

Albumin Polymorphism in Nigeria Local Ecotype and Exotic Breed

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ABSTRACT

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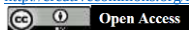
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All agricultural animals have experienced a growing loss of genetic diversity. Nigerian local ecotypes are valuable dual-purpose birds possessing highly conserved genetic systems and adaptive potentials to varied ecological conditions. Furthermore, albumin polymorphisms have been utilized as markers to compare allele frequencies within and between these chicken populations. To properly take advantage of strain differences and facilitate genetic development in breeding, diversity research on these specific ecotypes is essential. This study investigated genetic diversity at the albumin locus to identify and quantify alleles within diverse chicken populations, specifically the Abuja, Yoruba, and Fulani ecotypes, alongside an Exotic breed. Typing 200 birds via cellulose acetate electrophoresis revealed two co-dominant alleles (Ab A and Ab B) and two present genotypes (Ab AA and Ab AB), while the Ab BB genotype was absent across all populations. The populations exhibited high observed heterozygosity (0.4725), indicating increasing genetic heterogeneity, while the genetic variance between the investigated populations was minor. Dendrogram analysis established that Yoruba and Fulani chickens share more genetic similarities with each other than with the exotic broiler breeds. These findings establish a baseline that could serve as a reference point for the genetic diversity improvement of both indigenous and exotic chicken breeds using biochemical markers.

Keywords: albumin; chicken; allele; polymorphism, genetic diversity, exotic breed

Introduction

Biodiversity refers to the distinct evolutionary histories of species, genetic variety within populations, and dispersion across habitats, ecosystems, landscapes, and continents/oceans (FAO, 2009). All agricultural animals have seen a growing loss of genetic diversity, and more than half of major livestock breeds, particularly poultry, are now endangered or at risk of extinction (Hoffman, 2005).

According to FAO (2000), Animal genetic enables farmers to choose stocks or establish new breeds in response to environmental change, disease threats, new understanding of human dietary requirements, changing market situations, and social demands. Fewer than 25 domestic plant and animal species generate about 75% of the world's food and agriculture. Unfortunately, genetic resources for farm animals are rapidly depleting. (FAO, 2007). The number of domestic animal species is down, possibly 40% in total, and less than 14% accounts for more than 90% of global productivity. (FAO, 2004).

The Nigerian local ecotype is a dual-purpose bird that is utilized for both meat and egg production in the rural and peri-urban parts of the country. They are found in vast numbers scattered over several agroecological categories under a traditional family-based scavenging management system Ajayi, (2010). They possess a highly conserved genetic system with significant degrees of heterozygosity. (Wimmers et al., 2000). These show that they are very significant agricultural animals, retained for a decent supply of animal protein, revenue, and sociocultural functions (Awobajo et al., 2020). Ajayi,

(2010) reported the adaptive potentials of the Nigerian indigenous chicken to varied ecological conditions, stresses and diseases. There have been various efforts to describe Nigerian local ecotypes. Adeleke (2011) found that major genes influence growth, fertility, hatchability, and semen quality. Hassan (2015) found that Nigerian indigenous chickens are more resistant to infectious disease agents than exotic equivalents.

To broaden the genetic basis, poultry breeding companies should use locally adapted chicken resources. In addition to phenotypic characterisation, molecular analysis can provide insights into phylogeny, diversification, and relatedness. To take advantage of the differences in the strain of chickens and bring about genetic development in breeding, diversity research is essential (Awobajo et al., 2020).

Albumin is a protein that's the most abundant protein in chicken blood plasma formed by liver and discovered in the blood which performs as a carrier protein, transporting various substances through the bloodstream. It binds to hormones, fatty acids, drugs, and other molecules, helping to distribute them to different tissues and organs. It also helps to maintain colloidal osmotic pressure (oncotic pressure) in the bloodstream which helps to retain water within the blood vessels and prevents excessive fluid leakage into tissues, which could lead to edema (swelling). Polymorphisms in the albumin gene can lead to variations in the construction and purpose of the albumin protein. For example, a mutation in the albumin gene might lead to altered binding properties, affecting the transport of substances in the bloodstream. Albumin polymorphisms have been used as symbols to compare allele frequencies within and between chicken populations (Hassan, 2015). This experiment is to identify and quantify the different alleles present in the albumin gene. The frequencies can then be calculated by dividing the quantity of each allele by the total number of alleles in that population. Gel electrophoresis is also one of the most realistic practical means of detecting genetic variation available (Jaayid et al., 2011) and it was made use of to provide estimates of variation. Akpa (2011) used the same technique to analyze genetic diversity in different poultry birds, but their emphases were macro geographic patterns and inter specific differences in allelic frequencies. This study is concerned with genetic diversity at albumin locus in Abuja, Yoruba, Fulani ecotype chickens in Nigeria and exotic chickens.

Methodology

Study Area

The experiment was conducted at University of Ilorin Biotechnology Laboratory and University of Abuja.

Experimented Animals

The sum of 50 blood samples each was extracted from a sum of 200 birds comprising of Abuja ecotype(G1), Yoruba ecotype(G2), Fulani ecotype(G3) and Exotic breed (G4) of chicken was used in the experiment.

Cellulose Acetate Electrophoresis

The Cellulose Acetate Electrophoresis was done using the Gallenkamp Model JY-SP7 Electrophoretic equipment located at the Molecular Evolution and Genome Diversity Unit of the Biotechnology Laboratory, University of Ilorin.

Blood Collection and Sample Preparation

Five milliliters (5ml) of blood were collected from the sampled animals individually by vein puncture by Inserting needles and syringes into test tubes containing Ethylene Diamine Tetraacetic Acid. (EDTA) as anticoagulant and samples were properly labeled. They were then refrigerated at 8⁰c for two hours and thereafter carried into the laboratory.

Preparation of Blood Haemolysates

The plasma fraction was divided from the erythrocytes fraction of the heparinized blood by centrifugation at 2500-3000 rpm for 10 minutes at 4⁰c.

Plasma

The liquid remaining above the solid called the supernatant was used to give result to the genetic variants in transferrin and Albumin.

Cellulose Acetate Paper Soaking

Cellulose acetate papers were soaked in the same buffer as the electrode buffer (Continuous buffer system). Papers were soaked for 20 minutes.

Band Scoring

Bands were scored visually as defined by RIKEN (2006) and Sola-Ojo et al. (2020). Direct counting was done for estimating gene frequencies.

Statistical Analysis

Population estimates were determined using PopGen 32.0 software, while the analysis of the morphometric parameters and phenotypic correlation were estimated using SPSS version 22.0 (2017).

The effect of breed type and blood enzyme polymorphism on measured traits and their interfaces were determined using the PROC Generalized Linear Model (GLM) of Statistical Analysis System (SAS) 9.2 (2003). Significant ($p < 0.05$) differences in means were divided using Duncan Multiple Range Test (DMRT) (Duncan, 1955).

Results

The observed Allele frequency is consistent with the findings of Johari et al. (2008), who discovered two Alleles A and B in chicken. Some species, including Muscovy and Pekin ducks (Azmi et al., 2006; Johari et al., 2012), has shown to have comparable albumin polymorphism, confirming that albumin is polymorphic in the populations studied.

Table 4.1. Allele frequency at Albumin for ecotypes

Population Ecotypes	Allele	Sample size	Allele Frequency
Fulani	A	200	0.5500
	B		0.4500
Yoruba	A	100	0.6000
	B		0.4000
Abuja	A	98	0.6531
	B		0.3469
Exotic	A	100	0.7400
	B		0.2600
Average	A	498	0.6358
	B		0.3642

The genotype frequency for AbAA ranges from 0.14, 0.21, and 0.20 in the Fulani, Yoruba, and Abuja ecotypes to 0.25 in the Exotic breed (Table 4.2). The AbBB genotype is missing in all indigenous and exotic bird populations.

The observed polymorphism may be attributed to a group of environmental and genetic factors. This is steady with the findings of Esmailkhanian et al., (2000), who identified three Albumin genotypes in chicken breeds, namely AA, AB and BB. Ismoyowati (2008) claims that.

Table 4.2. Genotype frequency at Albumin for poultry

Population Ecotypes	Genotype	Sample size	Genotype Frequency
Fulani	AA	200	0.14
	BA		
	BB		
Yoruba	AA	100	0.21
	BA		
	BB		
Abuja	AA	98	0.20
	BA		
	BB		
Exotic	AA	100	0.25
	BA		
	BB		
Average	AA	480	0.19
	BA		
	BB		

Table 4.3 shows the F-statistics estimates of population structure, and AB estimates of FIS, FIT, and FST were not important except for the FST value for 0.0214 and the FIT value for -0.0201, which were in agreement, indicating a small deviation from Hardy Weinberg's Equilibrium and a measure of outbreeding in the population (Weir and Cockerham, 2014).

Table 4.3. Wright F-Statistic analysis for Albumin for poultry

Population	(F _{IS})	F _(ST)	F _(FIT)	N _m
Average(ecotypes)	-0.0424	0.0214	-0.0201	11.4460

The high heterozygosity, detected HO, for all chicken kinds in all populations (0.4725), indicates that genetic heterogeneity in chicken populations is increasing at the Albumin locus (Table 4.4). The heterozygosity observed is higher than the expected.

The high heterozygosity, detected HO, for AB chicken kinds in AB populations, indicates that genetic heterogeneity in chicken populations is growing at the Albumin locus. This might be attributable to the chicken sample's population structure (Rychlik et al., 2011). The observed heterozygosity is more than the anticipated heterozygosity, indicating that the populations are outbred.

Table 4.4. Effective sample size (N) and expected and observed heterozygosity (HE and HO) at Albumin locus for poultry

Population	N	H _E	H _O
Fulani	200	0.4975	0.5600
Yoruba	100	0.4848	0.3600
Abuja	98	0.4578	0.4898
Exotic	100	0.3887	0.4800
Total	480	0.4572	0.4725

The genetic variance between the populations investigated was minor, but within the 0.0089 to 0.9911 range indicated by Nei (1976) for local breeds. The difference between Yoruba ecotype and Abuja ecotype was the greatest, while the distance between Abuja ecotype and Yoruba ecotype was the least. AB of the chicken types congregated until they reached a spot where the layers and indigenous

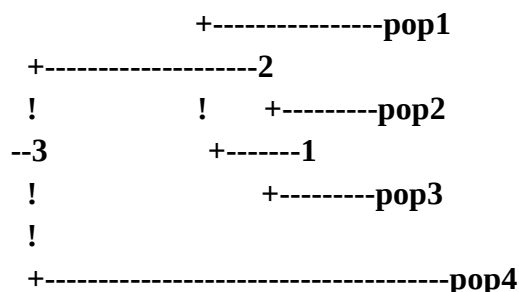
clustered. According to Nei, the genetic variance between AB breeds of birds from AB locations is the same.

Table 4.5. Genetic distance for AB breed of birds from AB location according to Nei 1972 identity (up) and distance (down)

Population ID	1	2	3	4
1	****	0.9816	0.9859	0.9432
2	0.0185	****	0.9911	0.9810
3	0.0142	0.0089	****	0.9699
4	0.0584	0.0192	0.0305	****

The dendrogram of the four chicken kinds indicates that the Yoruba and Fulani chickens have more genetic similarities than that of the broiler, all of the chicken types congregated until they reached a spot where the Fulani and Yoruba Ecotype clustered. According to Nei, the genetic variance between all breeds of birds from all locations is the same.

Figure 4.5a. The Dendrogram of the four chicken ecotypes.



Between	And	Length
3	2	0.98354
2	pop1	0.81923
2	1	0.37320
1	pop2	0.44603
1	pop3	0.44603
3	pop4	1.80277

Conclusion

In conclusion, our study of albumin polymorphism in Nigerian local chicken ecotypes and an exotic breed indicates a high level of genetic heterogeneity characterised by the presence of co-dominant alleles (Ab A and Ab B) with a very high observed heterozygosity (0.4725) indicative outbreeding within these populations [19], [22], [25]. In addition, dendrogram analysis showed that the genetic distance which existed between the eco-types of Yoruba and Fulani were more closer to each other than to 18 exotic broiler. This study provides important implications for genetic improvement as it establishes baseline information which can be used to harness biochemical markers to increase effective diversity and provide genetic gains of indigenous and exotic chicken populations. In order to take the next steps from this platform, it is worth directing future research in new directions such as integration of broader

molecular and genomic approaches at even larger extents and sample sizes to offer the deeper phylogenetic and relatedness resolution that will further capitalize on these locally adapted gene pools.

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