(CO)VARIANCE COMPONENT ESTIMATION FOR GROWTH WEIGHTS OF MONTANA TROPICAL®, A BRAZILIAN BEEF COMPOSITE

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INTRODUCTION
Composite cattle are hybrids that are expected to bred to their own kind, retaining a level of hybrid vigor we normally associate with traditional crossbreeding systems, but without the crossbreeding. After the formation of the composite, whether these breeds have been bred in such a way that they retain significant hybrid vigor (i.e. whether they have successfully avoided inbreeding), they can be called as composites, other way they are simply newer breeds. (Bourdon, 1999). It is an alternative to more complex systems of crossbreeding with management requirements that are similar to straight breeding (Cundiff and Gregory, 1999).

The concept of composite cattle come from plant breeders, where it resulted in synthetic varieties. A program that wishes to explore composites in beef production should consider several criteria to compare with traditional systems, to be evaluated. Bourdon (1999) highlights as such criteria the merit of component breeds, level of hybrid vigor produced, simplicity, replacement considerations, complementarity, constancy of performance and accuracy of genetic merit prediction. That author also emphasize that to maintain hybrid vigor, a composite program has to have a large herd, cooperate with other breeders and avoid inbreeding.

Based on the experiments of the U.S.D.A. Roman Huskra Meat Animal Research Center, Clay Center, Nebraska, lead by K. Gregory, R. Koch, L. Cundiff and staff, published in several papers (Gregory et al., 1993; 1994a,b) and on the evidence that the large beef production area of Brazil and other South American countries needs a large amount of replacement bulls per year, CFM-Leachman Pecuária Ltda., a joint venture between Agro-Pecuária CFM Ltda. (Brazil) and the Leachman Cattle Company (USA) stated that a tropical composite bull should be: a) genetically evaluated and considered superior; b) produce, in combination to genes of the regular zebu or crossbred cows that are the basis of the production system, significant values of heterosis in the progeny; c) adapted to tropical and subtropical conditions, breeding under pasture condition; d) show reproductive longevity under pasture condition and e) have a worth price, making superior genetic seedstock accessible to small and medium size producers, without the need of artificial insemination. That company started, in 1994, a program that resulted in Montana Tropical®, a composite beef cattle developed for tropical and sub-tropical beef cattle systems under grazing conditions. Details of the development of that composite was shown by Ferraz et al. (1999b) and Ferraz and Eler (2000).

The objective of this study was to estimate (co)variance components for some traits used in the genetic evaluation of the Montana Tropical® population.
MATERIAL AND METHODS

Material. The Montana Tropical® population started in 1994 from crossbred and Nelore cows from several farms around Brazil. The program has actually 24 farms spread from northern Uruguay and southern Brazil through northern Brazil. The majority of the ranches are located between 10°S and 24°S and 40°W and 70°W. The program uses a franchise system, with the main company holding, in a nucleus herd, 1.5% of better cows born. Genetic material from nucleus herd can be used by any franchise.

The holly system has, today, around to 60,000 cows and close to 35,000 crossbred calves were born in the crop of 2000. Bulls are sold between 18 and 24 months of age (1,800 in 2001, born in 1999) and the majority of females are kept and exposed to bull at 14 months of age.

Animal are kept grazing in tropical pastures, being the majority in acid soils with Brachiaria spp grass, with mineral and salt supplementation all around the year. Some farms supplement in dry season, with mineral salt enriched with a protein source.

Animals are identified and weighed at birth, weaning and at one year of age. At yearling, muscle score (varying from 1, very bad, to 9, very good), hump height (cm) and navel score (varying from 1, very short, to 5, very long) were taken for all animals. Scrotum circumference (cm) is taken for all males kept after 12 month of age. All the ages at measurements are also collected. At weaning, close to 50% of males are culled based on performance and genetic evaluation, expressed in EPD’s. In this study, (co)variance components were estimated only for weaning (WW) and yearling weight (YW) and weight gains from weaning to 12 and 15 month of age (WG160 and WG245).

Data collected are kept in a databank that has information on 153,000 records of animals measured, breed composition of around 215,000 males and females and pedigree information on 214,500 cattle. The calves were sired by 578 different bulls and 85,780 dams.

Animals are grouped in contemporary groups (CG) that consider the year and season of birth, farm, management group or lot within farm and sex. The number of CG varied from 1,965 (WW), 1,426 (YW), 1,414 (WG160) and 1,039 (WG245).

In order to make analysis feasible, the breed composition of a given animal, kept as fractions of one, were grouped in 4 different biological types, named NABC, as follows:

- Group N – a group of zebu cattle (Bos taurus indicus), from breeds originated in India and imported to Brazil. Breed fractions of Nelore (the vast majority), Guzerá, Gir, Boran, Tabapuã, and other composite cattle are grouped in this N group.
- Group A – a group of non-zebu breeds (Bos taurus taurus) adapted under tropical conditions over the time. This group, that includes the African Sanga group, holds animals from Afrikander, Barzona, Belmont Red, Bonsmara, Senepol, Tuli, Caracu and Romo-Sinuano (Criollo-type breeds from Brazil and Colombia).
- Group B – this group holds the breeds (Bos taurus taurus) originated in the British islands, like Aberdeen Angus, Devon, Hereford, Red Angus, Red Poll, South Devon, etc., with a very important participation of Red Angus and South Devon.
- Group C – This group keep the breed composition related to the European continental breeds, like Braunvieh, Charolais, Gelbvieh, Limousin, Simental and several others.

The average crossbred animal of the gene pool has the composition 0.37 N, 0.12 A, 0.30 B, 0.18 C 0.03 other (residual not defined breed composition, from old cows from foundation...
population. Although the breeds were grouped in biological types, several breeds participate on the foundation population. In the gene pool, more than 40 different breeds had contributed, mainly through crossbred cows.

Statistical analyses. In order to process genetic analysis, models were defined based on the considerations of Pollak and Qiaas (1998); Qiaas (1999) on the original methodology by Robison et al. (1981). Additional considerations can be found and Ferraz et al. (1999a) and Ferraz and Eler (2000). The mixed model methodology applied considered as fixed effects the age at measurement (covariate), and the effects of contemporary groups and class of age of dam (8 classes).

To take in account the effects of heterozigosity, that is supposed to be proportional to heterosis and complementarity, models considered, as covariates, the direct effects of outcrossing percentages of NxA, NxB, NxC, AxB, AxC, BxC and maternal effects of the outcrossing percentages (also NxA, NxB, NxC, AxB, AxC, BxC) of the cows, mothers of calves.

The random effects of direct additive genetic of animals (for all traits), maternal genetic effects (for birth and weaning weights) and permanent environmental effects of cows (for birth and weaning weights) were also considered. Analysis were processed using derivative-free REML methods, through MTDFREML (Boldman et al., 1995).

RESULTS AND DISCUSSION
The description of the dataset and the results of variance components estimated are shown in Table 1.

### Table 1. Means, number of observations, (co)variance components and genetic parameters for growth and production traits of Montana Tropical, a beef composite

<table>
<thead>
<tr>
<th>Trait</th>
<th>N</th>
<th>Mean</th>
<th>s.d.</th>
<th>$\sigma^2_p$</th>
<th>$\sigma^2_g$</th>
<th>$\sigma^2_m$</th>
<th>$h^2$</th>
<th>$h^2_m$</th>
<th>$c^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weaning weight $^a$, kg</td>
<td>132,674</td>
<td>190.7</td>
<td>37.6</td>
<td>522.59</td>
<td>73.22</td>
<td>82.93</td>
<td>.14</td>
<td>.16</td>
<td>.10</td>
</tr>
<tr>
<td>Yearling weight $^b$, kg</td>
<td>41,800</td>
<td>260.7</td>
<td>56.9</td>
<td>778.57</td>
<td>118.94</td>
<td>42.09</td>
<td>.15</td>
<td>.05</td>
<td>.00</td>
</tr>
<tr>
<td>Weight gain $^c$</td>
<td>40,067</td>
<td>63.3</td>
<td>36.8</td>
<td>365.68</td>
<td>28.13</td>
<td>13.28</td>
<td>.08</td>
<td>.04</td>
<td>.00</td>
</tr>
<tr>
<td>Weight gain $^d$</td>
<td>27,724</td>
<td>88.9</td>
<td>54.1</td>
<td>711.32</td>
<td>52.85</td>
<td>28.39</td>
<td>.07</td>
<td>.04</td>
<td>.00</td>
</tr>
</tbody>
</table>

$h^2$ = heritability for direct genetic effects; $h^2_m$ = heritability for maternal genetic effects; $c^2$ = fraction of phenotypic variance due to permanent environmental effects; $^a$ mean age of 206.2 days; $^b$ mean age of 376.1 days; $^c$ weight gain from weaning-12 month; $^d$ weight gain from weaning to yearling (15 mo).

The covariance between direct and maternal genetic effects of weaning and yearling weights were, respectively -35.75 and 14.70. Two trait analysis were not made.

The results obtained indicate that the heritabilities are lower than those described by Gregory et al. (1995), as well as other reports on Nelore cattle, raised in similar conditions in Brazil (Eler et al., 2001a,b). Maternal heritability reported for weaning and weights is larger than the direct estimate, due, probably to the wide range of crossbred cows used to produce the composite. Although heritabilities were low, they show that there is enough genetic variation to get genetic
progress under selection. The models used, where the effects of heterozigosity were removed by using as covariate the outcrossing percentage of biological types, showed to be capable to take those effects into account. Further studies, including other traits controlled in the population and two-trait analysis will be conducted in near future.

CONCLUSION
The observed values indicate that there is a large influence of environment in this early stage of foundation of Montana Tropical® composite, but the model proposed, that considered the outcrossing percentages among biological types of cattle breeds showed to be an adequate model to estimate (co)variance components in composite populations. This study will be repeated next year with more information, but also the variance components will be estimated again using sub datasets with lower variation in environmental conditions and also two-trait analysis will be conducted to get new (co)variance components to be used in genetic evaluation of that population.

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REFERENCES