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Genetic Divergence between the Indigenous Chickens of Nigeria

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Abstract

A total of 671 pedigreed chicks were artificially hatched from a controlled breeding population of Nigerian local chicken composed of three phenotypic groups namely the normal feathered (NF), frizzle feathered (FF) and the naked neck (Na). Hatch weights were recorded and the resulting chicks were reared in captivity on a standard farm-mix ration. Body weights were taken 4-weekly to 20 weeks of age. Twenty pullets from each of NF, FF and Na were randomly selected and monitored for part period egg production and progressive increase in egg weight to 280 days of age. Data collected were subjected to Mahalanobis D^2 discriminant analysis for genetic distance estimation. Six of the seven discriminating variables used in this study revealed that there was significant ($P<0.05$) genetic distance between the genetic groups. It is concluded that heterosis is expected to be higher for crosses between the NF and Na, and NF and FF than between the Na and FF.

Keywords: boiled mango, maize, broiler finisher, carcass indices, organ indices

Introduction

Genetic distance is that difference between two entities that can be described by allelic variation [1]. It is the extent of gene differences between populations or species that is measured by some numerical quantity [2]. Genetic divergence studies may be used to evaluate the behaviour of genotypes in different environments and to evaluate the superiority of some genotypes over others. Piassi further noted that genetic distance is important in identifying divergent genotypes that may be used as parents in breeding programs and to relate genetic divergence to heterosis [3]. Bruchi et al reported that the distribution of genetic diversity within and among populations is a function of the rate of gene flow between the populations. These authors further reported that the extent of gene flow in a population depends on the distribution of the habitat it occupies and the size and degree of isolation [4]. According to Eding and Laval genetic distances between breeds or populations are controlled by mutation, genetic drift, selection and migration. That a distance of zero implies no genetic difference between groups and a maximum value indicates fixation for alternate alleles [5]. FAO reported that characterization includes a clear definition of the genetic attributes of an animal species or breed, which has a unique identity and the environment to which the species or breed populations are adapted [6]. This was corroborated by the report of Salako and Ngere, that morphological distance is capable of providing a sound foundation and reference in the systematic evaluation and characterization of indigenous species, and will also save cost of experimental materials in terms of number of animals which may be required for evaluation [7]. Insight into breed diversity may be achieved by examining differences in phenotypic traits using certain cladistics or phenetic approaches [8,9]. Mahalanobis recommended the estimation of genetic distance using quantitative traits through development of a statistical model widely used today called Mahalanobis D^2 statistic [10].

Several authors have reported on the estimation of distance between populations in goats Salako and Ngere) and in fish [7,11]. However, there is paucity of information as to the genetic distance estimation in chickens, especially the Nigerian indigenous chicken. In the current study, the genetic diversity between the normal, frizzled and naked neck indigenous chickens of Nigeria is evaluated using traits that show continuous variation.

Materials and Methods

Experimental site

The experiment was carried out in Makurdi-Nigeria. The co-ordinates, rainfall pattern, humidity and temperature variations in Makurdi have already been described by Dzungwe [12].

Parental population and their management

The parental stock consisted of ninety female birds from each of the three phenotypic expressions (normal feathered, frizzled feathered and naked neck) obtained locally from

Makurdi and its environs and kept for an adaptation period of four weeks during which they were given prophylactics against common endemic diseases. At the end of the adaptation period, the birds were distributed randomly into breeding pens with a mating ratio of 1:10 cock to hen respectively in a like by like arrangement. Eggs from the breeding populations were collected, identified along side lines and set in an electric type incubator.

Hatched chicks were reared to 20 weeks of age during which increase in body weight was evaluated 4-weekly. Twenty randomly selected pullets at 20 weeks of age from each genetic group were monitored on deep litter for part period egg number and egg weight to 280 days of age.

Data collected were used as discriminant variables in Mahalanobis squared distant estimation using the SAS (2008) statistical software [13,14]. Pair wise squared distances between the genetic groups were calculated as:

$D^2_{(i/j)}$: $(X_i-X_j).cov^{-1}$ (X_i-X_j) where:

D^2: Squared distance;

Cov: covariance

i: i^{th} genetic group;

j: j^{th} genetic group

X_i: mean of the X parameter of the i^{th} genotype

X_j: mean of the X parameter of the j^{th} genotype

Results and Discussion

Table 1 Squared Mahalanobis Distance (D^2) between the Genetic Groups of the Nigerian Local Chicken.

Genotype	NF	FF	Na
NF	0	0.635	6.64642
FF	0.6352	0	5.31598
Na	6.6464	5.316	0

NF-Normal feathered genotype; FF- Frizzle feathered genotype; Na- Naked neck genotype

Table 2 Multivariate Statistics and F Approximations for the Discriminant Analysis.

Statistic	Value	F Value	Den DF	Pr>F
Wilk's Lambda	0.12303	20.37	2976.9	<0.0001
Pillai's Trace	1.44701	14.41	4176	<0.0001
Hotenlling-Lawley trace	3.39415	27.23	1976.8	<0.0001
Roy's greatest root	2.24037	146.18	522	<0.0001

Table 1 presents the pair wise squared distance between the genetic groups. There was a greater divergence between the NF chickens and the Na than between the NF and FF genotypes.

Thus, the normal NF is more closely related to the FF than to the Na bird. The multivariate statistics are presented in **(Table 2)**.

All test statistic revealed a significant (P<0.05) difference between the genetic groups. The univarvate test statistics for the discriminating variables are shown in **(Table 3)**.

All the variables significantly (P<0.05) discriminated between the genetic groups except for age at 20 weeks.

Table 4 presents the Mahalanobis squared distance for the discriminating variables. The squared distance ranged from 0.0001 to 0.0148 in the genetic groups.

The Mahalanobis squared distance for the genotypes revealed that there is no significant difference in distance between the normal feathered genotype and the naked neck genotype.

The various crossbreds exhibited similar pattern with those having the normal feathered gene showing no significant difference with crosses carrying the frizzle gene.

Table 3 Univariate test statistic for the discriminating variables.

Variable	TSD	PSD	BSD	R-Square	R-Square(I-RSQ)	F Value	P>F
EW	4.2268	3.8635	1.8851	0.1771	0.2153	14.05	<0.0001
HT	3.077	2.846	1.2936	0.1574	0.1868	12.19	<0.0001
W4	6.1387	5.1966	3.5284	0.2942	0.4169	27.2	<0.0001
W8	21.5533	20.5736	7.3158	0.1026	0.1143	7.46	<0.0001
W12	83.6003	56.8659	63.3569	0.5443	1.1944	77.93	<0.0001
W16	81.9948	61.5795	57.9272	0.4445	0.8001	52.21	<0.0001
W20	412.057	412.4019	50.6294	0.0134	0.0136	0.89	0.5252

TSD = Total Standard Deviation; PSD = Pooled Standard Deviation; BSD = Between Standard Deviation; W4 = 4 Weeks Weight; W8 = 8 Weeks Weight; W12 = 12 Weeks Weight; EW = Egg Weight; W16 = 16Weeks Weight; HT = Hatch Weight; W20 = 20 Weeks Weight

Table 4 Test of Significance of Squared Mahalanobis Distance.

Genotype	NF	FF	Na
NF	1	0.0148	<0.0001
FF	0.0148	1	<0.0001
Na	<0.0001	<0.0001	1

NF-Normal feathered genotype; FF- Frizzle feathered genotype; Na- Naked neck genotype

Conclusion

Six of the seven discriminating variables used in this study significantly (P<0.05) discriminated between the genetic groups. Results of the genetic distance estimation show a greater divergence between the NF and Na, and NF and FF relative to that between the Na and FF genotypes. It could therefore be inferred that Na and FF populations were distinctly separated from the NF birds with little or no interflow of genetic materials between them. Therefore, the fixation alternate for genes were more pronounced in the Na and FF populations when compared to of the NF genotypes. Fixation for alternate alleles in breeding populations is advantageous as this can promote heterosis when the populations are inter mated. Consequently, heterosis for the traits evaluated is expected to be higher for crosses between the NF and Na, and the NF and FF than between the Na and FF genotypes. Comparatively, the reduced genetic distance between the Na and FF genotypes depicts a reduced diversity between these genetic groups.

This could be the result of a greater flow of genetic materials between the breeding populations. In conclusion, a plausible way forward for improving the productivity of the native chickens of Nigeria for the traits evaluated in the current study is to cross breed the Na and FF with the NF genotype. It is also the opinion of this researcher that the results in the current research could further be buttressed using molecular techniques. This will be the first step toward the conservation of the inherent genetic resources in these local chickens.

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