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Genetic parameters for milk yield and composition of crossbred dairy cattle in Brazil*

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ABSTRACT

Data representing 20 dairy herds in Brazil from 1981 through 1992 were collected for study. After screening, 1430 to 2343 lactation records by 955 to 1402 cows were analyzed to estimate effects influencing milk, fat and protein yields and fat and protein percentages. Data represented total and 305 day performance. Animals were crossbreds, representing groups of daughters by 80 crossbred sires. Sires were from 5/8 to 7/8 European-Zebu crossbreds; daughters ranged from 2/8 to 7/8. European contribution was mostly Holstein; Zebu contribution was Gir and Guzera. Within crossbred groups, heritabilities ranged from 0.10 to 0.24, if records were not adjusted for days in milk, close to classic estimates for yields from temperate climates but lower than those for percentages. Heritabilities were slightly but consistently lower for 305 day records than for total records. Adjustment for days in milk lowered heritabilities to 0.06 to 0.22. Genetic correlations between total and 305 day performance were high, 0.84 to 1.00 (10 estimates); phenotypic correlations ranged from 0.52 to 0.99. Other estimates pooled within the crossbred groups were similar to those obtained in purebred groups within temperate areas. Estimates of genetic change from selection within crossbred groups would not be expected to differ widely from estimates obtained elsewhere for purebreds.

INTRODUCTION

Crossbred dairy cattle are used widely by dairy farmers in Brazil. Such animals have advantages in production systems because they utilize, to some degree, the Zebu's resistance to environmental stress, affecting health and well-being, and the milk producing ability of European dairy breeds. Certainly no unique system of crossbreeding or upgrading is best for all farms due to the diversity of management systems which exist in Brazilian tropical areas. Many small herds in this region cannot have more than one bull on the premises, and can cull only a very few cows, which makes it difficult to pursue a successful crossbred dairy cattle breeding system. Typically, artificial insemination services are not available. Thus a real problem exists for farmers who wish to create and maintain a productive and profitable crossbred herd.

Yet, use of crossbred sires may be a practical strategy for many small herds that wish to improve milk yield. However, selection for this trait also is necessary for this strategy to be successful. Milk yield doubtless is the most important single trait of dairy cows in Brazil, and major emphasis should be placed on it. There is little information available on milk fat and protein composition in tropical areas, especially in crossbred cattle.

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For development of an effective breeding program, knowledge of genetic parameters for the important traits is required. Under tropical conditions, and in crossbred populations, these may differ from those estimated in temperate environments. Heritability estimates from populations with low production may differ from estimates from those with high production.

Researchers in Brazil have found values for heritability of milk yield of between 0.16 and 0.30 for crossbred cattle (Lôbo *et al.*, 1984; Nobre *et al.*, 1984; Milagres *et al.*, 1988; Freitas *et al.*, 1991); for purebreds, values were between 0.23 and 0.37 (Ledic, 1992; Ribas *et al.*, 1993; Coelho *et al.*, 1993) for Holstein, Brown Swiss and Gir cows. Estimates of heritabilities of fat yield and percentage were between 0.28 and 0.47 (Ribas *et al.*, 1993); 0.19 and 0.46 (Coelho *et al.*, 1993) for Holsteins and within the range of 0.21 and 0.33 for Brown Swiss.

Chaudhry *et al.* (1993) found low heritabilities for total milk yield of 0.16, and 0.12 for 305 day milk yield, for Holstein-Sahiwal crossbreds in Pakistan. Others have shown low values for milk yield in tropical and subtropical areas (Rege and Mosi, 1989; Alba and Kennedy, 1993; Jairath *et al.*, 1994). Heritabilities of fat and protein yields were reported to be between 0.30 and 0.37 for milk yield, 0.40 and 0.59 for fat yield, and 0.26 to 0.43 for protein yield (Moya *et al.*, 1985; Campos *et al.*, 1994), in Florida's subtropical Holstein and Jersey herds.

Repeatability estimates in tropical and subtropical areas are not as common. They range between 0.28 and 0.51 for milk yield, 0.35 to 0.49 for fat yield, and 0.09 to 0.61 for fat percent in Brazil for crossbred and purebred herds. In other developing countries, values have been found to be 0.77 and 0.76 for milk yield in Jamaica Hope herds (Schneeberger *et al.*, 1982). Rege and Mosi (1989) and Alba and Kennedy (1993) estimated 0.49 and 0.44 for Holstein herds in Kenyan and Criollo cattle in Mexico.

Ribas *et al.* (1993), working with Holsteins in Brazil, found the genetic correlation between total milk yield and total fat yield to be 0.78, between total milk yield and fat percent -0.13, and between total fat yield with fat percent to be 0.52. Moya *et al.* (1985) and Campos *et al.* (1994) observed high correlations between milk yield and fat and protein yields and negative values between milk yield and fat and protein percentages. In other countries researchers have found similar values, such as Schneeberger *et al.* (1982), with Jamaica Hope cows, Strandberg and Danell (1989), with Swedish dairy cattle and Santus *et al.* (1993) and Jairath *et al.* (1994) with Brown Swiss in Italy and Holsteins in Canada, respectively.

In temperate areas, reliable estimates of genetic parameters in pure breeds were summarized by Wilcox (1992). Repeatabilities of lactation yields were 0.50 and percentages 0.75; heritabilities were 0.25 and 0.50. Yields were positively correlated with other yields, and percentages with other percentages. Correlations between yields and percentages were low and negative.

Objectives of the present study were to estimate genetic and environmental parameters for production in crossbred dairy herds under tropical Brazilian conditions.

MATERIAL AND METHODS

The data set consisted of 2343 lactation records of 1402 crossbred dairy cows maintained on 20 farms from 1981 to 1992. Daughters of 80 crossbred sires which participated in the progeny test program of Centro Nacional de Pesquisa Gado de Leite, EMBRAPA, Coronel Pacheco, MG, Brazil were represented. The main food source was pasture. Cows also received grass or corn silage, with mineral supplementation on some farms. In some cases they also received urea in the ration with sugar cane at milking time. Milking was twice a day with calf at side; calves were allowed to suckle after milking. Individual samples of milk were collected monthly for analyses of fat and protein contents; they were sent, with potassium dichromate preservative, to the central testing laboratory in Coronel Pacheco for chemical analysis.

Breed groups of sires were 5/8 to 7/8 European-Zebu, and daughters were 2/8 to 7/8 European-Zebu. The European contribution was mostly Holstein and the Zebu contribution was Gir and Guzera.

Total and 305 day records for milk, fat and protein yields and fat and protein percentages were evaluated. Records for 305 days were truncated at 305 days, but if the animal did not complete 305 days, due to her own inability to milk longer, the records were considered to be 305 day records. If the lactation was terminated by accident, disease, death or similar reasons, records were included in the data set. Lactations less than 120 days were not included. About 15% of all data were deleted from the original data available. Herd-breed groups with less than five observations also were eliminated, and these represented 2.3% of the total data set. The remaining data represented various numbers of observations for the different responses. The largest set therefore represented a screened data set. A reduced data set then was obtained for additional statistical analyses

Table I - Models for estimation of sums of squares using reduction notation.[1]

Source[2]	Reductions in sums of squares	Expectations of mean squares
S	R(u,S,B,F)-R(u,B,F)	$\sigma^2_R + k_{11}\sigma^2_{C(SHB)} + k_{12}\sigma^2_{SH} + k_{13}\sigma^2_S$
H	R,(u,H,B,F)-R(u,B,F)	$\sigma^2_R + k_8\sigma^2_{C(SHB)} + k_9\sigma^2_{SH} + k_{10}\sigma^2_H$
S*H	R,*u,S,H,SH,F)-R(u,S,H,F)	$\sigma^2_{12} + k_6\sigma^2_{C(SHB)} + k_7\sigma^2_{SH}$
B	R(u,S,H,SH,B,SB,HB,F)-R(u,S,H,SH,SB,HB,F)	Fixed effect
S*B	R(u,S,B,SB,F)-R(u,S,B,F)	$\sigma^2_R + k_4\sigma^2_{C(SHB)} + k_5\sigma^2_{SB}$
H*B	R(u,H,B,HB,F)-R(u,H,B,F)	$\sigma^2_R + k_2\sigma^2_{C(SHB)} + k_3\sigma^2_{HB}$
C:(SHB)	R[u,S,H,SH,B,SB,HB,C(SHB),F]-R(u,S,H,SH,B,SB,HB,F)	$\sigma^2_R + k_1\sigma^2_{C(SHB)}$
F	Adjusted for S,H,B	Fixed effects
R	R(y,Y)-R[u,S,H,SH,B,SB,HB,C(SHB),F]	σ^2_R

[1]S*H*B not estimable.
[2]S = sire, H = herd, B = breed group, C = cow, F = a set of fixed effects, R = residual.

which were complete for all response variables. These data included 1430 lactation records of 955 cows and were used to estimate heritabilities and genetic and phenotypic correlations; the overall screened data set represented up to 2343 records by 1402 cows and was used to estimate heritabilities and repeatabilities.

Estimates of components of variance were obtained by Henderson Method 3 (Henderson, 1953), with the series of mixed models presented in Table I. Included in the models were fixed continuous effects, such as age of cow at parturition and length of record (each to the third order of polynomial regression). Fixed classes effects representing month and year of calving also were included.

Repeatability was estimated by the following equation:

$$t = [\ \sigma^2_S + \sigma^2_{C(SHB)}\ ] \div [\ \sigma^2_S + \sigma^2_{C(SHB)} + \sigma^2_R\ ]$$

and heritability as:

$$h^2 = 4\sigma^2_S \div [\ \sigma^2_S + \sigma^2_{C(SHB)} + \sigma^2_R\ ]$$

where σ^2_S = sire variance, $\sigma^2_{C(S\ H)B}$= cow within sire-herd- breed variance and σ^2_R = residual variance.

Model 6 of Harvey's LSMLMM analysis (Harvey, 1990) was used to estimate all genetic and phenotypic correlations:

$$Y_{ijklm} = \mu + S_i + H_j + S^*H_{ij} + G_k + YS_l + Age + e_{ijklm}$$

where Y_{ijklm} is the response variable; S_i are effects of sire; H_j, herd effects; S^*H_{ij}, sire-herd interaction effects; G_k, genetic group effects; YS_l, year-season effects and age at parturition (linear, quadratic and cubic terms). Effects of S_i, S^*H_{ij} and e_{ijklm} were considered to be random. All other effects were fixed. Additional analyses (also Model 6) included length of lactation to verify effects of adjusting for number of days in milk.

Phenotypic correlations were estimated as

$$r_{P_{xy}} = (Cov_{P_{xy}}) \div (\sigma^2_{PX} \cdot \sigma^2_{PY})^{1/2}$$

where x and y represented any two response variables; σ^2_{PX} and σ^2_{PY} were the phenotypic variances for each. The total phenotypic variances and covariances were estimated as the sum of the three random terms of the model. Genetic correlations were obtained by

$$r_{A_{xy}} = {cov}_{S_{xy}} \div (\sigma^2_{SX} \cdot \sigma^2_{SY})^{1/2}$$

using sire components of variance and covariance.

RESULTS AND DISCUSSION

Observed means, standard deviations, ranges and coefficients of variation for traits studied are in Table II. Total and 305 day milk yields were similar to those obtained by Milagres *et al.* (1988) who worked with records from one herd which was participating in

Table II - Observed means, standard deviations (S.D.), minimum and maximum values, and coefficients of variation (C.V.)[1] for traits measured, n = 2343.

Trait	Mean	S.D.	Minimum	Maximum	C.V. (%)
Total milk yield[2]	1950	780	345	4630	39
Milk yield, 305 days	1695	640	345	4015	37
Fat yield	64	28	5	140	44
Fat yield, 305 days	60	25	4	136	42
Protein yield	54	22	4	124	43
Protein yield, 305 days	51	19	4	116	39
Fat percentage	3.60	0.60	0.33	7.03	23
Fat percentage, 305 days	3.55	0.59	0.19	8.98	32
Protein percentage	2.88	0.34	0.40	4.95	16
Protein percentage, 305 days	2.85	0.33	0.40	7.33	28

[1]Based on residual mean squares.
[2]All yields in kilograms.

Table III - Least squares analyses of variance (n=2343)[1].

Source	Milk		Milk (305)	Fat		Fat (305)	Protein		Protein (305)	Fat%		Fat % (305)	Protein %		Protein % (305)
	DF	MS	MS	DF	MS	MS	DF	MS	MS	DF	MS	MS	DF	MS	MS
Sire, S	79	438*	370	79	529*	609**	74	263	241	79	4653*	4560*	74	1937**	1939**
Herd, H	19	5093**	4747**	16	3905**	3993**	18	2591**	2405**	15	19883**	18741**	16	3910**	4024**
S*H	349	330**	436**	254	368	379	316	223**	200**	233	3385*	3347	284	1122*	1129*
Breed group, B	5	354**	300**	5	215	194	5	452**	412**	4	6269**	5459**	5	3066**	3127**
S*B	189	304**	388**	172	384*	386	187	234**	213**	162	4041**	4053**	180	1125*	1089
H*B	31	207**	507**	23	0	0	28	300**	337**	21	8128**	7891**	21	1077	1404
Cow (S*H*B)	722	177**	891	314**	325**	689	122**	118**	473	2699**	2744**	634	876	876	908
Residual	921	107	131	473	137	179	838	104	103	423	1743	1733	743	860	878

[1]Breed considered a fixed effect.

the same progeny testing program. Values were lower than those in some other studies with crossbred European-Zebu cows in Brazil, such as Schneeberger *et al.* (1982), Lôbo *et al.* (1984), Nobre *et al.* (1984) and Freitas *et al.* (1991).

On the other hand, our data included a majority of first lactation animals. Farmers were required to keep only daughters of sires in their herd until they completed their first lactation. There were 1294 first, (54.8%), 612 second (25.9%), 234 third (9.9%), and 203 fourth or higher lactation cows (9.4%). Also in Brazil, Ledic (1992) found average Gir production to be 2057 kg; but Ribas *et al.* (1993) reported 5296 kg for Holsteins.

Means of fat and protein yields and percentages were lower than most of those found in the literature. Ribas *et al.* (1993) found averages of 204 kg and 3.4% for fat in Holsteins, and Lôbo *et al.* (1984) 116 kg and 4.1% for Pitangueiras in Brazil. In other tropical and subtropical areas, fat and protein yields ranged from 173 to 497 kg, and 142 to 443 kg; those for fat and protein percentages were 3.4% to 4.6% and 3.3% to 3.6%, respectively (Moya *et al.*, 1985; Simianer *et al.*, 1991; Campos *et al.*, 1994).

Analyses of variance are presented in Table III. Estimates resulted from various combinations of the models shown in Table I. Most effects included in the model were statistically significant.

Sire by herd interactions (Table IV) were responsible for appreciable fractions of the variance in total milk and milk (305 days) yields and total protein and protein (305 days) yields. These interactions accounted for 16.7% and 18.2% of the variation in total

Table IV - Sire by herd interactions expressed as percentages of the total variance (n=2343).

Traits	Unadjusted[1]	Adjusted[1]
Total milk yield	14.8	22.0
Milk yield (305 days)	24.7	27.0
Total fat yield	16.2	17.9
Fat yield (305 days)	19.0	16.1
Total protein yield	10.4	17.2
Protein yield (305 days)	13.9	16.8
Total fat percentage	14.7	13.6
Fat percentage (305)	11.4	7.2
Total protein percentage	16.7	18.2
Protein percentage (305 days)	8.1	8.6

[1]Adjusted or unadjusted for days in milk.

Table V - Heritabilities (h^2) and repeatabilities (r) of yield and percentage traits (n=2343).

Trait	h^2	r
Milk yield	0.12	0.19
Milk yield (305 days)	0.00	0.17
Fat yield	0.14	0.49
Fat yield (305 days)	0.18	0.39
Protein yield	0.05	0.11
Protein yield (305 days)	0.05	0.10
Fat percentage	0.12	0.32
Fat percentage (305 days)	0.12	0.34
Protein percentage	0.15	0.05
Protein percentage (305 days)	0.15	0.06

protein percentage and 8.1% to 8.6% for 305 day protein percentage. Estimates for seven of the 10 traits were increased when records were adjusted for days in milk. These values are higher than most estimates from temperate areas (Verde *et al.*, 1972) which generally are < 10% and frequently < 5%.

Estimates of repeatability are in Table V. In Brazil, research has shown similar values for data from European-Zebu populations (Lôbo *et al.*, 1984; Nobre *et al.*, 1984; Milagres *et al.*, 1988; Freitas *et al.*, 1991). The average heritability obtained in their work was 0.22 and for repeatability 0.35. Our results were lower than those obtained by Ribas *et al.* (1993) and Coelho *et al.* (1993), for purebred Holsteins and Brown Swiss; they found values for heritability of milk, fat and fat percentage of 0.29, 0.23 and 0.42, and repeatabilities of 0.48, 0.44 and 0.48. In other countries, several authors have found estimates as low as ours (Rege and Mosi, 1989; Jairath *et al.*, 1994), but the majority obtained higher estimates; principally the higher estimates represented purebred cows at higher production levels. Estimates of heritability and repeatability are important in the estimation of sire breeding values and for predicting response to selection.

Estimates of heritability from the larger data set (Table V) ranged considerably. A value of 0 was found for 305 day milk yield. The reason for this value is unknown. There seemed to be no consistent pattern in the estimates related to whether they represented total lactations or 305 day lactations. The estimate was slightly higher for 305 day fat yield, but the remaining responses were the same. Additional estimates of heritability from the reduced data set are in Tables VI and VII.

Table VI - Phenotypic and genetic correlations for traits measured, unadjusted for days in milk, reduced data set (n=1430)[1].

Traits	MY	M305	FY	F305	PY	P305	F%	F%305	P%	P%305
Total milk yield (MY)	*0.19*	0.86	0.85	0.77	0.91	0.86	0.02	0.27	0.08	0.35
Milk yield, 305 days (M305)	0.84	*0.14*	0.59	0.66	0.64	0.74	-0.01	-0.21	0.04	-0.21
Total fat yield (FY)	0.87	0.72	*0.24*	0.91	0.92	0.86	0.51	0.53	0.40	0.48
Fat yield, 305 days (F305)	0.63	0.79	0.86	*0.23*	0.82	0.86	0.49	0.55	0.36	0.38
Total protein yield (PY)	0.91	0.72	0.93	0.72	*0.24*	0.95	0.28	0.40	0.45	0.54
Protein yield, 305 days (P305)	0.89	0.85	0.94	0.84	0.97	*0.20*	0.27	0.33	0.46	0.47
Total fat % (F%)	0.23	0.17	0.70	0.72	0.49	*0.18*	0.62	0.66	0.59	
Fat %, 305 days (F%305)	0.25	-0.52	0.69	0.74	0.52	0.55	0.95	*0.10*	0.41	0.80
Total protein % (P%)	0.30	0.25	0.60	0.53	0.64	0.67	0.74	0.73	*0.27*	0.56
Protein %, 305 days (P%305)	0.51	-0.28	0.70	0.37	0.76	0.67	0.64	0.61	0.84	*0.13*

[1]Heritabilities on, phenotypic correlations above, and genetic correlations below the diagonal.

Table VII - Phenotypic and genetic correlations between yield and percentage traits adjusted for days in milk (reduced data set) (n=1430)[1].

Traits	MY	M305	FY	F305	PY	P305	F%	F%305	P%	P%305
Total milk yield (MY)	*0.10*	0.72	0.58	0.56	0.74	0.73	-0.26	-0.07	-0.24	-0.03
Milk yield, 305 days (M305)	1.00	*0.06*	0.45	0.45	0.55	0.58	-0.15	-0.47	-0.37	-1.19
Total fat yield (FY)	-0.04	0.02	*0.08*	0.90	0.77	0.75	0.56	0.39	0.30	0.20
Fat yield, 305 days (F305)	0.13	0.32	0.89	*0.17*	0.70	0.71	0.49	0.49	0.25	0.16
Total protein yield (PY)	0.27	0.63	0.33	0.51	*0.06*	0.99	0.17	0.15	0.41	0.31
Protein yield, 305 days (P305)	0.25	0.63	0.28	0.49	0.99	*0.07*	0.16	0.13	0.40	0.29
Total fat % (F%)	-0.80	-0.74	0.69	0.48	- < 0.01	- < 0.01	*0.15*	0.60	0.64	0.30
Fat %, 305 days (F%305)	-0.53	-0.34	0.42	0.75	0.15	0.53	0.84	*0.09*	0.35	0.75
Total protein % (P%)	-0.70	-0.36	0.23	0.17	0.45	0.49	0.66	0.50	*0.22*	0.52
Protein %, 305 days (P%305)	-0.83	-0.56	-0.02	-0.15	0.19	0.15	0.56	0.34	0.86	*0.07*

[1]Heritabilities on, phenotypic correlations above, and genetic correlations below the diagonal.

Heritabilities for milk, fat and protein yields and for fat and protein percentages are in Table VI. They were decreased by adjustment for days in milk (Table VII). In the restricted sample the estimates of heritability were higher than those estimated from the complete data set. Madalena (1988) published a note on effects of variation of lactation lengths on the efficiency of tropical cattle selection for milk production. The overall effect of adjusting for lactation length was a reduction in the genetic variability between genetic groups of crossbred cattle. This would be expected if the length of record were heritable. His conclusions seemed to be confirmed in the present study.

Phenotypic correlations between milk yield and fat and protein yields were high (Tables VI and VII). Correlations between milk yields and component percentages were low or negative, and those between fat and protein yields with fat and protein percentages had intermediate values. These values agreed closely with those reported in the literature (Moya *et al.*, 1985; Strandberg and Danell, 1989; Jairath *et al.*,1994).

Adjustment for days in milk (Table VII) lowered estimates of correlations between milk, fat and protein yields. The principal effect of adjustment for days in milk on genetic correlations were reductions in the correlations between yields, causing them to become negative for yields and percentages. The latter change caused them to be in closer agreement with estimates from temperate areas.

CONCLUSIONS

Estimates of repeatabilities and heritabilities seemed lower in this crossbred population than in most temperate pure breeds. Adjustment of records for days in milk had variable effects on estimates; additional study on this point seems needed. Genetic change within crossbred groups can be obtained if selection pressure is adequate, as would be expected in purebred cattle in temperate areas.

RESUMO

Foram coletados para estudo, no período de 1981 a 1992, dados representativos de 20 rebanhos de leite no Brasil. Analisou-se 1430 a 2343 registros de lactação de 955 a 1402 vacas, para estimar efeitos que influenciam a produção de leite, gordura e proteína e porcentagens de gordura e proteína. Os dados representaram os níveis para lactação total e em 305 dias. Os animais eram mestiços, representando grupos de filhas de 80 touros mestiços. Os touros eram de 5/8 a 7/8 Europeu-Zebu e as filhas 2/8 a 7/8. A contribuição européia foi em maior parte Holandês e a contribuição zebuína, Gir e Guzerá. Dentro de grupos, as herdabilidades permaneceram entre 0,10 a 0,24, se os registros não foram ajustados para dias em lactação. Estas estimativas ficaram próximas das estimativas clássicas para produção em clima temperado, mas menores que aquelas obtidas para porcentagens. Herdabilidades foram levemente, mas consistentemente menores para registros aos 305 dias que para a produção total. Ajustamentos para duração da lactação diminuiram as herdabilidades para 0,06 a 0,22. As correlações genéticas entre o total e 305 dias de lactação foram altas, 0,84 a 1,00 (10 estimativas); correlações fenotípicas variaram de 0,52 a 0,99. Outras estimativas para grupos mestiços foram similares a aquelas obtidas em animais puros em áreas temperadas. Estimativas de mudanças genéticas por seleção dentro de grupos mestiços não devem ser muito diferentes das estimativas obtidas em outros lugares para raças puras.

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