Egyptian Journal of Sheep & Goat Sciences, Vol. 9 (3), P: 1- 15, December 2014

COMPARISON OF REPEATABILITY AND MULTIPLE TRAITS MODEL IN ESTIMATING HERITABILITY, BREEDING VALUES AND GENETIC CORRELATIONS FOR FOUR CONTINUOUS TRAITS USING DIFFERENT CRITERIA OF EVALUATION (A SIMULATION STUDY)

Manal Elsayed[1] and Reda Elsaid[2]

1 Department of Animal Production, Faculty of Agriculture, Ain Shams University, Shubra El-Khema, Cairo, Egypt

2 Department of Sustainable Development, Environmental Studies and Research Institute (ESRI), University of Sadat City, Egypt

ABSTRACT

The present study evaluated the multiple traits model, as opposite to repeatability model approach in estimating heritability, breeding values and genetic correlation for four continuous traits (represent four parities) using bias, Mean squared error (MSE), Akaike information criteria (AIC) and Bayesian information criteria (BIC). The simulated base population consisted of 20, 60 or 100 sires. Each sire mated to 50 females to produce 1000, 3000 or 5000 progenies. The variance components modified to simulate three levels of heritability (h^2), 0.05, 0.25 and 0.5. Genetic correlations (GC) among the four studied traits were 0.3, 0.5, 0.9 and one and residual correlation was 0.2. Twenty replicates were generated for each of the 36 combinations (three levels of h^2 * four levels of GC * three levels of number of animals). These data sets (36 set) divided into two scenarios. The first one (27 set) was simulated as multiple traits and the second scenario (nine sets) was simulated as repeated measures. Each set of data in each scenario analyzed by multiple traits model (MTM) and repeatability model (RM). Correlations between the true and estimated breeding values of studied trait(s) estimated for the two types of analysis. Then, bias, MSE, AIC and BIC for all estimated values calculated as measures for comparing models of estimation. The mean estimates of h^2 resulted from MTM and RM were 0.27, and 0.20, respectively. When level of GC increases, the mean estimate of h^2 increases and reaches to equal the estimate of h^2 resulted from MTM when GC=1. The bias and MSE of MTM are less than those of RM. The smallest estimates of bias and MSE were noticed at GC = 0.9 and 1. The lowest AIC and BIC values were observed when fitting RM with data of the two scenarios. Therefore, the two criteria favored RM. Correlations between true and estimated breeding values of the four traits in MTM were slightly better than in RM. The effect of type of model was significant (P<0.01). In addition, significant effects between number of animals levels, heritability levels and GC levels were observed (P<0.01). This study indicated that, multiple traits analysis is more accurate than repeated measurements analysis in estimating h^2 and breeding values as concluded from results of bias and MSE. AIC and BIC were not the suitable criteria for selecting the appropriate model under the circumstances of this study.

Keywords: Multiple traits model, Repeatability model, heritability, breeding value, Bias, Mean Squared error (MSE), Akaike information criteria (AIC), Bayesian information criteria (BIC).

INTRODUCTION

Satisfaction of animal breeding programs based on accurate estimation of genetic parameters (Sadegh Alijani et al., 2012). First, the best possible model must defined to establish the efficient selection program (István Nagy et al., 2011). For a model selection context assume, there are data, a set of models and that statistical inference is to be model-based (Burnham and Anderson, 2002).

Different models could use to analyze longitudinal data. One of them is the repeatability model. The RM used when multiple measurements recorded on an individual on the same trait. By using RM, it could assumed a genetic correlation of unity between all pairs of records, equal variance for all records and equal environmental correlation between all pairs of records (Mrode and Thompson, 2005). MTM could used to analyze repeated measures, which are determined during different times and assuming them as different traits. A multiple traits analysis involves the evaluation of animal for two or more traits and assumes the phenotypic and genetic correlations between the traits are different (Mrode, 1996).

Model selection is the task of selecting a statistical model from a set of potential model given data (Burnham and Anderson, 2002). When the set of possible models has selected, the mathematical analysis allows us to determine the best of these models. A good model select technique that will balance goodness of fit with simplicity. Model selection techniques can considered as estimators of some physical quantity (Burnham and Anderson, 2002).

Choice of an appropriate model to evaluate animal should base on the accuracy, which can achieved relative to computing facilities available, assumptions made implicitly in any of the models should be checked to be realistic in real life data case (Simianer, 1986).

The term model selection used to describe statistical estimation in a context when the focus is more on the fitted model than on the individual parameters (Kerby Shedden, 2011). AIC, BIC, MSE and bias provide means for model selection (Xiaochuan Qin and Robert Reed, 2008)

Akaike's Information Criteria developed by Hirotsugu Akaike under the name of "an information criteria" (AIC) in 1971 and proposed by Akaike (1974). AIC is a measure of the goodness of fit of an estimated statistical model. It is a measure of goodness of fit grounded in the concept of entropy offering a relative measure of the information lost when a given model used to describe reality and can said to describe the tradeoff between bias and variance in model construction, or that of precision and complexity of the model. So, AIC is a tool for model selection. Given a data set, several models ranked according to their AIC. The absolute values of the AIC for different models have no meaning, only relative differences can ascribe meaning (Akaike ,1974).

Bayesian Information Criteria (BIC) or Schwarz Criterion is another criterion for model selection among a class of parametric models with different numbers of parameters. When estimating model parameters using maximum likelihood estimation, it is possible to increase the likelihood by adding additional parameters, which may result in over fitting. The BIC resolves this problem by introducing a penalty term for the number of parameters in the model. The BIC was developed by Schwarz and Gideon (1978). It closely related to the AIC. In BIC, the penalty for additional parameters is stronger than that of the AIC (Mark and Bin, 2003). The model with lowest value of these estimates (bias, MSE, AIC and BIC) considered as the best model (Rozenn Dahyot (2011); Tiejun (Ty) Tong (2010) and Mekkawy et al. (2010)).

The purpose of this study was to evaluate the MTM, as opposite to RM approach in estimating heritability, breeding values and genetic correlations for four continuous traits using bias, MSE, AIC and BIC criteria.

MATERIALS & METHODS

Data Simulation

The simulated base population consisted of 20, 60 or 100 sires. Each sire mated to 50 females to produce 1000, 3000 or 5000 progenies. Each progeny had four traits (represent four parities) which have the same variances and covariances with each other. The variance components modified to simulate three levels of h^2 (0.05, 0.25 and 0.5). GC among the four studied traits was 0.3, 0.5, 0.9 and one and residual correlation was 0.2. Twenty replicates were generated for each of the 36 combinations (three levels of h^2 * four levels of GC * three levels of number of animals). These data sets (36 sets) divided into two scenarios. The first one consisted of 27 set of data represent the three levels of h^2, the three levels of genetic correlation and the three levels of number of animals. These sets of data simulated as multiple traits. The second scenario consisted of nine sets of data represent the three levels of h^2, one level of genetic correlation (GC=1) and the three levels of number of animals. These sets simulated as repeated measures. Each set of data in each scenario analyzed by multiple traits model and repeatability model. In addition, two fixed effects generated with four levels for each of them and each level had 25% of total records.

Multiple traits simulation

The phenotypic means in the first scenario were: parity 1=3000 kg, parity 2=3200 kg, parity 3=3400 kg and parity 4=3600 kg. The present study assumed that all traits have the similar phenotypic variance of $2*10^5$ kg^2. Genetic and residual variances calculated based on the assumed heritability. For example if the assumed heritability is 0.25, in that case the genetic variance is 200000*0.25=50000 kg^2 and the residual variance is 200000-50000= 150000 kg^2. Genetic covariance calculated based on the assumed heritability and genetic correlation. For example, if we assume a heritability of 0.25 and genetic correlation of 0.3, then genetic variance will be 50000 as explained in the previous section and the genetic covariance will be 0.3*50000= 15000. Genetic variances for both traits are equal because the same heritability and phenotypic variance used for simulated traits. The residual correlation assumed 0.2 and similar to the previous section, the residual covariance calculated as 0.2 * 150000= 30000. Table 1 shows the parametric phenotypic, genetic and residual variance in the case of multiple traits model.

Repeated measurements simulation

Phenotypic means were assumed to be: parity 1=3000 kg, parity 2=3200 kg, parity 3=3400 kg and parity 4=3600 kg. The Phenotypic variance for the simulated trait was 200000 kg^2. Genetic, permanent and residual variances calculated based on the assumed heritability and the proportion of the permanent environmental variance that was 0.2.

For example if the assumed heritability is 0.25, in that case, the genetic variance is 200000*0.25=50000 kg^2. Permanent environmental variance is 0.2 * 200000 = 40000 kg^2. Note that, the repeatability in that case is 0.25+0.2=0.45 and the residual variance is (200000-50000-40000) = 110000 kg^2.

Methods:

Two models used to analyze each replicate. The first model was the multiple trait animal model and was as follows:

$$\mathbf{Y = X\,\beta + Z_a\,a + e}$$

Where:

Y is N vector of observations of the four studied traits;

X is the incidence matrix for the two studied fixed effects;

β is the vector including the overall mean and the fixed effects;

Z_a is the incidence matrix for random effects;

a is the vector of direct genetic effect of animal and

e is a vector of random residuals normally and independently distributed with zero mean and variance σ^2_e I.

The second model was repeatability animal model which was as follows:

$$\mathbf{Y = X\beta + Z_a\,a + Z_c\,c + e,}$$

Where:

Y is the vector of observations;

X is the incidence matrix for fixed effects;

β is the vector of an overall mean and fixed effects;

Z_a is the incidence matrix for random effects;

a is the vector of direct genetic effects of animal;

c is the vector of permanent environmental effects and

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

Tables 2 and 3 represent the 36 studied cases for the two models (scenarios).

Estimates of h^2 of the studied traits and GC between them estimated from each studied case (36 cases) using repeated measurements analysis and multiple traits analysis with DFREML program (Misztal et al., 2002). In addition, the correlations between true and estimated breeding values of studied traits estimated from the two types of analysis.

Table 1. Means (kg) and phenotypic, genetic (GV) and residual (RV) variances (kg2) in the case of Multiple Traits Model

Parity(P)	**Mean**	**Phenotypic variance**	**$h^2 = 0.05$**		**$h^2 = 0.25$**		**$h^2 = 0.5$**	
			GV	**RV**	**GV**	**RV**	**GV**	**RV**
P_1	3000	200000	10000	190000	50000	150000	100000	100000
P_2	3200	200000	10000	190000	50000	150000	100000	100000
P_3	3400	200000	10000	190000	50000	150000	100000	100000
P_4	3600	200000	10000	190000	50000	150000	100000	100000

Table 2. Scenario of multiple traits model

Case	**Number of Animals**	**Number of Sires**	**Heritability**	**Genetic correlation**
1	1000	20	0.05	0.3
2	1000	20	0.05	0.5
3	1000	20	0.05	0.9
4	1000	20	0.25	0.3
5	1000	20	0.25	0.5
6	1000	20	0.25	0.9
7	1000	20	0.50	0.3
8	1000	20	0.50	0.5
9	1000	20	0.50	0.9
10	3000	60	0.05	0.3
11	3000	60	0.05	0.5
12	3000	60	0.05	0.9
13	3000	60	0.25	0.3
14	3000	60	0.25	0.5
15	3000	60	0.25	0.9
16	3000	60	0.50	0.3
17	3000	60	0.50	0.5
18	3000	60	0.50	0.9
19	5000	100	0.05	0.3
20	5000	100	0.05	0.5
21	5000	100	0.05	0.9
22	5000	100	0.25	0.3
23	5000	100	0.25	0.5
24	5000	100	0.25	0.9
25	5000	100	0.50	0.3
26	5000	100	0.50	0.5
27	5000	100	0.50	0.9

Table 3. Scenario of repeatability model

Case	**Number of Animals**	**Number of Sires**	**Heritability**	**Genetic correlation**
28	1000	20	0.05	1
29	1000	20	0.25	1
30	1000	20	0.50	1
31	3000	60	0.05	1
32	3000	60	0.25	1
33	3000	60	0.50	1
34	5000	100	0.05	1
35	5000	100	0.25	1
36	5000	100	0.50	1

Then, bias and MSE for all estimated values calculated as measures for comparing models of estimation. Bias calculated as the deviation of observed estimate from the true parameter. MSE calculated as the sum of the bias squared plus the variance of the estimated values. In addition, the two models were compared based on AIC and BIC. According to Rozenn Dahyot (2011) the AIC is:

$$\mathbf{AIC = 2k - 2 \log (L)}$$

Where:

K is the number of parameters in the statistical model, and

L is the maximized value of the likelihood function for the estimated model.

Also, According to Rozenn Dayhot (2011) BIC is:

$$\mathbf{BIC = -2 \log L + k \log N}$$

Where:

N is the number of observations,

L is the maximized value of the Likelihood function for the estimated model and

K is the number of parameters to be estimated in the model.

The following model was applied using SAS (1996) to analyze the estimates of bias, MSE and GC:

$$\mathbf{Y_{ijklm} = \mu + t_i + n_j + h_k + g_l + e_{ijklm},}$$

Where:

Y_{ijklm} is the estimate of bias, MSE or GC of ith type of model, jth level of number of animals, kth heritability level and lth genetic correlation level of mth progeney;

μ is the overall mean;

t_i is the fixed effect of the ith level of type of model (i = 1 for MTM and 2 for RM);

n_j is the fixed effect of the jth number of animals (j = 1 for 1000 animals, 2 for 3000 animals and 3 for 5000 animals);

h_k is the fixed effect of the kth heritability level (k = 1 for $h^2 = 0.05$, 2 for $h^2 = 0.25$ and 3 for $h^2 = 0.5$);

g_l is the fixed effect of the lth genetic correlation level (l = 1 for GC = 0.3, 2 for GC = 0.5, 3 for GC = 0.9 and 4 for GC = 1);

e_{ijklm} is the random error associated with each observation.

RESULTS AND DISCUSSION

Means and their standard errors (± SE) of main effects for h^2 estimates are shown in Table 4. The studied main effects were all significant (P<0.01) except the number of animals which was not significant.

Comparing estimates of h^2 resulted from MTM and RM for all traits (parities) confirm that the mean estimates resulted from MTM (0.27) was the average of the three simulated levels (0.05, 0.25 and 0.50) of h^2. Whereas the mean estimates of h^2 resulted from RM (0.2) was underestimate of the average. Van Vleck and Gregory (1992) summarized that, the estimate from the repeated records model seen to be approximately the product of the average genetic correlation and the average heritability from the multiple traits procedure. The same authors reported that such a result expected particularly if the environmental correlations are small among records of the same animal.

Means of h^2 for the three levels of number of animals for all studied traits were almost equal (~ 0.23). When level of GC increases, the mean estimate of h^2 increases and reaches to be equal the estimate of h^2 resulted from MTM when GC=1.

Tables 5 and 6 show the means and their SE of main effects for bias and MSE of h^2 estimates. The most noticeable pattern shown at these tables is that, the bias (in absolute estimate) and MSE of MTM are less than those of RM. The smallest MSE was noticed when number of animals was 5000, whereas the bias estimates were almost equal in all levels of number of animals. The smallest estimate of bias also noticed at h^2 level = 0.05, whereas MSE estimates varies from level of h^2 to the other. The bias decreases when GC increases and the smallest bias can be noticed at GC=1 (Table 5). The smallest estimates of MSE were noticed at GC = 0.9 and 1 (Table 6). Estimates of GC between traits in different parities may be lower than one especially between later parities, therefore MTM may be preferred in such situation (Serenius et al., 2002). Van Vleck and Gregory (1992) implicated that failure of a statistical model to account for covariance among genetic and environmental effects on repeated records can lead to biased estimates of parameters such as h^2. The same authors concluded that, such biases would result in serious errors in selection and require further analysis. In contrast, Lukovic et al. (2004) introduced that most studies use a RM due to its simplicity.

Table 7 indicated that, correlations between true and estimated breeding values of four traits in MTM were slightly better than in RM, the effect of type of model was significant ($P<0.01$). This result confirmed that MTM is better than RM in estimating breeding values. The results of Piles et al., 2006 indicated that, the predicted breeding values resulted from RM and MTM had nearly the same accuracies. In addition, the present study indicated that, significant effects between number of animals levels, h^2 levels and GC levels were observed ($P<0.01$).

Noticeable increase in correlations between true and estimated breeding values recorded with increasing number of animals, h^2 levels and GC levels.

Means and their Standard errors of main effects for genetic correlation between traits resulted from MTM are summarized in Tables 8 and 9. These tables introduced two main results, the first is that all main effects were significant ($P<0.05$) except for correlations between trait 1 with trait 3 and trait 1 with trait 4 for number of animals effect. The second main result was that, estimates of GC between all studied traits were < 1. The heterogeneity of genetic correlations between the four studied traits lower than one suggests that the four studied traits (even though they were the same trait measured in different parities) could considered as different traits when genetic evaluations are performed (Piles et al., 2006 and Serenius et al., 2002). Robertson (1959) suggested that, when GC between repeated records is > 0.8, there is no need to treat repeated measures as different traits.

The estimated means and their SE of the criteria AIC and BIC are presented in Table 10. Relying these criteria (AIC and BIC), MTM yield the largest values of both. The lowest AIC and BIC values were observed when fitting RM with data of the two scenarios. So that, the two criteria favored RM. These results of AIC and BIC disagree with the previous results of MSE and bias that suggest that, the use of MTM may be an appropriate choice. In addition, based on -2 log likelihood values (Table 10), the value of MTM (155974) is less than the value of RM (156343). Therefore, this criterion favored MTM. The present results are in agreement with Mekkawy et al. (2010). As reported by Kenneth and David (2004), there is ample and diverse of theory for AIC and BIC based model selection.

AIC and BIC are functions of the number of observations, the sum of the squared errors, the pure error variance fitting the full model, and the number of independent variables (Dennis J. Beal, 2007). Mekkawy et al. (2010) referred this result to the fact that AIC and BIC were highly affected by the number of parameters in the model and tend to choose the model with lower number of parameters. Mark and Bin (2003) explained that AIC and BIC have different penalties. AIC ads one for each additional variable included in the model, while BIC adds log n/2 where n is the sample size. So that, as mentioned by Mekkawy et al. (2010) may be the number of observations in the present study was not sufficient to overcome the penalization of the MTM for which more parameters have to be estimate.

The results of Table 10 also indicated that, AIC and BIC decrease as the level of h^2 and GC increase. It is noticeable that, the lowest values of both of them at GC equal one. This result affirmed that these criteria preferred the repeatability model. In contrary of this result, Andonov et al. (2013) indicated that, AIC and MSE of prediction favored more complex models.

CONCLUSION

Multiple traits analysis is more accurate than repeated measurements analysis in estimating h^2 and breeding values as concluded from results of bias and MSE. Although the four studied traits were the same trait measured in different times, they could considered as four different traits, because GC's between them were < 1 in both studied scenarios. AIC and BIC were not the suitable criteria for selecting the appropriate model under the circumstances of this study.

ACKNOWLEDGEMENT

The authors thank Dr. Wagdy Mekkawy for the simulation software.

REFERENCES

Akaiki, Hirotugu. 1974. A new look at the statistical model identification. IEEE Transactions on Automatic control 19 (6): 716-723.

Andonov S Ødegård J, M. Svendsen , T. Ådnøy, M. Vegara and G. Klemetsdal.2013. Comparison of random regression and repeatability models to predict breeding values from test-day records of Norwegian goats. J Dairy Sci. 2013 Mar; 96 (3):1834-43. doi: 10.3168/jds.2012-5910. Epub 2013 Jan 26.

Burnham, K.P., and D.R. Anderson. 2002. Model selection and multi model inference. A practical-theoritic approach, 2nd ed. Springer-verlag. ISBN 0 - 38799364-7.

Dennis J. Beal. 2007. Information criteria methods in SAS® for multiple linear regression models. Proceedings of the 15th Annual Conference of the South East SAS Users Group, http://analytics.ncsu.edu/sesug/2007/SA05.pdf (accessed July 14, 2009).

István Nagy, István Radnai, Henrietta Nagyné-Kiszlinger, János Farkas and Zsolt Szendrő. 2011. Genetic parameters and genetic trends of reproduction traits in synthetic Pannon rabbits using repeatability and multi-trait animal models. Archiv Tierzucht 54 (2011) 3, 297-307, ISSN 0003-9438.

Kenneth P. Burnham and David R. Anderson. 2004. Multi model Inference: Understanding AIC and BIC in model selection. Colorado cooperative fish and wild life research unit (USGS-BRD), Colorado state university. 970491-1413 (FAX). kenb@cnr.colostate.edu.

Kerby Shedden. 2011. Model selection. Creative Commons Attribution Share Alike 3.0 License: http://creativecommons.org/licenses/by-sa/3.0/. Department of Statistics, University of Michigan.

Lukovic, Z.; S. Malovrh; G. Gorjanc; M. Kovac. 2004. A random regression model in analysis of litter size in pigs. South Africa Journal of Animal Science 34, 4.

Mark H. Hansen and Bin Yu. 2003. Minimum description length model selection criteria for generalized linear models. Jstor: lecture notes-monograph series, vol. 40(2003), pp.145-163.

Mekkawy W., R. Roehe., R.M. Lewis, M.H. Davies, L. Bu¨nger, G. Simm and W. Haresign. 2010. Comparison of repeatability and multiple trait threshold models for litter size in sheep using observed and simulated data in Bayesian analyses. J. Anim. Breed. Genet. ISSN 0931-2668.

Misztal, I., S. Tsuruta, T. Strabel, B. Auvray, T. Druet, D. H. Lee. 2002. BLUF90 and related programs (BGF90). Proc. 7th World Congr. Genet. Appl. Livest. Prod., Montpellier, France. CD-ROM. Communication No. 28–07.

Mrode R.A., 1996. Linear models for the prediction of animal breeding values. CAB International Wallingford Oxon, UK .

Mrode, R.A., R. Thompson. 2005. Linear models for the prediction of animal breeding values. ISBN 0 85199 0002, chapter 1. CABI publishing CAB international Wallingford Oxfordshire OX10 8DE UK. Email cabi@cabi.org. Website: www.cabi-publishing.org.

Piles, M.; M.L. Garcia; O. Rafel; J. Ramon; M. Baselga. 2006. Genetic of litter size in three maternal lines of rabbits: Repeatability versus Multiple-trait models. J. Anim. Sci., 84, 9, 2309-15.

Robertson A., 1959. The sampling variance of the genetic correlation coefficient. Biometrics 15: 469–485.

Rozenn Dahyot. 2011. AIC and BIC. Assistant Professor in Statistics, School of Computer Science and Statistics. Room 128 Lloyd Institute. Trinity College Dublin 2, Ireland. Phone: (+353) 1 896 1760. Fax: (+353) 1 677 0711. e-mail:Rozenn.Dahyot@scss.tcd.ie. https://www.scss.tcd.ie/Rozenn.Dahyot/, http://people.tcd.ie/dahyotr, http://tcd.academia.edu/Rozenn Dahyot, http://www.linkedin.com/pub/rozenn-dahyot/16/71/A08.

Sadegh Alijani, Mehdi Jasouri, Nasrolah Pirany and Hossein Daghigh Kia. 2012. Estimation of variance components for some production traits of Iranian Holstein dairy cattle using Bayesian and AI-REML methods. Pak Vet J, 32(4): 562-566.

SAS, 1996. Statistical Analysis System, SAS User’s Guide : Statistics. SAS Institute Inc. Editors, Cary, NC.

Schwarz and E. Gideon. 1978. "Estimating the dimension of a model ". Annals of statistics 6(2):461-464.

Serenius, T.; M. L. Sevon-Aimonen; E.A. Mantysaari. 2002. Effect of service sire and validity of repeatability model in litter size and farrowing interval of Finnish Landrace and large white population. Livestock production Sci., 81, 2-3, 213-222.

Simianer, H., 1986. A general approach to the use of multiple traits with repeated measurements in estimation of breeding values. Livestock production Sci., 15, 4, 315-324.

Tiejun (Ty) Tong. 2010**. Variable Selection and Model Building. Department of Applied** Mathematics, www.peltarion.com,/answers Magazine siemens.com/answers/urban- mobility.

Van Vleck, L.D.; K.E. Gregory. 1992. Differences in heritability estimates from multiple-trait and repeated-records models. J. Anim. Sci., 70, 2994-2998.

Xiaochuan Qin and W. Robert Reed. 2008. A comparison of large number of model selection criteria. ESAM08 Conference, “Markets and Models: Policy Frontiers in the AWH Phillips Tradition”, Wellington, New Zealand, July 9-11, 2008. The contact author is W. Robert Reed, Professor, Department of Economics, University of Canterbury, email: bobreednz@yahoo.com.

Table 4. Heritability estimates (Mean ± SE) for the main effects in the model.

Factor	Parity 1	Pr.	Parity 2	Pr.	Parity 3	Pr.	Parity 4	Pr.
	Mean ±SE		**Mean ±SE**		**Mean ±SE**		**Mean ±SE**	
Type of model		0.0001		0.0001		0.0001		0.0001
Multiple traits model	0.270±0.002		0.269±0.002		0.269±0.002		0.270±0.002	
Repeatability model	0.201±0.002		0.201±0.002		0.201±0.002		0.201±0.002	
Number of animals		0.3451		0.8003		0.9447		0.7773
1000	0.238±0.002		0.236±0.002		0.234±0.002		0.235±0.002	
3000	0.235±0.002		0.234±0.002		0.235±0.002		0.235±0.002	
5000	0.234±0.002		0.234±0.002		0.235±0.002		0.237±0.002	
Heritability level		0.0001		0.0001		0.0001		0.0001
0.05	0.048±0.002		0.050±0.002		0.048±0.002		0.049±0.002	
0.25	0.222±0.002		0.220±0.002		0.219±0.002		0.222±0.002	
0.5	0.436±0.002		0.435±0.002		0.438±0.002		0.436±0.002	
Genetic correlation		0.0001		0.0001		0.0001		0.0001
0.3	0.194±0.002		0.194±0.002		0.195±0.002		0.197±0.002	
0.5	0.216±0.002		0.215±0.002		0.215±0.002		0.214±0.002	
0.9	0.263±0.002		0.262±0.002		0.261±0.002		0.262±0.002	
1	0.269±0.002		0.268±0.002		0.267±0.002		0.269±0.002	

Table 5. Bias of heritability estimates (Means ± SE) for the main effects in the model

Factor	**Parity 1**	**Pr.**	**Parity 2**	**Pr.**	**Parity 3**	**Pr.**	**Parity 4**	**Pr.**
	Mean ±SE		**Mean ±SE**		**Mean ±SE**		**Mean ±SE**	
Type of model		0.0001		0.0001		0.0001		0.0001
Multiple traits model	0.004±0.002		0.003±0.002		0.002±0.002		0.004±0.002	
Repeatability model	-0.066±0.002		-0.066±0.002		-0.066±0.002		-0.066±0.002	
Number of animals		0.3451		0.8003		0.9447		0.7773
1000	-0.029±0.002		-0.031±0.002		-0.032±0.002		-0.032±0.002	
3000	-0.032±0.002		-0.033±0.002		-0.032±0.002		-0.032±0.002	
5000	-0.033±0.002		-0.032±0.002		-0.032±0.002		-0.030±0.002	
Heritability level		0.0001		0.0001		0.0001		0.0001
0.05	-0.002±0.002		-0.000±0.002		-0.002±0.002		-0.001±0.002	
0.25	-0.028±0.002		-0.030±0.002		-0.031±0.002		-0.028±0.002	
0.5	-0.064±0.002		-0.065±0.002		-0.062±0.002		-0.064±0.002	
Genetic correlation		0.0001		0.0001		0.0001		0.0001
0.3	-0.072±0.002		-0.073±0.002		-0.072±0.002		-0.070±0.002	
0.5	-0.051±0.002		-0.051±0.002		-0.051±0.002		-0.052±0.002	
0.9	-0.004±0.002		-0.004±0.002		-0.005±0.002		-0.004±0.002	
1	0.002±0.002		0.002±0.002		0.001±0.002		0.002±0.002	

Table 6. Mean squared errors (MSE) of heritability estimates (Means ± SE) for the main effects in the model

Factor	Parity 1 Mean ±SE	Pr.	Parity 2 Mean ±SE	Pr.	Parity 3 Mean ±SE	Pr.	Parity 4 Mean ±SE	Pr.
Type of model		0.0017		0.3167		0.1825		0.0949
Multiple traits model	0.002±0.002		0.007±0.004		0.006±0.003		0.006±0.003	
Repeatability model	0.012±0.002		0.012±0.004		0.012±0.003		0.012±0.003	
Number of animals		0.665		0.1588		0.1715		0.2389
1000	0.009±0.003		0.017±0.004		0.015±0.004		0.014±0.004	
3000	0.007±0.003		0.007±0.004		0.007±0.004		0.007±0.004	
5000	0.006±0.003		0.006±0.004		0.006±0.004		0.006±0.004	
Heritability level		0.0002		0.16		0.0819		0.0496
0.05	0.001±0.003		0.008±0.004		0.007±0.004		0.005±0.004	
0.25	0.005±0.003		0.005±0.004		0.005±0.004		0.005±0.004	
0.5	0.017±0.003		0.017±0.004		0.017±0.004		0.016±0.004	
Genetic correlation		0.0019		0.4685		0.2765		0.1353
0.3	0.017±0.003		0.017±0.005		0.017±0.004		0.017±0.004	
0.5	0.009±0.003		0.009±0.005		0.009±0.004		0.009±0.004	
0.9	0.002±0.003		0.007±0.005		0.006±0.004		0.006±0.004	
1	0.002±0.003		0.007±0.005		0.006±0.004		0.004±0.004	

Table 7. Correlation between true and estimated breeding values of the four traits (Means ± SE) for the main effects in the model

Factor	Parity 1	Pr.	Parity 2	Pr.	Parity 3	Pr.	Parity 4	Pr.
	Mean ±SE		**Mean ±SE**		**Mean ±SE**		**Mean ±SE**	
Type of model		0.0001		0.0001		0.0001		0.0001
Multiple traits model	0.565±0.001		0.563±0.001		0.563±0.001		0.566±0.001	
Repeatability model	0.513±0.001		0.512±0.001		0.512±0.001		0.515±0.001	
Number of animals		0.0001		0.0001		0.0001		0.0001
1000	0.443±0.002		0.438±0.002		0.439±0.002		0.445±0.002	
3000	0.568±0.002		0.569±0.002		0.569±0.002		0.569±0.002	
5000	0.605±0.002		0.605±0.002		0.605±0.002		0.607±0.002	
Heritability level		0.0001		0.0001		0.0001		0.0001
0.05	0.363±0.002		0.360±0.002		0.361±0.002		0.366±0.002	
0.25	0.571±0.002		0.568±0.002		0.567±0.002		0.571±0.002	
0.5	0.683±0.002		0.684±0.002		0.685±0.002		0.684±0.002	
Genetic correlation		0.0001		0.0001		0.0001		0.0001
0.3	0.447±0.002		0.442±0.002		0.445±0.002		0.448±0.002	
0.5	0.490±0.002		0.488±0.002		0.487±0.002		0.493±0.002	
0.9	0.595±0.002		0.594±0.002		0.595±0.002		0.597±0.002	
1	0.625±0.002		0.624±0.002		0.624±0.002		0.625±0.002	

Table 8. Means and their standard errors (±SE) of main effects for genetic correlations of parity1 with the others for multiple traits model

Factor	**Parity 1 &2**	**Pr.**	**Parity 1&3**	**Pr.**	**Parity 1 &4**	**Pr.**
	Mean ±SE		**Mean ±SE**		**Mean ±SE**	
Number of animals		0.0001		0.0808		0.5553
1000	0.621±0.009		0.646±0.009		0.662±0.009	
3000	0.637±0.009		0.655±0.009		0.650±0.009	
5000	0.658±0.009		0.649±0.009		0.663±0.009	
Heritability level		0.0001		0.0001		0.0001
0.05	0.584±0.009		0.612±0.009		0.616±0.009	
0.25	0.664±0.009		0.661±0.009		0.680±0.009	
0.5	0.668±0.009		0.677±0.009		0.678±0.009	
Genetic correlation		0.0001		0.0001		0.0001
0.3	0.306±0.011		0.323±0.010		0.341±0.010	
0.5	0.484±0.011		0.493±0.010		0.515±0.010	
0.9	0.850±0.011		0.863±0.010		0.862±0.010	
1	0.916±0.011		0.921±0.010		0.915±0.010	

Table 9. Means and their standard errors (±SE) of main effects for genetic correlations among parity 2, 3 and 4

Factor	**Parity 2 &3**	**Pr.**	**Parity 2&4**	**Pr.**	**Parity 3&4**	**Pr.**
	Mean ±SE		**Mean ±SE**		**Mean ±SE**	
Number of animals		**0.0001**		**0.0183**		**0.0002**
1000	0.575±0.011		0.644±0.010		0.615±0.010	
3000	0.636±0.011		0.639±0.010		0.649±0.010	
5000	0.654±0.011		0.659±0.010		0.655±0.010	
Heritability level		0.0001		0.0001		0.0001
0.05	0.549±0.011		0604±0.010		0.590±0.010	
0.25	0.648±0.011		0.664±0.010		0.662±0.010	
0.5	0.668±0.011		0.674±0.010		0.668±0.010	
Genetic correlation		0.0001		0.0001		0.0001
0.3	0.264±0.013		0.304±0.012		0.313±0.012	
0.5	0.470±0.013		0.501±0.012		0.480±0.012	
0.9	0.843±0.013		0.861±0.012		0.850±0.012	
1	0.911±0.013		0.924±0.012		0.917±0.012	

Table 10. Means and their standard errors (±SE) of main effects for -2 log likelihood, Akaike (AIC) and Bayesian (BIC) information criteria

Factor	-2log L[a]	Pr	AIC	Pr	BIC	Pr
	Mean ±SE		Mean ±SE		Mean ±SE	
Type of model						
Multiple trait model	155974 ±15.52	0.0001	188910±15.52	0.0183	288974±15.52	0.0002
Repeatability model	156343 ±15.52		170583±15.52		223991±15.52	
Number of animals						
1000	51994±19.01		63382±19.01		93462±19.01	
3000	156180±19.01	0.0001	179768±19.01	0.0001	255542±19.01	0.0001
5000	260301±19.01		296089±19.01		420443±19.01	
Heritability level						
0.05	157543±19.01		181131±19.01		257867±19.01	
0.25	156452±19.01	0.0001	180040±19.01	0.0001	256776±19.01	0.0001
0.5	154480±19.01		178068±19.01		254804±19.01	
Genetic correlation						
0.3	157083±21.95	0.0001	180671±21.95		257407±21.95	0.0001
0.5	156710±21.95		180298±21.95		257034±21.95	
0.9	155600±21.95		179188±21.95		255924±21.95	
1	155240±21.95		178828±21.95		255564±21.95	

[a] L is the maximized value of the likelihood function for the estimated model