

Genetic and phenotypic trends for growth traits of buffaloes in Brazil

C.H. Mendes Malhado¹, A. Amorim Ramos², P.L. Souza Carneiro¹,
J.C. de Souza³, W.R. Lamberson⁴

¹ Universidade Estadual do Sudoeste da Bahia (UESB – DCB), Jequié-BA

² Universidade Estadual Paulista (UNESP), Botucatu-SP

³ Universidade Federal do Paraná (UFPR), Palotina-PR

⁴ Animal Science Department, University of Missouri - Columbia

Corresponding author: C.H. Mendes Malhado, Universidade Estadual do Sudoeste da Bahia, Departamento de Ciências Biológicas. Avenida José Moreira Sobrinho, s/n. Jequiezinho. Jequié - BA. Brazil. ZIP code: 45200-000 - Tel. 55-73-91919131 - Fax: 55,7335256683 - Email: carlosmalhado@gmail.com

ABSTRACT: The objectives this paper were to estimate genetic parameters and genetic and phenotypic trends of birth weight (BWT) and weights adjusted to 205 (WT205), 365 (WT365) and 550 (P550) days of age of beef buffaloes born from 1985 to 2003 in Brazil. For BWT and WT205 the model included direct and maternal genetic and maternal environment as random effects and contemporary and genetic groups as fixed effects. For WT365 and WT550 the same model was used except without direct maternal and maternal environmental effects. The genetic and phenotypic trends were estimated by regression of means of dependent variables on birth year of animals. Regressions were obtained by using two methodologies: 1) linear regression; and 2) non-parametric splined regression. The direct heritability estimates were 0.09, 0.45, 0.46 and 0.58 for BWT, WT205, WT365 and WT550, respectively. The direct genetic trends from linear regression were 0.01, 0.23, 0.58 and 1.40 kg per year for PN, WT205, WT365 and WT550, respectively ($P < 0.001$ for all). Phenotypic trends were strongly positive while genetic trends were consistently positive but small. Genetic parameters indicate potential for increased rate of genetic change with full implementation of genetic improvement programs.

Key words: Buffalo, Genetic trend, Genetic parameters, Heritability.

INTRODUCTION - Buffaloes of Murrah, Mediterrâneo, Jabarabadi and Carabao breeds were introduced in Brazil in the beginning of the 20th century. The population is now 2.8 million in Brazil and increasing at a faster rate than cattle. The productivity of this species has improved year by year. Livestock genetic improvement programs and improvement of the environment combined to improve the phenotype of animals. This background provided a place to initiate a national genetic evaluation program for buffaloes for milk and meat production. This resulted in publication in 2002 of the First National Buffaloes Summary – PROMEBUL (Ramos et al. 2002). Selection efficiency depends on identification of the best animals for economically important characteristics and the use of them in reproduction. After the start of a program of genetic selection and evaluation, it is necessary to perform periodic evaluations of the efficiency of the program. Along this line, evaluation of genetic progress has been the objective of studies in cattle in Brazil, see for example Ferraz Filho et al. (2002), and Malhado et al. (2005).

The objective of this paper was to evaluate genetic progress and estimate genetic parameters for use in future genetic evaluation programs for buffaloes in Brazil.

MATERIAL AND METHODS - The data used were from the Genetic Improvement Program of Buffaloes - PROMEBUL. The study used information from 6,992 buffaloes, born from 1974 to 2003 in Brazil, from three genetic groups (Jafarabadi – 1,413, Mediterrânea – 5,281 and Murrah 1,036) on 11 farms, located in the states of Bahia, Goiás, Pará, Paraná, Rio Grande do Sul and São Paulo. Estimates of variances and covariances were obtained using single trait analyses with the MTDFREML set of programs (Boldman et al., 1995). For birth weight (BWT) and weaning weight at 205 day of age (WT205) the model included direct and maternal genetic, and uncorrelated maternal random effects. Fixed effects were contemporary groups (sex, season, year, and farm) and genetic groups. The covariance between direct and maternal genetic effects was considerate null ($\sigma_{am} = 0$). For WT365 and WT550 the same fixed effects were used and maternal and uncorrelated random effects were dropped from the model. The genetic and phenotypic trends were estimated by regression of means of dependent variables on birth year of animal. Non parametric regression, SPLINE (articulate polynomials), was also used to describe genetic trends (Reinsch, 1967).

Table 1. Estimates of covariates components and heritability of birth (BWT), weight at 205 (WT205), 365 (WT365) and 550 (WT550) weights.

	σ_a^2	σ_m^2	σ_{am}^a	σ_{ep}^2	σ_e^2	σ_p^2	h_d^2	h_m^2
BWT	0,96	0,37	0	0,43	9,27	11,03	0,09 ± 0,03	0,03 ± 0,02
WT205	351,05	69,61	0	0,097	366,49	787,15	0,45 ± 0,06	0,09 ± 0,04
WT365	857,91	-	-	-	1017,63	1875,55	0,46 ± 0,04	-
WT550	2419,3	-	-	-	1785,41	4204,73	0,58 ± 0,10	-

σ_a^2 ; σ_m^2 ; σ_{am}^a ; σ_{ep}^2 ; σ_e^2 ; σ_p^2 ; h_d^2 ; h_m^2 = Direct variance component, maternal variance component, covariance direct maternal, dam uncorrelated permanent environmental, residual variance, phenotypic variance and heritability direct and maternal, respectively.

RESULT AND CONCLUSIONS - The (co)variance components and heritabilities of direct and maternal effects are presented in table 1. For BWT these heritabilities were low, direct (0.09) and maternal (0.03). The direct and maternal heritabilities for WT205 were 0.45 and 0.09, respectively. For WT365 and WT550 heritabilities were 0.46 and 0.58, respectively. The direct and maternal genetic trends (linear regression) of BWT were equal to 0.006 and -0.0104 kg per year, respectively ($P < 0.001$), and over the 18 years studied the genetic gain was 0.108 kg for the direct effect and the maternal effect lost 0.187 kg. For WT205 the genetic trends (linear regression) for direct and maternal effects were equal to 0.23 and 0.05 kg per year, respectively ($P < 0.01$). This represents genetic progress of 4.11 and 0.82 kg in the 18 years of study (Figure 1). The annual genetic trends are equivalent to 0.12 and 0.025% of the mean weight at 205 days respectively. The direct genetic trends (linear regression) for WT365 and WT550 were 0.58 and 1.40 kg per year, respectively,

($P < 0.001$) with genetic progress of 10.44 and 25.27 kg in the period (Figure 2). The genetic gain is equivalent to an annual increase of 0.22 and 0.35% of the means, respectively. The phenotypic trend (linear regression) for BWT was equal to -0.03 kg per year ($P < 0.05$). For WT205 the phenotypic trend (linear regression) was 2.70 kg per year ($P < 0.001$). For WT365 and WT550 phenotypic trends were equal to 5.42 and 12.40 kg per year ($P < 0.05$). The coefficient of heritability for weights at 205, 365 and 550 days of age show potential for genetic gain and indicate selection should be used for improvement of buffaloes. In the period of this study, the genetic trends were positive but very small. Phenotypic trends were positive indicating that buffalo breeders have improved the environment.

Figure 1. Direct (A) and maternal (B) genetic trends (linear and non parametric regression) for weight at 205 days of age (WT205) from 1985 to 2003.

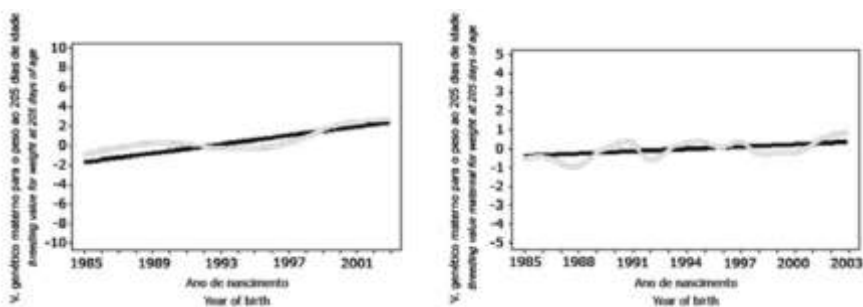
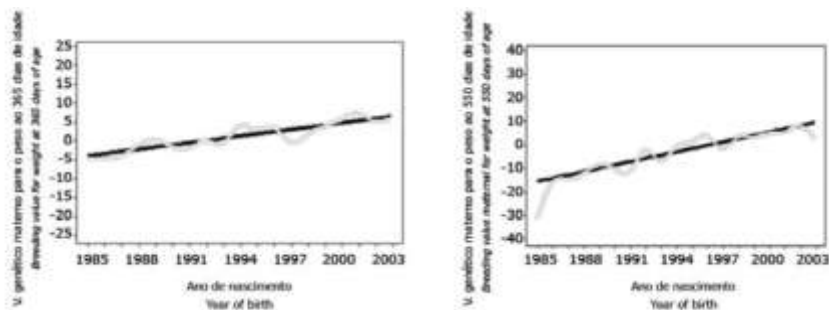


Figure 2. Direct genetic trends (linear and non parametric regression) to weights at 365 (A) and 550 (B) days of age, from 1985 to 2003.



REFERENCES - Boldman, K.G., Kriese, L.A., Van Vleck, L.D. Kachman S.D. 1995. A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances. ARS-USDA, Clay Center, NE. **Ferraz Filho, P.B. Ramos, A.A. Silva, L.O.C. Souza, J.C. Alencar, M.M., Malhado, C.H.M. 2002.** Genetic trends of direct and maternal effects on weaning weight and post weight of Tabapuã cattle in Brazil. *Revista Brasileira de Zootecnia*, 31 (2):637-642. **Malhado, C.H.M., Martins Filho, R., Lôbo, R.N.B., Facó, O. Azêvedo, D.M.M.R., Souza, J.C, Oliveira, S.M.P. 2005.** Genetic Trends for Traits Related to the Growth Rate in Nellore Cattle Raised in the Northeast Region of Brazil. *Revista Brasileira de Zootecnia*, 34(1): 60-65. **Ramos, A.A. 2002.** Buffaloes Summary – PROMEBUL, 1. **Reinsch, C. H. 1967.** Smoothing by spline functions. *Numerische Mathematik*, 10: 177-183.