COMPARATIVE EVALUATION OF GROWTH AND BIOCHEMICAL METABOLITES OF THREE TYPES OF INDIGENOUS CHICKENS AND THEIR CROSSES WITH HUBBARD BROILER

BY

ABDULKADIR AROME ODIBA

DEPARTMENT OF ANIMAL SCIENCE,

AHMADU BELLO UNIVERSITY,

ZARIA, NIGERIA.

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BY

Abdulkadir Arome ODIBA, B. AGRIC (KOGI STATE UNIVERSITY, ANYIGBA)
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DEPARTMENT OF ANIMAL SCIENCE,
FACULTY OF AGRICULTURE,
AHMADU BELLO UNIVERSITY,
ZARIA, NIGERIA

AUGUST, 2015

DECLARATION

I declare that the work in this thesis entitled "COMPARATIVE EVALUATION OF GROWTH AND BIOCHEMICAL METABOLITES OF THREE TYPES OF INDIGENOUS CHICKENS AND THEIR CROSSES WITH HUBBARD BROILER" has been carried out by me in the Department of Animal Science. The information derived from the literature has been duly acknowledged in the text and the list of references provided. No part of this thesis was previously presented for another degree or diploma at this or any other institution.

Abdulkadir Arome ODIBA	_____	_____
Name of Student	Signature	Date

CERTIFICATION

This thesis entitled "COMPARATIVE EVALUATION OF GROWTH AND BIOCHEMICAL METABOLITES OF THREE TYPES OF INDIGENOUS CHICKENS AND THEIR CROSSES WITH HUBBARD BROILER" by Abdulkadir Arome ODIBA meets the regulations governing the award of the degree of Masters of Science, of the Ahmadu Bello University, and is approved for its contribution to scientific knowledge and literary presentation.

Dr. (Mrs) M. Orunmuyi	_____	_____
Chairman, supervisory committee	(Signature)	(Date)
Prof. B. I. Nwagu	_____	_____
Member, supervisory committee	(Signature)	(Date)
Professor S. Duru	_____	_____
Head of department	(Signature)	(Date)
Professor K. Bala	_____	_____
Dean, School of Postgraduate Studies	(Signature)	(Date)

DEDICATION

This thesis is especially dedicated to my parents and siblings.

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ABSTRACT

A study was conducted on the comparative evaluation of growth and biochemical metabolites of three types of indigenous chickens and their crosses with Hubbard broiler. The indigenous types of chicken and their crosses with Hubbard broiler were naked neck x frizzle (NaF), normal feather x frizzle (NF), naked neck x normal feather (NaN), Hubbard broiler x naked neck/frizzle (B/NaF), Hubbard broiler x normal feather/frizzle (B/NF) and Hubbard broiler x naked neck/normal feather (B/NaN). A hundred and ten (110) birds were used as foundation stock in this study. This consisted of 90 pullets (30 from each genetic group), three cockerels each from NaF and NF, four cockerels from NaN and 10 male Hubbard broiler chickens. Ten pullets and the cockerels from each of the three genotypic groups were randomly mated, and the other 20 pullets from each of the three genotypic groups were mated artificially with pooled semen from the broilers. The resulting offspring were weighed on weekly basis, body linear measurements were also taken on weekly basis and blood samples were collected in two phases (5^{th} and 10^{th} week of age) with each phase consisting of 4 females and 5 male birds from each of the genetic groups. Data on growth traits and biochemical metabolites were subjected to one-way and three-ways ANOVA respectively. Biweekly body weight and growth rate differed significantly ($p<0.01$) among the six genetic groups. B/NaF had the highest performance for growth which range from 26.53g to 1084.13g. Similar trend was observed for growth rate except for bi-weekly growth rate at 70 days of age which did not differ significantly ($p>0.05$) with B/NF and B/NaN genetic groups. Bi-weekly phenotypic correlation of body weight and growth rate of indigenous chickens crossed with Hubbard broilers ranged from negative (-0.39) to positive (0.98). Similar magnitude and direction in phenotypic correlation was obtained for indigenous genetic groups without the

Hubbard broiler gene. The phenotypic correlation also ranged from negative to positive and high (-0.47 to 0.99). Blood biochemical metabolites (total protein, albumin, glucose and serum alkaline phosphatase) differed significantly ($p<0.05$) among the six genetic groups. Age and sex also had significant effects ($p<0.05$) on blood biochemical metabolites. NaF and NF had the highest values for biochemical metabolites except serum alkaline phosphatase which was lowest in NF (816.57 iu/l). Biochemical metabolites decreased in value as the birds increased in age except for serum alkaline phosphatase which increased with increased age. Female birds used in this study showed significantly ($p<0.05$) higher values of blood metabolites than their male counterparts. Correlation between blood metabolites at 5 and 10 weeks of age of indigenous chickens ranged from negative (-0.56) to positive (0.72). Same negative phenotypic correlation which ranged from low to high was also seen in indigenous chickens with broiler gene (-0.28 to 0.56). Parameters measured for proximate composition were dry matter, ash, ether, and crude protein. The results obtained indicated that there were significant ($p<0.05$) differences in proximate composition among the genetic groups and the values obtained are comparable to reference values in literature. It was therefore concluded that the naked neck and frizzle genes are important sources of variation in growth and biochemical metabolites as the genes were responsible for body weight, growth rate and normal biochemical values. Thus, the genes can be incorporated either singularly or in combination with Hubbard broiler in genetic improvement.

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CHAPTER ONE

1.0 INTRODUCTION

The indigenous chickens evolved through thousands of years of natural selection. They are well adapted to the local climatic conditions, feed and stress, with resistance to diseases. Though their peculiar extensive system of management is characterised by low input and corresponding low output, they provide food security, protein nutrition and women empowerment to the rural families besides alleviating poverty in developing countries (Gondwe, 2004).

Their wide distribution in villages demonstrates the importance of these small and easily managed farm animals. Large variations were reported to exist among the indigenous birds in conformation, plumage colour, immune response to various antigens, growth and reproductive performance (Peters, 2000; Msoffe *et al.*, 2001). This led to the conclusion that the indigenous chickens are repositories of unique genes that could be used in other parts of the world (Adebambo, 2005), hence the need for their conservation to keep genetic variation within and between local breeds. For any meaningful progress in the performance of the indigenous chickens to take place, there is a need for improvement in the characteristics of the local chicken including their body and egg sizes (Ndofor-Foleng *et al*., 2006). An important requirement for this improvement is an appropriate breeding method for bringing about rapid genetic changes.

Major genes of chicken are believed to confer not only adaptability to the tropical climate, but also resistance to diseases (Haunshi *et al*., 2002). The influences of major genes such as naked neck, frizzle, slow feathering and dwarfism on immune competence in chicken have been evaluated by Bacon *et al.* (1986)**.**

Crossbreeding can lead to production of birds that will be better in growth rate, feed efficiency and reproductive traits in the local environment. The outcome of crossbreeding is due to the phenomenon of heterosis, which is expressed in the performance of the hybrids. Quality meat-type chickens are developed from local breeds and taste better than fast-growing broilers. They are considered as alternatives to fast-growing broilers in some regions of the world, such as in Europe and East Asia, and the output of quality chicken meat is rising each year (Chin, 2003).

The potential use of biochemical blood metabolites as predictors of health status, genetic disease resistance, meat quality and performance traits depend on a better understanding of the causes of quantitative variation in the characteristics among indigenous chickens. Most of the investigated blood metabolites have been associated with diseases resistance, meat quality or performance trials (Ademola *et al*., 2009). For proper management, breeding, feeding, prevention and treatment of diseases, it is desirable to know the normal physiological values in the Tropical environment (Ibrahim *et al*., 2012).

1.1 Justification

The indigenous chickens are characterized by poor performance in terms of growth rate (hence meat production) and egg production. Most of them are of small adult size and lay small sized eggs and few egg numbers when compared to improved commercial broiler or layer birds respectively (Nwagu and Nwosu, 1994; Pedersen, 2002; Gondwe, 2004). In spite of the many problems associated with the rearing of indigenous chickens, almost all households in the villages rear them. Indigenous chickens are therefore considered as excellent resources in poverty alleviation due to their quick return on investment. Thus, if production could be improved, village poultry production would create an opportunity for

the development of the rural segments of society (Permin *et al.,* 2000). Stemming from the importance of indigenous chickens to the economy of the poor majority in Nigeria, this study was designed to evaluate the growth performance and blood biochemical metabolites of the offspring of local chickens crossed with Hubbard breed of broiler.

1.2 Hypotheses

H_o: There is no difference in the growth performance of three types of indigenous chickens and their crosses with Hubbard broiler.

Ho: There is no difference in the values of serum biochemical metabolites of indigenous chickens and their crosses with Hubbard broiler.

$H_{o:}$ There is no difference in the proximate composition of breast meat from indigenous chickens and their crosses with Hubbard broiler.

1.3 Objectives

The objectives of this study were to evaluate:

1. The growth performance of three types of indigenous chickens and their crosses with Hubbard broiler.
2. The blood biochemical values in three types of indigenous chickens and their crosses with Hubbard broiler.
3. The proximate composition of breast meat from three types of indigenous chickens and their crosses with Hubbard broiler.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin of Indigenous Chickens

According to modern ornithology, there are four species of the jungle fowl and the red jungle fowl (*Gallus gallus)* is found to be the major contributor or an ancestor to the domestic fowl (Crawford, 1990). It is believed that the other three wild species (*G. sonnerati, G. lafayettei and G. varius*) interbred with *Gallus gallus* and those domestic fowls are carriers of the inheritance from these three species. These fowls give rise to variety of domestic hens of all kinds. These "fancy" breed are of important value. It is very important that these breeds are maintained in the future as "gene bank" because they may comprise major genes that could be exploited cost-effectively (Smith, 1990). Indigenous chickens of today resulted from many cross-breeding with exotic breeds and random breeding within flocks of indigenous fowl. As a consequence, it is not possible to homogenize the characteristics and performance of indigenous chickens (FAO, 1998).

Mutant genes such as the frizzled feathers, naked neck, pea, rose and walnut combs are widespread within local birds (Anonymous, 2007). The Naked neck mutation originated in Transylvania, Romania and spread across Europe many centuries ago, while the frizzle feathered chicken was first described by Western explorers in Fiji during the seventeenth century (FAO, 2000).

2.2 Overview of Major Genes in Poultry

2.2.1 The naked neck (*Na*) gene

Naked-neck chickens look like a cross between a turkey and a chicken with their completely featherless necks and faces. They are often referred to as turkens, Transylvania Naked-necks, bare necks, Hackle-less and Rubber necks and are characterized by the naked-neck trait, caused by a single autosomal incompletely dominant gene (Nthimo, 2004). The naked-neck gene (*Na*) is incompletely dominant and the heterozygote (*Nana*) can be identified by a tuft of feathers on the ventral side of the neck above the crop. The homozygous dominant chickens (*NaNa*) however, either lack this tuft or it is reduced to just a few pinfeathers or small feathers (Crawford, 1976). Scott and Crawford (1977) demonstrated that the presence or absence of the tuft could be used to identify the two genotypes accurately at hatching. The resulting bare skin becomes reddish, particularly in males as they approach sexual maturity (Somes, 1990).

The naked-neck chicken is thought to have originated from Transylvania, Romania and was spread all over the world by a Dutch East Indian Company in the course of trading around the 17th century (Ramsey *et al*., 2000). The *Na* gene is associated with significantly less plumage cover than chickens not carrying the gene (Nthimo, 2004). They are very colorful – white, red, brown and black feather combinations are found. The autosomal incompletely dominant naked-neck (*Na*) gene is not only responsible for de-feathering the neck region, but it also restricts the feathered area around the body by 20 to 30% in heterozygous (*Nana*) and up to 40% in homozygous (*NaNa*) genotypes because of the incomplete dominance of the *Na* gene (Islam and Nishibori, 2009).

The *Na* gene received greater attention in the recent past in broiler production because of its association with heat tolerance (Merat, 1986; Cahaner *et al*., 1993); which is considered to be the most important inhibiting factor for poultry production in hot

tropical climate (Horst, 1987). In broiler chickens, the *Na* gene results in a relatively higher growth rate and meat yield than the normal birds at normal temperature and the effect is more pronounced at high temperature (Cahaner *et al*., 1993). Higher meat yields were reported for *Na* genotypes (Younis and Cahaner, 1999; Galal and Fathi, 2001; Patra *et al*., 2002; Fathi *et al*., 2008).

In expression of sex differences, *Na* females have 4.8% greater naked area compared to *Na* males (Howlider *et al*., 1995). Bordas *et al*. (1978) reported that the *Na* birds tend to have more feathers cover as compared to their *Na* counterparts (41 to 27%) and (33 to 22%) for males and females respectively. Normally, the apterium carry scattered down and semi-plume feathers, but the apterium of the naked-neck birds contain no feathers.

The feather tracts themselves are also either absent or reduced in area so that birds have greatly reduced feather cover (Nthimo, 2004). Feather pterylae are absent from the head and neck except around the comb, the anterior spinal tract and two small patches on each side around the comb. Islam *et al*. (2004) suggested that the *Na* gene and its effects on heat dissipation positively affect appetite and this happens for two opposing reasons; in cool climates, because of higher energy demands, and in hot climates because of an increase in the upper limits of the critical body temperature. Under such conditions, feed intake increases, resulting in improved body weight, egg sizes and livability. The introduction of the *Na* gene in chicken breeds seems to improve the resistance of the birds to heat stress (Islam and Nishibori, 2009).

The incorporation of *Na* gene in commercial breeds might contribute to the production of birds with a high genetic potential and better performance at high temperatures. The relationship between the presence of the *Na* gene and the resistance of the naked-neck

bird to heat stress is due to the fact that the gene reduces feathering by about 30% in the heterozygous birds (*Nana*) and 40% in homozygous birds (*NaNa*). The homozygous naked neck *(NaNa*) is slightly superior in most tests to the heterozygote (*Nana*) for body-weight and feed efficiency (Gowe and Fairfull, 1995). Eberhart and Washburn (1993) stated that feather reduction in naked-neck birds probably caused their greater ability in dissipating heat through exposed areas compared to birds not carrying the gene. Singh *et al*. (2004) reported that in India, the naked-neck and frizzle birds were not liked by most people because of their unfamiliar look but demand is increasing year after year realizing the advantage of these genotypes in tropical adaptation and productivity.

2.2.2 Frizzle (F) gene

The frizzle gene was first described by Aldrovandi in 1600, but it was Davenport who first suggested that it is a dominant gene in 1906 (Somes, 1990). According to Horst (1989) the frizzle condition is caused by a single incompletely dominant autosomal gene, symbolized *F*. The frizzle gene which controls frizzling is situated on chromosome 6. The gene is infrequently restricted by an autosomal recessive modifier (*mf*). As described by Somes (1990), in unmodified homozygous frizzled birds, the rachises of all feathers are extremely curved. These feathers are easily broken and therefore the birds appear quite bare. The modifying gene lessens the extreme aspects of the homozygote so that they appear less woolly. The unmodified heterozygotes have the feather shafts and barbs of contour feathers curved, to a much lower extent than the homozygote. The action of the frizzling gene has been shown to be localized in the feather follicle and does not result from a metabolic disorder (Somes, 1990). He further stated that the modifying gene modifies the heterozygotes making them less different from the normally feathered ones.

2.2.3 Normal feather chicken

Birds have evolved many unique and interesting features, allowing them to adapt and radiate into various ecological niches. They display a great degree of diversity in feathers and other body parts. Domesticated birds exhibit an even greater diversity in phenotypes than their wild ancestors, thus providing an excellent opportunity to explore the genetic basis underlying variation in morphology, physiology, and behaviour (Ng *et al*., 2012). The complex organization of feathers allows for a variety of potential morphological changes to occur. Modifications of the feather include deterrence of feather development, changes in feather structure, inhibition of feather molting, and alterations of feather growth rates. The Nigeria native chickens have very colourful plumage; solid white or black, brown, red and grey or combination of these. They possess different feather patterns, mostly, barred, pencilled, laced and partridge with skin and small almond shaped ear lobes that are white in colour. The colour of their egg shell is mainly white or tinted.

2.3 Characteristics of Nigerian Indigenous Chickens

The Nigerian indigenous chicken can be classified as a light breed, with small oblong head and vigorous outlook (Ibe, 1993). Hill and Modebe, (1996) reported that the neck of the indigenous chicken varied in length ranging from 5.6cm to 14cm with a mean of about 10.17cm. They further described the indigenous chicken as having pin lash-white skin, usually covered at a fairly long and densely covering fluff. Eshiette and Okere (1990) reported that the Nigerian chicken has multicoulored feather with several variation.

Peters (2000) reported the superiority of frizzled feathered birds over naked-neck birds with regards to body weight and chest girth. However, the naked-neck broiler had higher growth rate and meat yield compared to normal birds under high temperature, (Younis and Cahaner, 1999). He also reported that the frizzle feathered gene, increases heat conductivity of the feather coverage by affecting feather structure, and its effect on layers performance was reportedly significant.

2.4 Adaptation of the Chickens in the Tropical Environments

The strong nature of the local chicken as manifested in their resistance to certain diseases and their ability to thrive well under harsh condition had helped in their adaptation in the tropical environment which is characterized by heat stress (Horst, 1989).

Peters (2000) reported that the naked-neck chicken has the highest egg weight followed by frizzle feathered and lastly normal feathered chickens. Variation in egg weight/size, egg length and breadth is said to be influenced by the possession of major genes, dam's genotype and environmental factors. The possession of major genes influences the utilization of available food reserve for egg production as reported by Peters (2000). Peters (2000) attributed the superior performance of the naked-neck and the frizzle feathered birds when compared to the normal feathered birds in terms of feed efficiency to the thermoregulatory roles of the genes they possess.

2.5 Local Poultry as Sources of Pertinent Genetic Materials

Modern breeding strategies for profitable poultry centre on dedicated production lines derived by vigorous selection from a few breeds and a very large population with a great genetic uniformity of traits under selection (Ac Amovic *et al*., 2005). There are fancy breeds throughout the world that are characterized by medium or low performance and are often maintained in small populations (Horst, 1989). The genetic erosion of these local breeds may lead to the loss of valuable genetic variability in specific characteristics that are momentarily unimportant in commercial breeding strategies (Ladokun *et al*., 2008). It can be assumed that local breeds contain the genes and alleles pertinent to their adaptation to particular environments and local breeding goals. Local breeds are needed to maintain genetic resources permitting adaptation to unforeseen breeding requirements in the future and a source of rich material (Notter, 1999).

2.6 Crossbreeding

Crossbreeding is one of the tools for exploiting genetic variation (Adebambo, 2005). Crossbreeding, the mating of two individuals with different breed make-up is one type of a larger class of mating systems called outbreeding. Outbreeding has the opposite effect of inbreeding and hence results in increased heterozygosity in a population and decreased homozygosity. A crossbreed or crossbred animal usually refers to an animal with purebred parents of two different breeds, varieties, or populations. The intention is often to create offspring that share the traits of both parent lineages, and producing an animal with hybrid vigor.

Crossbreeding is beneficial for two primary reasons. First, a well designed crossbreeding system allows the producer to combine the desirable characteristics of the breeds involved in the cross while masking some of the disadvantages of the breeds. This is

frequently referred to as breed complementarity. The second benefit arises from heterosis, which is often referred to as hybrid vigor. In addition to these primary benefits, Adebambo (2005) reported that crossbreeding enables a producer to change a population rapidly with the introduction of new breeds. Adebambo (2005) further reported that crossbreeding is to produce progeny which are more disease resistant, healthier and hardier.

2.6.1 Breed complementarity

Breed complementarity, a major advantage of crossbreeding, is often very important to the success of crossbreeding programmes (Adebambo, 2005). It refers to the production of a more desirable offspring by crossing breeds that are genetically different from each other, but have complementary attributes. Breed complementarities is the result of mixing and matching the mean breeding values of different biological types of breeds.

2.6.2 Heterosis

The term heterosis, also known as hybrid vigor or outbreeding enhancement, describes the increased strength of different characteristics in hybrids; the possibility to obtain a genetically superior individual by combining the virtues of its parents (Shawn, 2012). It is a measure of the superior performance of the crossbred relative to the average of the purebreds involved in the cross. The probable cause of most heterosis is combination of genes from different breeds, concealing the effects of inferior genes. Heterosis may result in the crossbred being better than either paternal breed or simply better than the average of the two. Heterosis is measured by crossing populations to produce an F1 generation, which is compared to the parental populations (Shawn, 2012). Theoretically, the magnitude of heterosis is inversely related to the degree of genetic resemblance between

parental populations (Wilham and Pollak, 1985) and is expected to be proportional to the degree of heterozygosity of the crosses (Sheridan, 1981). Thus, heterosis is a result of non-additive genetic effects and may be viewed as overall fitness as well as an expression of a specific trait. It is usually greater for reproductive traits than for growth traits (Fairfull, 1990). Heterosis is influenced by maternal and dietary effects (Liu *et al*., 1995) and may vary with regard to complex traits (Gram and Pirchner, 2001). In addition, Lamont and Deeb (2001) reported that heterosis for body weight was age dependant. Generating hybrid vigor is one of the most important reasons for crossbreeding.

In Egypt, Sabra (1990) found that crossbreds obtained from crossing between local breeds (Silver Montazah and Dandarawi) had positive and high magnitude of heterosis for body weight at different ages. Saadey *et al*. (2008) found that crossbreds obtained from crossing between Sinai (S) and White Leghorn had positive and high heterotic percentage at all ages, except at 2 and 3 months of age. Malik *et al*. (2005) reported that strain cross pullets were lighter than purebreds at 20 weeks of age while Singh and Singh (2005) reported that crossbreds were superior than purebreds in body weight at 20 and 40 weeks of age.

Most reviewed studies show that body weights of crossbred chickens at different ages are associated with positive heterotic effects for growth traits (Sabri *et al*., 2000). Iraqi *et al*. (2002) indicated that heterosis estimates were generally positive and high for body weights of crossbreds obtained from crossings between Mandarah and Matrouh chicken strains. Heterosis for body weight was observed in chickens when there were small differences in body weight between parental lines (Yalcin *et al.*, 2000) and when there were large differences between the parental lines used in the cross (Liu *et al*., 1995).

Nagpure *et al.* (1991) demonstrated the effects of crossbreeding using the Japanese Shamo Game, a popular meat bird in Hawaii. This local breed was crossed with Rhode Island Reds, Barred Plymouth Rocks and White Leghorns. The four pure breeds were compared with crossbreds resulting from matings of the Shamo Game males to females of each of the other three mentioned breeds. There was definite improvement in hatchability of all crossbreds over the purebreds except in the case of the Rhode Island Reds. The crossbreds in each group had a lower chick mortality rate than the purebreds of the corresponding group. The crossbreds grew more rapidly than any purebred except the Shamo Game and ate less through the first eight weeks than did any of the purebreds.

Kitalyi (1998) outlined the importance of crossbreeding by crossing two strains of chickens. The offspring of the strain cross laid about 22 eggs per year more than offspring of the pure strains. In addition the hybrids laid larger eggs, matured earlier, and had a larger body size than the pure strain hens. There are three types of heterosis, which include Individual heterosis, maternal heterosis and paternal heterosis. Individual heterosis is the advantage of the crossbred individual relative to the average of the purebred individuals; maternal heterosis is the advantage of the crossbred mother over the average of purebred mothers; while paternal heterosis is the advantage of the crossbred sire over the average of purebred sires. Paternal heterosis generally has an effect only on conception rate and aspects of male reproduction. The male parent does not have any direct environmental effect on the survival of the offspring, so the benefits are more limited than those for maternal heterosis. However, the benefit in added conception rate can be substantial, particularly if young males are being used (Anonymous, 2007).

2.7 Effect of the Naked Neck Gene on Performance of Birds

The naked-neck genes conferred better feed conversion, growth rate, feed efficiency and dressing percentage than the normal feathered chicken. The feather structure and feather distribution genes are well adaptive to the harsh tropical environment; survive on low energy feed, highly resistant to diseases and superior to their exotic counterparts. Crossbreeding with the exotic breeds improved body weight greatly at 12 weeks of age. Merat (1986) and Horst and Rauen (1986) studied the effect of temperature variation on the egg production performance of two genotypes (naked-neck and normally feathered birds). Their studies showed that there was a different response of the naked-neck and normally feathered genotypes to high environmental temperature.

2.7.1 Carcass characteristics

The reduction of plumage (20 - 40%) gives 1.5 - 3.0% more carcass yields to the naked-neck genotypes than their normal feathered counterparts regardless of the temperature. Due to the higher proportion of muscle in the pectoral region of naked neck birds, there is 1.8-7.1 percent more meat in them than normal feathered birds when their carcasses are dressed (Merat, 1986). Fathi *et al.,* (2008) reported that the naked-neck genotypes (*NaNa* or *Nana*) exhibited higher relative weight of dressed carcass, drumstick and breast muscles compared to normally feathered individuals (*nana*) and that the proportion of abdominal fat was decreased in both naked-neck genotypes compared with normally feathered ones. Intramuscular and subcutaneous fat in naked-neck birds is low due to the utilization of a larger fraction of energy for thermoregulation (Merat, 1990). N'Dri *et al*. (2005) observed that slow growing homozygous and heterozygous naked-neck birds under fluctuating temperature, tended to reach the weight of 2 kg 3.3 days sooner than normally feathered birds and that carcass yield of *Na* birds was higher than that of

normally feathered birds (81.6 % vs. 80.0 %). Singh *et al*. (1996) reported that heterozygous naked-neck broilers gained about 3% more weight than their normally feathered counterparts under commercial conditions during the spring and summer months, and that this advantage was almost tripled at high ambient temperature of about 32°C.

2.7.2 Body weight and growth rate

At 20°C, adult body weight was lower in naked-neck hens, especially the homozygote, than in hens with complete plumage cover, but the trend reversed when the temperature increased above 30°C (Cahaner *et al*., 1993). The reduction of feather coverage provides relative heat tolerance and therefore, in high ambient temperature, heterozygous naked-neck chickens are superior to their normally feathered counterparts (Cahaner *et al*., 1993). The naked-neck gene has been associated with increased laying rate, egg size and egg mass in hot environments (Garces *et al.*, 2001; Younis and Galal, 2006). Abdel-Rahman (2000) researched into the effect of the naked-neck gene on the egg production performance of Sharkasi chickens under subtropical conditions and reported that the naked-neck birds showed significant increases in egg production, 90-day egg number and egg mass by 9.0, 17.80 and 13.30% for *Na/na* and 3.70, 7.30 and 7.30% for *Na/Na* respectively compared with the *na/na* genotype. Garces *et al.* (2001) and Younis and Galal, (2006) observed that the naked-neck birds also reached sexual maturity significantly earlier than the normally feathered birds by about 5 days. The naked-neck birds were also heavier at 24, 40 and 72 weeks than normally feathered birds ($P<0.05$ at 40 and 72 weeks of age). The average mortality rate during the laying season was less in naked-neck birds than normally feathered (*na/na*) ones; however, the differences were

not significant. Garces *et al.* (2001) and Younis and Galal, (2006) stated that the *Na* gene also reduced feed intake by 12.40 and 13.60% in *Na/na* and *Na/Na* genotypes, respectively. The naked-neck birds had a significantly better feed conversion than *na/na* genotypes. The *Na* gene led to a significant reduction in egg yolk and shell percentages. Eggs produced from naked-neck birds had a lower breaking strength and egg shell thickness compared with the *na/na* genotypes.

Other effects of this gene on productivity noted by other researchers include reduced effect of high ambient temperature on fertility, (Ladjali *et al*., 1995), less body weight loss under heat stress and superior levels of heat shock protein, Hsp 70 (Hernandes *et al*., 2002). Similarly, Fraga *et al*. (1999) observed the lowest incidence of diseases such as cloaca cysts, ascites, prolapse, Mareks disease, Coccidiosis, Osteodystrophy and Salmonellosis in the naked-neck birds studied. According to Yushimura *et al*. (1997) among the indigenous chickens, the naked-neck is found superior in terms of egg production, egg size and body weight in a hot and humid environment. Other positive effects associated with this gene on broiler stocks are increased body weight and meat yield, higher body weights, lower fat content and better feed efficiency (Merat, 1986).

A study by Njenga (2005) on productivity and socio-cultural aspects of local poultry phenotypes in coastal Kenya showed that the naked-neck phenotypes had significantly higher body weights compared to the normally feathered counterparts. Egg weights ranged from 38±2.9 g to 45±4.5 g, with the naked-neck phenotypes having the highest.

The overall mean eggshell thickness for the birds was 0.31mm. The naked-neck had the highest average daily gain among the other four phenotypes. The author concluded that the naked-neck phenotype is superior in productivity when compared to the other

phenotypes. Barua *et al*. (1998) showed that among the indigenous chickens of Bangladesh, the naked-neck fowl performed better in terms of egg and m eat production, and were more resistant to diseases than their fully feathered counterparts. They observed that the crosses between the indigenous naked-neck fowl and the exotic standard breeds performed better than similar crosses using fully feathered indigenous fowl.

2.8 Effects of the Frizzle Gene on Performance of Birds

There is not as much information on the effects of the frizzle gene on productivity as there are in the naked-neck gene. Nevertheless, there is evidence to indicate that the gene may be useful in stocks that have to perform under hot humid conditions (Gowe and Fairfull, 1995). Gowe and Fairfull, (1995) stated that the gene was capable of reducing the insulating properties of the feather cover thereby making it easier for the bird to radiate heat more efficiently from their body. Merat (1990) showed that the frizzling gene resulted in an increase in egg number and mass, alongside reducing mortality under hot and humid conditions. Work by Haaren-Kiso *et al.* (1988) on *F/f* and *f/f* progenies compared under two temperatures, (18-20°C) and (32°C), revealed that the birds carrying the *F* gene laid 24 more eggs over a 364 day laying period in the hot (32°C) environment. On the other hand, the *F* gene birds laid only 3 eggs less on average in the cooler (18°C) environment. There was also an increase in egg weight, feed efficiency and viability under the hot environment for the frizzled birds.

According to Horst (1988) the *F* gene is associated with increases in egg number, egg mass and reduction in mortality when the birds are raised under hot and humid conditions. Haunshi *et al.* (2002) worked on the effect of the naked-neck and frizzle genes on immune-competence in chickens and reported that there were significantly

higher haemolytic complement levels in serum observed for the frizzle feathered birds than their normally feathered sibs. Younis and Cahaner (1999) suggested that when reared at high ambient temperature (32°C), birds with frizzle genes perform better in terms of weight gain from 4-7 weeks than their counterparts which are normally feathered. The results indicated that the reduction in feather coverage by the frizzle gene provided relatively better heat tolerance, and therefore, under hot climates the *F/f* broilers were superior to their normally feathered counterparts. They concluded that frizzled broilers should be preferred in hot climates. Nwachukwu *et al.* (2006) also observed that the birds with the frizzle gene outperformed their sibs which were either naked-neck or normal feathered in body weights and most of the egg traits evaluated, thus indicating that the frizzle gene may be advantageous in poultry production in the humid tropics.

2.9 Interaction between the Naked-neck (*NA*) and Frizzle (*F*) Genes

According to Gowe and Fairfull (1995) some major genes like naked-neck and frizzling are used to improve heat tolerance and are often incorporated in breeding programs with local chickens to increase poultry production. Studies by Younis and Cahaner (1999) have shown that combining the naked-neck allele with another heat tolerant gene like frizzling resulted in a favourable additive effect on various productive parameters. Mathur and Horst (1992) reported that the three genes *Na*, *F* and *dw* interact so that the combined effects of two genes are lower than the sum of their individual gene effects. Mukherjee (1992) observed a positive additive effect on performance when Dahlem Red naked-neck strains were crossed with Dahlem White frizzle strains. Mahrous *et al*. (2008) observed that the naked-frizzle genotypes had significantly better egg performance, egg quality traits and attained sexual maturity earlier than the normally feathered females.

2.10 Growth Performance of the Indigenous Chickens

Although the Nigerian indigenous chickens possess small body size and grow slowly, it has been concluded that they reach point of inflection earlier than the exotic (Nwosu *et al.*, 1980). Body size of an individual chicken is also determined by its rate of growth (Ibe, 1993). Olawunmi *et al.* (2008) found that the Fulani ecotype chicken was bigger in size than the Yoruba ecotype chicken 1.76±0.4 and 0.79±0.21 kg respectively. Indigenous male chicken was also bigger in size than their female counterparts 1.5±0.06 kg versus 1.29±0.04 kg respectively (Ajayi *et al*., 2008). It has also been reported that the frizzle feathered and the naked neck genes conferred better feed conversion on these genotypes when compared to their normal feathered counterpart (Horst, 1997; Gunn, 2008).

2.10.1 Effects of day-old chick weight on subsequent growth of chickens

Due to the lovely appearance, wonderful taste and other unique characteristics, indigenous chickens are preferred to fast growing broilers in Nigeria (Chin, 2003). Genetic selection for high hatching egg number will results in smaller egg weight and thus decrease day-old chick weight (Yannakopoulos and Tserveni-Gousi, 1987). However, the effect of day-old weight on growth rate of indigenous chickens varied among different studies. Some researchers have found that day-old chick weight affect performance of broiler chicks to market age (Mendes *et al*., 2007), while other studies have shown that, for broiler, the advantage of initially higher chick weight diminishes rapidly during early growth period and has little influence on economic traits at market time (Pinchasov, 1991).

2.10.2 Body weight and body linear measurement

Series of techniques are available to gain information about an animals' body mass and body composition. Some of these techniques use simple, inexpensive equipments and others require sophisticated equipment (Lerner, 1973).

The animals' mass is usually directly determined by weighing. However, under some circumstances a scale may not be available. Alternative way is to measure body parts and relate them to body weight (Lerner, 1973). Shank length has been commonly related to body weight in poultry. This is simply because different coefficients and exponents are needed for different breeds of chickens.

Body Weight

Adeyinka *et al.* (2006) obtained body weight of naked neck broiler chickens at day old, 2, 4, 6 and 8 weeks as 37.22±0.32g, 210.46±1.97g, 744.33±4.31g, 1,351±7.91g and 2428.1±14.61g respectively. Okon *et al.* (1996) observed that live body measurement at 28 days (4 weeks) were 6.21 and 6.09 times their 7 days (1 week) old values for the Lohman Brown and Anak strains respectively and added that the chicks doubles its weight 3 to 5 times before 6 weeks of age. Mature body weight of indigenous chickens in Africa under scavenging system ranged from 1170g – 1500g, 1354g – 1652g for chickens under intensive management, while it was between 1140g - 2000g and 1125g – 2000g respectively in their Asian counterparts (Horst, 1989; Huque, 1999 as cited in Sonaiya and Swan, 2004).

Breast Girth

Continuous increase in breast girth from 3 – 12 weeks in broiler chicken has been reported (Okon *et al.,* 1996). They recorded a range of 15.59±0.08 to 37.08±0.24 from 3-

12 weeks of age. Essien and Adeyemi (1999) had also observed that breast circumference increased with age from 1 to 7 weeks in Lohman Brown and Anak broiler strains. Okpeku *et al.* (2003) obtained a slight difference in breast circumference between male and female local chickens in Edo state. 39.03±4.89cm was obtained for male while 38.01±4.50cm was obtained for female.

Shank Length

Essien and Adeyemi (1999) showed that shank length increases with age and was significantly different among broiler strains. According to Kabir (2006), Rhode Island chickens recorded the mean shank length values of 9.74±0.19 and 12.69±0.06 at 20 and 40 weeks of age respectively. Okoro and Ogundu (2006) observed that shank length varied between sexes in turkey and they recorded higher shank length for males than females. This was also observed in local chicken in Edo State as reported by Okpeku *et al.* (2003) with males recording up to 9.52±0.32cm and females 8.99±0.60cm.

Thigh Length

Essien and Adeyemi (1999) reported that thigh length increased with age and differed between strains of broilers. However, Okoro and Ogundu (2006) observed that thigh length differed between sexes in turkey and male had higher thigh length than females. The authors also noticed that breed had significant effects on thigh length.

2.11 The use of Blood Biochemical Values in the Improvement of Poultry

Physiology and chemistry of blood were used as indicators for various diseases in birds (Harr, 2002; Hauptmanova *et al*., 2006) and animals (Perelman, 1999). However, these

values were affected by different factors such as nutrition, age, sex and genotype (Fudge, 2000; Kececi and Col, 2011). In many species of bird, normal values for biochemical factors were measured and comprehensive data base was established as their blood profiles.

Growth and carcass traits are of primary concern in breeding programs because they are economically important traits in poultry. Biochemical traits have been reported by several authors to affect growth rate, carcass traits and feed efficiency in poultry (Amills *et al*., 2003; Zhou *et al*., 2005; Promwatee and Duangjinda, 2010). Such biochemical traits include enzymes, metabolites and electrolytes. The enzymes include Glutathione Peroxidase (GP), Aspartate Amino Transferase (AST), Alanine Amino Transferase (ALT) and Alkaline Phosphatase (AlP). The metabolites include Cholesterole (Cho), Glucose (Glu), Albumin (Alb) and Total Protein (TP); while the electrolytes include Sodium (Na), Potassium (K), Calcium (Ca) and Chlorine (Cl).

AlP is an enzyme which is found mostly in the duodenum and kidney. According to Harr (2002), AlP is considered to be a good indicator of osteoblastic activity. Its level increases in growing birds, egg laying birds when calcium metabolism is increased in the medullary bone and in some cases in liver disease, such as aflatoxin poisoning. Low levels of AlP may be seen in Zinc deficient diet.

Glucose is required for cellular respiration and is the preferred fuel for all body cells. Elevations in the blood glucose levels are the principal pathological change noted in avian species (Harr, 2002). Increased glucose level results in hyperglycaemia while decreased glucose level results in hypoglycaemia.

According to Harr (2002), normal values for cholesterol in birds are in the range 108-330 mg/dl. This substance is the precursor of all steroid hormones and bile acids. The remainder of the cholesterol is produced in the liver and is also gotten from the diet. Plasma levels of cholesterol are increased in cases of fatty liver and kidney syndrome. Very high levels of plasma cholesterol accompanied by a lipaemia indicate fatty acid degeneration of the liver.

Creatinine levels in avian serum samples typically fall below a measurable range and certain technical factors contribute to a high incidence of artefactual changes. Elevations have been associated with kidney disease, but creatinine is not considered to be a reliable indicator of renal function (Harr, 2002).

Electrolytes also play important roles in various physiological processes. Such processes include osmotic pressure maintenance, synthesis of tissue proteins, intra and extracellular homeostasis maintenance, maintenance of the electrical potential of cell membrane, acid-base homeostasis, as well as the functioning of the enzymes and nerves (Bounous *et al*., 2000).

2.12 Meat Quality of Birds

The production of broilers in free-range systems may pose a determined meat traits sought by consumers of chicken meat. The main differences in meat quality between free-range and conventionally reared chickens are related to colour, flavour and texture (Castellini *et al.,* 2002).

The differences may be related to sex, due to different growth and muscle development potential between males and females (LE Bihan Duval, 2004). However, the effects of

different genetic strains on meat quality characteristics are not well known, particularly in slow-growing strains. According to Souza *et al.* (2011), meat proximate composition was not influenced by genetic in all the broiler strains, however, ash content was affected by sex, with the highest values obtained in males.

Diaz *et al. (*2010) reported higher lipid content of the breast and drumstick meat of capons than that of the broilers and organic chickens. According to them, this fact could be attributed to caponization effects on the metabolism of the animals (their fat deposition is increased). However, dry matter and ash content of breast meat were similar to those described in broilers or indigenous chicken (Wattanachaut *et al.,* 2004). Diaz *et al.* (2010) also reported decrease in protein content of the capon with age and correlated with an increase in fat. In chickens, Thai indigenous breed meat contained higher protein content and lower fat and ash content when compared to broiler meat (Wattanachaut *et al.*, 2004).

Eva *et al.* (2011) reported that broiler chickens and pheasant differ to a large extent in the chemical composition of breast and thigh muscles. However, this finding is contrary to the results reported by Kuzniacka *et al.* (2007) who did not observe such differences. The most likely reason for this was related to the fact that the values obtained were related to the original weight of the muscles rather than the dry matter content. Eva *et al.* (2011) showed that pheasant and broiler meat significantly differ in their nutritional values. Such differences are determined genetically and may also be influenced by the diet as reported by Kokoszynski, *et al.* (2008). Eva *et al.* (2011) also reported that protein content in breast muscles was 5.16% higher in female pheasant and 7.95% in male pheasant than in broiler chicken.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Location

The experiment was carried out at the Department of Animal Science Teaching and Research Farm, Faculty of Agriculture, Ahmadu Bello University, Zaria located at Latitude 11° 11' N and Longitude 7° 38' E at an altitude of 706m above sea level (Akpa and Jokthan, 1996). The area is characterized by 6 to 7 months of rainfall ranging from 1100mm to 1250mm annually. The ambient temperature of Zaria is 26°C. The area has clear distinctive dry and wet seasons. The ambient temperature rarely falls below 26°C except during Harmattan period when temperature below 26°C may be recorded. However, annual temperature rarely exceeds 35°C (Akpa and Jokthan, 1996).

3.2 Source of Experimental Animals and Mating Procedure

The three genetic groups of indigenous chickens i.e. normal feather x frizzle feather (*NF),* naked-neck x normal feather (*NaN*) and naked-neck x frizzle feather (NaF) used in this study were generated from a main cross (at the Department of Animal Science farm, A.B.U) between normal feather and frizzle feather, naked-neck and normal feather, frizzle feather and naked-neck stocks. The genotypes were first generation (F_1) offspring generated through *inter* crossing between the pure normal feathers, frizzle feather and naked-neck chickens. On the other hand, Hubbard broiler foundation stock that was crossed with the indigenous chickens were sourced from the National Animal Production Research Institute (NAPRI), Shika, Zaria. A total of 110 foundation stock consisting of 90 pullets (30 from each genotypic group), three cockerels each from NaF and NF, four cockerels from NaN and 10 male Hubbard broiler chickens were used.

Mating commenced when the birds were 30 weeks of age. Ten pullets and the cockerels were randomly mated according to corresponding genotypes (Table 3.1), and the

remaining 20 pullets from each of the three genotypic groups were inseminated artificially with pooled semen from the Hubbard broilers chickens (Table 3.2).

Artificial insemination was done twice a week (Wednesdays and Saturdays) between the hours of 4pm and 6pm. Semen collection from the Hubbard broiler chickens were done by stimulating the copulatory organ (the phallus). This was followed quickly by pushing the tail forward with one hand, at the same time, using the thumb and forefinger of the same hand to apply pressure in the area. At this point the phallus was erected, the cloaca was everted and semen pulled out of the phallus following each squeeze of cloaca. Semen was carefully collected in calibrated test tube, making sure not to contaminate it with feacal material. Collected semen was diluted prior to insemination.

Insemination of hens involved holding a hen upright, and then pressure was applied to the abdomen around the vent, particularly on the left side. This caused the cloaca to evert and the oviduct to protrude, so that the insemination straw could be inserted into the oviduct and the appropriate amount (about 1ml) of semen deposited. As the semen was expelled, pressure around the vent was released, which enabled the hens in retaining the sperm in their oviduct.

Table 3.1 Mating Plan for Indigenous Chickens

Sire	Dam	Mating	Progeny
NaF	NaF	NaFxNaF	NaF

NF	NF	NFxNF	NF
NaN	NaN	NaNxNaN	NaN

Table 3.2 Mating Plan for Crosses between Indigenous Chickens and Their Crosses with Hubbard broiler

Sire	Dam	Mating	Progeny
B	NaF	BxNaF	B/NaF
B	NF	BxNF	B/NF
B	NaN	BxNaN	B/NaN

Collection of eggs commenced 24 hours after the first insemination. The eggs were collected on daily basis, marked according to genotype/treatment number and stored in a cool place for seven days before taken to the hatchery for incubation. Prior to incubation, eggs were fumigated with potassium permanganate and hydrogen peroxide for 30 minutes. Eggs in the incubator were maintained at a temperature of 37.8°C and a humidity of between 78-80%. Eggs were candled twice during the incubation period (at the 7^{th} and 18^{th} day) to determine infertile eggs and dead embryos. They were transferred for the last 3 days of incubation to the hatchers (90% humidity) into marked compartments according to genotype number. The model of incubator used was 1520 sportman®.

3.3 Brooding and Management Practices of Progenies

A total of 196 chicks were generated from the natural mating and artificial insemination. All chicks were brooded in carton boxes with electric bulbs and lanterns. Charcoal pots

were used at night to supplement heat source. The birds were wing tagged according to genotype at day old and vaccinated for Newcastle disease, Gumboro and Fowl Pox. An antibiotic mixed with multivitamin (Keproceryl®) and Coccidiostat (Kepcox®) were routinely provided in drinking water. Chicks were fed commercial broiler starter. The brooding phase lasted for 4 weeks. The chicks were transferred to open-sided houses for rearing at 6 weeks, during which the birds were fed commercial finisher ration.

3.4 Data Collection

3.4.1 Body weight and body linear measurements

Body weight (g) of individual chicken was taken at day old and subsequently on weekly basis with the aid of a top loading sensitive scale (Citizen Electronic Balance, Goldair) with the maximum weight of 3kg. This was done for a period of 10 weeks and the average body weight per genotype was recorded. Weight gain was determined as the difference between present body weight and the last body weight. Growth rate was therefore calculated according to Nwagu and Nwosu (1994) as the weight gain divided by age (14 days).

$$\text{Growth rate (g/d)} = \frac{\text{final weight} - \text{initial weight}}{\text{age}}$$

Tape rule was used to measure the following body linear traits (cm);

Body length: distance from the base of the neck to the uropygial gland at the base of the tail (Molenarr *et al*., 2008)

Breast girth: circumference of the breast around the deepest region of the breast

Shank length: distance of the tarso-metatarsus from the hock joint to the metatarsal pad

Thigh length: distance from the hock joint, through the thigh to the upper joint

3.4.2 Blood collection and analysis

At the end of fifth week of the study period, 54 blood samples (2mls each) were drawn from birds across the six genetic groups with each genetic group containing blood samples from four females and five males. Prior to blood collection, the birds were subjected to 12 hours fasting. Blood collection was carried out aseptically using a sterile syringe and needle via wing veins. Blood samples were collected into sterile test tubes without anticoagulant. Serum was obtained by centrifugation and part of it was analysed for Glucose (Glu) immediately (Trinder, 1969). The other serum samples were stored deep frozen (-10 ˚C) until analyzed for Albumin (Alb), Total Protein (TP) and Alkaline Phosphatase (SAP). Total protein was determined by the Kjedahl method as described by Kohn and Allen (1995) and albumin by the method of Doumas *et al*. (1971).

Total protein was analysed by mixing 0.02ml of serum substrate with Buiret reagent mixture containing sodiumhydroxide (100mmol/l), Na-K-tartrate (16mmol/l), potassium iodide (15mmol/l) and cupric sulphate (6mmol/l) and incubated for 30 minutes at 20-250C. Light of 1cm path with wavelength of 546nm was made to penetrate the mixture. Thereafter, the absorbance of the sample (A sample) and of the standard (A standard) against the reagent blank was measured. The principle behind this was that peptide bond reacts with cupric ions resulting in colour complex formation. Total protein concentration = A sample/A standard x standard concentration. The method above was in accordance with colorimetry methods described by Abd El Azim (2012).

The method of analysis used for the determination of plasma alkaline phosphatase was according to Kind and King (1954). The principle involved is that phenol released by enzymatic hydrolysis from phenyl phosphate, at pH 10 reacts with alkaline oxidizing

agent (4 aminophenazone), to give a red colour, the intensity of which is proportional to enzymatic activity.

All blood analyses were repeated at the end of the experiment (10th week) at the Ahmadu Bello University Teaching Hospital, Zaria.

3.4.3 Proximate analysis of breast meat

At the end of the study period (10th week), three birds from each of the six groups were randomly selected for slaughter and a portion of breast muscle was cut from the carcass for proximate analysis. Analysis of proximate composition of meat was carried out according to standard methods of AOAC (1995) at the central laboratory, NAPRI. The following proximate components were determined: dry matter, crude protein, ether extract, and ash.

Determination of Crude Protein (CP)

A portion of dried meat sample was digested in sulphuric acid (H_2S0_4) which converted all nitrogen (N) present into ammonia (NH_3). The ammonia was obtained by adding sodium hydroxide to the digest, distilled off and collected into standard acid. The quantity collected was determined by titration. The determined nitrogen (N) was multiplied by 6.25 for crude protein.

CP = Nitrogen concentration x 6.25 (AOAC 1995)

Determination of Fat (Ether Extract)

A portion of meat sample was subjected to continuous extraction with petroleum ether using Soxhlet apparatus for 24 hours period. The solvent was then evaporated and the residue was then referred to as resultant extract or crude fat (AOAC 1995).

Determination of Nitrogen Free Extract (NFE) and Metabolizable Energy (ME)

This portion was determined by taking the difference as follows:

Nitrogen free extract (NFE) = 100 - % (CP + EE + Crude fibre (CF) + ASH + Moisture). (AOAC 1995)

Metabolizable energy (ME) calculated according to the procedure of Pauzenga (1985) as:

ME (Kcalkg-1) = 37xProtein (%) + 81.8xFat (%) + 35.5xNFE (%).

3.5 Data Analysis

3.5.1 Analysis of variance of growth, blood and proximate composition traits

The data obtained on growth and proximate composition traits were subjected to one-way analysis of variance with genotype effect using General Linear Model (GLM) procedure of SAS (2002). Means were tested for significant differences by Duncan's multiple range tests (Duncan, 1955). The linear model below was used for the data analysis.

$$Y_{ij} = \mu + g_i + \varepsilon_{ij}$$

Where: Y_{ij} = *performance of the* j^{th} *bird of the* i^{th} *genotypic group*

μ = *overall mean common to all observations*

g_i = *fixed effect due to* i^{th} *genotype (i = 1, 2, 3,4, 5 and 6)*

ε_{ij} = *random error effects peculiar to each observation*

The model above has the following assumptions:

$E(\varepsilon ij) = 0$, the expectations of errors are zero

$Var(\varepsilon ij) = \sigma^2$, the variance of errors are constant across groups (homogeneous)

It was also assumed that errors have a normal distribution

For the biochemical parameters, a three-way analysis of variance with genotype, age and sex effects using General Linear Model (GLM) procedure of SAS (2002) were employed with the following model.

$$Y_{ijkl} = \mu + g_i + a_{ij} + s_{ijk} + \varepsilon_{ijkl}$$

Where: Y_{ijkl} = *performance of the* j^{th} *bird of the* i^{th} *genotypic group,*l^{th} *age and* k^{th} *sex*

μ = *overall mean common to all observations*

g_i = *fixed effect due to* i^{th} *genotype (i = 1, 2, 3,4, 5 and 6)*

a_{ij}= *fixed effect of* j^{th} *age (j= 2: 5 and 10 weeks)*

s_{ijk}= *fixed effect of* k^{th} *sex (k= 2: male and female)*

ε_{ijkl} = *random error effects peculiar to each observation*

The model above has the following assumptions:

$E(\varepsilon ij) = 0$, the expectations of errors are zero

$Var(\varepsilon ij) = \sigma^2$, the variance of errors are constant across groups (homogeneous)

The interaction model for the effects of genotype, age and sex is given below:

$$Y_{ijkl} = \mu + g_i + a_{ij} + s_{ijk} + (ga)_{ij} + (as)_{jk} + (gs)ij + (gas)ijk + \varepsilon_{ijkl}$$

where: μ = *overall mean common to all observations*

g_i = *fixed effect due to* i^{th} *genotype (i = 1, 2, 3,4, 5 and 6)*

a_j= *fixed effect of* j^{th} *age (j= 2: 5 and 10 weeks)*

s_k= *fixed effect of* k^{th} *sex (k= 2: male and female)*

$(ga)ij$= *interaction effect of genotype and age*

$(as)_{jk}$= *interaction effect of age and sex*

$(gs)ij$ = *interaction effect of genotype and sex*

ε_{ijkl} = *random error effects peculiar to each observation*

$E(iid) = 0, \sigma^2$

3.5.2 Phenotypic correlation estimates

The relationships of body weight and growth rate among the six groups were estimated using the PROC CORR procedure of SAS (2002).

$$r = \frac{cov_{xy}}{\sqrt{\sigma^2{}_x \sigma^2{}_y}}$$

Where r = pearson's product correlation coefficient

X = first random variable of the i^{th} body weight and biweekly body weight

Y = random variable of biweekly body weight

CHAPTER FOUR

4.0 RESULTS

4.1 Growth Performance of Indigenous Chickens and their crosses with Hubbard Broiler

Table 4.1 shows the least square means and coefficient of variation for body weight and body linear measurement of indigenous chickens and their crosses with Hubbard broiler chickens at 5 weeks of age. Genotype had significant effect ($P<0.05$) on body weight and body linear measurements among the indigenous chickens and their crosses with Hubbard broiler chickens. The crossbred genetic group appeared similar in body weight (Bw) and thigh length (Tl). However, birds crossed with Hubbard broiler genotype (BxNaF, BxNF and BxNaN) were generally superior in body weight (Bw) compared to genotypes that were not crossed with Hubbard broilers (NaF, NF and NaN). Body weight (Bw), body length (Bl), breast girth (Bg), shank length (Sl) and thigh length (Tl) recorded range of values of 207.07g - 402.70g, 28.35cm - 36.06cm, 11.25cm -15.66cm, 2.65cm - 4.45cm, 5.30cm - 7.34cm, respectively. Table 4.2 shows the least square means and coefficient of variation for body weight and body linear measurement of indigenous chickens and their crosses with Hubbard broiler chickens at 10 weeks of age. Body weight and body linear measurement recorded higher values for birds crossed with Hubbard broiler (BxNaF, BxNF and BxNaN) compared to birds that were not crossed with Hubbard broiler. Bw, Bl, Bg, Sl and Tl recorded the range of values of 442.93±132.28-1144.09±217.39g, 44.90±4.11-61.00±8.40cm, 18.47±2.50-30.69±5.79cm, 6.72±0.44-9.86±4.14cm and 10.10±0.65-12.62±1.15, respectively.

Table 4.1: Least square means (±Standard Error) and Coefficient of Variation for body weight and body linear measurement of indigenous chickens and their crosses with Hubbard broiler chickens at 5 weeks of age.

	Genotype						
Traits	NaF	NF	NaN	B/NaF	B/NF	B/NaN	CV(%)
Bw (g)	245.40^{b}±88	229.85^{b}±549	207.07^{b}±68.95	397.01^{a}±50.38	364.16^{a}±34.55	402.70^{a}±58.94	16.72
Bl(cm)	30.14^{c}±1.75	28.35^{c}±1.40	29.57^{c}±2.39	33.69^{b}±2.73	33.55^{b}±1.60	36.06^{a}±4.44	32.38
Bg(cm)	11.78^{c}±0.35	11.25^{c}±0.44	12.59^{a}±1.09	14.13^{b}±1.46	13.59^{b}±1.09	15.66^{b}±5.87	22.62
Sl (cm)	2.82^{b}±0.39	2.65^{b}±0.17	3.23^{b}±0.63	3.69^{a}±0.70	3.52^{b}±0.64	4.45^{a}±3.06	44.76
Tl (cm)	5.56^{b}±0.65	5.30^{b}±0.80	6.20^{b}±1.35	7.34^{a}±1.19	7.09^{a}±1.03	6.84^{a}±1.08	16.33

^{abc}Means with different superscripts on the same row are significantly different ($p<0.05$). CV= Coefficient of variation Bw= Body weight, Bl= Body length, Bg= Breast girth, Sl= Shank length, Tl= Thigh length. NaF= naked neck x frizzle feather, NF= normal feather x frizzle feather, NaN= naked neck x normal feather, B= broiler.

Table 4.2: Least square means (±Standard Error) body weight and body linear measurement of indigenous chickens and their crosses with Hubbard broiler at 10 weeks of age.

	Genotype					
Traits	NaF	NF	NaN	B/NaF	B/NF	B/NaN
Bw(g)	568.68^{b}±160.91	442.93^{b}±132.28	506.20^{b}±131.70	1144.09^{a}±217.39	1142.37^{a}±24.75	1112.50^{a}±184.36
Bl(cm)	45.92^{c}±4.84	44.90^{c}±4.11	51.28^{b}±5.54	58.63^{a}±4.88	61.00^{a}±8.40	58.01^{a}±5.24
Bg(cm)	20.60^{b}±1.52	18.47^{c}±2.50	24.19^{b}±8.48	29.36^{a}±5.34	30.69^{a}±5.79	30.44^{a}±3.29
Sl(cm)	6.72^{b}±0.44	5.67^{b}±0.78	8.74^{a}±5.79	8.18^{a}±1.09	9.86^{a}±4.14	8.19^{a}±1.07
Tl(cm)	10.10^{b}±0.65	10.10^{b}±1.35	10.70^{b}±1.50	12.62^{a}±1.15	12.40^{a}±2.04	12.53^{a}±0.89

Bw= Body weight, Bl= Body length, Bg= Breast girth, Sl= Shank length, Tl= Thigh length. ^{abc}Means with different superscripts on the same row are significantly different ($p<0.05$). NaF= naked neck x frizzle feather, NF= normal feather x frizzle feather, NaN= naked neck x normal feather, B= broiler.

Table 4.3 shows bi-weekly body weight and growth rate of indigenous chickens and their crosses with Hubbard broiler chicken. CV (%) values range from 11.79 – 64.82. Values obtained for body weight at day old (Bwt1) showed Broiler x Naked/Frizzle (B/NaF) having the highest weight of 26.53g and was similar to Broiler x Normal/Frizzle (B/NF) and Broiler x Naked/normal (B/NaN) which have 25.85g and 26.36, respectively, but differed significantly ($p<0.05$) from Naked/frizzle (NaF), Normal/frizzle (NF) and Naked/Normal (NaN). At week two (Bwt14), B/NaF had the highest mean of 102.32g which only differed from NaF (57.58g), NF (62.02g), and NaN (56.85g). The same trend continued till Bwt70. However, Bwt70 recorded the highest growth rate (28.70) for B/NF, though this was not different from B/NaF and B/NaN with growth rates of 27.17 and 23.18 respectively for Bwt70.

4.2 Blood Biochemical Metabolites of Indigenous Chickens and their crosses with Hubbard Broiler Chickens

Table 4.4 shows the main effects of genotype on blood biochemical metabolites. Genotype had significant effects ($p< 0.05$) on blood biochemical metabolites. The values obtained for total protein (TP), albumin (Alb), glucose (Glu) and serum alkaline phosphatase (SAP) range from 2.48(g/dl) – 3.94 (g/dl), 1.26 (g/dl) – 1.90 (g/dl), 71.54 (g/dl) – 88.64 (g/dl) and 816.57 (iu/l) – 985.40 (iu/l) respectively. However, observed value of TP was highest in NF compared to the other genotypes, but lowest in the value of SAP. It was also observed that the values of TP and Glu were lowest in B/NF. NaF recorded a significantly higher value of SAP among the genotypes.

Table 4.3: Bi-weekly body weight and growth rate of indigenous chickens and their crosses with Hubbard broiler

	Genotype							
Traits	NaF	NF	NaN	B/NaF	B/NF	B/NaN	SEM	CV(%)
Bwt1(g)	22.75^{b}	23.48^{b}	23.28^{b}	26.53^{a}	25.85^{a}	26.36^{a}	0.21	11.79
Bwt14(g)	57.58^{b}	62.02^{b}	56.85^{b}	102.32^{a}	95.95^{a}	100.43^{a}	1.48	24.15
Bwt28(g)	142.76^{b}	141.03^{b}	134.28^{b}	264.27^{a}	257.63^{a}	263.14^{a}	2.79	17.75
Bwt42(g)	291.27^{b}	299.35^{b}	307.47^{b}	477.39^{a}	492.13^{a}	487.74^{a}	5.22	17.35
Bwt56(g)	432.44^{b}	393.25^{b}	391.55^{b}	703.77^{a}	679.57^{a}	695.19^{a}	8.72	20.55
Bwt70(g)	545.55^{b}	476.81^{b}	510.20^{b}	1084.13^{a}	1081.33^{a}	1019.72^{a}	13.19	21.47
Gr1(g/d)	2.49^{b}	2.75^{b}	2.40^{b}	5.41^{a}	5.01^{a}	5.29^{a}	0.12	34.50
Gr2(g/d)	6.08^{b}	5.64^{b}	5.53^{b}	11.57^{a}	11.55^{a}	11.62^{a}	0.19	27.69
Gr3(g/d)	10.61^{c}	11.31^{c}	12.37^{bc}	15.22^{ab}	16.75^{a}	16.04^{a}	0.40	64.82
Gr4(g/d)	10.08^{bc}	6.71^{c}	6.01^{c}	16.17^{a}	13.39^{ab}	14.82^{a}	0.57	64.82
Gr5(g/d)	8.08^{b}	5.97^{b}	8.48^{b}	27.17^{a}	28.70^{a}	23.18^{a}	0.84	61.67

Bwt1-Bwt70= Bi-weekly body weight from day old to 70 days of age, Gr1-Gr5= Bi-weekly growth rate from day old to 70 days of age, g= Gram, g/d= Gram per day.^{abc}Means with different superscripts on the same row are significantly different ($p<0.05$) different. NaF= naked neck x frizzle feather, NF= normal feather x frizzle feather, NaN= naked neck x normal feather, B= broiler.

Table 4.4: Main effects of genotype on blood metabolites

	Genotype							
Traits	NaF	NF	NaN	B/NaF	B/NF	B/NaN	SEM	LOS
TP (g/dl)	3.20[a]	3.94[a]	3.25[a]	3.09[a]	2.48[ab]	2.95[a]	1.20	**
Alb(g/dl)	1.90[a]	1.47[b]	1.40[ab]	1.26[b]	1.27[b]	1.38[b]	0.28	**
Glu(g/dl)	88.64[a]	78.74[d]	88.28[b]	71.54[e]	71.54[e]	80.18[c]	0.21	*
SAP(iu/l)	985.40[a]	816.57[d]	938.36[bc]	941.36[b]	929.78[bc]	951.08[b]	12.09	***

[abc]Means with different superscripts on the same row are significantly different (P<0.05). TP= Total Protein, Alb= Albumin, Glu= Glucose, SAP= Serum Alkaline Phosphatase. NaF= naked neck x frizzle feather, NF= normal feather x frizzle feather, NaN= naked neck x normal feather, B= broiler. LOS= Level of significance, *= 0.05 LOS, **= 0.01 LOS, ***= 0.001LOS

Table 4.5 shows the main effects of age on blood biochemical metabolites. Significant ($P< 0.05$) age effects were observed for all metabolites, whereby the birds at week 5 had higher values except SAP which was recorded to be high at week 10. Thus, the values for TP, Alb and Glu decreased as the age increased while the value for SAP increased as the age increased.

Table 4.6 shows the effects of sex on blood biochemical metabolites. Sex effects were significantly different ($P<0.05$) for TP and Glu. Values for Alb and SAP were similar in both sexes. Values for TP and Glu were also significantly higher in females than their male counterparts.

The least squares means of biochemical metabolites for indigenous chickens and their crosses with Hubbard broiler chickens are shown in Table 4.7. Significant ($P<0.05$) effects of age, sex and genotype were observed for all biochemical metabolites with the chickens at week 5 producing higher values. Though values for SAP and few of the values for Glu were higher at week 10. Females recorded higher values in all metabolites than their male counterparts. Again, mean values for all metabolites were highest in NF, followed by NaN.

Table 4.5: Main effects of age on blood biochemical metabolites

	Age			
Traits	5	10	SEM	LOS
TP (g/dl)	3.68[a]	2.27[b]	1.21	**
Alb (g/dl)	1.53[a]	1.10[b]	0.29	**
Glu (g/dl)	88.64[a]	66.86[b]	0.22	**
SAP (iu/l)	903.19[b]	977.36[a]	12.10	***

[abc]Means with different superscripts on the same row are significantly different (P<0.05). TP= Total Protein, Alb= Albumin, Glu= Glucose, SAP= Serum Alkaline Phosphatase. LOS= Level of significance, *= 0.05 LOS, **= 0.01 LOS, ***= 0.001LOS

Table 4.6: Main effects of sex on blood biochemical metabolites

	Sex			
Traits	Male	Female	SEM	LOS
TP (g/dl)	2.57[b]	3.87[a]	1.21	**
Alb (g/dl)	1.25	1.43	0.29	NS
Glu (g/dl)	76.40[b]	80.54[a]	0.22	**
SAP (iu/l)	938.82	942.11	12.10	NS

[abc]Means with different superscripts on the same row are significantly different (P<0.05). TP= Total Protein, Alb= Albumin, Glu= Glucose, SAP= Serum Alkaline Phosphatase. LOS= Level of significance, *= 0.05 LOS, **= 0.01 LOS, ***= 0.001LOS

Table 4.7: Least squares mean (±Standard Error) of biochemical metabolites of crosses between indigenous chickens with different age and sex.

		Genotypes					
		NaF		NF		NaN	
Traits	Age	Male	Female	Male	Female	Male	Female
TP (g/dl)	5	$3.40^{b}\pm0.00$	$4.05^{b}\pm11.62$	$3.60^{b}\pm0.00$	$4.86^{a}\pm4.01$	$3.56^{b}\pm14.36$	$4.85^{a}\pm12.02$
Alb (g/dl)		$1.00^{c}\pm0.00$	$1.57^{b}\pm0.96$	$1.60^{ab}\pm0.00$	$1.76^{a}\pm2.08$	$1.64^{a}\pm3.97$	$1.75^{a}\pm3.02$
Glu (g/dl)		$65.60^{ab}\pm0.00$	$100.34^{b}\pm2.65$	$157.4^{a}\pm0.00$	$60.20^{b}\pm1.44$	$87.20^{b}\pm2.71$	$161.00^{a}\pm2.12$
SAP (iu/l)		$970.00^{a}\pm0.00$	$982.50^{a}\pm21.55$	$957.00^{a}\pm0.00$	$622.00^{c}\pm311.90$	$851.80^{b}\pm255.38$	$998.50^{a}\pm2.12$
TP (g/dl)	10	$1.97^{b}\pm6.95$	$3.10^{a}\pm0.00$	$2.50^{b}\pm14.85$	$4.10^{a}\pm0.00$	$2.27^{b}\pm9.93$	$3.65^{a}\pm9.91$
Alb (g/dl)		$1.07^{b}\pm2.87$	$1.30^{a}\pm0.00$	$1.05^{b}\pm0.71$	$1.20^{a}\pm0.00$	$1.26^{a}\pm3.61$	$1.00^{b}\pm1.41$
Glu (g/dl)		$93.50^{ab}\pm2.87$	$134.00^{a}\pm0.00$	$89.00^{b}\pm0.71$	$116.00^{a}\pm0.00$	$128.06^{a}\pm3.61$	$80.00^{b}\pm1.41$
SAP (iu/l)		$987.50^{b}\pm14.27$	$1004.00^{a}\pm0.00$	$964.50^{d}\pm0.71$	$964.00^{d}\pm0.00$	$978.67^{c}\pm17.43$	$1007.00^{a}\pm2.83$

^{abc}Means with different superscripts on the same row (within sex sub group) are significantly different ($p<0.05$). TP= Total Protein, Alb= Albumin, Glu= Glucose, SAP= Serum Alkaline Phosphatase NaF= naked neck x frizzle feather, NF= normal feather x frizzle feather, NaN= naked neck x normal feather.

The least square means of biochemical metabolites for indigenous chickens and their crosses with Hubbard broiler are shown in Table 4.8. Significant effects ($P<0.05$) of age, sex and genotype were observed for Alb, TP10 and SAP10. Five weeks old chickens produced higher values, though values of SAP were higher in chickens of week 10.

4.3 Estimates of Phenotypic Correlation for Growth and Blood Biochemical Metabolites

Tables 4.9 - 4.12 show estimates of phenotypic correlation for growth and blood biochemical metabolites of indigenous chickens and their crosses with Hubbard broiler chickens.

4.3.1 Growth trait

Table 4.9 shows the coefficient of phenotypic correlation between bi-weekly bodyweight and growth rate of indigenous chickens. Correlation varied in magnitude and direction. Positive, negative and significant relationship existed between bi-weekly body weight and growth rate. Bwt1 was negatively and significantly ($P<0.05$) correlated with Bwt56, Bwt70 and Gr4. The negative significant phenotypic correlation in growth rate diminished at the 56 days of age. However, Bwt1 had no significant correlation with growth rate from 14-42 and 70 days of age.

There were no significant correlations between Bwt14 and Bwt70, Gr3. Also, there were no significant correlations between Bwt28 and Bwt42, Bwt56, Bwt70 and Gr4. Positive correlations were observed between Bwt42 and Bwt56, Bwt70, though their corresponding growth rates not significant. Both Bwt56 and Bwt70 were positively and significantly correlated with Gr4 and Gr5 respectively.

Table 4.8: Least squares mean (±Standard Error) of biochemical metabolites of indigenous chickens crossed with Hubbard broiler with different age and sex.

		Genotypes					
		B/NaF		B/NF		B/NaN	
Traits	Age	Male	Female	Male	Female	Male	Female
TP (g/dl)	5	3.57±14.33	4.33±11.89	2.97±9.38	2.77±6.35	2.92±14.27	4.55±31.63
Alb (g/dl)		1.53^{a}±2.67	1.51^{a}±2.99	1.53^{a}±2.00	1.23^{ab}±3.21	1.48^{a}±2.67	1.61^{a}±3.92
Glu (g/dl)		77.30±1.39	95.30±3.12	103.22±2.10	90.80 ±1.54	85.94 ±2.51	86.84±2.32
SAP (iu/l)		850.25±231.76	970.67±19.22	899.00±177.25	980.33±20.55	907.14±192.19	947.33±36.73
TP (g/dl)	10	2.17^{ab}±7.99	2.96^{a}±5.77	1.90^{b}±7.16	2.40^{ab}±15.00	1.83^{b}±5.83	3.36^{a}±12.66
Alb (g/dl)		1.06^{ab}±2.68	1.20^{a}±1.73	1.04^{ab}±2.40	1.16^{a}±6.11	0.97^{ab}±2.73	1.43^{a}±2.08
Glu (g/dl)		53.00±2.52	76.40±1.51	42.02±2.29	57.14 ±1.10	76.22±1.99	65.06±2.51
SAP (iu/l)		980.86^{a}±15.00	974.67^{a}±13.28	973.89^{a}±44.43	944.00^{b}±54.81	978.00^{a}±34.60	980.33^{a}±18.23

^{abc}Means with different superscripts on the same row (within sex sub group) are significantly different ($p<0.05$). TP= Total Protein, Alb= Albumin, Glu= Glucose, SAP= Serum Alkaline Phosphatase NaF= naked neck x frizzle feather, NF= normal feather x frizzle feather, NaN= naked neck x normal feather B= broiler.

Table 4.9: Phenotypic correlation between bi-weekly body weight and growth rate of indigenous breeds of chickens

	Bwt1(g)	Bwt14(g)	Bwt28(g)	Bwt42(g)	Bwt56(g)	Bwt70(g)	Gr1(g/d)	Gr2(g/d)	Gr3(g/d)	Gr4(g/d)	Gr5(g/d)
Bwt1(g)	-	0.00^{NS}	0.02^{NS}	-0.15^{NS}	-0.28*	-0.27*	-0.10^{NS}	0.02^{NS}	-0.15^{NS}	-0.27*	-0.10^{NS}
Bwt14(g)		-	0.71***	0.23*	0.43***	0.18^{NS}	0.99***	-0.20*	-0.04^{NS}	0.42***	-0.31**
Bwt28(g)			-	-0.01^{NS}	0.06^{NS}	-0.18^{NS}	0.70***	0.55***	-0.37**	0.11^{NS}	0.44***
Bwt42(g)				-	0.76***	0.68***	0.25*	-0.29*	0.93***	0.14^{NS}	0.17^{NS}
Bwt56(g)					-	0.86***	0.46***	0.42***	0.68***	0.76***	0.14^{NS}
Bwt70(g)						-	0.21^{NS}	0.46***	0.70***	0.62***	0.62**
Gr1(g/d)							-	-0.20^{NS}	-0.02^{NS}	0.45***	-0.30*
Gr2(g/d)								-	-0.47**	-0.35**	-0.25*
Gr3(g/d)									-	0.09^{NS}	0.31**
Gr4(g/d)										-	0.04^{NS}
Gr5(g/d)											-

Bwt1-Bwt70= Bi-weekly body weight from day old to 70 days of age, Gr1-Gr5= Bi-weekly growth rate from day old to 70 days of age, g= Gram, g/d= Gram per day. NS= Not significant *= 0.05 LOS, **= 0.01 LOS, ***= 0.001LOS

Table 4.10 shows the coefficient of phenotypic correlation between bi-weekly bodyweight and growth rate of indigenous chickens crossed with Hubbard broiler. Correlation varied in magnitude and direction. Positive, negative and significant relationship existed between bi-weekly and growth rate. Bwt1 was positively and significantly ($P<0.05$) correlated with Bwt28 and Bwt42.The significant correlation diminished after 42 days of age. Furthermore, it was observed that Bwt1 had no significant correlation with growth rate from 14-70 days of age.

Bwt14 correlated positively and significantly ($P<0.05$) with Bwt28, Gr1 ($P<0.0001$) and Gr2 ($P<0.05$). Subsequently positive correlations were obtained between Bwt28 and Bwt42 with corresponding growth rate to 56 days (Gr3 and Gr4). Both Bwt56 and Bwt70 were positively and significantly correlated with Gr4 andGr5. Gr1 and Gr3, Gr1 and Gr5 and Gr4 and Gr5 were not significant and were negatively correlated, indicating that as the age of the birds advanced, the rate of growth decreased significantly. Also, Gr1 and Gr4 were positively correlated, though the positive correlation was not significant

4.3.2 Blood biochemical metabolites

Table 4.11 shows the phenotypic correlation between blood metabolites at 5 and 10 weeks of age for indigenous chickens. Correlation varied in magnitude and direction. Positive, negative and significant existed between biochemical metabolites with age. TP5 was positively and significantly ($P<0.05$) correlated with TP10, but negatively correlated with SAP5. The negative significant correlation diminished at 5 weeks of age. Furthermore, it was observed that TP5 had no significant correlation ($P>0.05$) with Alb5, Alb10, Glu5, Glu10, and SAP10. Alb10 correlated positively and significantly ($P<0.05$) with Glu10. Positive correlation was obtained between Glu5 and SAP5.

Table 4.10: Coefficient of phenotypic correlation between bi-weekly body weight and growth rate of indigenous chickens crossed with Hubbard broiler

	Bwt1(g)	Bwt14(g)	Bwt28(g)	Bwt42(g)	Bwt56(g)	Bwt70(g)	Gr1(g/d)	Gr2(g/d)	Gr3(g/d)	Gr4(g/d)	Gr5(g/d)
Bwt1(g)	-	0.07^{NS}	0.17*	0.24*	0.07^{NS}	0.16^{NS}	-0.11^{NS}	0.14^{NS}	0.12^{NS}	-0.06^{NS}	0.12^{NS}
Bwt14(g)		-	0.18*	0.09^{NS}	0.09^{NS}	-0.03^{NS}	0.98***	-0.23*	-0.02^{NS}	0.04^{NS}	0.09^{NS}
Bwt28(g)			-	0.20*	0.15^{NS}	0.10^{NS}	0.15^{NS}	0.16^{NS}	0.82***	-0.39**	-0.01^{NS}
Bwt42(g)				-	0.16^{NS}	0.09^{NS}	0.04^{NS}	0.16^{NS}	0.82***	0.39***	0.01^{NS}
Bwt56(g)					-	0.27**	0.08^{NS}	0.11^{NS}	0.06^{NS}	0.85***	0.33***
Bwt70(g)						-	0.06^{NS}	0.12^{NS}	0.12^{NS}	0.21*	0.82**
Gr1(g/d)							-	-0.26*	-0.05^{NS}	0.05^{NS}	-0.11^{NS}
Gr2(g/d)								-	-0.39**	0.02^{NS}	0.05^{NS}
Gr3(g/d)									-	-0.39**	-0.01^{NS}
Gr4(g/d)										-	-0.30^{NS}
Gr5(g/d)											-

Bwt1-Bwt70= Bi-weekly body weight from day old to 70 days of age, Gr1-Gr5= Bi-weekly growth rate from day old to 70 days of age, g= Gram, g/d= Gram per day. NS= Not significant *= 0.05 LOS, **= 0.01 LOS, ***= 0.001LOS

Table 4.11: Coefficient of phenotypic correlation between blood biochemical metabolites at 5 and 10weeks of age of indigenous chickens

	Tp5(g/dl)	Tp10(g/dl)	Alb5(g/dl)	Alb10(g/dl)	G5(g/dl)	G10(g/dl)	SAP5(iu/l)	SAP10(iu/l)
TP5(g/dl)	-	0.72**	0.47^{NS}	-0.20^{NS}	-0.23^{NS}	-0.33^{NS}	-0.56*	0.24^{NS}
TP10(g/dl)		-	0.44^{NS}	0.26^{NS}	-0.05^{NS}	-0.20^{NS}	-0.26^{NS}	0.30^{NS}
Alb5(g/dl)			-	0.56^{NS}	-0.06^{NS}	0.01^{NS}	-0.24^{NS}	0.20^{NS}
Alb10(g/dl)				-	-0.22^{NS}	0.50*	-0.28^{NS}	0.04^{NS}
Glu5(g/dl)					-	-0.27^{NS}	0.49*	0.46^{NS}
Glu10(g/dl)						-	0.22^{NS}	-0.17^{NS}
SAP5(iu/l)							-	0.40^{NS}
SAP10(iu/l)								-

TP= Total Protein, Alb= Albumin, Glu= Glucose, SAP= Serum Alkaline Phosphatase, NS= Not significant, *= 0.05 LOS, **= 0.01 LOS, ***= 0.001LOS

Table 4.12 shows the phenotypic correlation between blood biochemical metabolites at 5 and 10 weeks of age for indigenous chickens crossed with Hubbard broiler. Phenotypic correlation varied in magnitude and direction. TP5 was positively and significantly ($P<0.05$) correlated with Alb5 and Alb10. The significant correlation diminished between TP5 and Alb10. Also, the phenotypic correlation between TP10 and Alb10 was very high ($P<0.0001$) and positive. Alb5 and Alb10 were also correlated positively.

4.4 Proximate Composition of Breast Meat

The results for the proximate components of breast meat from indigenous chickens and their crosses with Hubbard broiler are shown in Table 4.13. The values obtained for dry matter (DM), Ash, ether extract (EE), and crude protein (CP) range from 92.60-95.48, 4.55-5.46, 7.08-17.98, and 63.25-70.06, respectively. There were significant differences ($P<0.05$) in all proximate components within and between indigenous chickens and their crosses with Hubbard broiler chickens, though DM was observed to show no significant difference ($P>0.05$) within indigenous chickens crossed with Hubbard broiler. NF recorded highest values in DM, Ash and CP, while B/NF recorded the lowest values in DM and Ash but highest in EE.

Table 4.12: Coefficient of phenotypic correlation between blood biochemical metabolites at 5 and 10 weeks of age for indigenous chickens crossed to Hubbard broiler chickens.

	Tp5(g/dl)	Tp10(g/dl)	Alb5(g/dl)	Alb10(g/dl)	G5(g/dl)	G10(g/dl)	SAP5(iu/l)	SAP10(iu/l)
TP5(g/dl)	-	0.28^{NS}	0.34*	0.40*	-0.16^{NS}	-0.05^{NS}	-0.28^{NS}	0.24^{NS}
TP10(g/dl)		-	0.10^{NS}	0.56***	0.21^{NS}	0.08^{NS}	-0.12^{NS}	-0.13^{NS}
Alb5(g/dl)			-	0.39*	-0.20^{NS}	-0.26^{NS}	-0.26^{NS}	0.04^{NS}
Alb10(g/dl)				-	-0.34^{NS}	-0.08^{NS}	-0.24^{NS}	-0.27^{NS}
Glu5(g/dl)					-	0.21^{NS}	0.04^{NS}	0.19^{NS}
Glu10(g/dl)						-	0.03^{NS}	-0.04^{NS}
SAP5(iu/l)							-	-0.08^{NS}
SAP10(iu/l)								-

TP= Total Protein, Alb= Albumin, Glu= Glucose, SAP= Serum Alkaline Phosphatase, NS= Not significant, *= 0.05 LOS, **= 0.01 LOS, ***= 0.001LOS

Table 4.13: Proximate composition of breast meat from indigenous chickens and their crosses with Hubbard broiler

	Genotypes							
Traits	NaF	NF	NaN	B/NaF	B/NF	B/NaN	SEM	LOS
DM(%)	94.86^{b}	95.48^{a}	95.42^{a}	92.82^{c}	92.60^{c}	93.18^{c}	0.42	*
Ash(%)	4.68^{c}	5.46^{a}	5.06^{b}	4.72^{c}	4.55^{d}	5.46^{a}	0.13	*
EE(%)	11.67^{c}	10.24^{d}	7.08^{e}	14.33^{b}	17.98^{a}	11.20^{c}	0.82	**
CP(%)	65.00^{cd}	70.06^{a}	68.47^{b}	63.25^{de}	66.16^{c}	63.53^{d}	1.14	*

^{abc}Means with different superscripts on the same row are significantly different ($p<0.05$). DM = dry matter, EE = ether extract, CP = crude protein. NaF= naked neck x frizzle feather, NF= normal feather x frizzle feather, NaN= naked neck x normal feather, B= broiler. LOS= Level of significance,*= 0.05 LOS, **= 0.01 LOS,***=0.001LOS

CHAPTER FIVE

5.0 DISCUSSIONS

5.1 Body Weight and Body Measurement

Body weight and body measurement observed in this study increased with increasing age. Significant difference within the genetic lines agrees with the report of Okon *et al.* (1996) who stated that body weights of crossbred chickens differed with breed and that Lohman brown broilers had higher body weight than Cobb broilers when crossed with the Nigerian indigenous chickens. Essien and Adeyemi (1999) also noted that body weight differed with breeds. Significant ($p<0.05$) differences obtained in body weight across groups in the two periods were not consistent with the observations of Oke (2011) that there were no significant differences in body weight and body measurement traits for most of the study periods. Range of values for BW5 (207.07-402.70g) were within the reported observations by earlier researchers (Essien and Adeyemi, 1999; Peters *et al.*, 2005 and Oke 2011) who worked on Nigerian indigenous chickens. Significant difference among the body measurement are in consonance with the reports of several researchers (Essien and Adeyemi, 1999; Peters *et al.,* 2005, Mahrous *et al.,* 2008 and Oke 2011). The present values are comparable to those reported by Fayeye *et al*. (2006). However, Patra *et al*. (2002) reported that naked neck chickens have heavier body weight compared to their normal feathered counterparts. Similarly, Galal (2001) reported the superiority of naked neck and frizzle genes over normal feathered chickens in body weight, shank length and comb length. Trend in this study indicated that B/NaF was more superior to other genetic combinations at 5 weeks of age. This is a clear indication that the Hubbard

broiler gene, when crossed with the *Na* gene or the *F* either singularly or in combination, confers better growth ability. At 10 weeks of age, body weight range (442.93 - 1144.09) observed fell within the values reported by researchers (Mahrous *et al.*, 2008 and Oke, 2011). This is consistent with the findings of Cahaner *et al.* (1993).

Observed values (22.75-26.53) of weight at day old were lower than the range of 24.68 to 27.83 g reported by Pinchasov (1991) and higher than the lower limit of 21.82 but lower compared to the upper limit of 28.06g recorded by Ndofor-Foleng *et al*. (2006) for light and heavy ecotype chickens. B/NaF were consistent in body weight and growth rate compared to other genetic groups. This might be due to the fact that the frizzle and naked neck genes conferred fast growing ability either singularly or in combinations with broilers.

5.2 Biochemical Metabolites

Blood are reliable health indicators. They are used for on the spot assessment of health status of animal. All biochemical parameters measured in the present experiment were within the normal physiological ranges reported for chickens in literature. Observed values for indigenous chickens were higher than their counterparts crossed with Hubbard broiler. Values for Alb, Glu and SAP were significantly highest in NaF compared to other genotypes, with TP values being similar among genotypes. NF recorded the highest and lowest values of TP and SAP respectively. The high TP value in this study could be as a result of the presence of keratin (a protein structure) in the uniformly distributed feather of the normal feathered chickens. The higher values in NaF (naked x frizzle) and NaN (naked x normal) are in agreement with the findings of Clubb and Schubot (1991), although they attributed this to higher weight gain as a result of reduction in heat load. In

a similar finding, El-Safty *et al*. (2006) reported the superiority of the naked neck gene in biochemical parameters compared to that of normal feathered. This could be a boost to the growth and reproductive life of the former.

Enzyme activities in this study ranged from 816.57-985.40 i.u/l among the six genetic groups. This range was above the values reported in the literatures (Orunmuyi, 2006, and Ladokun *et al*., 2008), but were within the normal range (568-8831 IUL-^{1}) reported for broilers (Clinical Diagnostic Division, 1990). The lowest value of SAP recorded for NF was obviously due to normal feather gene effect as this was also seen in the same gene combination crossed with broiler. Significant differences in albumin within the genetic groups was similar to the trend obtained by Simaraks *et al*. (2004) but lower than the value reported by El-Safty *et al*. (2006). This disparity might be due to source of experimental birds, where such birds might have undergone previous selection and improvement, unlike birds that were purchased fresh from the market as foundation stock. The choice of statistical package used for the analysis may also be a factor.

Schmidt *et al*. (2009) also reported that blood traits in birds may vary due to age, sex, and also season. In this study, age effects were observed for all blood traits whereby the birds at week 5 had higher values except SAP which was recorded to be higher at week 10. Though the increased SAP with age conforms with the report of Orunmunyi (2006), the decreased TP, Alb and Glu values were contrary to the findings of Awotwi (1990) who indicated higher TP, Alb, Cholesterol and Glu in growing Ghanian domestic chickens. The results were also contrary to the results of Ritchie *et al*. (1994) who asserted that serum glucose in adults were higher than that of young chickens. The drop in glucose level in older birds may also be attributed to the health condition or muscular activity

during the struggling and running that preceded the collection of blood samples. Total proteins for the six genetic groups according to age were higher than the normal range in domestic turkey (4.9-7.6mgdL-1) and pheasant (male=5.65 mgdL-1; female=6.06 mgdL-1), guinea fowl (3.5-4.4 mgdL-1) and common quail (3.4-3.6 mgdL-1) (Ritchie *et al*., 1994).

Activities of SAP were similar between the males and females. Values obtained for SAP in this study, according to sex effect were lower than values previously reported in literature for male and female broilers, but were within the normal range (568-8831 IUL-^{1}), Melluzzi *et al*. (1992). There were significant sex ($p<0.05$) effect in TP and Glu, with females chickens reported to have higher values in all blood traits. This result was similar to the findings of Simaraks *et al*. (2004) and Pampori and Iqbal (2007) who studied the serum total protein in broiler, and the native chickens of Kashmir respectively. The higher mean total protein value in female birds could be attributed to an estrogen-induced hyperproteinemia which is associated with the age at which egg production approaches (Simaraks *et al*., 2004). Sturkie (1965) reported that glucose levels of female (109 g/dl) are lower than that of male (114g/dl) chickens, which was not the case for this study.

5.3 Phenotypic Correlation of Body Weight and Growth Traits

The estimates of phenotypic correlation in the present study are comparable to those reported by earlier workers (Gueye, 1998). The strong relationship existing between body weight and growth rate may be useful as selection criterion. Traits that showed negative relationship imply that an increase in a particular trait may lead to a decrease in corresponding trait. This, therefore, provides a basis for the phenotypic manipulation and improvement of the native stock using improved broiler breed. Values obtained for

coefficients of phenotypic correlation at BW14 and GR1 agreed with literature values reported by Okon *et al.* (1996) where moderate to high and positive ranges of phenotypic correlations between body weight and relative growth rate were observed at this age in their study. This shows that favourable relationships exist among traits that had higher correlation coefficients. It further explains that such traits could be collectively included in the selection index to achieve positive phenotypic progress (Ali and Khalid, 2002). Okoro and Ogundu (2006) equally recorded high and positive coefficients of correlation between body weight and other growth traits and it was concluded that these traits are good indicators of body weight.

5.4 Phenotypic Correlation of Biochemical Metabolites at age 5 and 10 for Indigenous Chickens and Their Crosses with Hubbard Broiler

Positive and high phenotypic correlation was observed between TP5 and 10(r=0.72) with highly significant effect in the indigenous breed. The negative, positive, low and moderate association indicates that weak and inverse relationship existed between blood traits at 5 and 10 weeks of age. This implies that selection at early age of any of these traits will not lead to a significant improvement at later ages. Similar trend was observed from earlier work by Marcela *et al*. (2008) which agrees with the coefficients obtained from this study.

Highest association (Alb10 and Tp 10; r=0.56***) obtained for Indigenous and broiler crosses implies that at later ages, increase in the content of albumin will cause an increase in the quantity of total protein. This agrees with the report of several authors (Aengwanich *et al*., 2004), who obtained high relationship between albumin and total protein at several ages.

5.5 Proximate Analysis

Significant differences obtained in proximate analysis for meat quality traits contrast the observation made by Souza *et al.* (2011) who stated that meat proximate composition was not influenced by genetic in all the broiler strains. Significant difference obtained in protein, fat, ash and dry matter for all the genetic types is an indication that genotype showed effect on these traits. The fat content obtained in this study is higher than value obtained by Souza *et al.* (2011) and the normal levels (7.3%). This implies that the genetic types under study are of higher fat content which may be detrimental to the health of the consumers. The significant differences obtained in this study for protein, fat and ash content for all the groups considered also contrasts with the report of Elie *et al.* (2010) who stated that the mean of % protein, mean % fat and mean % ash did not differ regardless of the nature of the four treatments in their study. Also significant differences obtained in all the measured traits of meat quality traits in all the groups were in agreement with the report of Souza *et al.* (2011), and they suggested that meat composition was not influenced by genetic strains which converse with the report in this study.

CHAPTER SIX

6.0 SUMMARY, CONCLUSION AND RECOMMENDATION

6.1 Summary

This study was carried out to assess the growth and biochemical metabolites of three types of indigenous chickens and their crosses with Hubbard broiler.

A total of 110 foundation stock consisting of 90 pullets (30 from each genotypic group), three cockerels from naked/frizzle (NaF) and normal/frizzle (NF), four cockerels from naked/normal (NaN) and 10 male Hubbard broiler chickens were used for this study. Ten pullets and the cockerels from each of the three genotypic groups were randomly mated, and the other 20 pullets from each of the three genotypic groups were inseminated artificially with pooled semen from the broilers.

Growth and biochemical metabolites, including proximate compositions of breast meat were evaluated on the resulting progenies. Body weight and body linear measurements were significantly influenced ($p<0.05$) by the introduction of broiler gene, with BxNaN having the best performance at the 5^{th} week of age (402.70g). This was not the case at week 10 as BxNaF was superior (1144.09g). Significant differences in linear measurements were influenced by the growth rate of chickens crossed with broilers. Body weight of chicks at day-old had no effect on subsequent growth rate and final body weight of chickens as NaF which has the lowest body weight at day-old appeared superior (though not significantly different) in growth rate at some periods, and final body weight when compared to NF and NaN. This was also seen in chickens crossed with broiler.

Biochemical traits show that indigenous crosses showed greater values compared to their broiler crosses counterparts. Generally, naked/frizzle (NaF) had the greatest values except total protein (TP) which was highest in normal/frizzle (NF). It was also gathered that age and sex had significant effect on biochemical traits. Young female birds had significantly higher values than their male counterparts.

Values of dry matter (DM), Ash and crude protein (CP) were highest in naked neck/frizzle (NaF) followed by normal/frizzle (NF), with only ether extract (EE) which was highest in Hubbard broiler x normal/frizzle (BxNF).

6.2 Conclusion

The variations in body weight and linear measurements imply that genotype is a determining factor for growth. Hubbard broiler x Naked neck/Frizzle (BxNaF) was the most superior in body weight at 10 weeks compared to the other genetic groups.

Evaluated biochemical metabolites differ significantly among genotypes, ages and sexes. This indicates that genotype, age and sex determine biochemical values. However, biochemical values of investigated birds were within reference values.

The significant differences in proximate composition of meat were due to gene effect. Cross between naked neck/frizzle gene sires and naked neck/frizzle gene dams produced the best meat quality as the result suggests low fat level and high protein level.

6.3 Recommendations

From the results obtained in this study, the following recommendations were made:

1. As a result of the superior performance of the naked neck and frizzle birds, the genes should be incorporated into broiler genes for local breed development strategies.

2. The results of biochemical metabolites should be considered as added information towards the goal of understanding indigenous chicken physiology in order to produce individuals that are fit and more productive.

3. For quality meat consumption, crosses between the local genes are best due to low fat and protein contents in meat.

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