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GENETIC PARAMETERS OF TEST DAY MILK YIELDS OF HOLSTEIN COWS

S.G. Machado, M.A.R. Freitas and C.H. Gadini

ABSTRACT

Data were obtained from 17,968 records from 2,130 first lactations of Holstein cows calving between 1988 and 1991. The subjects were daughters of 136 sires monitored by Brazilian Breeders Association, Animal Science Institute, Department of Agriculture, a branch of the State of São Paulo. Data were divided into 10 subsets based on the number of days in milk yield. Test day milk yields (M1 to M10) and 305-day milk yield (M305) were the traits studied. These traits were adjusted for several environmental effects: class of cow age at calving, interval from calving to first test day, and herd-year-season. Restricted maximum likelihood estimates of (co)variance components were obtained from one and two-traits analysis under a sire model. Estimates of heritabilities for M ranged from 0.04 to 0.32. The highest values were found in the second half of lactation (M5 to M7). Heritability estimate for M305 was 0.32. Genetic correlations between individual test days and M305 ranged from 0.78 to 1.00. Results suggested that test day milk yields, mainly in mid-lactation, can be used instead of 305-day milk yield in genetic evaluations, because estimates of these two-trait heritabilities are nearly alike. Moreover, early selection can reduce generation intervals.

INTRODUCTION

In general, standardized 305-day (d) milk yield (M305) has been used in genetic evaluation of dairy sires. Heifers that did not complete first lactation or had lactation periods shorter than 305 days have had their lactations extended and then used in the prediction of genetic merit.

However, prediction of uncompleted lactations may be biased. The major cause of bias in sire evaluations seems to be related to culling of heifers before completion of their first lactation, instead of non-random matings (Fimland, 1983).

To avoid extending lactations to 305-day, individual test day milk yields can be used in genetic evaluation of dairy sires and cows. Models that include test day milk yields in statistical analysis provide an alternative to selection on 305-day milk yield (Swalve, 1995b). In these models, any information on production can be utilized, and the models become more flexible. Cows can be included in the evaluations if they have at least one test day yield, and sires can be evaluated more accurately based on a larger amount of data available from their daughters instead of only one lactation record per daughter (Ptak and Schaeffer, 1993). The increase in accuracy is due mainly to a better adjustment of test day yields.

In Brazil, several studies have been done on aspects of the lactation curve, including studies to model lactation curves (Madalena, *et al.* 1979; Queiroz, *et al.* 1991; Durães, *et al.* 1991; Freitas, *et al.* 1992; Mcmanus, *et al.* 1997). There is no report on test day milk yield in specialized dairy breeds, probably due to the difficulty of storing enough information about a large number of animals. Test day records usually are discarded after M305 is calculated. Increases in computer storage capacity would allow this kind of information to be used either in lactation curve studies or directly in genetic evaluations.

Genetic parameters for test day yields have been estimated by several authors (Van Vleck and Henderson, 1961; Keown and Van Vleck, 1971; Auran, 1976; Danell, 1982, Swalve, 1995b, Gadini, 1997). According to these authors, selection based on some test day records is as efficient as on all. This may reduce the number of tests in routine milk recording.

The present study aims to estimate components of variance and covariance for test day milk yields in first lactation of Holstein cows by the use of a multiple trait derivative-free restricted maximum likelihood procedure, evaluating the possibility of utilizing these test day records as a selection criterion.

MATERIAL AND METHODS

Data were obtained from first lactation Holstein cows calving between 1988 and 1991. The herds were part of the Dairy Recording Program developed by the Brazilian Breeders Association, in partnership with the Animal Science Institute, a branch of the São Paulo State Department of Agriculture. Only first lactation records from cows aged between 1.5 and 3.5 years at calving were considered in this study.

Test day milk yields, recorded at approximately monthly intervals throughout lactation (M1-M10), and milk yields up to 305-days (M305) were the traits under analysis. According to Pander *et al.* (1992), test day yield was defined as the sum of all weighings of milk in a 24-h period.

The first interval in days for the first test was defined as date of recorded test day minus date of calving. Records with a first interval less than four or greater than

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Estação Experimental de Zootecnia de Ribeirão Preto IZ/CPA/SAA-SP, Av. Bandeirantes, 2419, 14030-670 Ribeirão Preto, SP, Brasil. Send correspondence to M.A.R.F.

45 days were eliminated for further analysis. Because test days do not always follow a regular interval of 30 days, interval classes of 30 days were created to make the 10 test days uniform. Test day records after 305 days were eliminated. Lactations with at least two test day records were used (Meyer *et al.*, 1989), or heritabilities and correlations for the first two tests were taken from the analysis of records of cows with at least two valid tests. Lactation records were discarded when the sire had less than five daughters, or when all the daughters were in the same herd.

Finally, a data set (Table I) of 17,968 test day records from 2,130 first lactations of Holstein cows, sired by 136 bulls, was used for further analysis. The 305-d milk yield was computed according to the method proposed by the Ministry of Agriculture (MAARA, 1986).

Two calving seasons were considered: the rainy season, October through March, and the dry season, April through September. Herd-year-season subclasses with at least four observations were used in the analysis. Age at calving was split into five classes (1.5 to 2.1; 2.2 to 2.4; 2.5 to 2.7; 2.8 to 3.1, and 3.2 to 3.5 years). Four classes were defined for the calving to first test day interval (from day 4 to day 14; 15 to 24; 25 to 35, and 36 to 45). Data were analyzed under restricted maximum likelihood, with the software MTDFREML (Multiple Trait Derivative-Free Restricted Maximum Likelihood), by Boldman *et al.* (1995). A sire model was used:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Za} + \mathbf{e}$$

where **y** = vector of dependent variables (M1 to M10 and M305), β = vector of fixed effects (age class, herd-year-season, interval calving-first control class), **X e Z** = design matrices for fixed and random effects, **a** = vector of sire effects, **e** = vector of residual effects. $E(\mathbf{y}) = X\beta$; $E(\mathbf{a}) = E(\mathbf{e}) = 0$. $Var(\mathbf{a}) = G = G_0 \otimes I_t$ and $Var(\mathbf{e}) = R = R_0 \otimes I_n$, where $\mathbf{G_0}$ = matrix of additive genetic covariance between the traits within sire, $\mathbf{R_0}$ = matrix of residual covariance between traits within animal, **I** = identity matrix of order n (number of records) or t (number of sires), $\otimes$ = direct product operator.

Preliminary analysis on data set from Table I indicated that there was no significant effect of class of calving to first test day interval on test day milk yields from the third test day on, so that this effect was considered only for M1 and M2. Convergence criterion was defined for simplex variance below 10^{-9}.

RESULTS AND DISCUSSION

Mean milk yield has the typical form of a lactation curve with the highest value occurring at M3 (Table II). In general, standard deviations were similar across test day records except for M6 and M7.

Estimates of heritabilities and the genetic and phenotypic correlations between each M and M305 (Table III)

Table I - The data set structure for the analysis of test day milk yields (M1-M10) in first lactations of Holstein cows.*

	Test day									
	M1	**M2**	**M3**	**M4**	**M5**	**M6**	**M7**	**M8**	**M9**	**M10**
Number of records	1298	1674	1749	1650	1673	1594	1517	1535	1387	1291
Number of sires	136	136	136	136	136	136	136	136	134	130
Herd-year-season subclasses	138	164	168	159	159	153	153	145	138	132
Class of age at calving	5	5	5	5	5	5	5	5	5	5
Class of calving to first test day interval	3	4	4	4	4	4	4	4	4	4
Number of herds	56	64	60	61	64	60	61	60	57	52

* M1 was taken from the first 30 days of lactation, M2 from the second, etc.

Table II - Observed means ($\overline{X}$), number of observations (N) and standard deviations (SD) of test day milk yields (M1 to M10) of first lactation Holstein cows.

Trait	**M1**	**M2**	**M3**	**M4**	**M5**	**M6**	**M7**	**M8**	**M9**	**M10**
N	1298	1674	1749	1650	1673	1594	1517	1535	1387	1291
$\overline{X}$ (kg)	21.8	23.6	23.3	22.1	20.9	19.7	18.3	17.3	16.0	15.0
SD (kg)	4.7	4.6	4.5	4.4	4.3	4.3	4.3	4.3	4.3	4.2

Table III - Heritability estimates (h^2) of test day milk yields (M1 to M10), and genetic (r_g) and phenotypic (r_p) correlations of test day milk yields and 305-day milk yield (M305).

Trait	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M305
h_2	0.20	0.20	0.20	0.20	0.32	0.20	0.24	0.16	0.12	0.04	0.32
r_g	1.00	0.80	0.92	0.96	0.89	0.95	1.00	0.93	0.78	1.00	
r_p	0.56	0.64	0.97	0.97	0.76	0.78	0.95	0.91	0.74	0.73	

followed trends in the literature, with higher values found in the second half of lactation, between M5 and M7 (Meyer *et al.*, 1989; Pander *et al.* 1992). In most reports, estimates were similar to heritability for M305. These published results suggested that test day records for mid-lactation could be used instead of M305 in genetic evaluations of dairy animals, but in none of the studies mentioned the estimates of heritability exceed those obtained for M305. This early selection can reduce generation interval. For M9 and M10, heritabilities were lower than those presented by Meyer *et al.* (1989), Rekaya *et al.* (1995) and Danell (1982). However, Kathenbrink and Swalve (1993), cited by Swalve (1995b), found heritability estimates of 0.09 and 0.05 for the last two test day milk yields, respectively.

Considerable differences in heritability estimates are found in the literature, due to differences in populations, different methods of analysis and, especially, how a trait is defined. In a study where several definitions for test day milk yield were analyzed simultaneously, Swalve (1995a) noted that yields defined as the average yield in a standardized 30-day interval resulted in higher estimates of heritability than for a non-standardized interval. He indicate that the use of standardized intervals can remove some of the problems that arise when different intervals between test days are used, especially between calving and first test day. Selection of sires and dams also can affect estimates. Auran (1976) reported slightly larger estimates from data where cows were not culled.

Genetic correlations between M1 and M305 varied from 0.78 to 1.00. Also, higher values were found in mid-lactation. However, other reports (Keown and Van Vleck, 1971; Pander *et al.*, 1992; Ribas *et al.*, 1994) have found significantly lower values, with genetic correlations between M1 and M305 and between M10 and M305 equal to 1.0. Moreover, when MTDFREML is used in the estimation of genetic correlations, there is a tendency for the estimates to reach +1 or -1, and the convergence to reach a local maximum. This may indicate the need for a larger data set to obtain better estimates (Van Vleck, 1992).

Rekaya *et al.* (1995) found the highest genetic correlation between the first test and M305 (0.89), but in the second half of the lactation genetic correlations between test day milk yields and M305 tended to decrease. Estimates for genetic correlations were higher than those found for phenotypic correlations, which followed the same trend in the literature, where smaller values were found in first and last test days, and the largest were in mid-lactation.

Tabela IV - Estimates of (co)variance components for test day milk yields (M) and 305-day milk yield (M305) obtained from one- and two-trait analysis.

M	σ^2_{aM}	σ^2_{aM305}	σ^2_{eM}	σ^2_{eM305}	$\sigma_{aM.M305}$
M1	4.28	114790	20.33	1920399	349.99
M2	4.32	141337	19.19	1754041	314.31
M3	3.76	163465	18.23	1843858	361.25
M4	3.68	99591	17.88	1798534	291.25
M5	5.36	164170	17.02	1778038	424.44
M6	3.72	101610	16.60	1852868	291.33
M7	3.68	114085	17.14	1850793	387.47
M8	2.44	126534	17.22	1815131	281.22
M9	1.96	87981	17.13	1767947	164.51
M10	0.72	109261	17.23	1695703	143.29
MP305	-	163465	-	1843858	-

σ^2_{aM}: Additive genetic variance of M; σ^2_{aM305}: additive genetic variance of M305; σ^2_{eM}: residual variance of M; σ^2_{eM305}: residual variance of M305; $\sigma_{aM.M305}$: genetic covariance between M and M305.

Residual variances were significantly larger in the first three test days (Table IV). These results are in accordance with Meyer *et al.* (1989) and Gadini (1997). Meyer *et al.* (1989) used univariate models with age at the test and days in milk as covariables, and they used herd year season (HYS) and herd test date (HTD) as fixed effects to fit test day production traits. They observed that including HTD in the model considerably reduced residual variances. Unfortunately, in our study we could not include HTD as a covariable because of the small data set.

CONCLUSIONS

This study has shown that genetic correlations between test day milk yields and 305-day milk yield are high and positive, indicating that test day milk yields could be utilized in place of M305 in genetic evaluations of dairy animals. The highest estimates of heritability in mid-lactation suggested that these test day yields (M5-M7) could be used as the selection criteria, leading to a reduction in generation interval.

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RESUMO

No presente estudo foram utilizados 17.968 registros de produção de leite, referentes a 2130 primeiras lactações de vacas da raça Holandesa, paridas nos anos de 1988 a 1991, filhas de 136 touros e controladas pela Associação Brasileira de Criadores (ABC). Os dados foram distribuídos em dez sub-arquivos de acordo com o número do controle (M1 a M10). As características estudadas foram: produção de leite no dia do controle (M) e produção aos 305 dias de lactação (M305), as quais foram ajustadas para os seguintes fatores de variação: idade da vaca ao parto em classes, intervalo parto-primeiro controle e subclasses de rebanho-ano-estação de parto. Os componentes de (co)variância foram obtidos a partir de análises com duas características utilizando-se o método REML, sob um modelo de touro. As estimativas de herdabilidade para as M variaram de 0,04 a 0,32 sendo os maiores valores encontrados na segunda fase da lactação (M5 a M7), enquanto que para a M305 este valor foi 0,32. As correlações genéticas entre as M e a M305 variaram de 0,78 a 1,00. Os resultados sugerem que as M podem ser utilizadas em substituição à M305 nas avaliações genéticas dos animais, visto que as herdabilidades no meio da lactação foram semelhantes à encontrada para a M305. Além disso, a seleção antecipada pode levar a uma redução no intervalo de gerações.

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