Genetic parameters for growth traits of a Brazilian *Bos taurus* x *Bos indicus* beef composite

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ABSTRACT. The genetic analysis of composite data is very complicated, mainly because it is necessary to adjust data to the effects of heterosis and breed complementarity, and because there is usually considerable confounding of these data with several other effects, such as contemporary group effects, breed composition of the animal and maternal breed composition, among others. Data on birth weight (N = 151,083), weaning weight adjusted to 205 days (N = 137,257), yearling weight adjusted to 390 days (N = 61,410), weight gain from weaning to yearling (N = 56,653), and scrotum circumference (N = 23,323) and muscle score (N = 54,770), both adjusted to 390 days, from *Bos taurus x Bos indicus* composite beef calves born from 1994 to 2003 were analyzed to estimate (co)variance components and genetic parameters of growth traits. The animals belonged to the Montana Tropical® program. Estimation was made by three models that approach adjustment to heterozygosis in order to suggest the best model. The RM model included contemporary groups, class of age of dam, outcrossing percentages for direct and

maternal effects, and direct and maternal additive genetic breed effects as covariates; the R model was the same as RM, but without additive maternal breed effects, and H was the same as RM, but not considering any additive breed effect. Both R^2 values and consistency of genetic parameters indicate that the more complex model (RM), which considers maternal and individual additive genetic breed effect, produces the best estimates when compared to other models. The R model seems to overestimate (co)variance components. The magnitudes of direct and maternal heritability estimates, obtained in this study, would permit genetic improvement for weight and growth traits, as much by selection of direct genetic effects for weight and growth as for the improvement of maternal performance, but in different lineages. Therefore, the correlations between these effects were unfavorable.

Key words: Composite beef cattle, (Co)variance components, Growth, Tropics, Montana Tropical®

INTRODUCTION

The Brazilian beef industry is a very large business that involves close to 200 million head of cattle, 7.5 million jobs and generates more than US$25 billion revenues, and it has a need of around 450,000 young replacement bulls per year. However, Brazilian beef productivity is still low and there is a strong need of improvement in herds. One of the options available to the Brazilian beef industry is to explore beef composites. One *Bos taurus x Bos indicus* beef composite program started in 1994 (Ferraz et al., 2002), based on the experiments of the U.S.D.A. Roman Huskra Meat Animal Research Center, Clay Center, Nebraska (Gregory et al., 1993, 1994a,b). The main goals of the program were to produce bulls with the following features: a) they are genetically evaluated and considered superior; b) they produce, in combination with genes of the regular Zebu or crossbred cows which are the basis of the Brazilian production system, significant values of heterosis and complementarity in the progeny; c) they are adapted to tropical and subtropical conditions, breeding under pasture conditions; d) they show reproductive longevity under pasture conditions, and e) they should have a worth price, making superior genetic seed stock accessible to small and medium size producers, without the need of artificial insemination.

All selection procedures were based on data collection developed for tropical and subtropical beef cattle systems under grazing conditions. It is an alternative to more complex systems of crossbreeding with management requirements that are similar to straight breeding (Cundiff and Gregory, 1999). Details of the development of that composite were shown by Ferraz et al. (1999b), Ferraz and Eler (2000) and Mourão (2005).

However, the genetic analysis of composite data is very complicated, mainly because it is necessary to adjust data to the effects of heterosis and breed complementarity, and there is usually a considerable amount of confounding of these data with several other effects, such as contemporary group effects, breed composition of the animal, and maternal breed composition, among others. According to Gregory et al. (1991a,b) who suggested that heterosis

is linearly proportional to heterozygosis, which was confirmed by Arthur et al. (1999), several investigators have used regression on heterozygosis levels to adjust crossbred or composite data to make those non-additive factors (Arthur et al., 1994; Alencar et al., 1995; Ferraz et al., 1999a,b; Dal-Farra et al., 2002; Prayaga, 2003, 2004; Mourão, 2005).

However, depending on how the covariates are used, some additive breed effects can be removed with those covariates, which leads to underestimates of (co)variance components, bias in expected progeny difference estimation, and errors in selection procedures.

The objective of this paper was to estimate (co)variance components for growth traits of a *Bos taurus x Bos indicus* composite population, using three different models that approach the adjustment to heterozygosis and compare them to determine the best model for such population.

MATERIAL AND METHODS

The Montana Tropical® program started with Nellore and crossbred cows. The foundation population included more than thirty breeds, which should introduce considerable difficulties to analysis. In order to simplify the control of breed composition, the breeds were classified as follows according to their biological types, as described by Ferraz et al. (1999b). i) Biological type N - where the *Bos indicus* animals (Zebu breeds) were grouped, including the breeds Gyr, Guzerath, Indubrazil, Nellore, Tabapuan, and Boran (an African Zebu breed). Those breeds contributed to the project with high heat and parasite tolerance and carcass yield, besides very good maternal ability. ii) Biological type A - *Bos taurus* animals, adapted to tropical conditions by long time living in tropics. This group included breeds such as Afrikander, Belmont Red, Bonsmara, Caracu, Romosinuano, Senepol, and Tuli. They contributed to the project with high fertility and good meat quality, besides growth performance and a certain adaptation to tropical conditions. iii) Biological type B - *Bos taurus*, of British origin, included breeds such as Aberdeen Angus, Red Angus, Devon, South Devon, Hereford, and Red Poll, with an important contribution to sexual precocity, early fat deposition, very good carcass and meat quality, and also growth performance. iv) Biological type C - *Bos taurus*, of Continental European origin, included breeds such as Charolais, Gelbvieh, Limousin, Brown Swiss, Simmental, and others, that contributed with high growth performance, carcass yield and quality.

The breed composition system included the percentage of each breed for all animals, but for analysis purposes, those percentages were added within the NABC breed control system, ignoring intra-group heterosis and breed complementarity. The contribution from each biological type to breed composition of animals and dam was also calculated, and from the combination of different biological types, direct and maternal heterozygosis coefficients were calculated. The outcrossing percentage was defined as $h_{ij} = \Sigma r_i r_j$ for all i*th* sire breed different from j*th* dam breed, where r is the fraction of the biological type in NABC system.

Material

The Montana Tropical® composite program works as a franchise system started in 1994, using crossbred and Nellore cows from several farms spread from northern Uruguay and southern Brazil to northern Brazil. The majority of the ranches are located between 10°S and 24°S and 40°W and 70°W (Figure 1 and Table 1).

Figure 1. Geographic distribution of farms within Montana Tropical® program.

Table 1. Location of farms/Brazilian states regarding the farms where the animals were born, including relative (N%) and absolute (N) frequencies on data set.

State	Farms	N per farm	N% per farm	N total	N% total
MS	12	290 to 26,878	0.17 to 16.12	76,607	45.92
SP	6	889 to 11,999	0.53 to 7.19	36,206	21.70
GO	4	2483 to 9921	2.67 to 5.95	21,158	12.69
RS	6	277 to 5236	0.17 to 3.14	12,417	7.44
MG	2	3464 to 5069	2.08 to 3.04	8,533	5.12
MT	4	266 to 2711	0.16 to 1.63	5,404	3.25
Others	5	83 to 2685	0.05 to 2.87	4,787	2.87
Total	39	-	-	166,764	100.00

MS = Mato Grosso do Sul; SP = São Paulo; GO = Goiás; RS = Rio Grande do Sul; MG = Minas Gerais; MT = Mato Grosso.

Data on birth weight (BW, kg, N = 151,083), weaning weight adjusted to 205 days (WW, kg, N = 137,257), yearling weight adjusted to 390 days (YW, kg, N = 61,410), post-weight gain from weaning to yearling (WG, kg, N = 56,653), and scrotum circumference (SC, cm, N = 23,323) and muscle score (MUS, N = 54,770), both adjusted to 390 days, from calves born from 1994 to 2003 in that composite program were analyzed to estimate (co)variance components and genetic parameters.

The animals were kept grazing in tropical pastures, the majority in acid soils with *Brachiaria* spp grass. A salt and mineral supplementation was given during all the years. Some farms supplement with mineral salt enriched with a protein source in the dry season.

Animals were identified and weighed at birth, weaning and around one year of age. At around yearling, muscle score (varying from 1, very poor, to 6, very good) was taken for all animals. SC (cm) was taken for all males kept after 12 months of age. The databank controlled information on performance, breed composition and pedigree of all animals. Animals were

grouped in contemporary groups (CG) that consider the year of birth, farm, and management group within farm and sex.

Data culling criteria were as follows: a) animals with missing parents or from multiple sires or pastures; b) CG with less than five animals; d) CG with progeny from a unique sire; e) CG with all animals from a unique breed composition; f) data from animals with breed composition incompatible with parents, and g) outliers on box-plot by traits (Table 1). The number of CG varied from 1437 (BW), 2120 (WW), 1824 (WG), 1909 (YW), 820 (SC), and 1667 (MUS). The animals with records had 881 sires and 98,288 dams.

Ages of dams at calving (AOD) were grouped into seven classes, and adjustment factors were considered as deviation of least square solutions in relation to class 4, the class that represents the dam at physiological maturity. Table 2 shows the criterion utilized to group classes of AOD, and their absolute frequency. That criterion was defined by the biological behavior and data distribution.

Table 2. Minimum and maximum age (months) and observed number of birth weight (BW), at 205 days of age (weaning weight, WW) and at 390 days of age (yearling weight, YW) for each class of age of dam at calving (AOD).

Class of AOD	Age of dam at calving (months)		Absolute frequency		
	Minimum	Maximum	BW	WW	YW
1	-	≤27	18,077	17,833	9,193
2	>27	≤41	35,209	30,351	13,726
3	>41	≤59	27,040	25,657	12,199
4	>59	≤119	53,213	52,090	21,180
5	>119	≤143	6,599	6,574	2,928
6	>143	≤167	2,867	2,862	1,313
7	>167	-	1,425	1,890	871

The average contribution of each biological type to genetic group of animals (Table 3) and absolute frequencies according to genetic group in different traits (Table 4) were also obtained.

Table 3. The average and standard deviation (SD) of composition based on NABC system, as a percentage per genetic group (GG).

GG[1]	Average composition (SD)			
	N	A	B	C
3/4B	10 (13.1)	1 (4.2)	74 (7.8)	15 (10.6)
3/4N	72 (8.0)	7 (10.1)	11 (10.3)	10 (10.0)
M4444	25 (0.4)	25 (0.1)	25 (0.4)	25 (0.6)
M4480	25 (0.5)	25 (0.0)	50 (0.6)	0 (0.4)
M4804	25 (0.4)	50 (0.0)	0 (0.1)	25 (0.4)
M4840	25 (0.3)	50 (0.0)	25 (0.3)	0 (0.2)
MX	23 (10.5)	44 (18.1)	22 (15.6)	11 (9.1)
PB	0 (0.5)	0 (0.3)	100 (1.5)	0 (1.4)
PN	100 (0.9)	0 (0.0)	0 (0.5)	0 (0.6)
F$_1$ (N x A)	50 (1.6)	50 (0.3)	0 (1.1)	0 (1.0)
F$_1$ (N x B)	50 (0.7)	0 (0.3)	50 (0.6)	0 (0.5)
F$_1$ (N x C)	50 (0.4)	0 (0.2)	0 (0.8)	50 (0.7)
Others	35 (16.1)	11 (20.5)	32 (16.7)	22 (14.7)

[1]The animals were classified into genetic groups, using the breed composition (NABC system) as criterion for classification; other details can be obtained in Mourão (2005).

Table 4. The absolute frequencies according to genetic group (GG) in different traits.

GG[1]	Absolute frequencies					
	BW	WW	WG	YW	SC	MUSC
3/4B	2,855	1,876	533	743	294	495
3/4N	1,881	2,170	543	565	104	389
M4444	11,497	10,869	5,192	5,692	2,809	5,572
M4480	3,125	2,681	1,507	1,634	718	1,541
M4804	15,933	13,753	6,649	7,173	3,030	6,766
M4840	33,153	32,612	17,078	17,876	8,213	17,018
MX	31,235	27,288	12,611	13,521	5,956	12,385
PB	1,713	1,028	218	364	171	221
PN	2,047	1,225	111	113	42	45
F$_1$ (N x A)	2,394	1,709	540	629	121	499
F$_1$ (N x B)	32,271	29,836	8,297	9,339	1,058	7,045
F$_1$ (N x C)	5,114	5,407	1,123	1,316	174	913
Others	7,864	6,801	2,251	2,445	633	1,881
Total	151,083	137,257	56,653	61,410	23,323	54,770

[1]The animals were classified into genetic groups, using the breed composition (NABC system) as criterion for classification; other details can be obtained in Mourão (2005).

Estimates for direct and maternal heterosis effects, expressed as outcrossing percentages among N, A, B and C biological types, were obtained as means square solutions for linear covariates from analysis of variance, in a procedure similar to the proposed by Dickerson (1973) and used by Mourão et al. (2007).

Statistical analyses

(Co)variance components for BW, WW, WG, YW, SC, and MUS were analyzed with the help of the restricted maximum likelihood method (REML), using three different animal models and the software MTDFREML (Boldman et al., 1995), using as convergence criteria variation of 10^{-9} between log of likelihood function on different rounds. The models considered were: model RM which included CG, AOD, outcrossing percentages for direct and maternal effects and direct and maternal additive genetic breed effects (covariates); model R, the same as in model RM, but not considering the additive maternal breed effects, and model H, the same as in model RM, but not considering any additive breed effect. Total heritability (h^2_t) was calculated according to Willham (1972).

RESULTS AND DISCUSSION

Coefficients of determination (R^2, %) varied from 25.2 to 73.4 on the different traits and models, being always highest with model RM and lowest for model H. Residual coefficients of variation varied from 9.5 to 19.24% and averages of traits were 32.47 kg (BW), 192.16 kg (WW), 118.53 kg (WG), 270.7 kg (YW), 28.3 cm (SC), and 4.1 (MUS). (Co)variance components and genetic parameters for each trait and model and the glossary of symbols, are presented in Table 5.

Table 5. Estimates of (co)variance components and genetic parameters from models RM, R and H for growth traits in a *Bos taurus x Bos indicus* beef composite.

Model	σ^2_a	σ_{am}	σ^2_m	σ^2_{ep}	σ^2_e	σ^2_p	h^2_d	h^2_m	h^2_t	c^2	e^2
Birth weight (kg)											
RM	4.41	-0.75	0.71	0.45	8.65	13.47	0.33	0.05	0.27	0.03	0.64
R	4.47	-0.67	0.51	0.56	8.63	13.51	0.33	0.04	0.28	0.04	0.64
H	3.97	-0.52	0.48	0.54	8.87	13.35	0.30	0.04	0.26	0.04	0.66
Weaning weight at 205 days (kg)											
RM	136.97	-48.04	103.04	38.46	290.41	520.83	0.26	0.20	0.22	0.07	0.56
R	191.32	-36.07	59.09	52.23	266.55	533.13	0.36	0.11	0.31	0.10	0.50
H	134.63	-25.48	68.10	48.00	294.10	519.36	0.26	0.13	0.25	0.09	0.57
Yearling weight at 390 days (kg)											
RM	183.44	-27.27	68.63	-	470.56	695.36	0.26	0.10	0.25	-	0.68
R	190.45	-3.75	25.63	-	475.28	695.11	0.27	0.04	0.28	-	0.68
H	176.67	-1.15	34.85	-	480.84	691.20	0.26	0.05	0.28	-	0.70
Post-weight gain from weaning to yearling (kg)											
RM	70.85	-19.48	18.59	-	341.23	411.19	0.17	0.05	0.12	-	0.83
R	118.56	-37.59	24.76	-	318.42	424.15	0.28	0.06	0.18	-	0.75
H	65.81	-19.00	18.37	-	344.89	410.07	0.16	0.04	0.11	-	0.84
Scrotum circumference (cm)											
RM	2.03	-0.18	0.50	-	6.99	9.34	0.22	0.05	0.22	-	0.75
R	1.91	-0.12	0.46	-	7.05	9.30	0.21	0.05	0.21	-	0.76
H	1.84	-0.25	0.57	-	7.10	9.26	0.20	0.06	0.19	-	0.77
Muscle score											
RM	0.116	-0.013	0.009	-	0.542	0.654	0.18	0.01	0.15	-	0.83
R	0.144	-0.029	0.017	-	0.529	0.661	0.22	0.03	0.16	-	0.80
H	0.113	-0.014	0.010	-	0.544	0.653	0.17	0.02	0.15	-	0.83

σ^2_a - additive direct genetic variance; σ_{am} - genetic covariance between direct and maternal genetic effects; σ^2_m - additive maternal genetic variance; σ^2_{ep} - permanent environmental effect variance; σ^2_e - residual variance; σ^2_p - phenotypic variance; h^2_d - heritability for direct effect; h^2_m - heritability for maternal effect; h^2_t - total heritability; c^2 - proportion of phenotypic variance due to permanent environmental effect; e^2 - proportion of phenotypic variance due to residual effect.

Genetic parameters for BW in models RM and R were similar to those found by Rodríguez-Almeida et al. (1997). For WW, the results of this paper are similar to those reported by Gregory et al. (1995a-c). These authors estimated higher values for WG and YW. Moderate heritability coefficients for genetic parameters for SC and MUS were estimated. Maternal heritability coefficients were low for all traits, and due to negative covariance, total heritability coefficients were lower than for direct genetic effects. Environment permanent ratios (c^2) were of small magnitude.

Different models had an important impact on (co)variance estimation in this composite population. The model that considers covariates for heterozygosis and direct and maternal additive breed effects seems to present the best estimation for genetic parameters.

For BW, the genetic variance components, additive and maternal, were minor when estimated by the model H. The covariance direct-maternal effect was negative in all of the

models; however, the estimate of smaller magnitude was obtained by the model H. Small differences were observed between the estimates originating from the models RM and R, as well as for the coefficients of heritabilities and the permanent effect of environment.

The estimates of h^2_d and h^2_t for BW were of medium magnitude, varying from 0.27 to 0.33. The estimates h^2_m and c^2 were of small magnitude, varying from 0.03 to 0.05. However, Ahunu et al. (1997), working with adapted and composite breeds, not including breed additive maternal effects in the model, found for BW a heritability of 0.45, relatively higher than that obtained in this study. For both h^2_d and h^2_t, they estimated WW values of medium magnitude, varying from 0.22 to 0.36. The h^2_m varied then from 0.11 to 0.20 based on the model. The c^2 proportion varied from 0.07 to 0.10.

For WW, important differences were observed between models RM and H and model R, regarding the magnitude of the additive genetic variance and of the total and direct heritability, which were greater for model R. Also smaller estimates occurred for additive genetic variance, both direct and maternal, in models R and H, perhaps indicating that the adjustment factor for the heterozygosis may have removed inappropriately of the additive genetic variance. The maternal heritabilities estimated by these models were relatively small compared to model RM. Regarding the permanent environmental effect, the models provided similar estimates.

Gregory et al. (1995a), working with pure, crossbreed and composite, found heritabilities of 0.36 and 0.48 for BW, 0.21 and 0.38 for W200, 0.31 and 0.43 for W368, and 0.24 and 0.40 for W410, respectively, where estimates were always lower for the crossbreed animals.

Ahunu et al. (1997), working with adapted and composite breeds, found for WW estimates of 0.38, 0.32 and 0.39 for the direct, maternal and total heritabilities, respectively. This estimate of h^2_m reported (0.32) was much higher than the value found in the present study.

Both direct and maternal heritabilities estimated by Montaldo and Kinghorn (2003), who worked with data from the Santa Gertrudis and their crossbreed with European breeds, were respectively 0.38 and 0.02 for W200, 0.22 (direct heritability) for W400, being similar to what was found in this study for the direct heritabilities, presenting evidence of the absence or small importance of maternal genetic effect in weaning. The results of Ahunu et al. (1997), Sarmiento and Garcia (2007) and of this study show a high maternal effect.

Estimates h^2_d and h^2_t for the W390 were of medium magnitude, varying from 0.25 to 0.28; h^2_m varied then from 0.04 to 0.10 according to the models. Important differences were observed among the models studied regarding the magnitudes of the variance for YW as well as changes in the direct and maternal heritabilities, but very small differences regarding total heritability. Following the same pattern observed for WW, smaller maternal genetic variances were obtained with the R and H models.

The direct and total heritabilities found in this study for the traits of weight were higher than those found by Demeke et al. (2003) for a multiracial population in Ethiopia, who reported direct and total heritabilities of 0.15 and 0.24 for BW, 0.07 and 0.09 for WW, and 0.12 and 0.12 for YW, respectively. The estimates h^2_d and h^2_t for WG were of small to medium magnitude, varying from 0.11 to 0.28; h^2_m varied then from 0.04 to 0.06 according to the models.

For WG, important differences were observed with the RM and H models compared to the R model, regarding the magnitude of the additive genetic variance and of the direct heritability,

being higher for the R model. Gregory et al. (1995a,b) reported estimates of heritabilities for post-weaning weight gain, which varied from 0.36 to 0.39 for pure and composite animals, respectively, being much higher than the values found in the present study.

The smaller magnitudes of these estimates for WG are divergent from those found in the literature, for composite and pure breeds, where for pre-weaning weight gains, Meyer et al. (1994) found estimates of 0.26 and 0.40, and Gregory et al. (1995a), of 0.35 and 0.24, respectively, for pure and crossbreed animals. Such fact may be explained by the difficulty of the models in discerning between additive and non-additive effects.

The estimates h^2_d and h^2_t for SC were of medium magnitude, varying from 0.19 to 0.22; h^2_m varied then from 0.05 to 0.06 according to the models.

For SC, the RM model yields estimates of higher additive variance and direct heritability, with slight reduction in the residual variance. However, the models were equivalent regarding other heritabilities.

The estimates h^2_d and h^2_t for the MUS were of small magnitude, varying from 0.15 to 0.22; h^2_m varied then from 0.01 to 0.03 according to the models.

For MUS, similar variances and genetic parameters were estimated for all models, possibly by the small magnitude of the additives and non-additives effects among the biological types, despite of the relative importance of some heterozygosis.

For all growth traits evaluated, estimates of (co)variance components between additive and maternal genetic effects were negative. Meyer et al. (1994) obtained similar results to those found in that study, upon estimating covariance components for the weaning weight and pre-weaning weight gain in the Hereford breed and Wokalup Composite (Charolais, Brahman, Angus, Hereford, and Holstein) beef cattle in Australian herds. Montaldo and Kinghorn (2003) also found this pattern for W200.

Maternal heritabilities found in this study were smaller for the majority of the traits, but within the worthy variation found in the literature. Demeke et al. (2003) obtained estimates that did not surpass 0.06, while Meyer et al. (1994) estimated coefficients between 0.09 and 0.20. In agreement with the majority of the studies, the direct effect had higher heritability than the maternal effect.

The effect of permanent environmental variance as a proportion of the total variance (c^2) in this study was higher than those obtained by Demeke et al. (2003) who reported a value of 0.02 for weight traits and by Meyer et al. (1994) who reported a value of 0.05 for WW.

CONCLUSION

Both R^2 values and consistency of genetic parameter estimates indicate that the more complex model (RM), which considers maternal and individual additive genetic breed effects, results in better estimates when compared to other models. R model (which does not consider maternal additive genetic breed effect) seems to overestimate (co)variance components.

The magnitudes of direct and maternal heritability estimates obtained in this study would permit genetic improvement for weight and growth traits, as much by the selection of direct genetic effects for weight and growth as for the improvement of maternal performance, but in different lineages. Therefore, the correlations between these effects were unfavorable.

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