

CONSEQUENCES OF REMOVING THE VARIATION IN LACTATION LENGTH ON THE EVALUATION OF DAIRY CATTLE BREEDS AND CROSSES

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ABSTRACT

Three procedures commonly used for breed group comparisons were studied; (a) adjustment of milk yield for lactation length; (b) exclusion of short lactations considered abnormal; and (c) utilization of all available observations, unadjusted for lactation length. These three procedures were applied in a comparison of six Holstein-Friesian: Guzera crossbred groups at farms in the southeast region of Brazil. Genetic group effects on milk and component yields were attenuated by procedures *a* and *b*, compared to procedure *c*, and this resulted in underestimation of heterosis for those traits, as well as underestimation of the breed additive differences. These results were expected given the presence of genetic variation for lactation length and the high positive correlation between this trait and milk yield. This research suggests that procedures reducing variation in lactation length are inadequate for evaluation of breed groups. "Abnormal" lactation data also should be reported when "normal" lactations are analysed separately.

INTRODUCTION

The incidence of short lactations is a serious problem for tropical dairy production, as it increases the proportion of dry cows in the herd. Lactation length is highly correlated with lactation milk yield (Mahadevan, 1966). Although this is a long known problem (Rhoad, 1935), its implications on the procedures used to calculate yield have not always received adequate attention.

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Mahadevan (1966) discussed the validity of omitting from statistical analyses short lactation records, mentioning a personal communication by French, who considered that such a procedure would "mask the high resulting wastage" in cows which dried off early. Referring to individual selection, Mahadevan (1966) suggested deleting short lactation records "except when ... they are of genetic origin". He presented evidence of breed differences in lactation length. Briquet Jr. (1967) recommended not to extend short lactations of genetic origin, as occurs in zebu. Franklin *et al.* (1967) utilized all records, unadjusted, in the development of the AMZ, so as to be able to exercise indirect selection pressure against short lactations when selecting for yield. Other authors included all lactations, independent of length, in comparisons of breeds and crosses (e.g. Buvanendran, 1977). Madalena *et al.* (1990) also adopted this criterion, not even deleting records terminated by death, illness or accident, as their incidence is influenced by crossbred type (Madalena *et al.*, 1989).

Three basic procedures have been described in the literature on genetic analyses of milk yield:

- (a) To adjust lactation milk yield by regression on lactation length;
- (b) To exclude short lactation records (typically with lactation length shorter than 100 - 150 days), considering them as abnormal;
- (c) To use all available observations, not adjusting for lactation length.

If lactation length has a genetic component and its correlation with yield is not low, it should be expected that those procedures reducing the variation between genetic groups in lactation length also would reduce the between group variation in yield. As a consequence, procedures *a* and *b* would result in underestimation of breed additive differences and heterosis, in relation to procedure *c* estimates.

This paper presents an example of this situation, obtained by analyzing the same data set with the three procedures. The data are from a crossbreeding trial the results of which were reported by Madalena *et al.* (1990) and will not be discussed here, where only the methodology aspects will be considered. The effects of the three procedures on the efficiency of within population selection were analyzed separately (Madalena, 1989).

MATERIAL AND METHODS

First lactation records (403) were used, of cows kept on 61 farms in the states of Minas Gerais, São Paulo, Rio de Janeiro and Espírito Santo, between June 1980 and June 1985. The animals were of six groups of red and white Holstein-Friesian (HF) x Guzerá (Gu), with the following expected fractions of HF genes: 1/4, 1/2, 5/8, 3/4, 7/8 and $\geq 31/32$ (HF). Farms were grouped into two classes of high and low management. Records were grouped into year-season of calving classes, with two seasons, dry (April to September) and rainy (October to March).

Estimates of the individual breed additive differences and individual heterosis were obtained by multiple regression (Dickerson, 1973), utilizing each of the procedures. The following model was used with b and c :

$$Y_{ijklm} = b_0 + M_i + g_i q_j + h_i z_j + F_{ik} + YS_{il} + e_{ijklm}$$

where:

- Y_{ijklm} = lactation length, or milk, fat or protein yield of the i - j - k - l - m -th cow;
 b_0 = intercept;
 M_i = effect of the i -th management level ($i = 1, 2$);
 g_i = individual breed additive difference (HF-Gu) in the i -th management class;
 q_j = expected proportion of HF genes in an individual of the j -th crossbred group ($j = 1, \dots, 6$). For the HF group $q = 1$ was used;
 h_i = individual heterosis in the i -th management class;
 z_j = expected proportion of loci occupied with one allele of each breed in an individual of the j -th crossbred group. Values of z_j for crossbred groups 1/4, 1/2, 5/8, 3/4, 7/8 and HF were, respectively, 1/2, 1, 30/64, 1/2, 1/4 and 0;
 F_{ik} = effect of the k -th farm within the i -th management class;
 YS_{il} = effect of the l -th year-season of calving within the i -th management class;
 e_{ijklm} = random error assumed NID (0,1).

All effects were considered fixed. A second model was also utilized, considering crossbred group as a classification variable. In this model, the effect of crossbred group (G_j , $j = 1, \dots, 6$) and the $G \times M$ interaction substituted for the $g_i q_j + h_i z_j$ terms.

The analyses were performed with the SAS SYSTEM (SAS Institute, 1982).

To apply procedure a , lactation length was included as a covariable, with a separate regression within each management class.

When applying procedure b , 39 records were excluded with lactation length up to 120 days.

The correlations of lactation length with milk and component yield were estimated within management level, adjusting for farm and year-season effects but not for crossbred group effects.

RESULTS AND DISCUSSION

The distribution of lactation lengths by crossbred group is shown in Table I. Groups 1/4 and 5/8 had a higher incidence of short lactations than other groups under high management, whereas under low management the HF also had high frequency of short lactations.

Table I - Distribution of lactation lengths (%).

Lactation length (d)	Management level											
	High						Low					
	1/4 ¹	1/2	5/8	3/4	7/8	≥ 31/32	1/4	1/2	5/8	3/4	7/8	≥ 31/32
0 - 120	12	-	19	-	4	-	20	-	11	4	9	26
121 - 240	20	-	25	-	-	-	33	9	34	14	24	24
241 - 360	64	90	56	67	71	43	29	35	37	35	38	26
361 - 480	4	10	-	33	25	50	10	42	9	37	27	17
> 480	-	-	-	-	-	7	8	14	9	10	2	7
Total	100	100	100	100	100	100	100	100	100	100	100	100
Number	25	21	16	15	24	14	49	57	44	51	45	42

¹Genetic group, denoted by the proportion of Holstein-Friesian genes.

Correlations of lactation length with milk and component yield were very high (Table II), larger than those reported in the literature (Madalena, 1989), as would be expected since genetic group was here a source of covariation.

Table II - Phenotypic correlations between lactation length and lactation milk or component yields¹.

Trait	Management level	
	High	Low
Lactation yield		
Milk	0.849	0.855
Fat	0.813	0.847
Protein	0.854	0.846

P < 0.0001 for all coefficients.

¹All variables adjusted for farm and year-season effects.

Therefore, in the data set analyzed, the necessary conditions existed for procedures *a* and *b* to underestimate the effects of crossbred group on milk and component

yield. In Table III the F-values for crossbred group and its interaction with management were lower for procedures *a* and *b* than for procedure *c*, although the latter resulted in greater residual variance and a higher coefficient of variation, i.e. more genetic than non-genetic variation was removed by procedures *a* and *b*.

Table III - Residual standard deviation (σ_e^2), coefficients of variation (CV) and F-values for crossbred group (G) and its interaction with management (M x G), from analyses of variance in procedures¹.

		Source of variation			
		σ_e^2	CV (%)	G	M x G
		F			
Milk yield (kg)	<i>a</i>	441.2	21.87	20.86***	3.20**
	<i>b</i>	675.6	30.54	28.45***	7.50***
	<i>c</i>	772.7	38.30	32.83***	9.88***
Fat yield (kg)	<i>a</i>	19.9	24.21	27.52***	2.32*
	<i>b</i>	30.2	33.44	29.30***	5.60***
	<i>c</i>	34.1	41.41	33.40***	7.46***
Protein yield (kg)	<i>a</i>	14.1	22.33	22.31***	1.05 ^{ns}
	<i>b</i>	21.4	31.00	27.08***	5.40***
	<i>c</i>	24.6	39.01	31.38***	7.66***
Lactation length (d)	<i>b</i>	82.4	25.19	9.23***	3.05*
	<i>c</i>	104.2	34.61	10.56***	5.06**

¹ *a*) Adjusting yields by lactation length; *b*) Deleting lactations shorter than 121 d; *c*) Not adjusting nor deleting records.

* P < 0.05; **P < 0.01, ***P < 0.0001, ^{ns}P > 0.10.

The attenuation of crossbred group effects also may be observed in Table IV, where estimates of these effects are expressed relative to the mean of the 1/2 HF group for each procedure. Attenuation of crossbred group effects was reported by De Alba and Kennedy (1985) due to deletion of lactations shorter than 150 d and yielding less than 450 kg of milk.

Table IV - Crossbred group effects on dairy traits, estimated by three procedures, *a*, *b* and *c* (as in Table III). Effects expressed relative to the mean of the 1/2 HF group, which are shown in the last column.

		1/4 ¹	5/8	3/4	7/8	≥ 31/32	1/2
		%					Mean
		of 1/2 HF					
<i>High management level</i>							
Milk yield (kg)	<i>a</i>	72	77	95	98	91	2919
	<i>b</i>	55	59	101	98	106	2995
	<i>c</i>	47	47	101	96	107	2952
Fat yield (kg)	<i>a</i>	64	62	86	81	70	131
	<i>b</i>	48	44	92	81	85	134
	<i>c</i>	42	35	92	79	85	132
Protein yield (kg)	<i>a</i>	72	72	88	86	78	99
	<i>b</i>	55	54	94	87	94	101
	<i>c</i>	48	43	94	84	93	100
Lactation length (d)	<i>b</i>	76	75	108	100	119	310
	<i>c</i>	69	63	92	97	120	305
<i>Low management level</i>							
Milk yield (kg)	<i>a</i>	62	69	85	75	67	2205
	<i>b</i>	54	58	89	71	57	2637
	<i>c</i>	45	54	85	63	47	2636
Fat yield (kg)	<i>a</i>	69	67	81	69	63	95
	<i>b</i>	60	56	86	66	52	114
	<i>c</i>	50	52	82	58	43	114
Protein yield (kg)	<i>a</i>	66	69	83	72	64	70
	<i>b</i>	58	58	87	68	55	83
	<i>c</i>	48	54	84	61	45	83
Lactation length (d)	<i>b</i>	81	81	101	89	85	376
	<i>c</i>	71	75	98	81	69	375

¹Genetic groups, denoted by proportion of Holstein-Friesian genes.

The consequences of reducing the variation in lactation length on the estimates of g and h also may be analysed as follows. If g_y and h_y represent the lactation yield parameters and g_x and h_x the lactation length parameters, it is shown easily that the corresponding parameters for the adjusted yield, $y_a = y - bx$ are:

$$g_{y_a} = g_y (1 - b g_x / g_y)$$

$$h_{y_a} = h_y (1 - b h_x / h_y)$$

It then may be seen that procedure *a* leads to a biased estimate of g_y if $g_x > 0$, and to a biased estimate of h_y if $h_x > 0$, unless $b = 0$. Here $b = 7.68$ kg/d under high management and $b = 5.78$ kg/d under low management, and the parameters estimated with procedures *a* were much smaller than with procedure *c* (Table V).

Table V - Estimates of individual breed additive differences (g , HF-Gu) and of individual heterosis (h) for first lactation traits using procedures *a*, *b* and *c* (as in Table III). Standard errors between parentheses.

Management level	Milk yield (kg)		Fat yield (kg)		Protein yield (kg)		Lactation length (d)		
	<i>g</i>	<i>h</i>	<i>g</i>	<i>h</i>	<i>g</i>	<i>h</i>	<i>g</i>	<i>h</i>	
High	<i>a</i>	1371 (243)	899 (188)	50 (11)	63 (9)	31 (7)	36 (6)	- -	- -
	<i>b</i>	2783 (357)	1312 (296)	113 (16)	82 (13)	78 (11)	50 (9)	175 (43)	51 (35)
	<i>c</i>	3113 (390)	1502 (335)	126 (17)	90 (15)	90 (12)	57 (11)	212 (51)	73 (44)
Low	<i>a</i>	960 (155)	1199 (133)	24 (7)	47 (6)	23 (5)	36 (4)	- -	- -
	<i>b</i>	1559 (271)	1872 (212)	48 (12)	77 (10)	40 (9)	56 (7)	110 (32)	110 (25)
	<i>c</i>	1749 (275)	2251 (227)	58 (12)	93 (10)	47 (9)	68 (7)	135 (36)	180 (30)

$P < 0.005$ for all estimates.

Because procedure *b* also removes variation in lactation length, although not completely, it should be expected to result in underestimation of *g* and *h*. In Table V this was actually the case, the bias being less than for procedure *a*, as expected. The bias with procedure *b* was not negligible in the high management level in spite of only six percent (7/115) of lactations having been discarded.

CONCLUSIONS

1. Removing variation between genetic groups in lactation length will reduce group differences in milk and component yields, unless the correlation between lactation length and yield is very low.

2. Adjusting yields for lactation length will yield estimates of the breed additive difference in yield biased downward when the breeds differ in lactation length, and will yield estimates of heterosis biased downward when there is heterosis for lactation length.

3. Similar biased estimates are expected from the deletion of short lactations, the magnitude of this bias downward being dependent on the proportion of records deleted.

4. A more thorough evaluation of breeds and crosses will be obtained by not adjusting milk or component yield for lactation length. To the same end, all available records should be analyzed irrespectively of lactation length, or, alternatively, results for abnormal lactations should also be reported when only normal lactations are analyzed.

RESUMO

Estudaram-se as conseqüências de três procedimentos geralmente utilizados para a comparação de grupos raciais: (a) ajuste da produção de leite (ou de gordura ou de proteína) por lactação pela duração da mesma; (b) eliminação das lactações consideradas anormalmente curtas; e (c) utilização de todas as observações disponíveis, sem ajustar. Estes três procedimentos foram aplicados na comparação de seis grupos de cruzamentos de Holandês e Guzerá, em fazendas da região Sudeste do Brasil. Os efeitos de grupo genético sobre a produção de leite e seus componentes foram atenuados com os procedimentos *a* e *b*, em relação ao procedimento *c*, resultando em uma subestimativa da heterose para aquelas características, assim como das diferenças aditivas entre raças. Esses resultados eram esperados com base na existência de variação genética na duração da lactação e na alta correlação positiva entre esta característica e a produção de leite. Conclui-se que os procedimentos que reduzem a variação genética na duração da lactação são inadequados para a avaliação de grupos raciais. Os resultados relativos a lactações "anormais" deveriam também ser comunicados, quando se analisam por separado as lactações "normais".

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(Received March 22, 1991)