: is a vector of random errors normally and independently distributed with zero mean and variance σ_e^2 .

Estimates of h^2 and genetic correlations between Milk1 and Milk2 obtained from the analysis of each sample were subtracted from their corresponding parametric values used in the simulation procedure to obtain the bias. Also, MSE was used to compare between the different studied cases.

To obtain least squares means (LSMEANS) and standard errors (SE) of the estimates and to study the effect of levels of missing sire pedigree informations, SAS (1998) was used in this analysis according to the model:

$$Y_{ij} = \mu + m_i + e_{ij}$$

where,

Y_{ij} : is the j^{th} estimate genetic correlation or bias of i^{th} level of missing pedigree;

μ : is the mean;

m_i : is the effect of level of missing pedigree information; and

e_{ij} : is the effect of random error associated with each observation assumed to be normally and independently distributed with 0 mean and variance σ_e^2 .

Type of Analysis

Estimates of h^2 for Milk1 resulting from single and multiple analyses for level of simulated $h^2 = 0.3$ and at the four simulated levels of missing pedigree information were considered to calculate bias and MSE for these estimates and to test the effect of type of analysis and missing pedigree information levels on h^2 , bias and MSE estimates according to the following model and using SAS (1998):

$$Y_{ijk} = \mu + m_i + t_j + (m * t)_{ij} + e_{ij}$$

where,

Y_{ijk} : is the k^{th} estimate of h^2 , bias or MSE of i^{th} level of missing pedigree and j^{th} level of type of analysis;

t_j : is the effect of level of type of analysis ($j=1$ and 2);

$(m * t)_{ij}$ is the effect of the interaction between i^{th} missing pedigree level and j^{th} type of analysis level; and the rest of the effects in the model defined as those in the previous model.

The term of interaction was omitted from the analysis of MSE (refer to the single trait analysis section).

RESULTS AND DISCUSSION

Least Squares Means (LSMEANS) Estimates of Bias and Mean Squared Error for Milk1(single trait analysis)

Table 1 shows estimates of bias and MSE least squares means (LSMEANS) and their corresponding standard errors for the three levels of heritability and the four levels of missing pedigree information. Means of bias increased as the level of missing pedigree information increased from complete to 30%, then decreased at level of 50% (Table 1). Schenkel and Schaeffer (2000) summarized that randomly missing pedigree information (15%) caused slightly upward bias in the random mating data set. These authors also explained that part of σ_a^2 was retained by the

fixed effect solutions. In the random mating and with using random model (as in the present study), bias of σ_a^2 was smaller and positive. Weigel and Lin (2004) indicated that incomplete pedigree for service sires can lead to unexpected results. Results of analysis of variance indicated that the effect of level of missing pedigree information was not significant ($P>0.05$), whereas the effect of heritability levels was significant ($P<0.05$) on the estimates of bias. These results agree with Schenkel and Schaeffer (2000) that missing pedigree information levels did not cause biased estimates of variance components in random mating population (the case studied here). Also, Reverter and Kaiser (1997) reported that additional generations to the pedigree might not greatly enhance accuracy of genetic evaluation. The effect of interaction between levels of missing pedigree information and levels of simulated h^2 was not significant ($P>0.05$). The smallest bias (0.0147,0.0073) was observed in the case of complete pedigree and $h^2=0.1$, respectively (Table 1). The previous result was in agreement with Thomas *et al.* (2000) and Ahmed (2004) who reported that bias decreased with decreasing simulated heritability. Figure 1 showed the h^2 levels * m levels interaction for the bias estimates.

Table 1. Least squares means (LSMEANS) \pm standard error (SE) for bias and MSE estimates of Milk1

Factor	Bias	MSE
	Mean \pm SE	Mean \pm SE
μ	0.018 \pm 0.00034	0.0033 \pm 0.0013
Level of missing pedigree information	N.S.	S
Complete	0.0147 \pm 0.0068	0.0452 \pm 0.0027
10%	0.0153 \pm 0.0068	0.0441 \pm 0.0027
30%	0.0233 \pm 0.0068	0.0549 \pm 0.0027
50%	0.0187 \pm 0.0068	0.0607 \pm 0.0027
Level of heritability	S	S
0.10	0.0073 \pm 0.0059	0.0221 \pm 0.0023
0.30	0.0083 \pm 0.0059	0.0485 \pm 0.0023
0.50	0.0358 \pm 0.0059	0.0831 \pm 0.0023

MSE = Mean squared error

N.S. =Not significant($p>0.05$)

S. =Significant($p<0.05$)

Table 1 shows that MSE decreased as level of missing pedigree information decreased. The smallest value of MSE (0.0441) was observed at 10% of missing pedigree. This estimate was not significantly ($P>0.05$) different from the estimate of complete case (0.0452). The greatest value of MSE was observed at 50% of missing pedigree (0.0607) which was different from ($P<0.05$) the complete case and 10% missing pedigree level. Schenkel and Schaeffer (2000) reported that, higher MSE was found in random mating than when selection was practiced for the random model data sets. Also, table 1 shows that MSE increased as the level of simulated h^2 increased from 0.1 to 0.5 (0.0221, 0.0485 and 0.0831, respectively). The effect of missing pedigree information and h^2 on the estimates of MSE was significant ($P<0.05$). These results agree with Baumung and Slkner (2002) who indicated that most measures for genetic variability are very sensitive to completeness of pedigree

information. Also, Cassel (1999) summarized that complete, accurate pedigree data for cows to be mated and sires used as mates will be a necessary part of such mating decision.

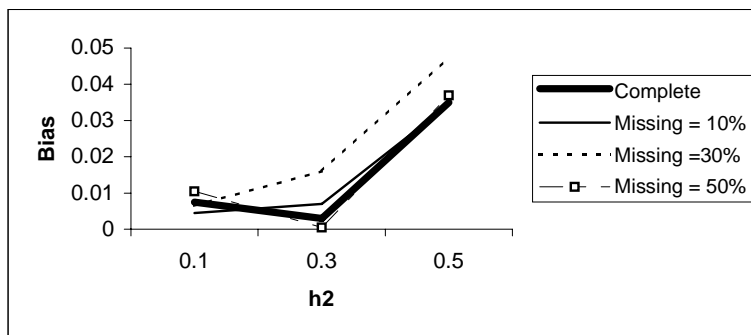


Fig. 1. Bias estimates of different levels of h^2 at each level of missing pedigree (m) for Milk1.

The previous results of MSE confirm that the best estimate of h^2 could be obtained from the smallest amount of missing pedigree information and for the smallest level of simulated h^2 . Under the circumstances of this study, up to 10% of missing sire pedigree caused no significant effect on the accuracy of estimating h^2 .

Fig. 2 shows that, as h^2 increased at any level of missing pedigree, the MSE increased. Also it could be concluded that the worst case was observed at $m=50\%$ and $h^2=0.5$ and that the trait with high heritability is more affected by the incomplete pedigree.

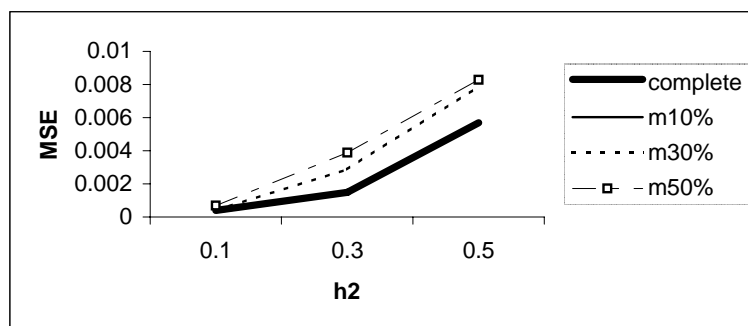


Fig. 2. MSE estimates of different levels of h^2 at each level of missing pedigree (m) for Milk1

Least Squares Means (LSMEANS) Estimates of Bias and Mean Squared Error for Milk1 and Milk2 (multiple traits analysis)

Table 2 shows estimates of bias and MSE least squares means (LSMEANS) and their corresponding SE for the four levels of missing pedigree information at $h_1^2 = 0.3$ and $h_2^2 = 0.28$ and $gc = 0.91$. All levels of missing pedigree information caused a negative bias. The least of bias was at complete pedigree information level (-0.0190 and -0.0035) for the two studied traits, respectively, whereas the greatest was at level 10% missing of pedigree information (-0.0295 and -0.0165) for the two traits, respectively. The analysis of variance of bias estimates indicated that the effect of missing pedigree information was not significant ($p > 0.05$). These results agree with Schenkel and Schaeffer (2000). The previous authors concluded that missing pedigree information did not cause biased estimates in random mating population. Fig. 3 shows the previous results.

Table 2 and Figure 4 show that MSE of the two traits decreased as the level of missing pedigree information decreased. The least MSE of the two studied traits were observed at complete pedigree information (0.0019 and 0.0014, respectively). The highest estimate were at 50% level of missing pedigree information (0.0028 and 0.0025, respectively). This result agrees with those of Baumung and Silkner (2002) and Cassel (1999). These authors indicated the importance of completeness of pedigree information for measuring genetic variability. These results of bias and MSE are compatible with those of the analysis of single trait discussed earlier.

Least Squares Means (LSMEANS) of Genetic Correlation, Bias and MSE Obtained From Multiple Traits Analyses

Table 3 shows LSMEANS of genetic correlation, bias and MSE of estimated genetic correlation for the different levels of missing pedigree information. The estimates indicated that the least estimate of bias was at 50% level of missing pedigree information. The greatest one was at complete pedigree information. The indicated biases could be attributed to missing pedigree information (Zwald *et al.*, 2003) and to the sample simulation process. The smallest MSE of genetic correlation was at 10% level of missing pedigree and the greatest one was at 50% level of missing pedigree.

Table 2. Least squares means (LSMEANS) \pm standard error (SE) for bias and mean squared error (MSE) of h^2 estimates of the two studied traits

Factor	Bias \pm SE		MSE \pm SE	
	Milk1	Milk2	Milk1	Milk2
μ	0.0243 \pm 0.0047	-0.0105 \pm 0.0047	0.0024 \pm 0.0002	0.0019 \pm 0.0002
Level of missing pedigree information	N.S.		N.S.	
Complete	-0.0190 \pm 0.0094	-0.0035 \pm 0.0093	0.0019	0.0014
10%	-0.0295 \pm 0.0094	-0.0165 \pm 0.0093	0.0022	0.0016
30%	-0.0255 \pm 0.0094	-0.0140 \pm 0.0093	0.0026	0.0020
50%	-0.0230 \pm 0.0094	-0.0080 \pm 0.0093	0.0028	0.0025

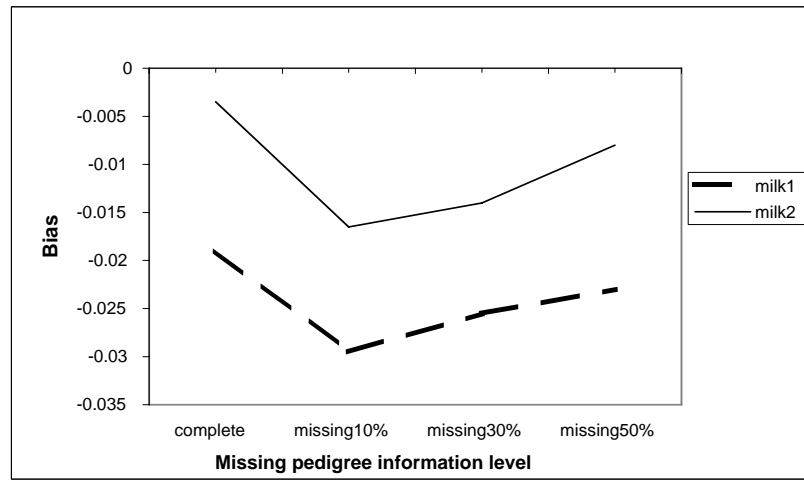


Fig.3. Bias estimates of different levels of missing pedigree information for Milk1 and Milk2

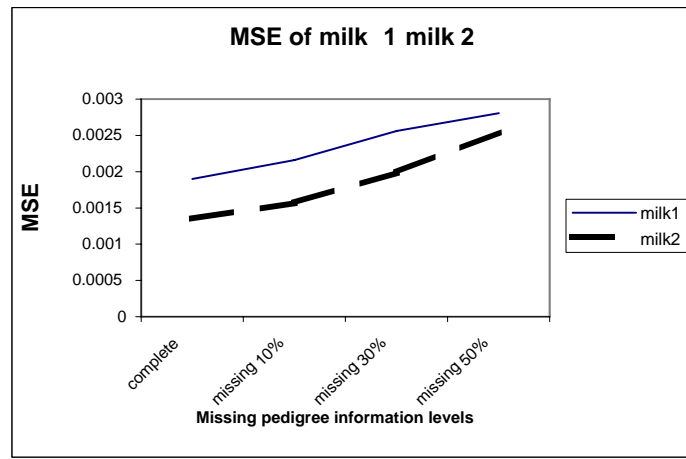


Fig. 4. Mean squared error estimates of different levels of missing pedigree information for Milk1 and Milk2

Table 3. Least squares means (LSMEANS) \pm standard error (SE) for estimates of genetic correlation, bias and mean squared error (MSE) of the genetic correlation between Milk1 and Milk2

Factor	Estimate \pm SE	Bias \pm SE	MSE \pm SE
μ	0.9116 \pm 0.0210	0.0016 \pm 0.0029	0.0008 \pm 0.0001
Level of missing pedigree information	N.S.	N.S.	
Complete			
10%	0.9180 \pm 0.0419	0.0180 \pm 0.0005	0.0009
30%	0.9145 \pm 0.0419	0.0145 \pm 0.0005	0.0007
50%	0.9095 \pm 0.0419	0.0095 \pm 0.0005	0.0008
	0.9045 \pm 0.0419	0.0045 \pm 0.0005	0.0011

Least Squares Means (LSMEANS) of h^2 , Bias and MSE for Milk1 obtained From Single and Multiple Traits Analyses

Table (4) shows LSMEANS \pm SE for the estimates of h^2 , bias and MSE of MILK1 resulting from single and multiple traits analyses, at the true level of h^2 (0.3). The results indicate that level of missing information had no significant effect ($P < 0.05$) on h^2 , bias or MSE estimates. The bias estimates of single and multiple traits analyses lead to unexpected result, where, the bias magnitude of single analysis was significantly lower than the bias of multiple trait analysis. The effect of type of analysis was significant on bias estimates and was not significant on the MSE estimates (0.05).

The two estimates of MSE were almost the same (0.0025, 0.0024). So that, in the case of missing pedigree, the change from single to multiple analysis does not enhance the accuracy of h^2 estimate under the circumstances of this study.

Table 4. Least squares means \pm SE for estimates of h^2 , bias and mean squared error (MSE) of simulated trait (Milk1) at $h^2 = 0.3$

μ	LSMEANS \pm SE		
	h^2	Bias	MSE
Level of missing pedigree information	NS	NS	NS
Complete	0.2913 \pm 0.0072	-0.0088 \pm 0.0072	0.0017 \pm 0.0044
10%	0.2888 \pm 0.0072	-0.0113 \pm 0.0072	0.0018 \pm 0.0044
30%	0.2953 \pm 0.0072	-0.0048 \pm 0.0072	0.0028 \pm 0.0044
50%	0.2928 \pm 0.0072	-0.0073 \pm 0.0072	0.0034 \pm 0.0044
Type of analysis	S	S	NS
Single trait Analysis	0.3083 \pm 0.0051	0.0083 \pm 0.0051	0.0025 \pm 0.0031
Multiple trait analysis	0.2758 \pm 0.0051	-0.0243 \pm 0.0051	0.0024 \pm 0.0031

CONCLUSION

For single trait analysis, in random mating, missing pedigree information does not cause biased estimates of heritability. Low heritability (0.1) and low amount of

missing pedigree information yielded the most accurate estimate of heritability as it had the smallest MSE. Under the circumstances of this study, up to 10% of missing sire pedigree caused no significant effect on the accuracy of estimating h^2 . As h^2 increases the effect of missing pedigree information becomes worse (trait with high heritability is more affected by incomplete pedigree) as indicated from the results of MSE.

However in the case of multiple traits analysis (under the circumstances of this study) as the amount of missing sires pedigree information increases, the estimates of MSE (accuracy) of heritability and genetic correlation decrease. The type of analysis (single or multiple) affected bias of h^2 estimates but it does not affect the accuracy of these estimates significantly.

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تأثير مستويات مختلفة من معلومات سجل النسب ومن المكافئ الوراثي علي جودة تقديرات المعالم الوراثية

منال السيد

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في هذه الدراسة تم عمل محاكاة لصفتي انتاج اللبن في أول وثاني موسم (Milk1, Milk2) بالكيلو جرام وقد كانت التباينات الوراثية والتغاير الوراثي بينهما كالتالي: 659202 ، 893572 ، 190612 أما التباينات البيئية والتغاير البيئي فكانت كالتالي: 139864 ، 153296 ، 687381 علي التوالي. مع العلم بأن المكافئات الوراثية للصفتين والارتباط الوراثي بينهما فكانت كالتالي: 0.3 ، 0.28 ، 0.91 علي التوالي. درست أربعة مستويات من الفقد في سجل نسب الطلوقة (m) (سجلات كاملة ، 10% فقد ، 30% فقد ، 50% فقد في سجل الطلوقة). بالنسبة للصفة الأولى (Milk1) فقد درست علي أساس نوعين من التحليل (t) وهما تحليل الصفة منفردة وتحليلها مع الصفة الأخرى (Milk2). في حالة دراسة الصفة منفردة فان مكونات التباين الحقيقية للصفة عدلت بحيث حوكت ثلاثة مستويات من المكافئ الوراثي وهي 0.1 ، 0.3 ، 0.5 .

درست عشرون عينة لكل من 12 توليفة من المكافئ الوراثي(3) – الفقد في سجل الطلوقة(4) وذلك للصفة الأولى فقط. أيضا درست عشرون عينة في حالة تحليل الصفة الأولى مع الصفة الثانية ولكن في مستوي واحد من المكافئ الوراثي (0.3) ومع وجود الأربعة مستويات من الفقد في سجل الطلوقة. في جميع هذه العينات كان يتم تقدير المكافئ الوراثي والارتباط الوراثي وقد استخدم الانحراف عن القيمة الحقيقية (bias) ومتوسط الخطأ مربعا (MSE) للحكم علي دقة التقديرات في كل حالة مدروسة.

استهدفت هذه الدراسة بدراسة تأثير مستويات المكافئ الوراثي المدروسة ومستويات الفقد في سجل الطلوقة علي التقديرات المختلفة للـ MSE ، bias ، كما اهتمت بدراسة تأثير نوع التحليل ومستويات الفقد علي تقديرات المكافئ الوراثي والارتباط الوراثي والانحراف ومتوسط الخطأ مربعا للصفة الأولى والثانية وعند مستوي واحد من المكافئ الوراثي (0.3، 0.28) للصفتين علي التوالي. استخدم برنامج MTDFREML لتقدير المكافئ الوراثي والارتباط الوراثي في الحالات المدروسة.

وقد لوحظ أنه في حالة تحليل الصفة الأولى منفردة فان أصغر قيمة لـ MSE (0.1220) كانت عند مكافئ وراثي يساوي 0.1 ونسبة فقد تساوي 10% وكانت (0.0441). ووجد أنه كلما زاد مستوي المكافئ الوراثي فان كلا من MSE ، bias ، تزيد بشكل معنوي ($p < 0.05$). مستويات الفقد في سجل الطلوقة كان تأثيرها غير معنوي ($p > 0.05$) علي قيم الانحراف bias ، ولكنه كان معنويا ($p < 0.05$) علي قيم الـ MSE حيث كانت هذه القيم تزيد بشكل عام مع زيادة m .

أما بالنسبة للارتباط الوراثي فان أدق قيمة لوحظت في حالة مستوي فقد يساوي 10% وأسوأ قيمة كانت في حالة 50% . كان تأثير m غير معنوي ($p > 0.05$) علي تقديرات المكافئ الوراثي والانحراف ومتوسط الخطأ مربعا بينما كان نوع التحليل معنويا ($p < 0.05$) علي كل من تقديرات المكافئ الوراثي والانحراف.

بينت هذه الدراسة من نتائج تحليل الصفة الأولى منفردة أن الصفة ذات المكافئ الوراثي المنخفض (0.1) وكمية الفقد المنخفضة (10%) تعطي أدق التقديرات للمكافئ الوراثي. بينما نتائج تحليل نفس الصفة (Milk1) مع الصفة الأخرى (Milk2) توضح أنه كلما زادت كمية الفقد في سجل الطلوق فإن تقديرات المكافئ الوراثي والارتباط الوراثي تصبح أبعد عن القيمة الحقيقية. أما بالنسبة لنوع التحليل فقد أعطي تأثير معنوي ($p < 0.05$) علي تقديرات المكافئ الوراثي والانحراف ولكن لم تؤثر بشكل معنوي علي تقديرات متوسط الخطأ مربعا تحت ظروف هذه الدراسة.