

MILK AND FAT PRODUCTION OF CROSSBRED HOLSTEIN-GIR COWS IN THE AGRESTE REGION OF THE STATE OF PERNAMBUCO, BRAZIL

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INTRODUCTION

Brazil produced in 2000 almost 20 billion liters of milk, which represents an increase of around 27% since 1995. In the state of Pernambuco, milk production is around 407 M liters (IBGE 95/96), placing the state as the second largest producer in the Northeast region of Brazil. Dairy herds are composed of a large variety of crossbred animals managed extensively. With the current crisis of sugarcane industry, crosses of Holstein and Gir are becoming new and interesting options in the Zona-da-Mata region. Different studies suggest the use of crossbred animals under tropical conditions to produce milk (Madgwick and Goddard, 1989; Ahlborn-Breier and Honenboken, 1991; Touchberry, 1992; Zarnecki et al., 1993); other studies support the use of purebred European cattle in the same regions (Swan and Kinghorn, 1992; Simpson and Conrad, 1993; McDowell *et al.*, 1996). It would appear that the particular environmental conditions may dictate which genetic solution is most appropriate.

To this end, the Empresa Pernambucana de Pesquisa Agropecuária (IPA) in the state of Pernambuco, northeast Brazil, initiated in the 80's a crossbreeding program to produce crossbred animals $\frac{5}{8}$ Holstein + $\frac{3}{8}$ Gir, using reciprocal or alternate crosses, with the objective of evaluating the performance of different genetic groups.

MATERIAL AND METHODS

Data were monthly test-day records on 1212 lactations of crossbred Holstein-Gir cows collected between January 1980 and December 1999. Initially, F1's ($\frac{1}{2}$ HG) were obtained by breeding Gir cows with Holstein sires. The following genetic group ($\frac{1}{4}$ HG) was obtained by back-crossing F1 cows to Gir bulls. Females of this group ($\frac{1}{4}$ HG) were then back-crossed to Holstein sires to obtain the third genetic group ($\frac{1}{4}$ HG). The fourth genetic group ($\frac{5}{8}$ HG) was obtained from the *inter-se* mating of $\frac{5}{8}$ HG. Between 5 and 10 sires were used in each genetic group over a number of years, so that there is a measure of overlap amongst the genetic groups.

A total of 7989 test-day records in 365 cows were analyzed using SAS/Proc MIXED. The statistical model included the effects of year of calving (19), genetic group of the cow (4), age of cow at calving (30 to 190 months), days in milk (5 to 330), year of birth of the cow (26), the random effect of sire (of cow), the random effect of cow (within genetic group) and the random residual. Test-days within lactation of a cow were treated as repeated records; compound symmetry, autoregressive (1) and spatial power covariance structures were tested. As might be expected (due to the variable intervals between test-days), the spatial power covariance

structure provided the best fit for the repeated records. Relationships amongst animals were not included.

The dependent variables were test-day milk and fat yields and fat percentage. Table 1 gives a summary of the data.

Table 1. Description of the data

Number of monthly records	7989
Number of cows	365
Number of lactations	1212
Number of sires	40

RESULTS AND DISCUSSION

Table 2 shows the F-tests and significance from the REML/GLS; all the fixed effects were statistically significant except for the effect of year of birth and genetic group on fat percent. These results agree with those of Lobo *et al.* (1984) and Martinez *et al.* (1988) for different crosses among Holstein and Zebu breeds in tropical areas. Table 3 shows milk yield, fat yield and fat percent for all genetic groups. The best productive performance was for the ½ HG group, followed by the ⅜ HG group. The *inter se* group (⅜ HGHG) was substantially below the performance of the ⅜ HG group probably by recombination loss (Willham and Pollak, 1985; Syrstad, 1989).

Table 2. F-tests for the three dependent variables

Variables	df	Milk yield	Fat yield	Fat %
Calving year	18	74.19**	30.81**	8.22**
Year of birth	26	1.70*	2.81**	1.12ns
Genetic group	3	18.77**	11.86**	2.49ns
Age at calving	156	5.26**	4.46**	1.44**
Days in milk	325	3.64**	2.43**	4.20**

* – significant ($P < 0,05$)

** – highly significant ($P < 0,01$)

Table 3. Least Squares Means of the four genetic groups for MY (kg), FY (kg) and FP (%)

	½HG	¼ HG	⅙ HG	⅙ HGHG
Milk yield	8.61± 1.16	5.34 ± 0.46	7.42 ± 0.39	5.76 ± 0.45
Fat yield	0.375 ± 0.052	0.231 ± 0.026	0.299 ± 0.025	0.231 ± 0.026
Fat percent	4.45 ± 0.29	4.08 ± 0.12	3.87 ± 0.10	3.89 ± 0.12

Table 4. Sire, cow and residual variances and correlations amongst monthly tests within a lactation for the three dependent variables.

	Milk yield	Fat yield	Fat percent
Sire variance	0.1091	0.000174	0.01054
Cow variance	1.3804	0.002074	0.07646
Correlation between tests	0.9707	0.9404	0.9755
Residual variance	3.2963	0.006787	0.2890

CONCLUSION

These results clearly shows that ½ HG yielded the best productive performance for all characteristics; it's very important to develop a breeding program in this genetic group. The ⅙ HG had a good performance, too; however, it is necessary to raise an intense selection because this genetic group is the genetic base for breeding *inter se*. The ⅙ HGHG require a rigorous evaluation and selection program.

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