GENETIC CHARACTERIZATIONS OF DIFFERENT PLUMAGE COLOUR OF NOILER CHICKEN.

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ABSTRACT
This study investigated the genetic characteristics of Noiler chickens of five different plumage varieties: brown, barred, black, black-white, and brown-white. A total of 195-day-old Noiler chicks were procured from a reputable hatchery and distributed into triplicate groups, with 13 birds per plumage variety. The chickens were raised at the Teaching and Research Farm of Adekunle Ajasin University, following standard management practices and fed a commercial diet ad libitum. At the 10th week of the study, 2 ml of blood samples was randomly collected from 10 birds per plumage variety for laboratory analysis. Protein separation was performed using the Bio-Rad Mini Protean II Cell electrophoresis system. The analysis revealed distinct protein bands, including myosin, bovine serum albumin, carbonic anhydrase, β-galactosidase, ovalbumin, and α-lactoglobulin. The detected bands were analyzed usi ng the Paleontological Statistics (PAST) software, and the resulting dendrogram illustrated the genetic similarities among the different plumage varieties. Notably, the brown and brown-white Noiler chickens exhibited the closest genetic relationship.
Keywords: Dendogram, Plumage, Noiler, SDS-PAGE,

INTRODUCTION

Amo Hatchery, also known as Amo Farm Sieberer Hatchery Limited, developed the Noiler chicken breed in Nigeria (Adamu *et al.*, 2021). The primary breeding objective of Noiler chickens was to create an improved breed that can replace indigenous chickens, which are known for their low-quality meat and egg production (Yakubu and Ari, 2010). Noiler chickens perform well under various production systems and demonstrate adaptability to poor feed conditions and suboptimal nutrition (Adetunji and Ola, 2020). Feathers are sclerotic structures with diverse developmental pathways, representing highly specialized integumentary appendages that have been the subject of extensive research for over 150 years (Prum and Brush, 2002). Recent advancements in genome-wide association studies, evolutionary developmental research, and phylogenetic comparative analyses have provided new insights into the evolutionary history and genetic mechanisms governing plumage variation (Cooke *et al.,* 2017). In poultry, particularly chickens, plumage colour serves as a genetic marker for identification due to its distinct characteristics (McGraw *et al.,* 2013). However, limited research has been conducted on the genetic basis of plumage variation in Noiler chickens.

MATERIALS AND METHODS

Experimental site

The study was carried out at the Teaching and Research farm of Adekunle Ajasin University Akungba Akoko, having a mean annual rainfall of 1500-2000mm and the average temperature ranging between 18°C and 35°C. Uniform plumage patterns were replicated, each of the plumage were housed in a wooden cage of 0.4m by 0.3m in a well-ventilated area

Experimental animals and management

A total of 195-day-old Noiler chicks were obtained from Amo Farm Sieberer Hatchery, Ibadan, Oyo State, Nigeria. The chicks were randomly distributed into triplicate groups, with 13 birds per plumage variety. The birds were fed *ad-libitum* without restrictions of light intensity for the periods of the experiment

Laboratory analysis

At the 10th week, 10 birds were randomly selected from each plumage variety and 2 ml of blood samples was collected from wing vein of each bird using syringes. The blood samples were taken to the laboratory for analysis. Serum was separated from the whole blood after centrifugation at 4000rpm. The Supernatant from the serum sample was carefully transferred into a clean 2.ml eppendorf microtube and stored at −4°C. The sodium dodecyl sulphate–polyacrylamide gel electrophoresis (SDS–PAGE)

analysis was carried out using the Bio-Rad Mini Protean II (10 ml capacity). The stacking gel contained distilled water (6.1 ml), 0.5 M Tris-HCl at pH of 6.8 (2.5 ml), 10 percent SDS (100 µl), acrylamide/bisacrylamide solution (1.3 µl), 10 percent ammonium tetraoxosulphate (vi) (50 µl) and Initiator or N,N,N',N'-Tetramethylethylenediamine (TEMED) (C6H16N2) (10 µl). B-mercaptoethanol (7.5 percent) in sample buffer was used for the preparation of the various plumage varieties. The serum and sample buffer were added at ratio 1:2 and heated at 95°C for 5 min in a water bath. The mixture was placed inside the deep freezer for 5 min and then loaded into the wells on the gel. The separation of protein was carried out with the aid of Bio-Rad Electrophoresis system using the Bio-Rad Mini Protean II Cell at 150 V for 2 h. The separating gel composed of 0.375 M Tris at pH of 8.8, distilled water (3.5 ml), 1.5 M Tris-HCl (2.5 ml), 10 percent SDS (100 µl), acrylamide/bisacrylamide (4.0 µl), 10 percent ammonium tetraoxosulphate (vi) (50 µl) and TEMED (5 µl). At the completion of the electrophoresis, the gels were carefully removed under water and placed in a staining solution of 0.1 percent Coomassie Blue in 1:4 glacial ethanoic acid (CH3COOH) and methanol (CH3OH). The staining solution was later removed and the gels were de-stained with a solution of 40 percent distilled water in 1:4 glacial ethanoic acid and methanol. The de-stained gels were then scanned and the bands visually scored (Adeleke *et al.*, 2012).

Data analysis

Data were analysed with paleontogical statistic (PAST). Employing its univariate and multivariate components

RESULTS

Using the molecular weight via SDS of the serum protein analysis, the comparative dendrogram for the Noiler plumage varieties (Figure 1) showed the polymorphic of the protein bands including myosin, bovine serum albumin, Carbonic anhydrase, Beta-galactosidase, alpha-lactoglobulin and ovalbumin. Comparing the proteins bands with the blue pre-stained standard, all plumage varieties: brown, back, black-white, barred, white-brown indicated a uniform abundance of myosin, galactose, albumin, ovalbumin, alpha-albumin with the exemption of black and black- white which possess aprotinin and glutamic dehydrogenase in their proteins band.

Dendrogram of Noiler chicken breed was differentiated based on the protein serum bands, utilizing the STATISTICA software and Euclidean correlated distances among the various plumage varieties. The dendrogram showed the relationship and genetic distance of different plumage varieties via their serum protein. Each plumage varieties showed a closed genetic distance similarity. Brown-white and brown plumage were observed to be more genetically closed with genetic distance value of 0.08, black plumage shared the nearest genetic distance with the closet plumage varieties relationship of about 0.40. Barred plumage varieties showed the most genetic distance from other plumage varieties of 1.36, emphasizing that their ancestors are moderately closed in the genetic distance from each Noiler plumage.

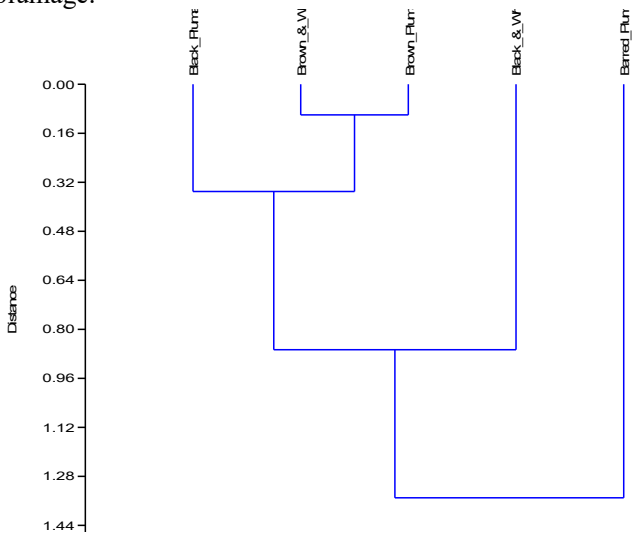


Figure 1: Comparative dendrogram for Noiler plumage varieties

DISCUSSION

The results indicated a high level of genetic similarity and general loss of genetic variation. This perhaps is as a result of reduced heterozygotes, heterogeneity, low polymorphism, and introgression among breeds of chicken (Betiku and Omitogun, 2006). Ensminge (1992) documented that plumage varieties had genetic and breeding functions to play other than camouflage and defense mechanism, influencing the molecular composition. The results indicated the abundance distribution of myosin, bovine serum albumin, Carbonic anhydrase, Beta-galactosidase, ovalbumin, and alpha-lactoglobulin among noiler chickens of different plumage varieties considered in this research. Variations in the bands may have to do with feather distribution gene that gives its characteristic phenotype (Adeleke *et al.*, 2011).

Adeleke *et al.,* (2011), all *Gallus. gallus* and chicken populations formed a common cluster on a dendrogram, with various geographic populations of *G. gallus* occupying different domains, this was in-line with the results of this research in that, though plumage varieties of noiler chicken had low disparities on the dendrogram clusters. Brown, white-brown plumage was observed to be more genetically closed in their genetic distance. Okamoto *et al.* (1999) had earlier affirmed a slight genetic difference in the polymorphic structure of local breeds of chickens. The low genetic disparity observed within various plumage, can be link to changes that have might occur in the nucleotide chain during protein synthesis. Mutation is largely responsible for genetic drift (Adeleke *et al.,* 2011).

CONCLUSION

This study affirmed that there is a low genetic distance between Noiler of different plumage varieties.

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