

ESTIMATES OF GENETIC CHANGES IN 365d-WEIGHT IN A BRAZILIAN NELLORE HERD

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ABSTRACT

Data for 1,753 calves born from 1975 to 1984 were used to estimate genetic change in weight at 365 days of age in a Nellore herd in northeastern Brazil. Three estimation procedures were used; two were based on repeated use of sires over successive years, and the third on comparison of mean yearly genetic gains. Mathematical model included sire effects (random), and a set of fixed effects (sex, age of dam at parturition, season, and year of birth). The overall mean weight and standard error were 190 ± 5 kg (CV = 15%). Heritability estimate from correlation among paternal half-sibs was $.27 \pm .08$. Estimates of genetic gain obtained by the three procedures agreed well, 1.38, 1.98 and 1.44 kg/year. Expected genetic gain was 1.68 kg/year. Results were very similar to larger studies done in temperate areas.

INTRODUCTION

Zebu cattle are the prevailing beef animals in the Brazilian cattle population, and the Nellore breed is the most widespread. Recent settlement and development of the northern (tropical) regions of the country has involved beef cattle, and Nellore have played an important role. Thus genetic improvement of this breed is of major

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importance. Considerable emphasis is placed in Brazil on breed standardization, with cattle shows and exhibits being highly valued. The need to produce more meat economically induces breeders to select individuals for increased weight gain. Thus separation of phenotypic changes over time into genetic and environmental portions to evaluate selection practices is important.

Using records for 29 Nellore herds under herd test by the Brazilian Association of Nellore Breeders, State of São Paulo, Pimenta Filho (1986) estimated phenotypic, genetic and environmental changes in weight at 365 days of age at .68 kg/year, 1.01 kg/year and -.33 kg/year. Since selection was practiced in these herds, the number of calves under test especially with males decreased after weaning, thus estimates obtained could be somewhat biased. However, using records of several breeds in Canada, Schaeffer *et al.* (1981) detected no significant differences in estimates of genetic change for weaning weight and weight at one year between groups of calves culled at weaning and groups maintained intact till one year of age.

The objectives of the present study were to estimate genetic change in weight at 365 days of age in a Nellore herd and to compare estimates obtained by three different procedures with each other and with estimates expected based on selection pressure, heritability and calving interval.

MATERIAL AND METHODS

Monthly weight data were obtained from a Nellore herd raised at a private farm in Northeastern São Paulo State. Climate, management and feeding conditions for this farm have been reported in detail by Amaral (1986). Records included 1,753 animals (853 males and 900 females), born from 1975 to 1984, sired by 29 bulls with a mean service time of 3.5 year. Weights obtained immediately before and after 365 days of age were used to calculate weight adjusted to 365 days (W365). Of the three procedures utilized to estimate genetic gain, the first and second are based on repeated use of sires over successive years (Smith, 1962), and the third was based on a comparison of mean yearly genetic gains (Henderson, 1973).

Procedure A. Two mathematical models were adopted; in the first:

$$Y_{ijk} = \mu + a_i + F_j + b_1 (X_{ijk} - \bar{X}) + b_2 (X_{ijk} - \bar{X})^2 + E_{ijk}$$

where Y_{ijk} is an observation on each animal; μ is a constant common to all observations; a_i is the random effect of the i^{th} sire; F_j is a set of fixed effects (sex of progeny, season and year of birth); b_1 and b_2 are the partial linear and quadratic regression coefficients of W365 on age of dam at parturition; X_{ijk} represent age at calving of the dam of each animal; \bar{X} is mean dam age at calving; and E_{ijk} represent random errors

associated with each observation. In the second model, the sire was deleted. Calculations were performed by the method of least squares analysis of variance, using the LSML76 computer program of Harvey (1977).

Since year effects estimated from the first model were adjusted for one half of the direct genetic (sire) effects, twice the difference in the two sets of year constants yields estimates of genetic trend. The least squares estimates for years from the second model were assumed to represent combined environmental and genetic effects on animals born during that year (Packer, 1977). In this case, the differences between means for two consecutive years measured the phenotypic change from one year to the other.

Procedure B: Genetic change was also estimated by the procedures of Zollinger and Nielsen (1984), a modification of the method proposed by Smith (1962). Weights were adjusted individually for effects of cow age at calving, using additive adjustment factors obtained by least squares analysis of variance. The means per group of same-sex animals of equal age were then calculated and each weight was expressed as a fraction of the group mean (W365R). Within-sire linear regression of W365R of the progeny over years was then used again to estimate $-(1/2)g$.

Procedure C: In this case, genetic change was estimated on the basis of sire contributions to genetic values of calves born each year. This is an adaptation of the method proposed by Henderson (1973), with estimates of predicted sire differences being calculated by least squares and not by BLUP procedures. Expected progeny differences (EPD) initially were estimated by the formula: $EPD = bs$, where b is the regression coefficient which depends on the number of calves and on the heritability of the trait, and s is the estimate of the sire constant, obtained by solving a model which included sires as fixed effects. Sire contributions to genetic value of calves born in a given year were calculated as:

$$SBV_j = \sum_i n_{ij} EPD_i / n_j$$

where SBV_j is the portion of mean genetic value in the j^{th} year, determined by sire contributions, EPD_i is the expected difference in progeny calculated for the i^{th} sire, n_{ij} is the number of calves sired by the i^{th} bull and born during the j^{th} year, and n_j is the total number of calves born during the j^{th} year. Regression of SBV over time estimates half the genetic gain in the herd, assuming that sire contributions are equal to cow contributions. Thus, genetic change was estimated as $g = 2bSBV.T$.

RESULTS AND DISCUSSION

Procedure A estimates of linear phenotypic, genetic and environmental changes in weight at 365 days of age were -3.92, 1.38 and -5.30 kg/year. The negative environmental change doubtless was due to pasture deterioration because of inadequate investment in pasture management. Phenotypic change also was negative. The low overall mean observed for the herd (190 ± 5 kg) was probably a reflection of overall management (Table I).

Table I - Means, standard errors, and coefficients of variation (CV) for weight at 365 days, by year of birth.

Year	Number of observations	Mean \pm SE	CV (%)
1975	131	199 \pm 17	14.6
1976	186	204 \pm 15	15.2
1977	151	207 \pm 17	13.0
1978	163	202 \pm 16	13.9
1979	209	189 \pm 13	12.7
1980	184	188 \pm 14	13.8
1981	154	182 \pm 13	14.3
1982	183	187 \pm 14	12.3
1983	227	166 \pm 13	12.1
Total/Mean	1,753	190 \pm 5	14.7

Heritability for W365, estimated by paternal half-sib correlation, was $.27 \pm .08$. On the basis of data reported here and in various studies on Nellore herds from different regions of Brazil, .17 to .36 is the probable range for heritability for Nellore or Zebu cattle reared under tropical Brazilian conditions.

Estimates of genetic change by procedures B and C (1.98 and 1.44 kg/year) agreed with those obtained by procedure A (Table II). The three values were .73, 1.04, and .76% of the overall mean. On this farm, selection was done on the basis of the ratio of individual weight to same-sex and age animal mean values, with 10% of the best males and 50% of the best females being selected. Expected genetic gain for W365 was estimated at 1.68 kg/year on the basis of the intensity of male and female selection, heritability, phenotypic standard deviations, and sire-and-dam-progeny generation intervals. Thus genetic gain was .88% of the overall mean. Results obtained

using the three different procedures agreed quite well with one another and also with expected genetic gain.

Table II - Estimates of genetic change in weight at 365 days obtained by three procedures.

Procedure	Change (kg/yr)	% of overall mean	Acumulated change (kg)
A	1.38	.73	13.88
B	1.98	1.04	19.80
C	1.44	.76	14.40

See text for description of procedures.

Procedures A and B are based on the fact that, when sires are constant, genetic change originates from the set of dams, whose contribution is equivalent to half the total genetic change. Harville and Henderson (1967) pointed out that a population needs to be in genetic equilibrium for genetic change in the sire population to be equal to genetic change in the cow population. However, conditions that allow a large cattle population to be in genetic equilibrium are unlikely to exist. Also, any factors independent of dam genetic composition which cause successive increases in calf means "within sire" lead to overestimates of genetic gain by procedure A and underestimates by procedure B. The inverse is also true. One of these factors is preferential mating, i.e. the fact that over the years some bulls are mated with older, selected cows (Smith, 1962). In procedure C, genetic change is estimated on the basis of the change in sire contribution to mean genetic values of calves born each year, and dams are also assumed to make an equal contribution. Studies involving data simulation are needed for a better judgment of the efficiency of these three procedures, which in the present investigation produced quite similar results.

Results obtained here suggested that the selection system utilized at this farm was adequate. Genetic gain in W365 could be higher if there were no interference by the process of bullock registration, which takes into consideration desired breed characteristics. Investment in pasture improvement is recommended, since it would certainly produce a profitable response by the herd in terms of weight gain.

ACKNOWLEDGMENTS

We thank CNPq Brazil for financial support.

Publication supported by FAPESP.

RESUMO

As mudanças genéticas foram estimadas em um único rebanho da raça Nelore, usando pesos de 1753 animais nascidos no período de 1975/84. A mudança genética para peso aos 365 dias foi estimada por três métodos; dois baseados no uso repetido de touros em anos sucessivos e o terceiro na comparação dos ganhos genéticos médios anuais. O modelo matemático incluiu os efeitos de touro (aleatório) e um conjunto de efeitos fixos (sexo, idade da vaca ao parto, estação e ano de nascimento). A média geral e o erro padrão para peso aos 365 dias foram de 190 ± 5 kg (CV = 15%). A estimativa de herdabilidade por correlação entre meio-irmãs paternas foi de $0,27 \pm 0,08$. As estimativas da mudança genética por três procedimentos foram da ordem de 1,38; 1,98 e 1,44 kg/ano, demonstrando concordância entre as mesmas. A mudança genética esperada foi de 1,68 kg/ano. Os resultados foram similares aos estudos realizados com grande volume de dados em áreas temperadas.

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(Received November 5, 1990)