

# Genetic parameters of test day milk yield in Brazilian Girolando cattle using an autoregressive multiple lactation animal model



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Costa, C. N.<sup>1,3</sup>, Freitas, A.<sup>1</sup>, Silva, M. V.<sup>1</sup>, Paiva, L.<sup>2</sup>, Thompson, G.<sup>3,4</sup>, Carnevalheira, J.<sup>3,4</sup>

<sup>1</sup>Embrapa Gado de Leite, 36038-330 Juiz de Fora, MG, Brazil, <sup>2</sup>Girolando Breeders Association, 38040-280 Uberaba, MG, Brazil; <sup>3</sup>ICETA/CIBIO, Universidade do Porto, 4485-661 Vairão o, Portugal; <sup>4</sup>ICBAS, Universidade do Porto, 4099-003 Porto, Portugal

## INTRODUCTION

The Girolando is a dairy cattle formed by crossing the Holstein and the Gir breeds. It is the most predominant cattle in dairy farming in Brazil. In the late nineties the Girolando Breeders Association (GBA) started running an AI progeny test of crossbred young sires. Genetic evaluation is currently based on fitting a lactation model.

This study was aimed to estimate variance components and genetic parameters for test day milk yield of Girolando cattle, using an autoregressive test day multiple lactations (AR) animal model.

## MATERIAL AND METHODS

**Data** - Test day (TD) records produced by Girolando cows under milk recording supervised by the GBA. After editing: 108,218 TD records from the first three lactations of 9,119 cows, sired by 1,284 bulls and calving from 1992 to 2008 in 214 herds.

**Averages and SDs for age at first calving, days in milk and milk yield in the first lactation were 34.0 ± 5.9 months, 142.6 ± 88.8 days and 13.8 ± 5.5 kg respectively.**

**Statistical analyses - Two AR models:**

**Model 1 – Breed Composition model (BCM):** included the fixed effects of herd, year-season of calving, days in milk within lactation order, regressions on age at calving (linear and quadratic) within herd and breed composition of the cow. The random effects were animal, long (LTE) and short term environmental (STE) effects (fitted with autoregressive covariance structures) and the residuals (accounting for heterogeneity of variance by parity number).

$$Y_{ijklmnpqo} = H_i + YS_j + DIM_m(H_k L_l) + \sum b_i Age_j(H_k) + C_m + A_n + LTE_p + STE_q + e_{ijklmnpqo}$$

**Model 2 – Genetic Model (GM):** the breed composition effect ( $C_m$ ) was replaced by regressions representing the additive (g) and non-additive (dominance (d) and recombination (r)) genetic effects.

(g) represents the expected contribution of Holstein genes, (d) the expected heterozygosity in the cow, calculated by  $p_p(1-p_p) + p_m(1-p_p)$ ; and (r) the expected average recombination effect of genes from the Holstein and Gyr breeds calculated by  $p_p(1-p_p) + p_m(1-p_p)$ , where  $p_p$  and  $p_m$  are, respectively, the proportion of Holstein genes in the sire and the dam of the cow.

**g + d + r**  
Dickerson et al., (1973)

Genetic gain estimated from PTAs of cows born from 1997 to 2005 was 5,1 kg/yr ( $R^2=0,79$ ), almost five times larger than 1,1 kg/yr ( $R^2=0,21$ ) obtained for the same period from the BC 305d model.

Genetic gain from 1997 to 2001 was 4,9 kg/yr ( $R^2=0,65$ ) and doubled in the last five years to 11,20 kg/yr ( $R^2=0,93$ ) (Figure 1).

## RESULTS AND DISCUSSION

Value of the Log-likelihood function was larger for the BCM than for the GM. LRT test was significant ( $P<0.005$ ,  $df=5$ ). Genetic and residual variances, heritabilities and other parameters practically did not differ between AR models (estimates for GM are shown in Table 1).

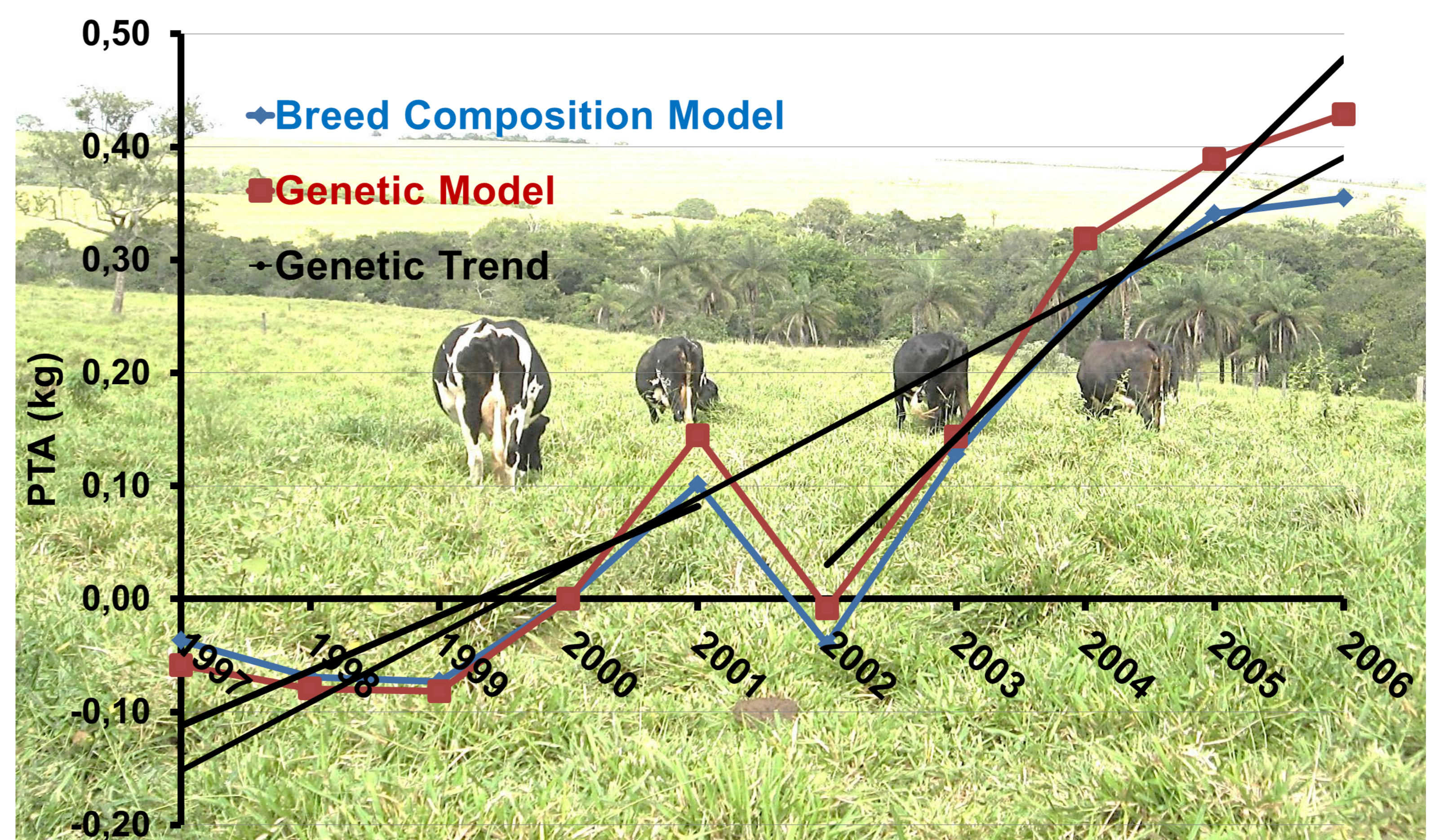
Heritabilities ranged from 0.17 to 0.27 (first lactation), on average larger than 0,19 obtained from previous analyses for 305-d models using the same BCM and GM with first lactation records only.

Average accuracies for BV predictions of Girolando sires from AR models were 0,86 and rank correlation between them was 0,975. Estimates of the same parameters for BV using 305-d records were 0,72 and 0,98.

**Table 1.** (Co)variance components, autocorrelations and genetic parameters for daily milk yields for Brazilian Girolando cattle, estimated by AR using the GM.

Parameter	Estimate
Genetic variance <sup>A</sup>	4.934
Error variances (L1; L2; L3) <sup>D</sup>	1.568; 1.789; 2.204
LTE <sup>B</sup> variance	< 0.0001
LTE autocorrelation	0.0002
STE <sup>C</sup> variance (L1) <sup>D</sup>	12.11
STE autocorrelation (L1)	0.798
STE variance (L2) <sup>D</sup>	17.86
STE autocorrelation (L2)	0.785
STE variance (L3) <sup>D</sup>	22.56
STE autocorrelation (L3)	0.821
Phenotypic variance (L1)	18.61
Phenotypic variance (L2)	24.58
Phenotypic variance (L3)	29.69
Heritability (L1)	0.265
Heritability (L2)	0.200
Heritability (L3)	0.165

<sup>A</sup>Variances (kg<sup>2</sup>); <sup>B</sup>Long term environmental effects; <sup>C</sup>Short term environmental effects; <sup>D</sup>L1, L2, L3= 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> Lactation.



**Figure 1:** Genetic progress for milk of Girolando cows born between 1997 and 2006 (base year = 2000) estimated by AR models.

## CONCLUSION

Larger heritability estimates, accuracies of breeding values predictions and realized genetic gains indicate large selection opportunities and recommend replacing the lactation model by the AR test day model for genetic evaluations of milk yield of the Girolando cattle.

Further studies are needed to compare simultaneous predictions of breeding values from these two models, their correlations and the impact on selection decisions made by breeders and on the expected genetic gain in milk production of dairy herds in Brazil.