

EMPIRICAL PROPERTIES OF SOLUTIONS FROM HENDERSON'S MIXED MODEL EQUATIONS WHEN SIRES ARE NON-RANDOMLY USED ACROSS CONTEMPORARY GROUPS

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- **ABSTRACT:** Stochastic simulations were carried out to investigate empirical properties of solutions from Henderson's Mixed Model Equations (HMME) under four different situations (ST1 to ST4) of sire by contemporary group (CG) association. Sires were used across CGs independently of their true breeding values (TBV) in ST1 and according to their TBV in ST2 to ST4, generating mean genetic differences between CGs in these latter situations. HMME were applied under a model including CG as fixed and sire and dam as random effects (M1). Three alternative models were used (M2 to M4). CG, sire, and dam were assumed as random effects in model M2, and as fixed effects in M3. For model M4, CG and sire were assumed as fixed and dam as random effect. Models M1, M2, and M4 showed similar results for situation ST1, whereas model M3 provided solutions with higher mean square error. In the presence of mean genetic differences between CGs, solutions from model M1 were biased. The bias reduced the ability of model M1 in properly ranking animals and its efficiency in selecting genetically superior sires. For situations ST2 to ST4, model M4 showed, in general, better properties than the other studied models.
- **KEYWORDS:** Bias, BLUP, genetic evaluation, mixed model

1 Introduction

In animal breeding, the currently most used model for genetic evaluation, proposed by Henderson (1963), relies on the assumption that the marginal expectation of the breeding value of each animal being evaluated is equal to zero ($E(a_i)=0$).

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Different types of selection or any force that results in non-random distribution or allocation of animals in levels of fixed effects can generate mean genetic differences between these levels and, consequently, invalidate the assumption that $E(a_i)=0$.

An effective selection of the parents, for instance, may create mean genetic differences over the time. In this case, the breeding values in later generations are expected to be higher than in the earlier ones. The effects of selection of the parents on genetic evaluation were investigated by several researchers (e.g., Sorensen and Kennedy, 1984; Van der Werf, 1990; and Schenkel, 1998) and will not be object of direct consideration in this study. The non-random association between sires and contemporary groups is another example where mean genetic differences can be generated.

The consequence of violating $E(a_i)=0$ is that solutions from Henderson's mixed model equations (HMME) are not guaranteed to be unbiased (Harvey, 1979; Fries and Schenkel, 1993). As a result, the ability to estimate environmental and genetic trends and to select better animals for reproduction may be reduced.

Henderson (1973, 1975) presented special conditions where solutions from HMME are unbiased even when $E(a_i)=0$ is violated. However, these conditions, such as full parental information, unselected base population and translation invariant selection, are rare to occur in practice, what highlights the importance of further studies to investigate how Henderson's Mixed Model behaves when the null expectation of breeding values is violated.

The objectives of this paper were to investigate, by stochastic simulation, empirical properties of solutions from HMME for situations where sires of different genetic merit are non-randomly used across contemporary groups (a type of $E(a_i)=0$ violation, where the expected values of distribution of a depend on the levels of fixed effects), and to evaluate alternative models under these situations.

2 Material and methods

2.1 Structure of the simulated populations

The base simulated population consisted of 250 sires and 2,500 dams, which were unrelated, unselected and assumed randomly sampled from a conceptually infinite population. Each dam was mated twice with randomly selected sires, producing two offspring. Only one generation of offspring was simulated. A total of 5,000 offspring were generated, which were distributed in 200 contemporary groups (CGs) according to four different situations (ST1 to ST4). Five sets of 40 CGs (sCG1 to sCG5) and five sets of 50 sires were formed based on either their identification number (ID) or on the rank of their true effects (rank), depending on the simulated situation. Sires were grouped according to their ID for ST1, and to their rank (based on the descending order of their true breeding values) for ST2 to ST4. CGs were grouped according to their ID for ST1 and ST2, and to the rank of their true effects for ST3 (descending order) and ST4 (ascending order). As shown in Table 1, the subclasses given by sets of sires by sets of CGs had different probabilities of occurrence due to a non-random distribution of the offspring in the CGs.

For ST1, the control situation, no mean genetic differences between CGs were expected as sets of sires were formed based on their ID. However, for ST2 to ST4, mean genetic differences between CGs were generated as sets of sires were formed based on the rank of their true breeding values, i.e., sCG1 and sCG2 had higher proportion of progeny

from better sires, whereas sCG4 and sCG5 had higher proportion of progeny from worse sires (Table 1).

Table 1 - Expected and observed probabilities (%) of occurrence of the subclasses given by sets of sire by sets of contemporary groups (CGs)

Set of sires ^b	Set of CGs ^a				
	1-40 (sCG1)	41-80 (sCG2)	81-120 (sCG3)	121-160 (sCG4)	161-200 (sCG5)
1-50	12 ^c (11.96 ^d)	6 (5.93)	2 (1.96)	0 (0.00)	0 (0.00)
51-100	6 (6.01)	8 (8.02)	4 (4.04)	2 (1.98)	0 (0.00)
101-150	2 (2.00)	4 (3.98)	8 (8.14)	4 (4.05)	2 (2.00)
151-200	0 (0.00)	2 (2.01)	4 (4.05)	8 (7.99)	6 (5.91)
201-250	0 (0.00)	0 (0.00)	2 (1.98)	6 (6.10)	12 (11.89)

^a Sets of CGs were formed according to their identification number for simulated situation 1 (ST1) and 2 (ST2), according to the descending rank of their true effects for ST3, and according to the ascending rank of their true effects for ST4.

^b Sets of sires were formed according to their identification number for ST1 and according to the descending rank of their true effects for ST2, ST3 and ST4.

^c Expected values (those used in the simulation process).

^d Observed values (average over 50 replicates).

No genetic and environmental correlation ($r_{G,E}$) was expected in ST2 as sets of CGs were formed with respect to their ID, while, for ST3 and ST4, positive and negative $r_{G,E}$ were generated as a result of grouping CGs according to their rank based on descending and ascending order of their true effects, respectively.

The connectedness of all CGs was guaranteed by imposing restrictions on a minimum progeny size per sire (5), number of young animals per CG (10), sires per CG (3), CGs per sire (3), and number of genetic links per CG (10). To satisfy this last restriction the program AMC (Fries, 1998; Roso et al., 2004) was used.

For each situation, 50 replicates were simulated. Base animal mates, size of progeny per sire, and number of young animals per CG varied across replicates.

2.2 Simulation model

For each replicate, observations of a fictitious trait (TRT) measured on young animals were simulated according to the model: $y_{ij} = b_i + a_{ij} + e_{ij}$, where y_{ij} is the TRT of animal j in CG i , b_i is the effect of CG i , a_{ij} is the additive genetic value of animal j in CG i and e_{ij} is the random residual term. Values for e_{ij} were independently drawn from a normal distribution with mean zero and variance of 180 kg^2 ($N(0,180)$). Values for b_i were drawn from a $N(172.5,300)$. Genetic values of base animals were generated from a $N(0,120)$ and of non base animals as $a_{ij} = \frac{1}{2}(a_{sj} + a_{dj}) + m_{ij}$, where a_{sj} and a_{dj} are the true breeding values (TBV) of the sire and dam of animal j , and m_{ij} is the Mendelian sampling effect of animal j drawn from a $N(0,60)$. These parameters used in the simulation process mimicked a trait with heritability equal to 0.4.

2.3 Statistical analyses

Analyses were carried out using four different models. All of them can be described by the equation:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_s\mathbf{s} + \mathbf{Z}_d\mathbf{d} + \mathbf{e},$$

where: \mathbf{y} is the vector of TRT, $\boldsymbol{\beta}$ is the vector of CG effects, \mathbf{s} and \mathbf{d} are, respectively, the vectors of sire and dam genetic effects, \mathbf{e} is the vector of random residual effects, \mathbf{X} , \mathbf{Z}_s and \mathbf{Z}_d are incidence matrices that relate elements of $\boldsymbol{\beta}$, \mathbf{s} , and \mathbf{d} to elements of \mathbf{y} , respectively. A sire and dam model was used because it is equivalent to the individual animal model when, for example, base animals have no record and all young animals with record have no progeny (Henderson, 1984), as in the present simulation study.

For model 1 (M1), $\boldsymbol{\beta}$ was considered a vector of fixed effects, and \mathbf{s} and \mathbf{d} vectors of random effects. The expectation and covariance matrices of the random variables were given by: $E(\mathbf{y}) = \mathbf{X}\boldsymbol{\beta}$, $E(\mathbf{s}) = E(\mathbf{d}) = E(\mathbf{e}) = 0$, $\text{Var}(\mathbf{y}) = \mathbf{V} = \mathbf{Z}_s\mathbf{Z}'_s\boldsymbol{\sigma}_s^2 + \mathbf{Z}_d\mathbf{Z}'_d\boldsymbol{\sigma}_d^2 + \mathbf{I}_n\boldsymbol{\sigma}_e^2$, $\text{Var}(\mathbf{s}) = \mathbf{I}_s\boldsymbol{\sigma}_s^2$, $\text{Var}(\mathbf{d}) = \mathbf{I}_d\boldsymbol{\sigma}_d^2$ and $\text{Var}(\mathbf{e}) = \mathbf{I}_n\boldsymbol{\sigma}_e^2$, where \mathbf{I}_s , \mathbf{I}_d and \mathbf{I}_n are identity matrices of orders equal to the number of sires, dams and observations, respectively, $\boldsymbol{\sigma}_s^2$ and $\boldsymbol{\sigma}_d^2$ are the genetic variances of sires and dams, which are equal to one fourth the direct additive genetic variance, and $\boldsymbol{\sigma}_e^2$ is the residual variance. Covariance matrices with a diagonal structure were used for \mathbf{s} and \mathbf{d} , because sires and dams were unrelated in the simulated populations. Solutions for $\boldsymbol{\beta}$, \mathbf{s} , and \mathbf{d} were obtained applying the HMME (Henderson, 1963).

Model 2 (M2) differed from M1 with respect to $\boldsymbol{\beta}$. In M2, $\boldsymbol{\beta}$ was considered as a vector of random effects. So, for M2, $E(\mathbf{y}) = \boldsymbol{\mu}$, $E(\boldsymbol{\beta}) = 0$, $\text{Var}(\mathbf{y}) = \mathbf{X}\mathbf{X}'\boldsymbol{\sigma}_{cg}^2 + \mathbf{Z}_s\mathbf{Z}'_s\boldsymbol{\sigma}_s^2 + \mathbf{Z}_d\mathbf{Z}'_d\boldsymbol{\sigma}_d^2 + \mathbf{I}_n\boldsymbol{\sigma}_e^2$ and $\text{Var}(\boldsymbol{\beta}) = \mathbf{I}_{cg}\boldsymbol{\sigma}_{cg}^2$, where: $\boldsymbol{\mu}$ is a vector of the overall mean, \mathbf{I}_{cg} is an identity matrix of order equal to the number of CGs, and $\boldsymbol{\sigma}_{cg}^2$ is the variance due to CG effects. The expectation and covariance matrices of the other random variables were as in M1. Solutions were also obtained by HMME, but, in this case, the value of the ratio between residual and CG variances ($\boldsymbol{\sigma}_e^2/\boldsymbol{\sigma}_{cg}^2$) was added to the diagonal elements of the coefficient matrix corresponding to the CG effects. Model M2 was used to investigate the considerations made by Van Vleck (1987), Ugarte et al. (1992), and Visscher and Goddard (1993) that benefits could arise by assuming CG as random effect in situations similar to ST3 simulated in the present study, this is, when there is a positive correlation between sire and CG effects.

For model 3 (M3), $\boldsymbol{\beta}$, \mathbf{s} , and \mathbf{d} were considered as vectors of fixed effects, so $E(\mathbf{y}) = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_s\mathbf{s} + \mathbf{Z}_d\mathbf{d}$, $E(\mathbf{e}) = 0$, and $\text{Var}(\mathbf{y}) = \text{Var}(\mathbf{e}) = \mathbf{I}_n\boldsymbol{\sigma}_e^2$. Expected progeny differences (EPD) for sires and dams were obtained by a two step procedure. Firstly, least square (LS) solutions were obtained imposing the restrictions that the sum of the elements in \mathbf{s} and \mathbf{d} were equal to zero. Secondly, solutions for \mathbf{s} and \mathbf{d} were multiplied by the regression factor: $np/(np+\boldsymbol{\sigma}_e^2/(1/4\boldsymbol{\sigma}_a^2))$, where np is the progeny size of the corresponding elements in \mathbf{s} and \mathbf{d} .

For the fourth model (M4), $\boldsymbol{\beta}$ and \mathbf{s} were assumed as vectors of fixed effects and \mathbf{d} as a vector of random effects. For M4, $E(\mathbf{y}) = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_s\mathbf{s}$, $E(\mathbf{d}) = E(\mathbf{e}) = 0$, $\text{Var}(\mathbf{y}) = \mathbf{Z}_d\mathbf{Z}'_d\boldsymbol{\sigma}_d^2 + \mathbf{I}_n\boldsymbol{\sigma}_e^2$, $\text{Var}(\mathbf{d}) = \mathbf{I}_d\boldsymbol{\sigma}_d^2$, and $\text{Var}(\mathbf{e}) = \mathbf{I}_n\boldsymbol{\sigma}_e^2$. Solutions for M4 were obtained from equations similar to those for M1, but without adding the value of the ratio between residual and sire variances ($\boldsymbol{\sigma}_e^2/\boldsymbol{\sigma}_s^2$) to the diagonal elements of the coefficient matrix corresponding to the sire effects. A restriction that the sum of the elements in \mathbf{s} was equal

to zero was imposed and, similarly to M3, solutions for *s* were regressed as a second step using the same regression factors defined for M3.

For all models, estimated breeding values (EBV) for sires and dams were obtained by multiplying EPD by two. The variance components used in the analyses were equal to the true values used to simulate the data, i.e., they were not estimated.

2.4 Model comparison criteria

Models were compared with respect to the biases and mean square errors (MSE) of their solutions. Spearman's rank correlations between TBV and EBV were calculated as an attempt to measure the ability of each model in properly ranking animals. Trying to measure the efficiency of each model in predicting genetic superiority, the means of TBV of sires selected according to the EBV provided by each model were also obtained. For this last criterion, paired t-tests at the 5% significance level were performed.

3 Results and discussion

3.1 Simulated data

Table 2 shows the means and variances of TBVs of young animals and of true CG effects (TCG) according to each simulated situation. As desired, the overall means and variances observed (last row of the table) were very close to the parameters used in the simulation process. Means of TBV by set of CGs were close to zero for ST1, and ranged from -5.52 to 5.36 kg for ST2 to ST4. The magnitude of the genetic differences generated among sets of CGs is plausible to occur with real data, for a trait with heritability close to 0.4.

Table 2 - Means (kg) (and variances (kg²)) of true breeding values (TBV) of young animals and of true contemporary group effects (TCG) by set of CGs and simulated situation – ST^a (average values over 50 replicates)

Set of CGs	TBV			TCG	
	ST1	ST2 to ST4	ST1 and ST2	ST3	ST4
1-40	-0.09 (120.58)	5.36 (102.06)	172.89 (292.50)	197.27 (68.16)	148.37 (64.65)
41-80	-0.07 (119.85)	3.07 (105.01)	172.73 (303.08)	181.97 (9.66)	163.30 (9.13)
81-120	-0.12 (118.71)	-0.13 (105.79)	172.64 (305.74)	172.55 (7.24)	172.55 (7.24)
121-160	-0.03 (119.52)	-3.20 (104.73)	172.50 (315.48)	163.30 (9.13)	181.97 (9.66)
161-200	-0.15 (119.60)	-5.52 (101.73)	172.70 (318.77)	148.37 (64.65)	197.27 (68.16)
Overall ^b	-0.09 (119.78)	-0.08 (119.60)	172.69 (307.44)	172.69 (307.44)	172.69 (307.44)

^a ST1: no mean genetic differences between CGs and no correlation between sire and CG effects.

ST2: mean genetic differences between CGs and no correlation between sire and CG effects.

ST3: mean genetic differences between CGs and positive correlation between sire and CG effects.

ST4: mean genetic differences between CGs and negative correlation between sire and CG effects.

^b Simulated mean and variance were 0 and 120 for TBV and 172.5 and 300 for TCG.

Variances of TBV within sets of CGs were reduced for ST2 to ST4, but they were almost the same among the sets of CGs, i.e., no heterogeneity of variance was generated. Means of TCG effects by set of CGs were close to 172.50 for ST1 and ST2, and ranged from 148.37 to 197.27 kg for ST3 and ST4. Heterogeneity of TCG variances among sets

of CGs was observed for ST3 and ST4. Following the simulation process, ST1 was characterized by no mean genetic differences among sets of CGs and no correlation between TBVs of young animals and TCG effects ($r_{G,E}$); ST2, ST3 and ST4 showed mean genetic differences among sets of CGs, and $r_{G,E}$ equal to 0.00, 0.34, and -0.34, respectively (correlation between TBV of sires and TCG effects were equal to zero for ST1 and ST2, 0.68 for ST3 and -0.68 for ST4).

3.2 Solutions for contemporary group effects

Table 3 shows bias and MSE of ECG effects given by each model. Overall values of bias and MSE and their corresponding values by set of CGs were obtained. According to the results of Table 3, ECG effects from model M1 were biased, except for situation ST1. M1 provided biased ECG effects for situations where mean genetic differences between CGs occurred (ST2 to ST4). Sets of CGs having animals with superior genetic merit had their effects overestimated (and vice versa), agreeing with the considerations of Harvey (1979) and Fries and Schenkel (1993) that solutions for fixed effects from HMME can be contaminated by the true breeding values. It is interesting to note that, if all CGs are jointly considered (overall bias), the bias is not observed.

Biases and MSE for M1 were exactly the same for situations ST2, ST3 and ST4, indicating that the main cause of the problem is the existence of mean genetic differences between CGs, and not due to genetic by environmental covariance. Even when $r_{G,E}$ was null, solutions from HMME were biased (solutions for M1 for situation ST2).

Considering CG effects as random (model M2) resulted in small reduction of bias in comparison to model M1 for situation ST2. The reductions in MSE for situations ST1 and ST2 were also small. These results are related to the relatively large size of the CGs and the small value of the residual by CG variance ratio used in the simulation process (Henderson, 1973). For situation ST3 ($r_{G,E} = 0.34$), in agreement with Ugarte et al. (1992) and Visscher and Goddard (1993), model M2 provided better results than M1 with respect to bias and MSE. The regressed solutions for CG effects, obtained when considering CGs as random effects, were less contaminated by the true breeding values in comparison with model M1. The same reduction in bias was not observed for situation ST4 ($r_{G,E} = -0.34$). For this situation, bias and MSE for model M2 were larger than for M1, as was also reported by Visscher and Goddard (1993). Therefore, these results suggest that the decision of treating CGs as fixed or random do not depend only on the size of the CGs and on the residual by CG variance ratio, but also on the direction of a possible genetic by environmental covariance (correlation).

In agreement with Harvey (1979) and Fries and Schenkel (1993), ECG effects from model M3, where all effects were treated as fixed, were not biased in all the simulated situations (ST1 to ST4). However, as expected (Henderson, 1978), model M3 had larger MSE than M1, due to higher prediction error variances (PEV; $PEV = MSE - bias^2$). Recall that LS solutions were obtained as a first step in M3 and that each dam had only two offspring, which likely contributed to the observed results. Bias and MSE in M3 were the same for ST1 to ST4, i.e., their values were independent of the presence of mean genetic differences and genetic by environmental correlation.

Table 3 - Bias and mean square error (MSE) of estimated contemporary group effects, given by each model, by set of CGs and simulated situation – ST^a (average values over 50 replicates)

ST1								
Set of CGs	Model 1 (M1)		Model 2 (M2)		Model 3 (M3)		Model 4 (M4)	
	bias (kg)	MSE (kg ²)	bias	MSE	bias	MSE	bias	MSE
1-40	0.13	10.92	0.11	10.43	0.06	23.74	0.15	11.30
41-80	-0.03	11.56	-0.03	10.90	0.04	22.59	-0.02	11.90
81-120	-0.07	11.87	-0.06	11.54	0.00	23.21	-0.06	12.10
121-160	0.07	11.03	0.08	10.64	0.05	22.95	0.04	11.20
161-200	-0.11	12.22	-0.09	12.04	-0.15	24.47	-0.12	12.57
overall	0.00	11.52	0.00	11.11	0.00	23.39	0.00	11.81
ST2								
Set of CGs	Model 1 (M1)		Model 2 (M2)		Model 3 (M3)		Model 4 (M4)	
	bias	MSE	bias	MSE	bias	MSE	bias	MSE
1-40	3.13	20.73	2.92	18.98	0.06	23.74	0.15	11.30
41-80	1.75	14.63	1.63	13.57	0.04	22.59	-0.02	11.90
81-120	-0.07	11.90	-0.07	11.56	0.00	23.21	-0.06	12.10
121-160	-1.73	14.18	-1.61	13.33	0.05	22.95	0.04	11.20
161-200	-3.08	21.54	-2.88	20.18	-0.15	24.47	-0.12	12.57
overall	0.00	16.60	0.00	15.52	0.00	23.39	0.00	11.81
ST3								
Set of CGs	Model 1 (M1)		Model 2 (M2)		Model 3 (M3)		Model 4 (M4)	
	bias	MSE	bias	MSE	bias	MSE	bias	MSE
1-40	3.13	20.73	1.48	12.36	0.06	23.74	0.15	11.30
41-80	1.75	14.63	0.96	11.56	0.04	22.59	-0.02	11.90
81-120	-0.07	11.90	-0.06	10.97	0.00	23.21	-0.06	12.10
121-160	-1.73	14.18	-0.94	11.18	0.05	22.95	0.04	11.20
161-200	-3.08	21.54	-1.43	13.39	-0.15	24.47	-0.12	12.57
overall	0.00	16.60	0.00	11.89	0.00	23.39	0.00	11.81
ST4								
Set of CGs	Model 1 (M1)		Model 2 (M2)		Model 3 (M3)		Model 4 (M4)	
	bias	MSE	bias	MSE	bias	MSE	bias	MSE
1-40	3.13	20.74	4.38	29.53	0.06	23.74	0.15	11.30
41-80	1.75	14.63	2.32	16.15	0.04	22.59	-0.02	11.90
81-120	-0.07	11.90	-0.06	11.07	0.00	23.21	-0.06	12.10
121-160	-1.73	14.18	-2.29	15.70	0.05	22.95	0.04	11.20
161-200	-3.08	21.54	-4.34	30.11	-0.15	24.47	-0.12	12.57
overall	0.00	16.60	0.00	20.51	0.00	23.39	0.00	11.81

^a ST1: no mean genetic differences between CGs and no correlation between sire and CG effects.

ST2: mean genetic differences between CGs and no correlation between sire and CG effects.

ST3: mean genetic differences between CGs and positive correlation between sire and CG effects.

ST4: mean genetic differences between CGs and negative correlation between sire and CG effects.

Similar to model M3, bias and MSE of ECG effects given by M4 were the same across all simulated situations. M4 showed no bias and a MSE similar to those from model M1 for situation ST1. Hence, for situations where dams have few progeny and are not expected to cause mean genetic differences between CGs, and where sires have progeny size relatively large, M4 seems to be a compromise in removing bias and not

providing CG solutions with inflated PEV. With respect to bias and MSE, model M4 showed better results than M1 for situations ST2 to ST4. Even when the usual assumption required by HMME to provide unbiased estimates of CG effects was met (ST1), model M4 was not inferior to M1 with respect to bias and MSE.

3.3 Solutions for sires

Table 4 shows values of bias and MSE of sires' EBVs given by each model. Sperman's rank correlation (CORR) between TBV and EBV is also shown. Overall bias, MSE and CORR, and values by set of sires were obtained.

For situations ST1, EBVs from all the studied models were unbiased. Model M3 had the highest MSE and the lowest CORR. All the other models showed similar MSE and CORR.

For situations ST2 to ST4, the observed biases in EBV from models M3 and M4 within sets of sires were likely due to the use of a regression technique, where extreme sires had their EBVs proportionally more regressed towards zero than intermediate sires. For models M1, EBV had an extra bias because, as previously shown, ECG effects for this model were confounded with genetic effects. The best sires showed downward biases because part of their effects was estimated as CG effect, while the worst sires showed upward biases.

When considering CG as a random effect (M2), part of true CG effects was incorporated into the EBV. In agreement with Visscher and Goddard (1993), the consequence of this confounding was that the results for M2 were, in comparison with M1, favorable (smaller bias and MSE and higher CORR) for situations ST2 and ST3 and unfavorable for ST4. Genetic by environmental correlation values for situations ST2, ST3 and ST4 explain these results. In ST4, for example, where best sires were associated with worst CGs, the part of true CG effects, which was incorporated into EBV, when treating CGs as random, resulted even more (in comparison to M1) in underestimation of the best sires and overestimation of the worst ones.

For situations ST1 to ST4, CORR by set of sires were smaller for model M3 than for M1, due to higher PEV. However, it is interesting to note that M3 had higher overall CORR than M1 for situations ST2 to ST4 due to a confounding of sire and CG effects in M1 solutions. Similar to the results reported by Harvey (1979), overall CORR of M3 remained constant for ST1 to ST4, while CORR of M1 was higher for ST1 than for the other situations.

Mean genetic differences between animals in CGs (situations ST2 to ST4) reduced the ability of M4 in properly ranking animals by set of sires, as happened with the other models, because sires of similar merit tended to be compared more frequently among themselves. However, the overall CORR of M4 remained the same (0.80) for all situations, and was superior to those of the other models for situations ST2 to ST4.

Trying to measure the efficiency of the models in predicting genetic superiority for each simulated situation, the average TBVs of top sires were calculated and shown in Table 5. Three selection intensities were applied, named 50% (top50), 20% (top20) and 2% (top2) of the best sires. The last 3 rows of the Table 5 shows the average TBV of top sires in a hypothetical situation where one would be able to select them according to their TBV.

Table 4 - Bias and mean square error (MSE) of estimated breeding values (EBVs) of sires and Spearman's rank correlations between EBVs and true breeding values (CORR) for each model, set of sires, and simulated situation – ST^a (average values over 50 replicates)

ST	Set of Sires	Model 1 (M1)			Model 2 (M2)			Model 3 (M3)			Model 4 (M4)		
		bias	MSE	CORR	bias	MSE	CORR	bias	MSE	CORR	bias	MSE	CORR
ST1	1-50	0.06	39.72	0.79	0.07	39.75	0.79	-0.06	72.27	0.67	0.02	40.45	0.79
	51-100	0.12	41.20	0.78	0.13	41.13	0.78	0.20	69.12	0.68	0.12	41.60	0.78
	101-150	0.05	38.92	0.80	0.05	38.85	0.80	0.01	69.81	0.67	0.04	39.23	0.80
	151-200	0.08	39.35	0.80	0.08	39.23	0.80	0.01	67.17	0.68	0.10	39.42	0.80
	201-250	0.35	39.57	0.80	0.33	39.58	0.80	0.49	67.41	0.69	0.37	39.75	0.80
	overall	0.13	39.75	0.80	0.13	39.71	0.80	0.13	69.16	0.69	0.13	40.09	0.80
ST2	1-50	-8.06	95.55	0.51	-7.84	92.18	0.51	-4.55	85.52	0.38	-4.46	53.45	0.51
	51-100	-3.59	40.53	0.21	-3.46	39.58	0.22	-1.41	58.99	0.18	-1.49	32.35	0.21
	101-150	0.00	26.51	0.22	0.00	26.46	0.22	-0.05	58.91	0.16	-0.02	28.92	0.22
	151-200	3.94	41.72	0.25	3.81	40.63	0.25	1.76	59.18	0.19	1.85	32.08	0.25
	201-250	8.38	99.73	0.51	8.16	96.12	0.51	4.92	83.76	0.40	4.80	54.72	0.51
	overall	0.13	60.81	0.65	0.13	59.00	0.66	0.13	69.27	0.69	0.13	40.30	0.80
ST3	1-50	-8.05	95.55	0.51	-6.40	71.68	0.51	-4.55	85.50	0.38	-4.46	53.44	0.51
	51-100	-3.59	40.53	0.21	-2.60	34.17	0.21	-1.41	58.99	0.18	-1.49	32.35	0.21
	101-150	0.00	26.51	0.22	-0.01	26.32	0.22	-0.05	58.91	0.16	-0.02	28.92	0.22
	151-200	3.94	41.72	0.25	2.96	34.83	0.25	1.75	59.17	0.19	1.84	32.08	0.25
	201-250	8.38	99.73	0.51	6.72	74.72	0.51	4.91	83.74	0.40	4.80	54.71	0.51
	overall	0.13	60.81	0.65	0.13	48.35	0.74	0.13	69.26	0.69	0.13	40.30	0.80
ST4	1-50	-8.06	95.57	0.51	-9.29	116.97	0.51	-4.55	85.54	0.38	-4.46	53.46	0.51
	51-100	-3.59	40.53	0.21	-4.33	46.53	0.21	-1.41	58.99	0.18	-1.49	32.36	0.21
	101-150	0.00	26.51	0.22	0.00	26.66	0.22	-0.05	58.91	0.16	-0.02	28.92	0.22
	151-200	3.94	41.72	0.25	4.67	48.08	0.25	1.76	59.18	0.19	1.85	32.08	0.25
	201-250	8.38	99.75	0.51	9.62	122.19	0.51	4.92	83.78	0.40	4.80	54.73	0.51
	overall	0.13	60.82	0.65	0.13	72.08	0.56	0.13	69.28	0.69	0.13	40.31	0.80

^a ST1: no mean genetic differences between CGs and no correlation between sire and CG effects.

ST2: mean genetic differences between CGs and no correlation between sire and CG effects.

ST3: mean genetic differences between CGs and positive correlation between sire and CG effects.

ST4: mean genetic differences between CGs and negative correlation between sire and CG effects.

For models M1 and M2, effects of mean genetic differences between CGs (comparing ST1 with ST2 to ST4) had, in general, a greater impact on average TBV of selected top sires when selection intensity was from low to moderate than when it was high. For model M1, average TBV of top50 and top20 were lower for situations ST2 to ST4 than for ST1 ($p < 0.05$). The same was observed for model M2 ($p < 0.05$). The ability of models M3 and M4 in selecting sires was independent of the simulated situations, i.e., results for situation ST1 and situations ST2 to ST4 were not different ($p > 0.05$). For situation ST2 to ST4, model M1 showed higher average TBV than M3 for top2, but lower for top50, and model M4 had higher average TBV than M1 for all selection intensities ($p < 0.05$). Contrasting models M4 and M2, model M4 was superior to M2 for top50 and top20 in situation ST3 and for all selection intensities in ST4 ($p < 0.05$).

Table 5 - Means (kg) of true breeding values (TBVs) of sires selected according to estimated breeding values, given by each model, for different selection intensities and simulated situations – ST^a (average values over 50 replicates)

		Model 1 (M1)			
N° of selected Sires	ST1	ST2 - ST4			
125 (50%)	6.92	5.61			
50 (20%)	12.28	10.37			
5 (2%)	20.73	20.64			
		Model 2 (M2)			
N° of selected Sires	ST1	ST2	ST3	ST4	
125 (50%)	6.90	5.73	6.40	4.84	
50 (20%)	12.29	10.53	11.47	9.23	
5 (2%)	20.68	20.59	21.11	20.26	
		Model 3 (M3)			
N° of selected Sires	ST1	ST2 - ST4			
125 (50%)	5.99	5.99			
50 (20%)	10.68	10.60			
5 (2%)	18.01	18.73			
		Model 4 (M4)			
N° of selected Sires	ST1	ST2 - ST4			
125 (50%)	6.93	6.92			
50 (20%)	12.28	12.28			
5 (2%)	20.94	21.29			
		Selection based on TBV			
N° of selected Sires	ST1 - ST4				
125 (50%)	8.52				
50 (20%)	15.05				
5 (2%)	25.84				

^a ST1: no mean genetic differences between CGs and no correlation between sire and CG effects.
 ST2: mean genetic differences between CGs and no correlation between sire and CG effects.
 ST3: mean genetic differences between CGs and positive correlation between sire and CG effects.
 ST4: mean genetic differences between CGs and negative correlation between sire and CG effects.

Empirical properties of dam solutions were not shown because all the models yielded similar results, regardless the simulated situation, as it was expected, because dams were not a source of mean genetic differences between CGs in this study.

Estimated breeding values of young animals were also obtained, by back-solving (Henderson, 1984), according to the solutions provided by each model. Considering model M1 and situations ST2 to ST4, EBVs of young animals were not as affected by bias

as sires' EBVs (results not shown). This can be explained by the opposite direction of biases found on sire and CG solutions, which tended to cancel each other off while estimating the Mendelian sampling effect.

3.4 General discussion

Empirical statistical and genetic properties of solutions from HMME were investigated for situations where sires were non-randomly used across CGs. Situations ST2 to ST4 are cases of "L'u type of selection" following Henderson's (1973) terminology, as sires were allocated to CGs based on "external" information (prior knowledge of their TBV). According to Henderson (1973), if sire's progeny were allocated to CGs based on the best linear unbiased prediction (BLUP) of their breeding values, solutions from model M1 would be unbiased.

In practice, mean genetic differences between CGs are usually generated as a result of farmers' decisions (e.g., which sires to use and how their progeny are allocated in different management groups), which are not based only on BLUP information. These decisions are also, obviously, not based on TBV, but maybe on other criteria that are correlated with TBV and which information is not available or not used in the evaluation, which ultimately may yield to genetic differences among levels of fixed effects and, as a result, to expected values of the distribution of genetic effects that are dependent on the levels of the fixed effects in the model. Using model M1 and regular HMME under these conditions resulted in biased solutions and reduced ability of properly ranking animals.

Henderson (1973) stated that biases due to differences in average merit of herds associated with sires would be eliminated if herds were treated as fixed effects (as CG effects in model M1). The results of the present study are not in disagreement with this statement because the situation which Henderson (1973) was referring to is not like ST3 or ST4, but another one where the average CG effects differ across sires, but the average merit of sires does not differ across CGs.

If one expresses breeding values solutions (\hat{u}) from HMME as $\hat{u} = \mathbf{GZ}'\mathbf{V}^{-1}(\mathbf{y}-\mathbf{X}\boldsymbol{\beta}^*)$, it becomes clearer that biases in $\boldsymbol{\beta}^*$ (ECG) can affect solutions for \hat{u} . If $\boldsymbol{\beta}$ (CG) is treated as fixed, Henderson (1973) mentioned that the expected value of \hat{u} provided by HMME is invariant to $\boldsymbol{\beta}$, what does not necessarily mean that \hat{u} is free from possible bias in $\boldsymbol{\beta}^*$.

Unbiased estimators may be inadmissible under the MSE criterion, i.e., biased estimators with smaller MSE may exist (Gianola, 1990). However, regarding HMME and the simulated situations ST2 to ST4, $\boldsymbol{\beta}^*$ was contaminated by genetic effects, what reduced the ability of HMME to discriminate better the animals, as can be observed in Table 4, contrasting CORR of model M1 for situation ST1 versus for situations ST2 to ST4. Biases in solutions from regular HMME were also reported by Harvey (1979), Simianer and Wollny (1989), Ugarte et al. (1992), Fries and Schenkel (1993), Visscher and Goddard (1993), Torres Jr. et al. (1997), and Täubert et al. (2002).

Simianer and Wollny (1989), for instance, stated that the strategy of treating daughters of genetically superior test bulls in order to improve their proofs was shown to have the opposite effect. Similar to the results of the present study, they observed that part of the genetic superiority of the best sires was interpreted as effect of treatment and, consequently, sires' breeding values were underestimated.

Torres Jr. et al. (1997) simulated a situation comparable to ST3 and observed higher biases in solutions from HMME when sires were unrelated, as was the case in the present

study. The presence of additive genetic relationship among sires reduced, but did not eliminate the biases.

Treating CGs as random (model M2) seems not to be a good alternative if there is evidence of a negative genetic by environmental covariance. Visscher and Goddard (1993) discussed some practical situations where sire and CG effects may be negatively associated and stated that, generally, in practice, the covariance between sires and CGs is merely the result of farmers choosing sires and this association should not be used to predict the performance of future progeny of the sires, as it is not a population parameter in the usual sense. When assuming CGs as random, in the presence of mean genetic differences between CGs, Ugarte et al. (1992) observed that the reduction in PEV did not trade off the increase in bias, for situations of CGs with small sizes and low values of residual by CG variance ratios.

The alternative models M3 and M4 (first step solutions) can be viewed as special cases of Henderson's Selection Model to account for "L'u type of selection" (Henderson, 1975), where the matrix which describes the "selection" process (L') was considered equal to an identity matrix for sires and dams in M3, and equal to an identity matrix for sires and a null matrix for dams in M4. This approach was suggested by Henderson (1973) when L' was difficult to define, as is usually the case with field data. Under the simulated situations, model M3 was not a good alternative model because its solutions showed higher PEV and MSE than the other models. On the other hand, model M4 seemed to be a model which compromises between removing bias and not providing solutions with inflated PEV.

Using genetic groups (Westell et al. 1988) could be an alternative to reduce or eliminate the bias observed with M1 in situations where mean genetic differences between CGs exist. This alternative was not investigated in the present study because with field data the proper definition of the genetic groups is usually not as straightforward as with simulated data (Kuehn et al., 2007). The definition of unnecessary genetic groups can reduce the prediction accuracy (Torres Jr. et al., 1997) and even result in estimability problems (Sullivan, 2002).

It is worthwhile to note that results of contrasting biased and unbiased methods of estimation can be highly dependent on the part of the parameter space that one is situated in (Gianola, 1990; Simianer, 1991), and generalizations with respect to the results of the present study should be made with caution.

Henderson (1973, 1975) presented some situations (e.g., when mean genetic differences are generated based on translation invariant function of the data) where solutions from models like M3 and M4 in the present study could be biased, what highlights that there is not a general statistical solution for the $E(a_i)=0$ violation problem, and the need for further studies.

Conclusions

Empirical evidences showed that solutions from regular Henderson's Mixed Model Equations, assuming genetic effects as random variables with null expectation and environmental effects as fixed variables, can have poorer statistical and genetic properties than anticipated when the expected values of the distribution of genetic effects depend on the levels of the fixed effects in the model and on information not available or not used in

the genetic evaluation process. Under these circumstances, alternative models fitting genetic effects or part of them as fixed variables can yield higher genetic response.

Results suggest that a dependence of expected values of the distribution of genetic effects with respect to the levels of the fixed effects in the model is a more important source of bias on estimated breeding values, given by Henderson's Mixed Model Equations, than a non-null correlation between genetic and environmental effects.

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CARVALHEIRO, R.; SCHENKEL, F. S.; FRIES, L. A.; QUEIROZ, S. A.; MILLER, S. P. Propriedades empíricas das soluções das equações de modelo misto de Henderson para diferentes situações de associação entre touros e grupos de contemporâneos. *Rev. Bras. Biom.*, São Paulo, v.25, n.3, p.7-21, 2007.

- *RESUMO: Simulações foram conduzidas objetivando investigar propriedades empíricas das soluções das equações de modelo misto de Henderson (EMMH) sob quatro diferentes situações (ST1 a ST4) de associação entre touros e grupos de contemporâneos (GC). Os touros tiveram progênie distribuída nos GCs independentemente de seus valores genéticos (VG) na situação ST1, e de acordo com seus VGs nas situações ST2 a ST4. As EMMH foram aplicadas sob um modelo que incluiu os efeitos de GC como fixo, e touro e vaca como aleatórios (M1). Três modelos alternativos foram usados (M2 a M4). GC, touro e vaca foram assumidos como efeitos aleatórios no modelo M2, e como efeitos fixos em M3. No modelo M4, consideraram-se os efeitos de GC e touro como fixos e vaca como aleatório. Na situação em que não houve diferenças genéticas entre GCs (ST1), os modelos M1, M2 e M4 apresentaram resultados semelhantes entre si, enquanto que M3 forneceu soluções com maior quadrado médio do erro de predição. Na presença de diferenças genéticas entre GCs (ST2 a ST4), as soluções do M1 foram viesadas, o que reduziu sua habilidade em classificar apropriadamente os animais. Nestas situações, o modelo M4 apresentou, no geral, melhores resultados que os outros modelos estudados.*
- *PALAVRAS-CHAVE: Avaliação genética, BLUP, modelos mistos, viés*

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