

**(CO)VARIANCE COMPONENTS FOR FIRST LACTATION MILK YIELD
AT THREE PRODUCTION AND VARIABILITY LEVELS IN
ARGENTINEAN DAIRY COWS**

A. Jara¹, D. Casanova², M. Elzo³ and N. Barriá¹

¹Departamento Fomento de la Producción Animal, Facultad de Cs. Veterinarias y Pecuarias,
Universidad de Chile, Chile

²Departamento de Zootecnia, Facultad de Ciencias Veterinarias, Universidad del Centro de la
Provincia de Buenos Aires, Argentina

³Department of Animal Sciences, University of Florida, USA

INTRODUCTION

The discovery of the deep freezing method of cattle semen preservation allowed for a world-wide exchange of genetic material and that the importation of semen from improved breeds have been often used in attempts to increase local livestock productivity. Frequently, this has been done without systematic evaluation of the introduced stocks in the new environment. In 1998, Argentina started a genetic evaluation procedure for yield traits in the Holando Argentino Dairy Cattle population through an animal model. This mixed model genetic evaluation procedure uses the simplifying assumption of equal genetic and residual variances across herds, and that the genetic correlation between genetic expression at different environments is equal to one. However, several studies in which variance components of milk yield were estimated from herds grouped by production and by variability levels have indicated a positive relationship between production level and variability level, and estimates of genetic and residual variances (De Veer and Van Vleck, 1987 ; Boldman and Freeman, 1990 ; Dong and Mao, 1990). The purpose of this work was to estimate (co)variance components for milk yield using a multiple trait model in which yields at three herd production and herd variability levels are considered as three correlated variables. The primary goal was to establish the patterns for variance components and heritability, and to estimate the genetic correlations between genetic expression at the three production and variability levels.

MATERIALS AND METHODS

The data were obtained from the official milk recording system of the Holando Argentino Breed Association in Argentina. Data set considered 145 050 305-d, ME first lactation milk yield records of daughters sired by 3 163 bulls, freshening between 1992 and 1998. The genotype by environmental interaction was evaluated by genetic correlation between herd production and between herd variability levels. Each record was assigned to a herd production level and to a herd variability level, using the average and the standard deviation of the milk yield of all first lactations initiated in the same herd-year (HY), respectively. Three levels of production and variability were considered ; low, medium, and high. Table 1, shows the limits used in defining levels for each group of data.

A multiple traits sire model was used to estimate (co)variance components in the different environments considered. Performance records from the environments described above were

explained by the following mixed linear model : $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$. Where, \mathbf{y} is the vector of observations in each environment ($\mathbf{y} | \mathbf{b}, \mathbf{u}, \sigma^2_{e1}, \sigma^2_{e2}, \sigma^2_{e3} \sim N(\mathbf{Xb} + \mathbf{Zu}, \mathbf{R})$), \mathbf{b} is the vector of herd-year-season (HYS) fixed effects ($p(\mathbf{b}) \propto \text{cte.}$), \mathbf{u} is the random vector of sire effects ($\mathbf{u} | \mathbf{G}_0 \sim N(\mathbf{0}, \mathbf{G} = \mathbf{A} \otimes \mathbf{G}_0)$), \mathbf{e} is the vector of errors, and \mathbf{X} , and \mathbf{Z} are known incidence matrices for fixed HYS and random sire effects, respectively.

Table 1. Upper and lower limits (kg) of production and variability levels

Group	Production Levels	Variability Levels
Low	< 6240.60	< 785.96
Medium	6240.60 – 7524.39	785.96 - 1062.65
High	> 7524.39	> 1062.65

The (co)variance components were estimated using a Bayesian and a Frequentist analysis. For the Bayesian analysis, an Inverted Wishart and three independent inverse chi-square distributions were used to describe the uncertainty of the previous knowledge of the genetic (co)variance components and the error variances, respectively. The prior distributions used were proper vague priors and were obtained by setting the degrees of belief so that the distributions were as flat as possible but with finite variance. The marginal posterior distributions were estimated through the implementation of a Markov Chain Monte Carlo (MCMC) algorithm, the Gibbs sampler (Gelfand and Smith, 1990). For each analysis, the Gibbs sampler was ran with a single chain length of 1 020 000. The first 20 000 iterations were discarded, and then samples were saved after each iteration. The chains were analyzed using the GIBANAL program (Van Kaam, 1997). In the frequentist analysis, REML (Patterson and Thompson, 1971) estimates of (co)variance components were obtained by using the MTDFREML (Boldman *et al.*, 1995) programs. For these analysis, it was assumed that the convergence was reached when the variance of the simplex values was less than 10^{-14} . In order to guarantee global maximum, analysis was restarted three times with previous converged values.

RESULTS AND DISCUSSION

A statistical description of marginal posterior distributions and REML estimates of additive genetic (co)variance components, heritability and, genetic correlations in different herd production and variability levels for milk yield are shown in table 2.

The sire variance component increased as production and variability level increased. However, the sire component of variance in the high group of variability and production was more than 3.5 and 1.8 times greater than that in the low group, respectively. In each of the herd-year stratification methods, the estimates of sire covariance components between groups were greater when higher levels were involved, especially when the herd-year standard deviation was the criterion.

Table 3, shows marginal posterior distribution features and REML estimates of error variance in different herd production and variability levels for milk yield. As observed for the genetic variance components, the error variance component increased as production and variability level increased. The error component of variance in the high group of variability and

production was 199 % and 72 %, approximately, greater than that in the low group, respectively. These results indicate that genetic variances increased at the greatest relative rate, and that stratifying records by herd-year standard deviation proved to be the most effective way to identify heterogeneous estimates of variance components. Similar results have been previously reported by Dong and Mao (1990) in the northeastern US.

Table 2. Statistical description of marginal posterior distribution and REML estimates of heritability and genetic correlations in different herd production (P) and variability (V) levels for milk yield

		Low		Medium		High	
		P	V	P	V	P	V
Low	mean	0.18	0.17				
	mode	0.17	0.16				
	median	0.18	0.17				
	sd	0.02	0.02				
	reml	0.16	0.16				
Medium	mean	0.94	0.99	0.21	0.21		
	mode	0.95	0.98	0.21	0.21		
	median	0.95	0.98	0.21	0.21		
	sd	0.02	0.01	0.02	0.02		
	reml	0.95	0.99	0.20	0.20		
High	mean	0.95	0.94	0.95	0.97	0.19	0.20
	mode	0.96	0.95	0.96	0.98	0.19	0.20
	median	0.96	0.95	0.95	0.97	0.19	0.20
	sd	0.03	0.03	0.02	0.01	0.02	0.02
	reml	0.96	0.95	0.96	0.97	0.20	0.20

The Bayesian points and REML estimates of heritability are in the lower limit of the range found in the literature for milk yield in the Holstein Breed using sire models, but they are lower than the observed values using animal models (Van Vleck and Dong, 1988 ; Albuquerque *et al.*, 1995). Heritability estimates were smallest for low average production and variability herd-year subclass while estimates for medium and high levels were similar. These results agree with the results previously reported by Boldman and Freeman (1990), working with three production levels for milk yield.

Table 3. Statistical description of marginal posterior distribution and REML estimates of error variance in different herd production and variability levels for milk yield (kg)

	Production level			Variability level		
	mean	sd	reml	Mean	sd	reml
Low	608 717	4 751	608 707	438 175	2 668	438 958
Medium	830 478	4 649	828 355	781 670	4 266	781 820
High	1 048 009	8 422	1 050 438	1 311 173	10 048	1 311 077

In each of the herd stratification methods, all genetic correlations between groups were close to unity. Therefore, sires were expected to be ranked similarly in different herd-year groups, but the magnitude of the sire differences was much greater in the high than in the low groups.

CONCLUSION

Variance components increased as production and variability level increased. However, stratifying records by variability is the most effective way to produce heterogeneous estimates. The results indicate that sires were expected to be ranked similarly in different herd-year groups and that the use of common heritability for all levels could result in the misranking of superior cows.

ACKNOWLEDGMENTS

This research was supported by the grants N° 1000794 and N° 7000794 from Fondo Nacional de Investigación Científica y Tecnológica de Chile, FONDECYT. Thanks are expressed to Asociación de Criadores Holando Argentino for providing the information used in this work.

REFERENCES

- Albuquerque, L.G., Dimov, G., Keown, J.F. and Van Vleck, L.D. (1995) *J. Dairy Sci.* **78** : 1591-1596.
- Boldman, K.G. and Freeman, A.E. (1990) *J. Dairy Sci.* **73** : 503-512.
- Boldman, K.G., Kriese, L.A., Van Vleck, L.D., Van Tassell, C.P. and Kachman, S.D. (1995) USDA, Agricultural Research Service.
- De Veer, J.C. and Van Vleck, L.D. (1987) *J. Dairy Sci.* **70** : 1434-1441.
- Dong, M.C. and Mao, I.L. (1990) *J. Dairy Sci.* **73** : 843-851.
- Gelfand, A.E. and Smith, A.F.M. (1990) *J. Am. Stat. Assoc.* **85** : 398-409.
- Patterson, H.D. and Thompson, R. (1971) *Biometrika* **58** : 545-554.
- Van Kaam, J.B.C.H.M. (1998) Dep. of Animal Breeding, Wageningen Agricultural University.
- Van Vleck, L.D. and Dong, M.C. (1988) *J. Dairy Sci.* **71** : 3040-3046.