

Influence of Breed and Hemoglobin Variants on Genotypic and Gene Frequencies and their Effect on Linear Body Measurements in Nigerian Local Chicken

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Abstract

This study investigates the effect of breed and hemoglobin (Hb) genotype on the phenotypic traits of 150 chickens, comprising 50 Naked Neck (NN), 50 Normal Feathered (NA), and 50 Frizzled Feathered (FF) individuals. Blood samples were collected via the wing vein for genetic analysis, while body weight, body length, wingspan, drumstick length, and shank length were measured. Genotypic analysis revealed that the NN and NA breeds had a higher frequency of the AA genotype (60%), while the FF breed exhibited a more balanced distribution (20% AA, 40% AB, and 40% BB). Allele frequency analysis showed a dominance of the A allele in NN (0.7) and NA (0.6), whereas the FF breed had a higher frequency of the B allele (0.6), indicating greater genetic diversity. The relationship between Hb genotypes and body measurements revealed that BB chickens exhibited superior growth traits, including body weight (1.08 kg), chest circumference (27.30 cm), and wingspan (35.50 cm), making them more suitable for meat production. AB individuals showed advantages in body length (28.83 cm) and shank length (8.43 cm), suggesting heterosis effects that enhance growth and adaptability. Conversely, AA chickens generally recorded lower values across most traits, indicating a potential disadvantage in productivity-focused breeding programs. These findings highlight the importance of genetic selection in shaping productivity and adaptability in poultry. Maintaining genetic diversity is essential for improving performance traits, and further research should explore the genetic markers influencing these traits to develop optimized breeding strategies.

Keywords: Chicken, Hemoglobin, Genotype, Gene, Phenotype.

Introduction

Genetic diversity plays a crucial role in livestock production, influencing adaptability, productivity, and resilience to environmental stressors (FAO, 2019). In poultry, genetic variations significantly impact growth performance, body conformation, and overall productivity (Ajayi et al., 2016). Among local chicken ecotypes, the Naked Neck (NN), Normal Feathered (NA), and Frizzled Feathered (FF) breeds exhibit distinct genetic structures and phenotypic traits that are shaped by selection pressures and breeding practices (Yakubu et al., 2020). Understanding these genetic differences is essential for optimizing breeding strategies and improving poultry production efficiency (Mpenda et al.,

2019). The genotype frequencies observed in different chicken breeds provide insight into the genetic structure and inheritance patterns that influence performance traits (Jaturasitha et al., 2017). The phenotypic evaluation of body weight (BW), body length (BL), wing span (WS), drumstick (DS), shank length (SHL), and chest circumference (CC) provides valuable insights into the relationship between genetic makeup and physical characteristics (Norris et al., 2017). The importance of genetic selection in poultry breeding has been widely documented, with studies emphasizing the need to maintain genetic diversity for improved resilience and production efficiency (Guni et al., 2022). The observed genetic variation in this study underscores the necessity of developing sustainable breeding programs that incorporate both adaptive and productivity-enhancing traits (Egbeyale et al., 2023). By leveraging genetic insights, poultry farmers can improve breed selection, ensuring higher growth rates, better feed efficiency, and increased adaptability to environmental conditions (Ademola et al., 2021). The objective of this study is to evaluate the effect of breed and Hb genotype on genotype frequency, gene frequency, and linear body measurements in Nigerian local chickens.

Statement of the Problem

Poultry production in Nigeria faces challenges related to low productivity and adaptability, particularly among indigenous chicken breeds. The Naked Neck (NN), Normal Feathered (NA), and Frizzled Feathered (FF) chickens are known for their unique morphological traits and potential resilience to heat stress. However, there is limited understanding of how these breeds' hemoglobin (Hb) genotypes influence their phenotypic traits, such as body weight, body length, wingspan, drumstick length, and shank length. This knowledge gap hinders the development of effective breeding programs aimed at improving productivity and adaptability. Recent studies have highlighted the significance of Hb polymorphism in poultry performance. For instance, Orunmuyi *et al.* (2020) reported that different Hb genotypes (AA, AB, and BB) in indigenous Nigerian chickens were associated with variations in body weight, breast girth, and tibia length, with heterozygotes (AB) demonstrating better adaptability and survival rates. Similarly, genomic analyses have revealed that Nigerian indigenous chickens possess substantial genetic diversity, which is crucial for adaptation to environmental stresses and for the improvement of production traits. Despite these insights, comprehensive studies examining the interplay between breed characteristics and Hb genotypes on phenotypic traits are scarce. Understanding this relationship is vital for optimizing breeding strategies that enhance both productivity and adaptability in poultry farming.

Research Objectives

1. To investigate the effect of breed on the phenotypic traits of chickens.
2. To examine the effect of hemoglobin (Hb) genotypes on the phenotypic traits of chickens.

3. To analyze the allele frequency distribution of Hb genotypes in the different chicken breeds.
4. To evaluate the heterosis effects of the AB genotype on growth and adaptability.
5. To provide insights for optimizing poultry breeding strategies based on genotype-phenotype relationships.

Research Questions

1. How does breed influence the phenotypic traits (body weight, body length, wingspan, drumstick length, and shank length) in chickens?
2. What is the relationship between Hb genotypes (AA, AB, BB) and the growth traits of chickens, including body weight, chest circumference, and wingspan?
3. What are the allele frequency distributions of Hb genotypes (A and B alleles) in Naked Neck, Normal Feathered, and Frizzled Feathered chicken breeds?
4. Do chickens with the AB genotype exhibit superior growth and adaptability traits (such as body length and shank length) compared to those with the AA or BB genotypes?
5. How can genetic selection based on Hb genotypes and breed-specific traits contribute to optimizing breeding strategies for enhanced poultry productivity and adaptability?

Materials and Methods

Study Location

This study was conducted in Calabar, the capital of Cross River State, Nigeria. Calabar is located in the southeastern region of Nigeria, between latitudes 4°57'N and 5°45'N and longitudes 8°18'E and 8°24'E. The city experiences a tropical rainforest climate with high humidity (above 80%) and an annual temperature range of 25°C to 30°C. The area receives an annual rainfall of approximately 2,500 mm, making it suitable for poultry farming due to the abundance of natural feed resources and a favorable environment for chicken rearing (Ekpo et al., 2018; Udo et al., 2021).

Experimental Birds and Sampling

A total of 150 local chickens were used for this study, consisting of 50 birds from each of three indigenous strains: Naked Neck, Frizzled Feathered, and Normal Feathered chickens. The birds were sourced from smallholder farms and local markets within Calabar and were raised under similar management conditions, including access to feed, water, and a well-ventilated housing system (Yakubu et al., 2020; Obike et al., 2023). The chickens were allowed to acclimatize for two weeks before sample collection to ensure they were stable and adapted to the study environment.

Hemoglobin Genotyping

Hemoglobin variants were determined using cellulose acetate electrophoresis at pH 8.6. Blood samples were hemolyzed, and a small volume was loaded onto cellulose acetate

strips. Electrophoresis was performed using a Tris-EDTA buffer system, and hemoglobin bands were visualized under appropriate lighting conditions. The genotypic frequencies of HbAA, HbAB, and HbBB were recorded.

Genotypic and Gene Frequency Determination

Genotypic frequencies were calculated by dividing the number of individuals with a specific genotype by the total number of individuals sampled. Gene frequencies were estimated using the Hardy-Weinberg equilibrium principle.

Phenotypic Measurements

Linear body measurements were taken using a flexible graduated tape to the nearest 0.1 cm. The following parameters were measured:

- **Body weight (BW):** Measured using a digital weighing scale to the nearest 0.01 kg.
- **Body length (BL):** Measured from the base of the beak to the base of the tail.
- **Wing span (WS):** Measured from the tip of one wing to the tip of the other when fully extended.
- **Shank length (SL):** Measured from the hock joint to the base of the toes.
- **Drumstick length (DL):** Measured from the hock joint to the knee joint.

Each measurement was taken three times per bird, and the average was recorded for statistical analysis to minimize measurement errors (Melesse et al., 2019; Olawunmi & Ibe, 2021).

Data Analysis

The data were analyzed using SPSS version 25.0 (IBM Corp, 2020) and SAS version 9.4. Descriptive statistics were used to summarize genotypic and gene frequencies to provide a foundational understanding of the distribution of alleles and genotypes within the population. The following statistical procedures were applied, each with specific underlying assumptions: ANOVA was employed to evaluate the effect of hemoglobin variants on linear body measurements. This method assumes: Each subject's measurements are assumed to be independent of others, ensuring unbiased variance estimates. The residuals (errors) from the model are assumed to be normally distributed. This assumption justifies the use of parametric tests and ensures reliable F-statistics. The central limit theorem supports this assumption, particularly with larger sample sizes. The variances of the dependent variable across the levels of hemoglobin variants are assumed to be equal. DMRT was used for post-hoc comparisons to identify statistically significant differences among group means. DMRT assumes the same conditions as ANOVA (particularly homoscedasticity and normality), and is particularly suitable for identifying where those differences lie after establishing significance in the ANOVA. Pearson's correlation coefficient was used to assess the relationships between hemoglobin variants and body traits. This method assumes: The relationship between variables should be linear; non-linear associations could distort the correlation value. While the test is somewhat robust to departures from normality,

significant deviations can affect the correlation estimate. The variance of one variable is assumed to be relatively constant across the range of the other. All assumptions were examined through diagnostic plots and formal statistical tests (e.g., Q-Q plots for normality, scatterplots for linearity, and Levene’s test for equality of variances) to ensure the robustness of the conclusions. These justifications support the validity of the inferential statistics applied to evaluate the effects and relationships among hemoglobin variants and linear body traits (Peters *et al.*, 2020; Ogundu *et al.*, 2024).

Results and Discussion

Table 1: Effect of breed on Genotype frequency

Genotype	AA (%)	AB (%)	BB (%)	Total (%)
NN	60	20	20	100
NA	60	0	40	100
FF	20	40	40	100

NN=Naked neck, NA=Normal, FF=frizzled feathered, AA=Homozygous genotype, AB= Heterozygous genotype, BB= Homozygous genotype, %=percent

Table 1 presents the genotype frequencies (AA, AB, BB) among three breeds normal feathered (NA), naked neck (NN) and frizzled feathered (FF). The findings highlight significant differences ($p<0.05$) in genotype distribution across breeds. NN Breed Shows a predominance of the AA genotype (60%), followed by an equal distribution of AB and BB genotypes (20% each). This suggests a strong homozygous presence of the AA allele in the population. NA Breed Similar to the NN breed, the AA genotype is dominant (60%), but this breed lacks heterozygous AB individuals (0%), while BB individuals make up 40% of the population. This might indicate selective pressures or breed-specific genetic influences that suppressed heterozygosity. FF Breed Shows a balanced distribution of genotypes, with BB and AB genotypes each at 40%, while AA is present at a lower frequency (20%). This suggests greater genetic diversity, potentially due to crossbreeding or polymorphic selection in this breed. Genetic frequency variations across breeds can be attributed to selection pressures, breeding practices, and genetic drift (Falconer and Mackay, 2015; Zhang et al., 2019).

The high AA genotype frequency in NN and NA breeds suggests a positive selection for AA-related traits, which could be linked to disease resistance, productivity, or adaptation to environmental conditions (Kim et al., 2017). Breed-specific genetic differences often arise due to natural selection and artificial breeding programs (Wang et al., 2020). The FF breed, which exhibits higher heterozygosity (40% AB), suggests that it might have undergone recent crossbreeding or genetic introgression, enhancing its adaptability (Santos et al., 2022). Studies have shown that different genotypes influence production traits such as growth rate, fertility, and disease resistance (Mukesh et al., 2018; Li et al., 2021). The predominance of AA genotypes in NN and NA could suggest a superior trait inheritance in

productivity-related genes, whereas the higher AB and BB frequencies in FF may imply diverse adaptive potential (Zhou *et al.*, 2023). Genotypic diversity is essential for maintaining heterosis (hybrid vigor), which enhances traits like fertility and disease resilience (Gurgul *et al.*, 2016). The lack of AB genotypes in NA suggests possible inbreeding or genetic fixation, which might reduce genetic adaptability and increase the risk of inherited disorders (Leroy *et al.*, 2017). Selective breeding programmes need to balance homozygosity and heterozygosity to optimize breed performance (Thornton *et al.*, 2016). The FF breed's higher heterozygosity (AB at 40%) indicates greater genetic diversity, which is beneficial for long-term breed sustainability (Kumar *et al.*, 2023). Conversely, NN and NA breeds may require controlled breeding strategies to prevent excessive homozygosity, which can lead to genetic bottlenecks (Osei-Amponsah *et al.*, 2020).

Table 2: Effect of breed on gene frequency

Genotype	A	B	Total
NN	0.7	0.3	1
NA	0.6	0.4	1
FF	0.4	0.6	1

NN=Naked neck, NA=Normal, FF=frizzled feathered, A=Allele, B=Allele

Table 2 presents the gene frequencies of alleles A and B in three different breeds (NN, NA, and FF). The total frequency for each breed is 1, indicating that these are the only two alleles observed in the population. The distribution of allele frequencies shows significant differences ($p < 0.05$) among the breeds. NN breed shows A allele is dominant (0.7), while B is less frequent (0.3), suggesting a selective advantage or preference for A in this breed. NA breed shows A allele (0.6) is still more frequent than B (0.4), but with a more balanced distribution compared to NN. FF breed shows the highest B allele frequency (0.6) and the lowest A allele frequency (0.4), indicating a shift in genetic composition compared to NN and NA. Gene frequencies in a population are influenced by natural selection, genetic drift, migration, and mutation (Falconer and Mackay, 2015; Osei-Amponsah *et al.*, 2020).

The high A allele frequency in NN (0.7) and NA (0.6) suggests that A is a favorable allele, possibly conferring advantages such as disease resistance, superior growth, or higher fertility (Wang *et al.*, 2019; Zhang *et al.*, 2023). On the other hand, the FF breed's higher B allele frequency (0.6) suggests a genetic shift, which may be due to crossbreeding, adaptive traits, or local selection pressures (Gurgul *et al.*, 2016; Li *et al.*, 2021). The increase in B frequency could be linked to traits such as heat tolerance, milk production, or meat quality (Kim *et al.*, 2017). Heterozygosity is an essential factor in maintaining genetic health and adaptation (Mukesh *et al.*, 2018). In the FF breed, a more balanced allele distribution (A = 0.4, B = 0.6) suggests a higher potential for heterozygosity, which can enhance hybrid vigor and adaptability (Thornton *et al.*, 2016). This supports previous research showing that balanced allele frequencies are associated with increased reproductive efficiency and

survival rates (Leroy et al., 2017). In contrast, NN and NA show higher A allele frequencies, indicating potential genetic fixation, which could limit adaptability (Kumar et al., 2023). Reduced genetic variation can make a breed more susceptible to environmental stressors and diseases (Santos et al., 2022). Breeding strategies must aim to balance genetic diversity while selecting for desirable traits (Wang et al., 2020). The NN and NA breeds, with higher A allele frequencies, may require genetic enrichment through selective breeding to maintain adaptability (Ahmed et al., 2022). Conversely, the FF breed's higher B frequency suggests genetic diversity, which may be beneficial for traits like heat resistance and disease resilience (Zhou et al., 2023). This aligns with recent studies showing that heterozygosity improves fertility and stress resistance in livestock (Mwacharo et al., 2019).

Table 3: Effect of Hb on linear body measurements

	Hb			
Parameters	AA	BB	AB	SEM
BW	0.99	1.08	1.00	0.07
BL	27.00	28.02	28.83	1.09
SHL	7.76	8.12	8.43	8.01
CC	25.79	27.30	24.67	0.74
WS	33.86	35.50	34.67	0.88
DS	13.04	13.30	12.87	0.40

AA=Homozygous genotype, AB= Heterozygous genotype, BB= Homozygous genotype, BW=body weight, BL=body length, SHL=shank length, CC=chest circumference, WS=wing span, DS=drumstick

Table 3 evaluates the effect of different hemoglobin (Hb) genotypes (AA, BB, and AB) on various linear body measurements in an animal population. The Standard Error of the Mean (SEM) is provided for each measurement, indicating the variation within the data. BB genotype (1.08 kg) has the highest body weight, followed by AB (1.00 kg) and AA (0.99 kg). The AB genotype (28.83 cm) shows the longest body length, followed by BB (28.02 cm) and AA (27.00 cm). The AB genotype (8.43 cm) has the highest shank length, while AA (7.76 cm) has the lowest. The BB genotype (27.30 cm) has the largest chest circumference, followed by AA (25.79 cm) and AB (24.67 cm). The BB genotype (35.50 cm) has the highest withers span, followed by AB (34.67 cm) and AA (33.86 cm). The BB genotype (13.30 cm) has the largest drum stick, while AB (12.87 cm) has the smallest. Hemoglobin (Hb) polymorphism has been linked to growth traits, adaptability, and metabolic efficiency in livestock (Oke et al., 2019; Ahmed et al., 2021).

The higher body weight (BW), chest circumference (CC), and wing span (WS) in BB genotype animals suggest that this variant enhances growth performance and body conformation (Yakubu et al., 2017; Li et al., 2020). The AB genotype's advantage in body length (BL) and shank length (SHL) indicates potential heterosis (hybrid vigor), where heterozygous animals exhibit improved growth characteristics (Musa et al., 2018). This aligns with studies showing that heterozygous Hb genotypes are associated with enhanced

oxygen transport and metabolic efficiency, leading to better growth rates (Gurgul *et al.*, 2016; Zhang *et al.*, 2022). Linear body measurements are critical indicators of productivity in farm animals, influencing meat yield, adaptability, and reproductive performance (Wang *et al.*, 2021). The BB genotype's superiority in chest circumference (CC) and wing span (WS) aligns with findings that suggest BB animals have enhanced muscle development and better adaptability to harsh environments (Thornton *et al.*, 2016; Santos *et al.*, 2022). In contrast, AB animals tend to exhibit balanced body proportions, which may be advantageous for endurance, reproductive efficiency, and adaptability (Mwacharo *et al.*, 2019). The AA genotype, having lower values in most parameters, may indicate a less efficient growth pattern and could be associated with lower meat yield potential (Leroy *et al.*, 2017).

The physiological role of hemoglobin variants extends beyond growth performance to adaptability, feed conversion efficiency, and disease resistance (Zhou *et al.*, 2023). Studies have shown that BB animals exhibit higher metabolic efficiency, making them well-suited for environments where high oxygen transport capacity is beneficial (Kim *et al.*, 2017). AB animals tend to have adaptive advantages, likely due to their balanced metabolic rate and efficient oxygen utilization (Li *et al.*, 2021). AA animals may be less efficient metabolically, leading to lower body weight and smaller body dimensions, which can be a disadvantage in meat production systems (Santos *et al.*, 2022).

Conclusion

The genotype frequencies in NN, NA, and FF breeds reflect distinct genetic structures shaped by selection, breeding, and environmental factors. NN and NA breeds show high homozygosity, favouring AA-linked traits, while FF exhibits greater genetic diversity with a higher B allele frequency. BB animals excel in body weight, chest circumference, and wing span, making them ideal for meat production. AB animals show advantages in body length and shank length, suggesting a heterosis effect for balanced growth. AA genotype generally performs lower, making it less suitable for productivity-focused breeding. These patterns highlight genetic selection and adaptability in livestock.

Recommendation

Based on the findings of this study, it is recommended that poultry breeding programs prioritize the incorporation of the BB hemoglobin genotype, particularly within the Frizzled Feathered (FF) breed, due to its superior growth performance in key traits such as body weight, chest circumference, and wingspan. The AB genotype also presents promising advantages, especially in body length and shank length, likely due to heterosis effects that may enhance adaptability and resilience. Therefore, balanced selection strategies that maintain genetic diversity while favoring performance-associated genotypes should be adopted. The lower growth metrics observed in AA individuals suggest that this genotype may be less favorable in productivity-focused systems. Continued genetic monitoring and the integration of molecular tools are essential to identify and select for desirable alleles

linked to growth and adaptability. Future research should aim to uncover specific genetic markers to guide more efficient and targeted breeding approaches for sustainable poultry production.

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