MORPHOLOGICAL AND GENETIC CHARACTERISATION OF DOMESTICATED GUINEA FOWL IN SOKOTO STATE, NIGERIA

BY

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ABSTRACT

Breed characterisation establishes genetic variability of organisms in a population which remains the basis for genetic improvement. Although, most poultry species have been largely characterised, little emphasis has been placed on domesticated Guinea fowl in Nigeria. Therefore, morphological and genetic characterisation of domesticated Guinea fowl was undertaken in Sokoto state, where there is a substantial population of the birds in Nigeria.

Guinea fowl varieties aged between 30 and 40 weeks: 425 pearl; 313 lavender; 271 black and 263 white were randomly selected from smallholders in Sokoto, Balle, Bodinga, Shagari, Goronyo, and Illela villages. Body Weight (BW), Head Thickness (HT), Helmet Length (HL), Helmet Width (HW), Wattle Length (WL), Wattle Width (WW), Keel Length (KL), Body Circumference (BC), Shank Length (SL), Shank Thickness (ST), Drumstick Length (DL), Thigh Length (TL) and Wing Length (WGL) were measured using standard procedures. Blood (5mL) samples were drawn by wing venipuncture from 50 randomly selected birds from each of the varieties for genetic studies. The blood samples were subjected to Cellulose Acetate Electrophoresis to determine genetic polymorphisms at haemoglobin, transferrin and Carbonic Anhydrase (CA) loci using standard procedures. Data were analysed using descriptive statistics, correlation, discriminant analysis, Principal Components Analysis (PCA), Euclidian distance, heterozygosity, Hardy-Weinberg's Equilibrium and ANOVA at $\alpha_{0.05}$.

The BW (kg) were 0.94±0.01, 0.93±0.01, 0.87±0.04 and 0.87±0.03 while HT (cm) were 0.32±0.00, 0.28±0.00, 0.27±0.01 and 26±0.01 for pearl, lavender, black and white varieties, respectively. The BW, HT, HL and WW differed between lavender and pearl varieties while KL was similar. However, WL and WGL differed among varieties. There was strong relationship between BW and TL (r=0.95), BW and BC (r=0.94), HL and WW (r=0.97), and BC and WL (r=0.96) for pearl, lavender, black and white Guinea fowl, respectively. The most discriminating of the birds' morphology was SL (0.9) followed by WGL (0.7), HW (0.6) and HT (0.5). Three PCA: PC1, PC2 and PC3 were extracted for lavender, PC1 and PC2 each for pearl and black and PC1 for white. The first factor explained 77.4, 61.2, 67.1, and 84.2 % of the generalised variance in pearl, lavender, black and white varieties respectively. The genetic distance between pearl and black (70.7) was highest and least between white and black (5.4) varieties. The allele frequencies

of haemoglobin A and B were 0.96 and 0.04 in pearl, 0.95 and 0.05 in lavender, 0.96 and 0.04 in black and 0.95 and 0.05 in white varieties. Two haemoglobin genotypes (AA and AB) were noticed in each of the four varieties. The transferrin (Tf^A) and CA (CA^F) were monotypic in all the varieties. The dendogram clustered all the varieties as two homogenous groups. The Chi-squared (χ^2) values showed departure from Hardy-Weinberg's Equilibrium in pearl (χ^2=62.0), lavender (χ^2=66.0), black (χ^2=39.0) and white (χ^2=39.0) varieties.

Morphologically, the pearl variety of Guinea fowl was superior to others. Biochemical parameters revealed high genetic similarities among the varieties. However, there is possibility of genetic improvement among the varieties through cross breeding.

Keywords: Guinea fowl, Bird morphology, Genetic distance, Breed characterisation

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'My Lord is so good; He is so good; My Lord is so good, He is so excellent' ----------

CERTIFICATION

I hereby certify that this work was carried out by Samuel Oladipo Kolawole Fajemilehin under mu supervision in the Department of Animal Science, University of Ibadan, Nigeria.

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DEDICATION

This project is dedicated to children who grew under the watch of ‘two eyes’

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CHAPTER ONE

1.0. Introduction

Agricultural animals, a renewable resource, have always made a major contribution to the welfare of human societies by providing food, shelter, fuel, fertilizer and other products and services. Of these, food is by far its most important contribution. Animals are a more important source of protein than they are of calories with meat, milk and fish, products from animals, supplying respectively 35 %, 34 % and 27 % of the world supply of total protein (Larry *et al*. 2005).

The Stewardship Community (2002) reported that, the diversity of farm animal breeds increases the farmers' ability to respond to changing environmental conditions, changes in production resources and market requirements, increase need for natural resistance to diseases and parasites and serve as information resource for the potential of protein variants in any animal species. Livestock keepers therefore need a broad gene pool to draw from if they are to improve the characteristics of their animals under changing conditions.

Thorough information is required for countries to make informed decisions about the future management of their animal genetic resources. It is apparent, that local breeds are being underused or ignored in favour of exotic breeds that appear to hold out the promise of increased productivity. Short-term economic growth has taken precedence over sustainable management of genetic resources for the future. Some countries like Ghana have already developed national action plans while others have increased their budgets for managing genetic resources. Better still, there must be a coherent and coordinated effort to stop the erosion of animal genetic resources for meeting future needs for food, fibre, fertilizer, draught power and to ensure that farmers have the flexibility to respond to changing production environments.

One of the important animal genetic resources in Nigeria is guinea fowls. Guinea fowls are wild animals which live in arid rural areas in many African countries and have been occurring in very considerable numbers in recent years with improving organic agriculture (Yildirim, 2012). Production of Guinea fowl has increased tremendously throughout the entire world because it can be successfully reared under semi-intensive conditions with less effort in the farms or

around villages. The bird is matured; reproductively efficient and resistant to diseases under different ambient temperatures (Boko, 2004). The bird, according to Embury (2001) and Champagne (2003) is widely bred in some European countries such as Belgium, Italy and France where strains producing up to 190 eggs per year (Muğlalı, 2001) have been bred.

Guinea fowl production is ubiquitous in northern Nigeria as backyard production unit where they are adapted to low input – low output production system like the H'mong chicken of northern Vietnam (Vo Van Su *et al.,* 2001). They produce meat and eggs and the meat are known to be tastier compared to that from other birds. However, evidence from literature shows that scientific interest in guinea fowl as an animal genetic resource date back to early 80's in Kanji Lake Research Institute, New Bussa, Niger State. It attracted a great deal of interest particularly in area of nutrition and performance characteristics but has since been jettisoned. It is worrisome to observe that this hardy bird has been relatively neglected even by African Network for Rural Poultry Development (ANRDP) because in almost all their newsletters, publications and books perused, it was all silence on the bird unlike chicken and pigeon.

For this animal to be relevant in large scale production, its performance characteristics should be improved. Improvement programmes depend on access to genetic variations and effective methods of exploiting these variations. These variations can be assessed at three levels: morphological, protein and nucleotide levels which are important means for detecting genetic relationships among breeds in different domestic species (Salako and Ngere 2002; Zaitoun *et al*., 2005 and Luc *et a*l., 2007).

Colour variation of indigenous guinea fowl is manifested in four feather colour variants, the pearl, lavender, black and white feathered groups (Ayorinde, 1987). It is however not clear whether the four colour variants are true representation of genetically distinct subpopulations within the guinea fowl community. It is therefore critical to characterize its genetic diversity as a prelude to its genetic improvement.

Biochemical polymorphism is a classical assay used in the study of population variability. Gel electrophoresis of protein coupled with histochemical visualization of locus-specific

allozyme offer a relatively cheap and fast method of analyzing single locus variability (May, 1998). Since the development of enzyme electrophoresis (Hunter and Markert, 1957), numerous animal populations have been investigated for genetic variation by using a range of protein loci (Nevo *et al.*, 1984). Analysis of genetic markers based on protein variants detected by electrophoretic method has been a tool for studying genetic differentiation among populations or phylogenic studies. It had become equally important in biosystematic and evolutionary studies. The phylogenetic relationships among indigenous Guinea fowl distributed in North West, Nigeria have not been surveyed using blood – protein polymorphic gene frequencies as no evidence was seen in literature search.

Both morphological and biochemical characteristics within a species, which are used in genetic appraisal of several species populations including poultry, are of great biological interest, both as observable facts (phenomena) and as descriptive and analytical tools. This approach to agriculture will ensure long-term productivity of animal resources to meeting food and fiber needs, so as to reduce importation and thus preserve foreign exchange. It is therefore the object of this study to fill these gaps.

1.1. Justification

1. In Nigeria, like other developing nations of the world, farmers tend to have a low appreciation of their own native breeds on the general assumption that exotic breeds are better. Consequently, in recent years in the poultry industry, only limited kinds of breeds, driven by economic demands are reared on a large scale. More worrisome is the introduction of exotic breeds into the rural communities which, as a result of interbreeding, could lead to the erosion of the genetic resource of the indigenous birds. It is therefore pertinent to conserve the local breeds as a genetic resource to fill unanticipated breeding demands in the future. The first step in accomplishing this is the objective description of body size and skeletal proportions of the indigenous stock. In general, the higher the maintained genetic diversity, the higher the adaptability and consequently the survival probability of species in a changing world which means that information on genetic variability of the species to be conserved is essential.

2. A proper knowledge of the genetic make-up and variability of any animal species will help in the management of such species.

3. The non diversification and over dependence on domestic fowl is certainly contributing to the scarce and costly animal protein supply in the country as other avian species like the guinea fowl constitute a huge potential. Thus, establishing the genetic variations between and within these promising species is important in strategic breeding improvement programme. Genetic markers based on morphological and biochemical polymorphism are valuable raw materials for mating system and selection to enhance improvement. Establishing the gene and genotype frequencies of protein molecules will contribute to the understanding of the level of relationship between the breeds, the justification of defining certain breeds and the endangerment of some genes due to sampling.

4. Such genetic resource information will enrich the databank of poultry birds and could be useful in generating future development initiatives.

5. The production of guinea fowl is gaining ground throughout the world, especially in developing nations with increasing demand for its meat because of the advantage of the gramy flavour *(*Mareko *et al., 2006)*. As a result of the increasing interest in the farming of guinea fowl and the gradual domestication of the bird, it is required to characterize the birds to bring about improvement in its performance and in supply of meat and egg.

6. The state of knowledge in the use of allozyme is still in its infancy in Nigeria as no literature was sighted in this field on guinea fowl.

1.2. Main Objective

The main objective of this study was is to characterize indigenous Guinea fowl in Sokoto State, Nigeria using morphological and geneticl markers.

1.3. Specific objectives

The specific objectives were to:

a. carry out morphometric measurements on adult birds of each of the available four varieties of Nigerian domesticated Guinea fowl, *Numidea meleagris galeata* pallas.

b. determine the relationship between their body weights and linear body measurements.

c. document quantitative variation and differentiation of the guinea fowl through the use of multivariate techniques.

d. calculate some body ratios and morphological indices for the varieties of Guinea fowl.

e. determine genetic variability, genetic distance and genetic differentiation at haemoglobin, transferrin, and carbonic anhydrase loci of the guinea fowl varieties.

CHAPTER TWO

2.0. Literature Review

2.1. Origin and domestication of Guinea fowl

Guinea fowl (*Numidia meleagris*), originated from Africa, where it exists in large number in the wild (Gracey *et al*., 1999; Saina, 2005). Ayorinde (2004) reported that Guinea fowl is believed to have evolved from a francolin-like Asiatic ancestor but the evolution, radiation and development to modern forms occurred solely in Africa. Embury (2001) believed that the domestic guinea fowl was derived from the helmeted guinea fowl of Africa.

Delacour, (1977) in his own submission stressed that, of the five world galliformes, it is only the Guinea fowl, *Numidinae*, which is endemic to Africa. Crowe (1978b) asserted that helmeted Guinea fowl is a sub-Saharan species occurring between Senegal in the west, Ethiopia in the east and extending southwards to South Africa. Church and Taylor (1992) posited that the birds are widespread and common at the continental scale, but a significant decline in parts of the range had occurred, probably due to habitat destruction, as well as hunting for their meat. Świreczewska *et al* (1999) wrote that domestication of Guinea fowl took place about 3000 years ago in Mediterranean countries, where ancient Greeks and Romans appreciated the taste of its meat; that the domesticated Guinea fowl is descended from wild guinea fowl (*Numidea meleagris*) that still inhabits the steppe regions of South Africa and Madagascar.

Sequel to all the literature above and evidentially from the name 'Guinea' in the taxonomy of the bird and 'Guinea' being a country on the sub-Saharan west coast of Africa, it will not be perfunctory to conclude that the bird originated from Africa.

2.2. Classification of Guinea fowl

Howard and Moore (1984) classified guinea fowls in the family *Phasianidae* and subfamily *Numidinae* but Belshaw (1985) placed them in the order *Galliformes*, family *Numididae.* There are four genera within this family: *Agelastes, Guttera, Numida and Acryllium* and six species within the genera: black, white-breasted, helmeted, plumed, crested and vulturine guinea fowls (Urban *et al*. 1986). Crowe (2000) used a simple classification of *Numidea*

meleagris involving nine well-marked subspecies which fall into three groupings: West African *Numidea meleagris galeata* and *Sabyi*, East African *Numidea meleagris meleagris* and *somaliensis*, and Central-South African *Numidea meleagris reichenowi*, *mitrata*, *marungensis*, *papillosa* and *coronate*. Ayorinde (1989) and Kozaczyński (1999) classified domesticated Guinea fowl of Nigeria into grey (pearl), white, black, lavender (light blue), and ash (pearling).

2.3. Morphology of Guinea fowl

It is a medium sized bird with strong legs and a bony crest (Sibley and Monroe, 1990). The trunk is oval shaped and oblique relative to the ground. Rectrices are carried low and almost fall to the ground (hump-backed posture). The head of an adult bird which is about 9 cm long is devoid of feathers**.** The bird has light blue skin and brown helmet on their heads: straight in females, larger and sloping in males. While in some birds certain shapes, colours and sizes of feathers vary with sex as a result of gonadal hormones, there is no striking plumage dimorphism in the guinea fowl (Ayorinde, 2004). The wattle is small and red. Legs are short, dark brown/green, without spurs. The lower leg (tibia) is about 12 cm in length and the shank is about 8 cm long. Mean body length is 55–61 cm; with wing span of 74–76 cm (Ayorinde, 2004). Guinea fowl has thick and dense plumage of various colours. Rounded wings make the bird poorly equipped for long flights. The helmeted Guinea fowl occasionally flies up into trees if chased by a predator. Helmeted Guinea fowl has conspicuous horny "helmet" on top of their naked heads which distinguishes it from others. The helmet is slightly larger in males than females but otherwise they exhibit almost no sexual dimorphism (Crowe, 1978a).

2.4. Habitat of Guinea fowl

Audran and Gain (2005) reported that guinea fowl are adapted to different environmental conditions and are therefore farmed all over the world. France is the world leading producer and consumer of guinea fowl meat in Europe, with Italy ranking second (Audran and Gain, 2005). Helmeted Guinea fowls breed in warm, fairly dry and open habitats with scattered shrubs and trees such as grasslands, savannah, bush land, woodland and farmland. Generally, they occur in moist areas, but usually absent from the rain forest and desert habitats (Grafton 1970).

The birds are affected primarily by the loss of feeding and nesting habitats. The habitats of helmeted Guinea fowls are degraded through intensive livestock grazing, settlement or agricultural expansion, or modified through human activities such as selective removal of vegetation for firewood and fence. They have numerous predators such as dogs, raptors, monkeys and other mammals which take the eggs and the chicks, and sometimes kill the adults and they suffer locally from hunting pressure. According to Lack (1968), terrestrial animals seek their habitats rather than dispersing randomly and birds are no exception. Brown *et al.* (2001) reported that animal species show a tendency to be confined to the habitat where they get their feeding and nesting sites.

2.5. Characterization of Guinea fowl

Guinea fowls are terrestrial, and fly when alarmed. It is, however, like most short and broad-winged birds, very agile and a powerful flyer, capable of hovering and even flying backwards when necessary. The helmeted Guinea fowls can run 10 km or more in a day (Crowe 1978a). They are omnivorous birds consuming a variety of animal and plant food: seeds, fruits, berries, green matters (bulbs and plant stems), snails, spiders, worms and insects (grasshoppers, termites, etc.), frogs, lizards, small snakes and even small mammals (Mentis *et al*. 1975). The helmeted Guinea fowl is equipped with strong claws and scratches the soil for food much like the domestic chicken (Farkas 1965). Farkas (1965) research on specimens from the Luangwa Valley also showed that this helmeted Guinea fowl does not damage crops. In fact, its primary diet consists of insects that feed on the crops and weeds surrounding crops. However after the harvest, it can consume waste maize or other crop seeds that are scattered on the soil surface (Ayeni, 1983).

Animals are broadly characterized at morphology, blood protein and molecular levels. Morphological characterization involves measurement of phenotypic characters. Phenotypic characters are those characters/traits that can be viewed and measured externally in animal species which includes visual appraisal and measurements of body dimensions. Genetic characterization is the embodiment of all available knowledge both published and unpublished which contributes to reliable prediction of genetic performance of an animal species in a defined environment.

2.6. Factors influencing body characteristics of Guinea fowl

Research to date have shown that body weight, dressing percentage, carcass composition and meat quality are mainly influenced by genotype (Ayorinde *et al.*, 1988 and Leterrier *et al.*, 1999) and age (Ayorinde *et al*., 1988; Mareko *et al.*, 2008; Porwal *et al.*, 2002; Pudyszak *et al.*, 2005 and Touraille *et al.*, 1981). In addition, the above traits are affected by diet composition (Ayorinde, 1989; Chiericato *et al*,. 2001; Frątczak *et al.*, 2002; Mazanowski *et al.*, 1982a and Mazanowski *et al.*, 1982b), housing system (Ayorinde and Ayeni, 1986; Mareko *et al.*, 2006 and Mareko *et al.*, 2008) husbandry system (Baéza *et al.*, 2001; Saina, 2005), environmental conditions (De Houx *et. Al.*, 1997 and Mareko *et al.*, 2006) and sex (Baéza *et al.*, 2001; Mareko *et al.*, 2006 and Mazanowski *et al.*, 1982a, 1982b).

Breeders generally produce well for 2 to 3 years (Ayorinde *et al*., 1989) while hens can lay up to 175-200 eggs per year. The hens after a 35-week-laying period can weigh up to 1.5-1.7kg of live weight and a ratio of 2.7-2.9 feed conversion within 11-12 weeks under intensive breeding and selection works (Le Coz-Douin, 1992). In France, strains are now developed than can produce 190 eggs per year (Muğlah, 2001).

2.7. Phenotypic characters

Phenotypic traits are the external features of living organisms which could be metric or non metric. Non metric traits are measured subjectively i.e. by visual appraisal while metric traits involve objective measurements of height, length and width. Phenotypic expression is the result of the genotype, environment and interactions between genotype and environment. Meghen *et al* (1994) reported that animals are often characterized based on their phenotypic characters which include coat colour, horns (shape and size), hair, live weight and body measurements. They stated that the priority elements in breed characterization include:

- General identification: Country, species, breed and location within country where breed is found.
- Population size during the reporting year, average herd size, average age of animals used for breeding by sex
- Physical characteristics including coat colour, horns, hair and other visible traits.

- Measures of adult size and weight including body measurements
- Current uses.
- Quantitative description of predominant system (nomadic, transhumance housing etc)
- Production traits

A careful search into body dimensions of farm animals in the tropics is vital and of great economic importance because majority of farmers in the sector are illiterates. They lack weighing scales and other equipment available for such exercise and even when the scales and other equipment are available the culture to manipulate them are not there (Gerald, 1994; Sharples and Dumelow, 1988). They therefore rely on visual appraisals of the variables particularly at the points of medication, feeding, sales and breeding

Phenotypic characterization is useful in obtaining a better understanding of the composition and developmental patterns of the breed and such understanding can aid in guiding a breeding programme. Phenotypic characteristics are often used to divide animals into species and it exhibits great diversity across species. However there may be limited genetic variation within any given species. Domestication of animals has led to the development of specific breeds, in the process increasing the within species variation. Animals are kept in environment ranging from temperate to tropical and for different purposes, resulting in selection for different characteristics in different locations and for different purposes.

2.8. Body weight

Body weight is a function of size of the animal and its condition. It is an important attribute of farm animals for making management, health, production and marketing decisions (Nwosu *et al*., 1985a). Smallholder farmers in the developing world are characterized by poor resource investment, therefore management decisions at this level is based on trial and error or on visual appraisal (Msanga, 1997). Consequently, impact of research findings have been lessened due to impracticability of relating visual appearance of the animal with their estimated live weights (Msanga, 1997). Given the right guidelines, farmers could visually relate body measurement of their animals with live weights by the use of simple techniques and facilities (Kyomo, 1978; Hassan and Ciroma, 1990).

Variation in body weight within a flock had been attributed to genetic variation and environmental factors that impinge on individuals (Ayorinde and Oke, 1995). Effects of age on body weight and body dimensions of Guinea fowl had been widely studied and documented (Sergejev *et al*. 1988; Salez and Du Preez, 1997; Saina, 2005; Nahashon *et al*. 2006; Nsoso *et a*l. 2006 and 2008 and Fajemilehin, 2010). Daria *et al*. (2011) reported sexual dimorphism on account of body weight of 13- week -old males and females pearl grey guinea fowl which accounted for 76% and 72.5% of the body weight of adult birds. Sergejev *et al.* (1988) and Nahashon *et al.* (2006) recorded 1289 g and 1352 g as adult body weights of female and male Guinea fowl respectively; Salez and Du Preez (1997) obtained body weights of 2208 g in males and 2300 g in females at adult age and much higher body weights were obtained by birds improved for meat traits (Leterrier *et al*. 1999 and Baéza 2001b).

2.9. Body linear measurements

Linear measurements could be divided into two groups: skeletal and muscular measurements. Skeletal measurements include all the height and length measurements while muscular measurements include measurements of width and depth. It is important to know that while height reflects skeletal size, width and body circumference tends to reflect animals' condition (Orheruata and Olutogun, 1994)..

In Skeletal development, there is a faster bone growth in length than in width and circumference (Brown *et al.*, 1956). Skeletal developments had been reported to be breed dependent as British breeds generally have longer body length than Nigerian breeds (Hall, 1991). Brown *et al.* (1984) in a study of skeletal growth pattern in Angus heifers showed that body parts in this breed matured in the following order: Hip height, shoulder width, hip width, width height, heart girth, chest depth, body length and loin width. Orheruata and Olutogun (1994) observed that body length, height at withers and shoulder to tail drop were about 40-50 percent matured in N'Dama cattle at birth. They put forward the following order of maturity among five body dimensions: Head to shoulder, Height at withers, Heart girth, shoulder to tail drop and Body Length in both sexes of N'Dama cattle. Green and Carmen (1976) positioned that in beef cattle, height at hips was the earliest to attain maturity followed by height at withers, width at shoulder, heart girth, depth of chest, depth of rear flank, body

length, width of hips and weight. They reported that skeletal development within a population became relatively more uniform with age. Monitoring these changes objectively with body dimensions and fat measurements can aid in guiding a breeding programme (Berg and Butterfield, 1976).

Daria *et al.* (2011) found that the body length of male and female guinea fowls at age 52 weeks were 35 cm and 34.7 cm respectively; Kozaczyński (1999) reported that adult guinea fowl had a body length of 58 cm. Daria *et al.* (2011) compared the chest circumference and sternum in female and male Guinea fowls and concluded that male had larger chest circumference and longer sternum at 52 weeks of age. They also found that lower leg length in males at 52 weeks was 12.0 cm and 12.7 cm in females; that male and female had similar shank length at 52 weeks of age (7.0 and 7.1 cm, respectively). Kozaczyński (1999) reported that tibia (lower leg) length is 12 cm and shank length is 8 cm in adult Guinea fowl.

Linear measurement can be used in assessing growth rate, weight, feed utilization and carcass characteristics of farm animals (Alderson 1999). Linear measurements have been used in determining the finishing process, carcass characteristics, production traits, genetic parameter estimates, type and conformation and pattern of development in cattle (Sharples and Dumelow, 1988). Linear body measurement is necessary in the formulation of programmes for selection and improvement of livestock and in predicting the direct and correlated responses due to selection (Alade *et al.*, 1999). Body measurements, because of their correlation with live weight, gives the livestock traders and buyers a fair idea of the value of their livestock in the absence of scales which is the case in most livestock markets in Nigeria.

2.10. Sources of error in taking body measurement in livestock

Errors involved in taking measurements is based on differences observable between repeated measurements on the same animal or on the differences observable between repeated measurements on different animal or on the differences observable between different operators taking the same measurement (Fisher, 1975). Fisher (1975) stated that there are three major sources of error in taking any one linear measurement. They are as follows:

a. Correct identification and location of the end reference points: In many ways circumferences are special measurements in that only one point is involved- the point at which measurements begins and terminates, but this may be anywhere in the correct plane of measurement and may vary from operator to operator, it may also vary between repeated readings

b. Anatomical distortions produced by changes in the animal's posture or muscular tone which actually alters the distance between the end points. The anatomical distortions may be dependent on the number of skeletal articulations between the two end points and the degree of movement at each joint

c. Error in the measurement of located distance which is minimal for callipers' measurement. It involves a constancy of tension in the measuring tape, used over convex surfaces like circumferences. This source because of the difficulty in ensuring that the tape follows the surface contours

2.11. Relationships among or between body weights and other body measurements

Correlation coefficient is a descriptive statistic which only indicates how closely associated two variables are (Wahua, 1999). Correlation analysis result is a single value, a dimensionless quantity that ranges from +1, through 0 to -1 (Brown *et al*., 1973; Wahua, 1999). When an increase or decrease in one trait brings about a corresponding increase or decrease in another trait, the two traits are said to be positively correlated. However when an increase in one trait brings about a decrease in another, they are said to be negatively correlated. The relationship between traits may be genetic, environmental or phenotypic. The relationship between traits calculated from observed or measurable values, is called phenotypic correlations. Age has a high and positive relationship with other body dimensions such that measurements taken at young age had higher and positive correlations than those taken at adult age (Orheruata and Olutogun, 1994).

Use of principal component analysis to examine the relationship between measurements of size and shape in poultry had been reported in chicken (Ibe, 1989; Yakubu *et al*., 2009) and duck (Shahin, 1996; Mc Cracken *et al*., 2000; Ogah *et al*., 2009). This multivariate procedure describes the total variation in a large system of body measurements in terms of a few of the

body measurements. The relationship that exist among linear body traits provides useful information on the performance, productivity and carcass characteristics of animals. Most of the linear measurements reflect primarily the length of the long bones of the animal and when taken sequentially over a period of time, they generally indicate the way in which the animal body is changing shape and have been used as predictors of live weight and carcass composition (Oke *et al.*, 2004).

Relationships between body weight and linear body measurements are important in genetic improvement strategies. In an organized livestock marketing system, weight ought to be taken to determine the market prices of animals. This requires the use of weighing scales which, quite often may not be available to the rural livestock and poultry farmers/traders. There are other indirect methods of assessing body weights in animals without recourse to the use of weighting scales. A lot of works have been done in this regard in larger animals, particularly cattle, sheep and goats (Nwosu *et al*., 1985a; Attah *et al.*, 2004; Sowande and Sobola, 2007 and Goe, 2007). In poultry, Oke *et al.* (2004) related body weight with some egg production traits in the guinea fowl while Teguia *et al.* (2008) reported significant associations between body weight and some body characteristics in the African muscovy ducks.

In vivo prediction of live weight based on single trait is usually discouraged because it is considered as not reliable. Raji *et al*. (2009) and Wawro (1990) proposed that more accurate results can be obtained when several parameters are used as independent variables in predicting weight performance in birds.

Body measurements can be useful in breeding work particularly in weight and carcass improvement (Wawro and Wawro, 1989; Wawro 1990; Wawro and Jankowski 1990). Most models were developed by multiple linear regression procedure where collinearity among the independent variables was not evaluated. However collinearity problem among independent variables should be expected as these are both genetically and phenotypically correlated (Simm and Dingwall, 1989) and it is known that model based on multicollinearity variable can limit inference and the accuracy of prediction (Chatterjee *et al.*, 2000). In fact the use of

collinear variables as independent variables does not improve the model precision, and create instability in the regression coefficient estimation (Shahin and Hassan, 2000).

2.12. Zoometrical indices and Body ratio

Zoometrical indices are currently receiving increased attention in birds (Lorentsen and Rov, 1994; Strelec *et al.*, 2005; Zenatello and Kiss, 2005 and Robertson *et al*., 2008). All the somatometric measurements taken according to the standard procedures described by Lohman *et al. (*1988) and Hall *et al.* (2003) can be used to estimate stature from different segments in human populations. Several major studies have assessed variation in cranial shape among and between populations (Lahr, 1996). In using, strictly skull based categorization method, anthropologists organized three facial groups: dolicocephalic, mesocephalic and brachycephalic (Umar *et al.* (2006). It had been reported in human that genotypic variation in human cranial shape is far greater within than between populations (Relenford, 1994). In parallelism with man according to Corey and Jantz (2002), cephalic indices could indicate an animal species to be dolichocephalic (long headed), mesaticephalic or mesocephalic or mesocranial (medium headed) or brachycephalic (short headed) if the ratio of the width and length are respectively less than 75%, between 75% and 83% and greater than 83%. It had been argued that cranial morphology provided a better means to model racial ancestry (Killgrove, 2005) and that local environmental conditions had a significant impact on the development of head shape (Ralph, 2002)

Corey and Jantz (2002) concluded that there was a "relatively high genetic component" of head shape. Ralph (2002) posited that the variations in skull shape have adaptive meaning and that normalizing selection might be at work on the trait, where extremes, hyperdolichocephaly and hyperbrachycephaly, are at a slight selective disadvantage.

Cephalic index or cranial index is the ratio of the maximum width of the head of an organism multiplied by 100 divided by its maximum length (i.e., in the horizontal plane, or front to back). The index was widely used by anthropologists in the early twentieth century to categorize human populations. Anthropology is the academic study of humanity. It deals with all that is characteristic of the human experience, from physiology and the evolutionary origins to the social and cultural organization of human societies as well as individual and

collective forms of human experience. It has origin in the humanities, the social sciences and the natural sciences. Today it is mainly used to describe individuals' appearances and for estimating the age of fetuses for legal and obstetrical reasons and to categorize animals, especially dogs and cats.

Zoometric indexes are relationships among body measurements that are used to describe the proportions and general size of the parts of animals. In the case of ethnological index, which are related to the origins and characterization of a breed (Cerqueira et al., 2011), a body index that is to determine an animal's proportions (Cerqueira et al., 2011) could be similar in male and in female birds.

2.13. Blood

According to Schalm (1975) blood can be defined severally as specialized connective tissue within the vascular system of animals, which transport oxygen, heat, nutrients, waste products of metabolism, hormones, enzymes and immune bodies within the body. Blood is the fluid medium with suspended cellular constituents, the latter being the product of the haematopoetic tissues, which is circulated round the body by the heart while being retained in the arteries and veins. Also blood can be defined as living tissue that consists of the plasma, red and white corpuscles and the platelets.

The blood is made up of the fluid (plasma) and the cellular portions (erythrocytes, leukocytes and the platelets). The fluid portion of blood is made up of serum and fibrinogen. Remain of blood after clotting is the serum. The plasma is made up of proteins, carbohydrates, lipids, non-protein nitrogenous materials like amino acids, waste products like urea and inorganic salts of sodium, potassium, calcium, magnesium etc. The cellular portion is made up of the erythrocytes, leukocytes and platelets. Haematology is the study of red and white blood cells and platelets. The analyses of these blood components reveal the health status of the animal.

The total volume of circulating blood is a function of the lean body weight. Blood function in the following ways according to Schalm (1975): absorption and transport of nutrients from the tract to the tissues; transport of gases to and from tissues; removal of metabolic wastes; regulation of body temperature; defence against infection; maintenance of constant

concentration of water and electrolytes in the cells; regulation of the body's H^+ concentration; defence against microbial invasion; hormonal transport and osmo-regulation.

Schalm (1975) asserted that the above functions were made possible by the individual and/or collective actions of the constituents. The erythrocytes are formed in the bone marrow and made up of 60 -70 % water, 28 – 35 % haemoglobin and a combination of organic and inorganic components. It is the carrier of haemoglobin (respiratory pigment) which in turn functions as carrier for oxygen and carbon dioxide.

Plasma forms about 66% of the total amount of the blood and consists of three proteins namely: fibrinogen, serum-globulin and serum –albumin (Schalm, 1975). While the blood is circulating the fluid protein is true plasma, but upon coagulation, it separates into two parts which is called serum and a solid, which is the fibrin clot. The fibrin clot contains two newly formed proteins fibrin- globulin and nucleo-protein.

Schalm (1975) identified the functions of plasma protein to include: transportation of blood cells and other particles like salts sugar and fats from the food animals eat and a store house of important dissolved protein. He stressed the functions of the 3 groups of plasma proteins as follows:

a. Globulins – This includes anti bodies (defensive) that attack invader.
b. Albumins – bind to toxic substances in the blood
c. Fibrinogen – essential for blood clotting.

Plasma protein had been reported to increase with advancing age and the most abundant protein. It is important in the regulation and maintenance of colloidal osmotic pressure of the blood. It has a large number of reactive groups causing it to bind reversibly with a large number of anions and cations. Hence albumen has an important transport function. It transports free fatty acids, the bile acids, bilirubin, the porphyrines keto steroids, many drugs such as penicillin, aspirin and barbiturates and cations such as Cu, Ca and Zn.

2.14. Genetic diversity of animal species

A Breed is a subgroup of a species. A breed is a specific variety of a particular domesticated animal species. It can also be defined as animals that through selection and breeding have come to resemble one another and pass those traits of resemblance uniformly to their offspring. All breeds within a species share common characteristics. However, each breed has certain unique traits. Breeds are created by natural and human selection. Each breed of a species has slightly different genetic traits, consequently, different breeds are better suited for different environmental conditions – certain breeds are adapted to withstand extreme cold, some extreme heat, some resistant to certain diseases while others are adapted to survive periods of drought. A **species** is a scientific classification used to group together plants and animals that have similar characteristics.

Species diversity/biodiversity refers to the number and distribution of species in one location that is, the measure of the number of different species within a given area. Humans have enormous effect on species diversity because they are involved in destruction, modification and/or fragmentation of habitat, introduction of exotic species, over harvest and global climate change. Genetic diversity is a level of biodiversity that refers to the total number of genetic characteristics in the genetic makeup of a species. The study of genetic variation in any animal species has proven to be valuable in the species management, for identification of stocks, selective breeding programmes, restoration of ecology and estimating contributions to stock mixtures. Generally, individuals with greater genetic variability have higher growth rates, developmental stability, viability, fecundity and resistance to environmental stress and diseases. The assessment of genetic diversity is required for the development of long-term disease management strategies.

2.15. Conservation of genetic diversity

Many local breeds represent a source of genes for improving health and performance traits for main stream breeds, and are well adapted to a specific environment (Ruan, 2002). They also utilize low quality feed and are effective from the view point of land cultivation (Zavodska and Urban, 2001). In most cases, a lack of economic profitability of local breeds is the main factor of rapid erosion of farm animals' diversity (Gandini and Oldenbroak, 2002). The use of few globally spread, highly productive breed dominates. Disappearance or

rapid modification of local breeds by crossbreeding and absorption or replacement of exotic breed would have a dramatic impact on the environment and human population.

Recognising the important roles farm animals play in food security, preservation of farm animal diversity has been a FAO initiative since 1990 when FAO's council recommended the preparation of a comprehensive programme for the sustainable use of farm animals at the global level (FAO, 2000).

Other reasons for conservation of genetic diversity include the following:

1. To take advantage of heterosis (hybrid vigour) - Heterosis is the increase above the average of the parent stocks obtained by crossing genetically diverse breeds. If only a few breeds are kept the opportunity to develop good crosses is lost

2. To overcome selection plateau- A selection plateau occurs when genetic variation is lost; no further change is possible because animals are genetically alike. If genetic variation exists in other breeds, crosses can be made to overcome this.

3. Provision of insurance policy - Insurance policy against climate change, spread of disease, changing availability of feeding stuffs, social change, such as issues of animal welfare and environmental sustainability and selection errors- a widely used sire may spread a genetic disease throughout a population before the problem is identified

4. For cultural reasons - Our history is closely linked to agricultural practices and the use of particular breeds.

5. For research - Unselected (control) lines are used to measure genetic progress in selection. Identification of specific genes, which regulate traits such as product quality and health, is made easier by comparing very different groups. Economic evaluation of breeding programmes now includes sociological aspects, as part of a focus on sustainable rural development. Research into the role of minor breeds in such production systems is needed.

6. Goals of conservation- To keep genetic variation as gene combination, in a form that is easily recovered and to keep specific genes

2.16. Biochemical Genetic studies of blood in farm animals.

The genetic variation of blood components is known more than any other animal tissue (Zaragora *et al*. 1987). Most blood protein polymorphisms are genetically controlled by allelic series which have dominance or co-dominance effect. Livestock breeds and populations are characterized using genetically controlled biochemical polymorphisms of blood proteins. Such studies contribute to the knowledge of genetic similarity and the distance between then (Zaragora *et al*. 1987).

Elctrophoretically detectable blood proteins have been widely studied and renewed in many livestock species (Agar, *et al*; 1972 and Manwell and Baker, 1980). Some of the blood proteins for which genetic and differences have been established have been shown to have fundamental physiological functions (Tunon, *et al*. 1989). The most important application of genetic polymorphism is in genetic improvement through loci affecting quantitative traits (Manwell and Baker, 1980).

2.17. Polymorphisms

A polymorphism is a genetic variant that appears in at least 1% of a population. By setting the cut off at 1%, it excludes spontaneous mutations that may have occurred in and spread through the descendants of a single family. Enzymes are frequently polymorphic. A population may contain two or more variants of an enzyme encoded by a single locus. The variants differ slightly in their amino acid sequence and often this causes them to migrate differently under electrophoresis. By treating the gel with the substrate for the enzyme, its presence can be visualized. Alleles can be distinguished by the speed with which their protein product migrates. Electrophoretic variants of an enzyme occurring in a population are called allozymes.

2.18. Allozyme

Allozyme electrophoresis denotes the technique for identifying genetic variation at the level of enzyme, which is directly encoded by DNA. The allelic variants give rise to protein variants called allozyme that differ slightly in electric charges. Allozymes are co-dominant Mendelian characters which are passed from parents to offspring in a predictable manner (May, 2003). Hunter and Markert (1957) described Isozymes and allozymes as different variants of the same enzyme having identical functions and present in the same individual. Isozymes are the multiple forms in which an enzyme may exist in an organism, the various forms differing chemically, physically, or immunologically, but catalyzing the same reaction and coded for by genes located at different loci. Allozymes are enzymes that differs in amino acid sequence, as shown by electrophoretic mobility or some other property, from other forms of the same enzyme and are coded for by different alleles at a single locus. Allozymes are products of alternative alleles at a locus encoding for a specific enzyme. Because allozymes are functional proteins, they can be subjected to selection (EOBRT, 2007).

Hamrick and Godt (1990) reported that allozymes may result from point mutations or from insertion-deletion events that affect the DNA coding sequence of the gene. He stressed that three things may happen in a new mutation:

a. The new allele may be non-functional in which case it will probably result in low fitness and be removed from the population by natural selection
b. If the amino acid residue that is changed is in a long way from the active site of the enzyme i.e. in a relatively unimportant part of the enzyme, the mutation may be selectively neutral and subject to genetic drift.
c. In rare cases, the mutation may result in an enzyme that is more efficient, or one that can catalyze a slightly different chemical reaction, in which case the mutation may cause an increase in fitness and be favoured by natural selection.

Population genetics is succinctly a study of the causes and effects of genetic variation within and between populations. In common use as molecular markers are isozymes and allozymes (Maria, 2005). Being co-dominant marker (May, 2003), allozymes are useful for assessing genetic variability and genetic identification of species (Dobrovolov *et al.*, 2012; Sujatha *et al.*, 2011). Stock identification of several species has been carried out using allozyme

technique (Shaklee *et al*., 1990; Ferguson *et al*., 1995). Allozymes were also found to be helpful in generating species-specific profiles and resolving taxonomic ambiguities in several species (Rognon *et al*., 1998; Gopalkrishnan *et al*., 1997; Pouyaud *et al*., 2000). The simplicity, speed, relatively low cost, little specialized equipment requirement (Ward and Grewe, 1995) and general applicability of the technique makes it one of the commonly studied forms of molecular variation. Maria (2005) asserted that isozymes and allozymes remain an excellent choice for projects that only need to identify low levels of genetic variation.

Except isozymes and allozymes are alike in terms of their biochemical properties, they may be separated by a biochemical assay. However, such differences are usually slight between allozymes which are often neutral variants. This subtleness exists because two enzymes that differ significantly in their functions are unlikely to have been identified as same enzyme whilst isozymes may be almost identical in function, they may differ in other ways such as the amino acid substitutions that change the electric charge of the enzyme and this forms the basis for the use of isozymes as molecular markers.

To identify isozymes, a crude protein extract is made by grinding animal or plant tissue with an extraction buffer, and the components of extract are separated according to their charge by gel electrophoresis. Historically, this has usually been done using gels made from potato starch, however, acrylamide gels provide better resolution. All the proteins from the tissue are present in the gel, so that individual enzymes must be identified using an assay that links their function to a staining reaction.

Wendel and Wendel (1990) gave a theoretical background of allozyme study as detailed below: A mixture of soluble enzymes is loaded on a gel (made of starch or cellulose acetate). Electric current causes each protein to move through the gel at a speed determined by its size and charge. The proteins are not visible as they move through the gel. To visualize them, they took advantage of the fact that they are enzymes. The substrate is added to the gel and anywhere an enzyme is present that reacts with that particular substrate, product will form. The product is generally not visible either. However, a stain that binds specifically to that product is also added, and any place where the enzyme was present will appear as a colored

band on the gel. In an allozyme gel, the lanes represent genotypes of different individual organisms. Each different zone of activity contains a different isozyme. By convention, they are numbered according to their position on the gel. Within the "A" zone of activity, the different bands represent allozymes coded for by different alleles. By convention, the alleles that code for these allozymes are named according to the speed at which their enzymes move through the gel (i.e. fast or slow).

An enzyme is said to be monomeric if it consists of a single polypeptide unit, each different band position in the zone of activity results directly from a different polypeptide coded for by a different allele while a dimetric enzyme has a quaternary structure consisting of two polypeptide units. The different band positions in the zone of activity represent the different combinations of polypeptide units. If there are two different alleles in an individual, there will be three positions because there are three possible combinations of the polypeptide subunits coded for by the alleles.

2.19. DNA MARKERS

The role of polymerase chain reaction based molecular markers like Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSR), Intersimple Sequence Repeats (ISSR), Single Nucleotide Polymorphisms (SNPs), microsatellites and so forth in the study of variability of the isolates of pathogen has been established (Chen *et al*., 1995; Chen *et al*., 1999; Chakraborty *et al*., 1999; Guzman *et al*., 1999; Pryor and Gilbertson, 2000; Kolmer and Liu, 2000 and Malvic and Grau, 2001) and to analyze virulence diversity related to genetic polymorphism (Chen *et al*., 1995; Chen *et al*., 1999; Chakraborty *et al*., 1999; Kolmer and Liu, 2000)..

Proteins are gene products and so polymorphic versions are simply reflections of allelic differences in the gene; that is, allelic differences in DNA. Often these changes create new or abolish old sites for restriction enzymes to cut the DNA. Digestion with the enzyme then produces DNA fragments of a different length. These can be detected by electrophoresis.

Developments in DNA sequencing now make it easy to look for allelic versions of a gene by sequencing samples of the gene taken from different members of a population (or from a heterozygous individual). Alleles whose sequence reveals only a single changed nucleotide are called single nucleotide polymorphisms. Single nucleotide polymorphisms can occur in non-coding parts of the gene so they would not be seen in the protein product and might not alter the cutting site for any known restriction enzymes so they would not be seen by Restriction Fragmented Length Polymorphisms analysis.

2.20. Haemoglobin

Haemoglobin is the iron-containing oxygen-transport metalloprotein in the red blood cells of vertebrates (Maton *et al*., 1993). Hemoglobin in the blood transports oxygen from the lungs in mammals and gills in aquatic animals to the rest of the body tissues where it releases the oxygen for cell use in exchange for carbon dioxide produced in the cells. The capacity of haemoglobin to bind oxygen according to Dominguez (1981) is between 1.36 and 1.37 ml of oxygen per gram of haemoglobin thus increasing the total blood oxygen capacity several folds (Constanzo, 2007)

The oxygen-carrying protein hemoglobin was discovered in 1840 (Hünefeld, 1840). Funke (1851) published a series of articles in which he described growing hemoglobin crystals by successively diluting red blood cells with a solvent such as pure water, alcohol or ether, followed by slow evaporation of the solvent from the resulting protein solution. Hoppe-Seyler (1866) described hemoglobin's reversible oxygenation and the molecular structure of hemoglobin was determined by x-ray crystallization (Perutz, 1960 and Perutz *et al*., 1960).

Hemoglobin consists mostly of protein (the "globin" chains), and these proteins, in turn, are composed of sequences of amino acids. These sequences are linear, in the manner of letters in a written sentence or beads on a string. In all proteins, it is the variation in the type of amino acids in the protein sequence which determine the protein's chemical properties and function. This is true of hemoglobin, where the sequence of amino acids may affect crucial functions such as the protein's affinity for oxygen. The amino acid sequences of the globin proteins in hemoglobins usually differ between species, although the differences grow with the evolutionary distance between species. Even within a species, different variants of

hemoglobin always exist, although one sequence is usually a "most common" one in each species. Mutation in the genes for the hemoglobin in a species results in haemoglobin variants. Variations in hemoglobin amino acid sequences, as with other proteins, may be adaptive.

According to Ajayi *et al* (2013), three types of haemoglobin were observed (AA, AB and BB) and were controlled by two autosomal alleles A and B in indigenous chicken in the Niger Delta region of Nigeria. Huisman, (1996) showed that Hb AA has a higher O_2 affinity than Hb BB Blood –typing tests. Most blood-typing tests are carried out as saline hemagglutination systems.

2.21. Transferrin

Yang *et al*. (1984) defined transferrin as a blood plasma protein for iron ion delivery that, in humans, is encoded by the *TF* gene. They stated further that transferrin is a glycoprotein that binds iron very tightly but reversibly. Although iron bound to transferrin is less than 0.1% (4 mg) of the total body iron, it is the most important iron pool, with the highest rate of turnover (25 mg/24 h). They asserted that transferrin has a molecular weight of around 80 kDa and contains 2 specific high-affinity Fe (III) binding sites. The affinity of transferrin for Fe (III) is extremely high (10^{23} M^{-1} at pH 7.4) but decreases progressively with decreasing pH below neutrality. When not bound to iron, it is known as apo-transferrin. (Yang *et al*. 1984). Yang *et al*., (1984) specified that the gene coding for transferrin in humans is located in chromosome band 3q21.

In humans, transferrin consists of a polypeptide chain containing 679 amino acids. It is a complex composed of alpha helices and beta sheets to form two domains (the first situated in the N-terminus and the second in the C-terminus). The N- and C- terminal sequences are represented by globular lobes and between the two lobes is an iron-binding site. The amino acids which bind the iron ion to the transferrin are identical for both lobes; two tyrosines, one histidine, and one aspartic acid. In order for the iron ion to bind an anion is required; preferably carbonate (CO_3^{2-}). Transferrin also has a transferrin iron-bound receptor; it is a disulfide-linked homodimer (Macedo and de Sousa, 2008). In humans, each monomer

consists of 760 amino acids. It enables ligand bonding to the transferrin, as each monomer can bind to one or two molecules of iron. Each monomer consists of three domains: the protease domain, the helical domain, and apical domain. The shape of transferrin receptor resembles a butterfly-like complex, due to the three clearly shaped domains (http://www.cs.stedwards.edu/chem/Chemistry/CHEM43/CHEM43/Projects04/ Transferrin / structure.htm). Transferring can bind to its receptor (Cheng *et al.* 2004) and when this happens, it forms transferrin receptor complex (Hafenstein *et al.* 2007).

Macedo and de Sousa, (2008) reported that the liver is the main source of manufacturing transferrin, but other sources such as the brain also produce this molecule. They asserted that the main role of transferrin is to deliver iron from absorption centres in the duodenum and red blood cell macrophages to all tissues. Predominantly, transferrin plays a key role where erythropoiesis and active cell division occur (Macedo and de Sousa, 2008). In order for iron ion to be introduced into the cell a carrier protein is used, known as a transferrin receptor. The receptor helps maintain iron homeostasis in the cells by controlling iron concentrations (Macedo and de Sousa, 2008).

Ritchie *et al.*(1999) reported that transferrin is associated with the innate immune system. That transferrin is found in the mucosa and binds iron, thus creating an environment low in free iron, where few bacteria are able to survive. The levels of transferrin reportedly decreases in inflammation (Ritchie *e tal.,* 1999), seeming contradictory to its function. Transferrin imbalance can have serious health effects for those with low or high serum transferrin levels. A patient with an increased serum transferrin level often suffers from iron deficiency anemia (Macedo and de Sousa, 2008). Macedo and de Sousa, (2008) revealed that a patient with decreased plasma transferrin can suffer from iron overload diseases and protein malnutrition. That an absence of transferrin in the body creates a rare genetic disorder known as atransferrinemia; a condition characterized by anemia and hemosiderosis in the heart and liver that leads to many complications including heart failure. Most recently, transferrin and its receptor have been tested to diminish tumour cells by using the receptor to attract antibodies (Macedo and de Sousa, 2008). Transferrin has been shown to interact with Insulin-like growth factor 2 (Storch *et al*, 2001) and IGFBP3 (Weinzimer *et al.* 2001). The Normal reference ranges for transferrin are 204 - 360 mg/dL (Kumar and Hagler,1999)

2.22. Carbonic anhydrase

The carbonic anhydrases (or carbonate dehydratases) form a family of enzymes that catalyze the rapid inter-conversion of carbon dioxide and water into bicarbonate and proton, a reversible reaction that occurs rather slowly in the absence of a catalyst (Badger and Price, 1994). The active site of most carbonic anhydrases contains a zinc ion; they are therefore classified as metalloenzymes. One of the functions of the enzyme in animals is to interconvert carbon dioxide and bicarbonate to maintain acid-base balance in blood and other tissues, and to help transport carbon dioxide out of tissues.

The reaction catalyzed by carbonic anhydrase is:

$$CO_2 + H_2O \xleftarrow{\text{Carbonic anhydrase}} H_2CO_3$$ (in tissues - high CO_2 concentration)

The reaction of carbonic anhydrase is one of the fastest of all enzymes, and its rate is typically limited by the diffusion rate of its substrates. Typical catalytic rates of the different forms of this enzyme range between 10^4 and 10^6 reactions per second (Lindskog, 1997). The reverse reaction is relatively slow in the absence of a catalyst. This is why a carbonated drink does not instantly degas when opening the container; however it will rapidly degas in the mouth when it comes in contact with carbonic anhydrase that is contained in saliva (Thatcher *et al.*, 1998).

An anhydrase is defined as an enzyme that catalyzes the removal of a water molecule from a compound, and so it is this "reverse" reaction that gives carbonic anhydrase its name, because it removes a water molecule from carbonic acid.

$HCO^-_3 + H^+ \longrightarrow H_2CO_3 \longrightarrow CO_2 + H_2O$ (in lungs and nephrons of the kidney - low CO_2 concentration)

A zinc prosthetic group in the enzyme is coordinated in three positions by histidine side – ch prosthains. The fourth coordination position is occupied by water. This causes polarisation of the hydrogen-oxygen bond, making the oxygen slightly more negative, thereby weakening the bond. A fourth histidine is placed close to the substrate of water and accepts a proton. The active site also contains specificity pocket for carbon dioxide, bringing it close to the

hydroxide group. This allows the electron-rich hydroxide to attack the carbon dioxide, forming bicarbonate.

According to Das and Deb (2008) the transport of CO_2, Heamoglobin utilization for controlling pH of body fluids and selection for the production of carbonate ions are facilitated by carbonic anhydrase. They observed six phenotypes viz. AA, BB, CC, AB, AC and BC controlled by three co-dominant alleles (CA-1A, CA-1B and CA-1C) located at an autosomal locus CA-1. They discovered no significant differences between various biochemical types and economic traits. However they reported that the activity of CA has been positively correlated with egg shell thickness.

2.23. Statistics

Statistics as defined by Dodge (2006) is the study of the planning of data collection in terms of the design of surveys and experiments, collection, organization, analysis, interpretation and presentation of data. The methods employed by statisticians in collecting, summarizing, analyzing, and interpreting variable numerical data are called statistical methods. Statistical methods are widely used in the life sciences, in economics, and in agricultural sciences to obtain approximate results. Applied statistics comprises descriptive statistics and the application of inferential statistics (Anderson *et al.*, 1994). Descriptive statistics summarizes the population data by describing what was observed in the sample numerically or graphically. Numerical descriptors include mean, standard deviation for continuous data types like heights and weights, while frequency and percentage are more useful in terms of describing categorical data. Inferential statistics involves drawing inferences about populations being studied from samples that were randomly drawn from them and subjecting the inferences made to statistical test to determine its validity or otherwise.

2.24. Experimental and observational studies

A common goal for a statistical research project is to investigate causality, and in particular to draw a conclusion on the effect of changes in the values of predictors or independent variable on dependent or response variables. There are two major types of causal statistical studies: experimental and observational studies. In both types of studies, the effect of

differences of an independent variable (or variables) on the behavior of the dependent variable are observed. The difference between the two types lies on how the study is actually conducted. Each can be very effective.

An experimental study involves taking measurements of the system under study, manipulating the system, and then taking additional measurements using the same procedure to determine if the manipulation has modified the values of the measurements. In contrast, an observational study does not involve experimental manipulation. Instead, data are gathered and correlations between predictors and response variables are investigated. The basic steps of a statistical experiment are: plan the experiments, design the experiment, perform the experiments, collect data, analyze the data, document and present the results of the study. Observational study typically uses a survey to collect observations about the area of interest and then performs statistical analysis.

2.25. Population and sample

In applying statistics to a scientific predicament, it is necessary to begin with a population to be studied. For practical reasons, a chosen subset of the population called a sample is studied as opposed to compiling data about the entire group. For a sample to be used as a guide to an entire population, it is important that it is truly a representative of that overall population. Unbiased representativeness assures that the inferences and conclusions can be safely extended from the sample to the population as a whole. A major problem lies in determining the extent to which the sample chosen is actually representative. Statistics offers methods to estimate and correct for any random trending within the sample and data collection procedures. The use of any statistical method is valid when the population under consideration satisfies the assumptions of the method. Misuse of statistics can produce subtle, but serious errors in description and interpretation.

2.26. Multivariate statistics and multivariate analysis

There are several body measurements that can be taken on an animal and for this reason many researchers used multivate techniques to simultaneously examine the relationship among them and production traits in West African Dwarf and Yankasa breeds of Sheep

(Salako and Ngere, 2002) and in beef cattle, these measurements have been reported to describe biological variations and to deduce their connection with production traits and carcass characteristics (Gilbert and Beerli 2001 and Nwosu *et al*, 1985b).

Multivariate statistics is a form of statistics encompassing the simultaneous observation and analysis of more than one outcome variable. It is concerned with multivariate probability distributions in terms of how these can be used to represent the distributions of observed data and how they can be used as part of statistical inference, particularly where several different quantities are of interest to the same analysis. Certain types of problem involving multivariate data, for example simple and multiple linear regressions, are not usually considered as special cases of multivariate statistics because the analysis is dealt with by considering the (univariate) conditional distribution of a single outcome variable given the other variables. The practical implementation of multivariate statistics to a particular problem may involve several types of univariate and multivariate analysis in order to understand the relationships between variables and their relevance to the actual problem being studied.

The application of multivariate statistics is multivariate analysis. Multivariate analysis is a generic term for any statistical technique used to analyze data from more than one variable. Multivariate analysis of variance (MANOVA) extends the analysis of variance to cover cases where there is more than one dependent variable to be analyzed simultaneously

2.27. Least squares and Coefficients of variation

Least squares method first described by Carl Friedrich Gauss around 1794 is a method of fitting a curve to data points so as to minimize the sum of the squares of the distances of the points from the curve (Al Kadi, 1992). The use of modern computers has expedited large-scale statistical computation, and has also made possible new methods that are impractical to perform manually. The method of least squares is a standard approach to the approximate solution of sets of equations in which there are more equations than unknowns. "Least squares" means that the overall solution minimizes the sum of the squares of the errors made in the results of every single equation.

Coefficient of variation (CV) is defined as the ratio of the standard deviation (ɗ) to the mean (μ). CV = $^{ɗ}/_{\mu}$

The coefficient of variation should be computed only for data measured on a ratio scale, as these are measurements that can only take non-negative values.

2.28. Cluster analysis

Cluster analysis or clustering is the task of grouping a set of objects in such a way that objects in the same group (called cluster) are more similar (in some sense or another) to each other than to those in other groups (clusters). It is a common technique for statistical data analysis used in many fields, including machine learning, pattern recognition, image analysis, information retrieval, and bioinformatics.

Cluster analysis itself is not one specific algorithm, but the general task to be solved. It can be achieved by various algorithms that differ significantly in their notion of what constitutes a cluster and how to efficiently find them. Popular notions of clusters include groups with small distances among the cluster members, dense areas of the data space, intervals or particular statistical distributions.

Clustering can therefore be formulated as a multi-objective optimization problem. The appropriate clustering algorithm and parameter settings (including values such as the distance function to use, a density threshold or the number of expected clusters) depend on the individual data set and intended use of the results. Cluster analysis as such is not an automatic task, but an iterative process of knowledge discovery or interactive multi-objective optimization that involves trial and failure. It will often be necessary to modify data pre-processing and model parameters until the result achieves the desired properties.

Besides the term clustering, there are a number of terms with similar meanings, including automatic classification, numerical taxonomy, botryology and typological analysis. The subtle differences are often in the usage of the results: while in data mining, the resulting groups are the matter of interest, in automatic classification primarily their discriminative power is of interest. This often leads to misunderstandings between researchers coming from

the fields of data mining and machine learning, since they use the same terms and often the same algorithms, but have different goals.

The term cluster analysis encompasses a number of different algorithms and methods for grouping objects of similar kind into respective categories. A general question facing researchers in many areas of inquiry is how to organize observed data into meaningful structures. In other words cluster analysis is an exploratory data analysis tool which aims at sorting different objects into groups in a way that the degree of association between two objects is maximal if they belong to the same group and minimal otherwise. Given the above, cluster analysis can be used to discover structures in data without providing an explanation/interpretation. In other words, cluster analysis simply discovers structures in data without explaining why they exist.

Note that the above discussions refer to clustering algorithms and do not mention anything about statistical significance testing. In fact, cluster analysis is not as much a typical statistical test as it is a "collection" of different algorithms that "put objects into clusters according to well defined similarity rules." The point here is that, unlike many other statistical procedures, cluster analysis methods are mostly used when we do not have any a priori hypotheses, but are still in the exploratory phase of our research. In a sense, cluster analysis finds the "most significant solution possible." Therefore, statistical significance testing is really not appropriate here, even in cases when p-levels are reported (as in *k*-means clustering).

2.29. Discriminant Analysis

Discriminant analysis is synonymous with classification. The term therefore refers to many techniques such as Logistic Regression, Decision Trees or Neural Networks. Discriminant Analysis or canonical variate analysis, attempts to establish whether a set of variables can be used to distinguish between two or more groups of cases. The common use of the term refers more specifically to two different approaches of classification: a descriptive approach (discriminant Function Analysis) and a predictive approach.

The goal of descriptive approach is to identify new variables called discriminant axes/functions from the linear combinations of original variables that are particularly effective at separating classes. Discriminant function analysis is used to determine which variables discriminate between two or more naturally occurring groups i.e. to determine whether groups differ with regard to the mean. Linear discriminant analysis is a method used in statistics and machine learning to find the linear combination of features which best separate two or more classes of objects or events. The resulting combination may be used as a linear classifier or more commonly, for dimentionality reduction before later classification.

2.30. Distance Measures and Genetic distance

The joining or tree clustering method uses the dissimilarities (similarities) or distances between objects when forming the clusters. Similarities are a set of rules that serve as criteria for grouping or separating items. These distances (similarities) can be based on a single dimension or multiple dimensions, with each dimension representing a rule or condition for grouping objects. The most straightforward way of computing distances between objects in a multi-dimensional space is to compute Euclidean distances.

It is computed as: distance $(x,y) = (\sum_i (x_i - y_i)^2)^{½}$

Note that Euclidean (and squared Euclidean) distances are usually computed from raw data, and not from standardized data. This method has certain advantages (e.g., the distance between any two objects is not affected by the addition of new objects to the analysis, which may be outliers). However, the distances can be greatly affected by differences in scale among the dimensions from which the distances are computed.

Genetic distance refers to the genetic divergence between species or between populations within a species which can be measured by a variety of parameters. Smaller genetic distances indicate a close genetic relationship whereas large genetic distances indicate a more distant genetic relationship. Genetic distance can be used to compare the genetic similarity between different species, such as humans and chimpanzees. Within a species genetic distance can be used to measure the divergence between different sub-species. In its simplest form, the genetic distance between two populations is the difference in frequencies of a trait. The

genetic distance of several individual traits can then be averaged to compute an overall genetic distance (Cavalli-Sforza, 2001)

2.31. Measures of genetic distance

Theoretically, there are several measures used to indicate genetic distance which include Fixation index, a commonly used measure of genetic distance which varies between 0 and 1. A value of 0 indicates that two populations are genetically identical whereas a value of 1 indicates that two populations are different species; Nei's standard genetic distance developed by Nei (1973) assumes that genetic differences arise due to mutations and genetic drift and Cavalli-Sforza and Edwards (1967) and Reynolds *et al.* (1983)) assume that genetic differences arise due to genetic drift only

Genetic drift or allelic drift is the change in the frequency of a gene variant (allele) in a population due to random sampling (Masel, 2011). The alleles in the offspring are a sample of those in the parents, and chance has a role in determining whether a given individual survives and reproduces. A population's allele frequency is the fraction of the copies of one gene that share a particular form (Futuyma, 1998). Genetic drift may cause gene variants to disappear completely and thereby reduce genetic variation. When there are few copies of an allele, the effect of genetic drift is larger, and when there are many copies the effect is smaller.

CHAPTER THREE

3.0. MORPHOLOGICAL CHARACTERIZATION OF PEARL, LAVENDER, BLACK AND WHITE GUINEA FOWLS.

3.1. MATERIALS AND METHODS

3.2. Distribution of experimental animal in Nigeria

Table 3.1 shows the distribution pattern of guinea fowl in Nigeria.

Table 3.1. Nigeria Guinea fowl population

State	Population	Percentage of total
Bauchi	5,748.469	13.15
Benue	1,997,184	4.60
Bronu	6,025,220	13.80
Gongola	2,008,684	4.60
Kaduna	6,016,342	13.76
Kano	5,115,958	3.16
Kwara	1,380,720	3.16
Niger	2,252,710	15.26
Plateau	5,793,166	15.26
Sokoto	7,349,350	16.81

Source: Akinwumi Iet al. (1979)

3.3. Description of study area

Nigeria is located between Latitudes 4^0-14^0N and Longitude 2^0-14^0E. It has a total area of 923,768km^2 (FOS, 1989). It is bordered by the Republic of Chad and Niger Republic in the north, Benin Republic in the west, the Republic of Cameroon in the east and by the Atlantic Ocean in the south. Nigeria has two broad belts of vegetation types, namely, the forest and savannah types. Savannah vegetation in Nigeria, as in other parts of West Africa, consists of three major belts, from south to north, viz: Guinea Savannah, Sudan Savannah; and Sahel Savannah.

The greatest number of the birds as shown in Table 3.1 are domicile in Sudan Savannah which is the vegetation belt found in the North-west stretching from the Sokoto plains in the west, through the northern sections of the central highland. It spans almost the entire northern states bordering the Niger Republic and covers over one quarter of Nigeria's total area. Sokoto State is located in the extreme northwest of Nigeria, near to the confluence of the Sokoto River and the Rima River. Sokoto State shares its borders with Niger Republic to the North, Zamfara State to the East, Kebbi State to the South-East and Benin Republic to the West. The sample sites were Sokoto, Bodinga, Goronyo, Balle, Shagari and Illela.

The geographical coordinates of Sokoto and other sampled settlements in the state were taken using Nokia E5.00 GPS/GSM instrument via its ovimaps/google imagery's search for placemarks. Sokoto lies within the co-ordinates of 13^0 3' 40" N and $5^0$14'20" E; Bodinga lies within 12^0 50' 49" N and 5^0 08' 44" E; Goronyo lies within 13^0 10' 58" N and 5^0 50' 47" E; Balle lies within 13^0 29' 24" N and $4^0$59'59" E; Shagari lies within 12^0 40' 55" N and 5^0 08' 41" E and Illela lies within 13^0 43' 42" N and 5^0 18' 01" E. Below is the detailed map of the study area.

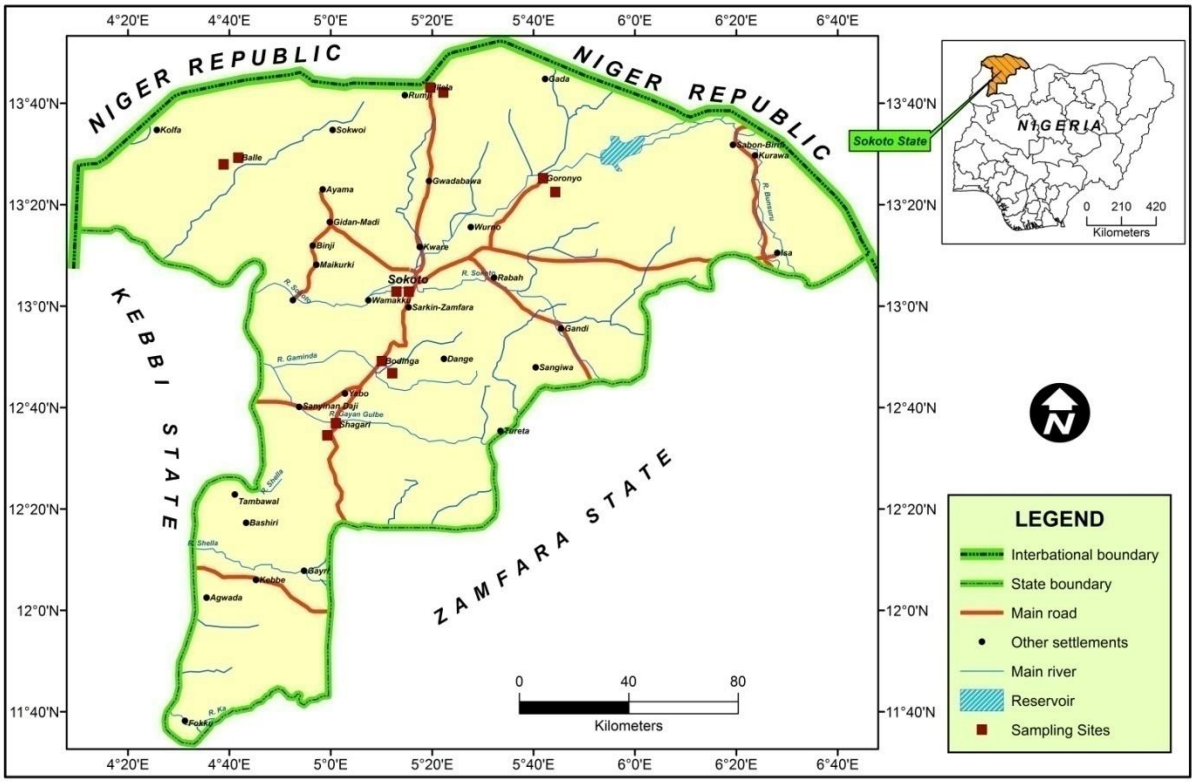


Figure 3.1: **Map of the Study area showing locations of sample sites**

3.4. Animals and management

The indigenous Guinea fowl population found in the study area are the Pearl, Lavender, Black and White varieties with the Pearl out numbering the other varieties. The birds were managed under the traditional semi-intensive system of animal husbandry at the backyard of the smallholders. At nights the birds were housed and in the morning, just before they were allowed to go out to scavenge for feed, they would be fed with grains like millet, rice, corn, other cereals and broken beans. During the day, the birds roam freely finding their own food such as insects, leaves, bulbs, seeds, worms etc around the owners' house. Water was provided in small pots under shade around the home stead for the birds to drink from at will. It is a production system that can be afforded by the rural poor because of its low input and it constitutes a significant part of the rural economy. No routine health management was imposed on the birds.

3.5. Identification

Five varieties of the grey helmeted guinea fowl were reportedly found in Nigeria: Pearl, White Breasted, Lavender, Black and White (Ogundipe, 1983). However, Ayorinde, (2004) from the breeding behaviour of the birds recognized only four varieties: Pearl, Lavender, Black and White. The plumage colourations of the varieties are as follows:

The Pearl is characterized with purplish grey plumage regularly dotted or pearled with small white circular spots or white feathers at the breast.

The Lavender has ash or light grey plumage dotted with white

The Black is entirely black in plumage but circular white dots may be present especially in the flight feathers.

The White variety has pure white

The photographs of the different varieties are presented in plates 1- 4.

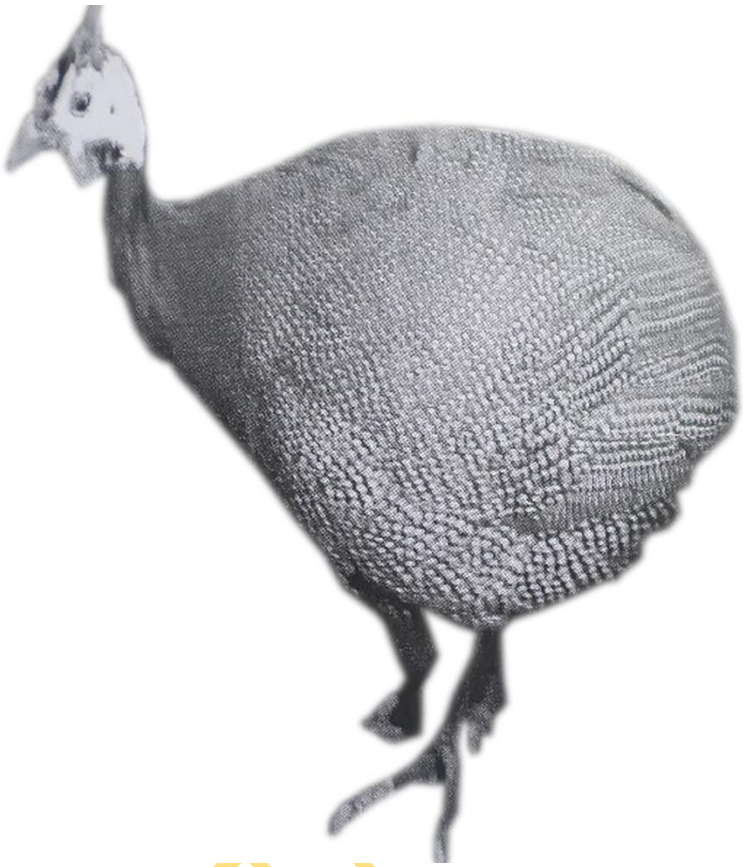


Plate 1: Pearl Guinea fowl

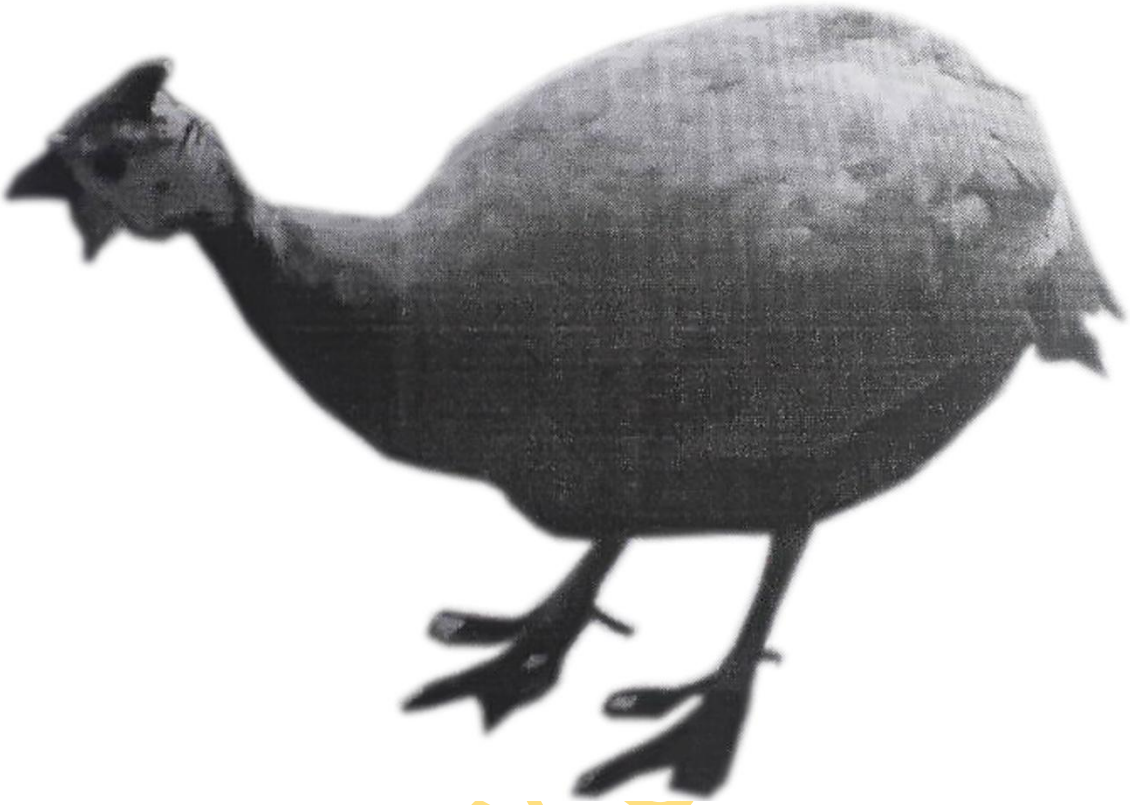


Plate 2: Lavender Guinea fowl

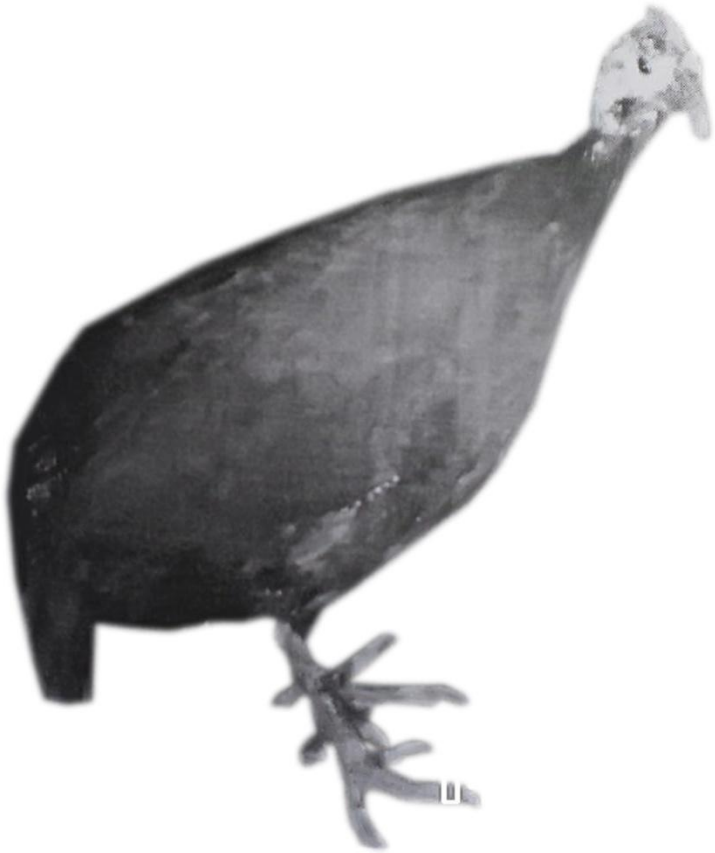


Plate 3: Black Guinea fowl

Plate 4: White Guinea fowl

3.6. Sample and sample size

A sample of one thousand, two hundred and seventy two (1,272) adult Guinea fowls comprising of four hundred and twenty five (425) pearl, three hundred and thirteen (313) lavender, two hundred and seventy one (271) black and two hundred and sixty three (263) white varieties were used for the study. Stratified Random Sampling technique was adopted to draw the samples from smallholders in Sokoto, Bodinga, Goronyo, Balle, Shagari and Illela villages as shown in Figure 3.1. The technique involved the division of the Sokoto State into three Senatorial districts and picking two villages from each of the districts. Random samples of the experimental units were then drawn from the villages. Data obtained from the different locations on each variety were pooled, because the locations are within the same ecological zone, and recorded according to varieties. Age determination was carried out by oral interview of stock owners through an interpreter that was vast and fluent in Hausa language.

3.7. Measurement of Quantitative traits

Body weight of individual bird was taken using a 5-kg weighing scale with sensitivity of 0.01 kg. The length and circumference measurements were effected using a measuring tape calibrated in centimetres (cm). Morphological variables were measured by the same trained operator (to eliminate error due to personal difference) in the mornings, before the animals were fed and allowed to leave the shelter to scavenge apparently to avoid undesirable variations because of changes in live weight and internal organs' volumes as a result of feeding. Each measurement was taken at least twice and the average of the measurements recorded as value for the variable.

3.8. Quantitative traits

Body weight (BWT) and thirteen primary biometric traits were taken on each of the animals. The biometric variables include; head thickness (HT), helmet length (HML), helmet width (HMW), wattle length (WL), wattle width (WW), body length (BL), keel length (KL), body circumference (BC), shank length (SL), shank thickness (ST), drumstick length (DL), thigh length (TL) and wing length (WGL). Data were categorized according to varieties

3.9. Description of reference points of measurements

The anatomical reference points used for measurements were according to standard descriptor (FAO, 1986) as shown in plate 5.

Body weight: The total weight of the live fowl

Head thickness: Head thickness was measured as the circumference at the middle of the head

Helmet length: Measured as the distance between the base of the head to the tip of the helmet

Helmet width: Measured as the distance between the broadest part of the helmet

Wattle length: Taken as the distance between the base of the beak and the tip of the wattle

Wattle width: Measured as the distance between the broadest part of the wattle

Body length: Body length was taken to be the distance between the posterior end of the pygostyle and the anterior of the nasal openings.

Keel length: Keel length was measured from the anterior point of keel to the posterior end.

Body circumference: The body girth was the circumference of the body around the breast region

Shank length: Shank length was measured as the distance between the foot pad and the hock joint when the tibio-tarsus and tarsometa-tarsus were held at right angles to each other

Shank thickness: Shank thickness was measured as the circumference at the middle of the shank

Drumstick length: The drumstick length was measured from the hock joint to the tibio-fibula-femora joint.

Thigh length: Measured as the distance between the knee and the hip

Wing length: The wing span was taken as the distance between the tip of the phalanges and the coracoids-humerous joint

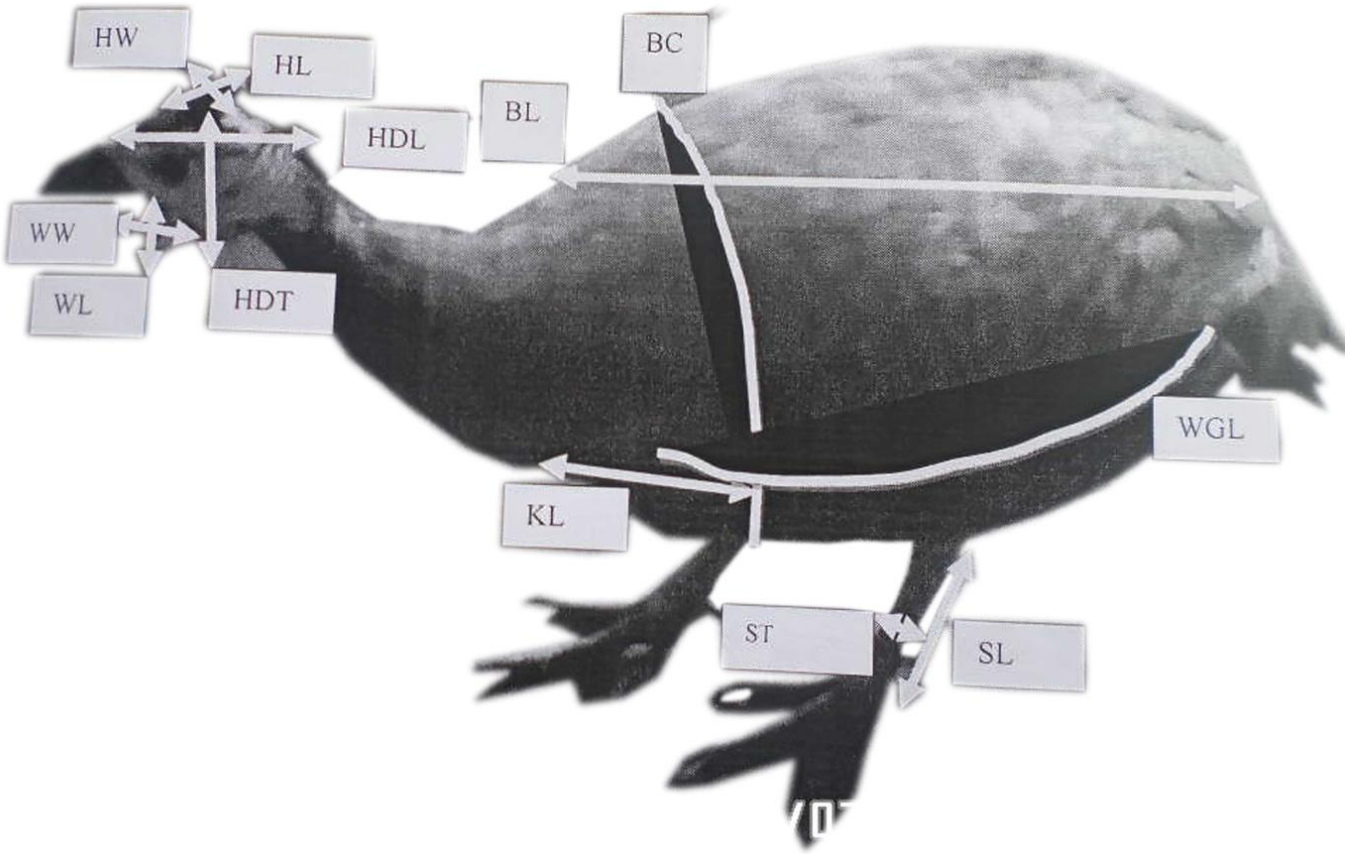


Plate 5: Reference points for body measurements of Guinea fowl

HW-Helmet width, HL-helmet length, WW-Wattle width, WL-Wattle length, HDT–head thickness, HDL –head length, BL - Body length, BC- Body circumference, KL- Keel length, SL –Shank length, ST-shank thickness, and WGL-Wing length

3.10. Statistical analyses.

3.11. Descriptive statistics

Means (*X*), standard deviation (SD), standard error (SE) and coefficients of variation (CV) associated with each zoometrical measurements were obtained. Varietal effects were determined by a one-way ANOVA and where significant differences occurred the means were separated using LSD procedure of SPSS (1989) statistical package.

3.12. Body Ratios, Body index and cranial indices of Guinea fowl

In the absence of body ratios used previously on Guinea fowl and after achieving the linear measurements, body ratio was obtained using the formular:

$$\text{Body ratio} = \frac{\text{Value of each variable}}{\text{The live weight of the bird}}$$

These principal selection indices state the ratio of measurements that characterize the proportionality of bird's body. Data collected on the body ratios were analyzed using the SPSS (1989) statistical package. Varietal effects were contrasted by a one-way ANOVA test followed by LSD test, implemented using the same statistical package.

A definition of each of these indices is shown below:

1. Body index $= \frac{\text{height}}{\text{body weight}}$

2. Skull index/cranial index $= \frac{\text{skull width}}{\text{skull length}}$

3. Helmet index $= \frac{\text{helmet width}}{\text{helmet length}}$

4. Wattle index $= \frac{\text{wattle width}}{\text{wattle length}}$

5. Shank index $= \frac{\text{skull width}}{\text{skull length}}$

The indices were meant to provide general information on the ethnological and functional attributes of the birds. Ethnological index was meant to contribute general information about varietal characteristics in terms of compactness, height, length and weight whereas functional index was meant to contribute information about the type, ability, purpose and production performance of the varieties. Data collected on these variables were analyzed using the SPSS (1989) statistical package. Varietal effects were contrasted by a one-way ANOVA test followed by LSD test, implemented in the same statistical package.

3.13. Correlation analysis

The degree of association between live weight and body measurements were computed for all the birds within each variety using Pearson's correlation subroutine. This was done to evaluate changing magnitude of association between the body weight and other zoometrical variables using SPSSCORR procedure of the SPSS, (1989).

3.14. Principal Component analysis

The principal component analysis (PCA) was performed in a single step using the Factor programme of the SPSS (1989) statistical package as reported by Mc Cracken *et al*., 2000 and adopted by Ogah *et al*., 2009. After the correlation matrix which was the primary data for the PCA analysis was generated, it was inspected for adequate determinant factor, sampling adequacy (Kaiser-Meyer-Olkin test) and sphericity (Battlet's test) of the same statistical package.

3.15. Discriminant analysis

Discriminant analysis was conducted to estimate the proportion of animals that were properly classified into their own variety as outlined by Snedecor and Cochran (1937). This was an additional way of evaluating within-flock resemblance and the degree of differences between flocks. Stepwise discriminant analysis of the SPSS (1989) Statistical package was used to screen for the most discriminating variables between the varieties. Wilks` lambda (U statistic) was used to test the significance of the discriminant function while the Bartlett`s V transformation of lambda of the same Statistical package was later used to compute the significance of lambda.

3.16. Cluster analysis

Cluster analysis was performed for classification of data to establish the optimum number of groups (i.e. subpopulations) using Cluster analysis of PAST Packages as outlined by Hammer *et al*., (2001).

CHAPTER FOUR

4.0. RESULTS

4.1. Descriptive statistics of body weights and different zoometrical measurements for the four varieties of Guinea fowls.

Descriptive statistics of body weights and different zoometrical measurements for the four varieties of guinea fowls are presented in Table 4.1.

The result of the descriptive statistics of live weights of pearl, lavender, black and white varieties of guinea fowl in the Table 4.1 showed significant ($p<0.05$) differences between pearl (0.94±0.01 kg) and the trio of lavender, black and white varieties. However, the black and the white varieties were similar ($p>0.05$). The body weight of the pearl variety was higher than that of lavender, black and white varieties by 10 g, 60 g and 60 g respectively. The range of the standard deviations among the four varieties was 0.07. The coefficient of variation was higher in black by 19.32 %, 4.63 % and 4.41 % respectively compared to pearl, lavender and white varieties.

The mean head thickness of pearl, lavender, black and white varieties of Guinea fowl were also presented in Table 4.1. Results in the table showed significant ($p<0.05$) differences between pearl and the three other varieties with the pearl variety having higher value than lavender, black and white varieties by 4 mm, 5 mm and 6 mm respectively. The range of the standard deviations in this trait among the four varieties was 0.04. The coefficient of variation ranged between 18.56 % in lavender to 34.64 % in the black variety

Results of helmet length in the Table 4.1 revealed significant ($p<0.05$) differences between pearl and the trio of lavender, black and white varieties. The helmet of the pearl variety was longer than that of lavender, black and white varieties by 2 mm, 3 mm and 3 mm respectively. The coefficient of variation was highest in the white variety with a value of almost 59 % and lowest in the black variety.

Results of Helmet width in the Table 4.1 clearly showed no significant ($p>0.05$) effect among pearl, black and white varieties while the lavender was significantly ($p<0.05$) different from them.

Table 4.1. Discriptive statistic of body weight and body measurements of Gunea fowl varieties

Traits		Pearl	Lavender	Black	White
$\bar{B}W$	X(kg)	0.94±0.01^{a}	0.93±0.01^{b}	0.87±0.04^{c}	0.87±0.03^{c}
	SD	0.17	0.21	0.24	0.20
	CV (%)	7.68	22.37	27.00	22.59
HT	$\bar{X}$(kg)	0.32±0.00^{a}	0.28±0.00^{bc}	0.27±0.01^{c}	0.26±0.01^{c}
	SD	0.09	0.05	0.09	0.06
	CV (%)	29.52	18.56	34.64	23.15
HL	$\bar{X}$(kg)	0.16±0.00^{a}	0.14±0.01^{bc}	0.13±0.02^{c}	0.13±0.01^{c}
	SD	0.07	0.06	0.07	0.07
	CV (%)	45.90	39.66	57.17	58.96
HW	$\bar{X}$(kg)	0.11±0.00^{b}	0.13±0.00^{a}	0.10±0.01^{b}	0.10±0.01^{b}
	SD	0.04	0.07	0.06	0.07
	CV (%)	41.93	58.40	66.23	63.56
WL	$\bar{X}$(kg)	0.21±0.00^{a}	0.21±0.00^{a}	0.16±0.01^{c}	0.15±0.01^{c}
	SD	0.06	0.04	0.07	0.05
	CV (%)	30.58	19.89	44.94	30.71
WW	$\bar{X}$(kg)	0.12±0.00	0.12±0.00	0.11±0.01	0.11±0.01
	SD	0.07	0.05	0.07	0.07
	CV (%)	56.11	45.94	63.75	58.47
SL	$\bar{X}$(kg)	6.87±0.04^{b}	6.61±0.06^{b}	6.89±0.41^{b}	7.32±0.19^{a}
	SD	1.03	1.01	1.58	1.95
	CV (%)	15.05	15.25	18.97	28.27
ST	$\bar{X}$(kg)	1.04±0.02^{b}	0.95±0.02^{c}	0.98±0.12^{c}	1.22±0.07^{a}
	SD	0.43	0.27	0.56	0.57
	CV (%)	41.27	28.66	45.96	58.19
DL	$\bar{X}$(kg)	12.23±0.04^{a}	11.80±0.09^{b}	11.62±0.26^{b}	12.44±0.18^{a}
	SD	1.38	1.66	1.47	1.25
	CV (%)	12.32	14.04	11.85	10.78
TL	$\bar{X}$(kg)	7.72±0.04^{b}	7.65±0.23^{b}	7.11±0.30^{c}	8.05±0.12^{a}
	SD	1.04	4.02	1.02	1.42
	CV (%)	13.43	12.52	12.70	19.96
WGL	$\bar{X}$(kg)	20.04±0.06^{a}	19.55±0.09^{b}	18.25±0.40^{d}	19.08±0.18^{c}
	SD	1.81	1.67	1.52	1.90
	CV (%)	9.03	8.57	7.97	10.39
BL	$\bar{X}$(kg)	37.47±0.21^{a}	36.39±0.19^{ab}	32.09±1.71^{c}	36.05±0.65^{b}
	SD	6.11	3.47	5.40	8.21
	CV (%)	16.31	9.53	14.98	25.59
KL	$\bar{X}$(kg)	13.16±0.05	12.72±0.11	12.19±0.37	13.06±0.16
	SD	1.34	1.86	1.33	1.75
	CV (%)	10.21	14.62	10.20	14.37
BC	$\bar{X}$(kg)	28 .07±0.12^{a}	27.15±0.18^{a}	25.41±0.96^{b}	28.141±0.43^{a}
	SD	3.61	3.16	3.60	4.59
	CV (%)	12.86	11.65	12.80	18.06

Figures in the same row bearing different superscripts differed significantly (P<0.05).

BW-Body weight, HT – Head thickness, HL-helmet length, HW-Helmet width, WL-Wattle length, WW-Wattle width, SL –Shank length, ST-shank thickness, DL – drumstick length, TL – Thigh length, WGL – Wing length, BL - Body length, KL- Keel length and, BC- Body circumference

The lavender variety was 15.38 %, 23.08 % and 23.08 % wider than the pearl, black and white varieties in helmet width. The coefficient of variation in each of the varieties examined were high ranging from 41.93 % in pearl to 66.23 % in black variety.

Mean Wattle length of pearl, lavender, black and white varieties of Guinea fowl were as indicated in Table 4.1. The Table revealed significant ($p<0.05$) differences among pearl, lavender, black and white varieties and statistical ($p>0.05$) similarity between black and white varieties. The pearl displayed superiority over lavender, black and white varieties by 2 mm, 5 mm and 6 mm respectively. Coefficients of variation ranged between 19.89 % and 44.94 % and the standard deviation estimates associated with the mean wattle length (0.04 – 0.07) could be regarded as small.

The mean shank lengths of pearl, lavender, black and white varieties were also presented in Table 4.1. The results on the table showed significant ($p<0.05$) differences between white variety and the three others with the white variety having higher value of 0.71 cm, 0.43 cm and 0.45 cm than lavender, black and pearl variety, respectively. The coefficient of variation ranged between 15.05 % in pearl to 28.27 % in the white variety.

Mean shank thickness of pearl, lavender, black and white varieties of guinea fowl were as revealed in the result presented on Table 4.1. The result showed that there were significant ($p<0.05$) differences between white variety and the other three varieties. Also, pearl variety was significantly ($p<0.05$) different from lavender and black variety. The shank of white variety was thicker than that of pearl, lavender and black variety by 1.8 mm, 2.7 mm and 2.4 mm, respectively. The coefficient of variation ranged between 28.66 % in lavender to 58.19 % in white variety and the sums of the square of deviates from the mean in all the four also ranged from 0.27 in lavender and 0.57 in white variety.

Also presented in the same Table 4.1 are the mean values of drumstick length of pearl, lavender, black and white varieties of Guinea fowl. The result showed similarities ($p>0.05$) between pearl and white on one hand and lavender and black varieties on the other hand. However, statistical ($p<0.05$) significance were recorded among the two pairs that were

similar. The coefficient of variation for the variable was generally low in the four varieties ranging from 1.32 % in pearl to 14.04 % in lavender.

The result presented on the Table 4.1 for thigh length revealed significant ($p<0.05$) differences between black and the other varieties and between white and the other varieties. The thigh length of the white variety was longer than that of pearl, lavender and black varieties by 0.33 cm, 0.40 cm and 0.94 cm respectively. The coefficient of variation was very high in lavender but comparatively low in the other varieties.

The mean wing length values of pearl, lavender, black and white varieties were as presented in Table 4.1. The result showed significant ($p<0.05$) differences among all the varieties with the pearl showing higher value over lavender, black and white varieties by 0.49 cm, 1.79 cm and 0.96 cm respectively.

The result of body length portrayed statistical significance ($p<0.05$) between black and the other varieties. The body length of the pearl variety was longer than that of lavender, black and white varieties by 1.08 cm, 5.38 cm and 1.42 cm respectively. The coefficient of variation ranged from 9.53 to 25.59 % among the varieties.

Lastly, the Table 4.1 showed the mean body circumference values of pearl, lavender, black and white varieties of guinea fowl. The result demonstrated statistical significance ($p<0.05$) between black and the other varieties. The body circumference of white variety was higher than that of pearl, lavender and black variety by 0.07 cm, 0.99 cm and 2.73 cm respectively. The coefficient of variation ranged from 11.65 % to 18.06 % among the different varieties of Guinea fowl.

4.2. Body Ratios and corporal indices

Tables 4.2 presented the standardization of body parameters by division with live weight. The results of ratios of body parameters divided by the live weights in all the varieties of Guinea fowl are statistically ($p>0.05$) similar.

Table 4.2. Ratio of zoometrical measurements to Body weight in four varieties of Guinea fowl

Traits	Pearl	Lavender	Black	White
Head circumference	8.42±0.05	9.08±0.05	8.94±0.09	9.08±0.15
Head thickness	0.32±0.01	0.36±0.01	0.40±0.01	0.37±0.01
Helmet length	0.23±0.01	0.23±0.01	0.23±0.02	0.27±0.04
Helmet width	0.15±0.01	0.12±0.01	0.14±0.01	0.13±0.01
Wattle length	0.05±0.01	0.06±0.01	0.06±0.01	0.06±0.01
Wattle width	0.18±0.01	0.18±0.01	0.15±0.01	0.17±0.01
Body length	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.00
Keel length	0.28±0.01	0.30±0.01	0.27±0.01	0.26±0.02
Body circumference	0.05±0.00	0.05±0.00	0.05±0.00	0.05±0.00
Shank length	0.41±0.01	0.41±0.01	0.34±0.01	0.38±0.01
Shank thickness	0.73±0.02	0.73±0.03	0.78±0.02	0.83±0.04
Shank circumference	0.03±0.00	0.04±0.00	0.04±0.00	0.04±0.00
Drumstick length	0.02±0.00	0.03±0.00	0.02±0.00	0.02±0.00
Wing length	0.06±0.00	0.06±0.00	0.07±0.00	0.06±0.00
Thigh length	0.26±0.00	0.26±0.00	0.24±0.01	0.26±0.01

Means along the same row with no superscripts are significantly (P>0.05) similar

4. 3. Body index and cranial indices

Table 4.3 presented the body index and cranial indices of the four varieties of guinea fowl. In the table five zoometric indices were analyzed with the aim of studying the ratio between the two principal dimensions of the structure and to learn about how the structure is. Its utility was derived from the relation between width and length.

The result as presented in Table 4.3 showed statistical ($p>0.05$) similarities among all the varieties.

Table 4.3: Body index and Cranial indices in four varieties of Guinea fowl

Traits	Pearl	Lavender	Black	White
Cranial index	0.18±0.01	0.16±0.01	0.29±0.01	0 .37±0.01
Body index	0.02.±0.00	0.03±0.00	0.01±0.00	0.00±0.00
Helmet index	0.69±0.03	0.89±0.03	0.76±0.03	0.82±0.05
Wattle index	0.57±0.002	0.60±0.04	0.72±0.02	0.64±0.02
Shank index	0.15±0.01	0.14±0.01	0.14±0.01	0.13±0.01

Means along the same row with different superscripts are significantly different (P<0.05)

4.4. RELATIONSHIP BETWEEN BODY WEIGHT AND ZOOMETRICAL MEASUREMENTS

4.4.1. Phenotypic correlations between weight and zoometrical traits.

Correlation between live weight and zoometrical measurements as described by phenotypic correlation coefficients are presented in Tables 4.3 and 4.4. Results showed that live weight was positively and significantly correlated with most zoometrical parameters in pearl, lavender, black and white varieties of guinea fowl.

In pearl variety, highest correlation value was obtained between body weight and thigh length (r=.95) followed by body circumference, body length, wing length, keel length, shank length, head thickness, helmet length, helmet width, wattle length, shank thickness, wattle width and lastly drumstick length (r=0.65).

In lavender variety, highest correlation value was obtained between body weight and body circumference (r=0.94), followed by body length, helmet length, shank thickness, wing length, keel length, shank length, wattle length, wattle width, helmet width, head thickness, drumstick length and the least value with thigh length (r=0.14).

In black variety, highest correlation value was obtained between body weight and head length and thickness (r=0.77), followed by wattle width, wattle length, helmet width, body circumference, wing length, keel length, drumstick length, body length, shank length, thigh length and lowest in shank thickness with a value of r=0.35.

In white variety however, the highest correlation value was obtained between body weight and keel length (r=0.91) followed by drumstick length, thigh length, head thickness, body circumference, helmet length, body length, wattle width, helmet width, shank length, shank thickness, wattle length and the least value of r=0.76 for wing length.

4.4.2. Phenotypic correlation among zoometrical traits.

4.4.2.1. Pearl variety

In pearl variety, the correlation coefficients ranged between 0.58 and 0.95. The correlation values obtained between head thickness and other zoometrical traits was highest with helmet length followed by wattle length, wing length, wattle width, helmet width, shank thickness, keel length, shank length, body circumference, body length, thigh length and drumstick length.

Helmet length had the highest correlation value with helmet width (r=0.89) followed by wattle length, wattle width, shank thickness, shank length, keel length, wing length, body circumference, body length, thigh length and drumstick length (r=0.57).

The correlation values obtained between helmet width and other zoometrical variables was highest with shank thickness (r=0.89) followed by wattle length, wattle width, shank length, keel length, wing length, body circumference, thigh length, body length and drumstick length (r=0.55).

Also, the correlation coefficients obtained between wattle length and other zoometrical parameters was highest with wattle width (0.91) followed by shank thickness, keel length, shank length, body circumference, thigh length, wing length, body length and drumstick length (r=0.55).

In the same variety, correlation values obtained between wattle width and other zoometrical parameters was highest with shank thickness (r=0.91), followed by keel length, shank length, thigh length, body circumference, body length, wing length and drumstick length (r=0.52).

The correlation values obtained between body length and other zoometrical parameters was highest with body circumference (r=0.94), followed by thigh length, wing length, keel length, shank length, shank thickness and drumstick length (r=0.64).

Table 4.4: Correlation of body weight and body traits of pearl and lavender varieties of Guinea fowl

	BW	HT	HL	HW	WL	WW	BL	KL	BC	SL	ST	DL	WGL	TL
BW		0.79**	0.76**	0.75**	0.75**	0.67**	0.94**	0.89**	0.94**	0.84**	0.72**	0.65**	0.91**	0.95**
HT	0.61**		0.93**	0.87**	0.90**	0.89**	0.74**	0.81**	0.74**	0.79**	0.86**	0.58**	0.73**	0.70**
HL	0.74**	0.86**		0.89**	0.89**	0.87**	0.73**	0.79**	0.74**	0.80**	0.86**	0.57**	0.75**	0.73**
HW	0.63**	0.78**	0.86**		0.88**	0.88**	0.70**	0.79**	0.73**	0.80**	0.89**	0.55**	0.74**	0.73**
WL	0.65**	0.70**	0.79**	0.72**		0.91**	0.71**	0.79**	0.73**	0.76**	0.86**	0.57**	0.72**	0.76**
WW	0.65**	0.75**	0.81**	0.89**	0.77**		0.63**	0.74**	0.67**	0.74**	0.91**	0.52**	0.62**	0.68**
BL	0.83**	0.46**	0.57**	0.31**	0.54**	0.36**		0.90**	0.94**	0.80**	0.68**	0.64**	0.91**	0.93**
KL	0.65**	0.60**	0.67**	0.59**	0.57**	0.65**	0.60**		0.91**	0.86**	0.79**	0.65**	0.87**	0.87**
BC	0.94**	0.59**	0.73**	0.57**	0.66**	0.61**	0.86**	0.69**		0.85**	0.72**	0.64**	0.91**	0.91**
SL	0.65**	0.67**	0.73**	0.64**	0.60**	0.67**	0.50**	0.69**	0.69**		0.83**	0.65**	0.85**	0.83**
ST	0.74**	0.72**	0.81**	0.80**	0.68**	0.76**	0.60**	0.69**	0.75**	0.77**		0.57**	0.71**	0.73**
DL	0.32**	0.16**	0.28**	0.18**	0.23**	0.19**	0.39**	0.27**	0.34**	0.26**	0.38**		0.66**	0.63**
WGL	0.85**	0.61**	0.73**	0.54**	0.68**	0.55**	0.84**	0.67**	0.87**	0.66**	0.74**	0.38**		0.88**
TL	0.14**	0.09	0.09	0.04	0.12*	0.07	0.14**	0.09	0.13*	0.19	0.09	0.01	0.13*	

** = (P<0.01) and * = (P<0.05)

Lower matrix = lavender variety; upper matrix = pearl variety

BW = Body weight, HT = Head thickness, HL= Helmet length, HW = Helmet width, WL = Wattle length, WW = Wattle width, BL = Body length, KL = Keel length, BC = Body circumference, SL = Shank length, ST = Shank thickness, DL = Drumstick length, WGL = Wing length, TL = Thigh length

For keel length and other zoometrical parameters, the correlation value was highest with body circumference (r=0.91) followed by thigh length, wing length, shank length, shank thickness, and drumstick length (r=0.65).

The correlation coefficients obtained between body circumference and other zoometrical parameters was highest with thigh length (r=0.91), followed by wing length, shank length, shank thickness, and drumstick length (r=0.64).

Shank length and other zoometrical parameters recorded highest correlation value with wing length (r=0.85) followed by thigh length, shank thickness, and drumstick length (r=0.65).

For shank thickness and other zoometrical parameters, the correlation values obtained was highest with thigh length (r=0.73) followed by wing length and drumstick length (r=0.57).

The values form drumstick length and other zoometrical parameters, was highest with wing length (r=0.66), followed by thigh length (r=0.63) and finally the correlation value recorded between wing and thigh lengths was r=0.88.

4.4.2.2. Lavender variety

In lavender variety, correlation coefficients obtained between head thickness and other zoometrical traits was highest with helmet length (r=0.86) followed by helmet width, wattle width, wattle length, shank thickness, shank length, wing length, keel length, body circumference, body length and drumstick length (r=0.16).

The correlation coefficients obtained between helmet length and other zoometrical parameters was highest with helmet width (r=0.86) followed by wattle width, shank thickness, wattle length, shank length, wing length, body circumference, keel length, body length and drumstick length (r=0.28).

Helmet width correlated with other zoometrical parameters recorded highest value with wattle width (r=0.89) chronologically followed by shank thickness, wattle length, shank

length, keel length, body circumference, wing length, body length and drumstick length (r=0.18).

The correlation coefficients recorded between wattle length and other zoometrical parameters showed highest value with wattle width (r=0.77) followed by shank thickness, wing length, body circumference, shank length, keel length, body length, drumstick length and thigh length (r=0.12). In the same variety, correlation values obtained between wattle width and other zoometrical traits was highest with shank thickness (r=0.76) followed by shank length, keel length, body circumference, wing length, body length and least with drumstick length (r=0.19).

The correlation values obtained between body length and other zoometrical traits was highest with body circumference (r=0.86) followed by wing length, shank thickness, keel length, shank length, drumstick length and least with thigh length (r=0.14). The highest correlation coefficients between keel length and each of body circumference, shank length and shank thickness gave the same value (r=0.69) followed by wing length and drumstick length (r=0.27).

Body circumference correlated with other zoometrical traits recorded highest correlation value with wing length (r=0.87) followed by shank thickness, shank length, drumstick length and thigh length (r=0.13). Correlation coefficients between shank length and other zoometrical traits showed highest value with shank thickness (r=0.77) followed by wing length and drumstick length (r=0.26).

Shank thickness correlated with drumstick length and wing length gave values 0f r=0.38 and r=0.74 respectively. The values obtained when drumstick length and wing length was correlated gave a coefficient of 0.38 and the correlation coefficient between wing length and thigh length was 0.13.

4.4.2.3. Black variety

In black variety, highest correlation values obtained between head thickness and other zoometrical parameters was highest with wattle length (r=0.96) followed by wing length, helmet length, wattle width, helmet width, drumstick length, keel length, shank thickness, body length, body circumference, thigh length and shank length (r=0.28).

Also, correlation values obtained between helmet length and other zoometrical parameters was highest with wattle width (r=0.97) followed by, helmet width, drumstick length, wattle length, wing length, keel length, shank thickness, body circumference, body length, shank length and thigh length (r=0.45).

Helmet width and other zoometrical parameters recorded highest correlation value with wattle width (r=0.92) followed by wattle length, drumstick length, keel length, shank thickness, wing length, shank length, body circumference, body length and thigh length (r=0.38).

Correlation of wattle length and other zoometrical parameters recorded highest value with wattle width (r=0.95) followed by drumstick length, shank thickness, wing length, body length, keel length, body circumference, shank length and thigh length (r=0.29). In the same variety, correlation values obtained between wattle width and other zoometrical parameters was highest with drumstick length (r=0.69) followed by shank thickness, wing length, keel length, shank length, body circumference, body length, and thigh length (r=0.42).

The correlation values obtained between body length and other zoometrical parameters was highest with body circumference (r=0.93) followed by thigh length, wing length, keel length, shank length, drumstick length and shank thickness (r=0.69).

Correlation values between Keel length and other zoometrical parameters was highest with wing length (r=0.85) followed by body circumference, thigh length, shank length, drumstick length and shank thickness (r=0.72).

Table 4.5: Correlation of body weight and body traits of black and white varieties of Guinea fowl

	BW	HT	HL	HW	WL	WW	BL	KL	BC	SL	ST	DL	WGL	TL
BW		0.77**	0.77**	0.69**	0.71**	0.76**	0.49**	0.56**	0.61**	0.45**	0.35**	0.50**	0.56**	0.42**
HT	0.88**		0.92**	0.82**	0.96**	0.92**	0.38**	0.41**	0.36**	0.28**	0.39**	0.52**	0.43**	0.29**
HL	0.86**	0.86**		0.89**	0.94**	0.97**	0.50**	0.59**	0.53**	0.47**	0.58**	0.67**	0.60**	0.45**
HW	0.81**	0.72**	0.85**		0.86**	0.92**	0.42**	0.59**	0.45**	0.45**	0.57**	0.71**	0.56**	0.38**
WL	0.76**	0.77**	0.91**	0.76**		0.95**	0.37**	0.41**	0.35**	0.31**	0.46**	0.56**	0.44**	0.29**
WW	0.82**	0.77**	0.94**	0.79**	0.93**		0.45**	0.54**	0.46**	0.47**	0.59**	0.69**	0.55**	0.42**
BL	0.85**	0.70**	0.84**	0.80**	0.79**	0.74**		0.88**	0.93**	0.85**	0.69**	0.71**	0.88**	0.91**
KL	0.91**	0.78**	0.86**	0.82**	0.69**	0.76**	0.87**		0.93**	0.81**	0.72**	0.77**	0.95**	0.87**
BC	0.87**	0.72**	0.89**	0.78**	0.77**	0.80**	0.93**	0.94**		0.87**	0.70**	0.73**	0.93**	0.89**
SL	0.79**	0.67**	0.85**	0.63**	0.83**	0.92**	0.74**	0.75**	0.85**		0.87**	0.86**	0.83**	0.92**
ST	0.78**	0.72**	0.92**	0.78**	0.86**	0.93**	0.76**	0.78**	0.85**	0.91**		0.91**	0.76**	0.78**
DL	0.90**	0.77**	0.94**	0.85**	0.88**	0.69**	0.84**	0.87**	0.88**	0.90**	0.93**		0.78**	0.75**
WGL	0.76**	0.88**	0.91**	0.85**	0.78**	0.79**	0.93**	0.95**	0.96**	0.96**	0.80**	0.87**		0.87**
TL	0.88**	0.79**	0.88**	0.67**	0.77**	0.85**	0.84**	0.88**	0.92**	0.93**	0.83**	0.88**	0.89**	

** = (P<0.01)

Lower matrix = white variety; upper matrix = black variety

BW = Body weight, HT = Head thickness, HL= Helmet length, HW = Helmet width, WL = Wattle length, WW = Wattle width, BL = Body length, KL = Keel length, BC = Body circumference, SL = Shank length, ST = Shank thickness, DL = Drumstick length, WGL = Wing length, TL = Thigh length

Body circumference and other zoometrical parameters when correlated showed highest value with wing length (r=0.93) followed by thigh length, shank length, drumstick length and shank thickness (r=0.70).

Shank length and other zoometrical traits when correlated showed highest value with thigh length (r=0.92) followed by shank thickness, drumstick length and wing length (r=0.83). Also, when shank thickness and other zoometrical parameters were correlated, the correlation values obtained was highest with drumstick length (r=0.91) followed by thigh length and wing length (r=0.76).

When drumstick length and other zoometrical parameters were correlated, the correlation value was higher wing length (r=0.78) followed by thigh length (r=0.75) and finally the correlation value between wing length and thigh length was r=0.87

4.4.2.4. White variety

In white variety, correlation values obtained between head thickness and other zoometrical traits was highest with helmet length (r=0.86) followed by wing length, body circumference, drumstick length, keel length, wattle length, wattle width, helmet width, shank thickness, body length, thigh length and shank length (r=0.67).

Also, correlation values obtained between helmet length and other zoometrical parameters was highest with wattle width (r=0.94) followed by drumstick length, shank thickness, wattle length, wing length, body circumference, thigh length, keel length, helmet width, shank length and body length (r=0.84). When helmet width and other zoometrical parameters were correlated, the correlation value was highest with drumstick length (r=0.85) followed by wing length, keel length, body length, wattle width, shank thickness, body circumference, wattle length, thigh length and shank length (r=0.63)

Wattle length and other zoometrical traits were correlated and the highest correlation value was recorded with wattle width (r=0.93) followed by drumstick length, shank thickness,

shank length, wing length, body circumference, thigh length, body length and keel length (r=0.69). In the same white variety, correlation values obtained between Wattle width and other zoometrical variables was highest with shank thickness (r=0.93) followed by shank length, thigh length, body circumference, wing length, keel length, body length, and drumstick length (r=0.69).

The correlation values obtained between body length and other zoometrical parameters was highest with body circumference (r=0.93) followed by wing length, keel length, thigh length, drumstick length, shank thickness and shank length (r=0.74). Values obtained when keel length was correlated with other zoometrical parameters recorded highest value with wing length (r=0.95) followed by body circumference, thigh length, drumstick length, shank thickness and shank length (r=0.75). The correlation coefficients obtained when body circumference and other zoometrical parameters were correlated was highest with wing length (r=0.96) followed by thigh length, drumstick length shank length, and shank thickness (r=0.85).

Also, when shank length and other zoometrical traits were correlated, the correlation value was highest with thigh length (r=0.93) followed by shank thickness, drumstick length and wing length (r=0.76). A similar exercise with shank thickness recorded highest value with drumstick length (r=0.93) followed by thigh length and wing length (r=0.80). When drumstick length and other zoometrical parameters were correlated, correlation values of r=0.88 and r=0.87 were obtained with thigh length and wing length respectively. The correlation value obtained between wing length and thigh length was r=0.89

4.5. Principal Component Analysis (PCA)

Tables 4.4-4.7 showed the rotated component matrix of the PCA showing the factor solutions to pearl, lavender, black and white varieties of guinea fowl. The Kaiser-Meyer-Olkin measures of sampling adequacy were 0.81, 0.89, 0.91 and 0.95 with the corresponding determinants of 2.24E-013, 1.98E-009, 4.25E-016 and 2.24E-013 in white, black, lavender and pearl varieties respectively. The result further showed that two principal components were yielded by the factor solutions for pearl and black; three for lavender and one principal component for white variety.

Table 4.6. Rotated Component Matrix of the PCA showing the factor solution in pearl variety.

Traits	PC1	PC2
Head circumference	0.97	0.00
Head thickness	0.91	-0.27
Helmet length	0.90	-0.34
Helmet width	0.89	-0.32
Wattle length	0.90	-.294
Body length	0.91	0.32
Keel length	0.94	0.12
Body circumference	0.92	0.28
Shank length	0.91	017
Shank thickness	0.89	-0.31
Shank circumference	0.54	0.41
Drumstick length	0.71	0.21
Wing length	0.90	0.23
Thigh length	0.92	0.26

PC 1 = Principal component one, PC 2 = Principal component two

Table 4.7. Rotated Component Matrix of the PCA showing the factor solution in lavender variety.

Traits	PC1	PC2	PC3
Head circumference	0.86	0.40	0.02
Head thickness	0.80	-0.36	0.05
Helmet length	0.90	-0.26	-0.01
Helmet width	0.80	-0.51	-0.01
Wattle length	0.81	-0.23	0.06
Wattle width	0.82	-0.46	0.01
Body length	0.77	0.56	-0.02
Keel length	0.79	-0.02	-0.03
Body circumference	0.91	0.31	-0.00
Shank length	0.80	-0.15	-0.03
Shank thickness	0.89	-0.13	-0.06
Shank circumference	0.64	0.06	0.05
Drumstick length	0.37	0.33	-0.37
Wing length	0.88	0.31	-0.03
Thigh length	0.86	0.40	0.92

PC 1 = Principal component one, PC 2 = Principal component two and PC 3 = Principal component three

Table 4.8. Rotated Component Matrix of the PCA showing the factor solution in black variety.

Traits	PC1	PC2
Head circumference	0.76	0.46
Head thickness	0.73	0.64
Helmet length	0.85	0.48
Helmet width	0.80	0.44
Wattle length	0.74	0.62
Wattle width	0.84	0.51
Body length	0.83	-0.42
Keel length	0.87	-0.33
Body circumference	0.86	-0.40
Shank length	0.84	-0.49
Shank thickness	0.81	-0.30
Shank circumference	0.84	-0.32
Drumstick length	0.89	-0.18
Wing length	0.88	-0.33
Thigh length	0.81	-0.51

PC 1 = Principal component one, PC 2 = Principal component two

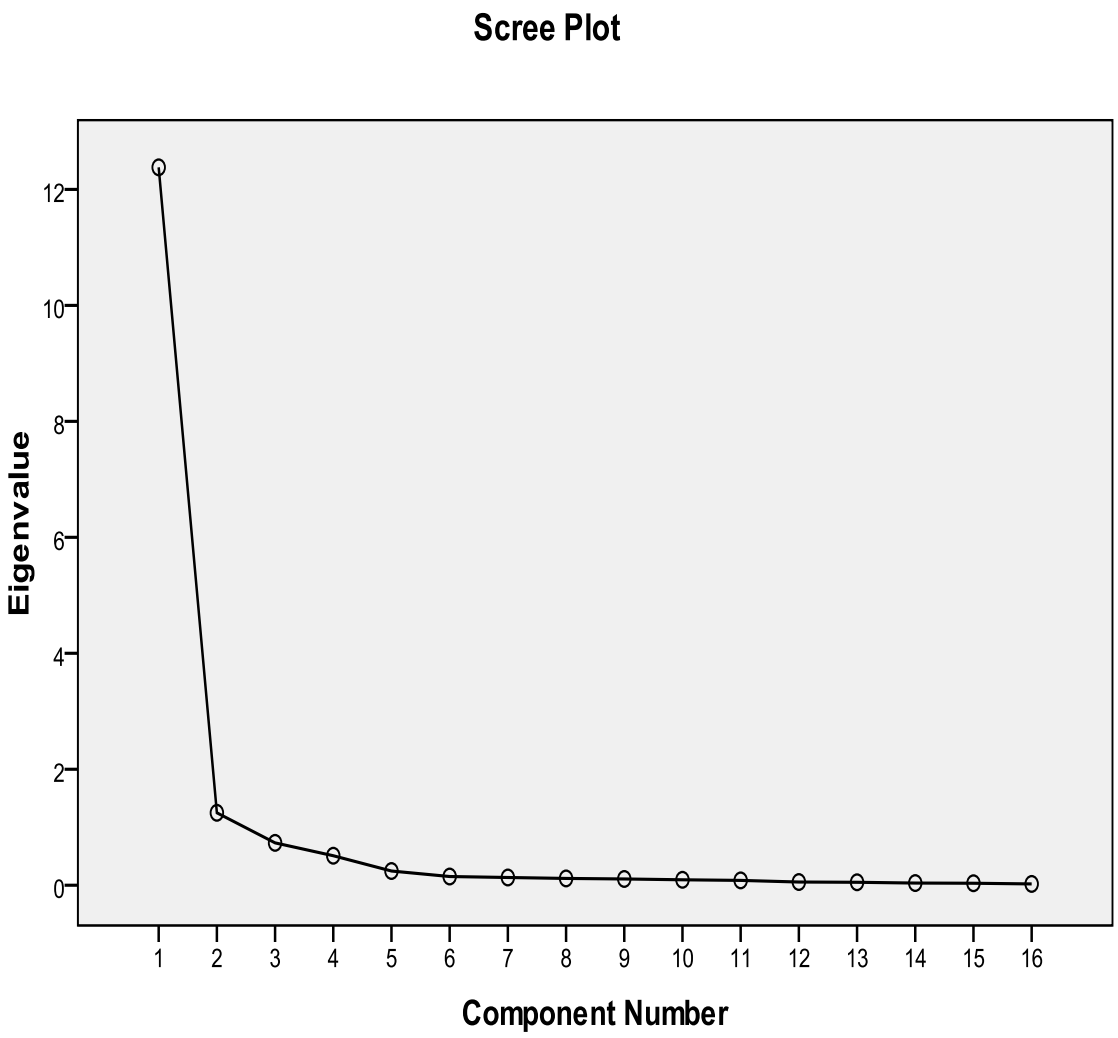
Table 4.9. Rotated Component Matrix of the PCA showing the factor solution in white variety.

Traits	PC1
Head circumference	0.93
Head thickness	0.85
Helmet length	0.97
Helmet width	0.85
Wattle length	0.88
Wattle width	0.93
Body length	0.90
Keel length	0.93
Body circumference	0.95
Shank length	0.90
Shank thickness	0.92
Shank circumference	0.91
Drumstick length	0.97
Wing length	0.95
Thigh length	0.94

PC 1 = Principal component one

4.6. The Scree plots

The scree plots of the eigenvalues for the four varieties of guinea fowl shown in Figures 2 – 5 were meant to get indications of the importance of each eigenvalue. In the figures most of the points on the graph tend to level out that the eigenvalues were very close to zero and therefore the variables can be ignored.



4.1. Scree plot for pearl variety

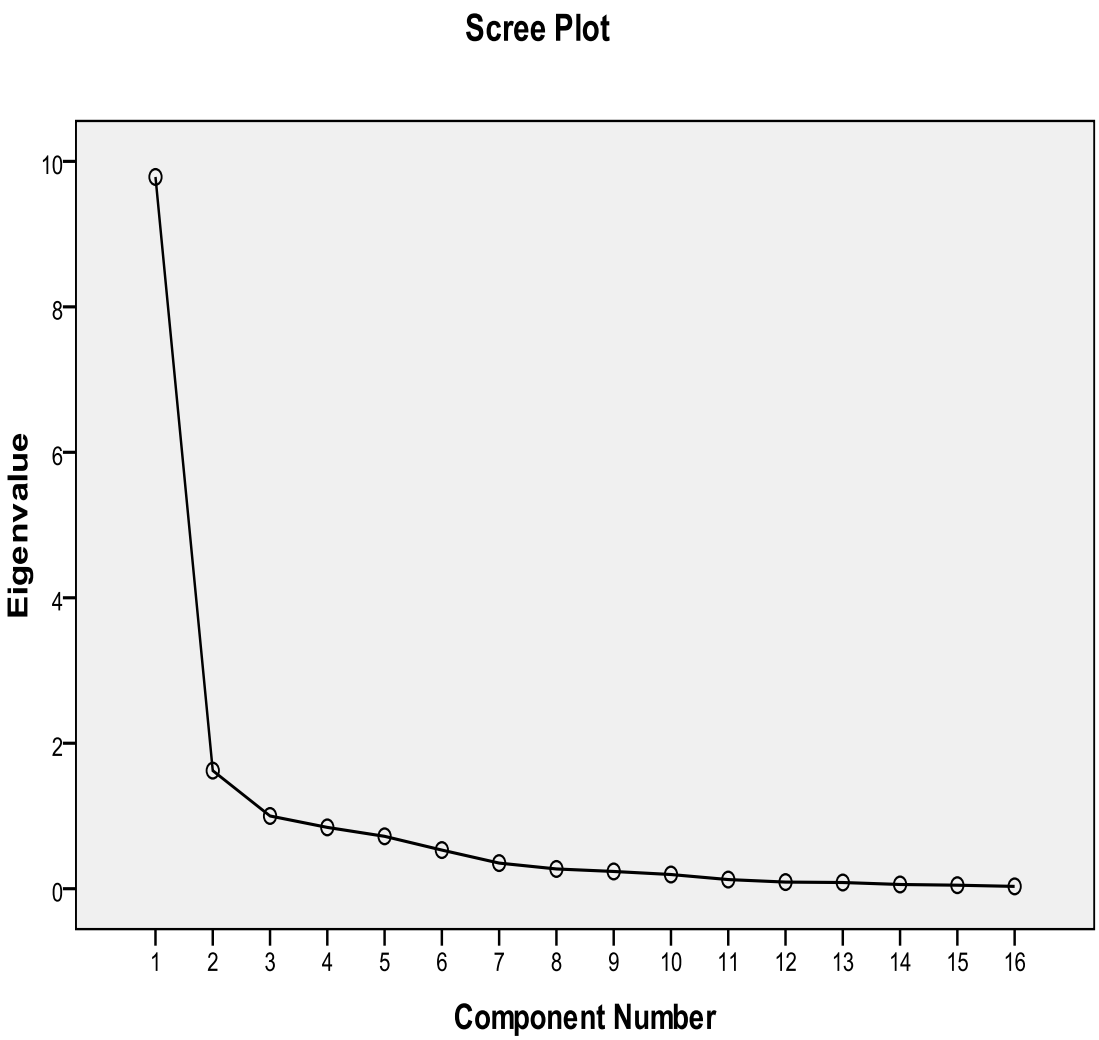


Fig 4.2. Scree plot for lavender variety

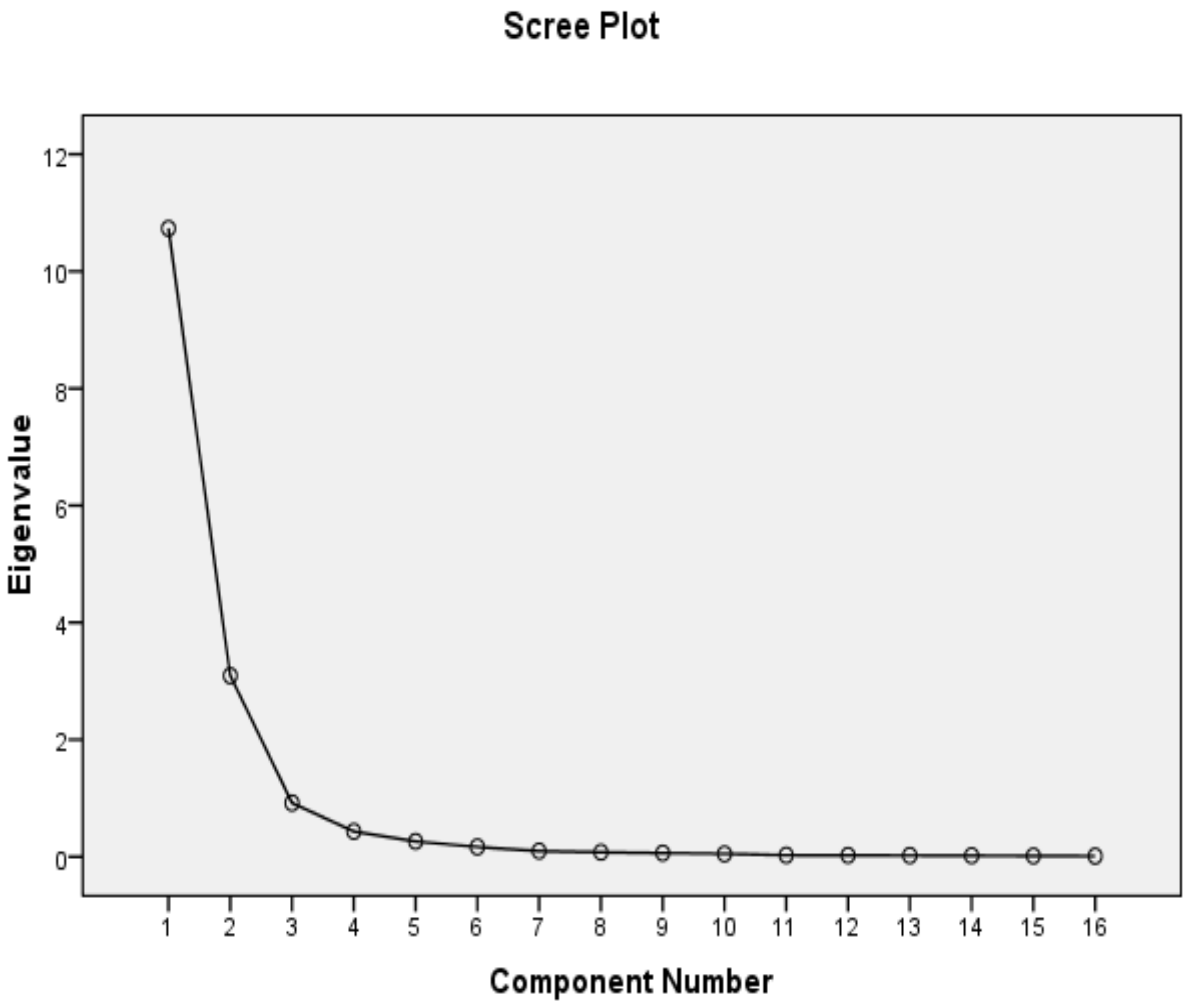


Fig 4.3. Scree plot for black variety

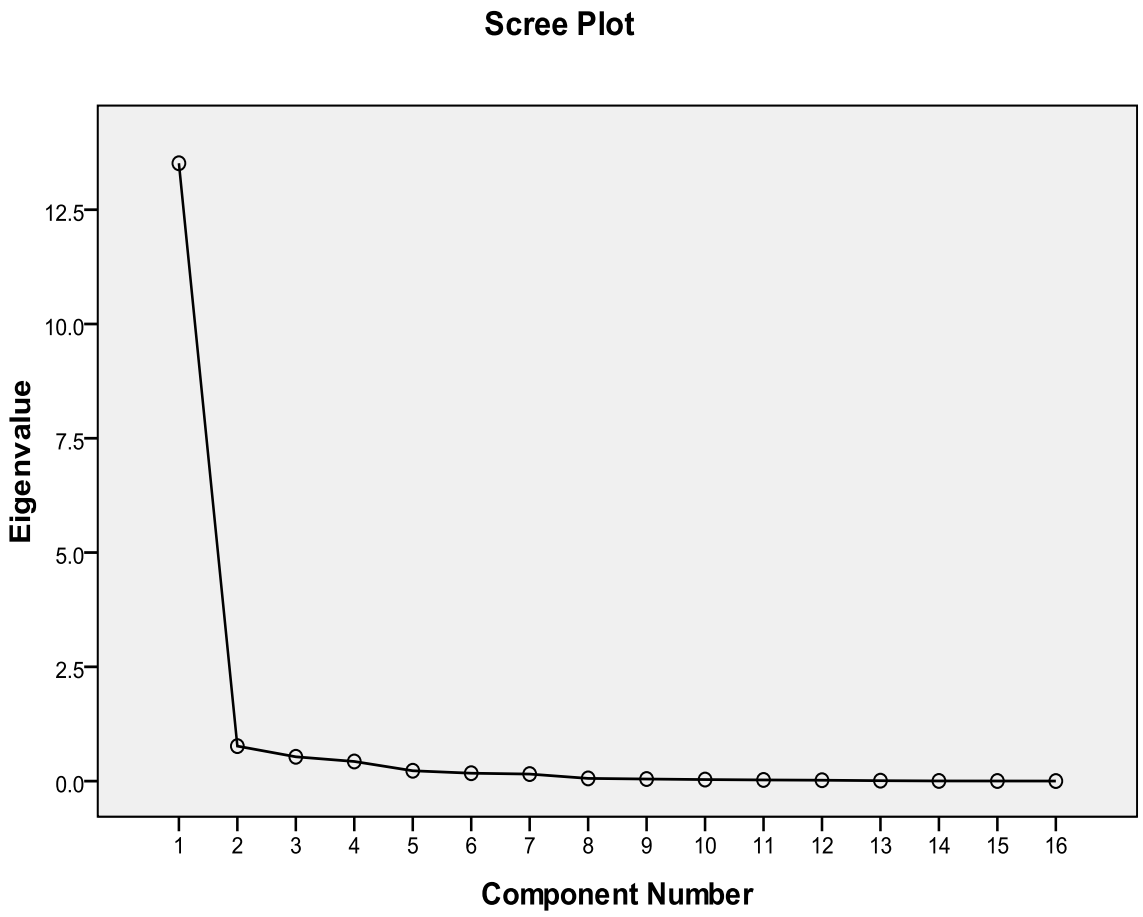


Fig 4.4. Scree plot for white variety

4.7. The Discriminants of body weight and body traits in Guinea fowl

The summary of stepwise selection among pearl, lavender, black and white varieties of Guinea fowl are presented in Table 4.8. In this study, 12 variables showed significant discrimination among the varieties. However, the most discriminating variables are: shank length, wing length and helmet width.

Table 4.10. Summary of stepwise selection among pearl, lavender, black and white varieties of Guinea fowl

Traits	Wilks' Lambda	F	Sig
SL	0.90	47.16	.00
WGL	0.66	149.99	.00
HW	0.57	64.06	.00
HT	0.50	68.91	.00
BL	0.47	20.87	.00
WL	0.46	12.91	.00
KL	0.45	11.48	.00
HL	0.43	10.44	.00
BW	0.42	6.97	.00
BC	0.41	6.51	.00
WW	0.41	4.21	.00
ST	0.41	2.38	.00

SL-Shank length, WLT- Wing Length, HW- Helmet Width, HT-Helmet Thickness, BL-Body length, WL-Wattle Length, KL-Keel Length, HL-Helmet Length, BW-Body weight, BC-Body Circumference, WW-wattle Width, ST-Shank Thickness

4.8. Morphological cluster analysis of the four varieties of Guinea fowl

The morphological parameters of the four varieties were used to generate a dendrogram by means of UPGMA cluster analysis as shown in Figures 4.5-4.8. Cluster analysis is an important approach to order genetic variability and relationships by using computer algorithms developed in the fields of multivariate statistics. The cluster analysis generated showed similarity coefficients which ranged from 0.45 to 0.85. The highest similarity index occurred between white and lavender varieties and between white and black varieties with a coefficient value of 0.85 and the lowest index of similarity occurred between black and white varieties with a coefficient value of 0.45. The detailed similarity index between black and pearl; white and lavender; lavender and pearl; white and black; black and lavender and white and pearl were 0.45, 0.85, 0.58, 0.85, 0.72 and 0.65 respectively as encapsulated in the figures below.

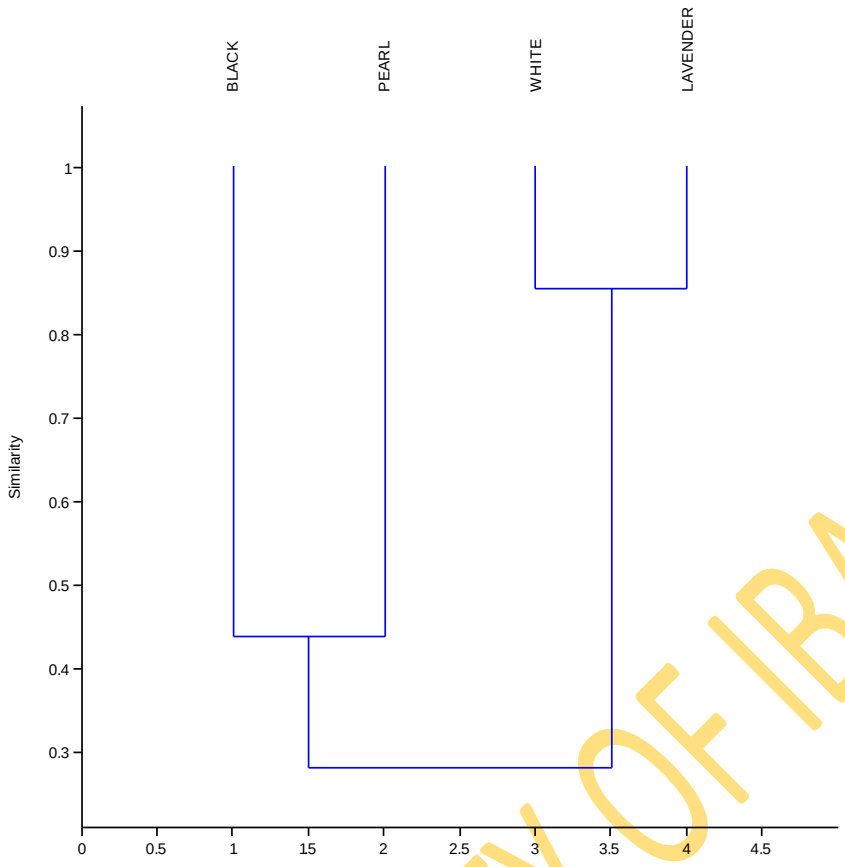


Fig. 4. 5. Cluster analysis of the morphometrical variables showing genetic relationship between black and pearl and between white and lavender varieties

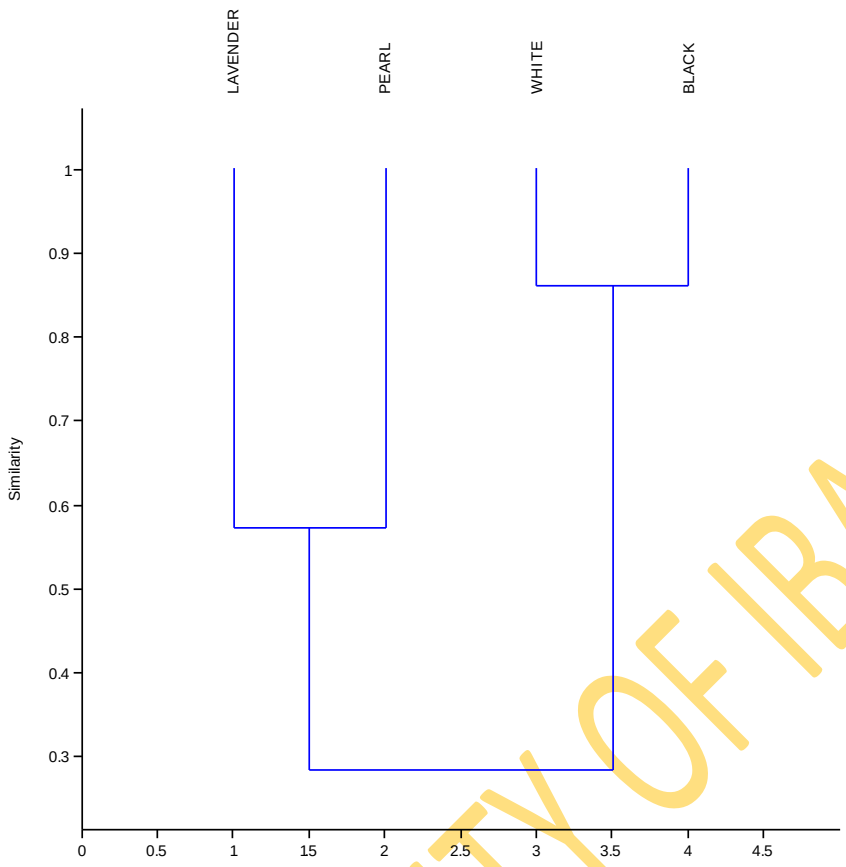


Fig 4. 6. Cluster analysis of the morphometrical variables showing genetic relationship between lavender and pearl varieties and between white and black varieties

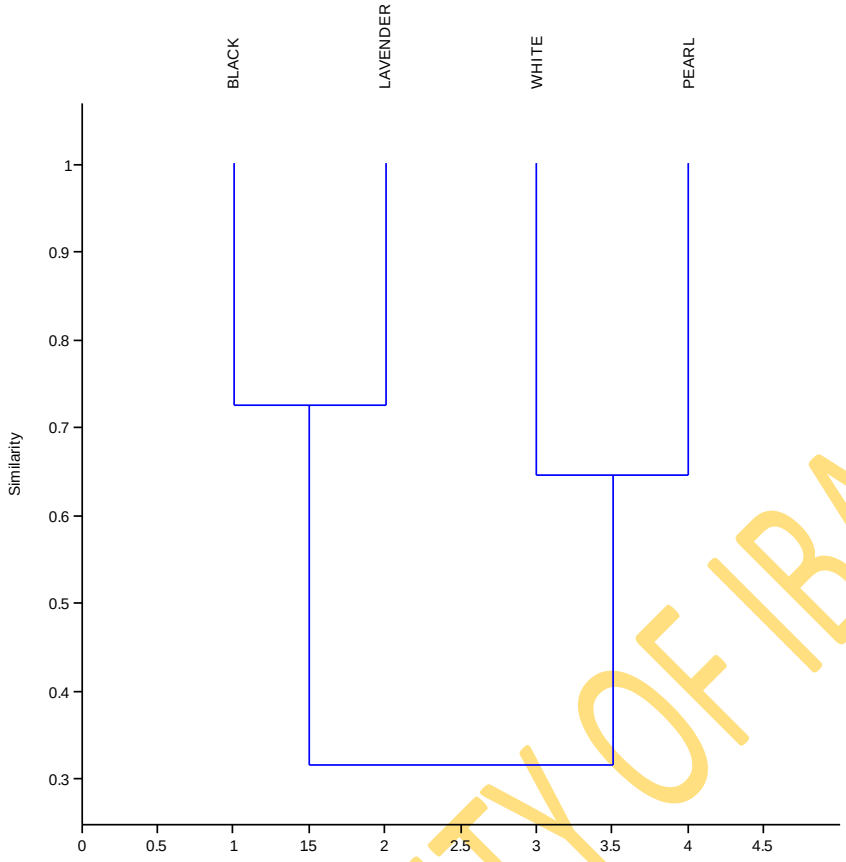


Fig 4.7. Cluster analysis of the morphometrical variables showing genetic relationship between black and lavender varieties and between white and pearl varieties

4.9. Genetic Distance determination

The Euclidean distance, a strong and broadly appropriate measure of genetic distance was used to calculate the distance among the varieties of guinea fowl. The result as presented in Table 4.16 showed white to be closest to black than the other varieties, with the genetic distance of 5.37. Pearl variety is closer to lavender than black and white varieties, with the distance of 15.82. The farthest genetic distance was between pearl and black (70.72) chronologically followed by pearl and white, lavender and white and lavender and black (55.02).

4.20. Euclidian Distance

Table 4.11: Genetic distances among the four varieties of Guinea fowls

	Pearl	Lavender	Black	White
Pearl	0.00	15.82	70.72	70.55
Lavender		0.00	55.02	57.77
Black			0.00	5.37
White				0.00

CHAPTER FIVE

5.0. DISCUSSION

5.1. Body weight

Body weight is a function of framework and condition of animals. It is an important attribute of farm animals as it forms the basis for not only assessing growth and feed efficiency but also in making economic decisions. It has been reported by Nwosu *et al*. (1985a) that live weight is the best parameter for making management, health, production and marketing decisions. The differences in the body weight as revealed in this study indicate inherent genetic constitution of each Guinea fowl variety. The variation in body weight could be quite useful for screening overall adaptive genetic diversity (Toro and Caballero, 2005).

The Mean bodyweights (kg) of 0.94±0.01, 0.93±0.01, 0.87±0.04 and 0.87±0.03 obtained for pearl, lavender, black and white varieties respectively in this study were similar to the values obtained for grey, blue, grey x blue, blue x grey and white x blue groups reported by Veicman (1969); 900 – 1020 g obtained by Oluyemi and Ogunmodede (1979) for female chickens in South Western Nigeria; Ayorinde and Okaeme, (1984) for adult body size of wild Guinea fowl and the values reported by Fajemilehin (2007) for pearl, ash/lavender and black varieties. However, the result on body weight obtained in this study were lower than the value of 1000- 1500g reported by Ayorinde (1999) for free ranging adult birds; 1175g reported for unselected Guinea fowl and1406 g for local Guinea fowls selected for body weight over three generations (Ayorinde and Oluyemi, 1991, Ayorinde, 1996); 1800 g for exotic breeds and the crosses of the breed with indigenous varieties and 1507 g for Pollastra guinea fowl imported from Galor and Pollastra x local selected guinea fowl (Ayorinde and Oluyemi, 1991, Ayorinde, 1996).

The value of 850 g obtained by Morathrop *et al*., (2007) for female decoy chickens in Upper North of Thailand corroborates the report of Ayorinde (2004) that the free ranging guinea fowls are slightly larger than the scavenging local chicken. The values obtained in this study lend further credence to the two assertions.

The variations between the results of this study and those reported by other authors could be attributed to differences in the genotype of the birds used, age of the birds, management practices employed, and differences in the environment where the researches took place and

a lot of other extraneous factors that are latent. These reasons are consistent with the observations of previous researchers who reported that variations in body weights of same animal species are mainly influenced by genotype (Ayorinde *et al.*, 1988; Culioli *et al.*, 1990 and Leterrier *et al.*, 1999) and age (Ayorinde *et al*., 1988; Mareko *et al.*, 2008; Porwal *et al.*, 2007; Pudyszak *et al.*, 2005 and Touraille *et al.*, 1981). In addition, the trait can be affected by diet composition (Ayorinde, 1989; Chiericato *et al.*, 2001; Frątczak *et al.*, 2002); Mazanowski *et al.*, 1982a and Mazanowski *et al.*, 1982b), housing system (Ayorinde and Ayeni 1986; Mareko *et al.*, 2006 and Mareko *et al.*, 2008), husbandry system (Baéza *et al.*, 2001 and Saina, 2005), environmental conditions (De Houx *et. al*, 1997 and Mareko *et al.* 2006) and sex (Baéza *et al.*, 2001; Mareko *et al.*, 2006 and Mazanowski *et al.*, 1982a, 1982b).

The low adult body weight obtained in this study could also be attributed to the birds used for this study which were obtained from the stock of small farm holders who most probably must have gathered them from the wild and kept them in the home stead for breeding purpose. In the wild, small body size is advantageous for the birds for rapid flight and fast running to escape predators and to struggle for feed. It is therefore not only that the indigenous stocks had not been selected for heavy adult body weight but had been selected against it because in the wild, the heavy ones are preyed over by predators most probably because they cannot run fast enough to avoid them and at the home stead, the fleshy ones are either slaughtered to entertain visitors or taken to market for sales in time of the slightest provocative need for money. The net effect is the availability of only the small-body-sized birds for breeding. It is therefore safe to conclude that the small body size characteristic of the indigenous birds is an adaptive feature to the environment for survival.

This is consistent with the report of Olawunmi (2008) who reported that the small body size of local chicken is important in reducing feed requirement for maintenance and increase feed efficiency in the tropics where the birds free range for limited feed resources in terms of quantity and quality and because no deliberate selection process had been embarked upon. The variations in the body weights in the four varieties suggests prospect of genetically improving the low body weight of the birds through systematic selection.

The coefficients of variation in body weight which ranged between 7.68 and 27.00 % across the varieties suggested absence of selection of this primary production trait. Generally, a high phenotypic variation of traits indicates a higher genetic variation which guarantees a sufficient selection opportunity. This is more so important because directional selection for morphological traits which commonly occurs in natural populations rarely operates on only one character at a time.

5.2. Head thickness, helmet length, helmet width, wattle length and wattle width

The variations in head thickness, helmet length, helmet width, wattle length and wattle width of the indigenous Guinea fowl with the pearl showing superiority in most of the traits as evidenced in this study. These variations are pointers to the prospect of genetically improving the adaptive features of the birds through selection. The values ranging between 0.126 - 0.160 for helmet length and 0.097 - 0.125 for helmet width in this study were considerably lower than the value of 3.2 cm and 2.0 cm reported by Ayorinde (2004) on the same trait, though he did not report the extent of selection on the birds on which the trait was measured. The wattle length 0f 0.149 – 0.208 cm obtained in this study was low compared with the value of 0.59 cm obtained by Bogale (2008) though in chicken.

In all these traits high coefficient of variations were recorded indicating that these traits were genetically sensitive. High coefficient of variation is a pointer to the capacity of an isolated allele to have more than one distinguishable effect (pleiotropic) on an organism.

5.3. Shank length, shank thickness, drumstick length, thigh length and wing length

The mean shank length, shank thickness, drumstick length, thigh length and wing length for pearl, lavender, black and white Guinea fowls recorded in this study were shorter compared to the values reported by Fajemilehin (2010). The differences recorded in these variables could be attributed to different management practices involved in the two studies. In the case of Fajemilehin (2010), the birds were reared intensively while birds in the present study were reared semi-intensively. The similarities in the shank lengths of three of the four varieties suggest similarity in the gene responsible for the shank length in these varieties. This is consistent with the findings of Ayorinde (2004) who reported that similarity of body parameters suggests similarity in the gene responsible for growth in animal species.

The shank length recorded in this study is similar to a length of 6.3 cm reported by Marathrop *et al.*, (2007) for female decoy in upper North of Thailand chickens but lower than the value of 8.14 cm reported by Halima, (2007) for Ethiopia indigenous chickens. The value recorded for Shank circumference in this study was higher than the value of 0.87 cm reported for indigenous chicken from Ethiopia (Halima, 2007).

The leg length of the ash and pearl varieties were longer than that of the black guinea fowls while the leg length of the white variety was longest. This is a pointer to the fact that the white variety has the potentials of fast growth rate than the other varieties suggesting that it is probably more suitable for higher body weight development. This assertion is consistent with the report of Maciejowski & Zieba, (1982) that rapid leg development is a criterion used for assessing growth rate.

The Wing lengths of 20.04 cm, 19.55 cm, 18.25 cm and 19.08 cm for pearl, lavender, black and white varieties of guinea fowl obtained in this study when compared with the values of 16.79 cm and 18.80 cm for mixed population of chicken by Fayeye *et al.*, (2006) and 57 – 15.88 cm by Bogale (2008) are longer. However, they are shorter than the values of 23.99 cm – 31 .01 cm reported for Muscovy ducks by Raji *et al*., (2009). Although guinea fowl is essentially a terrestrial bird, its characteristic large and strong wing confers on it a feature suited for rapid flight required to escape predators.

5.4. Body length, Keel length and Body circumference of pearl, lavender, black and white varieties of Guinea fowl

The mean Body length, Keel length and Body circumference obtained in this study for the four varieties of Guinea fowl were inferior to the values reported by Fajemilehin (2010) . The Keel length and the Body circumference taken around the chest region indicate breast development. Breast development is a good measure of meatiness in poultry. The Body length of the Guinea fowl (32.09 – 37.47 cm) reported in this study is much more than the value of 15.6 – 20.7 cm reported by Badubi *et al*., (2006) for indigenous chicken of Bostswana but much more inferior to the values of 45.51 – 59.25 cm reported by Raji *et. al*., (2009) for Muscovy ducks in Borno State, Nigeria.

It could be Inferred from long legs and wings and the compact shape of this bird in terms of short Body length and circumference, that the features required for survival in the wild or semi-wild life are still retained. Fajemilehin (2010) reasoned that the low body weight and body linear measurements of indigenous guinea fowl suggest that the indigenous Guinea fowls are the light strain types that are likely suitable for egg rather than for meat production.

The variability associated with the measurements in this study can be a reflection of little variation among actual ages of the birds sampled. Positive and highly significant ($P<0.01$) correlations among the measurements suggest high predictability among the measurements. It also suggests absence of selection in the birds, or the parts measured respond more to the environment than others

5.5. Body ratios and cranial indices

Comparison of the four varieties of Guinea fowl when their body parameters were standardized by division with Body weight did not show a definite pattern in all the varieties. Though there was no literature to discuss this result, it is important that the pattern might be considered as a base line for future studies on body ratios in the birds.

Body weight was corrected for body size using weight/ wing ratio. This, according to Owen and Cook (1977), gave a better indication of a bird's ability to meet its present and future energy requirements than using body weight alone. This is physiologically important because standard measures of metabolic activities are frequently expressed as a function of body size, and it is often useful to examine the relationship of structures or organs relative to overall body size (Blem, 1984). Metabolism is the set of life-sustaining chemical transformation within the cells of living organisms. These enzyme-catalyzed reactions allow organisms to grow and reproduce, maintain their structures, and respond to their environments. It can also refer to all chemical reactions that occur in living organisms, including digestion and the transport of substances into and between different cells. In the present study this index was found to be highest in black (7 %) than the other varieties (6%). The generally low metabolic value obtained in this study suggests that birds in arid environments, where primary productivity is low and surface water is scarce, have reduced energy expenditure. It is suggested that the black variety possesses higher metabolic rate which is capable of giving

the variety a competitive edge in feeding on abundant resources in highly competitive situations. On rarer resources, the metabolically more conservative varieties can support larger populations on a given amount of resource and expend less energy during the time spent looking for these rarer resources. This argument is extended to limited situations where the maintenance of adequate stocking rate through stress periods is crucial to the survival of a species. Because of their more conservative metabolic demands, the pearl, lavender and white varieties can achieve higher stocking rate on a given amount of resource and should be favoured over time.

Body weight, shank length ratio is an index of density (Melesse and Negesse, 2011). It is an indicator of degree of fleshing in relation to body size which usually increases with body size. The current study revealed that pearl and lavender varieties possessed better genetic potentials for table meat production under scavenging feeding system and the lower values obtained for black and white varieties suggest their suitability for egg production purpose. This assertion is in consonance with the findings of Melesse and Negesse, (2011) though in local chickens of Ethiopia.

The zero value reported for Body index using Body weight/Body length ratio in this study indicate that the birds are closer to being rectangular in shape and is indicative of better conformation for meat production (Cerqueira *et al.*, 2011). The low values between the ratios of Body weight and Keel lengths in the four varieties were indicative of the low massiveness and stockiness of the birds. Massiveness and stockiness which, are used to assess muscular development, are traits for solidity of the body and clearly defined traits for meat-type birds. In the present study, meatiness trait was best described in lavender (0.30± 0.01) chronologically followed by pearl (0.28± 0.01), black (0.27± 0.01) and white (0.26± 0.01) varieties using body weight and keel length ratio.

The cranial index which showed low values in all the varieties is of ethnological importance, particularly because its variation is not influenced by environmental factors and animal's management but by its genotype. In the individuals studied, the length of the head was predominant over the width, so much so that it can be classified as dolichocephalic. Based on their head structure, it can further be classified as mesocraniot (head width and length

similar). The result of the cranial index suggests that the different varieties of the birds are closely related and are well adapted to their environmental conditions.

5.6. Variation among body measurements

Data from this study demonstrated wide variations among body parameters. Correlation coefficients associated with all the traits measured in the pearl and white variety were highly and positively correlated ($P<0.01$) ranging from 55 to 95 % in pearl and 67 to 95 % in white variety. In the case of the lavender variety, very low, low, moderate and highly and positively correlated ($P<0.01$) coefficients of variation were observed among the assessed variables ranging from 7 to 94 %. Finally, the black variety revealed moderate to high values of coefficient of variation ranging from 29 to 96 %. The high correlation coefficients recorded in this study suggest that most of the traits measured were under the influence of same genes meaning that selection for an improvement of one trait may lead to a positive improvement in the other traits. This finding is in agreement with the work of Gueye *et al,* (1998) who reported that all significant values of correlation coefficients in matured Senegalese indigenous fowls were positive.

5.7. Body Weight and linear body measurements.

Correlation is the degree of relationship or association between or among variables. It is a measure of the degree to which variables vary together. It is a quantity having a value between -1 and 1. A negative correlation coefficient implies that an increase in one variable tends to be associated with a decrease in the other; while a positive correlation means that the values of both variables rise or fall together. The magnitude (high or low) of the correlation coefficients is an indication of how closely linear the variables are. In the present study, highly positive relationships among the traits measured were recorded. This suggests that the traits affected are likely to be under the effect of same gene action. This finding is in consonance with the report obtained by Ngapongora *et al*. (2004) and Ogah *et al*. (2009); Hassan and Adamu (1997) in indigenous pigeons. They observed that body length as well as chest width were strongly and significantly correlated to body weight.

Gueye *et al.* (1998) noted that all significant values of correlation coefficients were found to be positive in matured Senegalese indigenous fowls. Similarly the result of this study agree with the report of Tamer *et al*, (2011) who noted that correlation coefficients between live weights and body measurements in the rock partridge (*Alectoris graeca*) ranged from 0.016 to 0.832. He reported highest correlation coefficient (0.832) between live weight and shank width, whilst the lowest correlation coefficient (0.016) was between live weight and head length. Also, a positive and significant correlation was obtained between live weight and body measurements by Yang *et al.* (2006) in chickens; Raji *et al*. (2009) in Muscovy ducks; Saatci and Tilki (2007) in native geese ($p<0.01$), and Saatci (2008) in geese ($p<0.01$). However, the result of this study contradicts the report of Sheila *et al.*, (2009) who investigated the relationship of body weight to external body measurements such as body length, thoracic girth, abdominal girth, tibiotarsal, tarsometatarsal, wing length, and height from ground to the top of the back in adult fighting cocks and found that the correlation analysis showed a weak relationship between body weight and external body measurements.

5.8. Principal component analysis (PCA)

Principal component analysis (PCA) is a mathematical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal component. The number of principal components is less than or equal to the number of original variables. This transformation is defined in such a way that the first principal component has the largest possible variance (that is, accounts for as much of the variability in the data as possible), and each succeeding component in turn has the highest variance possible under the constraint that it be orthogonal to (i.e., uncorrelated with) the preceding components. PCA is the simplest of the true Eigen vector-based multivariate analyses. Often, its operation can be thought of as revealing the internal structure of the data in a way that best explains the variance in the data. Principal components are guaranteed to be independent only if the data set is jointly normally distributed.

In this study, Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (0. 95) revealed the proportion of the variance in the body measurements of pearl variety caused by the underlying factor and the Bartlett's test of sphericity (P<0.01), communalities (0.46-0.94), which is the explained variance together with the determinant (2.24E-013) obtained from the correlation matrix permitted all body measurements into reasonable factor analysis-PCA. After a high promax rotation (>0.5) of the component matrix, two principal components were yielded by the factor solution as presented in table 3.7. The first principal component explained 73.38 % of the generalized variance in the body measurements giving nearly equal emphasis to each body measurement (0.89-0.97) except Shank circumference and Drumstick length which gave emphases of 0.54 and 0.71 respectively. These can be considered as generalized size factors. The second principal component explained only 7.81 % of the generalized variance.

Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (0.91) revealing the proportion of the variance in the body measurements of lavender variety caused by the underlying factor and the Bartlett's test of sphericity (P<0.01), communalities (0.42-0.92), which is the explained variance together with the determinant (1.98E-009) obtained from the correlation matrix permitted all body measurements into reasonable factor analysis-PCA. After a high promax rotation (>0.5) of the component matrix, three principal components were yielded by the factor solution as presented in table 3.8. The first principal component comprising fourteen measurements (Body weight, Head circumference, Head thickness, Helmet length, Helmet width, Wattle length, Wattle width, Body length, Keel length, Body circumference, Shank length, Shank thickness, Shank circumference and Wing length) explained 61.16 % of the generalized variance in the body measurements giving nearly equal emphasis to each body measurement (0.64-0.91). Drumstick length and Thigh length gave emphases of 0.34 and 0.41 respectively. These can be considered as generalized size factors. The second and third principal components explained only 10.15 % and 6.25 % of the generalized variances respectively.

Clearly, two major underlying factors are responsible for the observed clusters (Table 3.6). These may be related to the different association of each measurement with bone,

environmental components or the time taken to reach maturity. These in turn will be expected to change with time. More importantly, the elements present in each cluster probably have common genomic sites for their genetic control. In other words, pleiotropic is likely implicated.

Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (0.89) revealing the proportion of the variance in the body measurements of black variety caused by the underlying factor and the Bartlett's test of sphericity (P<0.01), communalities (0.73-0.94), which is the explained variance together with the determinant (4.25E-016) obtained from the correlation matrix permitted all body measurements into reasonable factor analysis-PCA. After a high promax rotation (>0.5) of the component matrix, two principal components were yielded by the factor solution as presented in table 3.9. The first principal component comprising fourteen measurements (Body weight, Head circumference, Head thickness, Helmet length, Helmet width, Wattle length, Wattle width, Body length, Keel length, Body circumference, Shank length, Shank thickness, Shank circumference and Wing length) explained 67.09 % of the generalized variance in the body measurements giving nearly equal emphasis to each body measurement (0.73-0.89). These can be considered as generalized size factors. The second principal component explained only 19.30 % of the generalized variances.

Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (0.95) revealing the proportion of the variance in the body measurements of white variety caused by the underlying factor and the Bartlett's test of sphericity (P<0.01), communalities (0.54-0.93), which is the explained variance together with the determinant (2.24E-013) obtained from the correlation matrix permitted all body measurements into reasonable factor analysis-PCA. After a high promax rotation (>0.5) of the component matrix, one principal component was yielded by the factor solution as presented in table 3.10. The only principal component comprising fourteen measurements (Body weight, Head circumference, Head thickness, Helmet length, Helmet width, Wattle length, Wattle width, Body length, Keel length, Body circumference, Shank length, Shank thickness, Shank circumference and Wing length) explained 84.48 % of the generalized variance in the body measurements giving nearly equal emphasis to each body measurement (0.85-0.97).

The results may be related to the different associations of each measurement with bone, environmental components or the time taken to reach maturity. These in turn will be expected to change with time. More importantly, the elements present in each cluster probably have common genomic sites for their genetic control. In other words, pleiotropic is likely implicated.

5.9. Discriminant and morphological cluster analyses

Discriminant analysis is one of the most promising tools for predicting and solving problems of discriminating between groups. In this study, twelve (12) of the measured variables were found to show significant discrimination among the varieties ($P<0.01$). However, the most discriminating variables are: shank length and wing length. Two other variables namely the drumstick length and thigh length not fitted to enter the model were removed. The implication of this result is that taking these two basic measurements (shank and wing lengths) consistently could be more important in differentiating between the four varieties than acquiring numerous additional measurements. The reduction in the number of measurements saves time and energy required to distinguish between the varieties. No literature was available for comparisons in the variety discriminants, however, the use of discriminants analysis has been successfully used to differentiate within and between livestock breeds (Jordan *et al*. 1993 and Herrera *et al*. 1996).

The result of this study thus showed close similarities (85 %) between the pairs of white and lavender and white and black. The black and lavender are 72 % similar; white and pearl 65 % similar; lavender and pearl 58 % similar and black and white 45 % similar.

5.10. Genetic Distance

Genetic distance is the extent of genomic difference among and within breeds that is measured by some numerical quantity. Genetic differences between varieties and populations are controlled by mutation, genetic drift, selection and migration (Eding and Laval, 1999). Therefore, the evaluation of guinea fowl populations as genetic resources includes the determinations of genetic distance between the available populations. In this study a distance of 15.82, 70.72, 70.55, 55.02, 57.77 and 5.37 was obtained between pearl/lavender,

pearl/black, pearl/white, lavender/black, lavender/white and black/white varieties respectively. The low genetic distance obtained in the pairs of pearl/lavender and black/white indicates little genetic effects of drifts or mutation. It also reflects that these populations are not genetically isolated from each other. However, the high genetic distance between the pairs of pearl/black and pearl/white implies high levels of genetic flow among the varieties resulting in admixed populations.

The greatest genetic distance observed in this study between pearl and black suggests that an appreciable heterosis, especially with regard to most body traits which are of economic importance can be obtained by crossing the two varieties. This is in line with the report of Sharp (1987) that potential gains from crossbreeding which is now widely utilized for animal improvement, may be related to the genetic distance between the populations utilized.

CHAPTER SIX

6.0. BIOCHEMICAL VARIATION IN PEARL, LAVENDER, BLACK AND WHITE GUINEA FOWL VARIETIES

6.1. Introduction

Genetic variation offers opportunity for improving animal species. These variations can be assessed at three principal levels viz-a-vis morphological, protein and molecular. While morphological variations underestimate the true level of genetic variation or genetic diversity of any animal species, the other two are more resolute in determining these variations. Allozyme characteristics of an animal species depict monomorphic or polymorphic nature of the protein or enzyme in question. Biochemical diversity prevalently described as biochemical polymorphism is the occurrence of protein/enzyme variants attributed to biochemical difference, which are under genetic control. A population is said to exhibit genetic polymorphism when two or more distinct inherited variants co-existed in the same individuals. A genetic character is known to be polymorphic when the rarest phenotype has a frequency greater than one percent (Des and Dab, 2008). Gene-controlled-biochemical-polymorphism identified so far has motivated many discussions as touching its derivation/source, preservation and maintenance of heterozygosity. However, it is widely believed that the equilibrium between the adaptive values of dissimilar gene types under varying environments would be responsible for its maintenance.

Biochemical characterization of blood proteins as a useful tool in measuring genetic differentiation in domestic animals had been reported in sheep (Di Stasio, 1997) and in chicken (Lee *et al.*, 2000 and Esmaeilkhanian *et al.*, 2000). Its importance in genetic improvement of livestock because of its association with economic traits had been documented (Braend, 1971 Rendel, 1967; Vicovan and Rascue, 1989 and Charon *et al*., 1996). Its usefulness in the study of genetic relationship among livestock breeds had also been documented (Esharatkhah *et al*., 2007; Ibeagha-Awemu and Erhardt, 2004, Mwacharo *et al*., 2002).

It is therefore the objective of this study to analyze and document the genetic variations at haemoglobin, transfferin and carbonic anhydrase loci in pearl, lavender, black and white helmeted Guinea fowls and to estimate the genetic relationships of the varieties.

6.2.0. LABORATORY PROCEDURES

6.2.1. CELLULOSE ACETATE ELECTROPHORETIC ANALYSIS

6.2.2. Sampling

A total of two hundred visually healthy birds comprising fifty pearl, fifty lavender, fifty black and fifty white varieties were randomly selected from smallholders in Balle, Bodinga, Sokoto, Shagari, Goronyo, and Illela villages for the biochemical evaluation.

6.2.3. Equipment and background information

The Cellulose Acetate Electrophoresis was carried out using the Gallenkamp Model JY-SP7 Electrophoretic equipment at the Genetics Laboratory of the Department of Animal Science, University of Ibadan. The theoretical principle behind the protocol is that all organisms will produce multiple forms of some allozymes and all diploid organisms have two alleles at each locus.

6.2.4. Blood collection

Five millilitres (5mL) of blood was drawn from each of the birds by wing venipuncture using needle and syringe. The drawn blood was dispensed into heparinized tubes to prevent coagulation. The blood samples collected were refrigerated.

6.2.5. Samples preparations

The erythrocytes and the plasma fractions of the blood samples were separated by centrifuging at 2500-3000 rpm at 4^0c for 10mins.

6.2.6. Preparation of Blood haemolysates

Red blood cells were prepared from the erythrocytes fraction of the heparinized blood by centrifuging at 2500-3000rpm for 10 minutes at 4^0c. The RBCs were washed in saline (0.155m NaCl) three times and centrifuged at 2500-3000rpm for 5 minutes at 4^0c. The RBCs were then dissolved with a fourfold volume of distilled water to release haemoglobin. The

red blood cells were used to determine the genetic variants in haemoglobin and carbonic anhydrase.

6.2.7. Plasma

The plasma fraction was separated from the erythrocytes fraction of the heparinised blood by centrifugation at 2500-3000rpm for 10 minutes at 4^0c. The liquid remaining above the solid called the supernatant was used to determine the genetic variants in transferrin.

6.3. Procedures of Electrophoresis

6.3.1. Gel Soaking

A continuous buffer system whereby the Cellulose acetate plates and filter paper were soaked in the same buffer as the electrode buffer was employed in this study. The soaked filter paper serves as a bridge between the electrode and the loaded Cellulose acetate paper. Multiple gel were concurrently soaked in a 800ml capacity beaker with each gel plate separated by glass rods to ensure complete soaking of every plate. The plates were submerged at a slow and constant rate into the gel plate to prevent formation of bubbles on the gel plate. The soaking lasted for twenty five minutes

6.3.2. Sample loading

Prepared blood samples were added into the wells of the sample plates. The soaked Cellulose Acetate plate was blotted dry between two sheets of filter papers to remove excess moisture. Caution was taken to ensure that the Cellulose Acetate paper did not shift when the samples were loaded. To prevent movement, the aligning plate was moistened with a drop of gel buffer before the Cellulose Acetate plate was set on it. The plate was also centred on the aligning base to ensure that all samples were applied. Using the applicator, samples were applied twice to the same position on the plates. Once loaded, plates are rested on the wicks in the tank (without current been applied) while subsequent plates are loaded. The teeth of the applicator were blotted each time before other applications were made.

6.3.3. Gel running

The side bearing the cellulose acetate was placed on the wick that had already been wedged with glass side to prevent the paper from shifting. Care was taken to prevent the loaded zone

on the paper to touch the wick. For haemoglobin and transfferin, the loaded zones were positioned at the cathodal end of the tank to run since current runs from negative to positive while the zone loaded with carbonic anhydrase was positioned anodally since in its own case, current flow from positive to negative.

6.3.4. Gel staining

On completion of the gel run, the plate was removed from the tank and placed in an empty petri-dish to effect staining. Here, caution was taken to ensure that the Cellulose Acetate plate lies horizontally. Once plates have been removed from the tank, they were stained with Ponceau stain before they dry out.

6.3.5. Gel scoring

After twenty minutes, the plate was sufficiently stained. Thereafter, the plate was destained several times until it was clear and sharp bands appear. The bands were scored visually based on their migratory patterns as described by RIKEN (2006).

6.4. Electrophoretic conditions

The method employed in this study was as described by RIKEN (2006) as shown in Table 6.1

Table 6.1: Electrophoretic conditions

	BUFFER	TIME (mins)	pH	VOLTAGE	STAIN
Haemoglobin	Tris-EDTA - borate	40	8.4	350	Ponceau
Carbonic anhydrase	EDTA sodium acetate	45	5.6	200	Ponceau
Transferrin	Tris glycine	15	8.5	150	Ponceau

6.5. Estimation of gene and genotype frequencies

Direct counting was used for calculating genotypic frequencies and gene frequencies were calculated from it using the expression provided by Roughgarden (1977) as follows:

$$P = \frac{2(N_{xx}) + N_{xy}}{2N} \qquad Q = \frac{2(N_{yy}) + N_{xy}}{2N}$$

Where Q = allele frequency of allele y, Q = allele frequency of allele y, N = total number of individual, N_{xx} = observed genotype from xx, N_{xy} = observed genotype from xy, = N_{yy} = observed genotype fro yy

Genotypic frequency was prepared using the formular below:

$$\frac{\text{Number of xx or xy or yy x 100}}{\text{Total number of individual}}$$

PAST software package (PAleontological STatistics) (Hammer *et al.*, 2001) was used to analyse data obtained from the electrophoretic analysis to generate dendograms at each of the loci investigated.

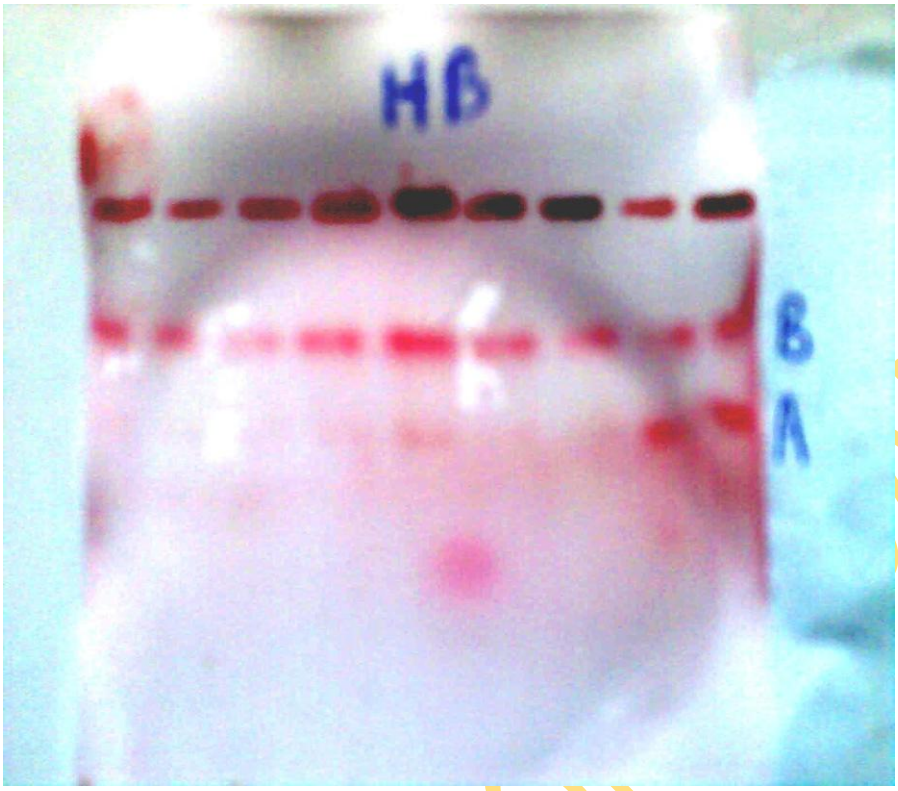


Plate 6.1: Electropherogram showing migration of haemoglobin genetic types on cellulose Acetate gel

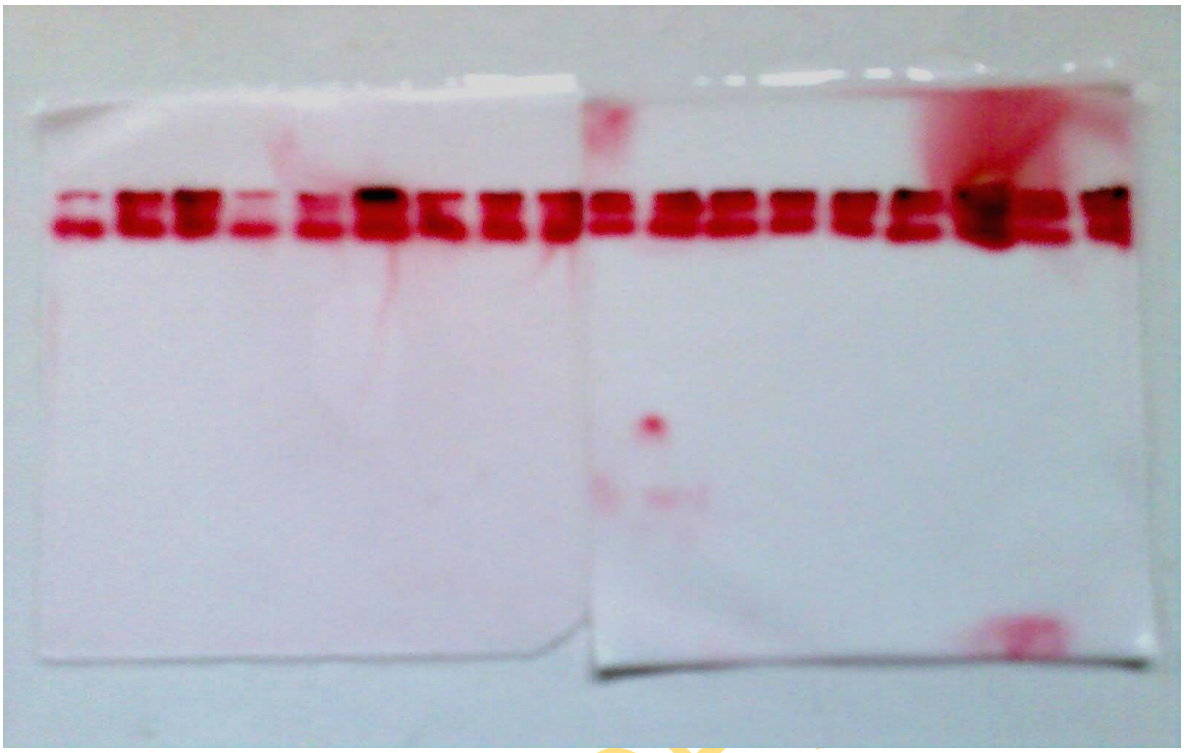


Plate 6.2: Electropherogram showing migration of Caebonic anhydrase genetic types on cellulose Acetate gel

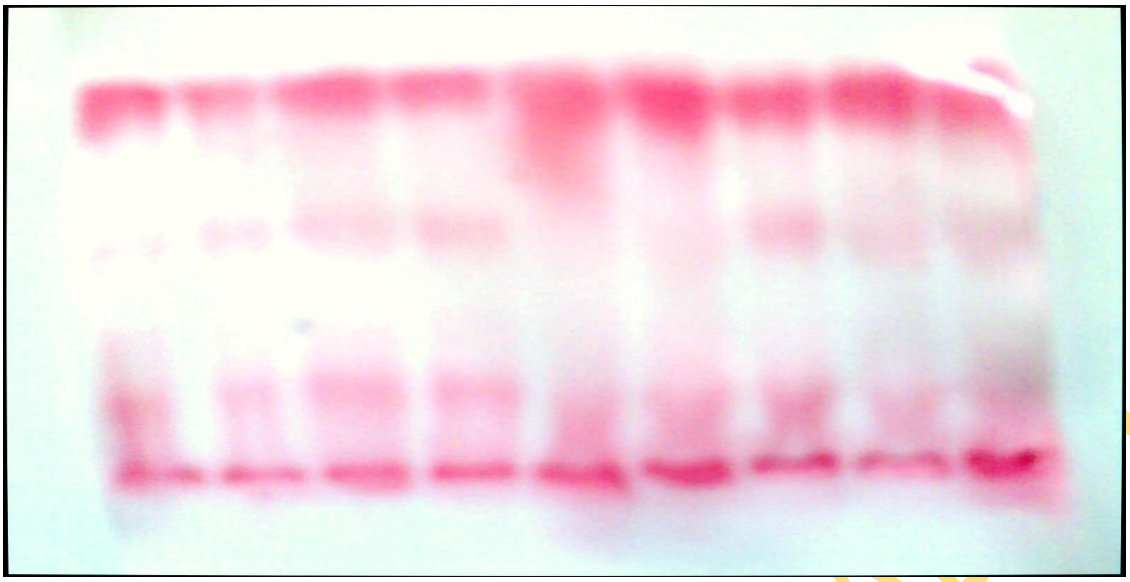


Plate 6.3.: Electropherogram showing migration of transfferin genetic types on cellulose Acetate gel

CHAPTER SEVEN

7.0. RESULTS

7.1. Genotypes and allele frequencies at haemoglobin, transferrin and carbonic anhydrase loci

Tables 7.1-7.3 show the genotype and allele frequencies of the four varieties of Guinea fowl.. The table revealed that the allele frequencies of Haemoglobin A and B in pearl, lavender, black and white varieties were 0.96 and 0.04, 0.95 and 0.05, 0.96 and 0.04 and 0.95 and 0.05, respectively. The frequency of Haemoglobin A was higher than for Haemoglobin B in all the varieties. Two genotypes were noticed in each of the four varieties at haemoglobin locus. HbAA and HbBB were found in pearl and black varieties, while HbAA and HbAB were found in the lavender and white varieties. Transferrin and Carbonic anhydrase were monotypic in all the varieties.

Table 7.1: Genotype and gene frequencies at haemoglobin locus in the four varieties of Guinea fowl

		Genotype frequency						Gene frequency	
Varieties	Number	HbAA	%	HbAB	%	HbBB	%	A	B
Pearl	50	48	96	-	-	2	4	0.96	0.04
Lavender	50	45	90	05	10	-	-	0.95	0.05
Black	50	48	96	-	-	2	4	0.96	0.04
White	50	45	90	05	10	-	-	0.95	0.05

Table 7.2: Genotype and gene frequencies at transferrin locus in the four varieties of Guinea fowl

	Genotype frequency			Gene frequency	
Varieties	Number	TfAA	%	A	B
Pearl	50	50	100	1.000	-
Lavender	50	50	100	1.000	-
Black	50	50	100	1.000	-
White	50	50	100	1.000	-

Table 7.3: Genotypes and gene frequencies at Carbonic anhydrase locus in the four varieties of Guinea fowl

	Genotype frequency			Gene frequency	
Varieties	Number	F	%	F	S
Pearl	50	100	100	1.000	-
Lavender	50	100	100	1.000	-
Black	50	100	100	1.000	-
White	50	100	100	1.000	-

7.2. Test of Hardy-Weinberg equilibrium at haemoglobin locus.

Tables 7.4 showed the Chi-squared test of haemoglobin phenotype in the Guinea fowl varieties under study. The table revealed that the Chi-squared (χ^2) values showed departure from Hardy-Weinberg's Equilibrium in pearl (χ^2=62.0), lavender (χ^2=66.0), black (χ^2=39.0) and white (χ^2=39.0) varieties suggesting that the samples studied deviated significantly from Hardy-Weinberg theory.

Table 7.4: The Chi-squared statistics at haemoglobin locus of the four varieties of indigenous Guinea fowl.

	Genotypes	Observed (O)	Expected (E)	$(O-E)^2/E$	HWE Chi-squared values	p-value
Pearl	AA/AB	48	37.50	2.940	62.02	0.00
	BB	02	12.50	8.820		
Lavender	AA/AB	50	37.50	4.167	66.02	0.00
	BB	00	12.50	12.500		
Black	AA/AB	48	37.50	2.940	39.03	0.00
	BB	02	12.50	8.820		
White	AA/AB	50	37.50	4.167	39.03	0.00
	BB	00	12.50	12.500		

7.3. Test of heterozygosity at haemoglobin, transferrin and carbonic anhydrase loci

Table 7.5 showed the degree of heterozygosity at haemoglobin, transferrin and carbonic anhydrase loci.

Table 7.5: Summary of heterozygosity at haemoglobin, Transferrin and Carbonic Anhyrase loci of the four varieties of indigenous Guinea fowl.

	Sample size	Observed heterozygosity	Expected heterozygosity	Nei value	Average heterozygosity
Haemoglobin locus					
Pearl	50	00	37.50	0.08	0.09
Lavender	50	05	37.50	0.08	0.09
Black	50	00	37.50	0.10	0.09
White	50	05	37.50	0.10	0.09
Transferrin locus					
Pearl	50	00	37.50	0.00	0.00
Lavender	50	00	37.50	0.00	0.00
Black	50	00	37.50	0.00	0.00
White	50	00	37.50	0.00	0.00
Carbonic anhydrase locus					
Pearl	50	00	37.50	0.00	0.00
Lavender	50	00	37.50	0.00	0.00
Black	50	00	37.50	0.00	0.00
White	50	00	37.50	0.00	0.00

7.4. Cluster Analysis

Figures 4.1 – 4.3 show the cluster analyses at the three loci investigated. At the haemoglobin locus, the black and the lavender/ash are absolutely the same with similarity index of "1" while the white and the pearl are 0.91 similar. The similarity between the two pair is 0.85. At the transferrin and Carbonic Anhydrase loci, the four varieties have similarity index of 0.50.

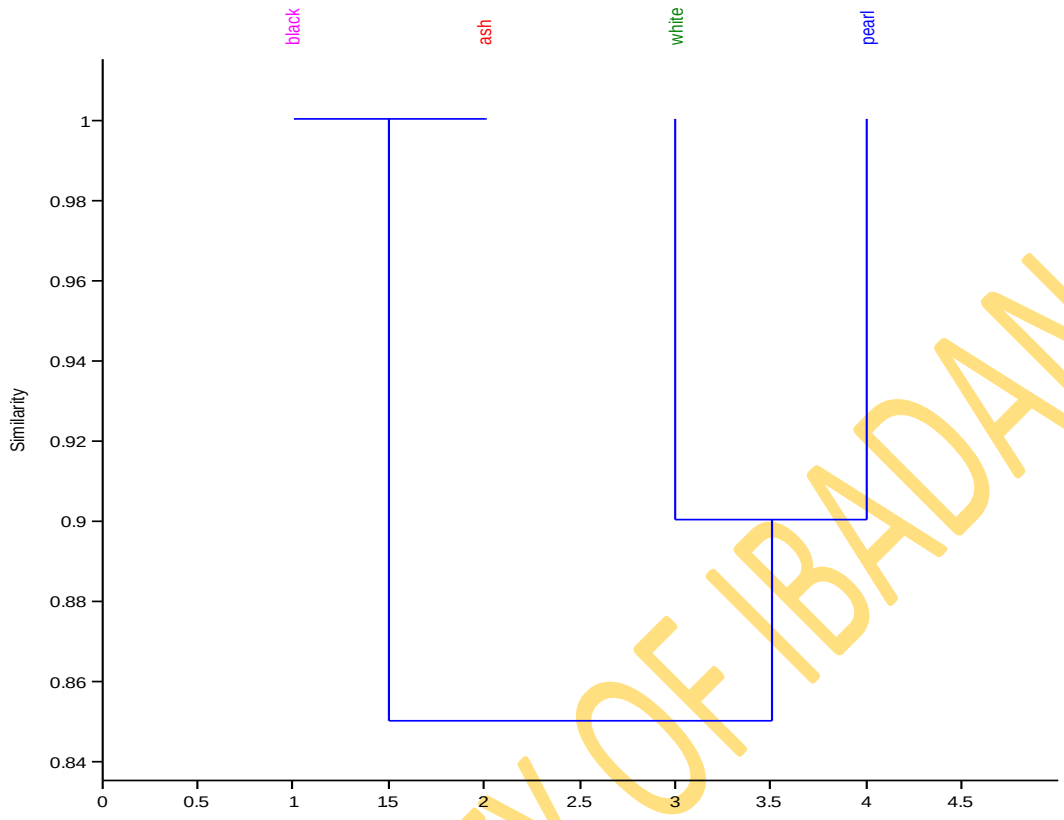


Fig. 7. 1: Cluster analysis of the biochemical variables showing genetic relationship among the varieties at haemoglobin locus

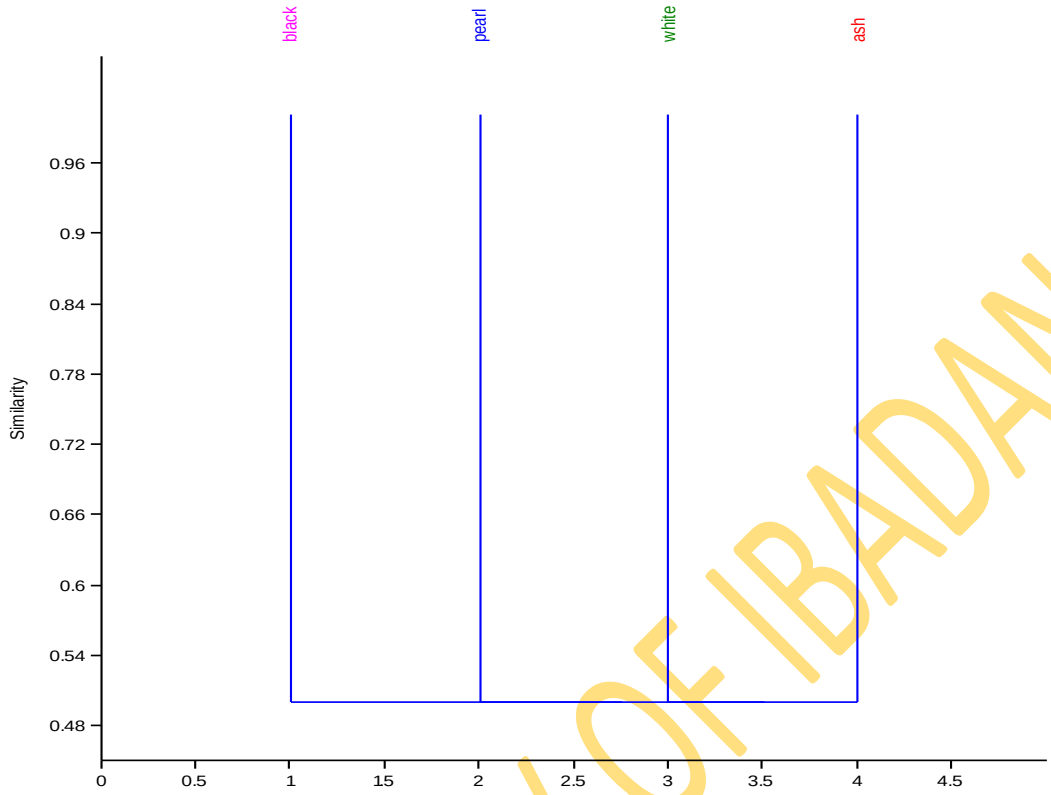


Fig.7. 2: Cluster analysis of the biochemical variables showing genetic relationship among the varieties at transferrin locus

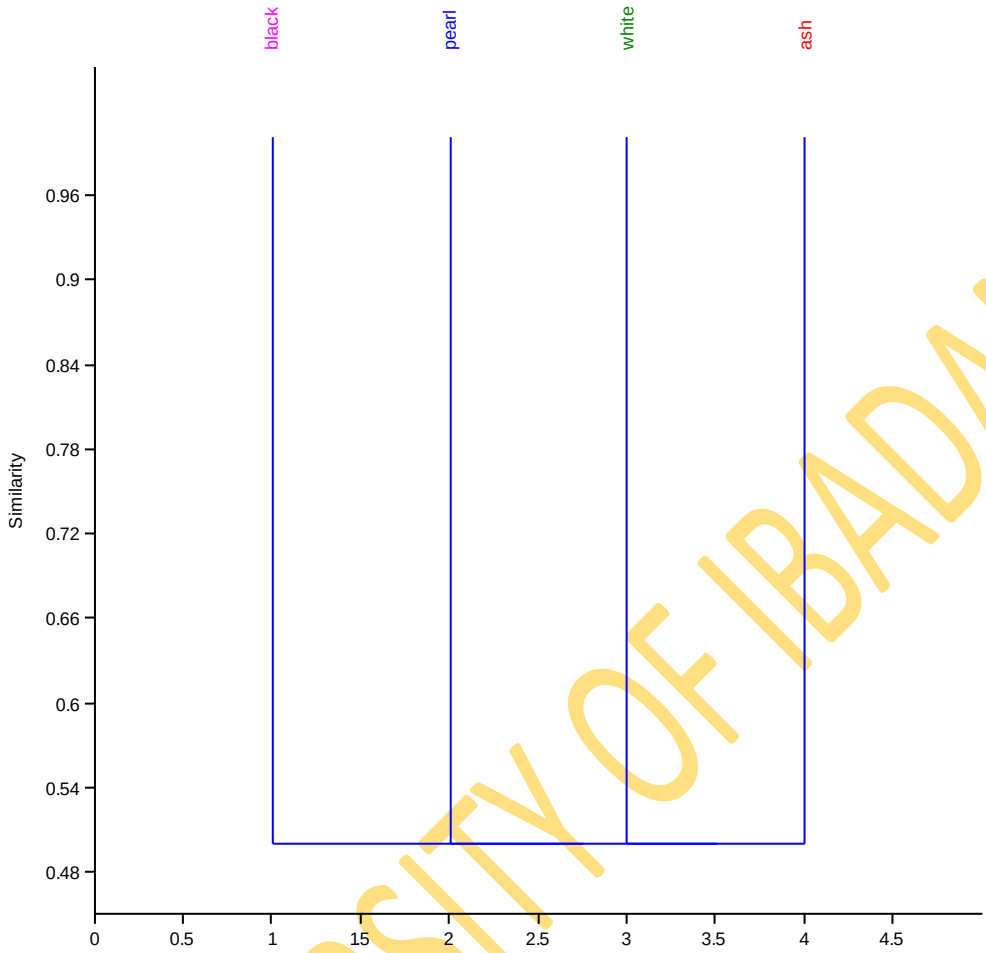


Fig.7.3: Cluster analysis of the biochemical variables showing genetic relationship among the varieties at carbonic anhydrase locus

CHAPTER EIGHT

8.0. Discussion

8.1. Haemogiobin

Livestock breeds and populations are characterized using genetically controlled biochemical polymorphisms of blood proteins and fortunately most of these blood protein are genetically controlled by allelic series which have dominance or co-dominance effect. This marker has been extensively used for documenting genetic diversities of different populations (Washburn *et al*., 1971, Dimri,1978, Mazumder *et al.*, 1989, Lee *et al*., 2000, Salako and Ige, 2006, Das and Deb, 2008). It had been stressed that the most important application of genetic polymorphism is in genetic improvement through loci affecting quantitative traits. Haemoglobin is the principal molecule for transport of carbon dioxide in blood. Although enough literature were not found on this subject but reports close to it in the poultry world were used. The reports of several workers have identified three types of haemoglobin which are controlled by two autosomal alleles A and B (Dimri, 1978 in Indian native chickens, Mazumder *et al*., 1989 in white leghorn chickens and quails, Lee *et al*., 2000 in Korea native chicken, Salako and Ige, 2006 in Nigeria mixed population of indigenous chicken and Ajayi *et al.*, 2013 in indigenous chicken in the Niger Delta region of Nigeria). Similar results were observed in the four populations studied. Mazumder and Mazunder (1989) reported that the frequency of the normal haemoglobin gene of guinea fowl is fixed and reported similar complete gene fixation in broiler and local fowl in India. Also, Nordlong (1981) reported complete gene fixation for haemoglobin in inbred line of chickens. The two results contradict the result of the present study as frequency of HbA were 0.95, 0.90, 0.95 and 0.90 while frequency of HbB were 0.05, 0.10, 0.50 and 0.10 in pearl, lavender, black and white varieties respectively. It is significant to note that in the present study, the frequencies of HbA allele predominated over the HbB allele in the four populations. The divergence in results obtained from this study and the result of Nordlong (1981) is that while in the latter case intensive selection through inbreeding which favoured homozygosity had taken place; in the later no selection has taken place at all. It is therefore safe to ascribe the differences obtained in these studies to differences in the genetic conditions of the species. In chickens, it had been demonstrated that Hb AA has a higher O_2 affirmably than Hb BB (Huisman, 1996); that the

homozygous mutant haemoglobin genotypes were approximately 20% less susceptible to Marek's disease (Washburn *et al*., 1971); that Hb genotypes affect growth rate and hatchability (Dimri *et al.* 1981). Hatchability was reported to be highest in AA (62.20%) followed by AB (48.20%) and BB (31.50%) genotypes. This advantage, particularly in area of hatchability should be explored in guinea fowl as it has poor hatchability features. Pattern of cluster at this locus grouped black and lavender/ash on one part and white and pearl on the side suggesting that genetically, for traits for which Hb is a marker, the similar black or lavender/ash should be bred with either white or pearl to get maximum vigour expressed. In general, the physiological vigor of an organism as manifested in its rapidity of growth, its height and general robustness, is positively correlated with the degree of dissimilarity in the gametes by whose union the organism was formed. The more numerous the differences between the uniting gametes, at least within certain limits, the greater on the whole is the amount of stimulation.

8.2. Transferrin

Transferrin is the blood plasma protein for iron ion (Fe^{3+}) delivery. It is a glycoprotein that binds iron very tightly but reversibly. The main role of transferrin is to deliver iron from absorption centres in the duodenum and red blood cell macrophages to all tissues. Predominantly, transferrin plays a key role where erythropoiesis and active cell division occur. The receptor helps maintain iron homeostasis in the cells by controlling iron concentrations. In birds transferrin is known to function as bacteriostatic agent in eggs by altering the Fe++/Co++ ratio. Several workers have reported Biochemical polymorphisms at transferrin locus in poultry (Ogden *et al*., 1962, Lush, 1966, Jain, 1977, Stratil, 1968, Okada *et al*., 1980, Tanabe et al, 1991, Montag, 1993 and Esmaeilkanian *et al*., 2000) which disagrees with the result of the present study. The differences observed in these studies might be largely due to differences in genetic background of the breeds under study and their purity. This study demonstrates complete gene fixation for the structural marker under investigation which is in tandem with the work of Lee *et al*., (2000) who reported the presence of complete gene fixation for yellow line in Korean native chicken and all the foreign breeds they investigated for transfferin. This comparison of chickens with guinea

fowl finds congruence in the report of Dessauer *et al.* (1962) that in many cases transferrin patterns for closely related genera and species could be quite similar.

A probable reason for this fixation might be due to any or more of the following; heterozygote scored incorrectly as homozygotes or selection against heterozygote for breeding; strong inbreeding within these varieties of indigenous Guinea fowl presumably resulting in some way from the indiscriminate and uncontrolled mating (Devendra and Nozowa, 1976) characteristic of free ranging animals, leading to small effective population sizes, breeding between relatives and consequent genetic drift. The implication of the fixation therefore, is that, at the transfferin locus in guinea fowl, there is no improvement programme that can be initiated. Transferring has been linked with some traits of economic importance in poultry. It has been reported that chickens with 'TfB' have the advantage of higher egg production over chickens with 'TfA' as the latter appeared to have delayed sexual maturity while the former has earlier age of sexual maturity (Stratil (1968). According to Lush (1966) the effect of heterozygous transferrin (TfBC) appeared to be significant including variability in fertility, hatchability and egg production (at least 90 days' production).

8.3. Carbonic anhydrase

The carbonic anhydrases form a family of enzymes that catalyze the rapid inter-conversion of carbon dioxide and water into bicarbonate and proton, a reversible reaction that occurs rather slowly in the absence of a catalyst. The transport of CO_2, Hb utilization, control of body fluids pH and selection for the production of carbonate ions are facilitated by carbonic anhydrase. The result of this study showed complete gene fixation at the carbonic anhydrase locus among the four varieties. No literature was sighted on carbonic anhydrase types in guinea fowl but the one reported on chickens showed six phenotypes which is not in agreement with the value recorded in this study (Das and Deb, 2008). The monotypism at this locus maybe because of the non-functionality of other alleles which probably result in low fitness and their removal from the population by natural selection or the amino acid residues responsible for other alleles is in a long way from the active site of the enzyme thus enhancing selective neutrality which are subject to genetic drift.

Again it might be that the monotypism is more efficient, or can catalyze a slightly different chemical reaction, in which case it may cause an increase in fitness and be favoured by natural selection. Additionally, the monotypism might be, in parallelism with transferrin, as a result of scoring bias or selection against heterozygote for breeding; strong inbreeding within and between these varieties of indigenous guinea fowl presumably because they are geographical neighbours. The implication of the fixation therefore, is that, at the carbonic anhydrase locus in guinea fowl, there is no improvement programme that can be initiated. No significant differences were detected between various biochemical types and economic traits. However the activity of CA has been positively correlated with egg shell thickness.

CHAPTER NINE

9.0. Summary, Conclusion and Recommendation

In this study, morphological and biochemical indicators were used to characterize the pearl, lavender, black and white varieties of indigenous Guinea fowl in Sokoto state, Nigeria. On the subject of morphology, Body weight and fourteen measurable (metric) characters/traits were considered to supply information on genetic distinction of the different varieties on the subject. Variables measured include Body weight, Head thickness, Helmet length, Helmet width, Wattle length, Wattle width, Body length, Keel length, Body circumference, Shank length, Shank thickness, Drumstick length, Thigh length and wing Length. The biochemical characterization involved the use of cellulose acetate electrophoretic procedures to separate the genetic types of haemoglobin, transferrin and carbonic anhydrase to provide information on variation in gene and genotype frequencies at the three different loci in the four different populations.

Although low values were accomplished in the morphological measurements, no defined patterns of differences or similarities were observed among the varieties. It is therefore difficult to categorize their supremacy or otherwise using these parameters. Coefficients of correlations between body weight and body measurements among the four different populations were generally high, suggesting a capacity of an isolated allele to have more than one distinguishable effect between Body weights and body measurements. Two principal components were yielded by the factor solution in the pearl variety with the first and second principal components explaining 73.38 and 7.81 % of the generalized variances respectively. In the lavender variety however, three principal components were yielded by the factor solution. The first, second and third components respectively explained 61.16 %, 10.15 % and 6.25 % of the generalized variances. Two principal components were yielded by the factor solution in the case of black variety. The first principal component explained 67.09 % and the second explained only 19.30 % of the generalized variances. Finally in the white variety only one principal component was yielded by the factor solution and it explained 84.48 % of the generalized variance in the body measurements giving nearly equal emphasis to each body measurement.

In this study, 12 variables showed significant discrimination among the varieties, however, the discriminating power of Shank length was highest, chronologically followed by Wing length, Helmet width, Head thickness, Body length, Wattle length, Keel length, Helmet length, Body weight, Body circumference, Wattle width and Shank thickness. Two other variables (Drumstick length and Thigh length) not fitted to enter the model were obliterated. Similarity index of 85 % was recorded between the pairs of white and lavender and white and black varieties. The black and lavender are 72 % similar; white and pearl 65 % similar; lavender and pearl 58 % similar and black and white 45 % similar. Comparison of the four varieties of Guinea fowl when their body parameters were standardized by division with live weight did not show a definite pattern in all the varieties. The Cephalic index in this study indicated that the head shape of the four varieties is dolichocephalic.

Using the biochemical indicator for characterization of Guinea fowl at haemoglobin, transferrin and carbonic anhydrase loci, haemoglobin locus was the only polymorphic locus among the three loci, the other two were fixed. Haemoglobin exhibited two genotypes and the inheritance was genetically controlled by two co-dominant alleles. The frequency of Haemoglobin A was significantly higher than for Haemoglobin B in all the varieties. The gene frequencies for Transferrin and Carbonic anhydrase were monotypic in all the varieties.

Although allozyme can be analyzed rapidly and inexpensively, there are limitations as the number of polymorphic loci are low and some enzyme proteins are more polymorphic and evolve at faster rate than the other. It is therefore recommended that a more objective approach to assessing genetic variation like Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSR), Intersimple Sequence Repeats (ISSR), Single Nucleotide Polymorphisms (SNPs) or microsatellites is strongly advocated to access the diversity in the four varieties if any. Also, the immunological differences in the varieties should be investigated.

Important findings in the study

1. Genetic variation was observed at the morphological level suggesting prospect of genetic improvement of the birds
2. Most of the traits investigated favour pearl variety suggesting that the pearl variety is more adaptive, the reason it was more frequently encountered during the sampling stage
3. The white variety grow faster as indicated by its superior leg and wing lengths
4. The low body weight and body linear measurements suggest that the birds are the light strain type suitable for egg production
5. The body weight shank length ratio being index of fleshiness suggest that the pearl and lavender are superior to the two others therefore could be better suited for meat production than the two.
6. The birds were found to be dolicocephalic
7. Most of the traits because they were highly and positively correlated were under the influence of the same gene action
8. The most discriminating traits in the varieties are the shank length, wing length and helmet width
9. The similarity index ranged between 58 and 85 %
10. Genetic distance was highest between pearl and black varieties while the least was between black and white varieties
11. Genotype and gene frequencies at haemoglobin locus are polymorphic
12. The genotype and gene frequencies at transferring and carbonic anhydrase loci are fixed

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