Genetic Diversity of the Nigerian Indigenous Chicken Population: A Review

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Abstract

Genetic diversity is crucial for enhancing adaptability, improving disease resistance, and ensuring the long-term survival and productivity of animal species. Assessing genetic diversity of the Nigerian indigenous chickens is essential to understand their genetic resources, adaptability, and unique traits. It provides insights into their conservation and sustainable utilization, aiding in the improvement of productivity and preventing genetic erosion. This will also provide information that will support breeding programmes aimed at enhancing food security and rural livelihood, while preserving the genetic heritage of the native chickens. The aim of this paper was to review genetic diversity studies of the Nigerian indigenous chicken population. The Nigerian indigenous chickens are found in different parts of the country and theses chickens have been characterized by researchers into different ecotypes such as Fulani, Yoruba, Owerri, Nsukka, Agwu, Olori and Tiv ecotypes. Characterization of the Nigerian indigenous chickens into various ecotypes has not been clearly delineated with DNA-based data. Studies on phenotypic assessment of Nigerian indigenous chicken populations revealed a lot of phenotypic variations, which perhaps do not delimit the chickens into different breeds. Studies on blood protein polymorphism revealed moderate to high genetic variations within the indigenous chicken populations in Nigeria. Studies using microsatellite markers revealed high level of genetic variability among the naked neck, normal and frizzled-feathered Nigerian indigenous chickens. Reports on genetic analysis of mtDNA D-loop sequences in Nigerian indigenous chickens revealed high genetic diversity and differentiation among the indigenous chicken populations, although phylogenetic analysis grouped the chickens to a single clade.

Keywords: Characterization, chickens, diversity, phenotype, polymorphism.

Running title: The Nigerian Native Chicken Genetic Resource

Diversité génétique de la population de poulets indigènes du Nigéria : Une revue

Résumé

La diversité génétique est cruciale pour améliorer l'adaptabilité, renforcer la résistance aux maladies et assurer la survie et la productivité à long terme des espèces animales. L'évaluation de la diversité génétique des poulets indigènes du Nigéria est essentielle pour comprendre leurs ressources génétiques, leur adaptabilité et leurs traits uniques. Cela permet de mieux gérer leur conservation et leur utilisation durable, en contribuant à améliorer la productivité et à prévenir l'érosion génétique. Cela fournira également des informations soutenant les programmes de reproduction visant à améliorer la sécurité alimentaire et les moyens de subsistance ruraux, tout en préservant l'héritage génétique des poulets indigènes. L'objectif de cet article est de passer en revue les études sur la diversité génétique de la population de poulets indigènes du Nigéria. Les

poulets indigènes du Nigéria sont présents dans différentes régions du pays, et ces poulets ont été caractérisés par les chercheurs en différentes écotypes tels que les écotypes Fulani, Yoruba, Owerri, Nsukka, Agwu, Olori et Tiv. La caractérisation des poulets indigènes du Nigéria en différents écotypes n'a pas encore été clairement définie par des données basées sur l'ADN. Les études sur l'évaluation phénotypique des populations de poulets indigènes du Nigéria ont révélé de nombreuses variations phénotypiques, qui peut-être ne permettent pas de délimiter les poulets en différentes races. Les études sur le polymorphisme des protéines sanguines ont révélé des variations génétiques modérées à élevées au sein des populations de poulets indigènes du Nigéria. Les études utilisant des marqueurs microsatellites ont montré un niveau élevé de variabilité génétique parmi les poulets indigènes à cou nu, normaux et à plumes frisées du Nigéria. Les rapports sur l'analyse génétique des séquences du D-loop de l'ADNmt chez les poulets indigènes du Nigéria ont révélé une grande diversité génétique et une différenciation parmi les populations de poulets indigènes, bien que l'analyse phylogénétique ait regroupé les poulets dans un seul clade.

Mots-clés : Caractérisation, poulets, diversité, phénotype, polymorphisme

Introduction

Nigeria as a tropical country has two major vegetation regions, which include rainforest region of the south and savannah region of the north, with two prevailing seasons (wet and dry seasons) (Ayanlade *et al*., 2021). Nigerian indigenous chickens are widely found across the two vegetation regions mostly on free range with little or no housing (Ekeocha *et al*., 2021). Over the years, the Nigerian indigenous chickens have been under the influence of the prevailing and ever-changing climatic conditions in their various ecosystems, as well as direct effects of diseases, natural and artificial selection, mutation, migration and genetic drift (Ukwu *et al*., 2017b). Consequently, the Nigerian indigenous chickens may have evolved adaptive features over time in response to pressures from evolutionary forces, in order to survive under their ever-challenging environmental conditions (Qanbari *et al*., 2019; Malomane *et al*., 2021; Kpomasse, 2023).

It is therefore pertinent to note that there exists genetic diversity within and between the Nigerian indigenous chicken populations in different regions of the country. Since genetic diversity is a heritable variation (Delany, 2003), it is an indispensable tool for selection and improvement of the Nigerian indigenous chicken genetic resource. Genetic diversity of the Nigerian indigenous chickens could be assessed phenotypically (qualitative and quantitative approach) or at the molecular level (i.e., DNA-based approach). There are reports on variations in colours of plumage, shank, beak, ear lobe, eyes, comb type, and body size among the Nigerian local chicken populations (Egahi *et al*., 2010; Gwaza *et al*., 2015).

The Nigerian indigenous chicken genetic resource is endowed with several genes including naked neck (Na), frizzling (F), recessive sex-linked dwarfism (dw), spur (Sl), polydactyly (Po), and ptilopody (Fsh). The operation of these genes in the Nigerian indigenous chicken populations has been reported (Sonaiya and Olori, 1990; Ibe, 1993; Peters *et al*., 2004). The influence of naked neck and frizzling genes, both singly and in combination, on productive performance of Nigerian indigenous chickens has been extensively studied (Ibe, 1993; Peters *et al*., 2004; Fayeye *et al*., 2006). Several indigenous chicken ecotypes such as Fulani, Yoruba, Owerri, Nsukka, Agwu, Olori and Tiv ecotypes have been identified and linked to particular tribes in Nigeria. The naked neck and frizzling genes can be found in each indigenous chicken ecotype in Nigeria. The objective of this paper was to review

reports on phenotypic and molecular genetic diversity investigation of the Nigeria indigenous chicken population.

Phenotypic Analyses of the Nigerian Indigenous Chickens

Several researchers have studied the Nigerian indigenous chicken populations based on morphology, ecological location, and measurable traits. The Nigerian indigenous chickens are generally small in body size when compared to their exotic counterparts. Ibe (1992) studied three Nigerian indigenous chicken genotypes (frizzle-feathered, naked neck and normal-feathered chickens) and reported that frizzle-feathered and naked neck chickens mature earlier than normal-feathered chickens. According to that report, there was no significant difference in body weight of frizzle-feathered, naked neck and normal-feathered chickens at all ages, but chickens with normal feathering were generally superior in body weight. Ibe (1992) further noted that naked neck chickens showed superiority over frizzle-feathered birds from week one to week ten. The reverse was the case between weeks eleven and eighteen, according to that report. Ibe (1992) therefore opined that non-significant difference in body weight of frizzle feathered, naked neck and normal-feathered chickens showed that any advantage the naked neck and frizzling genes may have as a consequence of their direct effect in efficiency of thermoregulation in hot environment would probably be manifested after the growth period. Ibe (1992), therefore, suggested that frizzle and naked neck genes should be fully exploited in order to broaden the genetic base of the Nigerian indigenous chicken population for selection for productive adaptability in a heat-stressed environment. Ibe (1993) also noted the advantages of body size reduction of Nigerian indigenous chickens from the point of view of lower maintenance requirement and greater efficiency of thermoregulation, which has informed the use of sex-linked dwarf gene that causes 20 – 30% reduction in body size. Ibe and Nwohu (1999), however, reported superiority of frizzle and naked neck male indigenous chickens for early growth parameters (18-week), namely body weight, shank length, thigh length, keel length and breast width, over their normal-feathered counterparts, but superiority of normal female indigenous chickens over their frizzle and naked neck counterparts. Ibe and Nwohu (1999), therefore, opined that frizzle and naked neck genes did not improve growth of pullets as they did in cockerels, which is desirable since fast growth is usually discouraged in the management of growing pullets to avoid precocious maturity with its attendant disadvantages during the laying period. Ibe (2007) also reported that frizzling and naked neck genes cause a reduction in tropical heat stress by improving the chicken's ability for convection, resulting in improved feed conversion and better performance. Fayeye *et al*. (2006) studied the frequency, influence of some major genes on body weight and body size parameters of Nigerian indigenous chickens, and reported that polydactyl birds were significantly superior in body girth and shank length compared to ptilopody and normal birds. Fayeye *et al*. (2006) further reported that both polydactyly and ptilopody birds were superior to normal-feathered birds in all measured traits except shank length, while normal-feathered birds were superior to naked neck and frizzle-feathered birds in most of the metric traits, although not statistically significant. Fayeye *et al*. (2006) therefore concluded that the potential of thermoregulatory naked neck and frizzling genes to improve body weight and body size may not be realized in Nigerian indigenous chickens because of their small body size which confers them with a general adaptation.

Orheruata *et al*. (2006) investigated morphological, reproductive and egg quality characteristics of Nigerian indigenous chickens in Edo State, Nigeria, and reported that adult indigenous chickens of Nigeria had mean values

of 1.01kg, 7.00cm, 8.82cm, 12.61cm, and 3.43 cm for body weight, shank length, thigh length, breast length, wing length, and comb length, respectively. According to Orheruata *et al*. (2006), the Nigerian indigenous chicken population was predominated by normal-feathered chickens with a few numbers of frizzle-feathered and naked neck chickens. Orheruata *et al*. (2006) further reported that plumage colour varied from brown, black, white to mixed colour, while comb type varied from predominantly single to few pea, walnut and combless. Orheruata *et al*. (2006) also reported that shank colour varied from white, yellow, to black; ear lobe colour varied from red, white, to black. They reported mean values of 34.90g, 5.50cm, 3.66cm, 0.31mm and 8.6 for egg weight, egg length, egg width, egg shell thickness, and yolk colour score, respectively, while mean values reported for reproductive traits were 8.39, 12.31days and 76.70% for number of eggs per clutch, clutch period, and hatchability, respectively. Orheruata *et al*. (2006), therefore, concluded that Nigerian indigenous chickens showed wide morphological differences that can be exploited for the development of new breeds and strains.

Yakubu *et al*. (2008) investigated the productivity and egg quality traits of free-range naked neck and normal-feathered Nigerian indigenous chickens in Nasarawa State, and reported that mean body weight of 1.30kg recorded for naked neck chickens was significantly higher than the value 1.16kg recorded for normal-feathered chickens. According to Yakubu *et al*. (2008), average egg per clutch was significantly higher in naked neck (11.63 eggs) genotype than the normal-feathered (9.71 eggs) birds, while hatchability, shell weight and yolk index did not differ significantly between the naked neck and normal-feathered Nigerian indigenous chickens. Yakubu *et al*. (2008) further reported that mean values for egg weight, egg length, egg width, egg shape index, shell thickness, albumen weight, albumen height, yolk weight, yolk height, yolk width, and Haugh unit were significantly higher in naked neck hens than normal-feathered hens. Yakubu *et al*. (2008) concluded that the introgression of the naked neck gene into chicken breeding could play a pivotal role in the genetic improvement of traditionally managed flocks.

Oguntunji and Ayorinde (2009) evaluated the frequency and influence of the spur gene on body weight and metric traits in the Nigerian indigenous chickens in Oyo State and reported that 37.15% of the sampled indigenous chickens were spurred with estimated gene frequency of 0.61. They also reported highly significant incidence of the spur gene in male chickens (70.73%), against 29.27% for females. Oguntunji and Ayorinde (2009) concluded that incidence of spur gene seems to be sex-influenced, higher than expected but had no effect on body weight, body length, wing length, shank length, shank thickness and breast girth.

Momoh *et al*. (2010) grouped the Nigerian indigenous chickens based on body weight into heavy and light ecotypes, and compared their performance on deep litter system. According to Momoh *et al*. (2010), body weight of heavy ecotype chickens of Nigeria at 0, 4^{th}, 8^{th}, 12^{th}, 16^{th} and 20^{th} weeks of age were 30.2±0.06, 157.0±0.45, 350±3.01, 720±9.47, 840±9.35 and 976±11.2g, respectively, while those of light ecotype at similar ages were 24.2±0.05, 139±2.24, 299±3.01, 560±4.31, 707±4.89 and 831±5.52g, respectively. The results of investigation by Momoh *et al*. (2010) showed that the heavy ecotype chicken of Nigeria performed better than the light ecotype in terms of body weight from 0 – 20 weeks of age. Momoh *et al*. (2010), therefore, concluded that the heavy ecotype chicken of Nigeria has potential to be developed as meat-type chicken.

Egahi *et al*. (2010) investigated variations in qualitative traits in the Nigerian indigenous chickens in Makurdi area of Benue State Nigeria, and reported that comb type varied from

predominantly single to few of pea, Rose and walnut. According to Egahi *et al*. (2010), shank colour varied from predominantly black, white to yellow; while plumage colour varied from black, white, light brown, mottled to spotted. Egahi *et al*. (2010) also reported that crested head shape was least frequent relative to the plain head shape, while ptilopody occurred in 5.56% of the populations studied. Egahi *et al*. (2010) further reported that ear lobe was present in 70% of the population studied, and ear lobe colour varied from predominantly white, red to black. Egahi *et al*. (2010) concluded that the Nigerian indigenous chickens showed heterogeneity in phenotypic traits.

Egena *et al*. (2011) investigated the incidence of spur gene and its effect on metric parameters in male and female Nigerian indigenous chickens in Niger State and reported that among the Nigerian indigenous chicken population sampled, spurred chickens predominated their spurless counterparts. Egena *et al*. (2011) also reported that spurred male chickens were significantly better in body length, wing length and shank length than spurred females and spurless males and females.

Sola-Ojo *et al*. (2011) investigated the occurrence and frequencies of adaptive genes (dwarfism, naked neck, frizzling, silkiness, crest, pea com, ptilopody and polydactyly) in intensively raised Fulani ecotype chickens of Nigeria and found that the adaptive genes showed very low occurrence among Fulani ecotype chickens. According to Sola-Ojo *et al*. (2011), the incidence of dwarfism, naked neck, frizzling, silkiness and crest genes were 1.81, 1.21, 0.60, 0.60 and 9.10 %, respectively, while the incidence of pea comb, ptilopody and polydactyly genes were 1.81, 4.24 and 3.60 %, respectively. Sola-Ojo *et al*. (2011) also reported that the observed frequencies of these genes ranged from 0.006 to 0.091 while the calculated gene frequencies ranged from 0.011 to 0.078.

Apuno *et al*. (2011) characterized the Nigerian indigenous chickens in Shelleng and Song local government areas of Adamawa State, Nigeria and reported that eye colours were either brown, red, light green, pink, or ash, while comb type was mostly single, rarely rose and pea. According to Apuno *et al*. (2011), plumage colours were black and mottled, dark red/golden, dark brown, and brown/mottled. Other plumage colours reported by Apuno *et al*. (2011) were ash, white, white/mottled and black. They also reported that observed shank colours were pink, ash, dark ash, and light yellow, while the remaining had either milky, red, light pink or ash and yellow shanks. Apuno *et al*. (2011), therefore, opined that those distinct phenotypic differences in almost all measurable parameters among the Nigerian indigenous chickens provide the basis for which they could be classified into breeds.

Ige *et al* (2012) performed qualitative traits characterization of Yoruba ecotype (YEC) and Fulani ecotype (FEC) indigenous chickens in derived savannah zone of Nigeria and reported that highest percentage of large comb size was observed for male chicken in YEC (67.57%) and FEC (71.32%) chickens. Ige *et al*. (2012) observed that highest proportion of large wattle size favoured male chickens in YEC (51.13%) and FEC (49.38%) chicken. Ige *et al*. (2012) also recorded three different comb types (single, rose and pea) with preponderance of single comb type (94.29% in YEC and 80.44% in FEC) and obscurity of other comb types. Ige *et al*. (2012) further reported that among the naked neck, normal and frizzle-feathered genotypes observed in derived savannah region of Nigeria, normal-feathered chickens had the highest proportion (YEC: 83.99%, FEC: 83.05%) in both populations. Ige *et al*. (2012) also noted that plumage colour varied widely between the two populations, while three colour patterns (red, white and ash) of ear lobe were observed in FEC and YEC, in addition to brown and yellow ear lobes observed in FEC.

Adekoya *et al*. (2013) carried out morphological characterization of five Nigerian indigenous chicken phenotypes (naked neck, frizzle-feathered, featherless wing, rose comb and wild type) in Lagos State Nigeria, and reported that the rose comb and wild type were mostly isolated from each other and from other genotypes. Adekoya *et al*. (2013) also reported that the proportion of individuals correctly classified into their original group was highest in the wild type (78.6%), then naked neck (63.6%) and featherless wing (60.0%), indicating that the wild type is highly divergent from other types. Adekoya *et al*. (2013), therefore, suggested that application of molecular genetics technique could be useful in confirming the detected phenotypic differentiation of Nigerian indigenous chicken types.

Gwaza *et al*. (2015) evaluated the genetic distance between populations of the Tiv ecotype chickens in the derived Guinea savannah zone of Nigeria and reported significant genetic distances between Tiv ecotype chickens in different locations. According to Gwaza *et al.* (2015), there were significant variation in body length, shank length, tail length, tail width and comb length of the Tiv ecotype chickens due to location. Gwaza *et al*. (2015) therefore concluded that there was significant genetic diversity in body dimensions between isolated populations of the Tiv ecotype chickens.

Gwaza and Eje (2015) investigated within ecotype genetic divergence of the Yoruba ecotype chickens in selected populations in Kwara State, Nigeria, and reported that significant differences existed in linear body measurements between the populations. They also reported that body height, comb length and wattle height exhibited high variability with equally highest discriminant ability to differentiate between the populations. Gwaza and Ejeh (2015), therefore, opined that the increase in size of the comb and wattle between the populations of Yoruba ecotype chickens was an adaptive divergence among the populations to enhance thermoregulatory efficiency compensating for lower relative heat loss due to lower surface area to mass ratio as body height and size increase.

Ukwu *et al*. (2017b) compared the Nigerian indigenous chickens in south eastern Nigeria with the Nigerian indigenous chickens in north-central Nigeria and reported that indigenous chickens in North central were better than their counterpart in south eastern Nigeria in terms of body weight, shank length, wing length and toe length. Ukwu *et al*. (2017b) therefore concluded that the Nigerian indigenous chickens in southeast and north-central Nigeria were heterogeneous in terms of body weight and linear body measurements, which is an indication of genetic diversity within the Nigerian indigenous chicken populations.

It is worthy of note that reports on phenotypic assessment of the Nigerian indigenous chicken populations revealed a lot of phenotypic variations, which perhaps do not delimit the chickens into different breeds. However, these reports need to be properly verified using DNA-based information in other to accurately delineate the genetic diversity status of the indigenous chicken populations in Nigeria, and probably classify them into a breed or different breeds.

Genetic Analysis of the Nigerian Indigenous Chickens Using Physiological and Biochemical Markers

Physiological and biochemical markers have been tried out extensively in genetic analysis of farm animals, but have not been found encouraging as they are often sex-linked, age-dependent, and are significantly influenced by the environment (Mitra *et al*., 1999). Although protein polymorphisms were among the first markers used to estimate genetic variation within and between chicken populations, however, they show low degree of polymorphism reflected by a high degree of similarity in gene frequencies among populations and lines, especially when

these are closely related (Weigend and Romanov, 2001; Weigend *et al*., 2004). In the recent past, physiological and biochemical markers (blood protein polymorphisms) have been relatively used for genetic analysis of farm animals, especially in the developing countries very recently, including Nigeria, although there are more advanced tools for genetic analysis. Blood protein markers such as haemoglobin, transferrin, albumin, globulin, and carbonic anhydrase have been employed in genetic diversity studies of Nigerian indigenous chicken populations by some researchers. The central hypothesis in the use of blood protein markers in genetic analysis of farm animals is that existence of molecular and structural differences in these markers could be neutral, or translate phenotypically to functional variants by conferring certain advantages to individual in a population or limit their productivities.

Ladokun *et al*. (2008) evaluated the haematological and serum biochemical indices of naked neck and normal-feathered Nigerian indigenous chickens in a sub-humid tropical environment and reported non-significant differences between the genotypes in the mean values of white blood cells, mean corpuscular volume and mean corpuscular haemoglobin concentration. Ladokun *et al*. (2008) reported that naked neck cocks were significantly superior in packed cell volume, haemoglobin and red blood cells when compared with their normal-feathered counterparts. Ladokun *et al*. (2008) also reported non-significant differences in total protein, albumen, urea, glucose, cholesterol, serum alanine amino transaminase (SALT) and serum aspartate amino transferase (SAST) of the naked neck and normal-feathered indigenous chickens. According to the report of Ladokun *et al*. (2008), normal-feathered cocks had significantly higher globulin content and lower creatinine value than naked neck cocks; plumage colour did not significantly affect haematological and serum biochemical indices of the Nigerian indigenous chickens, except packed cell volume, which was significantly higher in brown cocks than white cocks.

Salako and Ige (2006) studied the Nigerian indigenous chickens and exotic (meat-type) chicken at the haemoglobin locus using cellulose acetate electrophoresis and reported that exotic birds were the same in phenotypic characteristics and haemoglobin genotype (Hb^{AA}), while the Nigerian indigenous chickens varied in their haemoglobin genotypes (Hb^{AA} and Hb^{AB}) and phenotypic characteristics. According to Salako and Ige (2006), the frequencies of haemoglobin alleles Hb^{A} and Hb^{B} in the Nigerian indigenous chickens were 0.68 and 0.33 respectively, with corresponding genotype frequencies of 0.35 and 0.65 for Hb^{AA} and Hb^{AB} respectively, while the frequency of Hb^{A} in exotic chicken was fixed (1.00 or 100%). Salako and Ige (2006) therefore concluded that the Nigerian indigenous chicken population was in Hardy-Weinberg equilibrium while the exotic birds were not.

Adeleke *et al*. (2011) carried out preliminary screening of genetic lineage of three Nigerian indigenous chicken strains (normal feathered, frizzle feathered and naked neck) and one exotic strain (Anak Titan) based on blood protein (globulin, transferrin and albumin) polymorphism, using Sodium dodecyl-sulphate polyacrylamide gel electrophoresis (SDS-PAGE) and reported that the strains were clearly separated from one another. Adeleke *et al*. (2011) also reported that mean genetic similarity among the four strains was 55% with naked neck chicken being the most diverged. Adeleke *et al*. (2011) therefore concluded that low polymorphism exists among the Nigerian indigenous chickens and Anak Titan with respect to the blood proteins examined.

Yakubu and Aya (2012) analyzed three indigenous chicken populations in Nigeria (naked neck, normal and Fulani-ecotype chickens) at the haemoglobin locus using cellulose acetate electrophoresis and reported two co-dominant

haemoglobin alleles (Hb^A and Hb^B) with three genotypes (Hb^{AA}, Hb^{AB} and Hb^{BB}) in the populations. According to Yakubu and Aya (2012), there was preponderance of haemoglobin alleles Hb^A over the Hb^B allele in the populations of normal-feathered, naked neck and Fulani-ecotype chickens. Yakubu and Aya (2012) also reported the preponderance of haemoglobin genotype Hb^{AA} in the three Nigerian indigenous chicken populations. Yakubu and Aya (2012) further stated that the gene and genotype frequencies of naked neck and Fulani-ecotype chickens of Nigeria were in Hardy-Weinberg equilibrium, while those of normal-feathered chickens of Nigeria deviated from the theoretical proportions.

Ajayi *et al.* (2013) analyzed haemoglobin polymorphism in three Nigerian indigenous chicken populations (frizzle feathered, naked neck and normal chickens) in the Niger Delta region using cellulose acetate electrophoresis and found three haemoglobin genotypes namely Hb^{AA}, Hb^{AB} and Hb^{BB} controlled by two haemoglobin alleles, Hb^A and Hb^B, in each of the populations. According to that reports of Ajayi *et al*. (2013), the frequency distribution of haemoglobin genotypes among the three indigenous chicken genotypes in the Niger Delta region did not follow any pattern. Ajayi *et al*. (2013) concluded that the Nigerian indigenous chickens in the Niger Delta region are characterized into frizzle-feathered, naked neck and normal-feathered, and are a mixture of Hb^{AA}, Hb^{Ab} and Hb^{BB} genotypes. These findings suggest that the Nigerian indigenous chickens in the Niger Delta region are polymorphic at the haemoglobin locus.

Ige *et al*. (2013) characterized indigenous Fulani and Yoruba ecotypes chicken of Nigeria at two blood protein loci (haemoglobin, Hb and carbonic anhydrase, CA) using cellulose acetate electrophoresis. Ige *et al*. (2013) reported three haemoglobin genotypes (Hb^{AA}, Hb^{AB} and Hb^{BB}) genetically controlled by two co-dominant alleles Hb^A and Hb^B, and three carbonic anhydrase genotypes (CA^{FF}, CA^{FS} and CA^{SS}) genetically controlled by two co-dominant alleles CA^F and CA^S. Ige *et al*. (2013) reported the preponderance of Hb^B allele in Yoruba ecotype chicken as well as in Fulani ecotype chicken. Ige *et al*. (2013) also reported that CA^S allele was more frequent in Yoruba and Fulani ecotype chickens than CA^F allele. Ige *et al*. (2013) concluded that genetic similarity within ecotype indicated 60% in Fulani ecotype chicken, 80% in Yoruba ecotype chicken and 40% between Yoruba and Fulani ecotypes at Hb locus, while at CA locus, genetic similarity was 69% in Fulani ecotype, 50% in Yoruba ecotype and 42% between Yoruba and Fulani ecotypes chicken. Ige *et al*. (2013) also concluded that the Fulani ecotype chicken and Yoruba ecotype chicken were genetically related at Hb and CA loci.

Ige *et al*. (2014) also investigated genetic similarity of Yoruba ecotype indigenous chickens in derived Savannah region of Nigeria at four blood protein loci (globulin, transferrin, albumin and post albumin) using Sodium dodecylsulphate polyacrylamide gel electrophoresis (SDS-PAGE) and reported that the Yoruba ecotype chickens were genetically similar at transferrin (58%) locus. They, however, reported low genetic similarity at albumin (19%), globulin (18%) and post albumin (40%) loci within the Yoruba ecotype indigenous chicken population.

Ige and Salako (2014) studied genetic variation at transferrin (Tf) locus in Fulani and Yoruba ecotypes chicken in Nigeria and reported six (6) transferrin genotypes (Tf^{AA}, Tf^{AB}, Tf^{AC}, Tf^{BB}, Tf^{BC} and Tf^{CC}) genetically controlled by three co-dominant alleles (Tf^A, Tf^B, and Tf^C). According to the report of Ige and Salako (2014), frequency distribution of Tf^A, Tf^B and Tf^C alleles among the Yoruba and Fulani ecotype chickens did not follow any defined trend. Ige and Salako (2014) also reported 72% genetic similarity within Fulani ecotype chickens, 58% genetic similarity within Yoruba ecotype chickens, 78% genetic

similarity between Fulani ecotype and Yoruba ecotype chickens, and therefore concluded that the two Nigerian indigenous chicken populations were closely related at transferrin locus.

Ukwu *et al*. (2017a) analyzed within-ecotype genetic diversity at the haemoglobin locus in the Tiv ecotype chickens in Benue State and reported three haemoglobin genotypes Hb^{AA}, Hb^{AB} and Hb^{BB} with genotype frequencies 0.44, 0.32 and 0.24 respectively. Ukwu *et al*. (2017a) also reported heterozygosity value of 0.48, gene frequencies of 0.60 and 0.40 for Hb^{A} and Hb^{B} alleles respectively at the haemoglobin locus in the Tiv ecotype chicken population in Benue State. This report suggests the preponderance of Hb^{A} allele among the Tiv ecotype chickens of Nigeria.

The results of these investigations that focused on blood protein loci (haemoglobin, transferrin, globulin, albumin, post albumin and carbonic anhydrase) in the Nigerian indigenous chicken populations, therefore, suggest that there exist low to moderate polymorphisms at the loci studied. However, studies of the Nigerian indigenous chicken populations based on blood protein polymorphism are fragmented since none attempted to integrate all the indigenous chicken ecotypes found in different regions of Nigeria into a detailed study to estimate their distinctiveness and diversity. Consequently, it is difficult to integrate these results in order to make a substantive conclusion about the Nigerian indigenous chicken genetic resource. These results, therefore, need to be further verified using more informative methods of genetic analysis that employ DNA-based markers in high throughput genetic analysis of chicken populations in order to precisely delineate the Nigerian indigenous chicken genetic resource.

Molecular (DNA-based) Analyses of the Nigerian Indigenous Chickens

The analysis of the Nigerian indigenous chicken genetic resource using molecular genetics approach, although cost intensive, is a more realistic approach than quantitative genetics approach, which anchors in physically observable characteristics. This is because molecular characterization provides in-depth information of polymorphisms existing among individuals within or among populations. However, the Nigerian indigenous chicken genetic resource has not been relatively exploited for genetic polymorphisms using molecular genetics approach, although some investigators have attempted to study the indigenous chicken ecotypes in different regions of Nigeria using blood protein polymorphisms, microsatellite markers and mitochondrial DNA D-loop. This situation is worsened by inadequate funding and lack of advanced technologies for high throughput genome analyses in Nigeria and other African countries.

Molecular Genetic Analyses of the Nigerian Indigenous Chickens Using Microsatellite Markers

Microsatellites are tandem DNA repeats of 2 to 5 bp (FAO, 2011) and are highly polymorphic markers. However, microsatellites do not encode proteins, and are thus assumed to be selectively neutral (FAO, 2011). Microsatellite markers have been extensively used in determining measures of genetic diversity such as allele number (N_a), effective number of alleles (N_e), observed and expected heterozygosity (H_o and H_e), polymorphism information content (PIC), and genetic distances within and between chicken populations (e.g. Takahashi *et al*., 1998; Hillel *et al*., 2003; Parmar *et al*., 2006; Qu *et al*., 2006; Zanetti *et al*., 2007; Suh *et al*., 2014; Abebe *et al*., 2015).

The analysis of genetic diversity of the Nigerian indigenous chicken populations using microsatellite markers have also been tried out by some investigators. For example, Ohwojakpor *et al*. (2012) studied three Nigerian indigenous chicken populations (normal feathered, frizzle-feathered and naked neck) in South-south region of Nigeria using eight microsatellite markers and

reported that mean allele number (N_a) for all loci ranged from 5.6250 (Naked neck) to 9.8750 (normal-feathered), and mean effective number of allele (N_e) ranged from 5.0133 (naked neck) to 7.1637 (normal-feathered). They also reported that mean polymorphism information content (PIC) was between 0.7588 (naked neck) and 0.8282 (normal-feathered), averages of observed heterozygosity among loci were 0.5068, 0.5236 and 0.5755 for naked neck, normal-feathered and frizzle-feathered chicken populations, respectively. Ohwojakpor *et al.* (2012) further reported that genetic distance estimates revealed that the normal-feathered and frizzle-feathered Nigerian indigenous chicken populations were closely related with genetic distance value of 0.5183, while genetic distance between normal-feathered and naked neck, and between frizzle-feathered and normal feathered chicken populations were 0.6177, and 0.6306, respectively. Ohwojakpor *et al*. (2012) concluded that naked neck chickens were genetically diverse from other indigenous chicken populations.

Olowofeso and Ohwojakpor (2016) studied genetic diversity among three Nigerian indigenous chicken populations (naked neck, frizzle-feathered and normal-feathered) obtained from South-south geo-political zone of Nigeria, based on eleven microsatellite markers and reported that mean number of allele N_a were 7.0±0.82, 8.09±0.82 and 9.55±0.66 for naked neck, frizzle-feathered and normal-feathered chickens, respectively. They also reported that mean expected heterozygosities (H_e) were 0.76, 0.84 and 0.84 for naked neck, frizzle-feathered and normal-feathered chickens, respectively. Olowofeso and Ohwojakpor (2016) concluded that there is high level of genetic variability among the naked neck, normal and frizzle-feathered chicken populations.

It is evident, based on microsatellite analysis, that there is moderate to high genetic diversity within the Nigerian indigenous chicken populations, and this could be exploited in genetic improvement and conservation programmes.

Molecular Genetic Analyses of the Nigerian Indigenous Chickens at the Mitochondrial DNA D-loop Region

The mitochondrial DNA (mtDNA) D-loop region has been widely used in genetic diversity studies of chicken populations (e.g. Liu *et al*., 2006; Muchadeyi *et al*., 2008). It has been reported that mtDNA markers may also provide a rapid way of detecting hybridization between livestock species or subspecies (Nijman *et al*., 2003). However, there is limited information on the use of mtDNA markers in genetic analysis of the Nigerian indigenous chicken populations.

For example, Adebambo *et al*. (2010) studied the Nigerian indigenous unrelated chickens from four geographical regions in Nigeria (Northwest, Northeast, Southeast and Southwest) using mtDNA D-loop and identified 35 haplotypes from 36 polymorphic sites. According to Adebambo *et al*. (2010), phylogenetic analysis of mtDNA D-loop sequences revealed that the Nigerian indigenous chickens were grouped to a single clade, and 97.8% of the total maternal variation occurred within populations, while the remaining was found among populations. Adebambo *et al*. (2010) concluded that lack of substructure in the Nigerian indigenous chicken populations is evidence of a single maternal origin and extensive genetic intermixing in the past and present times.

Ajibike *et al*. (2017) assessed maternal genetic diversity at the mitochondrial DNA D-loop region of indigenous chickens from Northeast, Northwest, Northcentral and Southeastern Nigerian and reported 28 haplotypes majorly of haplogroup D, which originated from Indian subcontinent, hence an indication of single maternal lineage. Ajibike *et al*. (2017) further reported that mean haplotypic and nucleotide diversity at the mtDNA D-loop region of the Nigerian indigenous chicken populations were 0.39±0.05 and 0.02±0.02 respectively, while

genetic variation within and between the chicken populations accounted for 97.30 and 2.70 % of the total genetic variation. Ajibike *et al*. (2017) therefore concluded that there was relatively high genetic diversity and differentiation among the indigenous chicken populations in Nigeria.

Thus, reports on genetic variability at mtDNA D-loop region revealed moderate to high genetic diversity within the Nigerian indigenous chicken populations, which is in agreement with reports based on microsatellite analysis as well as reports on phenotypic assessment.

Molecular Genetic Analyses of the Nigerian Indigenous Chickens Using Single Nucleotide Polymorphism (SNP) Markers

Although SNPs have been used in genetic analyses of chickens (Riztyan *et al*., 2011a, 2011b; Jalving *et al*., 2004), turkey (*Meleagris gallopavo*) (Aslam *et al*., 2012) and cattle (Gorback *et al*., 2010), there is dearth of information on the use of SNPs in genetic analysis of the Nigerian indigenous chicken populations. This situation could be because of inadequacy of funding and advanced technology for high-throughput genome analysis in Nigeria. However, the existence of single nucleotide polymorphism (SNP) within the Nigerian indigenous chicken population has been reported. For example, Ilori *et al*. (2016) investigated the polymorphism of IGF-1 gene in the Nigerian indigenous chickens and identified eight SNPs across the populations. The report further stated that small genetic differentiation exists among the Nigerian indigenous chicken populations as revealed by phylogenetic tree.

There is, therefore, need for further investigation of the Nigerian indigenous chicken populations to uncover single nucleotide polymorphisms (SNP) that may exist within the indigenous chicken population, and subsequently investigate their associations with some economically important traits.

Conclusion

There exists moderate to high genetic diversity within the Nigerian indigenous chicken genetic resource, which is yet to be fully exploited for the purpose of genetic improvement. Phenotypic assessment of the Nigerian indigenous chicken populations revealed a lot of phenotypic variations, which perhaps do not delimit the chickens into different breeds. Microsatellite studies and mtDNA D-loop analysis also revealed high level of genetic diversity and differentiation within the indigenous chicken populations in Nigeria. Since genetic diversity enables perpetuation of species in the presence of changing climatic conditions, the Nigerian indigenous chicken genetic resource needs to be further exploited for its valuable arrays of allelic forms pertinent to tropical environmental conditions.

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