Within-herd genetic and phenotypic analysis of selected production and fertility traits of multibreed commercial dairy cows in Kenya

Within-herd genetic and phenotypic analysis of selected production and fertility traits of multibreed commercial dairy cows in Kenya

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Executive summary

The purpose of this study was to estimate within-herd genetic and phenotypic trends of test day milk yield, age at first calving and calving interval in two commercial multibreed dairy herds in Kilifi and Nakuru counties of Kenya and to determine the optimum proportion of exotic and indigenous cattle crosses that best suit the different ecologies, considering the above traits. Genetic and phenotypic trends are indicative of the changes that have occurred in the herds because of selection and/or breed combination practices and the overall respective breeding strategies that have been adopted over time.

Lactation and calving records of 436 and 191 cows in both the Kilifi commercial dairy farm and Kenya Agricultural & Livestock Research Organization (KALRO's) Naivasha herd in Nakuru county, were collected from 2000 to 2019 for this study. For milk yield in both herds, a fixed regression animal model was used to analyse the data. The model was adjusted for fixed effects of year and season of calving, year and season of milking, parity, age nested within parity, days in milk nested within parity and degree of exoticness of the cow. Legendre polynomials of order three was used to model fixed regressions of the lactation curves. Mean daily milk yield was 15.06±4.92 kg and 7.24±3.62 kg for the Kilifi and Naivasha herds, respectively.

The model used for analysing age at first calving included degree of exoticness, year and season of birth, and the repeatability model fitted to calving interval included year and season of calving, degree of exoticness, and calving age. Mean age at first calving was 28.85±4.10 months for the Kilifi herd and 37.98±5.57 months for the Naivasha herd while mean calving interval was 447.5±96.86 days and 512.4±170.16 days for the Kilifi and Naivasha herds respectively.

Breed proportion of cows generated from the information provided in the data was used to group the animals into three breed classes, based on the proportion of exotic dairy breed into exotic class 1 (EC1) made up of animals having 0–50% exotic breed proportion (n=481), exotic class 2 (EC2) with animals having between 50 and 75% exotic breed composition and exotic class 3 (EC3) with animals having over 75% exotic dairy breed proportion (n=1,009). Adjusted means of the breed classes were calculated and contrasted for the different traits. There was no significant difference (p < 0.05) between breed types for age at first calving and calving interval, but significant differences were observed for milk yield in both herds with EC2 cows having the highest milk production across breed group in both the Kilifi herd (9.93±0.26 for EC2 vs 8.24±0.39 and 8.67±0.4 for EC1 and EC3) and Naivasha herd (15.9±0.34 for EC2 vs 15.4±0.4 and 14.9±0.27 for EC1 and EC3), respectively.

These results suggest the breed makeup of EC2 cows might be more suitable for sustainable and profitable dairy farming under the dairy farming context of both herds since they produced more milk.

The heritability (h^2) estimates for test day milk, age at first caving and calving interval were 0.27±0.06, 0.31 ± 0.13 and 0.14±0.12, respectively, for the Kilifi data and 0.20±0.09, 0.24±0.27 and 0.03±0.13 for the Naivasha data, respectively. Estimated breeding values (with accuracy of prediction) for milk yield, age at first calving and calving interval in the Kilifi herd ranged from -6.88 to 4.6 kg (0–88.9%), -3.92 to 5.91months (0–84.8%), -75.5 to 80.7 days (0–71.3%), respectively and in the Naivasha herd, it ranged from -3.61 to 1.65 kg (0-81.7%), -6.82 to 4.87 (0-74.6%) and -78.97 to 87.55 (0–72.6%), respectively.

At herd level, phenotypic and genetic trends for milk yield was significantly positive (+0.97 litres per year) and negative (-0.26 litres per year) respectively for the Kilifi herd although both trends showed no significant change for the Naivasha herd. Phenotypic and genetic trend for age at first calving and calving interval for the Kilifi herd did not show significant change over time, and for the Naivasha herd, both trends showed no significant change over time for age at first calving although there was a significant favourable negative phenotypic trend for calving interval (-10.54±4.5). No significant increase in breeding value was observed for the sire and dam population over time in both herds for these traits.

Despite the favourable phenotypic changes which occurred in milk yield in the Kilifi herd and calving interval in the Naivasha herd, genetic trend for all traits analysed did not significantly improve in both herds over time indicating that these favourable phenotypic changes were not accompanied by improvement in breeding values for both traits, but likely reflect improvement in herd management practices over the past 19 years.

Genetic improvement for these traits in the herds may be achieved and accelerated by increasing selection pressure on them, followed by wide-ranging use of the selected bulls and cows as sires and dams.

1   Introduction

The fundamental aim of any animal breeding program is to increase productivity of the animals and profitability of the farm (Kosgey and Okeyo 2007). Increase in production efficiency could be achieved either by improving the environmental conditions of the animals, improving the mean breeding value of the population, or by combining of both (Katkasame et al. 1996). Estimating of genetic and phenotypic trends (i.e. computing the change in mean breeding values and phenotypic values over the years) indicates the progress made in the herd over time and helps in understanding to what extent selection and breeding programs have been effective (Oldenbroek and van der Waaij 2014). It conveys a quick assessment of how successful or not a breeder has been in achieving the intended selection goals over the generations. Analyses of such trends may reinforce or optimize selection and management goals established by a breeder or even signal the need to change/redesign the selection and/or management strategy. A comparison of genetic trends to phenotypic trends would help in understanding whether the progress observed could be attributed to the genetic improvement of the herd or to improvement in management practices (Javed et al. 2007). Continuous genetic and phenotypic evaluation to monitor whether desirable trends are being realized for each trait is important for sustaining herd improvement and profitability.

Data generated in two multibreed commercial dairy cattle herds in Kilifi county and Naivasha sub-county in Nakuru county of Kenya between 2000 and 2019 has not been genetically evaluated to establish if indeed progress has been made or is being achieved. Specifically, this assessment was to obtain estimates of genetic parameters and assess the phenotypic and genetic trends for total milk yield, age at first calving and calving interval and to estimate breeding values for comparative ranking by genetic merit of all animals in the herd for selecting superior replacement breeding stock within a multibreed-herd of cattle in the Kilifi and Nakuru counties of Kenya. The optimum proportion of exotic x indigenous dairy crosses suited to the herds for the different traits was explored. Information generated is useful for optimizing herd operations and to give direction for future crossbreeding programs for genetic improvement of the herds, especially because these two herds are significant sources of breeding bulls and heifers to neighbouring smallholder dairy farmers. Progress made in these herds or lack of it, has cascading consequences to the dairy sector in these regions.

2   Materials and methods

2.1 Geographical locations and climatic conditions

The Naivasha herd is in Nakuru county which lies approximately 90 km northwest of Nairobi at an altitude of 1,829–2,330m founf above sea level. The region falls within agro-ecological zone UM 5 (Upper Midland-Livestock) and is defined as a semi-arid pasture-based zone. Annual mean temperatures range between 18.3 and 19.6°c with an annual average rainfall of 650–750 mm. The region receives bimodal rainfall with a main rainy season from March to June and a short rainy season from October to December (Jaetzold et al. 2010). The Kilifi herd is in the Kilifi County, which is located about 120 km north of Mombasa with a usually hot and humid climate all year round. It falls under the coastal lowland semihumid agroecological zone. The mean daily temperature ranges from a minimum of 22°c to a maximum of 29.5°c. It has two rainy-seasons with the long rains occurring between April to June, and short rains between October to December. The average rainfall ranges from 400 mm in the hinterland to over 1,200 mm along the coastal belt (Hoorweg et al. 1995).

2.2 Herd management and crossbreeding strategies

The Naivasha herd is kept under both extensive (controlled) and zero-grazing production systems, with the latter including supplementation with high-quality feeds and concentrates. Grading up and rotational crossbreeding was practiced in this herd where the respective indigenous cows were crossed with mainly Holstein Friesian bulls through artificial insemination. Indigenous and crossbred bulls were also used for mating to achieve the required exotic breed persentages. The Kilifi herd is made up of an intermating population of composite cattle originating from crossbred parents. It is managed under an extensive system supplemented with natural grass silage, giant panicum and Napier grass, maize stover, and fodder trees. The farm produces synthetic lines of cattle, which are continuously maintained when interbred, hence stabilizing new composite breeds.

2.3 Phenotype, genotype, pedigree data

The data used in this study was lifted from historical farm records for periods between 2000 and 2019 from two multibreed commercial dairy farms located in Kilifi and Nakuru counties of Kenya. Farm records from both herds were first lifted from paper copies and converted to digital records before data analysis. The data included a total of 208,634 milk records and 824 calving records of 436 cows from the Kilifi herd and 10,160 milk records and 490 calving records of 191 cows from the Naivasha herd. The data was accessed for quality and cows with missing dates of birth and calving dates were excluded from the analysis while outlying data were replaced with trait means. Age at first calving and calving

interval were calculated from the data received using dates of birth and calving. Age at first calving was defined as age from birth to first calving in months and calving interval was defined as the interval between two consecutive calving events in days. Age at first calving was restricted to 48 months and parity was grouped into parities 1, 2 and 3+ because fewer numbers of cows were observed in later parities.

The Kilifi pedigree file had a total of 1,015 animals (754 females and 261 males) born between 1992 and 2020 while the Naivasha pedigree had a total of 1,496 animals (984 females and 512 males) born between 1985 and 2018. In addition, the Naivasha herd had 200 cows genotyped with the GeneSeek Genomic Profiler Bovine 50K chip. These were imputed to the Illumina HD chip using a reference population consisting of crossbred cattle from east Africa and several European purebred animals (Aliloo et al. 2018). After quality control, 684,183 single nucleotide polymorphism markers (SNPs) remained for inclusion in the analysis. Breed proportions of the cows were generated from the information provided by the farmers and used to group the animals into three breed classes, based on the proportion of exotic dairy breed. Exotic class 1 (EC1) was made up of animals having 0–50% exotic breed proportion, exotic class 2 (EC2) with animals having between 50 and 75% exotic breed composition and exotic class 3 (EC3) with animals having over 75% exotic dairy breed proportion. Available breed composition data for the Kilifi herd show that Sahiwal, Ayrshire and Holstein breeds have the most penetrance in the herd (Figure 1). The breed composition data for the Naivasha herd (Figure 1) showed that most of the animals in this herd had their breed information defined. However, due to unplanned mating during grazing, the sires of some animals are not known, thus represented as unknown in the chart below (Figure1). The exotic dairy breeds included Holstein Friesian, Jersey, Guernsey, Ayrshire, Brown Swiss, Fleckvieh, Milking Shorthorn, Meuse Rhine Issel, Scandinavian Redwood and Montbéliarde. Non-exotic or zebu dairy breeds in both populations included Sahiwal, Boran and Gir.

Figure 1. Per cent of breed presence in crossbred cow population in the Kilifi and Naivasha herds.
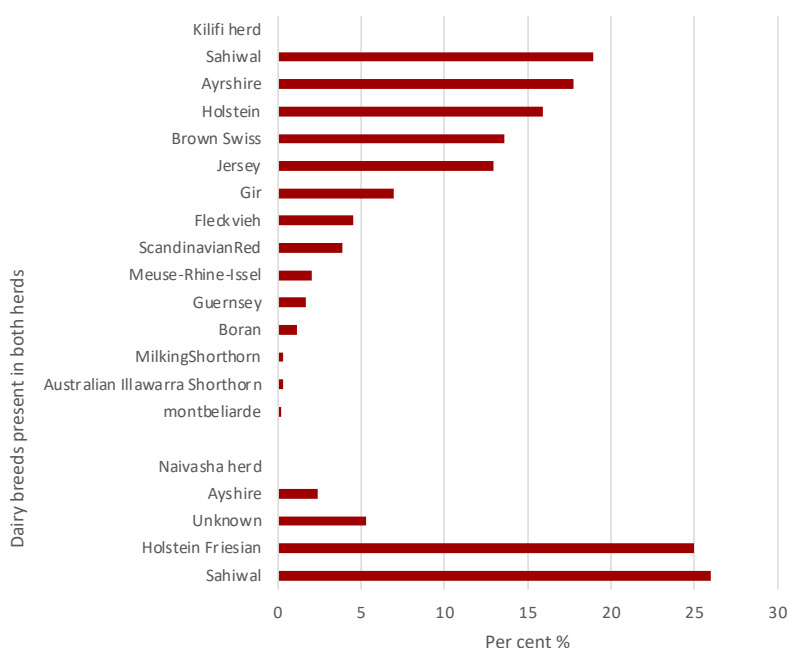
2.4 Statistical analysis

Variance components and corresponding genetic parameters and breeding values were estimated for each trait using the Average Information Restricted Maximum Likelihood (AIREML) algorithm of the Wombat program (Meyer 2007) by fitting three single trait animal models. The model used for analysing age at first calving included degree of exoticness, year and season of birth as fixed effects and animal effect as random while the repeatability model fitted to calving interval included fixed effects of year and season of calving, degree of exoticness, parity and age nested within parity with permanent

environment and animal effects fitted as random. For milk yield, a fixed regression animal model was used to analyse the data, which was adjusted for fixed effects of year and season of calving, year and season of milking, parity, age nested within parity, days in milk nested within parity and degree of exoticness. Legendre polynomials of order three was used to model the fixed regressions of lactation curves. The pedigree-derived relationship matrix, A and the pedigree-genomic relationship matrix H (pedigree relationships [A] combined with genomic relationship matrix based on SNP information [G]) were used to describe covariance among individuals for breeding value estimation in both a classical and single step best linear unbiased prediction (BLUP) procedure for the Kilifi and Naivasha herds, respectively.

Estimates for genetic change in the herds and within sire and dam groups over time was obtained by averaging breeding values within year of birth and regressing them on years of birth and regressing least square means within year of calving on years of calving for phenotypic change.

Adjusted means of the breed classes were calculated and contrasted for the different traits.

3   Results and discussion

3.1   Mean phenotypic values for milk yield, age at first calving and calving interval

The mean daily milk yield was 15.06±4.92 kg, mean age at first calving was 28.85±4.10 months and mean calving interval was 447.5±96.86 days for the Kilifi herd and for the Naivasha herd, mean daily milk yield was 7.24±3.62 kg, mean age at first calving was 37.98±5.57 months and mean calving interval was 512.4±170.16 days.

There was no significant difference (p < 0.05) between breed types for age at first calving and calving interval, but significant differences were observed for milk yield in both herds with EC2 cows having the highest milk production across breed group in both herds (9.93±0.26 for EC2 vs 8.24±0.39 and 8.67±0.4 for EC1 and EC3 cows in the Naivasha herd and 15.9±0.34 for EC2 vs 15.4±0.4 and 14.9±0.27 for EC1 and EC3 cows in the Kilifi herd, respectively see Table 1).

Table 1. Least square means (LSM) for age at first calving (AFC), calving interval (CI), and milk yield (MY) by breed class in the Kilifi and Naivasha herds

Herd	Trait	Breed classes		
		LSM±SE		
		EC1	EC2	EC3
Kilifi	AFC	30±0.59	29.6±0.42	28.5±0.37
	CI	445±11.9	437±10.7	450±10.2
	MY	15.4±0.4ab	15.9±0.34a	14.9±0.27b
Naivasha	AFC	37±1.25	37.9±0.7	37.1±1.19
	CI	496±39.3	489±17.1	527±35.3
	MY	8.24±0.39a	9.93±0.26b	8.67±0.4a

Note: Exotic class 1 (EC1) was made up of animals having 0–50% exotic breed proportion, exotic class 2 (EC2) with animals having between 50 and 75% exotic breed composition and exotic class 3 (EC3) with animals having over 75% exotic dairy breed proportion.

These results suggest that since the breed groups did not differ across herds for age at first calving and calving interval; EC2, which are cows having between one half and three-quarters of exotic blood in their breed makeup might be more suitable for sustainable and profitable dairy farming under the context of both herds since they produced more milk (Figure 2). It is valuable for farmers to understand the types of crossbred cows they need to keep, to produce more milk for increased profitability.

Figure 2. Milk yield of cows by proportion of exotic genes in the Naivasha and Kilifi herds.
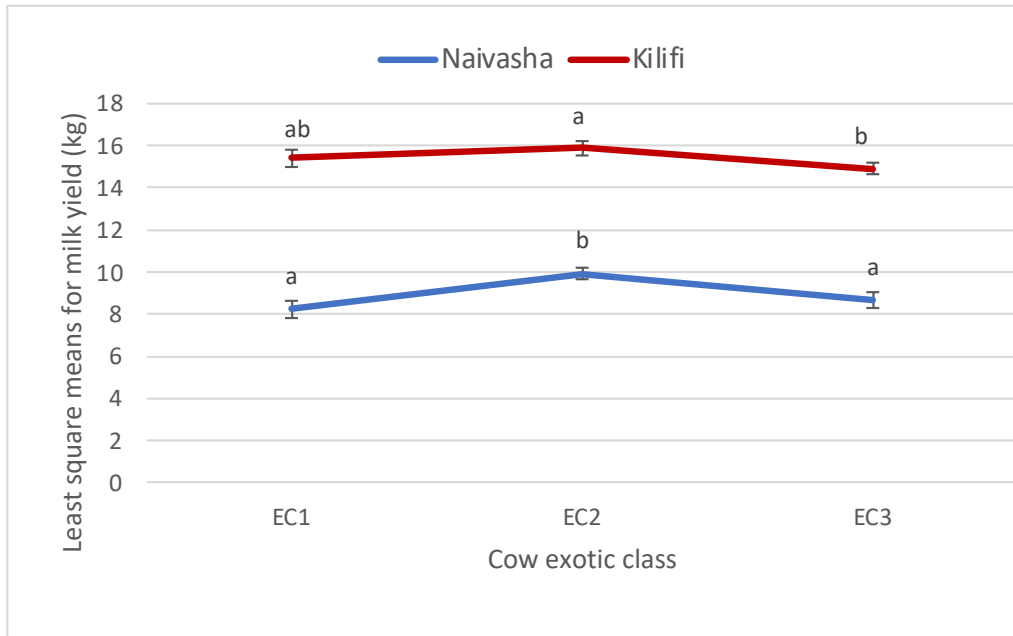
3.2 Heritability and repeatability estimates

Heritability summarizes how much of the variation in a trait is due to variation in genetic factors and is important in animal selection/genetic improvement programs because response to selection depends on it (Bourdon 2000). Heritability for milk yield and age at first calving in the Kilifi herd were moderate at 0.27±0.06 and 0.31±0.13, respectively, suggesting that breeding values for milk yield and age at first calving have a moderate influence on its phenotypic values. Heritability estimates for calving interval was lower at 0.14 ± 0.12. In the Naivasha herd, heritability for milk yield was moderate, at 0.20±0.09. Heritability estimates for age at first calving and calving interval were 0.24±0.27 and 0.03±0.13, respectively. Low heritability estimate for calving interval suggests that non-additive genetic effects such as dominance or non-genetic factors such as herd management had a greater influence on this trait as is expected in crossbred populations.

Repeatability is an indicator of changes in traits over time and measures consistency between repeated records for a trait and the tendency of animals to maintain their ranking over time (Bourdon 2000). Moderate to high repeatability values suggest that the first record on an animal's performance is a good indicator of its second and subsequent records. Thus, an animal's single performance for a trait is on average a good indicator of its producing ability. In the Kilifi herd, repeatability for milk was moderate at 0.45±0.03, and low at 0.14 ± 0.12 for calving interval. An awareness of the repeatability of a trait is useful in making culling decisions. In the Naivasha herd, repeatability for milk was moderate at 0.39±0.03, and low for calving interval at 0.03±0.15. Low repeatability for calving interval might be due to the data structure as records of individuals for these repeated records were not consistent across parities. It might also be due to changes in herd management and environment over time.

3.3 Genetic merit of animals—estimated breeding value

Estimated breeding values (EBV) reflect the genetic potential or transmitting ability of animals. They are estimated for individual animals based on own performance records, that of their parents, siblings, and/or progenies (Satpal et al. 2012) after correcting for various environmental and management factors like season of calving, age at calving, breed,

etc. For a trait such as milk yield, animals with the highest breeding values are genetically superior, while for traits such as calving interval and age at first calving, those with least breeding values, are genetically superior and are selected as parents for breeding the next generation of animals to ensure faster genetic progress is made in the herd.

All animals in the pedigree were evaluated and ranked based on their breeding values for daily milk yield, age at first calving and calving interval. Superior animals would have high EBVs for milk and low (negative) EBVs for age at first calving and calving interval. It is important to consider the accuracy of each EBV during selection as this provides a measure of its reliability. The accuracy of an animal's EBV is the correlation between its true value and the estimated one (Mrode 2014). The higher the accuracy of an EBV, the lower the likelihood that it will change as more information is gathered and analysed for that animal.

EBVs are reported in plus or minus values, in the same units of measurement as the recorded trait and are easy to interpret. For example, a bull/cow with +8 breeding value for milk means that on average the daughters of this bull/cow have a genetic capacity to produce 4 litres more milk per day compared to the population of daughters of all other bulls in the herd. A bull/cow will pass on half of its genes to its calves so its EBVs is halved to estimate the average genetic worth of its progeny. The absolute value of an EBV indicates magnitude and the sign indicates direction of the breeding value effect. A positive sign indicates increase and a negative sign, decrease.

When selecting a bull to breed heifers and cows, positive values are preferable in certain situations such as milk yield or growth and negative values are preferred for traits such as birth weight or calving interval. Where bulls do not have a favourable combination for all traits of interest, corrective mating strategies should be employed by pairing the bulls and cows/heifers in such a way that weaknesses in the genetic attributes of either the bull or the cow are corrected or compensated for by either party or mate (Allaire 1977), this way, the overall positive breeding goals are achieved.

3.4 Genetic and phenotypic trend over time

One way of monitoring herd progress over time is by evaluating genetic and phenotypic trends for traits of interest. A genetic/phenotypic trend measures change in performance over time (typically years) due to change in mean breeding value or phenotypic value for the trait of interest in the population (Herbert and Bhatnagar 1988).

Information from trends give direction for future definition of breeding goals to support profitable and sustainable dairy business. Assumptions underlying trend analysis is that if animals with superior genetic merit have been used for breeding each year, then phenotypic and breeding value averages should increase over time. Regression coefficients of genetic and phenotypic trends for the entire population in both herds are represented in Table 2 and trendlines (only significant trends) in Figures 3 and 4. Annual genetic change was also calculated separately for bulls and cows in both herds and presented in Table 3.

Table 2. Mean, standard deviation (std-dev), heritability, repeatability, estimates of annual phenotypic and genetic changes

Herd	Trait	No.	Mean	Std-dev	Heritability	Repeatability	Δ phen	Δ gen
Kilifi	MY (kg)	161,322	15.06	4.92	0.27±0.06	0.45±0.03	0.97±0.07***	-0.26±0.02***
	AFC (months)	341	28.85	4.10	0.31±0.13	-	-0.12±0.07	-0.005±0.02
	CI (days)	295	447.5	96.86	0.14±0.12	0.14±0.12	2.72±1.77	0.67±0.40
Naivasha	MY (kg)	10,160	7.24	3.62	0.20±0.09	0.39 ± 0.03	0.29±0.59	-0.008± 0.009
	AFC (months)	163	37.98	5.57	0.24±0.27	-	0.14±0.19	0.003±0.007
	CI (days)	216	512.4	170.16	0.03±0.13	0.03 ± 0.15	-10.54±4.5*	0.19±0.58

(Δ), MY-milk yield, AFC- age at first calving and CI calving interval. *, **, ***mean significant at p<0.05, 0.01 and 0.001 respectively.

Table 3. Annual genetic gain for bulls and cows

Herds	Animal	Annual genetic gain		
		MY (kg)	AFC (months)	CI (days)
Kilifi	Sires	0.07	0.006	0.168
	Dams	-0.17***	0.008	0.030
Naivasha	Sires	-0.006	0.007	0.18
	Dams	-0.008	0.003	0.21

MY-milk yield, AFC- age at first calving and CI calving interval. *, **, ***mean significant at p<0.05, 0.01 and 0.001 respectively.

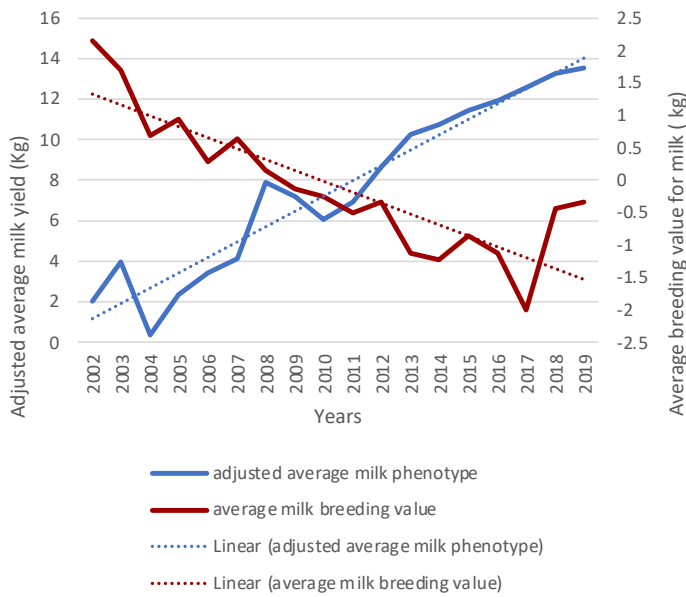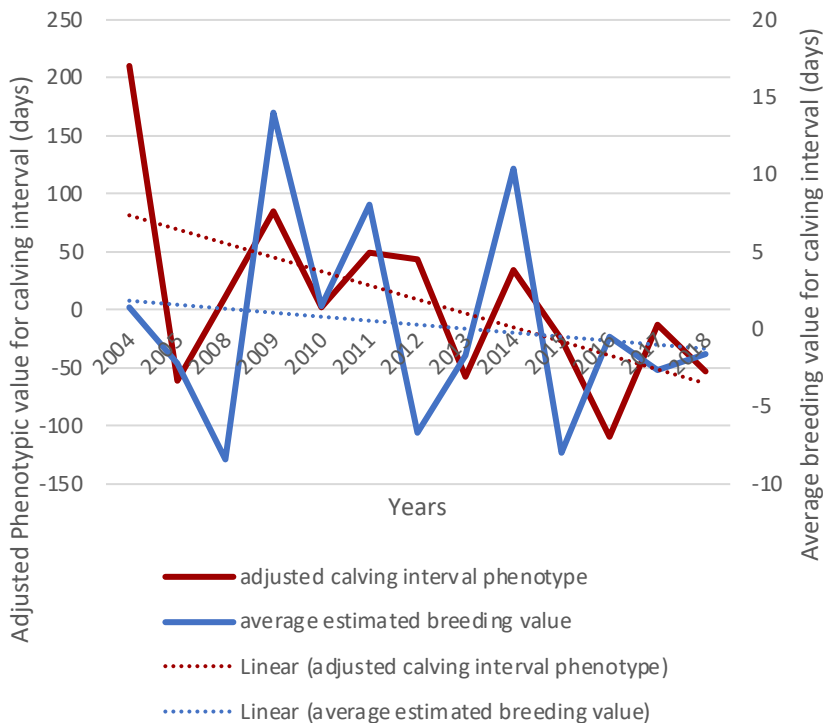Figure 3. Genetic and phenotypic trend for milk yield in the Kilifi herd.

Figure 4. Genetic and phenotypic trend for calving interval in the Naivasha herd.

In the Kilifi herd, the results indicate a significant increase in milk yield over time with a regression coefficient of 0.97 litres/year and a decline in milk breeding value with regression coefficient of -0.26 litres/year. Figure 1 shows that phenotypic and genetic trends for milk yield for the Kilifi herd changed in reverse direction over the course of time suggesting that phenotypic increase in milk yield is mostly due to management. Phenotypic and genetic trend for age at first calving and calving interval did not show significant change over time.

In the Naivasha herd, genetic and phenotypic trends for milk yield and age at first calving, showed no significant change over time (Table 2) but there was a favourable significant negative phenotypic trend for calving interval (-10.54±4.5) suggesting a reduction of about 10 days in calving interval over time in the herd although the genetic trend did not show a significant change over time.

No significant increase in breeding value was observed for sires and dams over time in both herds for these traits. Since these are mainly crossbred animals, this result suggests that no significant genetic gains were being achieved among the parental population or that sires and dams of similar or worse genetic merit have been used in the herds from year to year.

These results suggest that except for significant phenotypic improvement and decline in milk yield and calving interval, in the Kilifi and Nakuru herds, respectively, performance traits considered in this analysis have remained relatively unimproved over the period of herd data analysed. This might be an indication that selection pressure on these traits is low in the respective herds. However, considering these trends within breed groups might reveal a different picture even though this is not feasible in the present analysis due to the low within group sample sizes.

4 Conclusions and recommendation

Herd genetic trend showed no significant genetic progress made for milk yield, age at first calving and calving interval over the period of study (i.e. period covered by the data used in the analysis for both herds). Also, no significant increase in breeding value was observed within sires and dam populations over the same period in both herds.

Routinely calculating of breeding values for both herds is recommended to provide insights for designing optimal breeding plans and enable restricted selection of genetically superior breeding parents (bulls and replacement heifers) to ensure genetic progress is made in desired directions for all the traits.

While there was no genetic progress for any of the traits in both herds, there was a significant phenotypic increase in milk yield in the Kilifi herd and a significant decrease in calving interval in the Naivasha herd. Significant phenotypic improvement in these traits outside of genetic progress suggests proper management of the herd.

Farm records from both herds were first taken from paper copies and converted to digital records before data analysis. Digital record management is advised for improved efficiency of record-keeping, analysis and monitoring of animal performance. Digital tools eliminate time consumed in searching for historical farm records needed to make decisions and readily delivers accurate information needed to improve overall farm productivity.

A more complete delivering farm data management solution would involve integrating a trusted third-party platform which acts as a central hub in keeping farm records accessible and sharable, secure, and confidential and produces summaries for more efficient farm operations. The African Dairy Genetics Gain program (ADGG - https://www.ilri.org/research/projects/african-dairy-genetic-gains) has developed a farm management data platform for medium- and large-scale farms which stores farm data, analyses and generates reports on herd basis and on individual animal basis to support data driven decision-making on the farm for increased productivity and profitability. It has validation checks built in and can capture errors in spelling, dates and correct them in real time and flag important details which are missing at data entry point, thus ensuring high standards of data accuracy and consistency. The database also helps with scheduling and assigning tasks and activities on the farm.

Collectng of hair samples and subsequent genotyping of active bulls and their known relatives across herds in Kenya to optimize genetic linkages for better prediction and increased accuracy of breeding values is underway. Genotype information will help verify pedigrees, and farmer declared breed compositions to inform proper management of the animals for optimum extraction of their genetic potential.

Data management support and training will be provided to medium- and large-scale farms in Kenya as a guide on how to use the ADGG database and how to conduct genetic evaluation using freely available animal breeding and genetic software to determine genetic merit of animals for selection and breeding.

5 References

Aliloo, H., Mrode, R., Okeyo, A.M., Ni, G., Goddard, M.E. and Gibson, J.P. 2018. The feasibility of using low-density marker panels for genotype imputation and genomic prediction of crossbred dairy cattle of east Africa. *Journal of Dairy Science* 101(10): 9108–9127.

Allaire, F.R. 1977. Corrective mating methods in context of breeding theory. *Journal of Dairy Science* 60(11): 1799–1806.

Bourdon, R.M. 2000. *Understanding animal breeding*. 2nd ed. Hoboken, New Jersey, USA: Prentice Hall.

Herbert, S. and Bhatnagar, D.S. 1988. Genetic trends of economic traits in dairy cattle: A review. *Agricultural Reviews* 9(4): 200–216.

Hoorweg, J., Foeken, D. and Klaver, W. 1995. *Seasons and nutrition at the Kenya Coast*. The Hague, the Netherlands: African Studies Centre: Avebury.

Jaetzold, R., Schmidt, H., Hornetz, B. and Shisanya, C. 2010. *Farm management handbook of Kenya: Subpart B1a, Southern Rift Valley Province*. 2010, II, 213.

Javed, K., Babar, M.E. and Abdullah, M. 2007. Within-herd phenotypic and genetic trend lines for milk yield in Holstein-Friesian dairy cows. *Journal of Cell and Animal Biology* 1(4): 066–070. https://d-nb.info/1097289923/34

Katkasame, S., Tumwasorn, S., Thaninndratarn, B. and Pasanpanich, S. 1996. Trend analysis on milk production traits in the dairy farming promotion organization of Thailand. *Agriculture and Natural Resources* 30(2): 211–219.

Kosgey, I.S. and Okeyo, A.M. 2007. Genetic improvement of small ruminants in low-input, smallholder production systems: Technical and infrastructural issues. *Small Ruminant Research* 70(1): 76–88.

Meyer, K. 2007. WOMBAT—A tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *Journal of Zhejiang University Science B* 8(11): 815–821.

Mrode, R.A. 2014. *Linear models for the prediction of animal breeding values.* Cabi.

Oldenbroek, K. and van der Waaij, L. 2014. *Textbook animal breeding: Animal breeding and genetics for BSc students*. Wageningen, the Netherlands: Centre for Genetic Resources and Animal Breeding and Genomics Group, Wageningen University and Research Centre.

Satpal, D., Sivalingam, J. and Dinesh, K. 2012. Chisinau, Republic of Moldova: *Genomic and phenomic tools for livestock genome analysis*. Lap Lambert Academic Publishing GmbH KG.