ORIGINAL ARTICLE

Genetic diversity of poultry chicken types reared in Ogun state using albumin polymorphism

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ABSTRACT

The study was carried out to examine the genetic diversity in different chicken types reared in Ogun State using Albumin. A total of 80 birds which include: 25 broilers, 25 layers and 30 indigenous chickens from Abeokuta North, Ado odo Otta, Sagamu and Ijebu Imushin were purposely sampled. 5mL blood samples were drawn per individual from the wing vein via 2mL hypodermal needle into anticoagulant treated (heparinized) vials. Albumin polymorphism was investigated using cellulose acetate paper electrophoresis. Based on the estimate allele frequencies the population was characterized by their genetic distance (D) among the populations. The estimates of heterozygosity were 0.28, 0.40, and 0.55 for layers, broilers and indigenous chicken populations. Two alleles were reported for each of the population (A and B in Albumin). The closest genetic distance relationship was found between the indigenous and layers chicken populations (D=0.0038), while population from broilers and indigenous were more genetically distance (D=0.8948). The relationships among the chicken population were consolidated by the dendrogram that emanated from their genetic distance. The result obtain will be useful as an initial guide in defining objectives for future investigations of genetic integrity and developing conservation strategies for chicken species.

Keywords: Genetic diversity; Albumin; Chicken; Heterozygosity; genetic distance; Polymorphism

INTRODUCTION

Biodiversity encompasses not only the world's species with their unique evolutionary histories, but also genetic variability within and among populations of species and the distribution of species across local habitats, ecosystems, landscapes and whole continents or oceans (FAO, 2009). An increasing loss of genetic diversity has been observed for all agriculturally used species, and more than half of common livestock breeds especially poultry are now endangered or at risk of extinction, (Hoffman, 2005). Acording to FAO (2000), animal genetic diversity allows farmers to select stocks or develop new breeds in response to environmental change, threat of disease, new knowledge of human nutrition requirements, changing market conditions and societal needs. Over 75 percent of the world's food and agriculture is produced by fewer than 25 domestic plant and animal species and unfortunately, global farm animal genetic resources are disappearing very fast (FAO, 2007). The number of domestic animal species is low perhaps 40% in total, and with less than 14% accounting for over 90% of global production (FAO, 2004).

The Nigerian indigenous chicken is a dual-purpose bird that is used both for meat and egg production in the rural and peri-urban areas of the country; they are found in large numbers distributed across different agroecological categories under a traditional family based scavenging management system Ajayi, (2010). They contain a highly conserved genetic system with high levels of heterozygosity (Wimmers et al., 2000). These indicate that they are highly important farm animals, kept for good source of animal protein, for income and socio-cultural roles. Ajayi, (2010) reported the adaptive potentials of the Nigerian indigenous chicken to varied ecological conditions, stresses and diseases. There have been some efforts at characterizing the Nigerian indigenous chickens. These efforts include classification based on ecotypes (Sonaiya and Olori, 1990), plumage and shank colour (Ebozoje and Ikeobi, 1995; Ikeobi et al., 1996), possession of the major genes of feather distribution and feather structure (Ibe, 1993, Ebozoje and Ikeobi, 1995; Peters et al., 2002, 2005, 2007, 2008a, 2008b). Major genes effect on growth, fertility, hatchability and semen quality characteristics have also been reported (Peters et al., 2002, 2005, 2008a, 2008b). Wekhe (1992) earlier reported that Nigerian indigenous chickens are more resistant to infectious disease agents than their exotic counterparts. These chicken population estimated at about 140 million (FAO, 2006) is currently underutilized in the development of acceptable improved breeds. There is a need to expand the narrow genetic base in which the world's poultry breeding company currently operates by including local chicken resources that has been widely reported to be well adapted to the local conditions. In addition to the phenotypic characterization that has been done and reported above, there is a need to perform molecular characterization for information with regard to phylogeny, diversity and relatedness. To take advantage of the differences in the strain of chickens and bring about genetic progress in breeding, a diversity study is imperative. Protein polymorphisms have been used as marker systems to estimate genetic variation within and between chicken populations (Mina et al., 1991; Romanov, 1994) there is a need to use protein markers to do a preliminary screening on genetic diversity of Nigerian local chickens. This investigation therefore sought to find the genetic diversity, as a preliminary assessment, among Nigerian indigenous chickens broiler and layers reared intensively using blood protein polymorphisms by estimating genetic similarity. Gel electrophoresis is also one of the most realistic practical means of detecting genetic variation available (Hubby and Lewontin, 1966) and it was used to provide estimates of variation. Dessauer and Nevo (1969) 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 various chicken types in Ogun State, Nigeria. The main objective of this research is to examine genetic diversity in different chicken types using Albumin in Ogun State, while the specific objectives are; to evaluate albumin alleles and genotypes frequencies, to evaluate Hardyweinberg equilibrium for the four populations, estimate heterozygosity of allele and testing Hardy-Weinberg's equilibrium.

MATERIALS AND METHODS

The study was carried out within the four province of Ogun State. Four areas were randomly selected and they are Abeokuta-North, Ado-OdoOtta, Sagamu and Ijebu Mushin. Blood samples were obtained from each of the sampling area making a total of 80 blood samples in all comprising of 25 broilers, 25 layers and 30 indigenous chickens. 5ml of whole blood was collected from the wing vein into heparinized bottle and stored at 4°C and transported to the animal science genetic laboratory. 5 ml of blood was drawn into tube containing Lithium Heparin as anticoagulant. Blood plasma was separated from blood cell by centrifugation at 3500 rpm at room temperature for 10 minutes. Blood plasma was drawn into labeled sample tube after centrifugation and stored in the freezer until tested. Cellulose Acetate Electrophoresis was performed according to (RIKEN (2006) with minor modifications. Band scoring was carried out to visualize the protein bands at the albumin (Al) locus. They were destained several times until clear and sharp bands appear, the bands were scored visually based on their migratory pattern as described by RIKEN (2006) and direct counting was used for calculating gene frequencies. Tools for Population Genetic Analyses (TFPGA)

software was used to generate the genetic distance according to (Nei's Original 1972), the allele frequency, observed and expected heterozygosity, Hardyweinberg's Equilibrium coefficient, Wright's F_{IS}, F_{IT} and F_{ST} estimated and drawing UnPaired Group Method of Algorithm (UPGMA) dendrograms.

RESULTS AND DISCUSSIONS

The highest frequency was observed in Alb^{A} from Abeokuta North population with 1.00 while the lowest frequency was obtained in Alb^{B} (0.10) from Ijebu Imushin, (Table 1). This aligns with the work of Johari et al., (2008) who reported the presence of two alleles A and B in Kedu chickens. Other species such as the Muscovy and pekin ducks (Azmi et al., 2006 and Johari et al., 2012) have also been reported to exhibit similar albumin polymorphism and this confirmed that albumin as a good marker is polymorphic in the various populations sampled.

Table 1. Allele frequency at Albumin for poultry birds from Abeokuta North, Ado odo Otta, Sagamu and Ijebu Imushin.

Population Location	Allele	Sample size	Allele Frequency (Types)			Average allele frequency
			Layer	Broiler	Indigenous	
Abeokuta	A	19.00	1.00	0.79	0.80	0.87
North	B		0.00	0.21	0.20	0.13
Ado-odo Otta	A	17.00	0.59	0.25	0.50	0.44
	B		0.41	0.75	0.50	0.56
Sagamu	A	17.00	0.67	0.33	0.70	0.56
	B		0.33	0.67	0.30	0.44
Ijebu Imushin	A	17.00	0.83	0.50	0.90	0.73
	B		0.17	0.50	0.10	0.27
Average for all location	A	70.00	0.78	0.48	0.72	0.66
	B		0.22	0.52	0.28	0.34

The genotype frequency ranges from 0.14 for Alb^{AB} in (Abeokuta North) broilers to 0.80 for Alb^{AA} in (Ijebu Mushin) indigenous birds (Table 2). Alb^{BB} genotype does not exist in indigenous birds from all the population and in layers from Abeokuta North and Ijebu Mushin. This is similar to the report of Esmailkhanian et al., (2000) with three albumin genotypes i.e AA, AB and BB observed in Iranian native poultry breed. Ismoyowati, (2008) reported Alb^{AA}, Alb^{AB}, Alb^{AC}, Alb^{BB} and Alb^{BC} Albumin genotypes in Kampung chicken. This further confirmed that albumin is polymorphic among the populations sampled. Hardy-Weinberg Equilibrium exact test of various types of chicken was not Significant ($p<0.05$) in all the sampled populations (Table 3). This implied that there is no significant ($p<0.05$) deferent in the Hardy-Weinberg Equilibrium for all the populations sampled.

Table 2. Genotype frequency at Albumin for poultry birds from Abeokuta North, Ado odo Otta, Sagamu and Ijebu Imushin.

Population Location	Genotype	Sample size	Genotype Frequency			Average Genotype frequency
			Layer	Broiler	Indigenous	
Abeokuta	AA	19.00	1.00	0.72	0.60	0.79
North	AB		0.00	0.14	0.40	0.16
	BB		0.00	0.14	0.00	0.05
Ado-odo Otta	AA	17.00	0.33	0.50	0.00	0.24
	AB		0.50	0.50	1.00	0.64
	BB		0.17	0.00	0.00	0.12
Sagamu	AA	17.00	0.50	0.50	0.40	0.36
	AB		0.33	0.33	0.60	0.41
	BB		0.17	0.17	0.00	0.23
Ijebu Imushin	AA	17.00	0.67	0.17	0.80	0.53
	AB		0.33	0.66	0.20	0.41
	BB		0.00	0.17	0.00	0.06
Average for all location	AA	70.00	0.64	0.32	0.45	0.46
	AB		0.28	0.40	0.55	0.40
	BB		0.08	0.28	0.00	0.14

Table 3. Test for Hardy Weinberg Equilibrium for poultry birds from Abeokuta North, Ado odo Otta, Sagamu and Ijebu Imushin.

Population	Allele	Sample size	Hardy Weinberg's Equilibrum			Average
			Layer	Broiler	Indigenous	
Abeokuta North	A	19.00	__	0.24 ^{NS}	1.00^{NS}	0.26^{NS}
	B					
Ado-odo Otta	A	17.00	1.00^{NS}	1.00^{NS}	0.13^{NS}	0.34^{NS}
	B					
Sagamu	A	17.00	1.00^{NS}	1.00^{NS}	1.00^{NS}	0.62^{NS}
	B					
Ijebu Imushin	A	17.00	1.00^{NS}	1.00^{NS}	1.00^{NS}	1.00^{NS}
	B					
Average	A	70.00	0.55^{NS}	0.42^{NS}	0.26^{NS}	0.43^{NS}
	B					

The F-statistics estimates of population structure are presented in table 4 and all estimates of $F_{IS,}$ F_{IT} and F_{ST} were not significant (P<0.05) except for F_{ST} value for population from Abeokuta North and F_{IT} value for population from Ijebu Imushin that were significant (P<0.05) indicating small deviation from Hardy-Weinberg's Equilibrium and a measure of outbreeding in the population, (Weir and Cockerham, 2014). The high heterozygosity, observed H_O, for all the chicken types in all populations (0.60) points to increasing genetic variability in the chicken populations at the Albumin locus (Table 5). This may be due to the population structure of the chicken sample (Rychlik et al., 2011). The observed heterozygosity is higher than expected heterozygosity implying an out bred populations.

Table 4. Wright F-Statistic analysis for Albumin for poultry birds from Abeokuta North, Ado odo Otta, Sagamu and Ijebu Imushin.

Population	f(F_{IS})	F(F_{ST})	F(F_{IT})
Abeokuta North	0.32^{NS}	0.03*	0.34^{NS}
Ado-odo Otta	0.35^{NS}	0.07^{NS}	0.26^{NS}
Sagamu	0.15^{NS}	0.07^{NS}	0.21^{NS}
Ijebu Imushin	0.17^{NS}	0.16^{NS}	0.02*
Total for all location	0.06 ^{NS}	0.10^{NS}	0.15^{NS}

Table 5. Effective sample size (N) and expected and observed heterozygosity (H_E and H_O) at Albumin locus for poultry birds from Abeokuta North, Ado odo Otta, Sagamu, Ijebu Imushin and average sample.

Population	Observed and Expected Heterozygosity									Average for all population		
	Layers			Broilers			Indigenous					
	N	H_E	H_O	N	H_E	H_O	N	H_E	H_O	N	H_E	H_O
Abeokuta North	7	0.86	0.14	7	0.14	0.86	5	0.40	0.60	19	0.15	0.85
Ado odo Otta	6	0.50	0.50	6	0.50	0.50	5	1.00	0	17	0.64	0.36
Sagamu	6	0.33	0.67	6	0.33	0.67	5	0.60	0.40	17	0.41	0.59
Ijebu Imushin	6	0.33	0.67	6	0.67	0.33	5	0.20	0.80	17	0.41	0.59
Total	25	0.28	0.72	25	0.40	0.60	20	0.55	0.45	70	0.40	0.60

The genetic distance among the population studied were small but within the range of 0.001 and 0.046 reported by Nei, (1976) for local breeds. The longest distance was observed between indigenous chicken and broiler chicken while the shortest distance was observed between layers and indigenous. For identity, layers and indigenous are 99.92% closer to each other while indigenous and broiler chicken were 95.51% closer to each other.

The dendrogram of the three chicken types reared in Ogun State revealed that the layer and the indigenous are genetically closer than the broiler (Fig 1). All the chicken type where together until they get to a point where the layers and indigenous cluster together and the broiler on another node, later the layer and the indigenous separated to add different nodes.

Table 6. Genetic distance for all breed of birds from all location according to Nei 1972 identity (up) and distance (down)

Breed	Layers	Broilers	Indigenous
Layers	*****	0.1598	0.1112
Broilers	0.8523	*****	
Indigenous	0.9962	0.8948	*****

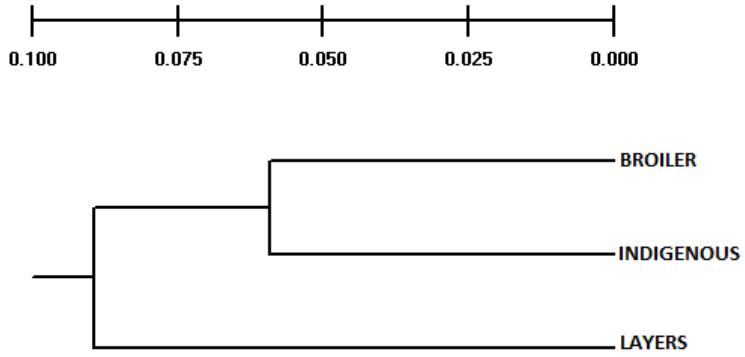

Figure 1. The Dendrogram of the three chicken types reared in Ogun State.

CONCLUSION

This study revealed that there is a low diversity among the different poultry chicken typed reared in Ogun State based on the value of their expected gene diversity on the population studied which give room for improving the chicken types reared in Ogun State. The result from this study is of important as a guide in defining objectives for designing future investigations of the genetic integrity and developing conservation strategies for chicken species. Genetic characterization of animals is the first step in considering sustainable management or conservation of a particular population and it is important to know how different and unique each population is. Data on species to species and even location to location variation for important genes and their frequencies can help to understand dynamics of genetic change owing to factors such as natural selection, breeding strategies and genotype environment interaction.

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