

GENETIC PARAMETERS OF FIRST LACTATION MILK YIELD UNDER LOW, MEDIUM AND HIGH PRODUCTION SYSTEMS IN KENYA, USING TEST-DAY RANDOM REGRESSION MODEL

P.K. Wahinya^{1,2}, T.M. Magothe³, A.A. Swan¹ and M.G. Jeyaruban¹

¹Animal Genetics & Breeding Unit*, University of New England, Armidale, NSW, 2351 Australia

²Karatina University, Department of Agricultural Sciences, Kenya

³Livestock Recording Centre, Ministry of Agriculture, Livestock and Fisheries, Kenya

SUMMARY

The aim of this study was to estimate genetic parameters for test-day milk yield in different production systems in Kenya. 10,923, 19,049 and 26,287 first lactation test-day records from multiple breeds under low, medium and high production systems, respectively, were analysed. On average cows under high production systems were younger and had a higher test-day milk yield than in low and medium production systems. A model fitting fourth order Legendre polynomials was found to be the most parsimonious and was therefore used to model the data. Additive genetic and permanent environmental variances were heterogeneous along different days in milk and between production systems. Heritability and repeatability were also different between days in milk and production systems. Heritability was on average 27%, 48% and 48% and repeatability 72%, 83% and 78% under low, medium and high production systems, respectively. Genetic correlations ranged from -32%, 34% and 45% to unity between daily milk yield in different days in milk under low, medium and high production systems, respectively. These parameters indicate that random regression using Legendre polynomial order four can be used to model test-day milk yield under the three production systems in Kenya. The observed heterogeneity of variance indicates that genetic parameters should be estimated within production systems for sustainable genetic improvement.

INTRODUCTION

Genetic evaluation using test-day milk yield allows better modelling of environmental factors affecting yield and variation in the lactation curve in addition to providing accurate genetic evaluation (Ptak and Schaeffer 1993). Random regression models using orthogonal Legendre polynomials are commonly used to model the covariance structure between test-day records. The models should include the general shape of the lactation curve, variation in test-day yields, effects specific to cows on the same test-day, and production levels if known (Ptak and Schaeffer 1993). In Kenya dairy production systems vary in terms of the level of inputs and outputs such that production systems can be classified into low, medium and high production systems (Wahinya *et al.* 2018). Genetic parameters of milk yield and persistency using test-day records under these production systems are not available. This paper, therefore, aims at estimating genetic parameters for milk yield using test-day Legendre polynomial random regression models.

MATERIALS AND METHODS

Data. 56,259 first lactation test-day records were received from the Livestock Recording Centre (LRC) in Kenya. The records were observed from 5,179 multi-breed cows in 142 herds from 1990 to 2014. The cows were managed under different production systems and in different geographical regions of the country. Records that were retained for this analysis ranged from 5 to 365 days post-partum with twelve records on average per cow and a range of three to twenty two records per

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cow. Test-day yields were cleaned for outliers using a threshold of four standard deviations from the mean within the production systems.

Classification of herds into production systems was done in a separate analysis using average predicted herd 305-day milk yield. To obtain the predicted herd milk yield productivity level, individual cows 305 days milk yield were estimated using a linear mixed model with calving year, parity and breed group as fixed effects and herd as a random effect. K-means cluster analyses in R software (R Core Team 2017) using the Hartigan and Wong (1979) algorithm was then used to group predicted herd means into three groups here described as low, medium and high production systems, as summarised in Table 1.

Statistical analysis. Variance components were estimated using univariate animal test-day models using the ASReml software package (Gilmour *et al.* 2015). Contemporary group (CG) was defined based on herd-test month of milk sampling. Test-day milk yield was regressed on days in milk to account for the lactation curve. A random regression test-day model was fitted as:

$$y_{ijkl} = CG_i + Age + \beta t_j + g_i + \alpha_{kn} \varphi_n(t_j) + p_{kn} \varphi_n(t_j) + e_{ijkl}$$

where y_{ijk} is the test-day milk yield sampled on animal k , on t_j days in milk within the i^{th} CG, with age at calving (Age) and in genetic group g_i ; β , α_{kn} and p_{kn} are regression coefficients for days in milk, additive and permanent environmental random effects of each cow k , respectively; $\varphi_n(t_j)$ is the covariate of the regression function of n^{th} Legendre polynomial order for the day in milk; and e_{ijkl} is the residual term. Seventy-four g_i were defined separately for sires and dams within six categories based on year of birth: before 1986, between 1986 to 1990, 1991 to 1995, 1996 to 2000, 2001 to 2005 and after 2005, and Friesian, Ayrshire, Guernsey, Jersey, Sahiwal, Brown Swiss, and Unknown breeds using Westell-Quaas method (Westell *et al.* 1988). Residual variance was assumed to be heterogeneous considering 11 classes of 5 – 15, 16 – 30, 31 – 60, 61 – 90, 91 – 120, 121 – 150, 151 – 180, 181 – 210, 211 – 240, 241 – 270, and 271 – 365 days in milk, however, genetic parameters were estimated up to 305 days in milk.

Based on log likelihood ratio test, AIC, BIC and variance estimates, a model fitting Legendre polynomial order 4 (LP4) was found to be the most parsimonious and therefore, was used to estimate genetic parameters.

Table 1. Test-day data structure and average age (days) and test-day milk yield (kg) (standard deviation in brackets) under low, medium and high production systems

System	Records	Cows	Herds	Sire	Dam	CG	Age	Milk yield
Low	10,923	1,034	50	385	916	587	1,112(277)	7.9(3.6)
Medium	19,049	1,659	55	450	1,283	638	990(228)	12.3(4.8)
High	26,287	2,486	37	626	1,580	434	910(140)	16.5(5.8)

RESULTS AND DISCUSSION

Low, medium and high production systems had different phenotypic means and variances for test-day milk yield (Table 1). Table 2 illustrates variance components, heritabilities and repeatabilities from model LP4 for selected test-days under the low, medium and high production systems. Variance components were heterogeneous between and within production systems. Additive genetic variances ranged from 1.3 to 6.7, 6.9 to 14.6 and 7.9 to 17.2 under low, medium and high production systems, respectively. Within low and medium production systems, additive genetic variance was highest at the beginning of the lactation period which is consistent with other reports in the literature (Muasya *et al.* 2014). In the high production system additive variance increased from the beginning of lactation to a peak on day 100 then gradually decreased towards the end of the lactation. Andonov *et al.* (2013) reported higher additive variance in the mid-lactation while Berry *et al.* (2003) observed a

similar trend to what was observed in this study. The trend for permanent environmental variance was different between production systems. In the low production system, it was highest around day 60 then it decreased to the end of the lactation. A similar trend was observed by Andonov *et al.* (2013) although in their study they estimated peaks at the beginning and end of the lactation period. Permanent environmental variance increased gradually from the beginning to the end of the lactation under the medium production system while under the high production system, it remained constant with peaks at the beginning and end of the lactation period as reported by Muasya *et al.* (2014). Residual variance was constant along the days in milk except for higher residual variances observed in the early stage of the lactation in high production systems.

Table 2. Additive, permanent environment (Pe) and residual variances, heritability (h²) and repeatability (r) for daily milk yield in selected days in milk (DIM) under low (L), medium (M) and high (H) production systems (variances are rounded to the nearest whole number)

DIM	Additive			Pe			Residual			h ² (%)			r (%)		
	L	M	H	L	M	H	L	M	H	L	M	H	L	M	H
5	7	15	8	4	2	14	2	3	4	53	74	30	84	85	84
60	2	7	15	5	6	7	2	3	13	22	46	43	79	81	63
100	1	7	17	4	6	7	2	2	7	18	47	55	71	86	76
180	1	8	14	3	6	7	2	3	5	23	46	53	70	81	80
260	2	7	11	2	6	8	2	2	5	32	44	47	70	82	80
305	2	8	11	3	7	8	2	3	5	28	45	47	66	85	81

Heritability estimates in this study ranged from 18% to 53%, 44% to 74% and 30% to 55% under low, medium and high production systems respectively. Similar results have been reported in literature (Costa *et al.* 2005). Higher estimates, especially for the medium production system, were reported here than were reported for Holstein-Friesian cattle in Kenya (Muasya *et al.* 2014). This can be attributed to the multi-breed data used in this study which is expected to have a higher genetic variance than in a single breed population (Gebreyohannes *et al.* 2016). Heritability estimates were highest at the beginning of the lactation under low and medium production systems (Bignardi *et al.* 2009). Under the high production systems heritability estimates were lowest at the beginning of the lactation, increased to a peak then gradually decreased to the end of the lactation period. Daily milk yield was highly repeatable (63% – 87%) and decreased from the start of the lactation to the end in low production systems but increased gradually from the beginning to the end of the lactation in the medium and high production systems.

Genetic correlations estimated using model LP4 for test-days up to 305 days are illustrated in Figure 1. The trend of correlation was different between production systems. In general, correlations were higher between adjacent days in milk but declined with increasing distance between days of lactation in all production systems. Most of the correlations were positive except for correlations between milk yield at the beginning and end of lactation in the low production system. Negative correlations have been reported in literature (Rekaya *et al.* 1999) indicating that improvement of yield at the beginning of the lactation would result in reduced yield at the end and therefore lower persistency. Positive correlations indicate that selection for high milk yield at the end of the lactation can be effective based on yield at the beginning of the lactation especially under medium and high production systems with moderate correlations up to 0.3 and 0.5 respectively.

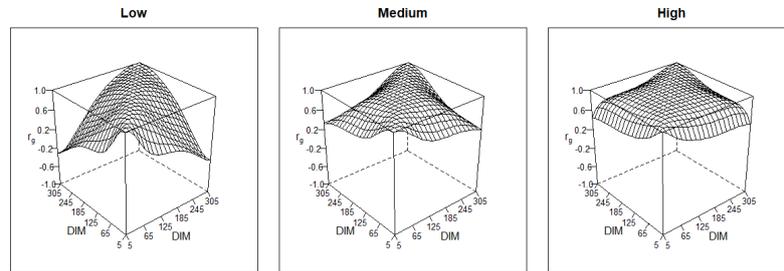


Figure 1. Genetic correlation (r_g) between milk yields in different days in milk (DIM) under low, medium and high production systems

CONCLUSIONS

A fourth order random regression model was most appropriate for modelling milk yield test-day records in this study. Genetic and permanent environmental variances were heterogenous along the trajectory of days in milk. Genetic and permanent environmental variances, heritabilities and repeatabilities were different in low, medium and high production systems. Genetic correlations between milk yields in different days of a lactation indicate that selection for improved milk yield at the beginning of the lactation period in the medium and high production systems would result in improved yield at the end of the lactation and therefore improved persistency, whereas under low production systems negative correlations were estimated between early and late lactation. Further analysis of the test day records is recommended using alternative models such as cubic splines. This study showed that genetic parameters should be estimated within production systems for sustainable genetic improvement and selection for milk yield can be effective based on yield at the beginning of the lactation.

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