

## **UNIVARIATE VS BIVARIATE ANALYSES OF WEANING AND 18-MONTHS WEIGHTS IN TROPICARNE CATTLE**

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### **INTRODUCTION**

Tropicarne is a composite beef breed developed by a group of cattle breeders at the Northeast of Mexico, based on the productive and reproductive performance of the animals, and their capacity to survive in tropical environments. After several years of crossing and performance evaluation, the first Mexican cattle breed was formed, containing approximately 63% Senepol, 23% Barzona, 9% Brahman and 5% Charolais.

In tropical areas, postweaning performance of heifers and bulls is usually recorded at 18-mo of age, because food resources in extensive production systems are of lower quality than those in temperate areas. Usually, some selection is practiced by breeders at weaning time, having a reduction on the amount of information, from weaning to postweaning weights. Univariate analyses assume that correlation among traits is zero; however, according to selection index procedures, multivariate analyses of correlated traits use all the information available to get more accurate estimates of breeding values for a specific trait (Van Vleck, 1994). Additionally, when data has been subjected to selection, univariate analyses may be biased, while multivariate analyses are expected to account for selection (Thompson and Meyer, 1986).

Given that Tropicarne is a new breed that begins to be evaluated, it is important to investigate the effect of performing univariate vs bivariate animal models on the magnitude of estimates of genetic parameters, and on the prediction of breeding values for weaning and 18-mo calf weights.

### **MATERIAL AND METHODS**

Data for this study came from two herds of the Mexican Association of Tropicarne Cattle Breeders, located in the Northeast part of the country (temperatures from 15 to 40 °C and annual rainfall from 700 to 1200 mm). This Association carries three herd books for grading up cattle (1/2, 3/4, and 7/8 of Tropicarne, respectively), and two herd books for straightbred cattle (15/16 and 31/32 of Tropicarne, respectively). In these books all pedigree and performance information of animals overcoming the breed standards are recorded.

Cattle production systems utilized by the Tropicarne breeders are those common for tropical areas, that is, grazing based food resources; breeding season during the year but tending to concentrate in two seasons, July and August, and February and March; and mating a sire to 25-30 cows. These cattle are treated against external parasites when required, but rarely are being treated against internal parasites. Calves are weaned at about 8-mo of age. After weaning, heifers and bulls are separated and fed only on forage based, plus vitamins and minerals.

The information analyzed included 1522 records of weaning weight (WW) adjusted to 8-mo of age and 1142 records of weights at 18-mo of age (W18M). The pedigree file included 1895 animals born from 1965 to 1998. In a previous study (Dominguez-Viveros *et al.*, 2001), univariate analyses were carried out to identify the model that best fit the data. The model for WW included the fixed effects of contemporary group (herd-year-season-sex subclasses), plus cow age and proportion of Tropicarne genes as linear and quadratic covariates; and as random the additive direct and maternal genetic effects, ignoring their covariance. For W18M the random effects considered were additive direct and maternal permanent environmental; fixed effects were the same as for WW. Based on the selected models from univariate analyses, the bivariate animal model included the effects described before, plus the covariances between direct genetic effects and between residual effects for the two traits.

Variance components were estimated using multiple-trait derivative-free restricted maximum likelihood (MTDFREML) programs (Boldman *et al.*, 1995). The method involves maximizing the likelihood function ( $L$ ) given the data, or equivalently minimizing  $-2 \log L$ . Iterations were stopped when the variance of function values in the simplex were less than  $1 \times 10^{-6}$ . The program was restarted using the resulting estimates of the parameters as new priors until function values did not change to the third decimal after consecutive restarts.

Correlations between estimates of breeding values from univariate *vs* bivariate animal models were calculated. Averages of estimated breeding values from bivariate analysis for the top 20% sires selected based on univariate and bivariate models were also obtained.

## RESULTS AND DISCUSSION

Means and standard deviations were  $220.19 \pm 27.04$  kg for WW, and  $323.42 \pm 49.38$  kg for W18M. Estimates of (co)variance components and genetic parameters from univariate and bivariate analyses for WW and W18M are shown in Table 1. A large increase on estimates of variance components for direct genetic and a reduction on variances of residual environmental effects were observed, when changing from univariate to bivariate analyses. Bennett and Gregory (1996) observed similar results when comparing univariate *vs* multivariate animal models for 200-d weight and postweaning gain.

Estimates of direct heritability for WW and W18M from bivariate analyses were larger (0.11 and 0.07, respectively) than those from univariate analysis, partially due to reductions on estimates of maternal heritability for WW, and a decrease of the fraction of the total variance due to permanent environmental effects for W18M. Eler *et al.* (1995), analyzed growth data of Nelore cattle under univariate and multivariate animal models, and observed that estimates of direct heritabilities from multivariate analyses were a bit higher for WW and yearling weight, with the largest increase for birth weight. Estimates of direct heritability for W18M (Table 1) were higher than those reported (0.11 to 0.12) by Lee *et al.* (2000), who evaluated various single trait models.

Improvement of the size of direct heritabilities from bivariate analysis, may also be the result of the high and positive estimate of direct additive genetic correlation between WW and W18M (0.85), indicating that a large proportion of the genes explaining the variation for one

trait, are also causing variation on the other trait. Therefore, in bivariate analysis each trait is used as an additional source of information for predicting breeding values of the other trait. A similar estimate of the genetic correlation between WW and yearling weight (0.74) was reported by Eler *et al.* (1995).

**Table 1. Estimates of variance components (kg<sup>2</sup>) and genetic parameters from univariate and bivariate analyses for weights at weaning (WW) and at 18-mo of age (W18M)**

Item	Univariate		Bivariate		
	WW	W18M	WW	WW-W18M	W18M
Variance components <sup>A</sup>					
$\sigma_g^2$	35.42	282.80	85.08		337.71
$\sigma_g$				143.25	
$\sigma_m^2$	61.84		30.18		
$\sigma_p^2$		93.51			44.95
$\sigma_e^2$	359.81	642.05	337.59		592.48
$\sigma_e$				174.17	
Genetic parameters <sup>B</sup>					
$h_g^2$	0.08	0.28	0.19		0.35
$h_m^2$	0.14		0.07		
$c^2$		0.09			0.05
$r_g$				0.85	
$r_e$				0.39	

<sup>A</sup> $\sigma_g^2$  = direct additive genetic variance,  $\sigma_g$  = direct additive genetic covariance between WW and W18M,  $\sigma_m^2$  = maternal additive genetic variance,  $\sigma_p^2$  = permanent environmental variance,  $\sigma_e^2$  = residual environmental variance, and  $\sigma_e$  = residual environmental covariance between WW and W18M.

<sup>B</sup> $h_g^2$  = direct heritability,  $h_m^2$  = maternal heritability,  $c^2$  = fraction of the total variance due to permanent environmental effects,  $r_g$  = direct additive genetic correlation between WW and W18M, and  $r_e$  = residual environmental correlation between WW and W18M.

As a consequence of higher estimates of direct heritabilities for WW and W18M from bivariate analysis as compared to univariate analyses, accuracies of estimated breeding values were also higher; specially for direct WW (means of 0.53 *vs* 0.40 and ranges of 0.87 *vs* 0.72). The estimate of correlation between residuals of WW and W18M was 0.39, which may have also contributed to the increase of accuracy, due to a better connectivity among contemporary groups (Thompson and Meyer, 1986).

Ranges of estimated breeding values from univariate analyses were 16.44, 24.67 and 79.61 kg for direct WW, maternal WW and W18M, respectively; and the corresponding ranges from bivariate analysis were 43.13, 15.84 and 102.98 kg. Therefore, when using bivariate analysis, a

larger proportion of phenotypic differences were accounted for differences in breeding values for direct WW and W18M.

Estimates of rank and product-moment correlations between estimated breeding values obtained from univariate and bivariate analyses are presented on Table 2. Rank and product-moment correlations were of similar size for direct WW and W18M. Assuming that the bivariate animal model is the true model, reranking of selected animals based on estimates of breeding values from univariate models will be highest for maternal WW and lowest for W18M. When the top 20% of sires were selected under each type of analyses, but the means of estimated breeding values were calculated from bivariate analysis, those means for direct WW, maternal WW and W18M were 13, 18 and 7% higher, respectively, than the means when sires were ranked based on univariate analyses

**Table 2. Comparison of univariate vs bivariate analyses when sires were selected based on estimated breeding values (kg) for direct (WW-d) and maternal weaning weight (WW-m), and for weight at 18-mo of age (W18M)**

Type of analysis	WW-d			WW-m			W18M		
	RC <sup>A</sup>	PC <sup>A</sup>	Mean <sup>B</sup>	RC	PC	Mean	RC	PC	Mean
Univariate	0.84	0.85	8.06	0.82	0.87	2.19	0.95	0.94	18.71
Bivariate			9.13			2.58			20.06

<sup>A</sup>Rank (RC) and product-moment (PC) correlation coefficients between estimated breeding values with univariate and bivariate analyses.

<sup>B</sup>Mean of estimated breeding values from bivariate analysis for the top 20% sires selected based on this type of analysis.

## CONCLUSIONS

Genetic improvement of growth at weaning and at 18-mo of age in Tropicarne cattle will be faster if breeding animals are selected based on a bivariate instead of univariate animal models.

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