

Genetic parameters of milk, fat, and protein yields in the first three lactations, using an animal model and restricted maximum likelihood*

L.G. Albuquerque^{1,2}, J.F. Keown² and L.D. Van Vleck³

ABSTRACT

Milk, fat, and protein yields of Holstein cows from the States of New York and California in the United States were used to estimate (co)variances among yields in the first three lactations, using an animal model and a derivative-free restricted maximum likelihood (REML) algorithm, and to verify if yields in different lactations are the same trait. The data were split in 20 samples, 10 from each state, with means of 5463 and 5543 cows per sample from California and New York. Mean heritability estimates for milk, fat, and protein yields for California data were, respectively, 0.34, 0.35, and 0.40 for first; 0.31, 0.33, and 0.39 for second; and 0.28, 0.31, and 0.37 for third lactations. For New York data, estimates were 0.35, 0.40, and 0.34 for first; 0.34, 0.44, and 0.38 for second; and 0.32, 0.43, and 0.38 for third lactations. Means of estimates of genetic correlations between first and second, first and third, and second and third lactations for California data were 0.86, 0.77, and 0.96 for milk; 0.89, 0.84, and 0.97 for fat; and 0.90, 0.84, and 0.97 for protein yields. Mean estimates for New York data were 0.87, 0.81, and 0.97 for milk; 0.91, 0.86, and 0.98 for fat; and 0.88, 0.82, and 0.98 for protein yields. Environmental correlations varied from 0.30 to 0.50 and were larger between second and third lactations. Phenotypic correlations were similar for both states and varied from 0.52 to 0.66 for milk, fat and protein yields. These estimates are consistent with previous estimates obtained with animal models. Yields in different lactations are not statistically the same trait but for selection programs such yields can be modelled as the same trait because of the high genetic correlations.

INTRODUCTION

Dairy sire evaluations mainly use first lactation records or repeated records assuming correlation of unity among yields in different lactations. These two procedures assume that first lactation yields can

provide adequate information about later lactation yields, implying that the same genes influence first and later lactation yields. The main benefit obtained by using later lactations for sire evaluation is the increased accuracy of evaluation that occurs mainly due to the increase in the number of ties among sires (Ufford *et al.*, 1979 and Meyer, 1983). Advantages and disadvantages of using first lactation only, or including later lactations, for dairy cattle evaluation have been extensively discussed (e.g., Cassell and McDaniel, 1983). There is reasonable agreement to include later lactations in dairy cattle evaluation (Cassell and McDaniel, 1983 and Meyer, 1983). Estimates of genetic correlations for yields across lactations have been estimated with sire

* Nebraska Agricultural Research Division. Journal Series No. 10794, University of Nebraska, Lincoln, NE 68583-0908, USA.

¹ Departamento de Melhoramento Genético Animal, Faculdade de Ciências Agrárias e Veterinárias de Jaboticabal (FCAVJ), Universidade Estadual Paulista (UNESP), 14870-000 Jaboticabal, SP, Brasil.

² Department of Animal Science, University of Nebraska, Lincoln, NE 68583-0908, USA.

³ Roman L. Hruska US Meat Animal Research Center, ARS, USDA A218 Animal Sciences, University of Nebraska, Lincoln, NE 68583-0908, USA

models (Rothschild and Henderson, 1979; Tong *et al.*, 1979; Meyer, 1984 and 1985) and animal models (Swalve and Van Vleck, 1987 and Visscher and Thompson, 1992). In general, estimates are similar and above 0.80. However, a repeatability model assumes not only genetic correlations of unity, but also equal variances and similar influences of fixed effects across lactations. Since 1987, dairy cattle evaluations in the US have used a repeated records animal model with a scale factor to adjust for higher phenotypic variances in later lactations (Wiggans *et al.*, 1988). Multiple-trait analysis, considering different lactation yields as different traits, would be more demanding in computational time but could take into account differences in variances, fixed effects, and possible bias in later lactations from selection in early lactations. Estimates of genetic and phenotypic parameters for yields across lactations based on an animal model using REML with large data sets have not been available in the US. Thus, objectives of this study were to estimate genetic and phenotypic variances and covariances among lactations separately for milk, fat, and protein yields using an animal model and REML for much larger samples than previously used in such analyses, and to determine if yields in different lactations can be considered to be one trait.

MATERIAL AND METHODS

The data consisted of 305 days, twice daily milking, mature equivalent yields for milk, fat, and protein in the first, second and third lactations of California (CA) and New York (NY) Holstein cows

calving from 1986 to 1990 and from 1981 to 1990, respectively. The yields were preadjusted for age using multiplicative factors currently applied by US Department of Agriculture. There is indication that age factors should be developed within parity group (Wiggans and VanRaden, 1994). However, these factors were not available and the inclusion of age-season effects in the model for each trait would drastically increase computational time making the analysis impractical. Lactations with less than 240 days or without protein records were excluded. First lactation yield was required for all cows, and additional lactations were used only if the previous one was recorded. Only cows first freshening by 1988 were used so that each cow had the opportunity for a second and a third lactation. All herds had cows recorded in at least 3 years. The minimum acceptable number of cows for a herd to be included in the study was 100 for CA and 50 for NY. After editing, the data consisted of 110,777 records of 54,634 cows from CA and 118,820 records of 55,427 cows from NY. The records from each state were randomly assigned to 10 subsets according to the herd code so that all animals in the same herd were kept in the same sample. The structure of the samples is summarized in Table I.

Yields for first, second, and third lactations were considered as different traits. Milk, fat, and protein yields were analyzed separately because a nine trait analysis was not possible. Therefore, not all yields on which selection might have been practiced were included in the analyses. The percentages of cows having second and third lactations were, respectively, 66 and 36 for CA data and 70 and 45 for NY data. The

Table I - Summary of the data structure.

Order or number	California			New York		
	Mean	Minimum	Maximum	Mean	Minimum	Maximum
Records						
First lactation	5463	4611	5940	5543	5296	5876
Second lactation	3629	3067	4129	3860	3580	4048
Third lactation	1985	1700	2307	2479	2308	2653
Herd-year-seasons						
First lactation	130	97	168	1111	932	1244
Second lactation	159	122	209	1080	891	1233
Third lactation	122	96	161	904	744	1043
Animals in relationship matrix	9220	7080	10,438	9275	8883	9722
Mixed model equations	28,070	21,663	31,752	30,920	29,471	32,231

structure of the samples from CA and NY was similar, but the number of herd-year-season effects was larger in NY due to smaller mean herd size.

Sample means for yields of milk, fat, and protein for first, second, and third lactations for CA and NY data are shown in Table II. Means for the three traits were larger for CA than for NY data, as reported by Dong *et al.* (1988).

The analyses were done using REML (Smith and Graser, 1986 and Graser *et al.*, 1987) with a multiple-trait animal model utilizing a derivative-free algorithm developed by Boldman and Van Vleck (1991) and Boldman *et al.* (1993).

The model was:

$$y = X\beta + Za + e$$

where y is a vector of yields in the first three lactations, β is a vector of fixed effects (herd-year-season), a is a vector of additive genetic values of animals, e is a vector of residual effects, X and Z are incidence matrices for fixed and random effects. $E(y) = X\beta$; $E(a) = 0$; and $E(e) = 0$. $\text{Var}(a) = G = G_0 \otimes A$ and $\text{Var}(e) = R = R_0 \otimes I_N$, where G_0 is the variance-covariance matrix for additive genetic effects among traits within animals; \otimes is the direct product operator; A is the numerator relationship matrix; R_0 is the variance-covariance matrix for residual effects among traits within animals; and I is an identity matrix of order equal to the number of animals. Covariances between genetic and environmental effects

and between environmental effects for records of different animals were assumed to be zero.

Three seasons of freshening were defined for CA (January to April, May to August, and September to December) and four seasons for NY (January to March, April to June, July to September, and October to December). Seasons were selected based on the average yield distribution by year and month of calving and agree with the seasons used for National Evaluation for cows and sires.

Convergence was assumed when the simplex variance reached less than 10^{-9} . All analyses were restarted to check for occurrence of local maxima. The time necessary for each likelihood evaluation was much larger for NY than for CA data, because of the larger number of herd-year-season effects in NY. Estimates of variances and covariances from each sample were pooled by arithmetic averaging and were used to calculate empirical SE of the averages.

Log-likelihood ratio tests, according to Dobson (1990), were used to test the hypothesis that the genetic correlations among yields in different lactations were unity. Two models were fitted: first, a model assuming genetic correlations equal to 0.998 and second, a complete model, using estimates of all genetic and environmental (co)variances. Twice the difference between the minimized log-likelihoods from the first and second models, respectively, was compared to a chi-square distribution with degrees of freedom equal to the difference in number of parameters estimated in each model.

Table II - Sample means, maximums, and minimums of yields (kg) for milk, fat, and protein in first, second, and third lactations.

	California			New York		
	Mean	Minimum	Maximum	Mean	Minimum	Maximum
Milk						
First lactation	10,198	9,885	10,485	8503	8320	8715
Second lactation	10,923	10,596	11,170	8927	8728	9163
Third lactation	10,796	10,624	11,050	8960	8808	9165
Fat						
First lactation	368	354	391	309	299	316
Second lactation	388	379	396	324	317	332
Third lactation	383	361	396	325	317	333
Protein						
First lactation	313	303	323	270	264	276
Second lactation	338	329	349	285	281	294
Third lactation	340	334	352	288	282	294

RESULTS AND DISCUSSION

Pooled estimates of genetic, environmental, and phenotypic (co)variances for yields of milk, fat, and protein in the first, second, and third lactations are presented in Table III.

For CA, the genetic variance of yield traits increased from first to second lactation and remained the same for the third lactation, except for milk yield. Environmental variance increased with lactation number; the largest change occurred from first to second lactation. Environmental variance increased in magnitude more than genetic variance; consequently, heritabilities for yields of milk, fat, and protein from CA

Table III - Mean^a estimates of genetic (g), environmental (e), and phenotypic (p) variances (σ^2), and covariances (σ) for yields of milk ($\text{kg}^2/1000$), fat, and protein (kg^2) in the first (1), second (2), and third (3) lactations for 10 samples from each state.

	California			New York		
	Milk	Fat	Protein	Milk	Fat	Protein
σ_{g1}^2	656	855	625	517	772	412
σ_{g2}^2	725	1073	790	573	1097	587
σ_{g3}^2	615	1046	766	527	1072	573
σ_{e1}^2	1293	1602	927	951	1126	813
σ_{e2}^2	1587	2219	1211	1130	1383	928
σ_{e3}^2	1600	2285	1290	1095	1393	930
$\sigma_{g1,2}$	596	851	636	472	836	430
$\sigma_{g1,3}$	481	784	575	424	782	397
$\sigma_{g2,3}$	629	1021	751	533	1066	567
$\sigma_{e1,2}$	651	803	427	450	468	379
$\sigma_{e1,3}$	600	712	359	387	380	304
$\sigma_{e2,3}$	793	1025	578	497	504	414
$\sigma_{p1,2}$	1247	1654	1064	922	1304	809
$\sigma_{p1,3}$	1081	1496	933	811	1162	701
$\sigma_{p2,3}$	1422	2046	1329	1030	1570	981

^a Empirical standard errors varied from 22 to 129 for estimates of genetic variances; from 24 to 89 for estimates of environmental variances; from 21 to 126 for estimates of genetic covariances; from 18 to 76 for estimates of environmental covariances, and from 14 to 56 for estimates of phenotypic covariances.

data decreased with lactation number (Table IV). Similar patterns were described by Rothschild and Henderson (1979), Meyer (1984), and Visscher and Thompson (1992). Tong *et al.* (1979), using a sire model, also reported an increase in environmental variance with the order of lactation, but sire variances remained constant across lactations. The increase in environmental variance in later lactations can be caused by various factors that do not influence first lactation, such as days dry, days open, and injuries (Tong *et al.*, 1979 and Cassell and McDaniel, 1983). Estimates for NY showed almost the same pattern as for CA except that the increase in the environmental variance was not proportionally larger than for the genetic variance. Consequently, heritability estimates did not decrease with lactation number.

Heritability estimates for milk yield (Table IV) were similar for both data sets. These estimates were larger than those obtained by Tong *et al.* (1979) and Meyer (1984), but smaller than those reported by Rothschild and Henderson (1979) using a sire model. However, Rothschild and Henderson (1979) used a maximum likelihood method, which does not account for the loss in degrees of freedom associated with fixed effects; they also performed only three rounds of iteration. Heritability estimates of milk yield across lactations for US Holstein cows, obtained with animal model and REML, were reported by Swalve and Van Vleck (1987) and Dong and Van Vleck (1989). Swalve and Van Vleck (1987) reported mean heritability estimates of 0.33, 0.33, and 0.34 after only 18 rounds of iteration for milk yields of first, second, and third lactations, using two data sets with 3070 and 2900 cows. Dong and Van Vleck (1989) estimated heritabilities of 0.27 for first and 0.25 for second lactation milk yield after only 20 rounds of iteration for two samples with 2137 and 2190 cows. In those studies, relationships across herds were ignored. Estimates obtained using an animal model by Visscher and Thompson (1992) for British Holstein cows were 0.40, 0.33, and 0.30 for milk yields of first, second, and third lactations.

Heritability estimates for fat yield were larger but not significant for NY data than for CA data. Heritabilities of protein yield were larger for CA than NY in the first lactation but were almost the same for both data sets in the second and third lactations. The present estimates were larger than those estimated with a sire model (Tong *et al.*, 1979 and Meyer, 1984). The only previous estimates obtained using an animal model for fat and protein yields were, respectively, 0.37 and 0.36 for first, 0.31 and 0.30 for second, and 0.29 and 0.31 for third lactations (Visscher and Thompson, 1992). Heritability estimates for yields of fat and protein in the

Table IV - Means^a and (ranges) of estimates of heritabilities (h^2) and genetic (g), environmental (e), and phenotypic (p) correlations (r) for milk, fat and protein yields in the first (1), second (2), and third (3) lactations for 10 samples from each State.

	California			New York		
	Milk	Fat	Protein	Milk	Fat	Protein
h_1^2	0.34 (0.23 - 0.53)	0.35 (0.19 - 0.48)	0.40 (0.21 - 0.63)	0.35 (0.29 - 0.41)	0.40 (0.33 - 0.48)	0.34 (0.26 - 0.46)
h_2^2	0.31 (0.18 - 0.55)	0.33 (0.22 - 0.42)	0.39 (0.22 - 0.63)	0.34 (0.20 - 0.43)	0.44 (0.25 - 0.58)	0.38 (0.27 - 0.61)
h_3^2	0.28 (0.16 - 0.41)	0.31 (0.22 - 0.44)	0.37 (0.22 - 0.59)	0.32 (0.23 - 0.39)	0.43 (0.22 - 0.62)	0.38 (0.23 - 0.61)
$r_{g1,2}$	0.86 (0.74 - 0.97)	0.89 (0.81 - 0.97)	0.90 (0.81 - 0.98)	0.87 (0.74 - 0.96)	0.91 (0.80 - 0.97)	0.88 (0.79 - 0.95)
$r_{g1,3}$	0.77 (0.65 - 0.87)	0.84 (0.67 - 0.95)	0.84 (0.72 - 0.94)	0.81 (0.72 - 0.90)	0.86 (0.76 - 0.95)	0.82 (0.73 - 0.89)
$r_{g2,3}$	0.96 (0.88 - 1.00)	0.97 (0.93 - 1.00)	0.97 (0.93 - 1.00)	0.97 (0.92 - 1.00)	0.98 (0.94 - 1.00)	0.98 (0.94 - 1.00)
$r_{e1,2}$	0.44 (0.22 - 0.54)	0.42 (0.34 - 0.47)	0.38 (0.04 - 0.52)	0.43 (0.37 - 0.47)	0.37 (0.21 - 0.47)	0.43 (0.32 - 0.51)
$r_{e1,3}$	0.42 (0.31 - 0.49)	0.37 (0.31 - 0.46)	0.32 (0.12 - 0.43)	0.38 (0.32 - 0.42)	0.30 (0.14 - 0.39)	0.35 (0.21 - 0.41)
$r_{e2,3}$	0.50 (0.39 - 0.56)	0.46 (0.38 - 0.51)	0.45 (0.13 - 0.56)	0.45 (0.38 - 0.54)	0.35 (0.14 - 0.51)	0.42 (0.19 - 0.53)
$r_{p1,2}$	0.59 (0.55 - 0.62)	0.58 (0.56 - 0.60)	0.60 (0.57 - 0.63)	0.58 (0.55 - 0.60)	0.60 (0.57 - 0.62)	0.59 (0.56 - 0.63)
$r_{p1,3}$	0.52 (0.50 - 0.55)	0.52 (0.50 - 0.56)	0.52 (0.48 - 0.55)	0.53 (0.50 - 0.55)	0.55 (0.50 - 0.70)	0.52 (0.49 - 0.55)
$r_{p2,3}$	0.63 (0.59 - 0.65)	0.62 (0.58 - 0.65)	0.66 (0.62 - 0.69)	0.62 (0.59 - 0.65)	0.63 (0.61 - 0.67)	0.65 (0.61 - 0.69)

^a Empirical standard errors varied from 0.01 to 0.04 for heritability estimates; from 0.01 to 0.03 for estimates of genetic correlations; from 0.01 to 0.05 for estimates of environmental correlations; and from 0.01 to 0.02 for estimates of phenotypic correlations.

first lactation using an animal model have varied from 0.26 to 0.46 for fat and from 0.22 to 0.40 for protein (Dong *et al.*, 1988; Van Vleck and Dong, 1988; Van Vleck *et al.*, 1988 and Misztal *et al.*, 1992).

According to various reports (DeVeer and Van Vleck, 1987 and Boldman and Freeman, 1990) heritability estimates may increase with production level and phenotypic variance. Average production levels were larger for CA data but heritability estimates were not consistently larger for CA than MY. These results may be associated with more complete relationship matrices for NY than CA because there was a difference in the period for which yields were measured, 9 and 4 years, respectively. In addition, a smaller fraction of non-zero off-diagonal elements was in the inverse of relationship matrix for CA data than for NY data, respectively, 1.33 and 1.71 on average, similar to those reported by Dong *et al.* (1988).

The magnitude of heritability estimates (Table IV) for the three yield traits varied widely among samples but, on average, agreed with REML estimates obtained using an animal model with fewer data and only a few rounds of iteration and, as expected, were larger than those estimated from sire models.

The genetic, environmental, and phenotypic covariances (Table III) were consistently larger between

adjacent and later lactations as observed by Majjala and Hanna (1974), Tong *et al.* (1979), and Meyer (1984). Estimates of correlations were similar for both data sets (Table IV). All estimates of genetic correlations, except those between milk yield for first and third lactations in CA, were greater than 0.80. A summary of estimates of correlations from the literature is presented in Table V. The results of the present paper agreed with those obtained with maximum likelihood and sire model (Rothschild and Henderson, 1979), REML and sire model (Tong *et al.*, 1979; Meyer, 1984 and 1985 and Banos and Shook, 1990), REML and animal model (Dong and Van Vleck, 1989; Swalve and Van Vleck, 1987 and Visscher and Thompson, 1992), and other methods (Majjala and Hanna, 1974). All estimates are similar and greater than 0.80, although Cassell and McDaniel (1983) indicated that conclusions varied. If the genetic correlations are indeed equal to 1, then yields in different lactations can be considered to be the same trait. First lactation yields would provide accurate information about later lactations. The use of a repeatability model for sire evaluation also would be justified (Tong *et al.*, 1979; Meyer, 1983 and 1984, and Swalve and Van Vleck, 1987). However, Majjala and Hanna (1974), Banos and Shook (1990), and Visscher and Thompson (1992) reported that yields for first and

later lactations cannot be considered to be the same trait, because the genetic correlations among lactations are not equal to 1. In such a case, the use of first lactation yields only or a repeatability model for sire evaluation is not appropriate and would reduce genetic progress (Visscher *et al.*, 1992). In the present study, the results of likelihood ratio tests indicated that genetic correlations among yields in different lactations are significantly different from one. Thus, in a statistical sense, yields across lactations are not the same trait. However, Robertson (1959) suggested that a genetic correlation must be less than 0.80 to be considered important for purposes of selection. The use of first lactation yields and a repeatability model for sire evaluation have been compared with a multiple-trait model, and the increase in accuracy was not large. Meyer (1983) compared first lactation versus first and second lactation multiple trait models for sire evaluation, using a genetic correlation of 0.91 between milk yield across lactations. Meyer found an increase in accuracy of 5 to 6% using multiple-trait analysis; half of this increase was due to stronger connections among sires. The rank correlations

between the breeding values estimated using those two models were close to 1. Visscher *et al.* (1992) reported that the use of a modified repeatability model for sire evaluation, with different variances and heritabilities across lactations, was as efficient as a multiple-trait model. However, they also found that the predicted response to selection obtained using the modified repeatability model was overestimated by 10%.

Environmental correlations were larger between second and third lactations and were similar for NY and CA data, except that correlations among fat yields for NY data were smaller but not significant (Table IV).

Phenotypic correlations varied, on average, from 0.52 to 0.63 for milk and fat yields and from 0.52 to 0.66 for protein yield. These results are larger than the average repeatability estimates between consecutive records summarized by Majjala and Hanna (1974) of 0.49 for milk and fat yields. Estimates of phenotypic correlations between yields of first and second lactation and between first and third lactation agree with those estimated with sire and animal models (Table V).

Table V - Previous estimates of genetic and phenotypic correlations for yield traits.

Trait and references	Genetic correlation for lactations			Phenotypic correlation for lactations		
	1 and 2	1 and 3	2 and 3	1 and 2	1 and 3	2 and 3
Milk						
Majjala and Hanna (1974)	0.81 - 0.87	0.80 - 0.85	0.99 - 1.03			
Tong <i>et al.</i> (1979)	0.89	0.85	0.89			
Rothschild and Henderson (1979)	0.92			0.56		
Meyer (1984)	0.92	0.91	0.96	0.54	0.54	0.58
Meyer (1985)	0.96			0.58		
Banos and Shook (1990)	0.82 - 0.86	0.77 - 0.84	1.00 - 1.10			
Swalve and Van Vleck (1987 ¹)	0.86	0.85	0.87	0.57	0.52	0.65
Dong and Van Vleck (1989 ¹)	0.82			0.58		
Visscher and Thompson (1992 ¹)	0.87	0.84	0.98	0.58	0.54	0.60
Fat						
Tong <i>et al.</i> (1979)	0.90	0.87	0.90			
Meyer (1984)	0.92	0.91	0.99	0.52	0.50	0.55
Meyer (1985)	0.98			0.54		
Visscher and Thompson (1992 ¹)	0.86	0.85	0.97	0.56	0.51	0.57
Protein						
Tong <i>et al.</i> (1979)	0.83					
Meyer (1984)	1.00			0.52		
Visscher and Thompson (1992 ¹)	0.86	0.82	0.98	0.58	0.52	0.61

¹Estimates obtained with animal models.

Phenotypic correlations between second and third lactations are larger than those obtained with a sire model but agree with estimates with an animal model.

The model used in these analyses did not include group effects to account for selection prior to when the records were made. For both states not many years were involved, especially for CA because of lack of protein testing in earlier years. Incorporation of selection group effects in the model would substantially increase computer time. A study of whether the heritability and correlation estimates would change in any important way is suggested as a future, although time-consuming, project.

CONCLUSIONS

Estimates of heritability for yields of milk, fat, and proteins were moderate and consistent with previous estimates obtained with animal models. Genetic and environmental variances were not the same for the three lactations. Genetic correlations among yields in different lactations were consistently close to unity, indicating that yields in all lactations were determined to a large extent by the same genes. However, the genetic correlations were significantly different from one. Thus, multiple-trait models considering yields in different lactations as different traits for sire evaluations could be considered. There is evidence that because of the high correlations, in terms of accuracy, a modified repeatability model, considering different variances across lactations, is as efficient as a multiple-trait model (Visscher *et al.*, 1992). The practical aspects of using multiple-trait models for genetic evaluations, considering the increase in computer time and costs versus the potential increase in accuracy and genetic response, must be investigated.

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RESUMO

Produções de leite, gordura e proteína no leite de vacas da raça Holandesa mantidas nos estados de Nova York

e Califórnia foram utilizadas com o objetivo de estimar (co)variâncias entre produções nas primeiras três lactações usando modelo animal e máxima verossimilhança restrita e verificar se produções em diferentes lactações são a mesma característica. Os dados foram divididos em 20 amostras, 10 de cada estado, com média por amostra de 5463 vacas da Califórnia e 5543 vacas de Nova York. As médias das estimativas de herdabilidade para produção de leite, gordura e proteína nos dados da Califórnia foram, respectivamente, 0,34; 0,35 e 0,40 para a primeira; 0,31; 0,33 e 0,39 para a segunda; e 0,28; 0,31 e 0,37 para a terceira lactação. Nos dados de Nova York, as estimativas foram: 0,35; 0,40 e 0,34 para a primeira; 0,34; 0,44 e 0,38 para a segunda; e 0,32; 0,43 e 0,38 para a terceira lactação. As médias das estimativas de correlações genéticas entre produções na primeira e segunda, primeira e terceira e segunda e terceira lactações, na Califórnia, foram: 0,86; 0,77 e 0,96 para a produção de leite; 0,89; 0,84 e 0,97 para a produção de gordura e 0,90; 0,84 e 0,97 para a produção de proteína. Para o estado de Nova York as médias destas estimativas foram: 0,87; 0,81 e 0,97 para leite; 0,91; 0,86 e 0,98 para gordura; 0,88; 0,82 e 0,98 para proteína. As correlações ambientais variaram de 0,30 a 0,50 e foram maiores entre a segunda e terceira lactações. As correlações fenotípicas foram similares nos dois estados e variaram de 0,52 a 0,66 para produções de leite, gordura e proteína. As estimativas são consistentes com as obtidas com modelos animais. Estatisticamente, produções em diferentes lactações não são a mesma característica. Entretanto, para seleção, podem ser modeladas como sendo a mesma característica, já que as correlações genéticas entre elas foram altas.

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