



Report

# The second round of genomic evaluation of dairy animals from Makitosha Farm, Kenya

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## Introduction

Smallholder dairy production dominates in Kenya. Dairy farmers keep a wide range of crossbred dairy animals, which are derived from different exotic commercial dairy and local breeds, some of which are locally selected. Until recently, crossbred bulls were not included in the Kenya National Genetic Resource Centre (KAGRC)'s bull stud, more so because such animals were not subjected to requisite national performance recording and genetic evaluations. Makitasha Farm is one of the private farms which has been breeding crossbred dairy animals, for the hot and humid coastal areas of Kenya, and selling such breeding stock to the neighboring farmers. It was therefore strategic for Makitasha to partner with the Africa Asia Dairy Genetic Gains (AADGG) project. As part of the AADGG project's remit within the CGIAR's Sustainable Animal Productivity for Livelihoods, Nutrition and Gender inclusion (SAPLING) initiative, historical pedigree and production data of the animals at Makitasha Farm were collected using the AADGG's ICT data capture tools and selected bulls and cows genotyped as part of the broader AADGG platform activities (<https://hdl.handle.net/10568/134784>), within the Kenya's dairy recording database.

This report presents the evaluation and ranking of the animals at the Makitasha Farm following the analysis of this data, and it gives recommendations of the top ranked bulls for recruitment into the KAGRC bull stud for semen production and wider use and access by farmers through artificial insemination (AI). This report therefore documents the scaling of AADGG innovations following its initial successful piloting in Ethiopia and Tanzania (<https://hdl.handle.net/10568/136083>; and <https://hdl.handle.net/10568/116186>).

## Materials and methods

This report summarizes results from genetic and phenotypic analysis of Makitasha Farm across 19 years, from 2004 to 2023. The files received had 680 calving records and 210,607 milk records from 505 cows. The associated pedigree dataset contained a total of 1,206 records, with 233 recorded fathers and 573 recorded mothers. The maximum paternal family size was 62, while the maximum maternal family size was 9. Results from the analysis is presented in three parts. Part I includes results from breed composition analysis. Part II gives an overview of the pedigree structure and part III presents results on genetic parameters for milk yield, age at first calving and calving interval, associated genetic and phenotypic trends as well as estimated breeding values of bulls and cows.

### I. Breed composition

Principal component analysis (PCA) was performed with a total of 686,119 imputed marker SNPs shared among 366 individuals to cluster animals and explore the relationships among and within breeds. Each data point on the plot represents an individual animal within its respective breed and different breeds are color-coded for clarity. The green data points correspond to European taurine animals. The PCA of this taurine cattle breeds formed overlapping clusters along the upper and lower left quadrant and were not clearly separated suggesting that this group did not constitute a homogenous population. Indicus cattle color coded blue clustered closely in the lower right quadrant, indicating genetic similarity while the African taurine cattle color coded red clustered in between the indicus and European taurine cattle. They were, however, closer to the taurine cattle in their grouping.

Makitasha cattle population has notable diversity in breed composition, indicating a mix of genetic backgrounds. Color coded purple, the animals showed clear separations towards the indicus, European and African taurine cattle clusters suggesting genetic diversity and showing the the genetic influences of these breeds on the Makitasha Farm cattle population. Some individuals

exhibit a dominant presence of a specific breed, while others show a more balanced combination of multiple breeds. There is variability in the contribution of each breed, suggesting a heterogeneous population structure.

Following are some key observations according to breed:

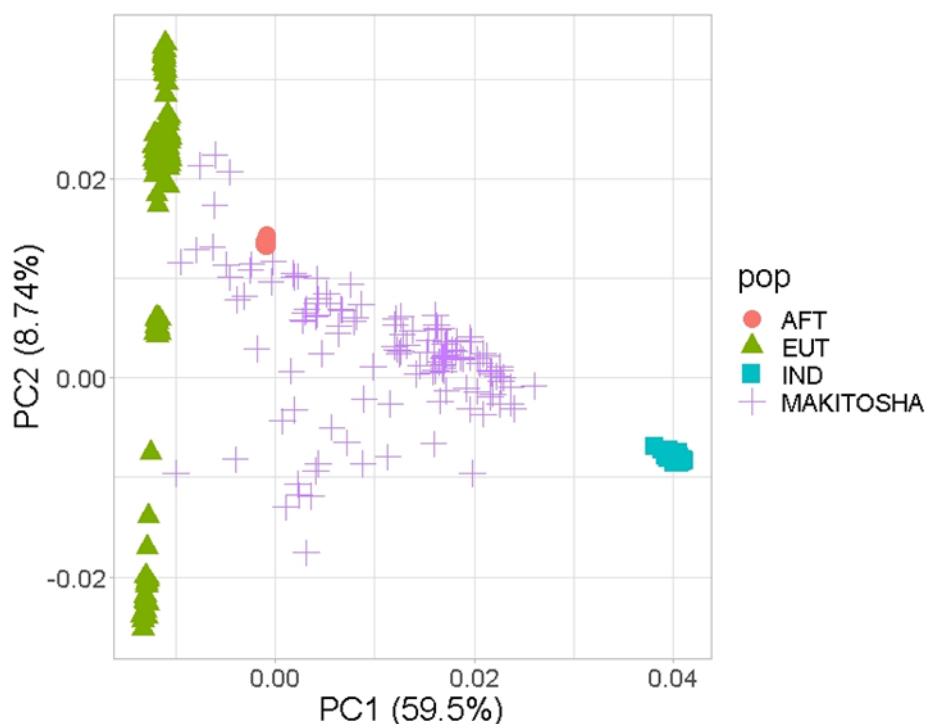
**Holstein:** The population exhibits a wide range of Holstein proportions, ranging from very low (e.g., 2.03%) to dominant percentages (e.g., 68.76%). The mean Holstein proportion across the population is approximately 14.64%.

**African taurine:** African taurine proportions vary, with some individuals having very low or negligible African taurine genes (e.g., 0.0%) and others showing more substantial percentages (e.g., 8.77%). On average, the African taurine contribution across the population is around 1.16%.

**Ayrshire:** Ayrshire proportions are diverse, spanning from minimal values (e.g., 6.86%) to higher percentages (e.g., 55.01%). The average Ayrshire proportion for the population is approximately 20.08%.

**Gir:** Gir proportions also vary widely, with some individuals having low Gir percentages (e.g., 1.28%) and others having a significant contribution (e.g., 66.82%). The mean Gir proportion across the population is roughly 21.45%.

**Jersey:** Jersey proportions show a broad range, from minimal values (e.g., 0.97%) to substantial percentages (e.g., 32.94%). The average Jersey proportion in the population is approximately 14.66%.



- i. Figure 1. PCA (Principal Component Analysis) plotted to visualizes the genetic relationship and diversity among various animal in the herd.

## II. Herd composition

Trends observed in the data showing farm breed composition of bulls and cows from 2013 to 2022 are presented below.

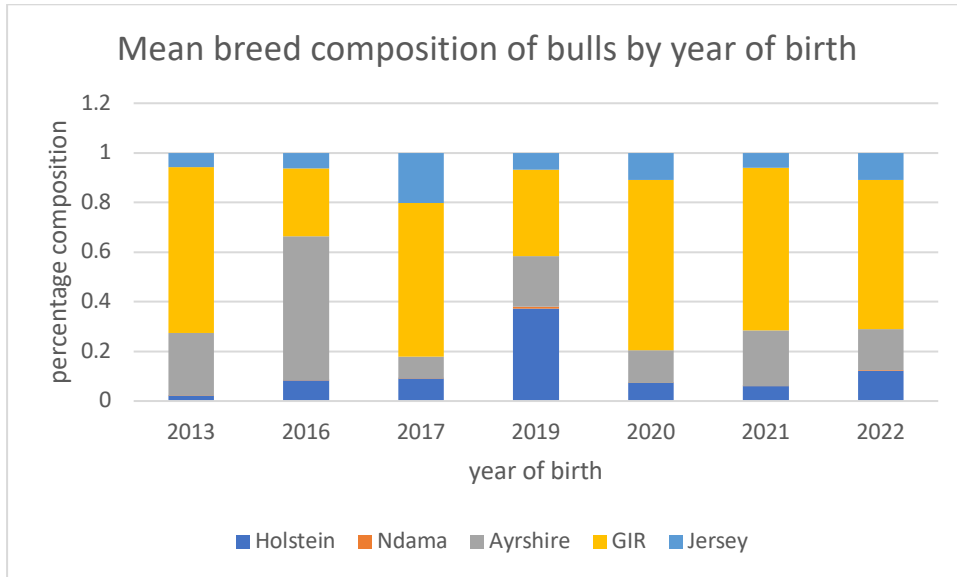


Figure 2. Mean breed composition of bulls by year of birth.

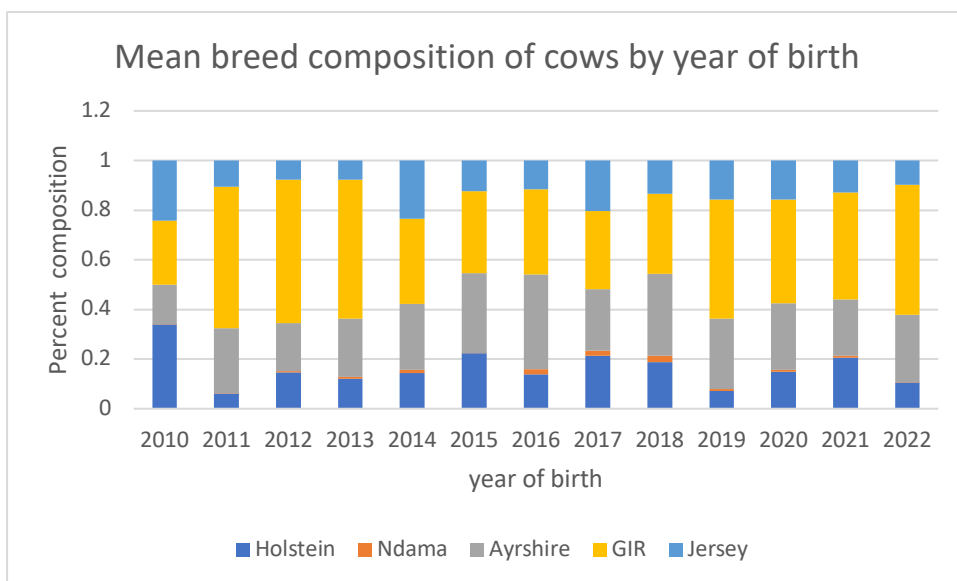


Figure 3. Mean breed composition of cows by year of birth.

Following are some key observations:

For bulls, proportions of Holstein ranged between approximately 2% and 37%, and in cows, proportions varied from 6% to 34% showing fluctuations without a clear upward or downward trend across years. African taurine consistently maintained a minimal presence, remaining close to 0% in both bulls and cows. Ayrshire displayed proportions fluctuating between 9% and 58% in bulls, whereas cows showed variations from around 16% to 38%. Gir showed fluctuations in proportions for bulls, varying between 27% and 69%, while for cows, it fluctuated from about 26% to 58%. For Jersey, bulls showed proportions varying between 6% to 20%, similar to cows, which fluctuated between 10% and 24%. Overall, both bulls and cows displayed fluctuating proportions for Holstein, Ayrshire, Gir, and Jersey breeds without a specific consistent trend of increase or decrease over the reported years while African taurine consistently maintained minimal representation. The proportion of Gir cattle across the years in both bulls and cows indicated a relatively stable and higher representation compared to the other listed breeds.

### III. Performance traits

#### *Summary statistics*

Table 1. Summary statistics for MY, AFC and CI.

Trait	n	mean	std-dev	min	max
MY (Liters)	210607	14.37	5.25	0.5	39.5
AFC (Months)	558	29.31	5.11	18	48
CI (Days)	679	445.87	97.71	265	730

#### *Pedigree data*

Pedigree data for the herd had 1,206 animals and after pruning, 940 individuals remained with 233 sires and 573 dams with a maximum sire family size of 62 and a maximum dam family line of 9. Average inbreeding coefficient across the herd is 0.61% and 5.21% among inbred animals.

### IV. Phenotypic and genetic parameters and herd progress for milk yield (MY), age at first calving (AFC) and calving interval (CI)

Estimates for genetic change over time was obtained by averaging breeding values within year of birth and regressing them on years of birth. For phenotypic change, means within year of birth was regressed on years of birth. Furthermore, an evaluation of the genetic diversity among bulls and cows born before and after 2010 was carried out to.

Table 2. Heritability repeatability estimates of annual phenotypic and genetic changes ( $\Delta$ ) for MY, AFC, CI.

Trait	heritability	repeatability	$\Delta$ phen	$\Delta$ gen
MY (Liters)	0.50 $\pm$ 0.05	0.55 $\pm$ 0.02	-0.36 $\pm$ 0.03*	0.02 $\pm$ 0.01
AFC (Months)	0.31 $\pm$ 0.11	-	-0.18 $\pm$ 0.07*	0.008 $\pm$ 0.009
CI (Days)	0.27 $\pm$ 0.17	0.27 $\pm$ 0.12	0.84 $\pm$ 0.8	0.14 $\pm$ 0.12

\*Statistically significant change across years at  $p < 0.05$ .

Table 3. Estimates of annual genetic changes in breeding value pre and post 2010 ( $\Delta$ ) for MY, AFC, CI.

Trait	Bulls $\Delta$ ebv		Cows $\Delta$ ebv	
	pre-2010	post-2010	pre-2010	post-2010
MY (Liters)	-0.11	0.03	-0.11**	0.15**
AFC (Months)	-0.02	-0.05	-0.02	0.03
CI (Days)	0.34	0.87	0.26	0.23

\* Statistically significant change across years at  $p < 0.05$ .

For milk yield (MY), a fixed regression animal model was used to analyze the data. The model was adjusted for fixed effects of year and month of calving, parity, age nested within parity and breed group. Mean daily milk yield was 14.36 liters with a standard deviation of 5.25 liters. The highest recorded milk volume reached 39.5 liters, while the lowest was 0.50. Heritability for milk yield in this herd was moderate, at  $0.50 \pm 0.05$  and repeatability was high at  $0.55 \pm 0.02$ , suggesting that breeding values for milk has a moderate influence on the phenotypic values for milk yield. The phenotypic trend for milk yield suggests a significant decrease (0.36 liters/year) over the years but considerable genetic change was not observed (Table 2). This suggests the decrease in milk yield can be attributed to alterations in management practices as farm genetics seem to have remained relatively stable over time. Moreover, genetic evaluation of the variation within bulls and cows born pre and post 2010 revealed bull genetics used in the farm herd have remained consistent overtime and for cows, before 2010 (Table 4, Figure3), a decrease in breeding value was noted, which was subsequently followed by an increase post 2010 (Table 3, Figure 3). This indicates that the decline in milk yield may be linked to alterations in farm management practices as genetics of cows has seemingly increased over time after 2010.



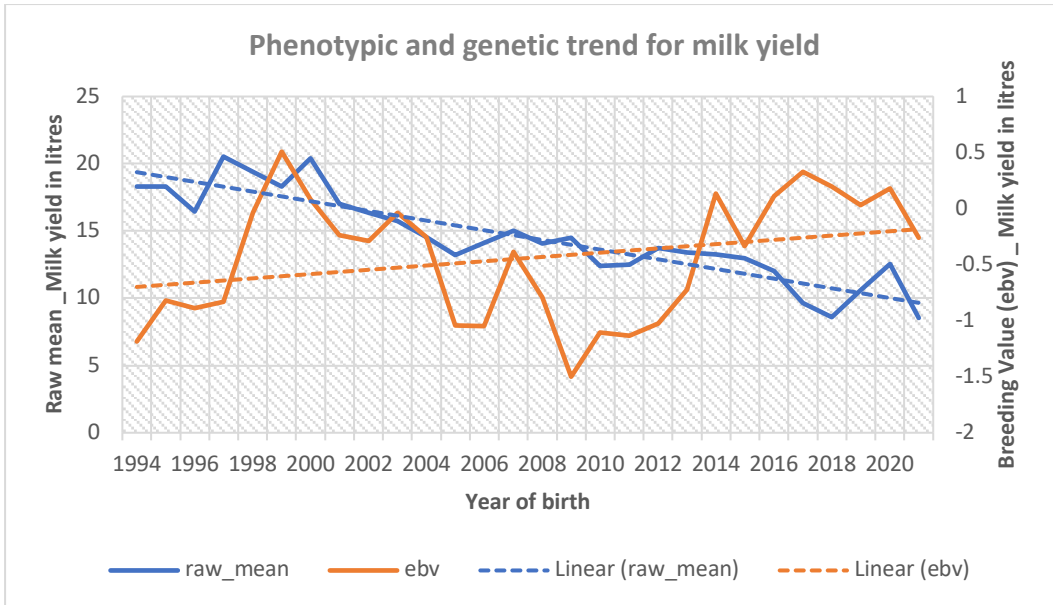


Figure 4. Phenotypic and genetic trend for milk yield

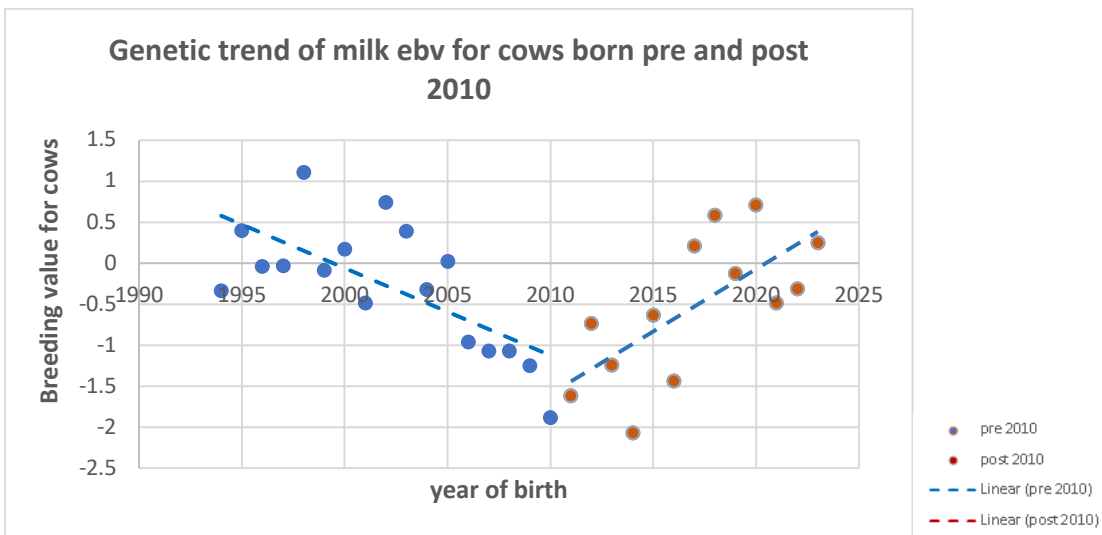


Figure 5. Genetic trend of milk yield for cows born pre and post 2010

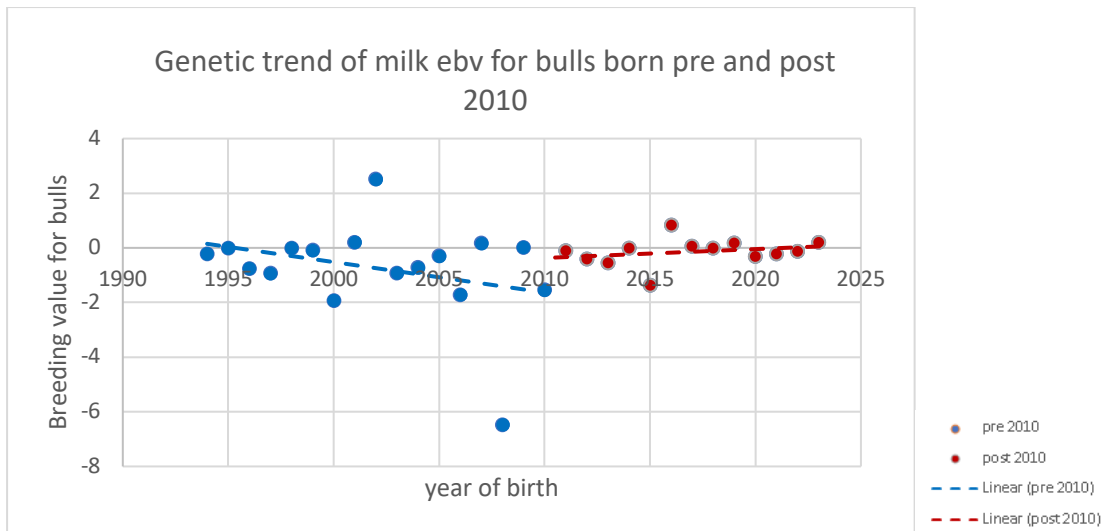


Figure 6. Genetic trend of milk yield for bulls born pre and post 2010

For age at first calving (AFC), the model included breed group, year and month of birth. Average AFC ranged between 18 to 48 months and mean AFC was 29.31 months with a standard deviation of 5.10 months. Heritability estimates for AFC was 0.31, while the phenotypic trend showed a significant reduction of 0.18 months (approx. 5.4 days), over the years, there was no notable change in breeding values, suggesting that the reduction in AFC might be due to change in management practice over time. Assessment of genetic variation among bulls and cows born before and after 2010 demonstrated that the breeding value related to AFC have remained consistent over time.

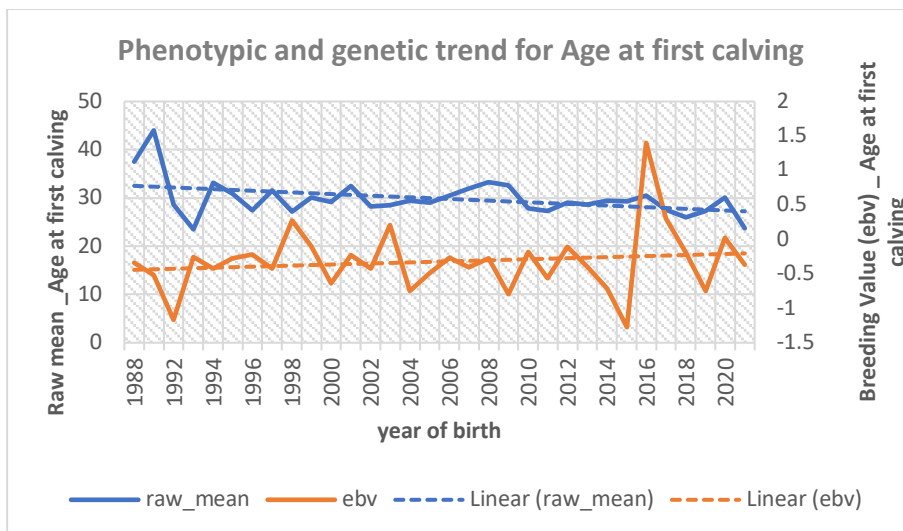


Figure 7. Phenotypic and genetic trend for age at first calving

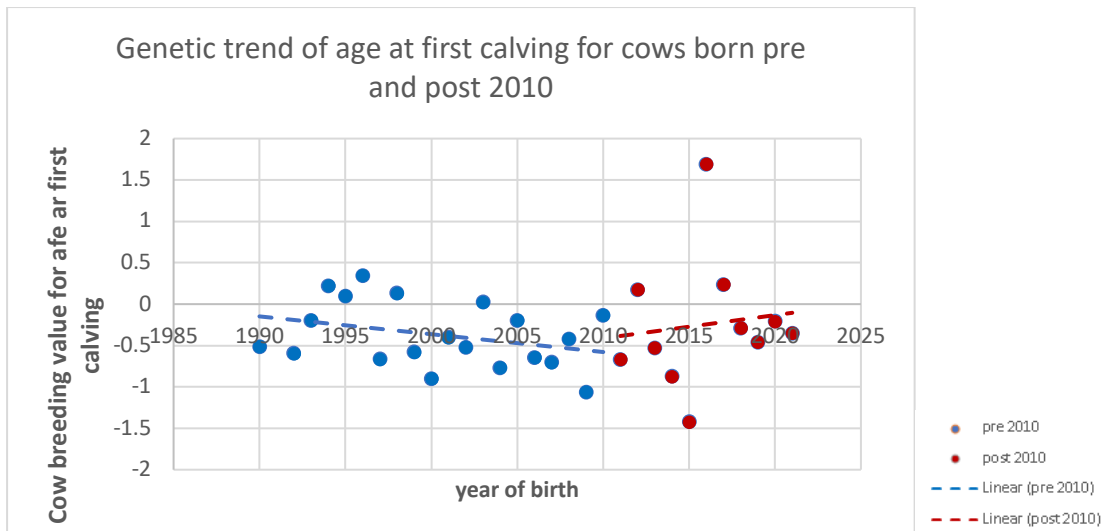


Figure 8. Genetic trend of age at first calving for cows born pre and post 2010

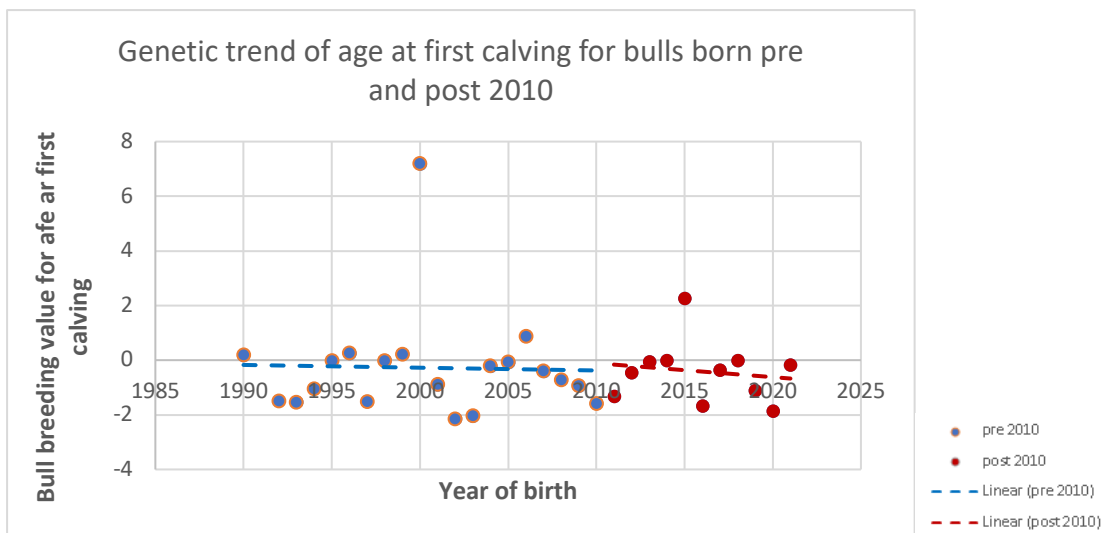


Figure 9. Genetic trend of age at first calving for bulls born pre and post 2010

The model fitted to calving interval (CI) included year and month of calving, breed group, parity and age nested within parity. and mean CI was 445.869 days (approx. 15 months) with a standard deviation of 97.71 days (approx. 3.26 months) and it ranged from 265 days (approx. 9 months) to 730 days (approx. 24 months). Both phenotypic and genetic trend for calving interval shows no significant change ( $0.14 \pm 0.12$ ) in breeding value and phenotypic trend ( $0.84 \pm 0.80$ ) over time. The evaluation of genetic diversity among bulls and cows born prior to and after 2010 showed breeding value associated with CI has remained relatively unchanged.

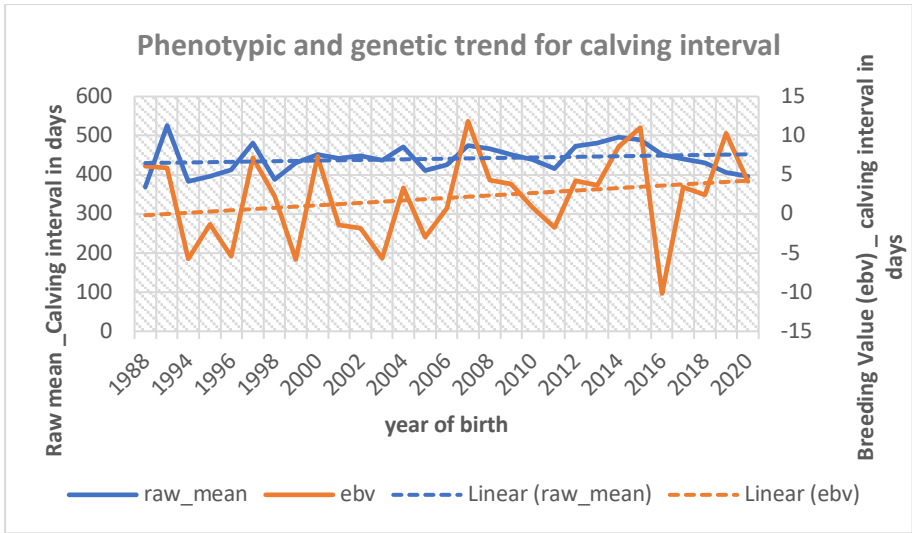


Figure 10. Phenotypic and genetic trend for calving interval

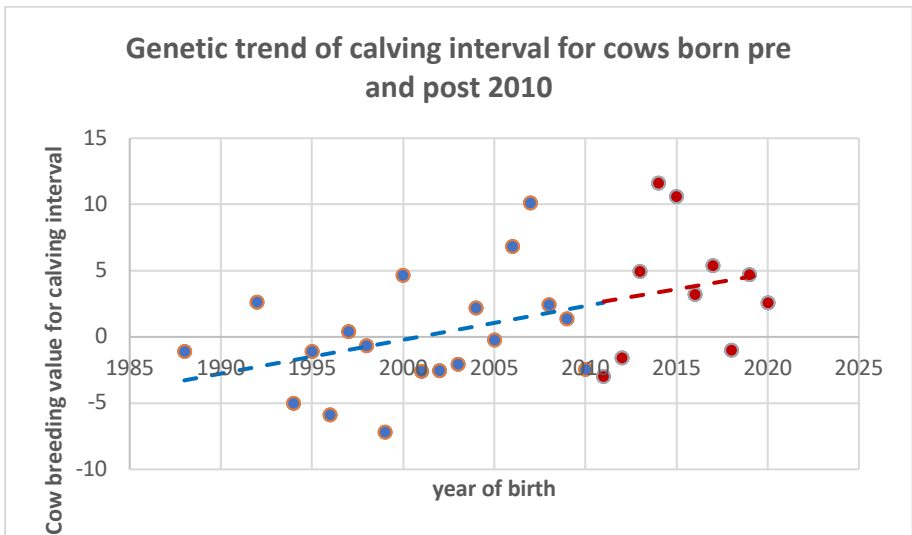


Figure 11. Genetic trend of calving interval for cows born pre and post 2010

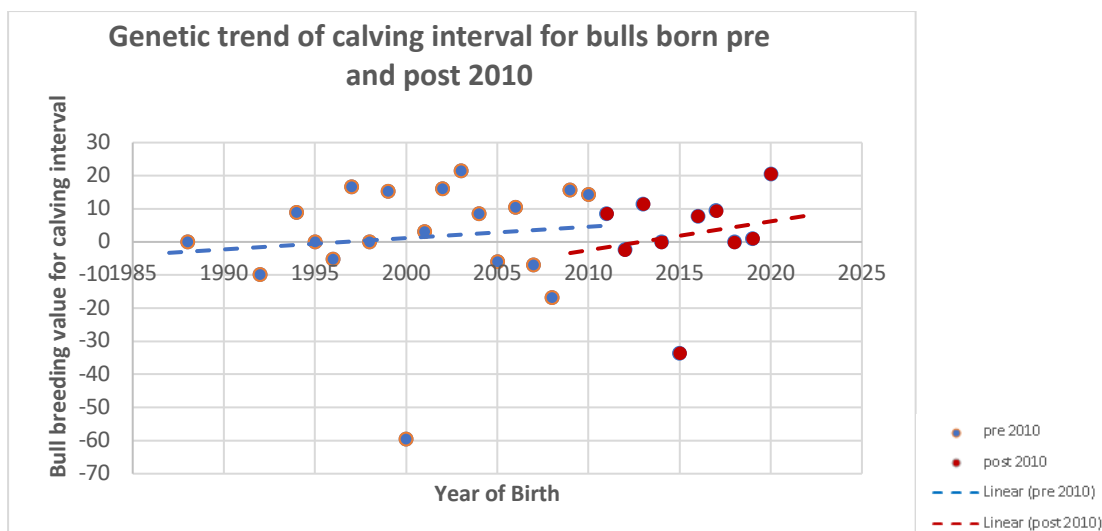


Figure12. Genetic trend of calving interval for bulls born pre and post 2010

### Genetic merit of animals – breeding value

Breeding values are indicators of an animal's genetic potential or ability to pass on desirable traits. These values are calculated for each animal by taking into account their own performance data as well as the performance of their parents, siblings, and offspring, while also adjusting for various environmental and management factors such as the month or season of calving, parity, age at calving, breed, and more. Animals with the highest breeding values are regarded as genetically superior and are chosen as breeding stock for the next generation. It is crucial to accurately estimate these breeding values to facilitate rapid genetic improvement within the herd.

All cows with milk yield and all animals in the pedigree have been evaluated and ranked based on their breeding values for daily milk yield, age at first calving and calving interval and results are in a separate document named "Bulls\_Cows\_EBVs\_Ranking 2023."

### Interpreting breeding values

If a bull or cow has a breeding value of +8 for milk yield, it indicates that, on average, their offspring (daughters) possess a genetic potential to produce an additional 4 liters of milk per day compared to the daughters of all other bulls in the population. As a parent, an animal passes on half of their estimated breeding value (EBV) to their progeny. Mean EBV for the top 20% (67) bulls 1.28 is and 1.83 for cows and the average milk yield of these top 20 cows is 16.59 liters. For continued herd genetic progress, only bulls with EBVs higher than this mean should be selected and used with replacement cows having ebv or milk yield that are equal to or exceed the benchmark for cows. Additionally, average ebvs for AFC and CI for the top 20 bulls were - 2.01 and -13.57 for cows, it was -2.84 and -22.09. AFC and CI are typically measured in units of time and negative values generally indicate a propensity for earlier or shorter time, suggesting a favorable genetic predisposition for these specific traits in the offspring. A negative breeding value for both AFC and CI suggests that the offspring of this animal would likely calve at an earlier age or would tend to have a shorter period between calvings compared to the population average. To ensure continued genetic herd progress for these traits, only bulls with EBVs lower than the mean (-2.97 and -4.4989 ) should be used and with replacement cows that possess EBVs equal to or lower than the stipulated benchmarks (-23.46 and -49.2683).

## Conclusion and recommendations

Genetic trend analysis revealed limited herd genetic progress and assessment of genetic variation within bulls and cows born before and after 2010 showed bull genetics used in the Makitasha Farm have remained consistent over time. For cows, a decline in breeding value was observed before 2010 followed by an increase post 2010. Nonetheless, significant phenotypic changes were noted for milk yield and age at first calving and these might be attributed to alterations in management practices and cow genetics.

To ensure ongoing enhancement of herd genetics, it is recommended to exclusively utilize bulls and cows whose breeding values (EBVs) for milk yield, age at first calving, and calving interval meet or exceed the predefined benchmark set by the average of the top 20% bulls and cows in the population.

In cases where obtaining enough animals becomes challenging due to strict standards, there is room to slightly adjust the minimum standards for traits. However, caution must be exercised in selecting animals with a favorable combination of traits, such as a positive breeding value for milk yield but negative breeding values for age at first calving and calving interval. This approach ensures that selected bulls and cows will produce offspring with increased milk yield but lower age at first calving and calving interval, contributing to desired genetic outcomes.



The CGIAR Research Initiative on Sustainable Animal Productivity for Livelihoods, Nutrition and Gender inclusion (SAPLING) is working in seven countries focusing on livestock value chains to package and scale out tried-and-tested, as well as new, innovations in livestock health, genetics, feed and market systems. SAPLING aims to demonstrate that improvements in livestock productivity can offer a triple win: generating improved livelihoods and nutritional outcomes; contributing to women's empowerment; and reducing impacts on climate and the environment. Its seven focus countries are Ethiopia, Kenya, Mali, Nepal, Tanzania, Uganda and Vietnam.

It forms part of CGIAR's new Research Portfolio, delivering science and innovation to transform food, land, and water systems in a climate crisis.

