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# VARIANCE COMPONENTS AND GENETIC PARAMETER ESTIMATES UNDER VARYING DEFINITIONS OF CONTEMPORARY GROUPS

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## Abstract

A total of 19 385 test day (TD) milk yield records were used to determine the effect of contemporary group (CG) on estimates of variance components and genetic parameters for test day milk yield (TMY) data of Sahiwal cattle in Kenya. Variance components and genetic parameters were estimated based on a derivative free restricted maximum likelihood procedure (DFREML) using multivariate and univariate TD models that defined CG either based on the year-season of calving (YSCV) or on the year-season of TD milk sampling (YSTD). Additive genetic and permanent environmental variances were higher under the YSTD model than YSCV model across the 3 lactations. The estimates of heritability were higher in the YSTD model than in the YSCV model in all lactations under both analyses. The study has shown that fitting YSTD as CG allows for a direct correction for environmental affects specific to the day of recording of a cow's performance.

## Introduction

Genetic evaluation of dairy cattle is commonly based on either standardised or total lactation milk yield. This does not effectively account for effects that are specific to the changing production environment because contemporary groups (CG) are formed based only on the year-season of calving (Jamrozik and Schaeffer, 1997; Rekaya *et al.* 1999; Serrano *et al.* 2001). Use of test day (TD) milk yield data for genetic evaluations considers both genetic and environmental factors that are unique to a particular TD, which gradually and continuously change over the lactation period (Ptak and Schaeffer, 1993; Van der Werf *et al.*, 1998). In this case, CG can either be defined based on the year-season of calving (YSCV) or on the year-season of TD milk sampling (YSTD). Use of TD milk yield (TMY) data in genetic evaluation programmes requires accurate estimates of variance component and of genetic and phenotypic parameters of specific TD records. The accuracy of such estimates can be determined by the definition of CG in the model of analysis. The aim of this study was to determine the effect of CG on estimates of variance components and genetic parameters for TMY of Sahiwal cattle in Kenya.

## Materials and methods

### Data collection and editing

Data were obtained from the National Sahiwal Stud (NSS), which is maintained by Kenya Agricultural Research Institute at the National Animal Husbandry Research Centre in Naivasha. Test day records from the first 3 lactations obtained from 1978 to 2002 were used in this study. First TD was sampled between day 2 and 15 post partum, while the second TD was sampled between day 16 and 31. Time interval between successive tests was approximately 30 days allowing for a maximum of 8 TD. Test day milk yield was defined as the total sum of milk recorded in the morning and evening. Table 1 shows the characteristics of the data in different TD and in the first 3 lactations. Milk records of animals receiving special treatment were not included e.g. cows under training for livestock exhibitions and shows, and records of cows used in feeding experiments. Animals whose lactation was terminated by death, sale or due to bad temper and difficult milking were also removed. Lactations initiated as a result of abortions were also eliminated. As a result of these edits, the number of TD milk yield records was variable throughout the 8 TD (Table 1). The final analysis consisted of a total of 19 385 TD milk yield records from the first 3 lactations of daughters from 1,618 cows and 162 sires.

### Statistical methods

Variance components and genetic parameters were estimated using univariate and multivariate TD models. All runs were carried out using the DFREML software package (Meyer, 1989). Animal models were used throughout, incorporating all the pedigree information available. Variance components and genetic parameters were estimated based on 2 different definitions of CG. Contemporary groups were defined either based on the year-season of calving (YSCV) or on the year-season of TD milk sampling (YSTD).

Two sets of analyses were performed. In the first analysis, 2 multivariate repeatability models differing in the definition of CG were used. The repeatability TD model proposed by Ptak and Schaeffer (1993) was extended to a multiple trait model under which the TD milk yield records within lactation were considered as repeated traits and the 3 lactations treated as separate traits (Reents *et al.* 1995; Rekaya *et al.* 1999).

**Table 1**—Characteristics of data on different test days and in the first 3 lactations of Sahiwal cows at KARI Naivasha Kenya.

Data	TD								Lactation		
	1	2	3	4	5	6	7	8	1	2	3
No. of records	3259	2678	2330	2330	2397	2194	2016	2171	8403	6448	4534
Average DIM	7	23	53	83	117	147	178	212	-	-	-
% missing records <sup>1</sup>	0.0	17.8	28.5	28.5	26.4	32.7	38.1	33.3	0.0	23.3	46.0
Milk yield	6.0	6.4	5.6	4.8	4.2	3.7	3.4	3.0	4.4	5.0	5.0
SD	2.5	2.6	2.5	2.3	2.1	1.9	1.8	1.6	2.3	2.7	2.7
Min	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Max	17.0	17.0	14.5	14.5	12.0	10.5	10.5	11.5	14.5	14.5	17.0

<sup>1</sup>Percent missing records as compared with first lactation and TD milk yield records, TD-test day, DIM-days in milk, SD-Standard Deviation.

The shape of the lactation curve was accounted for by fixed regression of yield on days in milk (*DIM*), while the additive genetic effect of the animal was modelled as a constant for each *DIM*. The covariances between the residuals were assumed to be zero. The equation of the model applied in this case was as follows:

$$y_{ijklm} = \mu + CG_{im} + age_j + b(DIM_{klm}) + b^2(DIM_{klm}) + g_{km} + p_{km} + e_{ijklm} \quad 1$$

where  $y_{ijklm}$  is the TD milk yield in animal  $k$ , in lactation  $m$  ( $m = 1, 2, 3$ ) and TD  $l$  ( $l = 1, \dots, 8$ ),  $\mu$  is the population TD mean for cows in lactation  $m$ ,  $CG_{im}$  is the effect of CG  $i$  for cows in lactation  $m$  (in the first multivariate repeatability model,  $i = \text{YSCV}$  while  $i = \text{YSTD}$  in the second model),  $age_j$  is the fixed effect of age class  $j$  ( $j = 1, \dots, 8$ ),  $b$  and  $b^2$  are the linear and quadratic effect of *DIM* in animal  $k$  and lactation  $m$  on TD  $l$ , respectively,  $g_{km}$  is the additive genetic effect of animal  $k$  in lactation  $m$ ,  $p_{km}$  is the permanent environmental effect of animal  $k$  in lactation  $m$  and  $e_{ijklm}$  is the residual term. The year of calving or of TD sampling were from 1978 to 2002 each with 4 seasons: January to March for the first dry season; April to June for the main wet season; July to September and October to December as the secondary dry and wet seasons, respectively. Age at calving was grouped into 8 classes as; 30 to 39 months, 40 to 49 months, 50 to 59 months, 60 to 69 months, 70 to 79 months, 80 to 89 months, 90 to 99 months and >100 months.

In the second analysis, a univariate repeatability model was used within each lactation with CG alternatives defined as above. The model applied in this case was similar to that used in the first analysis but the effects were fitted within each lactation.

## Results and discussion

Table 2 shows the estimates of variance components and of heritability, repeatability and genetic and phenotypic correlations from multivariate models under 2 alternatives of CG (i.e., YSCV and YSTD). The estimates of variance components and of heritability and repeatability from univariate models under 2 alternatives of CG are shown in Table 3. Additive genetic and permanent environmental variances were higher under the YSTD model than YSCV model across the 3 lactations. This implies that detection of differences among animals, both at genetic and individual environmental level, is enhanced by assigning cows to YSTD than YSCV. The residual variances were lower in the YSTD model than in the YSCV model in all lactations and under both analyses. This indicates that more environmental variation is removed by comparing cows based on the TD than on the period of calving. Similar findings have also been reported in the Holstein-Friesian cattle (Rekaya *et al.* 1999) and in Machenga dairy ewes (Serrano *et al.*, 2001). A comparison of residual variances between lactations showed that they were highest in the third lactation in both models under both multivariate (Table 2) and univariate (Table 3) analyses. The large residual variance associated with lactation 3 could be due to changes in the mean lactation milk yield and other sources of variation not accounted for in the 2 models such as length of the dry and gestation periods influencing subsequent lactations. Increased residual variance in later lactations has also been reported elsewhere (Teepker and Swalve, 1988; Rekaya *et al.* 1999).

The estimates of heritability were higher in the YSTD model than in the YSCV model in all lactations under both multivariate (Table 2) and univariate (Table 3). This was attributed to a proportionally large increase in the additive genetic variance with a corresponding reduction in the residual variance in the YSTD model. Heritability estimates obtained under the YSTD model are within the range of estimates obtained for TD milk yield in Holstein-Friesian (Rekaya *et al.* 1999). Repeatability estimates were higher in the YSTD model apart from lactation one and 3 under both multivariate (Table 2) and univariate (Table 3) analyses. Repeatability estimate in the present study were comparable to those reported by Lidauer *et al.*, (2003). Genetic correlations were moderately high in the 2 models (Table 2). Phenotypic correlations were correspondingly lower than genetic correlation estimates. Genetic correlations were higher between lactation one and 3 in both models than between lactations one and two. To the contrary, phenotypic correlations were higher between adjacent lactations than non-adjacent ones. This is consistent with the results of Rekaya *et al.* (1999) in the Holstein-Friesian population in Spain.

**Table 2**—Additive genetic ( $\sigma_a^2$ ), permanent environmental ( $\sigma_{pe}^2$ ) and residual ( $\sigma_e^2$ ) variances, heritability ( $h^2$ ), genet and phenotypic correlation and repeatability (r) in the first 3 lactations under different multivariate repeatability models<sup>3</sup>

Model <sup>1</sup>	Lactation	Component			Lactation <sup>2</sup>			r
		$\sigma_a^2$	$\sigma_{pe}^2$	$\sigma_e^2$	1	2	3	
YSCV	1	0.78	1.32	1.86	0.20	0.63	0.66	0.53
	2	0.77	1.65	1.95	0.27	0.18	0.53	0.55
	3	0.94	1.39	2.11	0.24	0.30	0.20	0.54
YSTD	1	0.85	1.40	1.68	0.22	0.60	0.61	0.58
	2	1.32	1.45	1.67	0.29	0.30	0.61	0.52
	3	0.97	1.63	1.83	0.27	0.37	0.22	0.59

<sup>1</sup>See text for description of models.

<sup>2</sup>Heritabilities (diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations.

<sup>3</sup>Standard errors for heritability estimates and genetic correlations ranged from 0.04 to 0.06 and from 0.10 to 0.14 in the 2 models, respectively.

**Table 3**—Additive genetic ( $\sigma_a^2$ ), permanent environmental ( $\sigma_{pe}^2$ ) and residual ( $\sigma_e^2$ ) variances, heritability ( $h^2$ ) a repeatability (r) in the first 3 lactations under different univariate repeatability models<sup>2</sup>

Model <sup>1</sup>	Lactation	$\sigma_a^2$	$\sigma_{pe}^2$	$\sigma_e^2$	H <sup>2</sup>	r
YSCV	1	0.67	2.14	1.79	0.15	0.61
	2	0.62	2.40	1.94	0.13	0.60
	3	0.35	2.36	2.03	0.07	0.56
YSTD	1	0.78	2.02	1.62	0.18	0.64
	2	0.72	2.46	1.68	0.15	0.66
	3	0.44	2.44	1.83	0.09	0.61

<sup>1</sup>See text for description of models.

<sup>2</sup>Standard errors for heritability estimates ranged from 0.04 to 0.05, and 0.05 for the YSCV and YSTD mode respectively

## Conclusion

In this study it has been observed that variance components were affected by the CG (YSTD or YSCV) in both multivariate and univariate repeatability TD models. These resulted in differences in heritability and repeatability estimates between models. The results clearly show the importance of environmental effects specific to the season of test. Models in which YSTD was fitted were found to be superior to models in which YSCV was fitted. This was in terms of reduction in residual and increase in additive genetic variances.

Therefore, fitting YSTD as CG effect is recommended because it allows for a direct correction for effects specific to the day of recording of a cow's performance.

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