In order to estimate (co)variance components and genetic parameters of weaning weight, at seven months of age (WW), and of final weight, at 18 months (FW), a sample was used from 67,373 records of WW and 7,990 records of FW of Cuban Zebu breed animals. They were born between 1988 and 2006, in five genetic centers of the country. The statistical model for WW included the effects of the group of contemporaries (herd–year–trimester–sex, weaning weight as linear covariable and the age of the mother as linear and quadratic), the random effect of the animal, the maternal random effect, the permanent environment effect and the error. The model for FW included the group of contemporaries (herd–year–four-month period), the animal effect and that of the permanent environment. The variance components, estimated through animal model for the direct effect of WW by univariate and bivariate analysis, were similar and did not tend to change significantly the magnitude of the heritability for the direct (0.06 vs. 0.08) and maternal effects (0.06 ± 0.01 vs. 0.05 ± 0.01). However, for the FW, the variance components for the direct effect had important changes. As a result, the $h^2$ was higher when using the bivariate model (0.26 ± 0.05) than when applying the univariate (0.16 ± 0.03). The genetic correlation between the direct and the maternal effect for the weaning weight reached a value of -0.37 ± 0.08 in the univariate analysis, and of -0.21 ± 0.07 in the bivariate. It was concluded that the utilization of an animal model, considering simultaneously weaning weight and final weight, increased the efficiency in the selection of this latter character.

Key words: Cuban Zebu cattle, variance components, genetic parameters, growth.

**Materials and Methods**

Weaning weight and final weight are the most important traits in the genetic improvement of beef cattle. However, the maternal effects affect the weaning weight, and it is evident that for attaining genetic progress, the direct and maternal genetic components should also be considered, especially if there is antagonist relation between them (Backer 1980, Bertrand and Benyshek 1987, Cantet et al. 1988, Bijma 2006 and Heydarpour et al. 2008).

In Cuba, the weaning of animals is conducted at seven months of age. Around 25 % of the male calves are selected to run tests of behavior, that ended at 18 months of age, and that are performed in extensive production systems, based on pastures and mineral salts. The selection can decrease the variability in the weight at 18 months, because the analyses performed currently are based on a single trait, thereby assuming that the genetic correlation is zero, between the weight at seven and 18 months. Schaeffer (1999) reported that when the data have been subject to selection, the univariate analyses can be biased, whereas the multivariate are expected to consider this bias.

The aim of this work was to compare the univariate and the multivariate analyses, based on the magnitude of the estimates of the genetic parameters and the forecast of the breeding values for the weight, at seven and 18 months of age.
Where,

\[ y = \text{dependent variable (weight at seven months)} \]

\[ b = \text{vector of fixed effects (combination herd-year-four-month period-sex plus weaning age, as linear covariable and age of the dam, as linear and quadratic covariable)} \]

\[ a_d = \text{vector of the random additive genetic effects} \]
\[ a_m = \text{vector of the random maternal genetic effects} \]
\[ a_e = \text{vector of the random permanent environment effects} \]
\[ x, Z_d, Z_m, y_w, \theta_w = \text{matrices of design or of incidence} \]

The matrices of design or of incidence connect the vector of the observations with the fixed and random effects, respectively. This model assumes the following distributions for the random effects:

\[
\begin{bmatrix}
    A \hat{d}_d \quad A \hat{d}_h \quad 0 \quad 0 \quad AZ_d^t \hat{d}_d^t \\
    0 \quad 0 \quad I \hat{c}_c^2 \quad 0 \quad W_c^t \hat{c}_c^2 \\
    Z_d A \hat{d}_d \quad Z_m A \hat{d}_m \quad W_c^t \hat{c}_c \quad I \hat{c}_e^2 \\
    0 \quad 0 \quad 0 \quad 0
\end{bmatrix}
\]

With:

\[ A = \text{matrix of relations between the individuals in groups of contemporaries} \]

\[ Z_d, Z_m = \text{matrices of design or of incidence} \]

\[ \Sigma = \text{the known matrixes of incidence}. \]

All the random effects in the model have mean zero. The structure of (co)variances assumed was the following:

\[
\begin{bmatrix}
    \sigma_d^2 & \sigma_d \sigma_m & \sigma_d \sigma_e & \sigma_d \sigma_c & \sigma_d \sigma_e & \sigma_d \sigma_c & \sigma_d \sigma_e & \sigma_d \sigma_e & \sigma_d \sigma_e & \sigma_d \sigma_e & \sigma_d \sigma_e & \sigma_d \sigma_e & \sigma_d \sigma_e \\
    \sigma_d \sigma_m & \sigma_m^2 & \sigma_m \sigma_e & \sigma_m \sigma_c & \sigma_m \sigma_e & \sigma_m \sigma_c & \sigma_m \sigma_e & \sigma_m \sigma_e & \sigma_m \sigma_e & \sigma_m \sigma_e & \sigma_m \sigma_e & \sigma_m \sigma_e & \sigma_m \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e^2 & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c & \sigma_e \sigma_c \\
    \sigma_d \sigma_c & \sigma_m \sigma_c & \sigma_e \sigma_c & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_c & \sigma_m \sigma_c & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2 & \sigma_c \sigma_e \\
    \sigma_d \sigma_e & \sigma_m \sigma_e & \sigma_e \sigma_c & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c \sigma_e & \sigma_c^2
\end{bmatrix}
\]

\[ \begin{bmatrix}
    [\theta^2] & Z_d^t y_d - [\theta] \\
    Z_d^t y_d - [\theta] & V
\end{bmatrix}
\]

Where,

\[ \theta^2 = \text{vector of the observations for WW (FW)} \]

\[ b^2 = \text{vector of solutions for the fixed effects of the groups of contemporaries} \]

\[ a_d^2(d_d') = \text{vector of the additive genetic effects for WW (FW)} \]

\[ a_m^2(d_m') = \text{vector of the maternal genetic effects of WW (FW)} \]

\[ a_e^2 = \text{vector of the residual effects for WW (FW)} \]

\[ \Sigma = \text{are the known matrixes of incidence}. \]

Table 1. Number of observations (n), means (\(X\)), standard deviation (\(\sigma\)) and coefficient of variation (CV %).

<table>
<thead>
<tr>
<th>Traits</th>
<th>N</th>
<th>X</th>
<th>(\sigma)</th>
<th>CV (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>WW (kg.)</td>
<td>67 373</td>
<td>150.7</td>
<td>28.8</td>
<td>19.1</td>
</tr>
<tr>
<td>FW (kg.)</td>
<td>7 990</td>
<td>326.5</td>
<td>57.5</td>
<td>17.6</td>
</tr>
<tr>
<td>WA (days)</td>
<td>67 373</td>
<td>199.7</td>
<td>18.2</td>
<td>9.1</td>
</tr>
<tr>
<td>FA (days)</td>
<td>7 990</td>
<td>552.0</td>
<td>16.1</td>
<td>2.9</td>
</tr>
</tbody>
</table>

WW= weaning weight; FW= final weight; WA= weaning age; FA= final age
Results and Discussion

The estimates of the (co)variance components from the univariate and bivariate analyses for WW and FW are provided in table 2.

The additive component for WW in the bivariate analysis was somewhat superior than the univariate, although this did not affect considerably the magnitude of the heritability of the direct effects ($h^2_d$) on the uni and bivariate analyses (0.06 and 0.08, respectively) (table 3). They were in the lower limit of those published in the international literature (Quintanilla and Piedrafita 2000) for different breed and methodologies.

In a population of Cuban Zebu breed cattle, Guerra et al. (2010) found similar values in weaning weight (0.06 ± 0.01) through the application of the unitrait animal model. According to Elzo et al. (2001), the production systems based on grazing, with access only to mineral salts and water, are a limitation for the dams (milk yield) and the calves (growing) may express all their genetic potential. Therefore, low heritabilities were found for the direct and the maternal genetic effects of WW.

Núñez-Domínguez et al. (2002) published for the Tropicarne breed important changes for $h^2_d$ in the weaning weight, when estimated through univariate (0.08) and bivariate analyses (0.19). Similar results were found by Bennett and Gregory (1996) and Garnero et al. (2000), when comparing an univariate animal model with a multivariate for weaning weight. In similar studies, Eler et al. (1995) used an animal model in the Nelore breed and reported slight differences, favoring the multivariate analysis.

For FW, the variance components (table 2) and the heritability value (table 3) for the direct effect had important changes. The heritability was higher with the utilization of the bivariate model (0.26), compared with the univariate (0.16). This was mainly due to the relative increment of the variance component of the additive effect. This result assumes a rise in the accuracy of the estimation of the breeding value, when using the bivariate analysis. González et al. (2009) estimated values of 0.21 ± 0.01 for FW in a Zebu cattle population, in a herd of the Pinar del Río province. Similar outcomes were reported by Garnero et al. (2000) and Núñez-Domínguez et al. (2002).

The genetic correlation between the additive values of WW and FW were of 0.86 ± 0.03, and between the residuals were of 0.47 ± 0.01. Schaeffer (1999) stated that the models for multiple traits are useful for the characters with differences between the genetic and residual correlations superior to 0.5, or where a trait has a $h^2$

<table>
<thead>
<tr>
<th>(co)variance components</th>
<th>WW</th>
<th></th>
<th>FW</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma^2_d$</td>
<td>26.7</td>
<td>36.9</td>
<td>145.6</td>
<td>270.9</td>
</tr>
<tr>
<td>$\sigma^2_m$</td>
<td>30.1</td>
<td>22.7</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>$\sigma^2_{d,m}$</td>
<td>-10.4</td>
<td>-6.14</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>$\sigma^2_e$</td>
<td>47.7</td>
<td>48.6</td>
<td>94.5</td>
<td>39.3</td>
</tr>
<tr>
<td>$\sigma^2_p$</td>
<td>475.3</td>
<td>478.2</td>
<td>933.6</td>
<td>1029.6</td>
</tr>
</tbody>
</table>

$\sigma^2_d$ = variance of the direct effects; $\sigma^2_m$ = variance of the maternal effects; $\sigma^2_{d,m}$ = additive covariance between the direct and maternal effects; $\sigma^2_e$ = variance of the permanent environment effects; $\sigma^2_p$ = residual variance; $\sigma^2_p$ = phenotypic variance

<table>
<thead>
<tr>
<th>Genetic parameters</th>
<th>WW</th>
<th></th>
<th>FW</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>$h^2_d$</td>
<td>0.06 ± 0.01</td>
<td>0.08 ± 0.01</td>
<td>0.16 ± 0.03</td>
<td>0.26 ± 0.05</td>
</tr>
<tr>
<td>$h^2_m$</td>
<td>0.06 ± 0.01</td>
<td>0.05 ± 0.01</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>$r_{g,d,m}$</td>
<td>-0.37 ± 0.08</td>
<td>-0.21 ± 0.07</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>$c^2$</td>
<td>0.10 ± 0.01</td>
<td>0.10 ± 0.01</td>
<td>0.10 ± 0.03</td>
<td>0.04 ± 0.02</td>
</tr>
</tbody>
</table>

$h^2_d$ = heritability of the direct effects; $h^2_m$ = heritability of the maternal effects; $r_{g,d,m}$ = additive genetic correlation between the direct and maternal effects and $c^2$ = rate of the permanent environment effects in respect to $\sigma^2_p$.
very superior to the other. All the traits were benefitted, somehow, by the simultaneous analysis. This author also noted that, in instances where the h² are similar and there are not differences between the genetic and the environmental correlations, the analysis for multiple traits is also useful, when there id bias due to selection. In this instance, it may have occurred because there is pre-selection of the calves (23.7 %) before they are taken to the behavior test.

Table 3 presents the genetic correlation between the direct and maternal effect, with a value of -0.37 ± 0.08 in the univariate analysis, and of -0.21 ± 0.07 in the bivariate. In several studies it has been proved the existence of antagonism between the direct and the maternal effects, in characters such as the weaning weight in the beef cattle (Bertrand and Benyshek 1987, Cantet et al. 1988, Garrick et al. 1989 and Robinson 1996). Quintanilla and Piedrafita (2000), in a wide review of 40 papers, noted that in 36 of them the genetic correlation between the direct and the maternal effect was negative. This implies that in an improvement program these effects should be taken into account simultaneously.

Heydarpour et al. (2008) reported that if these correlations are calculated from the data obtained in the herds, where there is good control of the genealogy, they turn to be small and positive. However, in field data, with lost connection between the identification of the animal, when weaned and when becoming mother, these correlations tend to be very negative, depending on the animal, when weaned and when becoming mother, these with lost connection between the identification of the

Acknowledgements

Thanks are given to Eng. Franky Ramos, from the National Genetics Direction, and to Eng. Roberto Peinado, from the National Center of Cattle Control for facilitating the access to the information.

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Received: February 12, 2010