

ESTIMATION OF VARIANCE COMPONENTS AND GENETIC PARAMETERS FOR VISUAL SCORES IN A NELORE ZEBU CATTLE POPULATION

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INTRODUCTION

Brazil holds the largest bovine commercial herd involved in beef production in the world, with more than 157 million head (Anualpec, 2000). Josakhian (2000) reported that around 80% of the Brazilian beef herd has some fraction of Zebu breeds. More than 70% of purebred animal registered by the Zebu Breeders Association (ABCZ) consist of animals from Nelore breed, as a result of the adaptability of those animals to tropical and subtropical conditions. The Brazilian beef industry is based on Zebu cows, mainly originated in Nelore breed. The breed shows a large variability in several economic relevant traits and that indicates good opportunities for genetic improvement (Eler *et al.*, 1995). There are several genetic evaluation and breeding projects running in Brazil at present time, the vast majority evaluating growth traits, besides scrotal circumference. Few programs consider other traits, such as reproduction or type traits.

Improving efficiency of beef cattle industry is a primary condition for any country to be competitive in a globalized world market. It is believed that the inclusion of visual evaluation scores and weight characteristics as auxiliary tools to identify precocious animals could help breeders. They could select for animals more adapted to the environment why they are being raised, with a shorter production time and with a desirable frame resulting in a more benefited activity and a better quality of the final product, that is bovine meat.

Visual scoring has advantages such as an inexpensive implementation, an easy management, but and also has some disadvantages, such as the need to be done by a skilled professional, and the need for very well defined references or models of the type conformation, because the quality of information and consistence of the data collected depends a lot on the classifier due to the subjectivity of the methodology. Anyway, visual score evaluation can add very important information to genetic improvement programs, as shape and distribution of muscle content, and be very useful as auxiliary tools in those programs.

The objectives of this research were to estimate variance components and genetic parameters of visual scores evaluations of Nelore, the largest Zebu breed in Brazil, so that these information can be used in animal breeding programs and also to create scientific subsidies that can help to justify and/or to redirect the criteria used in cattle exhibitions and shows because that the animal favoured in exhibitions should be the same as the one looked for by industry, *i.e.*, a more productive beef cattle livestock.

MATERIAL AND METHODS

We used 2,146 records of visual scores of carcass conformation (C), trait assessing the compatibility of the development of the animal in agreement with the chronological age; 2,146 records of precocity of finishing (P), *i.e.* an appraisal of capacity of animal to accumulate subcutaneous fat in earlier age and 2,146 records of muscle scoring (M), (volume and convexity of muscles); 3,479 weaning weights (WW) and 2,097 yearling weight (550W) of Nelore Zebu cattle, raised under pasture conditions, with mineral supplementation. The regular pasture is *Brachiaria spp.* The ranch, Fazenda Paredão, is located in the state of São Paulo, Brazil, close to 22° 09'S and 50° 05'W, between 600 and 700 m above sea level. Annual rain fall fluctuates between 1,400 and 1,500 mm/m²/year.

The methodology used for the visual evaluation for C, P and M was applied at weaning and the technique consisted in the attribution of scores to the animals, within a contemporary group. Animals were compared and each trait was graded with scores varying in a scale from 1 to 5, giving the value 1 to the worst animals and 5 to the best ones. A detailed description of the methodology applied to visual evaluation, including pictures, schemes and standards, can be obtained in Koury Filho (2001). That methodology can be easily adapted to other breeds and market conditions.

The estimation of variance components and genetic parameters of the analyzed weight traits and the visual scores was made with the use of REML method, in a two-trait model, where the basic characteristic were weaning weight and the yearling weight, in separate analysis. The model considered the fixed effects of contemporary groups (that included the effect of sex and management group) and the random genetic direct effect. In the case of weaning weight, model also considered the fixed effect of age of dam and the random effect of genetic maternal effect and permanent effects of dam. All the analyses were made using the program MTDFREML (Bolman *et al.*, 1995).

The dataset analyzed had a total of 4,867 animals in pedigree, including foundation animals, born in 10 different crops. The number of contemporary groups included in the analysis was 215 for WW, 176 for 550W and 102 for the visual scores.

RESULTS AND DISCUSSION

Table 1 presents the estimates of the variance components and genetic parameters for visual evaluation C, P and M, WW and 550W, obtained in two-trait analyses. The estimates shown in that table represent the results for each trait, when analyzed with the anchor traits. Table 2 displays the estimates of heritability for direct genetic effects in the diagonal of all the variables and the value given to the genetics correlations just below.

Table 1: Variance components and genetics parameters of visual evaluation of carcass conformation (C), precocity of finishing (P), muscle score (M), weaning weight (WW) and yearling weight (550W) from two-trait REML analysis in Nelore cattle

| Analyses | Variance components* | | | | Genetic parameters** | | | | |
|----------|----------------------|--------------|--------------|--------------|----------------------|---------|----------|-------|-------|
| | σ_d^2 | σ_m^2 | σ_c^2 | σ_e^2 | h_d^2 | h_m^2 | r_{dm} | c^2 | e^2 |
| C + WW | 0.27 | - | - | 0.39 | 0.41 | - | 0.61 | - | 0.59 |
| C + 550W | 0.27 | - | - | 0.40 | 0.40 | - | - | - | 0.60 |
| P + WW | 0.34 | - | - | 0.38 | 0.47 | - | 0.80 | - | 0.53 |
| P + 550W | 0.35 | - | - | 0.36 | 0.49 | - | - | - | 0.51 |
| M + WW | 0.24 | - | - | 0.45 | 0.35 | - | 0.58 | - | 0.65 |
| M + 550W | 0.18 | - | - | 0.36 | 0.33 | - | - | - | 0.67 |
| WW + C | 157.16 | 6.84 | 37.83 | 503.71 | 0.22 | 0.01 | 0.46 | 0.525 | 0.70 |
| WW + P | 110.79 | 39.99 | 19.57 | 528.43 | 0.15 | 0.06 | 0.25 | 0.027 | 0.74 |
| WW + M | 125.97 | 32.46 | 32.42 | 511.72 | 0.18 | 0.05 | 0.15 | 0.052 | 0.71 |
| 550W + C | 413.52 | - | - | 1085.78 | 0.28 | - | - | - | 0.72 |
| 550W + P | 396.09 | - | - | 1107.06 | 0.26 | - | - | - | 0.74 |
| 550W + M | 358.91 | - | - | 1113.89 | 0.24 | - | - | - | 0.76 |

* σ_d^2 = variance component for genetic additive direct effect; σ_m^2 = variance component for genetic additive maternal effect; σ_c^2 = variance component for additive permanent environment of cow; σ_e^2 = residual variance component;

** h_d^2 = heritability coefficient for genetic additive direct effect; h_m^2 = heritability coefficient for genetic additive maternal effect; r_{dm} = correlation among direct and maternal genetic effects; c^2 = proportion of the total variance due to the permanent environment of cow effect ; e^2 = proportion of the total variance due to residual effect.

Table 2: Maximum and minimum estimates for Heritability (in diagonal) and genetic correlations (bellow diagonal) obtained in two-traits REML analysis in Nelore cattle

| TRAIT 1 | TRAIT 2 | | | | | |
|----------|-------------|-------------|-------------|--------------|-------------|-------------|
| | P | M | C | MATERNAL | WW | 550W |
| P | 0.47 / 0.49 | | | | | |
| M | | 0.33 / 0.35 | | | | |
| C | | | 0.40 / 0.41 | | | |
| MATERNAL | 0.80 | 0.58 | 0.61 | 0.01 / 0,06 | | |
| WW | 0.77 | 0.74 | 0.89 | -0.29 / 0.25 | 0.12 / 0.22 | |
| 550W | 0.80 | 0.33 | 0.69 | | | 0.24 / 0.28 |

Heritability estimates for C, P and M were a little larger than described by Eler *et al.* (1996), that also worked with herds of Nelore cattle in Brazil. Those authors obtained estimates of 0.34 (C), 0.29 (P) and 0.33 (M). The results of this research are much larger than the ones described by Cardoso *et al.* (1998), who analyzed data of a Santa Gertrudis herd in Brazil, finding

estimates of 0.10 (C), 0.15 (P) and 0.11 (M). That great variation can be explained by the lack of methodology standardization and among the appraisers and/or the difference among the variability of the compared herds.

The correlations of C, P and M and the weight traits, all positive and of high magnitude, are not supported by the literature, but confirm the expectation that there is no important genetic antagonism between visual scored and growth traits. Then, those traits as auxiliary traits should be used as auxiliary traits in selection.

CONCLUSION

The estimates of heritability for genetic direct effect for C, P and M, and the correlation among them and weaning and yearling weights indicate that those traits can be selected.

The correlations with C, P and M and WW and 550W indicate that selection for the appraised visual traits should lead also to heavier animals, however with a more appropriate frame, shape and conformation, with a higher proportion of carcass and muscles.

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