International Journal of
Veterinary Sciences
and Animal Husbandry

ISSN: 2456-2912
VET 2021; 6(2): 31-34
© 2021 VET
www.veterinarypaper.com
Received: 21-01-2021
Accepted: 23-02-2021

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Genetic evaluation of daily milk yield across days in milk of the Sahiwal cattle in Kenya

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DOI: https://doi.org/10.22271/veterinary.2021.v6.i2a.341

Abstract
Animals with the same lactation breeding value can have different shapes of the additive genetic lactation curve, implying differences in persistency of lactation. Since environmental conditions change across lactation, animals can re-rank through the lactation, leading to genotype by environment interaction for daily milk yield. The objectives of this project is to describe the genetic curve pattern of daily estimated breeding values and to assess the extent of sire and cow re-ranking for daily milk yield across lactation in Sahiwal cattle in Kenya. Random regression coefficients for each animal were obtained from random regression test day models using Legendre polynomials. Animals were ranked within day and rank correlations estimated using spearman's rank correlation. The best cows and sires were those from cluster 1. Based on the results, cluster analysis can be used to pre-select cows and sires before ranking and selection is carried out.

Keywords: Breeding values, lactation curve, random regression test day models, sahiwal

Introduction

Worldwide, random regression test day models (RRTDMs) are being widely adopted for genetic evaluation of dairy cattle (Interbull, 2014) [1]. This trend is because RRTDMs are able to more precisely define contemporary groups, enabling to directly account for short-term environmental factors specific to individual yields, a feature lacking in lactation models. This leads to improvements in the properties of the statistical model. RRTDMs use complete as well as incomplete lactations records, thereby overcoming the need to predict lactation milk yields. Additionally, use of incomplete lactation records provides an opportunity of shortening generation intervals. From a management perspective solutions obtained from RRTDMs can be used in decision making leading to improvements in herd management.

The feasibility of implementing RRTDMs in genetic evaluations in Sahiwal cattle in Kenya has been evaluated (Ooko *et al*., 2016) [2]. However, the extent of re-ranking of animals across lactation was not evaluated. This is preferred that animals selected based on lactation breeding values have superior daily breeding values across lactation. It has been shown that animals with different additive genetic curves can have similar lactation breeding values. This implies the possibility of selection animals with poor lactation persistency (Khorshidie *et al*., 2012) [3]. Such animals require supplementation with concentrates to maintain milk yield at desired levels, leading to increased cost of production. Those that are more persistent utilize more roughages that concentrates, and are therefore more economical milk producers (Dekkers *et al*., 1998) [4]. Genotype by environment interaction for daily milk yield across lactation has not been investigated and it is therefore not known whether cows or sires will re-rank across lactation. Random regression test day models are more efficient than lactation models in identifying superior animals in breeding programmes. However, the environmental sensitivity of daily milk yield across a lactation have been estimated. It is therefore not known whether sire and cow will re-rank across lactation, thereby hampering use of RRTDMs in Kenya's Sahiwal cattle breeding programme.

Materials and Methods

Source of data

First lactation test day milk yield (TD) records of Sahiwal cattle breed were obtained from the

National Sahiwal Stud, Naivasha. Each cow had at least 5 test day records, a sire and/or dam. Contemporary groups (CG) was determined as year-month of test day. Each contemporary group had at least 4 animals.

Statistical model and data analysis

To estimate covariance components for daily milk yield across first lactation

A random regression model with a 4^{th} order for the fixed, additive genetic and permanent environmental effects was fitted as follows:

$$y_{ijkl} = HTD_i + AC_j + \sum_{m=0}^{4} \beta_{jm} X_m(t) + \sum_{m=0}^{p} \alpha_{km} \phi_{a,m}(t) + \sum_{m=0}^{q} \gamma_{km} \phi_{p,m}(t) + (e_{ijkl})r$$

where y_{ijkl} = l^{th} TD milk yield for cow k; HTD_i = fixed effect of i^{th} herd-year-test day; AC_j =fixed effect due to the j^{th} age calving class; β_{jm} = m^{th} fixed regression coefficient describing the average population curve; $X_m(t)$= m^{th} covariate evaluated at DIM t; α_{km} = m^{th} random regression coefficient associated with daily additive genetic (AG) variance for animal k; γ_{km} = m^{th} random regression coefficient associated with daily permanent environmental (PE) variance for animal k; $\phi_{a,m}(t)$ and $\phi_{p,m}(t)$= m^{th} covariates depending on DIM, t; and $(e_{ijkl})r$ = error term, assumed to be independent and normally distributed and r=residual variance class assumed to be constant throughout lactation (Ooko *et al*., 2016) [2].

To explore the genetic curve pattern of EBVs for TDMY in Sahiwal cows

Cluster analysis was used to group individual animals based on their EBVs for daily milk yield along the lactation curve. Two cluster analyses: hierarchical and non-hierarchical, was performed to describe the additive genetic pattern of daily milk yield in the population. Hierarchical cluster analysis was used to choose the number of clusters into which the population can be grouped. The Euclidian distance was used to measure the distance between the cows and the ward (1963) cluster algorithm was then used to form the clusters. Non-hierarchical clustering using k-means method was then carried out to explore the genetic curve patterns based on EBVs for 30, 60, 90, 120, 150, 180, 210 and 240 DIM.

Estimated daily breeding values for sires and cows were estimated from the random regression coefficients. If $\hat{a}_i$ is a $K_a \times 1$ vector of additive random regression coefficients for animal I, and Z_t is a $K_a \times 1$ vector of Legendre polynomial coefficients evaluated at day t, in matrix notation, $\hat{a}_i$ and Z_t are:

$$\hat{\alpha}_i = \begin{bmatrix} \hat{\alpha}_{i0} \\ \hat{\alpha}_{i1} \\ \hat{\alpha}_{i2} \\ \hat{\alpha}_{i3} \end{bmatrix}, \ Z_t \begin{bmatrix} \phi_{0t} \\ \phi_{1t} \\ \phi_{2t} \\ \phi_{3t} \end{bmatrix}$$

then the EBV of an animal I for the t^{th} day was:

$$EBV_{it} = \hat{Z}_t \hat{\alpha}_i = \sum_{j=0}^{K_a - 1} \alpha_{ij} \phi_j (DIM_t)$$

The EBV for such an animal for 305-day milk yield was given by:

$$EBV_{LMY_i} = \sum_{t=5}^{305} (\hat{\alpha}_{0i}\phi_{ot} + \hat{\alpha}_{1i}\phi_{1t} + \hat{\alpha}_{2i}\phi_{2t} + \hat{\alpha}_{3i}\phi_{3t})$$

$$= \left(\sum_{t=5}^{305}\phi_{0t}\right)\left(\sum_{t=5}^{305}\phi_{1t}\right)\left(\sum_{t=5}^{305}\phi_{2t}\right)\left(\sum_{t=5}^{305}\phi_{3t}\right)\hat{\alpha}_i$$

$$= Z_{c_{305MYg}} \hat{\alpha}_i$$

where $Z_{c_{305MYg}}$ =vector of Legendre polynomial coefficients summed over the total lactation. The EBV for an animal i was calculated as:

$$t_i = Z_{c_{t_i}} \hat{\alpha}_i$$

Assessment the extent of cow and sire re-ranking for daily milk yield

Sires and cows were arranged within DIM based on daily EBV from largest to the smallest and assigned ranked such that the sire with the largest daily EBV was ranked first while the one with the least EBV was ranked last. The rank correlation was estimated using Spearman's rank correlation (SAS, 2002) [5]. Top ten (10) sires and cows for daily milk yield from each DIM were identified.

Results and discussions

Sires and cows were ranked based on their estimated breeding values at different DIM from the largest to smallest as presented in Table 1. All spearman rank correlations were significantly different from zero ($P<0.05$). The spearman correlations values indicate that there was a strong correlation between ranking for sires and cows based on EBVs accept for DIM2 and DIM 235 which recorded low correlations. All other DIM had high rank correlations, implying that ranking of sires and cows remained fairly constant across DIM. However, the rank correlations between DIM 235 and late-lactation (DIM 150 to 210) were low and negative, but significantly different from zero ($P<0.05$).

Table 1: Rank correlations for sires (above diagonal) and cows (below diagonal) for Sahiwal cows in Kenya

	Days in milk								
	2	**30**	**60**	**90**	**120**	**150**	**180**	**210**	**235**
2		0.44	0.30	0.26	0.25	0.24	0.23	0.28	0.38
30	0.48		0.98	0.97	0.97	0.97	0.96	0.98	0.09
60	0.33	0.98		1.00	1.00	0.99	0.97	0.99	0.07
90	0.28	0.97	1.00		1.00	0.98	0.96	0.98	0.10
120	0.27	0.97	1.00	1.00		0.98	0.96	0.99	0.08
150	0.27	0.97	0.99	0.99	0.99		1.00	1.00	-0.05
180	0.27	0.96	0.98	0.97	0.97	1.00		0.99	-0.12
210	0.31	0.98	0.99	0.99	0.99	1.00	0.99		-0.03
235	0.47	0.27	0.24	0.26	0.24	0.13	0.06	0.15	

Shifts in rank for various top listed sires and cows were studied in order to determine the changes in both the rankings across lactation. The ranking of Sahiwal sires across selected days in milk is shown in Table 2a and Table 2b shows the ranking of cows for daily milk yield for selected days in Kenya. Relative to DIM2, only 4 sires 4, 2, 1, 1 sires appeared among the top ten superior sires in DIM 30, 60, 90 and 120, respectively. Days in milk 150, 180, 210 and 235 had 2 sires appearing in the top 10 across all days. The ranking of Sahiwal cows shows that Relative to DIM2, only DIM235 had one cow that appear in the top 10 in both days. The values show that cows underwent more shifting in ranks across the lactation compared to sires. This is similar to the findings of Khan *et al*. 2008 [6] in relation to Sahiwal. The Sahiwal sires under this study could be considered generalists as they maintained their superior rank performance across the lactation. Similar results were reported by Swalve (1995) [7], Kaya *et al*. (2003) [8] Khan *et al*. (2008) [6]. Swalve (1995) [6] reported that the largest rank shift in cows seemed to be associated with lactation curves that deviated greatly from standard lactation curve.

Table 2a: Ranking of Sahiwal sires across days in milk for selected days in Kenya

ID	2	30	60	90	120	150	180	210	235
1081	1	4	12	13	13	13	13	12	6
36391	2	7	14	18	18	14	14	13	48
47491	3	73	97	102	103	104	107	101	13
30951	4	19	25	24	27	34	41	30	3
35781	5	52	72	79	80	80	78	73	51
53061	6	43	66	68	68	73	75	70	16
5141	7	12	13	14	14	15	16	15	20
48001	8	13	16	16	16	16	18	16	41
13321	9	5	7	8	8	8	8	8	47
45621	10	6	10	11	11	9	9	9	74

Table 2b: Ranking of Sahiwal cows across days in milk for selected days in Kenya

ID	2	30	60	90	120	150	180	210	235
47952	1	122	284	322	354	453	530	368	8
52182	2	247	514	643	650	604	580	520	312
48712	3	205	390	466	485	532	551	443	83
52682	4	32	92	122	121	107	97	87	378
50122	5	92	187	236	247	274	293	222	62
66102	6	83	183	247	252	220	209	184	292
66852	7	401	688	779	801	805	805	724	164
38622	8	82	167	223	230	203	206	176	228
50522	9	690	996	1097	1111	1083	1068	1015	308
73472	10	57	131	163	168	151	152	136	286

This study also attempted to explore the genetic curve pattern of EBVs for TDMY in Sahiwal cows. Considering that Sahiwal cattle are dual purpose breeds, milk production level are still low, this implies that milk production level continues to be the main selection criterion. Therefore, emphasis should be given to persistency of lactation as a way of correcting long-term problems related to lower lactation persistency and shorter lactation length in animals of such a breeds (Cruz *et al*., 2016) [9]. To achieve this, cluster analysis was done based on the EBVs and days in milk with an aim of grouping those individual animals who are persistent throughout the lactation period to be used for selection purposes in Sahiwal breeding programmes.

Based on cluster analyses, three non-overlapping clusters were identified as shown in Figure 1. The EBVs were higher at the beginning of lactation, decreasing then slightly increases thereafter decreasing to lowest values at the end of lactation. These trend support those obtained by spearman correlation analysis in this study (Table 1), in which higher correlations were observed between 30-210 DIM for a lactation period. Although the shapes and their respective curves across DIM were similar, clusters 1 had higher average daily EBV across lactation for sires, while for cows, cluster 2 and three had the highest average EBVs. Each cluster with specific animals presented a different genetic curve pattern based on the milk yield. Based on the results, cluster analysis can be used to pre-select cows and sires before ranking and selection is carried out with the cluster with the highest performance.

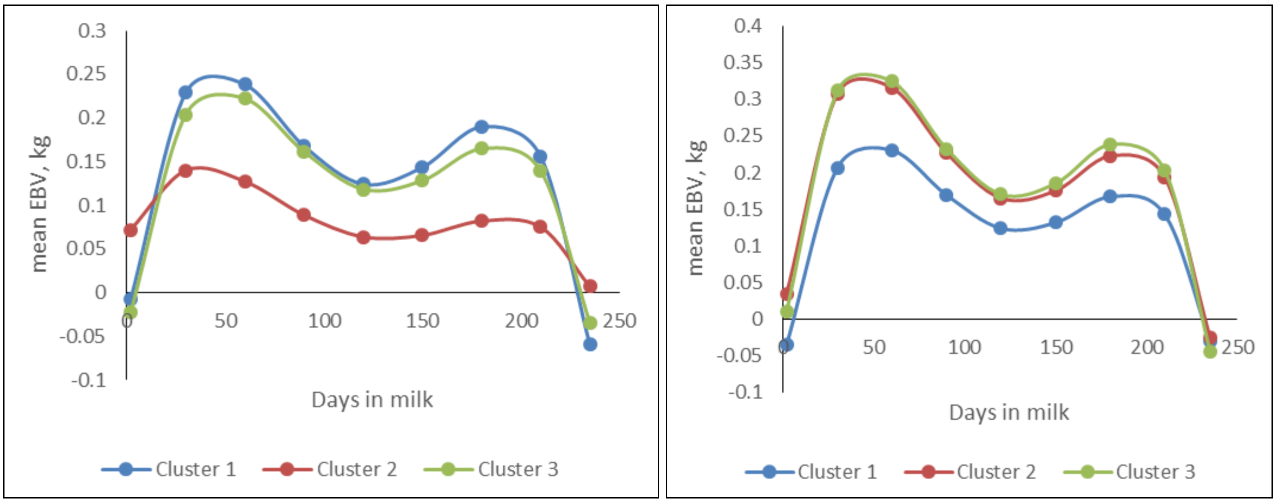

Fig 1: Cluster means for sires (a) and cows (b) for Sahiwal cattle across days in milk

This is attributed to the fact that cows with smoother production curves can be more persistent than cows exhibiting the same milk production with peak yields, but a sudden decline in production after peak lactation (Harder *et al*., 2006) [10]. Animals which are persistent throughout lactation have been reported to be requiring less feed and medication, therefore profiting the farmer in economic aspect (Cruz *et al*. 2016) [9].

Conclusions

Cluster analysis can be used to choose individuals for selection based on the shapes of the genetic curve patterns for milk yield estimated breeding values at day 235 for Sahiwal cows and sires. Therefore, the more productive animals can be selected at the same time on genetic curve patterns using random regression test day models. The cluster analysis should be used as an exploratory analysis to choose the best group or cluster that meets the breeding goals and thereafter choose the best animals at specific times on the cluster chosen.

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