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QUALITY OF VARIANCE COMPONENTS ESTIMATED BY GIBBS SAMPLING IN POPULATIONS WITH AND WITHOUT SELECTION AND VARYING HERITABILITY

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SUMMARY

Ten replicates were generated for each 30 combination of generation (5 generations) heritability levels (3 levels), type of mating (random mating and selective mating).

GS, REML and MIVQUE were used to calculate the variance components (VC) and heritabilies. The trait considered was lamb weaning weight with total phenotypic variance of 14.00 kg.^{2} .The real variance components were modified to simulate three levels of heritability (0.1, 0.3 and 0.5). Data were analyzed to compare the quality of GS estimator with those of REML and MIVQUE according to the mean squared error (MSE) of the estimates of these estimators.

The effects of heritability levels, generation number (1 to 5), selection (random mating and selective mating), method of analysis and all 2-way interactions on the estimates of variance components were examined. In the case of continuous variable (weaning weight), it could be concluded that in MIVQUE mean estimates appeared to overestimate of residual variance σ_e^2 for all three levels of heritability under selection or no selection and underestimate heritabilities in the case of h^2 =0.3 and 0.5 under selection or no selection.

*Estimates of VC and heritabilities by GS were closer to the real values of parameters than those by REML and MIVQUE. There were significant differences ($p<0.05$) between the mean estimates of heritabilities within heritabilities levels, generation number, type of mating and within method of analysis. All the 2-way interaction showed significant differences ($p<0.05$) except the term generation *method of analysis and generation * levels of heritability interactions ($p>0.05$).*

REML and GS estimates were not affected by selection but those by MIVQUE method were. Overall, under random mating, the GS and REML estimates seemed to be similar for continuous variable (weaning weight), especially at higher heritability. The GS had consistently smaller MSE than REML and MIVQUE due to the influence of the prior distribution of the variance component on the posterior distribution.

GS was a more suitable method in most cases and especially for the case of low heritability than REML and MIVQUE as it yielded estimates with smaller MSEs.

Keywords: *Gibbs sampling, MIVQUE, REML, Mean squared error, Monte-Carlo simulation procedure, continuous variable, variance component, and heritability.*
Abbreviation key: GS =Gibbs Sampling, REML= Restricted Maximum Likelihood, MIVQUE= Minimum Variance Quadratic Unbiased Estimator, MSE= Mean squared Error

INTRODUCTION

Estimation of variance components (VC) has long been an important aspect of animal breeding. Mean squared error for variance component increases as estimated values move away from the true values. Accurate estimates of variance components are important for genetic parameter estimation (Henderson, 1975; Schaeffer, 1984).

Computer simulation of genetic systems attempts to use knowledge of gene action along with modern computers to model actual systems. Simulation and theoretical results have been main tools in evaluating the impact of selection in most domestic species. The most common type of selection, as it relates to variance component estimation and genetic prediction, is the selection of animals to be parents. When data have been selected, there are concerns about the quality of parameter estimates and predicted genetic values.

The current method of choice for estimating VC is restricted maximum likelihood (REML) (Meyer, 1990). But, computational limitations have restricted the size of the data sets that can be considered for variance component estimation. However, VC estimation is now facilitated by many protocols provided with using derivative-free algorithms (Smith and Graser, 1986;), the use of sparse matrix techniques (Misztal and Perez-Enciso, 1993), or both (Boldman and Van Vleck, 1991; Boldman et al., 1993).

However, Gibbs Sampling (GS) is useful in that it yields direct and exact estimates of variance components and breeding values, and is suitable to run on microcomputers and workstations because the relatively little information it needs to be kept in memory (Schaeffer and Kennedy, 1986). GS is based on Bayesian variance component estimation method. The main objective of this study was to compare the quality of variance-component GS estimators compared with those of the restricted maximum likelihood and minimum variance quadratic unbiased estimation especially when selection is applied with different levels of heritabilities and different number of generation in the continuous trait of weaning weight trait.

MATERIALS AND METHODS

Material

Data used in the animal model were generated using a Monte Carlo simulation procedure. This simulation method generated five generations of animals. The first generation (base population) consisted of 100 sires; each mated to 10 females to produce 2 progenies from each mating (one male and one female). The first generation was sampled from a conceptually infinite population of unrelated animals (Mousa, 1989). Both additive genetic and residual effects were distributed normally, and covariances among base additive genetic and residual effect were all null. For generations after the first, a fraction of the males was chosen as sires of the next

generation (250 sires), and each sire was mated to 4 females assigned randomly to the sires once the sires were chosen. Each female was mated only once. The mode for choosing the sires was varied, once at random and once phenotypically selected. The real variance components were modified to simulate three levels of heritability, 0.1, 0.3 and 0.5. The trait considered was lamb weaning weight with a total phenotypic variance of σ_p^2 assumed to be 14.00 kg^2 in the base generation according to estimates from local Egyptian sheep data on the Ossimi breed (Mousa, 1989). Base generation additive genetic variance σ_a^2 levels were 1.4 kg^2, 4.20 kg^2 and 7.0 kg^2 and residual variance σ_e^2 levels were 12.6 kg^2, 9.8 kg^2 and 7.0 kg^2 for heritabilities of 0.1, 0.3 and 0.5, respectively. Ten replicates were generated for each of 30 combinations of generation (5 generations), heritability level (3 levels) and type of mating (random mating and selective mating). The simulated formula (Analla *et al.*, 1995) was used.

$$g_i = 0.5(g_s + g_d) + x * sqrt(0.5h^2\sigma_p^2)$$

Where,

g_i is the additive genetic values of an individual i a progeney of sire (g_s) and dam (g_d);

X is a random number taken from normal distribution with mean 0 and variance 1;

h^2 is the heritability; and

σ_p^2 is the phenotypic variance.

The bias (the deviation of observed estimate from the true parameter) in h^2, σ_a^2 and σ_e^2 was calculated. Also, the variances of estimates obtained were calculated. Mean squared error (MSE), calculated as the sum of the bias squared plus the variance of the estimated values, was used as the measure for comparing methods of estimation (GS, REML and MIVQUE), i.e.

$$MSE = E(b^r - \beta)^2 = \sigma^2(b^R) + [E(b^R) - \beta]^2$$ (Neter *et 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.

Methods

The usual mixed linear model with one random effect was employed to analyze the simulated data. The form of the model used was:

Y = XB + Zu + e, where Y is an nx1 vector of observations of weaning weight, B is kx1 vector of fixed effects, treated in the Bayesian setting as a vector of random effect with a flat prior distribution representing no prior knowledge about the values, u is an rx1 vector of random effects, e is an nx1 vector of random residual, X, Z, are appropriately dimensioned incidence matrices. In this situation, the only fixed effect considered will be that of sex. REML, GS and MIVQUE [using SAS (1996)] programs were used to calculate variance components and heritability. The same data set was used for all methods of estimation.

RESULT AND DISCUSSION

1-Mean Estimates of Variance Components

1.1 Effect of Selection

Means of estimates of heritabilities and variance components for all three methods REML, GS and MIVQUE with empirical standard errors under random mating are given in Table 1 and in Table 2 under selective mating. The MIVQUE mean estimates appear to underestimate of heritabilities in the case of $h^2 = 0.3$ and $h^2 = 0.5$ (Table 1) but the underestimation due to consistently higher σ_a^2 and σ_e^2 that was higher than its true values. The remaining estimators appeared to be relatively less unbiased, but, in general the estimates of VC by GS is closer to the real parameters than the REML.

The MIVQUE mean estimates appear to underestimate variance components in the case of $h^2=0.5$ and $h^2=0.3$ (table 2). The trends are similar to those under random mating. The remaining estimators appeared to be relatively less unbiased. So, non-of REML and GS estimators seemed to be superior based on the mean estimates.

Table 3 shows the least squares means of heritablity eatimates of the main studied factors (levels of h^2, generation, selection and method of analysis). There were observed differences between GIBBS and each of REML and MIVQUE in estimating heritability in the case of $h^2 = 0.1$ (Figure 1b). In contrast, there was no observed difference between REML and MIVQUE at the same level of heritability $h^2 = 0.1$. There were no differences in heritability estimates in generations 1 and 2 between select and random mating populations ($p>0.05$) , but starting from generation 3 that difference rose up to a peak in generation 4 ($p< 0.05$) (figure 1c). This may be due to that the responds to selection became less than first generation. It is possible more than 5 generations may be needed to investigate the effect of interaction. Figure 1d shows the differences between all methods of analysis and type of mating.

Although, GS gave consistently higher heritability estimates, the differences between these and these by REML were similar under selection or no selection (figure 1d). But the differences between estimates of REML and GS on one hand and those of MIVQUE on the other hand were smaller under selection than the no selection scenario. This is because both of REML and GS procedures are corrected for effect of selection on the additive genetic, thus described as most suitable methods to estimate variance component in animal breeding data (Sorensen , 1996) and Van der werf *et al.* (1993)).

Table 1. Mean and empirical standard errors [1](SE) for estimates of heritabilities, additive genetic and residual variances under random mating

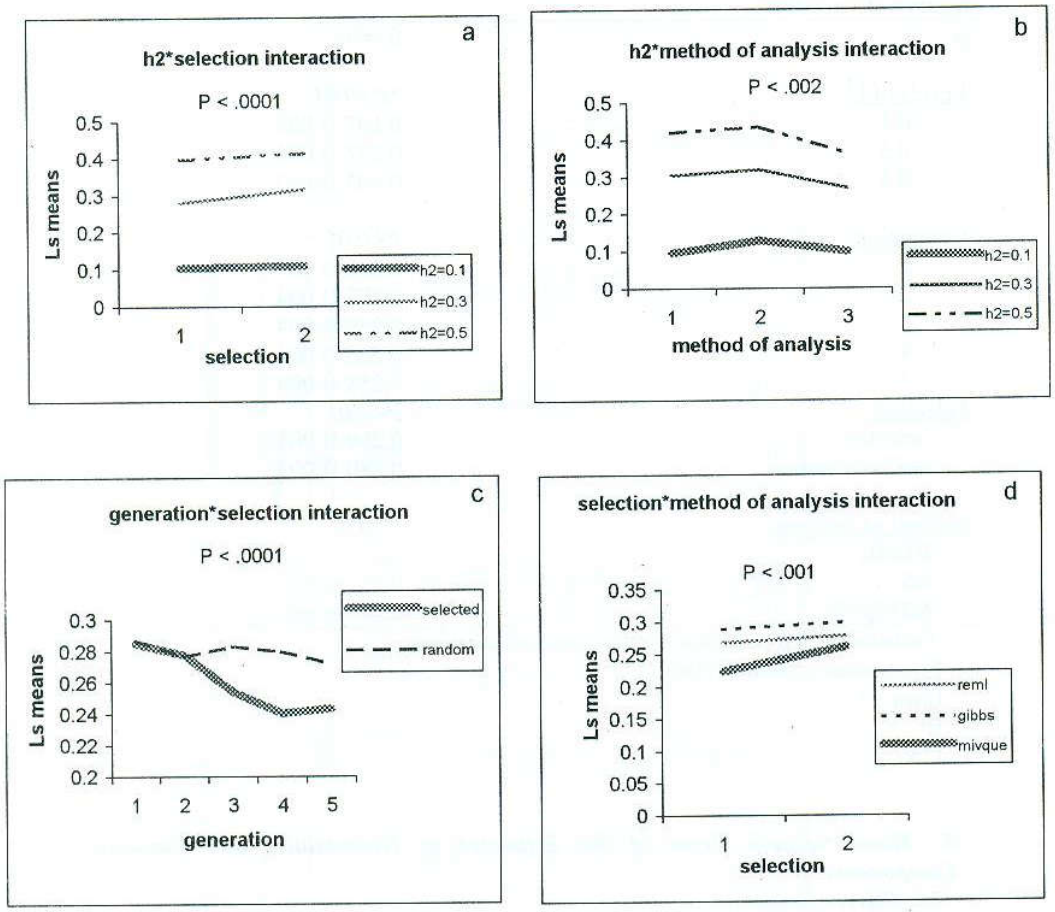
Parameter level	Generation	Mean ± SE								
		[3]REML			[4]GS			[5]MIVQUE		
		$\hat{h}^2$	[6]$\hat{\sigma}^2_a$	[7]$\hat{\sigma}^2_e$	$\hat{h}^2$	$\hat{\sigma}^2_a$	$\hat{\sigma}^2_e$	$\hat{h}^2$	$\hat{\sigma}^2_a$	$\hat{\sigma}^2_e$
	1	0.08±0.03	1.15±0.48	12.88±0.79	0.11±0.03	1.60±0.36	12.52±0.86	0.08±0.03	1.13±0.49	13.76±0.61
$\sigma^2a = 1.4$	2	0.09±0.05	1.22±0.64	12.74±0.66	0.12±0.03	1.68±0.71	12.34±0.57	0.09±0.04	1.40±0.71	13.62±0.42
$\sigma^2e = 12.6$	3	0.10±0.04	1.35±0.60	12.81±0.65	0.13±0.03	1.82±0.68	12.4±0.52	0.10±0.04	1.50±0.82	13.78±0.36
$h^2 = .1$	4	0.11±0.04	1.53±0.58	12.39±0.66	0.13±0.03	1.99±0.77	12.0±0.55	0.12±0.04	1.92±0.77	13.57±0.46
	5	0.10±0.04	1.19±0.60	12.74±0.59	0.14±0.03	1.69±0.81	12.3±0.51	0.10±0.05	1.48±0.81	13.57±0.37
	1	0.31±0.07	4.41±1.12	9.80±0.69	0.32±0.07	4.72±1.13	9.59±0.69	0.27±0.06	4.82±1.49	13.04±0.37
$\sigma^2a = 4.2$	2	0.29±0.03	3.98±0.40	9.93±0.47	0.29±0.02	4.11±0.37	9.84±0.40	0.25±0.04	4.28±0.78	12.83±0.46
$\sigma^2e = 9.8$	3	0.29±0.06	4.06±0.92	9.92±0.73	0.31±0.06	4.31±0.91	9.74±0.71	0.25±0.04	4.35±0.90	12.88±0.26
$h^2 = 0.3$	4	0.25±0.07	3.47±1.05	10.04±0.75	0.27±0.06	3.69±0.94	9.88±0.66	0.22±0.06	3.30±1.33	12.58±0.39
	5	0.29±0.06	3.99±0.84	09.72±0.73	0.33±0.10	4.22±0.90	9.55±0.78	0.25±0.06	4.37±1.31	12.61±0.55
	1	0.50±0.06	7.14±0.88	09.72±0.73	0.52±0.06	7.40±0.88	6.93±0.74	0.38±0.03	7.40±0.93	12.27±0.27
$\sigma^2a = 7$	2	0.49±0.04	6.70±0.59	07.04±0.73	0.49±0.04	6.90±0.58	6.91±0.42	0.39±0.04	7.59±1.22	11.84±0.40
$\sigma^2e = 7$	3	0.40±0.03	5.40±0.57	07.99±0.73	0.42±0.03	5.60±0.54	7.85±0.47	0.31±0.05	5.34±1.02	12.01±0.49
$h^2 = 0.5$	4	0.38±0.07	4.96±0.99	08.57±0.72	0.38±0.07	5.17±1.10	8.43±0.77	0.30±0.09	5.15±0.74	12.22±0.28
	5	0.37±0.06	4.92±0.06	08.51±0.73	0.38±0.06	5.11±0.97	8.37±0.75	0.27±0.05	4.66±1.06	12.21±0.48

[1]SE : Standard error, [2]h^2 : heritability; [3]REML : Restricted Maximum Likelihood; [4]GS : Gibbs Sampling , [5]MIVQUE : Minimum Variance Quadratic Estimation; [6]σ^2a : Additive genetic variance ; [7]σ^2e : residual variance.

Table 2. Mean and empirical standard errors [1](SE) for estimates of heritabilities, genetic variances and residual variances under selective mating

Parameter level	Generation	Mean ± SE								
		[3]REML			[4]GS			[5]MIVQUE		
		$\hat{h}^2$	$^{6}\hat{\sigma}^2_a$	$^{7}\hat{\sigma}^2_e$	$\hat{h}^2$	$\hat{\sigma}^2_a$	$\hat{\sigma}^2_e$	$\hat{h}^2$	$\hat{\sigma}^2_a$	$\hat{\sigma}^2_e$
$\sigma^2a = 1.4$	1	0.08±0.03	1.15±0.48	12.88±0.80	0.11±0.03	1.60±0.36	12.52±0.86	0.08±0.03	1.13±0.49	13.75±0.64
$\sigma^2e = 12.6$	2	0.11±0.05	1.47±0.72	12.44±0.77	0.13±0.04	1.88±0.80	12.1 ±0.62	0.11±0.05	1.70±0.80	13.49±0.37
$h^2 = .1$	3	0.1 ±0.03	1.39±0.45	12.29±0.49	0.13±0.03	1.82±0.49	11.89±0.42	0.11±0.03	1.67±0.49	13.26±0.24
	4	0.11±0.04	1.57±0.51	12.41±0.55	0.14±0.03	2.01±0.68	12.04±0.49	0.10±0.04	1.57±0.68	13.59±0.33
	5	0.1 ±0.04	1.34±0.59	12.92±0.75	0.13±0.03	1.84±0.36	12.50±0.55	0.10±0.04	1.57±0.62	13.87±0.43
$\sigma^2a = 4.2$	1	0.31±0.07	4.41±1.12	9.80±0.69	0.33±0.07	4.72±1.13	9.59±0.69	0.27±0.06	4.82±1.49	13.04±0.38
$\sigma^2e = 9.8$	2	0.31±0.08	4.51±0.98	9.68±1.1	0.32±0.07	4.45±1.03	9.51±1.04	0.27±0.05	4.86±1.20	12.69±0.47
$h^2 = 0.3$	3	0.34±0.07	5.06±1.45	9.2±0.91	0.35±0.07	4.97±1.05	9.06±0.94	0.30±0.04	5.43±1.12	12.62±0.38
	4	0.33±0.07	4.70±1.15	9.46±0.85	0.34±0.07	4.92±1.14	9.30±0.84	0.31±0.05	5.69±1.26	12.75±0.54
	5	0.34±0.09	4.70±1.27	9.29±1.28	0.33±0.06	4.88±1.27	9.17±1.27	0.30±0.06	5.54±1.48	12.61±0.46
$\sigma^2a = 7$	1	0.50±0.06	7.14±0.88	6.95±0.78	0.52±0.06	7.40±0.88	6.93±0.74	0.38±0.05	7.40±0.93	11.89±0.47
$\sigma^2e = 7$	2	0.42±0.06	5.78±0.83	8.03±0.87	0.43±0.05	5.93±0.77	7.92±0.87	0.39±0.05	7.77±1.69	11.89±0.47
$h^2 = 0.5$	3	0.37±0.13	5.89±0.86	8.43±0.72	0.42±0.05	6.12±1.00	8.21±0.71	0.31±0.04	8.66±1.43	12.29±0.37
	4	0.39±0.07	5.48±1.10	8.54±0.83	0.40±0.07	5.64±0.82	8.92±0.86	0.30±0.05	8.02±1.52	12.12±0.40
	5	0.38±0.05	5.22±0.81	8.53±0.62	0.39±0.05	5.36±1.13	8.44±0.66	0.39±0.04	7.76±1.20	11.92±0.34

[1]SE: Standard error, [2]h^2 : heritability; [3]REML : Restricted Maximum Likelihood; [4]GS : Gibbs Sampling , [5]MIVQUE : Minimum Variance Quadratic Estimation; [6]σ^2a : Additive genetic variance ; [7]σ^2e : residual variance.



*P probability of type I error

Fig. 1. Effect of significance 2-way interaction on h2 least squares means

Table 3. Source of variation and LsMean±SE of heritabilities

Source of variation	
μ	0.2699
Levels of h^2:	**P<0.01*
0.1	0.107 0.003
0.3	0.297 0.003
0.5	0.405 0.003
Generation:	*P<0.01*
1	0.286 0.004
2	0.277 0.004
3	0.269 0.004
4	0.260 0.004
5	0.258 0.004
Selection:	*P<0.01*
Selective	0.260 0.003
Random mating	0.280 0.003
Method of analysis:	*P<0.01*
REML	0.273 0.003
GS	0.293 0.003
MIVQUE	0.243 0.003

* Probability of type I error for the source of variation
Error means square = 0.003
Error d.f
R^2 = 0.856
C.V. = 20.0%

2- Mean Squared Error of the Estimates of Heritabilities and Variance Components

2.1. Effect of selection

Mean squared errors (MSE) of estimates of VC for all three procedures (REML, GS and MIVQUE) are presented in Table 4 for random mating and Table 5 for selective mating. MSEs for GS and REML estimates were smaller than those for MIVQUE.

Table 4. Mean squared errors ([1]MSE) for heritabilities, genetic and residual variances under random mating

Parameter level	Generation	Mean ± SE								
		[3]REML			[4]GS			[5]MIVQUE		
		$\hat{h}^2$	[6]$\hat{\sigma}^2_a$	[7]$\hat{\sigma}^2_e$	$\hat{h}^2$	$\hat{\sigma}^2_a$	$\hat{\sigma}^2_e$	$\hat{h}^2$	$\hat{\sigma}^2_a$	$\hat{\sigma}^2_e$
	1	0.001	0.29	0.71	0.001	0.17	0.47	0.002	0.17	1.74
$\sigma^2a = 1.4$	2	0.002	0.43	0.46	0.002	0.34	0.4	0.002	0.34	1.21
$\sigma^2e = 12.6$	3	0.002	0.36	0.46	0.002	0.35	0.31	0.002	0.35	1.52
$h^2 = .1$	4	0.002	0.35	0.48	0.003	0.52	0.66	0.003	0.52	0.84
	5	0.002	0.40	0.37	0.001	0.27	0.34	0.002	0.27	1.14
	1	0.005	1.29	0.48	0.005	1.54	0.52	0.005	1.54	10.61
$\sigma^2a = 4.2$	2	0.001	0.21	0.24	0.001	0.14	0.17	0.004	0.14	9.41
$\sigma^2e = 9.8$	3	0.004	0.87	0.54	0.004	0.85	0.51	0.004	0.85	9.56
$h^2 = 0.3$	4	0.007	1.63	0.62	0.005	1.15	0.44	0.010	1.15	7.9
	5	0.003	0.75	0.54	0.010	0.81	0.67	0.005	0.81	8.2
	1	0.003	0.8	0.62	0.004	0.94	0.56	0.017	0.94	27.85
$\sigma^2a = 7$	2	0.001	0.44	0.21	0.001	0.35	0.19	0.014	0.35	23.57
$\sigma^2e = 7$	3	0.010	2.9	1.19	0.008	2.25	0.94	0.040	2.25	25.34
$h^2 = 0.5$	4	0.022	5.14	3.0	0.019	4.34	0.64	0.043	4.34	27.35
	5	0.021	5.01	2.81	0.018	4.21	0.43	0.054	4.21	27.34

[1]MSE : Mean squared error; [2]h^2 : heritability; [3]REML : Restricted Maximum Likelihood; [4]GS : Gibbs Sampling ,
[5]MIVQUE : Minimum Variance Quadratic Estimation ; [6]σ^2a : Additive genetic variance ; [7]σ^2e : residual variance.

Table 5. Mean squared errors for heritabilities, genetic variances and residual variances under selective mating

Parameter level	Generation	Mean ± SE								
		[3]REML			[4]GS			[5]MIVQUE		
		$\hat{h}^2$	$^{6}\hat{\sigma}_a^2$	$^{7}\hat{\sigma}_e^2$	$\hat{h}^2$	$\hat{\sigma}_a^2$	$\hat{\sigma}_e^2$	$\hat{h}^2$	$\hat{\sigma}_a^2$	$\hat{\sigma}_e^2$
$\sigma^2a = 1.4$	1	0.001	0.29	0.71	0.001	0.17	0.47	0.002	0.31	1.74
$\sigma^2e = 12.6$	2	0.002	0.52	0.46	0.001	0.22	0.40	0.002	0.72	1.21
$h^2 = .1$	3	0.001	0.21	0.46	0.009	0.19	0.31	0.002	0.32	1.52
	4	0.002	0.29	0.48	0.001	0.23	0.36	0.003	0.49	0.84
	5	0.002	0.35	0.37	0.001	0.31	0.34	0.002	0.42	1.14
$\sigma^2a = 4.2$	1	0.005	1.29	0.48	0.005	1.24	0.52	0.005	2.59	10.61
$\sigma^2e = 9.8$	2	0.006	1.05	1.23	0.006	1.12	1.17	0.004	1.88	8.54
$h^2 = 0.3$	3	0.007	2.84	1.20	0.006	1.71	1.04	0.002	2.78	8.09
	4	0.006	1.57	0.83	0.005	1.81	0.66	0.002	3.80	8.98
	5	0.010	1.87	1.91	0.005	1.08	1.02	0.004	3.97	8.11
$\sigma^2a = 7$	1	0.003	0.8	0.62	0.002	0.94	0.56	0.015	3.46	24.16
$\sigma^2e = 7$	2	0.010	2.19	1.82	0.008	1.74	1.57	0.015	3.46	24.16
$h^2 = 0.5$	3	0.033	1.99	2.57	0.009	1.56	1.99	0.010	4.81	28.10
	4	0.017	3.52	3.07	0.015	3.08	2.76	0.013	3.36	26.42
	5	0.017	3.75	2.72	0.015	3.32	2.50	0.013	2.02	24.31

[1]MSE : Mean squared error, [2]h^2 : heritability; [3]REML : Restricted Maximum Likelihood; [4]GS : Gibbs Sampling ,
[5]MIVQUE : Minimum Variance Quadratic Estimation , [6]σ^2a : Additive genetic variance ; [7]σ^2e : residual variance.

However, since the same data were used for all the methods of estimation, this will tends to cause similar pattern for each of the estimation methods.

Under selection GS estimator yielded more estimates with smaller MSEs in most cases than REML and MIVQUE estimators (Table 5). MIVQUE estimator had larger MSEs than GS and REML estimators (Table 5). These results agree with those observed in previous studies (Sorensen and Kennedy, 1984; Pieramati and Van Vleck, 1993).

2.2. Effect of Estimation Methods

Under random mating, the MSE tended to be smaller estimates for GS based estimators, especially for low heritability data. This is due, at least in part, to the impact of prior information used in GS estimates. These results agree with those observed in previous studies (Van Tassel, 1994). There was no consistent pattern in the differences in MSE when one up to five generations were applied. From these results, it appears that using .the prior information will improve VC estimate precision (based on MSE) over current methods.

The effect of the prior distribution magnified in this study may be because relatively small data sets (3250) animals in each population were used.

Under selective mating, the GS and REML mean estimates of VC were similar for different heritability levels, whereas the MIVQUE mean estimates were underestimated. The estimates of MSEs for GS were smaller than those by REML in most cases. The MSEs for MIVQUE estimates were greater than those by GS and REML estimates. These results agree with those reported by Van Tassel, 1994.

CONCLUSION

In the case of continuous variable (weaning weight), it could be concluded that MIVQUE mean estimates appear to underestimate of heritabilities in the case of h^2 =0.3 and 0.5 under selection and no selection and overestimate residual variances σ_e^2 for all three level of heritabilities under selection and no selection . Estimates of VC and heritability by GS were closer to their real respective values of parameters than REMl and MIVQUE.

Overall, under random mating, the investigated GS and REML estimates seemed to be similar for the continuous variable (weaning weight), especially at high heritability level. The GS had consistently smaller MSE than REML and MIVQUE due to the influence of the prior distribution of the variance component on the posterior distribution.

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جودة تقدير مكونات التباين فى العشائر باستخدام طريقة جبس فى وجود أو عدم وجود الانتخاب واختلاف المكافئ الوراثي

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في هذه الدراسة تم عمل محاكاة لعشرة مكررات لكل من ٣٠ توفيقة كل منها عبارة عن رقم الجيل (٥ أجيال) ومستوى المكافئ الوراثي (ثلاثة مستويات) ونوع التزاوج (عشوائي وبالانتخاب). استخدمت طريقة جبس وطريقة الاحتمال العظمى المحددة وطريقة أقل تباين تربيعي غير متحيز فى تقدير مكونات التباين وكذلك المكافئات الوراثية فى كل عينة من العينات الثلاثمائة المخلقة السابقة، بحيث أصبح لدينا ٩٠٠ تقديراً باستخدام الطرق الثلاثة السابقة. كانت الصفة التي خلقت منها البيانات هي صفة وزن حملان الاوسيمى عند الفطام بتباين مظهري كلى قدره ١٤كيلو جوام. تم تحوير مكونات التباين الحقيقية وذلك لخلق ثلاثة مستويات مختلفة من المكافئ الوراثي (٠,١ ، ٠,٣ ، ٠,٥) . حللت البيانات لمقارنة جودة تقديرات طريقة جبس بتلك المقدرة باستخدام REML و MIVQUE عن طريق تقدير قياس متوسط الخطأ مربعا (MSE) فى كل طريقة عند استخدامها فى تقدير المكافئ الوراثي أو مكونات التباين.

تم عمل تحليل التباين لمعرفة تأثير كل من مستويات المكافئ الوراثي وعدد الأجيال وطريقة التزاوج وطريقة التقدير وكذلك كل التداخلات الممكنة بين كل التأثيرات السابقة على تقديرات المكافئ الوراثي .

أوضحت النتائج أنه فى حالة الصفات المستمرة (وزن الفطام) تكون تقديرات مكونات التباين باستخدام طريقة MIVQUE أقل من المتوقع

كانت تقديرات مكونات التباين وكذلك المكافئات الوراثية باستخدام طريقة جبس (GS) أقرب إلى القيم الحقيقية من REML و MIVQUE.

كان هناك تأثير معنوي لجميع مصادر الاختلاف السابقة الذكر (احتمال<٠,٠٥) على تقديرات المكافئ الوراثي وكذلك على التباينات الوراثية .

جميع التداخلات كانت معنوية التأثير على المكافئ الوراثي ماعدا تداخل (عدد الأجيال * مستويات المكافئ الوراثي) وكذلك (عدد الأجيال *طريقة التحليل) باحتمال > ٠,٠٥ .

أوضحت الدراسة أن طريقة جبس (GS) كانت أنسب الطرق فى معظم الحالات وبخاصة فى حالة المكافئ الوراثي المنخفض من طريقة REML و MIVQUE لأن تقديرات GS أعطت أقل متوسط خطأ مربعاً (MSE) .

أظهرت الدراسة أن طريقة GS و REML لا تتأثران فى تقديراتهما بالانتخاب بينما تتأثر طريقة MIVQUE به .

عموماً فأن تقديرات GS و REML تحت التزاوج العشوائي للصفات المستمرة تكون متقاربة وخصوصاً فى مستوى المكافئ الوراثي العالي (٠,٥ ، ٠,٣) .

تقديرات جبس (GS) لها متوسط خطأ مربعاً أقل من REML و MIVQUE وهذا راجع إلى تأثير التوزيع المبدئى على التوزيع اللاحق ، على العكس منه فإن التوزيع المبدئى فى طريقة REML و MIVQUE يكون مسطح .