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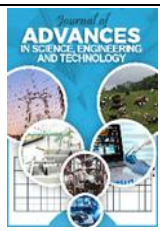

Performance of Improved Indigenous Chicken Genotypes in Kenya

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ABSTRACT

The Kenyan poultry industry contributes significantly to food security, nutrition, and economic development, with indigenous chicken constituting more than 84% of the country's chicken population. The low productivity of these indigenous breeds, primarily due to poor genetics, has hindered their potential. The Kenya Agricultural and Livestock Organization (KALRO) developed three breeding lines of chicken: KC1, KC2, and KC3. This study aimed to evaluate the effect of genetics on the performance of two KALRO breeding lines, KC1 and KC3, and the control. This study employed a completely randomized design with four replicates per genotype. Daily feed intake and weekly body weight were recorded for 135 chicks per genotype (KC1, KC3, and control F2) from hatch to 18 weeks. General Linear Model (GLM) determined the effects of genetics, temporal factors, and their interaction on chicken performance during the chick and grower stages. Results from the study showed genetics played a major role in the amount of feed KC3 consumed, while the KC1 breeding line achieved better live weight than the control group ($p < 0.001$). Growth was substantially affected by both time and genetics. The performance evaluation in the breeding lines revealed that the KC1 and KC3 breeding lines showed a superior outcome than the control. Therefore, farmers can use the KC1 and KC3 lines as they enable better production levels. Future studies should consider evaluating the adaptability and performance of KC1 and KC3 breeding lines across diverse agroecological zones to support widespread adoption.

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1. Introduction

Poultry is the leading and crucial livestock industry segment. Globally, it plays a major role in improving food security, nutrition, and strengthening economic growth through income generation. It is the most rapidly growing subsector in the agriculture line, especially in developing countries (Mottet & Tempio, 2017). Demographic factors such as increasing populations, urbanization, and rising incomes have contributed significantly to the growth of this sector. In low-income countries, it provides an affordable source of animal protein and essential nutrients for vulnerable populations.

According to the Kenya National Bureau of Statistics (KNBS), Livestock Statistics (2020), Kenya's Indigenous chicken (IC) constitutes 84.6% of the national population, estimated to be 47 million. These chicken have unique attributes to withstand harsh environmental conditions, poor quality feeds, scavenging resources, disease challenges, and poor management practices (Irene et al., 2022). They have developed these qualities over the years due to natural selection (Padhi, 2016). IC serves as a reservoir of genomes to improve yield in exotic germplasm for tropical adaptability and disease resistance(Padhi, 2016). They are found in all ecological zones of Kenya, contributing about 46% and 58% of the country's total meat and egg consumption, respectively (Cheruiyot & Adhiaya, 2021). However, they have slow growth rates and lay relatively fewer eggs due to natural selection and lack of inputs (Dessie et al., 2011).

Studies have demonstrated that genetic factors play a significant role in determining chicken growth potential and performance. Traits such as body weight, body size, and feed efficiency have moderate to high

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heritability, indicating a strong genetic influence on growth (Nawaz et al., 2025). Selective breeding is also a pivotal genetic strategy for enhancing chicken growth traits (Kenchaiwong et al., 2026). This understanding has paved the way for selective breeding programs to improve growth traits in commercial chicken breeds. KALRO developed three breeding lines of chicken, namely KC1, KC2, and KC3. KALRO Chicken (KC) is a synthetic breed population that originated from a dual-purpose hybrid subjected to a systematic and continuous inter-se mating, resulting in highly segregated individuals in subsequent generations (Wambua et al., 2021). Based on plumage dominance, three distinct groups were isolated: black and white barred plumage (KC1), black plumage (KC2), and brown and white barred plumage (KC3). The three KALRO breeding lines were subjected to within-line mating to stabilize their respective plumage color. This breeding strategy aimed to address poor genetics, feed intake, slow growth rate, and low productivity. These breeding lines may differ in their performance, and therefore, there needs to be more information regarding the genetic implications of these chicken lines in terms of their performance in feed intake and growth. This study aims to fill this gap by evaluating the genetic effects on the performance of KALRO genotypes on feed intake and growth during the chick and grower stages.

2. Material and Methodology

2.1. Study location

On-station studies were conducted at the Non-ruminant Research Institute (NRI), KALRO Kakamega, located in Kakamega town along the Kisumu - Webuye highway. Kakamega town is in western Kenya, about 30 km north of the equator and approximately 50 km north of Kisumu. It is situated at 37° 75'E 20°15'S and 1585m a.s.l., and experiences mean annual temperatures of 25°C and rainfall ranging from 1850 to 1916 mm (Burgin et al., 2018)

2.2. Experimental birds and sampling strategy

In this study, the experimental birds were two breeding lines of Improved Indigenous Chicken of KALRO, KC1, KC3, and F2, the control group. F2 consisted of the second-generation progeny resulting from crossing KC1 and KC3 lines. A sample of 135 chicks from each test breeding line was randomly selected from the KALRO NRI poultry hatchery. This method ensured equal chances for each chick's inclusion in the trial (Tipton et al., 2014). This approach ensured a representative and unbiased sample, reducing bias or systematic errors. Chicks were weighed individually upon hatching using a digital Ken Trac weighing balance and placed in a circular brooder with wood shavings as litter. The diameter of the brooder was approximately 1.8 - 2.1 m, recommended for 135 chicks (Alade, 2013). Infrared heating lamps were also placed in the brooder to provide warmth for the chicks. The brooding period was 28 days, and three brooders were used for each test genotype.

After the brooding phase, the birds were sexed on day 28 and transferred to pens, where an equal number of males and females belonging to each genotype were placed in each pen from the growing phase to the point of lay. Using a Completely Randomized Design (CRD), daily feed intake and weekly weight data were collected across four replicates for each genotype. The birds were reared on deep litter from 4 to 18 weeks of age in separate pens, but using similar feeding management.

2.3. Management of the experimental birds

For each treatment, birds were offered clean water ad libitum and a measured quantity of feed at 10% above the recommended intake, taking into account feed wastage due to the behavior of the birds. The amount of feed was adjusted weekly based on the feed intake of the birds and the development stages of the birds. A starter ratio of 18% Crude Protein and 2800 Kcal/kg Metabolizable Energy (ME) was given to the chicks up to eight weeks of age, and from eight weeks onwards, feed was changed to a grower ration of 16% CP and 2800 Kcal/kg ME.

Vaccinations were administered, ensuring optimal health. At day old, the chicks were vaccinated against Marek's disease through subcutaneous injection and against Newcastle disease and infectious bronchitis through aerosol spray. These vaccinations were carried out at the hatchery. On days 14, 21, 42, and 56, the chicks were administered the Gumboro, Newcastle live, fowl pox, and fowl typhoid vaccine respectively. Additionally, they were given anti-coccidial medications when necessary.

2.4. Data collection

The study involved weekly weighing of all the birds in each pen and allocation, collection, and weighing of feed in each genotype as suggested by Negash et al. (2023). Accurate weights and feed amounts were recorded using an electronic weighing scale. The data was used to track chick growth and monitor feed intake. Microsoft Excel and data sheets were used to organize and visualize data. The experiment calculated parameters between feed intake and growth rate through specific measurements for each genotype. The total feed distribution to birds minus their leftover amount resulted in the calculation of feed intake while considering the pen's bird population. In recognizing that birds in the three breeding lines could have varying phenotypes segregated across sex, they were physically assessed for secondary sexual characteristics soon after the brooding. Sexual dimorphism was subsequently accounted for by maintaining a 1:1 male-to-female ratio across the replicates and genotypes. Growth was tracked at the pen level to capture overall flock productivity. The mean weekly weight was computed by taking the total biomass of the pen and dividing it by the bird count. Although sexual dimorphism naturally causes males and females to grow at different rates, using pooled pen averages provided a more realistic metric for dual-purpose systems where mixed-sex management was the standard. Enforcing a strict 1:1 sex ratio in every pen ensured that these mean weights remained a reliable, normalized baseline for comparing the genetic potential of the three lines.

2.5. Data Analysis

Stata/IC 15.0 facilitated data analysis, with the Generalized Linear Model (GLM) used to compare performance across the three breeding lines. Considering the repeated-measures nature of the data arising from weekly metrics, both categorical and temporal variations were accounted for in the model. Consequently, the fixed effects model was conceptualized as represented in Eq.1

$$Y_{ijk} = \mu + G_i + W_j + (G + W)_{ij} + \varepsilon_{ijk} \quad (1)$$

Where Y represents mean live weight or feed intake, all measured in grams and computed at pen-level, G is the fixed effect of the genotype, W represents time/age, i is the genotype (KC1, KC3, or F2), j is the age of the bird when measurement was done, and k represents the specific pen. Y_{ijk} gives a specific result such that, for instance, references a bird taken from KC1, measured at week 4, and chosen from pen 2.

The study focused on mean feed intake and mean live weight, analyzed as pen-level averages. Sexual dimorphism was controlled for by the strict 1:1 ratio of male and female birds in each pen. Age was the main covariate for mapping the growth curves. Data were assessed for normality and variance homogeneity using Shapiro-Wilk and Levene's tests. For significant differences across genotypes, Tukey's Honestly Significant Difference (HSD) test was run to identify the exact point of significant difference.

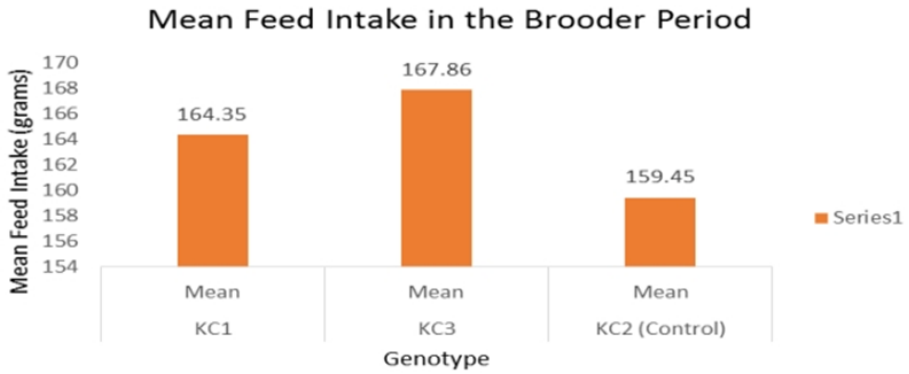

Fig. 1: Comparing Mean Feed Intake across Genotype.

3. Results

The examination determined whether genetic makeup, alongside time, affected the feed intake and weight increase of KC1, KC3, and the control group. The animals' genetic makeup significantly influenced their feed consumption and weight development during the chick and grower stages ($p < 0.001$)

3.1. Feed intake in chicks

All three variables of genetics and temporal factors, along with interaction terms, produced significant effects on feed consumption during the growth period. The genetic factors examined through KC1, KC3, and the control group ensured 73.6% of total feed intake variability ($\eta^2 p = 0.736$, $p < 0.001$). KC3 showed the highest average feed intake, consuming 8.4g more than the control group during the entire brooder period, followed by KC1, which consumed 4.9g more than the control group in the same period (Fig. 1). These results suggest that the KC3 line is genetically predisposed to higher feed consumption during early growth. The interaction between genetics and time was also significant ($\eta^2 p = 0.758$, $p < 0.001$), indicating that feed intake increased across all genetic lines as the chicks aged, with KC3 consistently consuming more feed than both KC1 and the control group throughout the eight weeks, as summarized in Table 1

Table 1: Tests of Between-Subjects Effects: Brooder Feed Intake.

Source		Df	Mean Square	F	Sig	Partial Eta Squared
Intercept	Hypothesis	1	5754043.12	25.218	.001	.759
	Error	8	228174.196[a]			
Genetic Factor	Hypothesis	2	1090.168	22.471	.001	.736
	Error	16	48.515[b]			
Temporal Factor (Weeks)	Hypothesis	8	250098.639	4720.294	.001	1.000
	Error	16	52.984[c]			
Genetic *Temporal Factors	Hypothesis	16	52.984	26.394	.001	.758
	Error	135	2.007[d]			

a = MS(Error) for testing the intercept effect, computed using the between-subjects error term (df = 8).
b = MS(Error) for testing the main effect of the genetic factor, based on the between-subjects error term (df = 16).
c = MS(Error) for testing the main effect of the temporal factor (weeks), based on the within-subjects error term (df = 16).
d = MS(Error) for testing the interaction effect between genetic and temporal factors, based on the residual within-subjects error term (df = 135).
KC1, KC3, and F2 represent the genetic lines evaluated. Week represents age in weeks. The statistical significance was performed at $P \leq 0.05$

3.2. Live weight in chicks

Genetic factors significantly impacted chick weight, with apparent differences emerging between the KC1, KC3, and control groups. KC1 had the highest average weight gain, with chicks weighing 40.4g more than the control group ($p < 0.001$), while KC3 chicks weighed 28.4g more than the control group ($p < 0.001$) (Fig. 2).

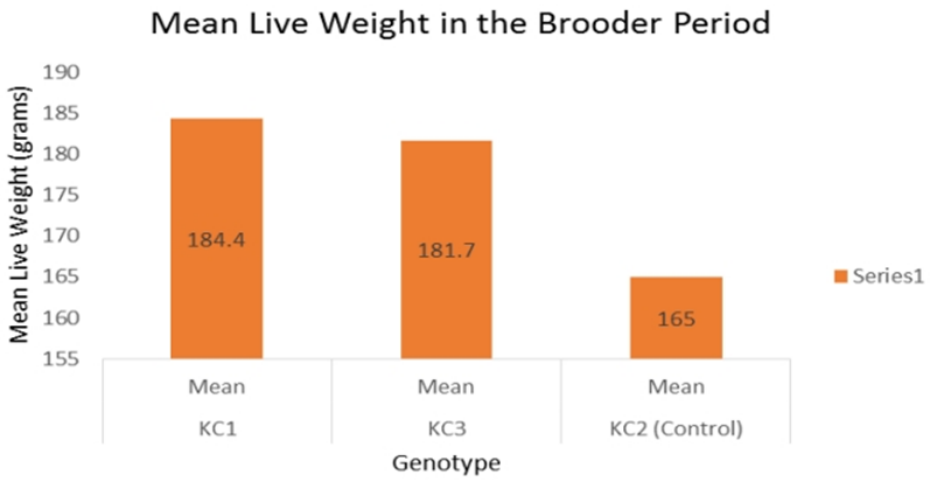

Fig. 2: Comparing Mean Live Weight across Genotype.

Genetics accounted for 44.8% of the variance in chick weight (η^2p = 0.448). These findings suggest that KC1 and KC3 outperformed the control group, with KC1 having a slight advantage. Meanwhile, the temporal factor accounted for 99.4% of the variance in chick weight (η^2p = 0.994), showing that age strongly influences growth across all genetic lines (Table 2).

Table 2: Tests of Between-Subjects Effects: Brooder Live weight

Dependent Variable: Live weight (grams)						
Source		**Type III Sum of Squares**	**df**	**Mean Square**	**F**	**Sig.**	**Partial Eta Squared**
Intercept	Hypothesis	6977664.207	1	6977664.207	20.526	.002	.720
	Error	2719659.079	8	339942.319[a]			
Genetic factor	Hypothesis	12935.218	2	6467.609	6.582	.008	.448
	Error	15965.424	16	982.605[b]			
Week	Hypothesis	2980785.527	8	372598.191	348.625	.000	.994
	Error	17100.229	16	1068.764[c]			
Genetic factor* week	Hypothesis	17100.229	16	1068.764	12.438	.000	.596
	Error	11600.480	135	85.929[d]			

a. .912 MS (week) + .088 MS(Error)
b. .912 MS (Genetic factor * week) + .088 MS(Error)
c. MS (Genetic factor * week)
d. d. MS(Error)

KC1, KC3, and F2 represent the genetic lines evaluated (F2 = control). Week represents age in weeks. Superscript letters (a, b, c, d) denote corresponding error terms in the GLM. Statistical significance was performed at $P \leq 0.05$. Partial Squared represents the effect size, indicating the proportion of variation explained by each factor. However, as seen in Table 3, the differences between KC1 and KC3 were not statistically significant ($p = 0.279$).

Table 3: Multiple Comparisons: Brooder Live Weight.

Dependent Variable: Weight (grams)				
Tukey HSD				
(I) Genetic factor	**(J) Genetic factor**	**Mean Difference (I-J)**	**Std. Error**	**Sig.**
KC1	KC3	2.7324	1.78398	.279
	F2	19.4524*	1.78398	.000
KC3	KC1	-2.7324	1.78398	.279
	F2	16.7200*	1.78398	.000
F2 (Control)	KC1	-19.4524*	1.78398	.000
	KC3	-16.7200*	1.78398	.000

Based on observed means.
The error term is Mean Square (Error) = 85.929.
*. The mean difference is significant at $P \leq 0.05$ level and was compared using Tukey's HSD test.

3.3. Feed Intake in Growers

In the grower stage, feed intake remained significantly influenced by both genetics and temporal factors. The genetic factor explained 70.8% of the variance in feed intake among growers ($\eta^2p = 0.708$, $p < 0.001$). The temporal factor accounted for 96.8% of the variance in feed intake ($\eta^2p = 0.968$), and the interaction between genetics and time accounted for 70.5% of the variance ($\eta^2p = 0.705$, $p < 0.001$), as

shown in Table 4. Mean differences were compared using Tukey's HSD test. Partial Eta Squared represents the effect size. The error terms (a, b, c, d) correspond to model-specific components in the GLM.

KC3 growers consumed significantly more feed than both KC1 and the control group ($\Delta M = 100.6g,\ p < 0.001$), while KC1 growers consumed more feed than the control ($\Delta M = 75.8g,\ p < 0.001$)(Fig. 3). The higher feed intake in KC3 during the grower stage suggests that this line continues to exhibit strong feed consumption patterns as the birds mature. KC1 and KC3 outperform the control group, indicating that either line is suitable for production.

Table 4: Tests of Between-Subjects Effects: Grower Feed Intake

Dependent Variable: Feed (grams)							
Source		**Type III Sum of Squares**	**df**	**Mean Square**	**F**	**Sig.**	**Partial Eta Squared**
Intercept	Hypothesis	56265332.311	1	56265332.311	186.270	.000	.954
	Error	2718575.583	9	302063.954[a]			
Genetic factor	Hypothesis	219792.882	2	109896.441	21.819	.000	.708
	Error	90661.970	18	5036.776[b]			
Week	Hypothesis	2718575.583	9	302063.954	59.972	.000	.968
	Error	90661.970	18	5036.776[b]			
Genetic factor* week	Hypothesis	90661.970	18	5036.776	11.946	.000	.705
	Error	37945.539	90	421.617[c]			

a. MS (week)
b. MS (Genetic factor * week)
c. MS(Error)

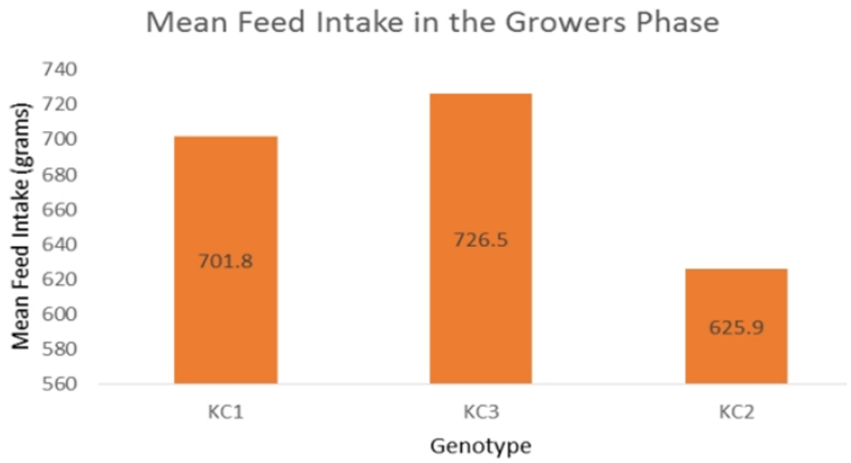

Fig. 3: Comparing Mean Feed Intake in Growers across Genotype

3.4. Live weight in growers

Live weight in growers also varied significantly by genetic line, with KC1 showing the highest growth, as illustrated in Fig. 4. KC1 growers gained an additional 75g per bird compared to the control group ($p = 0.016$), while KC3 growers gained 61.9g more than the control group, though this was not statistically significant ($p = 0.422$). The genetic factor accounted for 88.4% of the variance in grower weight ($\eta^2 p = 0.884$), indicating a strong genetic influence on weight gain. These results show that KC1 consistently demonstrates superior growth efficiency during the grower stage, making it the most efficient line for weight gain. The temporal factor explained nearly all the variance in grower weight ($\eta^2 p = 0.999$), while the interaction between genetics and time had no significant effect on weight gain ($\eta^2 p = 0.094,\ p = 0.941$) (Table 5).

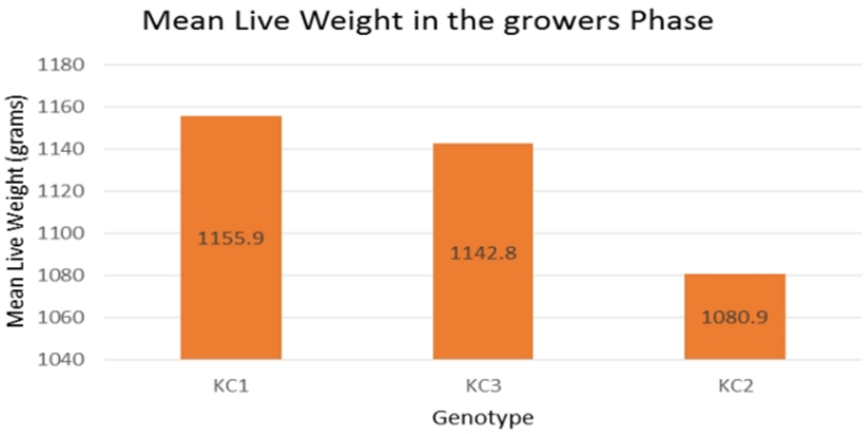

Fig. 4: Comparing Mean Live Weight in Growers across Genotype

Table 5: Tests of Between-Subjects Effects: Grower Live Weights

Source		Df	Mean Square	F	Sig	Partial Eta Squared
Intercept	Hypothesis	1	152285384.353	82.815	.000	.902
	Error	9	1838857.349[a]			
Genetic Factor	Hypothesis	2	64121.792	68.352	.000	.884
	Error	18	938.107[b]			
Temporal Factor (Weeks)	Hypothesis	9	1838857.349	1960.178	.000	.999
	Error	18	938.107[b]			
Genetic *Temporal Factors	Hypothesis	18	938.107	.521	.941	.094
	Error	90	1800.451[c]			

Statistical significance was set at $P \leq 0.05$. Superscript letters (a, b, c, d) denote model-specific error terms in the GLM

Although better models exist through which to visualize change with time, we reckoned that interacting genotype with time offered an avenue for analyzing temporal variation. Longitudinal data were used to see how genetic potential impacts growth and final weight. By looking at the interaction between Genotype (G) and Time (T), we were able to map out how these biological lines differ as they develop. In the first eight weeks, the three genotypes did not grow in parallel. The interaction between genetics and age, represented by a highly significant partial eta squared ($\eta^2 p = 0.736,\ p < 0.001$), was responsible for their diverging trajectories. The KC3 line had a high feed intake, consuming up to 8.4g more than F2. But the KC1 line had a higher weight of 40.4g, more than F2, even though it had a relatively lower feed intake. The huge F-value for time ($F = 4720.2$) highlights a very steep, exponential gain in early growth. From a production standpoint, KC1 reached its inflection point much faster than F2, gaining weight rapidly before the slower grower phase could even begin. Once the birds moved into the grower stage, genetics became dominant, explaining a massive 88.4% of the weight variance. Looking at the mean square variances, KC1 clearly has a higher biological potential for meat production. The interaction between age and genetics was at its lowest during the grower stage ($p = 0.941$). This suggests that the growth potential was determined during the brooder stage. Once KC1 established the early lead in weight gain, it followed a steady, predictable trajectory toward its maximum weight capacity. Looking at the full 18-week cycle, two distinct profiles emerge. The KC3 line had a higher feed intake compared to KC1 and F2. The high feed intake drive gives KC3 an advantage in free-range settings where it has to scavenge. In contrast, the KC1 line has a better growth coefficient. It reaches peak weight faster and maintains it without a massive feed intake. Mathematically, it could represent the best choice for semi-intensive meat production in the Kenyan market.

4. Discussion

The findings of this study showed that genetics played a crucial role in feed intake and weight gain in the three breeding lines. The KC1 and KC3 lines outperformed the control group in both traits, thus supporting genetic influences in poultry production as evidenced by previous studies (Miyumo et al., 2023; Tallentire et al., 2016). In particular, KC1 gained a significantly higher weight, while KC3 had comparatively higher feed intake. It can be concluded that different genetic lines have certain advantages in terms of production goals. The study findings matched those presented by Wambua et al. (2022), who found that improved indigenous chicken lines achieved better productivity results than standard chicken breeds.

The research indicates that breeding KC1 and KC3 selectively resulted in higher feed consumption and weight gains compared to the control group because selective breeding works to improve the indigenous chicken. Multiple studies have established that the proper breeding approach enhances poultry growth rates together with better feed efficiency and tissue features (Saxena & Kolluri, 2018; Tallentire et al., 2016). The variation between KC1 and KC3 genetic makeup allowed KC1 to gain more weight while KC3 consumed more feed. Miyumo et al. (2023) established that body weight and feed efficiency show substantial heritability, enabling an effective response to breeding selection practices. Genetic factors act as the probable cause for the variable growth results and feed efficiency shown by KC1 and KC3, as well as the control group.

The research findings demonstrated both the importance of temporal aspects and the combined effect of genetics on age development. Age proved to be a significant factor that impacted both feed consumption and animal weight, demonstrating that growth performance depends equally on age and genetics. Studies by Amusan et al. (2020) confirm that birds display rising feed intake and growth patterns with aging. The relationship between genes and time shows that genetic feed intake and growth levels become actualizable only when birds reach their specific developmental periods. This highlights that age management is crucial in realizing the potential of improved indigenous chicken breeds.

In comparison to previous studies, this study supports the findings of Fang et al. (2023), who demonstrated that growth traits in poultry are highly influenced by genetics and temporal factors. The significant interaction between genetics and time observed suggests that breeding programs should not only focus on genetic selection but also on management practices that support optimal growth in different development stages. This is relevant to poultry farmers seeking to maximize production throughout their birds' production cycle.

Despite the genetic advantages of KC1 and KC3, this study experienced a few limitations. The environmental factors, such as housing conditions, management, and

feed composition, were controlled but could have influenced the results. Also, evaluating the performance of these genetic lines in various ecological zones would provide crucial information on their productivity under varying environmental conditions.

The research results bring considerable helpful information to the practical operations of the Kenyan poultry industry. By selecting improved indigenous chicken lines, KC1 and KC3 farmers obtain increased growth rates, leading to reduced production costs and higher profitability. Improving Indigenous chicken productivity, as the hardy local breeds, presents a sustainable path to boost poultry production instead of continuing imports of exotic breeds. Research at the molecular level enables scientists to discover genes connected to feed consumption and growth, which will help breeding programs (Khobondo et al., 2014). Knowledge about these traits' genetic foundations will enable a more effective approach to advancing Indigenous chicken productivity in Kenya.

5. Conclusion

This study demonstrates that genetic makeup determines feed consumption patterns and growth performance of improved indigenous chicken strains, KC1 and KC3 breeding lines. The experimental lines KC1 and KC3 exceeded the control group in all performance metrics, from the chick to the grower stage. Selective breeding affects productivity levels according to the results measured by KC1, KC3, and the control group. Research data shows that KC1 exhibited heavier weight, but KC3 consumed greater amounts of feed, thus indicating distinct production capabilities among different breeding lines. The research demonstrates how the genetic advancement of native chicken breeds leads to enhanced feed processing alongside productivity development in Kenyan poultry agriculture. Based on the findings of this study, farmers can consider rearing the KALRO Improved Chicken breeding lines, especially the KC1 and KC3, given that these breeding lines have growth rates under experimental conditions. However, it is important to replicate these results in various farming environments to enhance their effectiveness. Hence, further research is recommended to compare the performance of these breeding lines on various ecological regions and management systems to provide comprehensive guidance to poultry farmers. Agricultural extension services should disseminate these findings to support farmers in adopting these improved breeds.

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