

Estimates of genetic parameters and evaluation of genotype x environment interaction for weaning weight in Nelore cattle

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ABSTRACT: Records of 105,645 Nelore calves born from 1977 to 1994 in eight different regions of Brazil were used to estimate genetic and environmental parameters and evaluate genotype x environmental interaction for weaning weight (kg). Estimates were obtained using MTDFREML with a sire model. Mathematical model included random effects of sire and dam, and fixed effects of sex, month and year of birth, herd, and age of dam at calving. Estimates of phenotypic variances were 375, 431, 431, 407, 409, 400, 413, and 336 for the eight different regions and 420 over all regions. Estimates of heritability were, respectively, 0.22, 0.26, 0.16, 0.29, 0.34, 0.38, 0.37, 0.26, and 0.26. Heritability estimates for weaning weights from two trait analyses with measurements in different regions considered as different traits varied from 0.17 to 0.38 and estimated genetic correlations among weaning weights in different regions varied from - 0.03 to 1.00. Spearman rank correlations between EPDs for weaning weight from different regions were calculated to verify whether sires ranked differently in different regions. The correlations ranged from - 0.25 to 1.00 between pairs of regions. Estimates of heritability suggest that mass selection could result in genetic gain under a breeding program that utilizes weaning weight as a selection criterion. The apparent importance of genotype x environment interaction detected by this study suggests a need to choose sires appropriate for the region where they will be used, since relative performance of progeny of a sire appears to change from one region to another.

Key Words: Beef cattle, Genetic evaluation, Zebu, Regions of Brazil.

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Estimativas de parâmetros genéticos e uma avaliação da interação do ambiente x genótipo para o peso ao desmame no gado Nelore

RESUMO: Dados de 105.645 bezerros da raça Nelore, nascidos no período de 1977 a 1994 em oito diferentes regiões no Brasil foram usados para estimar parâmetros genéticos e ambientais e avaliar a interação genético x ambiente para peso ao desmame. As estimativas foram obtidas usando programa MTDFREML, através de modelo touro. O modelo matemático continha os efeitos aleatórios de touro, vaca e o erro. Como efeitos fixos usou sexo, mês e ano de nascimento do bezerro, fazenda e idade da vaca ao parto (linear e quadrático). As variâncias fenotípicas estimadas foram 375; 431; 431; 407; 409; 400; 413; e 336 para as oito diferentes regiões e 420 para todas juntas. As estimativas de herdabilidades foram 0,22; 0,26; 0,16; 0,29; 0,34; 0,38; 0,37; 0,26; and 0,26, respectivamente. Estimativas de herdabilidade para o peso ao desmame quando as regiões foram analisadas duas a duas, os valores variaram entre 0,17 a 0,38, e a estimativa da correlação genética entre o peso ao desmame estimado para as regiões duas a duas variaram - 0,03 a 1,00. Ao analisar usando a correlação de Spearman para avaliar se houve variação da ordenação das DEPs de do peso ao desmame, para cada touro dentro das regiões duas a duas, constatou-se variação destes de região para região. As correlações estimadas para os pares de região encontram-se em uma faixa de - 0,25 a 1,00. As estimativas de herdabilidade sugere que a seleção massal pode resultar em ganho genético dentro de um programa de melhoramento que utilize o peso ao desmame como critério de seleção. A aparente importância da interação genótipo x ambiente detectada nesse estudo sugere a necessidade de se escolher corretamente os touros apropriados para região específica.

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Palavras chave: Bovino de corte, avaliação genética, Zebu, Regiões no Brasil.

Introduction

An option to improve productivity indices in beef cattle in Brazil is to define some traits of economic importance, select animals based on those traits and outline a breeding program. Knowledge of genetic parameters such as heritability is essential for the success of these programs. Estimates of heritability for weaning weight in Nellore cattle in Brazil indicate that, for some regions or herds, a selection program can be effective to improve weaning weight. Eler *et al.* (1989) found a value of 0.24 ± 0.02 for the heritability of weaning weight for Nellore calves, and Silva (1990), Euclides Filho *et al.* (1991), Eler *et al.* (1995), Souza and Ramos (1995) and Souza *et al.* (1996a) reported estimates of 0.35 ± 0.02 ; 0.28 ± 0.02 ; 0.14 ± 0.02 ; 0.18 ± 0.05 and 0.29 and 0.26 , respectively.

Another parameter to be considered in a breeding program is repeatability of weaning weight. Cardellino and Castro (1987), Souza *et al.* (1994), Souza and Ramos (1995) and Souza *et al.* (1996b), in the Nellore breed, obtained estimates of 0.31, 0.18, 0.32, 0.27 and 0.45, respectively.

Permanent environmental effects due to the dam is another important factor acting on weaning weight. A low estimate of .06 relative to phenotypic variance was found by Van Vleck *et al.* (1996) for the Simmental breed, indicating that permanent environmental effects are not important for weaning weight. He also suggested as a guideline a larger estimate (0.39) for Hereford cattle. Meyer *et al.* (1993) reported estimates of 0.29, 0.13, and 0.23 for Hereford, Angus and crossbred cattle, respectively.

Accurate prediction of breeding values is the basis for any breeding plan. Furthermore, increased production and productivity are fundamental goals of integrated plans involving animal breeding, nutrition, management, reproduction, and disease control. Knowledge of genetic and non-genetic effects acting on the traits and of effects of genetic x environment interactions also can provide for more effective overall herd management.

Studies of genotype x environment interaction evaluate performance of genetic groups in different environments. Hammond (1947), Falconer (1952) and Falconer and Latyszewsky (1952) were pioneers in studies of genotype x environment effects. Procedures to estimate a genetic correlation for the same trait in two different environments were introduced by Falconer (1952), Robertson (1959), Dickerson (1962) and others. These procedures are similar to estimation of the genetic correlation between two sexes for the same trait. Robertson (1959) presented the theoretical basis for Falconer's ideas, with several formulas for

estimating genetic correlation. He also suggested a guideline that genotype x environment interaction may be of practical importance when the genetic correlation observed for the same trait in different environments is less than 0.80.

Northcutt *et al.* (1990) found significant interactions between sire x location and calf genetic group x location for weaning weight in the USA. In the same country, Tess *et al.* (1979) estimated genetic correlations for performance (weaning weight) in two regions from progeny of several sires and obtained estimates at 0.90 ± 0.20 between Montana and the Midwest, 0.42 ± 1.70 between Montana and Texas, and 0.48 ± 1.10 , between the Midwest and Texas. Buchanan and Nielsen (1979) found significant sire x region interactions and estimates of genetic correlations of sire breeding values in different regions of 0.77 and 0.32 for weaning weight for Simmental and Maine-Anjou breeds, respectively.

Nobre *et al.* (1985), studying Nellore cattle in northeast Brazil, reported that sire x herd interactions were significant for 205-d weight, which suggests variation in sire performance across herds. Nobre *et al.* (1987) also observed that interaction of sire x microregion significantly affected 205-d weight.

Euclides Filho *et al.* (1991), in Brazil, estimated effects of sire/herd x age of cow at calving on weaning weight of Nellore cattle, which agreed with results reported by Silva (1990).

The objective of this study was to estimate genetic and environmental parameters and to evaluate the importance of genotype x region interaction effects on weaning weight of Nellore calves across eight different regions of Brazil.

Materials and methods

Records were weaning weights of 105,645 Nellore calves from a very large geographical area. The eight regions used in the analyses were characterized by ARRUDA and SUGAI (1994) and differed from each other by one or more of the following: production system, technology level, and natural resources such as climate, rain, topography and quality of the soil (Figure 1 and Tables 1 and 2). The data were provided by the Brazilian Zebu Breeders Association (ABCZ) and by the National Beef Cattle Research Center (CNPGC) of the Brazilian Agricultural Research Corporation (Embrapa). Table 3 presents for each region the total number of animals, number of sires, number of calves per sire, number of farms, number of dams, number of calves per dam, average age of the dams, standard deviation of age of dams, and weaning weight means.

Estimates of variance components and genetic parameters were obtained by restricted maximum likelihood using a derivative free algorithm (Boldman *et al.*, 1995), with a sire model. All bulls were assumed to be unrelated.

The statistical model was

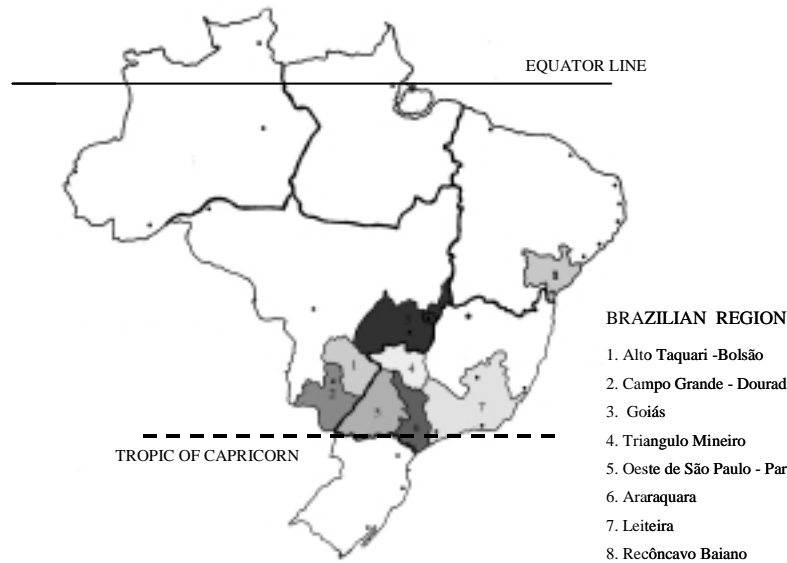


Figure 1. Brazilian regions of production characterized by Arruda and Sugai (1994)

Table 1. Distribution of the eight regions by total area, cattle density, pasture type and stocking rate at pasture (1ha = 10,000m²)

Region	Total Area (km ²)	Cattle density (head/km ²)	Pastures			
			Native pasture (%)	New pasture (%)	Total (ha)	Average cattle / ha
1	120 307	24.74	57.12	42.88	7 009 197	0.334
2	119 980	49.33	32.61	67.39	7 501 835	0.641
3	242 224	37.00	61.27	38.73	14 119 841	0.495
4	97 347	64.94	34.03	65.97	5 964 160	0.841
5	144 454	80.08	13.44	86.56	8 363 185	1.104
6	99 656	87.20	36.86	63.17	3 081 392	0.831
7	253 397	35.77	83.77	16.23	11 710 161	0.633
8	61 260	32.12	45.88	54.12	2 933 619	0.525

Source: Arruda e Sugai. 1994. Regions 1. Alto Taquari Bolsão; 2. Campo Grande - Dourados; 3. Goiás; 4. Triângulo Mineiro; 5. West São Paulo - Paraná; 6. Araraquara; 7. Leiteira; 8. Reconcavo Baiano.

$$y = X\beta + Zs + Wp + e$$

where,

y = vector of observations; X = design matrix for fixed effects; β = vector of fixed effects (sex, month and year of calving and herd, with age of dam as a covariate); Z = design matrix for the sires; s = vector of sire effects; W = design matrix for the dams; p = vector of effects due to

$$E \begin{bmatrix} s \\ p \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{Var} \begin{bmatrix} s \\ p \\ e \end{bmatrix} = \begin{bmatrix} I_s \sigma_s^2 & 0 & 0 \\ 0 & I_p \sigma_p^2 & 0 \\ 0 & 0 & I_e \sigma_e^2 \end{bmatrix}$$

dams; e = vector of random errors.

Also,

$$E(y) = X\beta$$

where:

2s = sire component of variance (1/4 of the additive genetic variance); 2p = variance of dams effects; 2e = residual variance; I_s, I_c, and I_n are identity matrices with orders equal to number of sires (s), number of dams (c), and number of observations (n), respectively.

Estimates of heritability for each region were calculated as four times the sire component of variance divided by the total (phenotypic) variance for each region separately. Repeatability was estimated as the sum of the sire and the dam components of variances divided by the total variance.

Weaning weights in different regions were considered different traits. Measures of genetic x environmental interaction were the genetic correlations between expression of sire effects in pairs of environments. Covariance components were estimated

$$S_o = \begin{bmatrix} \sigma_{e_1}^2 & \sigma_{e_1e_2} \\ \sigma_{e_1e_2} & \sigma_{e_2}^2 \end{bmatrix} \quad R_o = \begin{bmatrix} \sigma_{e_1}^2 & 0 \\ 0 & \sigma_{e_2}^2 \end{bmatrix} \quad \text{and} \quad P_o = \begin{bmatrix} \sigma_{e_1}^2 & 0 \\ 0 & \sigma_{e_2}^2 \end{bmatrix}$$

(Spearman correlations) also were calculated between the EPD for pairs of regions using SAS (1996).

Results and discussion

based on the same model using MTDFREML. In this case, the relevant covariance matrices for a pair of progeny of the same sire in two environments were:

The residual covariance (e_1e_2) is zero, since a calf has a record in only one environment (region).

Using the estimates of the covariance components at convergence, EPDs were estimated for sires with progeny in pairs of regions. Rank correlations

Estimates of genetic and phenotypic parameters are presented in Table 4. The smallest estimate of heritability (0.16) was for the Goiás region (central Brazil), while the largest estimate (0.38) was for the Araraquara region (southeast Brazil). The magnitude of the estimate for Goiás may be due to the size of the

Table 2. Relief, natural vegetation, climate and rainfall each region.

Regions	Relief	natural vegetation	Climates	Rainfall (mm)
1	- Plains	- Savanna - Tropical Forest	- Humid warmest	1250
2	- Uneven	- Savannah - Clean field - Forest tropical sub deciduous	- Humid warmest	1250 to 1500
3	- Uneven - Wavy plan	- Savannah - Native vegetation - Tropical Forest sub deciduous	- Humid warmest - Hot semi-humid	1750
4	- Smoothly wavy	- Savannah - Tropical forest	- Tropical humid the semi-humid	1500
5	- Underlain by eroded sedimentary rock with medium altitudes from 250 to 300 m	- Tropical forest sub deciduous - Savannah stains	- Tropical - hot humid, humid warmest and high humid	1250
6	- Wavy mountainous	- Tropical forests - Savannah - Subtropical forests. coasts and of Araucarias	- Tropical sub humid, humid and super humid	1100 to 1500
7	Mountainous	- Campos. savannah - Forest tropical deciduous - Forest leaf continual coastal hygrophilous	Tropical soft	1500
8	-	-	- Hot - Mediterranean - Humid Tropical	750 to 1750

Source: Arruda e Sugai. 1994. Regions 1. Alto Taquari Bolsão; 2. Campo Grande - Dourados; 3. Goiás; 4. Triângulo Mineiro; 5. West São Paulo - Paraná; 6. Araraquara; 7. Leiteira; 8. Reconcavo Baiano.

population in that region as compared with the others, by preferential mating of some sires, or by the small number of progeny of some sires.

Two regions, West São Paulo-Paraná and Araraquara, had the largest estimates of genetic variance and largest estimates of heritability, suggesting that selection based on weaning weight would be most effective in those regions. The larger estimates of heritability also may indicate more accurate

identification of sires.

Estimates of repeatability (Table 4) varied from 0.34, for Goiás region, to 0.57, for West São Paulo-Paraná and Araraquara regions. Estimates are higher than those found by Oliveira (1989) and Souza *et al.* (1994), but are similar to those reported by Cardellino and Castro (1987), Souza and Ramos (1995), and Souza *et al.* (1996b).

Estimates of relative variance due to dam effects (c_2)

Table 3. Numbers of animals (N), sires, dams, and farms and averages of age of dam (months) and weaning weight (WW) by region.

Region	N	Sires	KS	Farms	Dams	KD	AD ± SD	WW ± SE ⁽¹⁾
1	12 399	217	49.7	39	6 316	2.0	93 ± 42	149.89 ± 0.80 h
2	17 242	292	51.7	56	9 962	1.7	91 ± 42	153.12 ± 0.68 e
3	3 809	205	15.4	38	2 797	1.4	93 ± 42	150.08 ± 1.09 gh
4	25 614	445	50.5	95	14 326	1.8	93 ± 42	153.99 ± 0.57 de
5	25 380	336	64.5	91	14 515	1.7	95 ± 42	155.01 ± 0.50 cd
6	10 953	245	37.4	53	7 089	1.5	91 ± 39	157.08 ± 0.39 a
7	7 604	199	32.0	35	4 337	1.8	92 ± 40	155.38 ± 0.65 bcd
8	2 464	84	21.6	14	1 575	1.6	92 ± 40	152.04 ± 1.34 defgh
All	105 465	588	156.6	419	57 162	1.5	93 ± 42	153.33 ± 0.33

KS = number of calves per sire; KD = number of calves per dam and. SD = Standard Deviation; WW = weaning weight mean, adjusted by the least squares method; SE = Standard error. IV = age of dam. 1 Means followed by common letters do not differ significantly; The WW and SE were calculated using a SAS program.

Table 4. Estimates of components of variance and genetic and phenotypic parameters for weaning weight in Nellore cattle.

Region	σ_p^2	σ_s^2	σ_D^2	σ_e^2	h^2	c^2	e^2
1	375.11	20.33	74.99	279.79	0.22	0.20	0.75
2	430.87	28.08	69.30	333.49	0.26	0.16	0.77
3	430.65	17.72	76.88	336.05	0.16	0.18	0.78
4	406.63	29.80	69.94	306.89	0.29	0.17	0.75
5	408.89	34.36	92.25	282.25	0.34	0.23	0.69
6	400.44	38.08	71.99	290.37	0.38	0.18	0.73
7	412.71	37.72	68.35	306.64	0.37	0.17	0.75
8	335.74	21.44	75.84	238.47	0.26	0.23	0.71
All	420.04	27.00	77.11	315.93	0.26	0.18	0.75

σ_p^2 = phenotypic variance; σ_s^2 = sire variance; σ_D^2 = dam variance; σ_e^2 = error variance; h^2 = heritability; c^2 = fraction of variance due to dam; e^2 = fraction of variance due to residual for sire model.

are shown in Table 4, and varied from 0.16, for Campo Grande-Dourados region, to 0.23, for West São Paulo-Paraná and Recôncavo Baiano regions. Estimates were similar to those presented by Meyer (1992), Eler *et al.* (1995) and Van Vleck *et al.* (1996).

A genetic correlation is a measure of the influence of genes affecting two traits. Estimates of genetic correlations between weaning weights of progeny of the same sires raised in several regions are shown in Table 5. A genetic correlation of nearly unity was estimated between Leiteira (7) and Recôncavo Baiano (8) regions, and indicates absence of genotype x environment interaction, since sires would be evaluated similarly in both regions. However, for all other pairs of regions, estimates of genetic correlations were less than 0.80, suggesting, according to Robertson (1959), occurrence of genotype x environment interaction of practical importance.

A genetic correlation of near zero was observed between regions 2 (Campo Grande-Dourados) and 6 (Araraquara), suggesting that different sets of genes act

on weaning weight in those regions. If the correlation were really zero, superior sires in one region might not be superior in the other. Evidence of important genotype x environment interactions in Brazil has also been found by Nobre *et al.* (1987) and Silva (1990).

Results of this study suggest that some care must be applied when planning a comprehensive breeding program for weaning weight (weight at 205 days) in Brazil. Special consideration should be given to the environmental conditions where sires in the program were tested, because a sire that is satisfactory in one region may have progeny with less than ideal performance when used in another region.

Estimated progeny differences represent the differences in expected performance of a progeny of a sire compared to that of another sire participating in the same evaluation. An example of performance of two sires (A and B) in different pairs of regions (Figure 2) shows that there are differences in performance depending on the region where the progeny are raised. To evaluate the effect of genotype x environment

Table 5. Estimates of heritability (diagonal) and genetic correlations (above diagonal) for weaning weight in eight different regions.

		Region							
Region	1	2	3	4	5	6	7	8	
1	0.21	0.51	0.60	0.54	0.67	0.65	0.74	0.60	
2		0.26	0.70	0.61	0.40	-0.03	0.35	0.40	
3			0.17	0.74	0.45	0.61	0.49	0.66	
4				0.29	0.55	0.47	0.76	0.59	
5					0.34	0.40	0.72	0.67	
6						0.38	0.09	0.71	
7							0.35	1.00	
8								0.25	

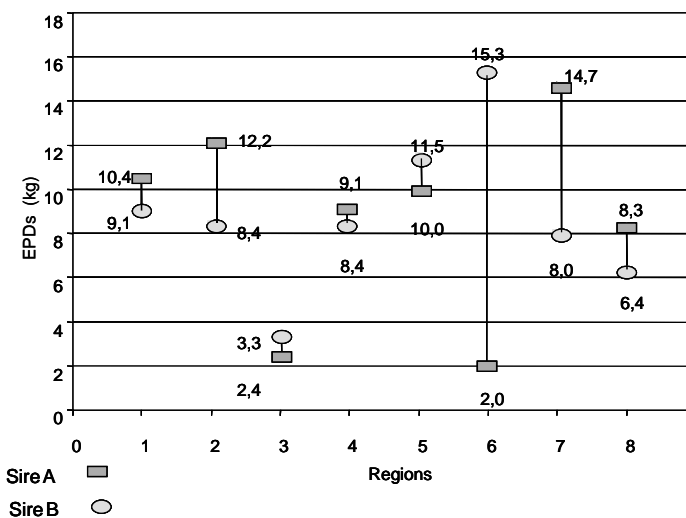


Figure 2. Differences in weaning weight EPD's for sires A and B in each of eight regions.

Table 6. Spearman rank correlations between sire EPDs1 in pairs of regions.

		Region						
Region	2	3	4	5	6	7	8	
1	0.79	0.88	0.84	0.89	0.88	0.92	0.91	
N ⁽²⁾	374	325	500	391	346	315	390	
2		0.94	0.84	0.67	-0.25	0.68	0.82	
N		390	507	454	393	391	310	
3			0.95	0.80	0.88	0.81	0.92	
N			471	409	339	313	227	
4				0.80	0.78	0.94	0.93	
N				539	507	478	457	
5					0.68	0.93	0.95	
N					349	399	351	
6						0.36	0.96	
N						325	274	
7							1.00	
N							233	

1EPD = Expected Progeny Difference; (2) = Number of sires (with progeny in both regions).

interaction on selection, rank correlations were computed between sire EPDs estimated for pairs of regions. The results, as seen in Table 6, indicate changes in ranks of the sires depending on the region. A negative rank correlation (-0.25) between regions 2 (Campo Grande - Dourados) and 6 (Araraquara) indicates that sires with good performance in region 2 were not the sires with good performance in region 6. For regions 6 (Araraquara) and 7 (Leiteira), the rank correlation was also low (0.36). On the contrary, in agreement with the estimate of the genetic correlation, a rank correlation of 1.00 was observed between EPD of sires from evaluations in regions 7 and 8.

Conclusions

The weaning weight can be considered a different trait in various regions of Brazil.

Genetic gains in weaning weight of Nelore cattle in Brazil are likely in view of the large genetics variations revealed in this study

Estimates of heritability for weaning weight suggest that mass selection could result in genetic gain under a breeding program that has the goal of improving this trait.

The genotype x environment interactions found in this study suggest the need to choose appropriate sires for the regions where they will be used.

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