Genetic analysis of growth traits in polled Nellore cattle from tropical region

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ABSTRACT: (Co)variance components and genetic parameters were estimated for weights at 120 (W120), 240 (W240), 365 (W365) and 450 (W450) days of age of Polled Nellore cattle born between 1987 and 2010 and raised on pasture. An animal model considering herd-year-season of birth and calf sex as fixed effects and age of cow as covariate was fitted by Gibbs Sampling. Direct heritabilities were estimated as 0.43, 0.61, 0.72 and 0.67 for W120, W240, W365 and W450, respectively. Maternal heritabilities were 0.07 and 0.08 for W120 and W240, respectively. Direct additive genetic correlations between weights at different ages ranged from 0.68 to 0.98. Direct-maternal genetic correlations for W120 and W240 ranged from -0.31 to -0.54. Estimates of maternal heritability ranged from 0.056 to 0.092 for W120 and from 0.064 to 0.096 for W240. This study showed that genetic progress is possible for early body weight.

Keywords: Growth; Heritability; Zebu

Introduction

Brazil ranks first worldwide in beef exports, and is the second largest producer (Brasil (2011)). Zebu breeds, primarily Nellore, account for more than 80% of beefproducing herds in Brazil. In Brazil, the Polled Nellore breed is considered as a distinct breed. However, performance data from Polled Nellore cattle have been scarce and insufficient to evaluate growth traits, such as the magnitude of (co)variance components.

Growth and production traits have a large impact on profitability of beef cattle production systems. Growth traits are influenced both by direct additive genetic effects and by maternal effects (Albuquerque and Meyer (2001)). When maternal effects are omitted from genetic evaluation due to data limitations (Wasike et al. (2009)), the genetic parameters are biased upwards (Dodenhoff et al. (1999), Maniatis and Pollott (2002)) and selection efficiency is reduced.

We carried out this study to estimate direct and maternal additive genetic (co)variance components and genetic parameters for weight at 120, 240, 365 and 450 days of age, specific for the Polled Nellore breed raised on pasture in tropical regions of Brazil.

Material and Methods

The data set was provided by Guaporé Pecuária Company (OB Group) together with the National Association of Breeders and Researchers (ANCP) and consisted of weight records collected between 1987 and 2010. The cattle were reared near Pontes e Lacerda, Mato Grosso, Brazil. It is a region of humid tropical climate, with an average altitude of 254 meters and average annual precipitation of 1,500 mm.

Weight information from every animal allowed estimation of the adjusted weights for 120 (W120), 240 (W240), 365 (W365) and 450 (W450) days of age. This was done because all breeding programs in Brazil function with standardized weights. Adjusted weight data were cleaned by excluding any adjusted weight more than three standard deviations from the mean. Contemporary groups presenting less than three records or sires presenting less than three offspring were also removed from the data set. The final data set was composed of 31,006, 33,595, 21,657 and 22,651 animals from seven herds with adjusted weights at 120, 240, 365, 450 days, respectively. The animals were progeny of 447, 461, 440 and 433 sires that descended from 11,771, 12,137, 9,684 and 9,705 cows, respective to the standard ages. The inverse relationship matrix was composed of 46,107 Polled Nellore individuals.

The genetic analyses were conducted by fitting multivariate animal models. The model for W120 and W240included herd-year-season (HYS) of birth, sex of the calf and herd as fixed effects, and cow age as a covariate. The maternal and the permanent environmental effects were not used for W365 and W450 because these effects were not significant (P > 0.05).

We assumed that the systematic effects listed above and the (co)variance components included in the fitted model have a uniform a priori Gaussian distribution, whilst the conditional distributions of the direct additive, maternal, permanent environmental and residual variances present inverse Wishart distribution (Sorensen and Gianola (2002)).

The marginal posterior distribution for each parameter was obtained via integration of multivariate density functions using a Gibbs sampling procedure, with a period of data collection for multi-traits of 1,500,000 iterates. The initial discard was 500,000 and the sampling interval was of 1000 iterations. Distributions (flat prior) were used to estimate (co)variance components, using the MTGSAM software (Van Tassell and Van Vleck (1996)). Serial correlation and convergence for the Gibbs sampler were obtained using the GIBANAL software (Van Kaam (1997)). Convergence was monitored using the Heidelberger and Welch diagnostic tests, available in CODA library (Convergence Diagnosis and Output Analysis) and implemented in the R software (R Development Core Team (2012)).

Results and Discussion

Average weights for W120, W240, W365 and W450 were 121.6, 183.8, 215.5 and 248.5 kg, respectively. Mean WADG and PWADG were 0.645 ± 0.124 and 0.288 ± 0.162 kg/d, respectively. Body weight is currently the selection criterion in Brazilian breeding programs, but if correlations are strong in all ages and heritabilities are high, animal selection at the age of W120 and W240 will probably result in more precocious and heavier animals at the time of slaughter. The selection for weight at older ages (W365 and W450) could result in animals with later maturation, with negative impacts on farm profits.

The (co)variance matrix of maternal and additive direct genetic effects, are shown in Table 1. The estimate of residual variance was 389.64 ± 12.74 , 573.05 ± 34.89 , 411.57 ± 18.91 and 561.91 ± 18.13 for W120, W240, W365 and W450, respectively. The variance estimates of maternal permanent environmental effects for W120 and W240 were 12.77 ± 1.71 and 15.87 ± 2.44 , respectively.

Table 1. Estimates of mean, standard-deviation, mode and bounds of highest posterior density intervals at 95% (HPD95 in brackets) of the marginal posterior distribution of (co)variance components due to direct additive genetic and maternal effect for weight at 120, 240, 365 and 450 days of age.

Doromotor	Mean	Standard Deviation	Mode	Credibility region		
Falameter				2.5%	97.5%	
σ_{a1}^2	299.1	9.08	298.8	282.2	318.9	
σ_{a1a2}	466.5	6.22	466.5	454.3	478.6	
σ_{a1a3}	442.4	6.47	442.2	430.3	455.2	
σ_{a1a4}	426.2	6.74	425.9	413.2	440.1	
σ_{alm1}	-52.6	5.85	-52.3	-64.6	-41.5	
σ_{a1m2}	-75.6	5.25	-75.6	-85.7	-65.7	
σ_{a2}^2	905.3	16.29	905.1	873.0	936.5	
σ_{a2a3}	812.3	9.52	812.2	793.8	831.0	
σ_{a2a4}	755.0	10.12	755.1	735.0	774.2	
σ_{a2m1}	-53.4	6.00	-53.4	-65.5	-41.3	
σ_{a2m2}	-164.2	10.85	-164.1	-185.8	-143.1	

σ_{a3}^2	1075.6	12.66	1076.1	1050.4	1098.8
σ_{a3a4}	1083.9	11.57	1083.9	1061.5	1105.8
σ_{a3m1}	39.3	5.84	39.4	27.8	50.6
σ_{a3m2}	21.1	7.05	21.2	7.3	34.7
σ_{a4}^2	1142.8	14.13	1143.3	1116.1	1170.9
$\boldsymbol{\sigma}_{a4m1}$	51.8	6.16	51.8	39.4	64.0
σ_{a4m2}	52.4	7.38	52.7	38.3	66.7
σ_{m1}^2	53.3	4.27	53.1	45.2	62.1
σ_{m1m2}	61.6	3.95	61.7	54.0	69.6
σ_{m2}^2	128.4	7.62	128.6	114.2	143.0

	1112	120.4	1.02	120.0	117.2	145.0	
Subscr	ipts 1, 2, 3	and 4 refer	to the we	ights at 120	, 240, 365	and 450	days
of age,	, respective	ely; σ_a^2 : a	dditive ger	netic varian	ice; σ_{am}	additive	and
matern	al genetic	covariance;	σ_m^2 : mat	ernal geneti	ic variance		

The estimates of direct heritability and genetic correlation for W120, W240, W365 and W450 are shown in Table 2. Maternal heritability for W120 and W240 was 0.07 \pm 0.006 and 0.08 ± 0.005 and the genetic correlation between the maternal and the direct effects was -0.42 ± 0.031 and - 0.48 ± 0.021 for weight at 120 and 240 days old, respectively. The estimates of the direct additive genetic correlations were greater than 0.70 at most ages and are in accordance with other studies in Brazil (Ferraz et al. (2002), Malhado et al. (2002)). Due to the strong genetic correlation between weights at different ages we suggest the selection of animals at W120 and W240. Although the direct heritability estimates for W365 (0.72) and W450 (0.67) were greater than W120 (0.43) and W240 (0.61), selection for post weaning weights may increase the age at slaughter and the production costs throughout the years. More criteria for the selection of these traits are therefore necessary. Similar results and arguments were reported for adjusted weights at 205, 365 and 550 days in Nellore cattle in Northern Brazil (Santos et al. (2012)).

Table 2. Estimates of mean, standard-deviation, mode and bounds of highest posterior density intervals at 95% (HPD95 in brackets) of the marginal posterior distribution of direct (h_a^2) and maternal (h_m^2) heritabilities, permanent environmental (c), estimates of genetic correlations (r_g) between direct genetic effects and esti-

mates of genetic correlations (Γ_{am}) between direct and maternal effect for weight at 120, 240, 365 and 450 days of age.

Parameter	Mean	Standard Deviation	Mode	Credibility region	
				2.5%	97.5%
h_{a1}^{2}	0.43	0.015	0.43	0.41	0.47

h_{a2}^2	0.61	0.018	0.61	0.58	0.65
h_{a3}^2	0.72	0.010	0.72	0.70	0.74
h_{a4}^2	0.67	0.008	0.67	0.65	0.69
h_{m1}^2	0.07	0.006	0.07	0.06	0.08
h_{m2}^2	0.08	0.005	0.08	0.07	0.09
r_{g12}	0.90	0.010	0.90	0.88	0.92
r_{g13}	0.78	0.012	0.78	0.76	0.80
r_{g14}	0.73	0.012	0.73	0.71	0.75
r_{g23}	0.82	0.007	0.82	0.81	0.84
r_{g24}	0.74	0.008	0.74	0.73	0.76
r_{g34}	0.98	0.001	0.98	0.97	0.98
r _{alm1}	-0.42	0.030	-0.42	-0.48	-0.36
r _{a2m2}	-0.48	0.020	-0.48	-0.52	-0.44
\mathbf{c}_1	0.032	0.004	0.031	0.023	0.040
c_2	0.027	0.004	0.027	0.019	0.036

Subscripts 1, 2, 3 and 4 refer to the weights at 120, 240, 365 and 450 days of age, respectively.

For weight at 120 and 240 days, the maternal effects accounted for a lower proportion of total variation than the direct additive genetic effects. At older ages, the maternal permanent environmental effect decreased, as the calves' diet changed from maternal milk to grazed forage. As expected (Rosales et al. (2004)), direct heritabilities for W120 and W240 were greater than maternal heritability. Direct maternal correlations for W120 and W240 were strong and negative (-0.21 to -0.28) but lower than some estimates reported in previous studies (Meyer (1992), Tawah et al. (1993), Elzo et al. (1998)).

The genetic correlation between direct additive genetic and maternal additive genetic effects suggests genetic antagonism between both effects. Therefore, selection for direct additive genetic effects would worsen the maternal ability, making it difficult to conduct joint selection for W120 and W240 (Vergara et al. (2009), Ferraz et al. (2002)). This may occur when some fixed effects that influence the trait are not considered in the model [39]. However, this could also indicate greater variation between sires and dams, due to either greater genetic variance or confounding environmental effects (Vergara et al. (2008)). The negative values of correlations may indicate antagonism between the effects of genes related to growth and the maternal ability, which is a major influence trait for optimal calf development (Souza et al. (2011)). However, negative correlations between direct additive genetic effects and maternal effects are frequent and often considered to be a statistical matter rather than a biological issue in animal breeding (Meyer (1997), Eler et al. (2000)). According to (Mercadante and Lôbo (1997)), non-inclusion of maternal genetic and permanent environmental effects can lead to overestimation of the direct additive component and therefore, result in decreased expected genetic gain. Thus, breeding programs that consider only the direct additive genetic effects will not necessarily guarantee increased maternal ability.

Conclusion

This study has revealed that genetic progress is possible for the accounted traits. The strong and positive estimates of direct additive genetic correlation for weight at 120, 240, 365 and 450 days old indicate that improvements in a trait should involve improvements in other traits. Maternal effects influenced the performance of weight at 120 and 240 days. Therefore, the maternal effect should be taken into account in genetic analyses of growth traits by fitting it as a genetic or a permanent environmental effect, or even both.

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