

Non-additive genetic effects on weights and performance of a Brazilian *Bos taurus* x *Bos indicus* beef composite

G.B. Mourão, J.B.S. Ferraz², J.P. Eler², R.S. Bueno³, J.C.C. Balieiro²,
E.C. Mattos² and L.G.G. Figueiredo⁴

Departamento de Ciências Exatas, Escola Superior de Agricultura

“Luiz de Queiroz”, Universidade de São Paulo, Piracicaba, SP, Brasil

²Departamento de Ciências Básicas, Faculdade de Zootecnia e Engenharia de Alimentos, Universidade de São Paulo, Pirassununga, SP, Brasil

³Universidade Tecnológica Federal do Paraná, Dois Vizinhos, PR, Brasil

⁴Departamento de Melhoramento e Nutrição Animal,

Faculdade de Medicina Veterinária e Zootecnia,

Universidade Estadual Paulista “Júlio de Mesquita Filho”, Botucatu, SP, Brasil

Corresponding author: G.B. Mourão

E-mail: gbmourao@esalq.usp.br

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ABSTRACT. The aim of the present study was to evaluate the heterosis effects on weaning weight at 205 days (WW, N = 146,464), yearling weight at 390 days (YW, N = 69,315) and weight gain from weaning to yearling (WG, N = 59,307) in composite beef cattle. The fixed models were: RM, which included contemporary groups, class of age of dam, outcrossing percentages for direct and maternal effects, and additive direct and maternal (AM) breed effects; R, RM model, minus AM breed effects, and H, RM model, minus additive breed effects. The estimates for W205 were in general positive ($P < 0.01$). The R and H models resulted in similar estimates, but they were very different from the ones estimated by the RM model. For W390, the R and H models resulted in general positive estimates ($P < 0.05$). For WG, the RM model resulted in

general significant heterosis effects ($P < 0.05$). It can be concluded that the RM model seems to supply estimates of better quality ($P < 0.01$).

Key words: Beef cattle; Crossbreeding; Heterosis; Performance

INTRODUCTION

Nowadays, in search of commercial advantages, cattle producers seem to be more aware of the need to utilize, more intently, enhancement tools, which may optimize gains and efficiency of herds. A natural option is the use of genetic improvement, which enables the identification of bulls with economic traits, thus allowing favorable changes in the current scenario of beef cattle raising.

Besides the direct selection of the best animals, it is also possible to explore the genetic differences existing between breeds through crossbreeding. A good alternative is the composite cattle called Montana Tropical[®], which has been developed in Brazil since 1994 (Luchiari Filho and Mourão, 2006), aiming to explore, in tropical and sub-tropical climates, the heterosis genetic effects and breed complementarities through the use of bulls for field reproduction in natural copulation.

There are favorable results in the literature, which indicate a heterosis effect on the main domestic species. For weight to weaning of beef cattle, the study of Arthur et al. (1994) reported effects of 19.7 to 24.9 kg for direct heterosis and 14.9 to 37.8 kg for maternal heterosis between Hereford and Brahman breeds, generally significant estimates ($P < 0.05$). Arthur et al. (1999) observed values of 28.0 and 53.5 kg ($P < 0.01$) for direct heterosis and 22.5 ($P > 0.05$) and 72.6 kg ($P < 0.01$) for maternal heterosis between Hereford and Brahman, respectively, in mild and subtropical weather, in a model which includes direct and maternal epistasis, being significant only in subtropical weather.

In Brazil, Perotto et al. (1999), studying the weight of crossbred young males of Red Angus and Nellore breeds, obtained significant values ($P < 0.05$) for individual and maternal heterosis.

More recently, a literature review by Burrow et al. (2001) found medium heterosis among young bulls of 7.4 kg (average of 16 studies) and among young bulls x young zebras (T x Z) of 21.7 kg (average of 10 studies), percent of 3.9 and 12.6%. Average maternal heterosis of 8.2 kg (3.9% in 13 studies) among young bulls and 31.1% kg (16.0% in 12 studies) among T x Z. In the same study the average weight heterosis between the young bulls for the year was 13.2 kg (27 studies), equivalent to 3.8% of the population average. The referred study does not mention results on composite cattle (young bulls x young zebras), nor does it refer to the maternal heterosis effect.

Weight traits to weaning (WW), at yearling 390 days (YW) and weight gain from weaning to yearling 390 days (WG) were studied, aiming to determine the contribution of the non-additive genetic effect on beef cattle.

MATERIAL AND METHODS

Material

Starting with the herd that originated a crossbred population, characterized by several

biological traits involved in the formation of a crossbred, information was analyzed regarding WW (N = 146,464), YW (N = 69,315) and WG (N = 59,307) of calves born between 1994 and 2004, distributed into 2,886, 1,934 and 1,985, respectively, of contemporary groups (CG).

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 years. Some farms supplement with mineral salt enriched with a protein source in the dry season.

Animals were identified and weighed at weaning and around one year of age. The databank controlled information on performance, breed composition and pedigree of all animals. Animals were grouped into CG that consider the year of birth, farm, management group within farm, and sex.

Breed composition was used to group breeds into biological types N (*Bos indicus*, zebu cattle), A (*Bos taurus*, breeds tropically adapted), B (*Bos taurus*, European cattle of British origin) and C (*Bos taurus*, European cattle of continental origin). Further details about the animal management techniques can be found in reports by Ferraz et al. (2002) and Mourão (2005).

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 single sire; e) CG with all animals from a single breed composition; f) data from animals with breed composition incompatible with parents, and g) outliers on box-plot by traits (Table 1). The animals with records had 881 sires and 98,288 dams.

Ages of dams at calving were grouped into seven classes, and adjustment factors were considered, such as deviation of least square solutions in relation to class 4, the class that represents the dam at physiological maturity, defined in accordance with Mourão et al. (2007).

Effects of maternal and direct heterosis were obtained from partial direct heterozygosity among biological types N, A, B, and C and total maternal heterozygosity among the biological maternal types, for example, $N \times A =$ breeding percentage between breeds of biological trait N and biological trait A found in the breed formation of the animal. The fractions of direct outcrossing were obtained from the formula, $H_{ij} = \sum_{i,j} (p_i m_j)$, where t is the number of biological traits of the system NABC and p_i and m_j are the contribution fractions to the i^{th} and j^{th} paternal and maternal biological traits, respectively.

The total maternal outcrossing (MT) was considered as the sum of partial direct outcrossing, as done before; however, being computed as a single total value for the animal's mother.

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

Statistical analyses

Based on the maximum likelihood and the genetic model methodologies proposed by Dickerson (1973), three mathematical models, which differ from one another according to the genetic effects, were studied: RM model - complete model, which includes fixed effects of CG, class of age of dam, and the covariates associated with maternal and direct additive genetic effects, and also covariates associated with non-additive genetic effects of outcrossing, for the direct effects as well as for the total maternal effect; R model - RM model minus additive effects of maternal breed, and H model - R model minus additive

breed effects. This last model was used in the process of genetic evaluation of the referred composite.

The likelihood logarithm ($\log_e L$) was used to determine the appropriate models for each trait. The best model for showing expressive influence was considered that showing a significant change in the $\log_e L$. To determine the most adequate model, the similarity test was applied to the models (Rao, 1973). The statistic of the likelihood rate (LR) was calculated to test the significance of the i^{th} model, containing additional effects, compared to the other j^{th} model, in which these effects were not present. The value was, then, at least twice as high as the natural logarithm of likelihood, that is: $LR_{ij} = -2 \log_e (L_i / L_j) = 2 \log_e L_i - 2 \log_e L_j$, in which L_j is the likelihood for model j and L_i is the likelihood for model i .

The value obtained was then compared with regard to the statistic of the likelihood test (LR) with the chi-squared value (χ^2) with $(l_i - l_j)$ degrees of freedom; the probabilities were determined, and conclusions were made about the significance of the effects included in different models.

RESULTS AND DISCUSSION

Table 1 shows the natural logarithm values of the likelihood function ($\log_e L$) for each model in each trait and values of the likelihood rate (LR_{ij}) for pairs of models in each trait studied, obtained through the use of maximum likelihood methodology.

The exclusion of covariates associated with maternal additive genetic effects (R model) and the exclusion of covariates associated with maternal and direct additive genetic effects (H model), in all traits, led to worse values of $\log_e L$, when compared to those obtained by the RM model.

Through the test of LR, the RM model demonstrated the best results, significant ($P < 0.05$) for all traits, showing the importance of including these effects to evaluate these productive traits in crossbred cattle.

Table 1. Natural logarithm values of likelihood function ($\log_e L$), for model and likelihood rate (LR) values for pairs of models, for weight to weaning at 205 days (WW), weight to yearling at 390 days (YW) and weaning weight gain at yearling at 390 days (WG).

Model	$-2 \log_e L$		
	WW	YW	WG
RM	1.348.258,0	647.995,3	515.726,1
R	1.349.410,0	648.219,9	515.734,5
H	1.350.326,0	648.357,1	515.839,8
	Likelihood rate		
$LR_{(RM-R), d.f.=3}$	1152,0	224,6	8,4
$P < \chi^2$	<0.0001	<0.0001	0.0384
$LR_{(RM-H), d.f.=6}$	2068,0	361,8	113,7
$P < \chi^2$	<0.0001	<0.0001	<0.0001
$LR_{(R-H), d.f.=3}$	916,0	137,2	105,3
$P < \chi^2$	<0.0001	<0.0001	<0.0001

d.f. = degrees of freedom.

The estimates of heterosis effects, obtained from the analysis of variance of models RM, R and H, related to direct and maternal outcrossing among the biological traits defined through the use of the NABC system, are shown in Table 2, expressed for 100% of the outcrossing.

For WW all models studied demonstrated positive heterosis effects, which were statistically significant ($P < 0.01$). Exceptions were N x A heterosis, which was negative ($P < 0.01$), and N x B, which was not significant ($P = 0.83$), estimated through the RM model.

Table 2. Estimates of non-additive effects (β) related to outcrossing, obtained through the least squares method, using three models (RM, R and H) for weight to weaning at 205 days (WW), weight to yearling at 390 days (YW) and weaning weight gain at yearling at 390 days (WG)*.

$H_{i \times j}$	Model RM**			Model R**			Model H		
	β	SE	$P < t $	B	SE	$P < t $	B	SE	$P < t $
WW (kg)									
N x A	-3.97	1.25	0.0015	24.83	0.76	<0.0001	19.09	0.73	<0.0001
N x B	-0.23	1.10	0.8327	7.70	0.74	<0.0001	19.51	0.62	<0.0001
N x C	7.83	2.08	0.0002	14.81	1.82	<0.0001	17.06	0.72	<0.0001
A x B	9.78	1.02	<0.0001	26.30	0.76	<0.0001	24.84	0.70	<0.0001
A x C	13.15	1.96	<0.0001	35.49	1.81	<0.0001	24.20	0.80	<0.0001
B x C	12.66	1.94	<0.0001	17.68	1.93	<0.0001	23.46	0.98	<0.0001
MT	4.51	0.39	<0.0001	3.16	0.38	<0.0001	3.57	0.37	<0.0001
YW (kg)									
N x A	-5.26	2.55	0.0390	21.05	1.47	<0.0001	15.82	1.31	<0.0001
N x B	11.93	2.47	<0.0001	25.71	1.55	<0.0001	30.67	1.22	<0.0001
N x C	2.68	4.37	0.5400	18.62	3.63	<0.0001	22.84	1.43	<0.0001
A x B	6.45	1.59	<0.0001	15.88	1.17	<0.0001	18.00	1.11	<0.0001
A x C	-0.64	3.65	0.8599	14.89	3.38	<0.0001	16.58	1.28	<0.0001
B x C	2.89	3.64	0.4269	8.12	3.61	0.0245	20.17	1.66	<0.0001
MT	1.72	0.58	0.0033	1.01	0.58	0.0815	1.70	0.57	0.0031
WG (kg)									
N x A	-5.86	1.93	0.0024	-2.46	1.12	0.0277	-3.31	1.02	0.0011
N x B	11.98	1.89	<0.0001	14.76	1.21	<0.0001	7.27	0.95	<0.0001
N x C	6.66	3.41	0.0510	11.78	2.86	<0.0001	4.12	1.10	0.0002
A x B	-0.83	1.26	0.5089	-0.57	0.93	0.5409	0.38	0.87	0.6603
A x C	-1.00	2.91	0.7312	-2.18	2.69	0.4189	-0.82	1.01	0.4169
B x C	-0.23	2.91	0.9379	-0.83	2.87	0.7732	-6.30	1.32	<0.0001
MT	-0.37	0.46	0.4141	-0.55	0.45	0.2193	-0.85	0.45	0.0569

*Estimates expressed for 100% of outcrossing; SE = standard error; $H_{i \times j}$ and MT are direct and maternal outcrossing, respectively, obtained for biological types N, A, B, and C. For example, N x A = percentage of crossbreeding between breeds of biological types N and A existing in the breed composition of the animal. **Estimates of maternal and direct additive genetic effects of biological types can be obtained in a report by Mourão et al. (2007).

R and H models seem to provide similar estimates *per se* and different ones in relation to the RM model. It is important to consider the impossibility of discriminating heterosis effects of maternal origin in R and H models, due to the fact that maternal biological effect was of great magnitude in this characteristic, as seen.

The direct heterosis effects varied from -3.97 to 13.15 kg, from 7.7 to 26.30 kg and from 17.06 to 24.84 kg for RM, R and H models, respectively. When Franke et al. (2001) analyzed the weight from weaning of crossbred Angus, Hereford, Charolais, and Brahman, raised

in subtropical weather, they found direct heterosis varying from 8.2 to 38.6 kg and maternal heterosis from -5.3 to 16 kg. These estimates show higher magnitudes than those obtained through the RM model, being closer to the R and H estimates and disagreeing with a possible inflation attributed to these models. Perotto et al. (1999), working on data from crossbred Red Angus and Nellore in Brazil, found maternal and individual heterosis effects ($P < 0.001$) equal to 30.5 and 27.2 kg, respectively.

Still in Brazil, Dal-Farra et al. (2002) estimated for weight gain pre-weaning an effect of 13.2 kg for maternal heterosis and 14.7 kg for direct heterosis in crossbred Angus x Nellore and Hereford x Nellore.

For maternal heterosis, the values varied from 3.16 to 4.51 kg in the different models. These were lower than those obtained by Prayaga (2003), in which direct heterosis among taurine (TT) and zebu (ZZ) and taurine x zebu (TZ) were 5.8 kg for ZZ, 11.4 kg for TZ and 6.2 kg for TT, and maternal heterosis varied from 1.4 kg for ZZ ($P > 0.05$) to 15.7 kg for TZ ($P < 0.01$). Small and very similar magnitudes compared to those found in this study, 5.34 and 2.19 kg for direct and maternal heterosis, were found by Abdel-Aziz et al. (2003), who worked on crossbreeding of Afrikander and European breeds in South Africa.

Teixeira (2004) estimated important non-additive effects between Hereford and Angus with Nellore, which were 19.6 and 9.6 kg, respectively, for direct heterosis ($P < 0.01$) and 14.7 and 17.3 kg for maternal heterosis ($P < 0.01$).

For yearling weight at 390 days, the R and H models estimated positive and significant heterosis effects ($P < 0.05$), except for MT, in which the effect estimated by the R model was not significant ($P = 0.08$). For RM model, they were significantly important ($P < 0.04$) only for the heterosis effects from outcrossing between N x A, N x B, A x B, and MT, respectively equal to -0.053, 0.119, 0.065 and 0.017 kg/%.

The R and H models, in general, estimate similarities of coefficients based on direction, and discordances based on greater magnitudes through the RM model, as observed for WW and YW.

According to Perotto et al. (1999), in a study conducted in Brazil using Red Angus with Nellore crossbreds, the individual and maternal heterosis effects on yearly weight were of great magnitude ($P < 0.001$), respectively equal to 55.0 and 19.3 kg. Later, according to Prayaga (2003), direct heterosis among and from young bulls (T) and young zebras (Z) were 8.6 kg (ZZ), 17.9 kg (TZ; $P < 0.01$), and 5.7 kg (TT; $P > 0.05$); the maternal ones were significant ($P < 0.05$) equal to 8.7 kg (ZZ), 9.9 kg (TZ) and 8.4 kg (TT). These values were very similar to the estimates from the R and H models, but higher than those from the RM model found in this study.

Still, according to Teixeira (2004), for post-weaning weight, heterosis between Hereford and Angus with Nellore breeds, were respectively 33.8 and 27.1 kg for direct heterosis ($P < 0.01$), again higher than the estimates found in this study. For maternal heterosis, results of -5.7 kg ($P < 0.01$) are contradictory to those found in the current study.

For WG, the RM model estimated significant heterosis effects ($P < 0.05$) provided by outcrossing among N x A, N x B and N x C, respectively equal to -0.059, 0.120 and 0.067 kg/%. For the R model, heterosis effects were significant ($P < 0.05$) also for outcrossing N x A, N x B and N x C, respectively -0.025, 0.148 and 0.118 kg/%. Finally, for the H model, heterosis effects were significant ($P < 0.05$), with coefficients equal to -0.0331, 0.0727, 0.0412 and -0.0630 kg/%, respectively, for outcrossing N x A, N x B, N x C and B x C. Heterosis effects

from A x B, A x C and MT were not significant ($P > 0.05$) in any of the models studied.

In Brazil, Perotto et al. (1999), studying Red Angus with Nelore crossbreds, obtained values of 23.3 and -5.4 kg ($P < 0.05$), respectively, for individual and maternal heterosis after the effects had been adapted for weight gain at 185 days. The original estimates were 0.126 and -0.029 kg/day.

Although the models provided estimates of heterosis effects relatively similar, in terms of numbers for WG, those derived from RM model showed higher estimates of standard error, which culminated with the absence of statistical significance. This may have occurred due to the great number of GCs and/or to the wide range of observations for this characteristic, along with the increase of parameter numbers in the model.

Using differently expressed data, kg/185 days instead of g/day, based on a review of Burrow et al. (2001), average heterosis was found among young bulls (T x T) of 0.6 kg (19 studies) and among young bulls x young zebus (T x Z) of 21.46 kg (6 studies), in percent terms equal to 2.6 and 16.2% of the parental average. Original estimates were equal to 0.003 g/day (T x T) and 0.116 g/day (T x Z), showing significance ($P < 0.05$).

Still, Burrow et al. (2001) reported that the maternal heterosis average, weight to weaning, was 8.2 kg (3.9% in 13 studies) among T x T and 31.1 kg (16.0% in 12 studies) among T x Z. With the same adjustment for gain in 185 days, with results from Prayaga (2003), direct heterosis among and within young bulls (T) and young zebus (Z) were 2.7 kg (Z x Z), 8.3 kg (T x Z) and 0.9 kg (T x T), and maternal heterosis was 3.8 kg (Z x Z), -4.8 kg (T x Z) and -0.2 kg (T x T). The original estimates were equal to: 14.5 g/day (Z x Z), 44.8 g/day (T x Z), showing significance ($P < 0.05$), and 4.9 g/day (T x T; $P > 0.05$), and maternal heterosis of 20.4 g/day (Z x Z) and -25.8 g/day (T x Z) were significant ($P < 0.05$), and of -1.2 g/day (T x T) non-significant ($P > 0.05$).

Teixeira (2004) estimated for weight gain from weaning to post-weaning, non-additive effects between Hereford and Angus with Nelore, which were respectively 25.2 and 15.7 kg for direct heterosis ($P < 0.01$), and -6.8 and -14.8 kg for maternal heterosis ($P < 0.01$).

Some of the above mentioned studies report estimates that contradict those found in this study for WG, maybe because of the differences in the calculation mode and evaluation period of weight gain.

Besides, this characteristic shows strong influences from environmental effects, which are difficult to control and/or measure.

As a whole, it is observed that the literature reports estimates similar to those found in this study for weight characteristics at different ages, in spite of the wide range among the studies with regard to models used and results obtained.

CONCLUSIONS

Estimating models, which are able to segregate and quantify outcrossing effects such as the RM model, should be selected in detriment of those that include singular estimating of heterosis effects, because in these cases the effects are inflated.

Overall, the linear relations between outcrossing and heterosis were important and should be considered in genetic evaluations, since the results support the evidence related to the contribution of genetic heterosis to production systems and animal improvements. Therefore, they can help establish and direct breeding and crossbreeding systems between breeds.

However, supplementary evaluations are required with more complete models or with other adjustment strategies, and thus, these studies will continue to be of great importance.

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