Livestock Research for Rural Development 16 (4) 2004 Citation of this paper

Variance heterogeneity for milk yield in Brazilian and Colombian Holstein herds

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(Part of doctoral Thesis of 1st author - FCAV-Unesp. Supported by FAPESP - Brazil.)

Abstract

Heterogeneity of variances for milk yield (MY) was determined for Brazilian and Colombian herds. The herds were grouped as high or low variability within each country, using as criterion the phenotypic standard deviation (**PSD**) of **MY** in the contemporary groups of cows, from the first to the sixth calving. Brazilian and Colombian herds with **PSD** greater than 1,168 kg or 1,012 kg, respectively, were classified as high variability while the herd groups with values lower than those were classified as low variability. The genetic parameters for **MY** within each herd group were estimated using bivariate analysis in an animal model and the restricted maximum likelihood method with a derivative free algorithm, using 72,280 first lactations of cows, daughters of 1,880 sires.

Heterogeneous variances were found, and Brazilian herds with high **PSD** had the greatest additive and residual genetic variances and heritability coefficients for **MY**. **MY** genetic correlation coefficients between herds of high and low variability within each country were 0.96 and 0.93 while between countries they varied from 0.72 to 0.81, suggesting that there was a reclassification of animals in the two countries and also heterogeneity of variances. This phenomenon leads to the questioning of the strategy of imported semen usage and the need to do genetic evaluations to identify sires with greater genetic potential for (sub) tropical environmental conditions.

Key words: Dairy cattle, genotype - environment interaction

Introduction

Animal genetic improvement programs involve comparisons among individuals of contemporary groups maintained in different environments, which could differ on averages as well as on variability among them; therefore, the animals could be erroneously classified, since the sires with most of their daughters in herds with greater variances would tend to have their genetic attributes overestimated (Hill 1984; Vinson 1987).

For Van Vleck (1988), genotypical and phenotypical variances are, in most cases, different from farm to farm. In studies referring to herd grouping by phenotypical standard error average of the contemporary groups (herd-year) done by Stanton (1990) in Colombia, Mexico, Puerto Rico and United States of America, by Costa (1999) in Brazil and USA, and by Cienfuegos-Rivas et al (1999) in Mexico and USA, it was concluded that the response differences to the use of sires in (sub) tropical countries seem to be associated with heterogeneous variances of the herds. This brings as a result wide phenotypical differences among the daughters. This problem becomes worse as the environment variation range increases where the improved genetic material would be used (Stanton 1990). Therefore, by ignoring variance heterogeneity, there will be consequences in resulting selection and genetic gain, reducing the effectiveness of the genetic breeding program (Vinson 1987; Van Vleck 1987).

In a study by Stanton (1990), the phenotypical responses of the daughters of different grouping classes in Latin American herds were smaller than those in American herds, suggesting that the genetic variances found in (sub) tropical environments are smaller than in temperate environments, since Holstein cattle under restricted management conditions did not present adequate physiological development and do not have the opportunity to express their production genetic potential. This phenomenon reduces population variability (McDowell et al 1976; Lopes-Villalobos et al 2001; Holmann et al 1990; Costa 1998).

Lopes-Villalobos et al (2001) and Holmann et al (1990) evaluated the profit of investing in North American semen for use in in (sub) tropical countries and concluded that these importations should be used strategically in environments with excellent feed and management, in order to obtain a positive response on the selection of imported genetic material.

This study had as objectives to determine the heterogeneity of genetic and residual variances in Brazilian and Colombian herds and to estimate the genetic correlation of milk yield between high and low variability herds.

Materials and Methods

The study was done based on 180,522 records of milk yield of 94,558 Holstein cows from 775 Brazilian and 317 Colombian herds, derived from the data bases of the State Associations affiliated to the Brazilian Holstein Cattle Ranchers Association (Associação Brasileira de Criadores de Bovinos da Raça Holandesa (ABCBRH)) and made available by the National Animal Sciences Archives (Arquivo Zootécnico

Nacional), managed by Embrapa Gado de Leite, Juiz de Fora, Minas Gerais, and from the archives of the Colombian Holstein Association (Asociación Holstein de Colombia (Asoholstein de Colombia)), from parities between 1980 and 1997. In Brazilian and Colombian Holstein dairy farms the cattle are mostly fed pasture and concentrates. Milk is produced on large and very intensive farms as well as in family systems.

Milk yield was adjusted for 305 day lactations, age, calving order and season, using correction factors suggested by Torres (1998) and Torres et al (2000a) for Brazil and by Cerón-Muñoz et al (2003) for Colombia.

The herds were grouped in high or low variability classes within each country, using as criterion the average phenotypical standard deviation (**PSD**) of milk yield for herd-year (**HY**) contemporary groups. For that purpose, **PSD** limits of 1,168 kg and 1,012 kg in Brazilian and Colombian herds, respectively, were considered. Herds with **PSD** values greater than those above mentioned were classified in the high **PSD**, while those with lower values were put in the low **PSD** group. The choice of **PSD** limits considered the condition of establishing in each group a similar number of sires, daughters and herds. Also, a minimum of 10 lactations of cows from the first to the sixth calving, by contemporary group, were considered.

After classifying the herds, only the information on the first lactation was used for genetic parameter estimation, discarding the contemporary groups with less than three records and sires with less than three daughters in by less than three herds. The numbers of herds were 307 and 468 in the high and low Brazil **PSD** and 139 and 178 in then high and low Colombian **PSD**, respectively.

The sires were grouped for origin and period of birth within origin (Table 1). Most of the Canadian and Americans sires had daughters in the two countries. The Brazilian and Colombian sires only had daughters in Brazil and Colombia, respectively; which, however, were descended from common ancestors (Canadian or American sires). The cows were grouped as: Holstein purebred or grade (genetic composition equal or less than 31/32 Holstein.

Table 1. Number of sires (S) and daughters (D) by sire genetic group in high and low variability herds from Brazil and Colombia

Genetic group	Brazil: High Variability (HB)		Brazil: Low Variability (LB)		Colombia: High Variability (HC)		Colombia: Low Variability (LC)		Common Sires: HB-LB	HB-HC	HB-LC	LB-HC	LB-LC	HC-LC
	S	D	S	D	S	D	S	D						
Br (≤79).....	73	838	50	1837	-	-	-	-	40	0	0	0	0	-
Br (80-84)..	168	1922	136	2909	-	-	-	-	94	0	0	0	0	-
Br (85-93)..	157	2007	189	1641	-	-	-	-	83	0	0	0	0	-
Ca (≤76)....	65	1057	61	1598	40	579	35	620	57	25	21	23	20	32
Ca (77-81).	32	1744	32	1326	33	880	34	1013	31	14	14	15	15	33
Ca (82-93).	51	1696	59	641	51	889	59	699	47	26	31	29	38	45
Co (≤79)....	-	-	-	-	44	448	39	445	-	0	0	0	0	31
Co (80-84).	-	-	-	-	66	1090	52	817	-	0	0	0	0	41
Co (85-93).	-	-	-	-	63	803	63	814	-	0	0	0	0	36
Eu (≤72)....	87	1582	84	2260	75	781	65	920	71	40	33	38	35	49
Eu (73-75).	87	1364	84	2274	87	1160	88	1596	78	51	49	50	49	72
Eu (76-82).	236	8196	251	7134	231	3575	230	3398	222	134	132	142	138	197
Eu (83-93).	139	4491	172	1698	140	2053	146	1485	132	62	58	80	77	112
Total sires	1095	24897	1118	21058	830	11098	811	11807						

Br= Brazilian sires; Ca= Canadian sires; Co= Colombian sires; Eu= North American sires.
HB = High variability Brazilian herds, LB = Low variability Brazilian herds, HC = High variability Colombian herds, LC = Low variability Colombian herds

The genetic parameters for milk yield in each herd group were estimated using bivariate analysis in an animal model and the restricted maximum likelihood method with an algorithm free of derivates. The fixed effects of **HY**, sire genetic group, and cow genetic group, and the random effects of animal and error were included. The model in a matrix notation for bivariate analyses of milk yield between Brazilian and Colombian herds of high and low **PSD**, can be represented as:

$$y_i = X_i b_i + Z_i a_i + e_i$$

with

$$y = \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

and X_i is the incidence matrix related to the fixed effects pertaining to b_i and Z_i is the incidence matrix related to the animal additive genetic random effect (a_i).

The assumptions in relation to the 1st and 2nd moments were:

$$\begin{bmatrix} a \\ e \end{bmatrix} \sim NMV\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix} \right)$$

considering that:

$G = A \otimes G_0$ is the additive genetic (co)variance matrix between the characteristics, and

$$G_0 = \begin{bmatrix} \sigma^2_{a_{11}} & \sigma_{a_{12}} \\ \sigma_{a_{21}} & \sigma^2_{a_{22}} \end{bmatrix};$$

where $\sigma^2_{e_{ii}}$ is the additive genetic variance for characteristic i=1,2, and is the additive genetic covariance between characteristics 1 and 2.

A is the relationship matrix and is the direct product; and

$R = I \otimes R_0$ is the residual (co)variance matrix between the characteristics, and

$$R_0 = \begin{bmatrix} \sigma^2_{e_{11}} & 0 \\ 0 & \sigma^2_{e_{22}} \end{bmatrix};$$

where $\sigma^2_{e_{ii}}$ is the residual variance for characteristic i=1,2.

The components of (Co)variance were estimated using the computer program MTDFREML (Boldman et al 1993).

Results and Discussion

Herds in the high variability group presented greater milk yield averages (Table 2). These results confirm that there is a positive relationship between the average and the phenotypical variance of the herds, as discussed by Hill et al (1983), Brotherstone and Hill (1986) and Boldman and Freeman (1988). Other studies did not highlight this relationship (Lofgren et al 1985).

In Brazil, genetic and residual variances of milk yield for herds in the group of low PSD were, respectively, 41% and 58% of the variances estimated for the herds in the group of high PSD. For low **PSD** in Colombia the respective values were 56 and 55% (Table 2).

Table 2. Estimates of (co) variance, heritabilities[1] and genetic correlations for milk yield in Holstein cattle according to the herd groups of high and low phenotipical standard-deviation in contemporary groups in Brazil and Colombia.

	Brazil		**Colombia**	
	High	**Low**	**High**	**Low**
Milk yield average, kg	6,932.47	6,174.69	6,416.23	5,196.63
Milk yield standard deviation, kg.	1,725.38	1,543.56	1,659.93	1.276.28
Coefficient of variation, %.	24.89	25.00	25.87	24.56
Additive genetic variance, kg^2.	678,195.25	278,279.23	320,302.25	180,602.68
Residual variance, kg^2	1,166,513.62	674,952.47	865,650.51	473,228.75
Heritability	0.37	0.29	0.27	0.28

Genetic correlations

	Brazil	**Colombia**	
	Low	**High**	**Low**
Brazilian herds with high standard deviation	0.96	0.81	0.73
Brazilian herds with low standard deviations		0.77	0.72
Colombian hers with high standard deviation			0.93

[1] *The variances and heritability estimations are the means of the bivariate analyses*

For Costa (1999), Stanton (1990) and Cienfuegos-Rivas et al (1999), differences in herd size and management practices have been associated with heterogeneous residual variances in Latin American herds. Smaller genetic variance in low **PSD** herds possibly could be due to the fact that the animals did not present the desired physiological development and did not have the opportunity of expressing their genetic production potential (McDowell et al 1976; Lopes-Villalobos et al 2001; Holmann et al 1990; Costa 1998).

However, in **PSD** herds of Latin American countries, animal performance is close to that of countries of origin, since the genetic potential is expressed and, consequently, the use of imported genetic material presents positive and expected results (Costa,1999; Stanton 1990; Cienfuegos-Rivas et al 1999). Greater variances in herds of high **PSD** than in low ones were also observed in exporting countries, indicating that in cattle populations, independently of country or genetic breeding program, the genetic potential is better expressed when environmental and management restrictions are less severe (Van Vleck 1988; Boldman and Freeman 1990; Sullivan and Schaeffer 1989; Hill et al 1983; Powell et al 1983; Dong and Mao 1990).

Greater heritability estimates were found in high **PSD** herds than in low ones in Brazil (0.37 and 0.29, respectively). A similar relationship of heritability estimates between groups classified by **PSD** was found by Torres et al (2000b), who used three herd classes (high, median and low **PSD**), finding heritability estimates of 0.30, 0.35, and 0.27, respectively and differed from the results found by Costa (1999), where herds of high **PSD** presented smaller heritability estimate (h^2=0.22) than those of low variability (h^2=0.30). In general, these differences can be caused by the distinct models used and the number of records considered.

In Colombia, the heritability was similar in the high and low **PSD** (0.27 and 0.28, respectively).

The genetic and residual variance were smaller in low **PSD** herds in both countries; however, as the herd variability increases, the genetic variance increases in the same proportion as the residual variance, which confirms that smaller variances are not necessarily associated to smaller heritability estimates for milk yield (Stanton 1990).

The observation of variance heterogeneity and/or different heritabilities in the high and low PSD, indicates that when ignoring the existence of heterogeneous variances, unexpected results are achieved by national genetic breeding programs (Hill 1984; Vinson 1987).

The genetic correlation coefficients for milk yield between high and low variability herds were 0.96 and 0.93 in Brazil and Colombia, respectively (Table 2). Although the genetic correlation estimates were close to unity, they were sufficiently low to significantly change the classification of sires between environments. Additionally, the existence of heterogeneous variances affects the performance magnitude of sires and cows in the environments where they are used (Costa 1999; Costa et al 2001).

The genetic correlation coefficients for milk yield between the high and low **PSD** groups of the two countries varied from 0.72 to 0.81. According to Falconer (1952) and Dickerson (1962), the genetic correlations minor to one, suggest that, possibly, there was reclassification of animals. In this investigation, the Brazilian and Colombian Holstein cattle populations, presented reclassification, potentially reducing the benefits of the global semen importation strategy for these countries. In this context, national genetic breeding programs should be aware of the differences among environments, since there would be an efficiency reduction of sire and cow selection by assuming homogeneous variances when they are evidently heterogeneous (Garrick and Van Vleck 1987).

Greater variances in high **PSD** herds were found in the two countries, and this phenomenon was also observed in other countries registered as importers of genetic material, which leads to the questioning about the best strategy for use of imported semen, which is evaluated only in environments favorable for yield. There is a present need to do genetic evaluation to identify sires of greater genetic value in the environmental condition of the (sub) tropical countries and, in these evaluations, to consider the marked differences in production systems within each country. As a contrast, there is an opportunity to develop genetic breeding programs at the national and regional levels that would benefit the low **PSD** herds, since the genetic value of the sires would not be masked in the conditions of unfavorable production environments.

Conclusions

- The results found in this study demonstrated different components of genetic and residual variances and the reclassification of the animals in Brazilian and Colombian herds of high and low phenotypical variability for milk yield.
- These countries should establish strategies for the use of imported genetic material, optimizing the progeny performance of sires for the many production systems, seeking for profits from the investment.

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Received 21 January 2004; Accepted 1 March 2004

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