

GENETIC RELATIONSHIPS FOR MILK AND FAT YIELDS BETWEEN HOLSTEIN POPULATIONS IN BRAZIL AND THE UNITED STATES

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SUMMARY

Genotype by environment interaction was investigated between Brazil and US Holstein populations. Genetic correlations for ME milk and fat yields between countries ranged from .79 to .90. Heterogeneous variances indicate differences among sire breeding values are compressed in low variance herd environments. Correlated response for milk and fat yields in Brazil from sire selection in the US are reduced to 1/2 to 2/3 that observed in the US.

Keywords: Genotype, environment, heterogeneity, genetic correlation, response.

INTRODUCTION

Development of the Holstein breed in Brazil has been based on continuous importation of live animals, embryos and semen mainly from the US, Canada, and Europe. About 50% of semen used in purebred herds is from North America (ASBIA, 1993). Availability of germ plasm from other countries with effective breeding programs provides opportunity for increasing genetic gain through importation. Besides other economically important factors, the presence of genotype by environment interaction would reduce potential benefits from a strategy based on importing germ plasm with superior genetic merit (Banos and Smith, 1991).

Genotype by environment interactions (GxE) may involve rank changes in genotypes or changes in the absolute and relative magnitude of the genetic variances between environments. Both changes have important implications in designing breeding programs: selection responses are unequal in the different environments.

The purpose of this study is to evaluate GxE in yields of milk and fat between the US and Brazilian Holstein cattle populations, and to examine their implications on improving the efficiency of production in Brazil through semen importation. The objectives include estimate components of (co)variance for yields of milk and fat, and calculate correlated responses for milk and fat yields between Brazil and the US.

MATERIALS AND METHODS

Data were provided by the Ministry of Agriculture of Brazil and the Brazilian Agricultural Research Organization (EMBRAPA) and by Animal Improvement Processing Laboratory (AIPL / USDA). First-lactation mature equivalent (ME) 305-day milk and fat yields of 726,932 daughters of 701 sires in the US and 29,413 daughters of 704 sires in Brazil were used. There were 358 sires with daughter records in both countries. Herds in Brazil were stratified by within herd-year standard deviation of ME milk (HYSD) into low and high HYSD classes.

A multiple trait sire model was used to estimate (co)variance components for milk and fat yields in different countries considered different traits. Performance records from Brazil and US are described by the following mixed linear model:

$$y = Xb + ZQg + Zu + e$$

where y is the vector of observations in each country; X , Q and Z are known incidence matrices for fixed, group and random sire effects respectively; and b , g , u and e are vectors of fixed, group, sire and residual effects respectively. It was assumed that

$$E \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \quad \text{and} \quad V = \text{var} \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} D & 0 \\ 0 & R \end{bmatrix}$$

where, $\text{var}(u) = D = \begin{bmatrix} \sigma_s^2 A & \sigma_{s\tau} A \\ \sigma_{s\tau} A & \sigma_\tau^2 A \end{bmatrix}$ where σ_s^2 and σ_τ^2 are respectively sire components of variance for Brazil and the US, $\sigma_{s\tau}$ is the sire covariance, and A is the genetic relationship matrix among sires.

$\text{Var}(e) = R = \begin{bmatrix} \sigma_e^2 \text{In1} & 0 \\ 0 & \sigma_e^2 \text{In2} \end{bmatrix}$ where σ_e^2 and σ_e^2 are the within-country residual variances, and In_i is an identity matrix of order equal to the number of records in country i .

These assumptions permit heterogeneous sire and residual variances. Components of (co)variance were estimated using MTDFREML programs (Boldman *et al.*, 1995). Convergence of the derivative-free iterative process was attained when the variance of the simplex values was less than 10^{-8} . In order to guarantee global maximum, analysis was restarted with previous converged values. Genetic correlations between countries were estimated by $\hat{r}_G = \hat{\sigma}_{s\tau} / (\hat{\sigma}_s^2 \hat{\sigma}_\tau^2)^{.5}$; and within-country heritability for each trait by $\hat{h}^2 = 4 \hat{\sigma}_s^2 / (\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$ and $\hat{h}^2 = 4 \hat{\sigma}_\tau^2 / (\hat{\sigma}_\tau^2 + \hat{\sigma}_e^2)$. Expected correlated response coefficients were estimated by the genetic regression $\hat{\sigma}_{s\tau} / \hat{\sigma}_\tau^2$, where $\hat{\sigma}_{s\tau} / \hat{\sigma}_\tau^2$ is the sire covariance and $\hat{\sigma}_\tau^2$ is the sire variance for the US in each joint analysis.

RESULTS AND DISCUSSION

Average HYSD in low, high and all data in Brazil were 1004 kg, 1319 kg and 1180 kg. Sire and residual variance components for ME milk (Table 1) in low, high and all data in Brazil for milk were 51% and 58%, 59% and 101% and 59% and 81% as large as corresponding estimates in the US. The proportional difference in sire variance of milk yield between Brazil and the US is larger than the difference between Colombia and the US (52%), but smaller than that between Mexico and the US (76%) reported by Stanton *et al.* (1991).

Table 1. Estimates of sire (co)variance and residual variances, heritability (h^2), and genetic correlation (r_g) for milk yields between the US and all and HYSD¹ data in Brazil.

Data	Sire	Residual	Cov	h^2	r_g
LOW HYSD					
Brazil	72,641	900,511	80,702	.30	.79
US	142,836	1,562,007		.34	
HIGH HYSD					
Brazil	85,570	1,580,357	96,761	.20	.87
US	144,400	1,562,015		.34	
ALL					
Brazil	87,592	1,263,474	97,267	.26	.85
US	148,194	1,562,007		.35	

¹HYSD classes: Brazil - Low, <1120 kg and High, >1150 kg of milk.

Estimated (co)variance for ME fat (Table 2) in low, high and all data in Brazil were 30% and 48%, 41% and 80% and 39% and 65% as large as estimates in the US. These results confirm that restricted environmental in tropical regions reduces the expression of genetic variance.

Table 2. Estimates of sire (co)variance and residual variances, heritability (h^2), and genetic correlation (r_g) for fat yields between the US and all and HYSD¹ data in Brazil.

Data	Sire	Residual	Cov	h^2	r_g
LOW HYSD					
Brazil	58	961	95	.23	.89
US	196	2001		.36	
HIGH HYSD					
Brazil	82	1610	115	.19	.90
US	198	2001		.36	
ALL					
Brazil	78	1307	111	.23	.89
US	200	2001		.36	

¹HYSD classes: Brazil - Low, <1120 kg and High, >1150 kg of milk.

Genetic correlation for ME milk between Brazil and the US ranged from .79 to .85. Estimates for ME fat were about .90. These estimates are large suggesting reranking of sires is unlikely. However, scale effects of small variance do not allow clear differentiation among breeding values in low HYSD environments. Under this scenario, less selection response from US sires is expected, reducing economic returns from genetic investment (Holmann et al., 1990).

Correlated response coefficients for milk and fat yields in all data in Brazil were .66 and .55 respectively. The coefficient for milk yield is smaller than reported by Stanton et al. (1991) for

Mexico (.78), but larger than in Colombia (.56). Correlated response coefficients for milk and fat yields were respectively .56 and .48 in low and .67 and .57 in high HYSD herds in Brazil.

Average milk HYSD for all data in Brazil was intermediate to values reported for Mexico (1413 kg) and Colombia (1024 kg). A positive trend of increasing sire and residual variances as average HYSD increases is clear in comparing estimates from these three countries (Figure 1). The estimates used in Figure 1 are from Table 1 and from Stanton et al. (1991). Large correlated responses in high variance herds indicate these herds will see larger correlated response from sire selection in the US than low variance herds.

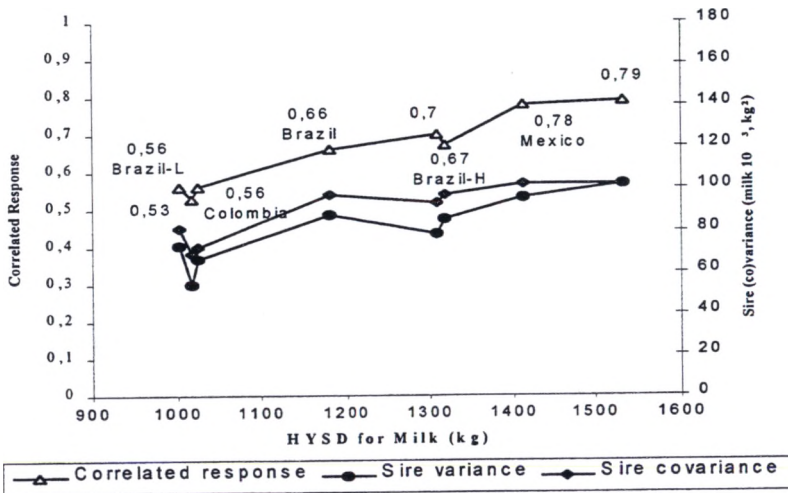


Figure 1. Sire (co)variances and correlated response coefficients for milk yield by HYSD for milk in Latin American herd environments.

Larger selection response and a faster rate of genetic improvement have been reported for herds with high HYSD in the US (Meinert et al., 1992). Therefore, efficiency of sire selection improves with increased HYSD suggesting that a strategy based on semen importation would be more effective in improving performance in high than in low HYSD herd environments.

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