

## **Genetic analysis of dairy cattle performance under extensive, semi-intensive and intensive production systems under tropical climate in Kenya**

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### **Summary**

Genetic parameters for milk and fertility traits of dairy cattle managed under extensive, semi intensive and intensive production systems in Kenya were estimated. Univariate and bivariate analyses were used to estimate genetic parameters for 305 days milk yield, lactation length, age at first calving, and calving interval. The heritability estimates for milk yield were moderate to high and ranged from 0.17 to 0.34. Estimated heritability for calving interval was low under all three production systems. Moderate to high heritability was estimated for lactation length and age at first calving. All the estimates varied among the production systems. Genetic correlation estimates among milk yield and fertility traits were negative. Production system specific parameters are essential to achieve optimum genetic gain under the three production systems in Kenya.

Keywords: dairy cattle, milk, fertility, genetic parameters, tropical production systems

### **Introduction**

Selection for dairy cattle performance in Kenya takes place in organized nucleus farms, usually large scale with high performance, while commercial production takes place in a range of intensive to extensive farms. To date, performance records from large scale herds have been used for genetic evaluation of dairy cattle from extensive, semi intensive and intensive farms (Musani & Mayer, 1997, Ojango & Pollott, 2001, Amimo, *et al.*, 2007, Ilatsia, *et al.*, 2007, Muasya, *et al.*, 2007, Ombura, *et al.*, 2007), but selecting sires using their EBVs based on performance in large-scale operations may be biased when used to predict production in more variable and less intensive environments, if there is significant genotype-by-environment interaction. This paper presents estimates of variance components for milk yield and fertility traits under extensive, semi-intensive and intensive production systems under tropical climate in Kenya, with a view to developing a unique genetic evaluation for each of the three production systems.

### **Materials and methods**

#### **Data structure and preparation**

Milk yield and fertility records were obtained from the Dairy Recording Services of Kenya

(DRSK), from 233 herds that participated in performances recording from 1983 to 2016. The records were obtained from farmers by the DRSK and then submitted to LRC for analysis and genetic evaluation. These records were from Friesian, Ayrshire, Guernsey, Jersey, Sahiwal cattle and their crosses raised under extensive, semi intensive and extensive production systems in Kenya. A total of 54,755 lactation records were available before data editing. Records were retained if breed, birth and calving dates, lactation length, parity and pedigree were correctly identified. Milk yield (MY) was standardized to a 305 day lactation length, and the fertility traits derived were age at first calving (AFC), lactation length (LL), and calving interval (CI).

To define production environments, herd means for 305 days milk yield were then used to form three data sets using the *K*-means clustering algorithm (Hartigan & Wong, 1979) in the statistical software R. The herd classification was then validated against groupings allocated by DRSK. Animals with outlier performance above three standard deviations from the individual herd means for each trait were removed. A total of 22,311 records from 86, 70 and 55 herds from extensive, semi-intensive and intensive production systems, with 4232, 3785 and 3640 animals respectively were finally used for analysis. The extensive, semi-intensive and intensive clusters had 932, 874 and 806 sires respectively with 120 sires in common across all three clusters.

## Statistical analysis

Mixed models were used to identify fixed effects, with major effects on the traits observations using the nlme package of Pinheiro, *et al.* (2017) in R. Only the interactions which were significant ( $P < 0.05$ ) on the selected traits were included in the model. Univariate and bivariate animal models were used to estimate phenotypic, additive genetic, residual variances and genetic and phenotypic correlations using the WOMBAT REML program (Meyer, 2007). The permanent environment effect of animal was fitted as an additional random effect for MY, LL and CI with multiple records. The basic model used for the estimation of genetic parameters was:

$$Y_{ijklmn} = \mu + H_i + Y_j + S_k + P_l + B_m + a_n + pe_o + e_{ijklmno} \quad 1$$

Where  $Y_{ijklmn}$  is the animals trait observation given  $\mu$  as the overall mean, in herd  $i$ , birth year  $j$ , birth season  $k$ , parity  $l$ , breed  $m$ , with  $a_n$  random additive genetic effect of the animal,  $pe_m$  the permanent environmental effect and  $e_{ijklmn}$  random error associated with the observation. Permanent environmental effect of animal was not fitted for age at first calving (AFC) with single record per animal. Common additive relationships were fitted and the breed effects were adjusted by fitting breed as a fixed effect in the model. Non-additive effects were assumed negligible.

## Results and discussion

### Estimates of heritability and variance ratio for permanent environmental effect

Trait means, standard deviations, and estimates of variance components, heritability and variance ratio for permanent environment are shown in Table 1. The mean production for milk traits increased with production level and decreased for fertility traits. The 305 day milk yield (MY) under three production systems was similar to results reported by Muasya, *et al.* (2007).

Lactation length (LL) was lower in the extensive production system indicating that the animals are milked for a shorter period of time compared to other two production system. The mean performance for all the traits was largely within the range of what has been reported for the Kenyan dairy cattle (Musani & Mayer, 1997, Ojango & Pollott, 2001, Ilatsia, *et al.*, 2007, Muasya, *et al.*, 2014).

Table 1. Descriptive statistics and estimated heritability for direct genetic effect ( $h^2$ ) and variance ratio for the permanent environment effects ( $c^2$ ) with standard error (SE) for milk and fertility traits of dairy cattle managed under extensive, semi-intensive and intensive production system in Kenya.

Traits	System	Record	mean	STD	Variance components <sup>3</sup>			$h^2 \pm SE$	$c^2 \pm SE$
					V <sub>a</sub>	V <sub>pe</sub>	V <sub>e</sub>		
MY	E	7348	2627.5	1007.2	85.5	24.4	387.6	0.17± 0.01	0.05± 0.02
	S	7196	4136.3	1202.8	254.3	128.0	715.4	0.23± 0.01	0.12± 0.01
	I	7766	5652.2	1514.0	652.0	147.6	1145.1	0.34± 0.01	0.08± 0.01
LL	E	7348	300.6	88.0	0.6	0.2	6.3	0.09± 0.03	0.02± 0.03
	S	7196	314.6	73.1	0.9	0.0	4.2	0.18± 0.03	0.03± 0.01
	I	7766	320.3	75.1	0.4	0.1	4.8	0.07± 0.02	0.02± 0.03
AFC	E	1217	1092.2	254.1	15.0	0.0	17.1	0.47± 0.13	
	S	1639	950.6	170.3	4.3	0.0	10.4	0.30± 0.09	
	I	2136	879.4	83.2	2.3	0.0	3.5	0.60± 0.09	
CI	E	2975	478.0	126.5	0.4	0.0	13.1	0.03± 0.04	0.05± 0.01
	S	3342	425.5	77.3	0.2	0.0	5.1	0.03± 0.03	0.04± 0.01
	I	4139	414.4	68.7	0.2	0.0	3.9	0.06± 0.03	0.03± 0.01

<sup>1</sup>MY – 305 days milk yield (kg); LL – lactation length (days); AFC – age at first calving (days); CI – calving interval (days).

<sup>2</sup> V<sub>a</sub> - additive genetic variance; V<sub>pe</sub> - permanent environment variance; V<sub>e</sub> – residual variance.

<sup>3</sup>Variance components are x10<sup>3</sup>

Heritability estimates for MY improved by 6 to 10% (0.17, 0.23, and 0.34 for extensive, semi-intensive and intensive respectively) between the production systems. This is due to differences in genetic and environmental variability across the production systems. Heritabilities estimated for LL were low in the extensive (0.09) and intensive (0.07) compared to the semi-intensive system (0.18). The variance ratio for permanent environmental effect for MY was low (0.02 – 0.03) in the three production systems with the lowest value for the semi-intensive system.

The heritability estimates obtained for age at first calving (AFC) ranged from 0.30 to 0.60. Estimated heritability for AFC under the extensive and intensive production systems were higher than those reported for AFC in Kenya (0.04 - 0.38) by Musani and Mayer (1997), Ilatsia, *et al.* (2007), Muasya, *et al.* (2014). High estimates indicate that there is potential to improve this trait in all production systems (Ojango & Pollott, 2001). The estimate for the semi-intensive production system (0.30) was within the range of other reported estimates. These higher estimates could be a result of differences in fixed effects used in the model. Age at first calving is influenced by breeding practices where some producers aim to breed animals to calve in

specific seasons while others breed their heifers based on attainment of a two thirds of the mature body weight (Ojango & Pollott, 2001).

The heritability estimates for calving interval (CI) under the three production systems were low ranging from 0.03 to 0.05 with variance ratio for permanent environmental effects of 0.03 to 0.05. The intensive production system had the highest heritability. The estimates were within the range of estimates previously reported from Kenya (0.02 – 0.05) Musani and Mayer (1997), Ilatsia, *et al.* (2007), Muasya, *et al.* (2014). Low heritability estimates indicate that deriving accurate records on this trait is difficult.

### Estimates of genetic and phenotypic correlations

Genetic and phenotypic correlation estimates between milk and fertility traits from bivariate analysis are presented in Table 2. The genetic correlations between milk yield and age at first calving were positive and ranged from 0.04 to 0.43. Breeding practices could contribute to the differences in the correlations between the production systems.

Table 2: Genetic ( $r_g$ ) and phenotypic ( $r_p$ ) correlations with their standard errors (SE) for milk and fertility traits of dairy cattle in extensive (E), semi-intensive (S) and intensive (I) production systems.

Traits <sup>1</sup>		$r_g$ (E)	$r_g$ (S)	$r_g$ (I)	$r_p$ (E)	$r_p$ (S)	$r_p$ (I)
MY	AFC	0.08±0.20	0.04±0.18	0.43±0.30	0.06±0.03	0.02±0.02	0.07±0.03
	CI	-0.53±0.59	0.03±0.00	0.14±0.20	0.00±0.01	0.01±0.00	-0.02±0.01
	LL	0.59±0.19	0.18±0.12	0.19±0.15	-0.01±0.01	0.04±0.01	0.03±0.01
LL	AFC	-0.21±0.19	0.04±0.34	-0.51±0.31	-0.00±0.02	0.01±0.03	-0.02±0.02
	CI	0.28±0.67	-0.10±0.07	0.58±0.10	0.07±0.01	0.00±0.00	0.00±0.00
AFC	CI	-0.01±0.01	-0.18±0.89	0.54±0.61	0.00±0.00	-0.12±0.03	-0.12±0.03

<sup>1</sup>MY – 305 days milk yield; LL – lactation length; AFC – age at first calving; CI – calving interval.

The genetic correlation between milk yield and calving interval was strongly negative for the extensive system but slightly positive for the other systems. This implies that selection for milk yield within the extensive system would result in a reduction in calving interval. These estimates are similar to those reported by Ojango and Pollott (2001). A positive correlation for semi-intensive and intensive production systems implies that an improvement in milk yield results an increase in calving interval. This has been reported in other studies associating the higher yielding animals to more days open which increase the calving interval.

Milk yield had moderate to high positive correlations with LL. The correlation ranged from 0.18 to 0.59 with the highest correlation of 0.59 in the extensive production system. This implies that genetic improvement in MY would result to an increase in lactation length in all three production systems.

The genetic correlation estimates between LL and AFC ranged from -0.51 to 0.04 and they were not significantly different from zero. Estimated genetic correlations between AFC and CI ranged from -0.01 to 0.54. However, due to high estimated standard error, they were also not significantly different from zero.

## **Conclusion**

This study found that the estimated heritability and genetic correlation between the traits were different across the production systems. This implies that sustainable genetic improvement for traits analyzed in this study could be achieved through genetic evaluation using production specific genetic parameters. Further study is required to explore the genetic control of economically important traits under the three production systems. This will eventually lead to a sustainable methods of genetic improvement under the three production systems. These parameter estimates will be used in constructing indices to optimize performance under extensive, semi-intensive and intensive production systems under tropical climate.

## **Acknowledgements**

The authors thank the University of New England-International Postgraduate Research Awards (UNE-IPRA), for funding the first author Ph.D. study and Dairy Recording Services of Kenya (DRSK) and Livestock Recording Center (LRC) of Kenya for supplying the dairy performance data.

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