GENETIC CHANGE IN THE NIGERIAN HEAVY LOCAL CHICKEN ECOTYPE THROUGH SELECTION FOR BODY WEIGHT AND EGG PRODUCTION TRAITS

BY

OGBU, COSMAS CHIKEZIE
PG/Ph.D/02/33657

DEPARTMENT OF ANIMAL SCIENCE
FACULTY OF AGRICULTURE
UNIVERSITY OF NIGERIA,
NSUKKA

MAY, 2010

GENETIC CHANGE IN THE NIGERIAN HEAVY LOCAL CHICKEN ECOTYPE THROUGH SELECTION FOR BODY WEIGHT AND EGG PRODUCTION TRAITS

BY

OGBU, COSMAS CHIKEZIE
DVM, M.Sc. (Animal Breeding/Genetics)

A THESIS
SUBMITTED TO THE DEPARTMENT OF ANIMAL SCIENCE, FACULTY OF AGRICULTURE, UNIVERSITY OF NIGERIA, NSUKKA IN FULFIMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF DOCTOR OF PHILOSOPHY (Ph.D) DEGREE IN
ANIMAL BREEDING AND GENETICS

PROJECT SUPERVISORS:

PROF. DR. C.C. NWOSU (PROF. EMERITUS)
PROF. L.N. NWAKALOR

CERTIFICATION

OGBU, COSMAS CHIKEZIE, a postgraduate student in the Department of Animal Science, Faculty of Agriculture, with Registration Number **PG/Ph.D/2002/33657,** has satisfactorily completed the requirement of research work for the award of the degree of Doctor of Philosophy in Animal Breeding and Genetics. The work embodied in this thesis is original and has not been submitted in part or full, for any other degree in this or any other university.

_____ _____

Supervisor(1) Supervisor(2)

_____ _____

Head of Department External Examiner

DEDICATION

To You Lord, Jesus. My Lord, and my God. My *Summun Puntum*

ACKNOWLEDGMENT

My deep gratitude and appreciation go to my supervisors, Professor, Dr. C.C. Nwosu (Professor Emeritus) and Prof. L.N. Nwakalor for their kind attention, guidance, support, encouragement and constructive criticisms. My lead supervisor, Prof. Dr. C.C. Nwosu was singularly outstanding. He shared in my worries and anxiety. May he also share in my triumph.

Mr Francis Aroh (retired) was completely wonderful in his service and support. He made sure my experimental birds were well taken care of especially in my moments of crisis (health problems, death, scarcity of water, feed raw materials etc). I am sincerely and immensely grateful.

I also wish to thank the heads of the Department of Animal Science over the period that this study lasted (2002 to 2010) namely Prof. G.C. Okeke, Prof. A.G. Ezekwe and presently Dr. S.O.C Ugwu for their wonderful support and encouragement.

I wish to thank my family members, namely my father Chief John Ogbu Okonkwo Anigweshi of blessed memory and my indefatigable mother, Mrs. Mary Nwankwo, Ogbu (*a.k.a Nwanyi nka*). My sibs: Comrade Peter Maduabuchi Ani, Bar. Simeon N. Ogbu, Mr. Simon Ogbu, Mr. Luke Achunike Ogbu, Benedeth, Nkechiyere Ogbu, and Mrs. Josephine Amamnke Ogbu-Agbodo for their support and encouragement. My father, Chief John Ogbu Okonkwo Anigweshi passed on towards the end of my field work. May I announce to you Dad, that this work has been completed.

This work would have been a lot more difficult to accomplish without the acceptance, and generous love showered on me by friends and members of the family of Mr. and Mrs. Maurice and Gloria Eze, Mr. Nicholas Eze, Mr. Uche Malachy Eze, Miss Anayo Odo, Miss Ogechukwu Eze. Little Oluchi and Chidimma Eze and a host of others. In addition to housing and feeding me all through this work they provided accommodation for my incubators and young chicks at some point and assisted in so many other ways too numerous and intricate to enumerate one by one. I will ever remain grateful to this Godly family. Mr. Maurice Eze passed on mid-way into this project. May his gentle soul continue to rest in the bosom of the Lord. So be it.

Finally, I prostrate in reverence and gratitude before God Almighty whose love, goodness and mercy have accompanied, covered and protected me these difficult and anxious years as I traversed the risky and dangerous road from Enugu to Nsukka in search of this academic laurel. I

hence dedicate this work wholly and entirely to you Lord Jesus. My Lord, and My God. My *Summum Puntum*.

ABSTRACT

The study was carried out to determine the genetic change in the Nigerian heavy local chicken ecotype (NHLCE) through selection for body weight and egg production traits. Progenies (G_0 generation) generated from breeding parents randomly selected from the parent stock of the NHLCE formed the materials for the research. On hatching, the chicks were grouped according to sire families using colour markers. The chicks were brooded and reared according to standard management practices. They were fed a starter mash containing 18% crude protein and 2800 Kcal/kgME from 0 – 8 weeks and a growers mash containing 15% crude protein and 2670 Kcal/ kgME from 8 weeks to 20 weeks. At 20 weeks, all pullets were moved into individual laying cages for short-term (16 weeks) egg production. From then the birds were fed layers mash containing 16.5% crude protein and 2600Kcal/kgME. Data were collected on body weight, egg weight and egg number. A control population was maintained for each generation and was used to measure environmental effects. At the end of the 16 weeks egg production period, hens were subjected to selection using a multiple trait selection index incorporating body weight at first egg (BWFE), average egg weight and total egg number. The relative economic weights of the traits and their heritabilities were used to weight the phenotypic values of each trait in the index. The index score of each bird became a univariate character, which enabled the hens to be ranked for purposes of selection. Males were selected based on their individual body weight performances at 39 weeks of age using mass selection. Selected parents from G_0 generation were used to generate the G_1 generation which in turn yielded the parents of the G_2 generation. Data on body weight, BWFE, egg weight and egg number were subjected to statistical analysis to obtain means, standard error of means and standard deviation using the SPSS 2001 statistical package. Analysis of variance yielded sire component of variance from which the additive genetic heritabilities of the traits were calculated. Genetic, phenotypic and environmental correlations between pairs of traits in the index were estimated. Indicators of selection response, namely, selection differential, expected, predicted and realized genetic gains were determined for each trait. There were significant increases ($P \leq 0.05$) in all the traits selected. Body weight performances (sexes combined) increased across the age periods (0 – 20 weeks) from the starting mean values in G_0 generation to the final values in G_2 generation. The body weight at hatch increased from a mean of 30.30g in G_0 generation to 33.48g in G_2 generation. Body weights at 4^{th}, 8^{th}, 12^{th}, 16^{th} and 20^{th} week of age also showed similar increases. Body weight of males and females were similarly significantly improved. Mean body weight of males at 12, 16, 20 and 39 weeks of age were 791.40 ± 8.79g, 932.25 ± 7.83g, 1112.60 ± 11.98g and 1693.75 ± 19.91g, respectively for G_0 generation as against 825.28±7.54g, 1027.83 ± 9.90g, 1156.69 ± 11.74g and 2000.00 ± 31.34g, respectively for G_2 generation. For females, body weights at 12, 16 and 20 weeks as well as BWFE were 667.98 ± 6.30g, 791.52 ± 6.24g, 911.59 ± 6.33g and 1330.44 ± 2.141g, respectively in G_0 generation. The corresponding values for G_2 generation were 673.94 ± 6.48g, 812.54 ± 7.72g, 939.64 ± 7.28g and 1428.48 ± 3.051g, respectively. For egg production, significant improvements were also made. Total egg number and average egg weight increased from 75.60 eggs and 41.27g, respectively in G_0 generation to 79.38 eggs and 43.18g, respectively in G_2 generation. Selection differential values were positive and high for 39 weeks body weight in males across the three generations (mean, 302.19g) as well as for total egg number (mean, 10.74eggs) and average egg weight (mean, 0.47g) in females. It was, however, negative on the average for BWFE (-5.41g). Selection intensity values for mass selection in males were 2.11, 1.75 and 1.16 for G_0, G_1 and G_2 generations, respectively. Mean selection intensity values for total egg number, average egg weight and body weight at first egg were 0.729, 0.106 and -0.277,

respectively. For index values, selection differentials (ΔS_I) were equally positive across the three generations and selection intensity (i_I) remained relatively stable viz. 0.703, 0.989 and 0.890 for G_0, G_1 and G_2 generations, respectively. Direct selection responses namely, expected, predicted and realized genetic gains were mostly positive for all traits selected. Expected average direct genetic gain per generation for egg number, egg weight and BWFE were 12.58 eggs, 2.98g and 25.04g, respectively. For gain in index traits due to selection on index score, a mean value of 1.705 eggs was obtained for total egg number, 0.949g for average egg weight and 43.93g for BWFE. The ratio of realized to expected genetic gain were positive across the three generations. Specifically, a mean ratio of 0.61 was obtained for 39 weeks body weight in males, 1.58 for BWFE, 1.70 for average egg weight and 1.75 for total egg number, for females. The estimate of additive genetic heritability (h^2) ranged from 0.12 to 0.24 for egg number, 0.34 to 0.43 for egg weight and 0.57 to 0.70 for body weight. Estimates of genetic correlation (rg) in whole populations across the three generations ranged from -0.01 to 0.01 for EN-EW, -0.06 to 0.01 for EN-BWFE, and 0.002 to 0.02 for EW-BWFE. For phenotypic correlation (rp), a range of -0.12 to 0.09, -0.04 to 0.08, and 0.21 to 0.23 were obtained for EN-EW, EN-BWFE, and EW-BWFE, respectively whereas, for environmental correlation, a range of 0.55 to 1.31, 0.52 to 0.69, and 0.38 to 0.85 were obtained, respectively for the same pairs of traits.

GLOSSARY OF TERMS

Control population: A random breeding population used to measure environmental variation from one generation to another in a selection programme.

Ecotype: A sub-species adapted to a particular habitat or ecosystem

Environmental variance: The value of the environmental variation.

Environmental variation: The differences among individuals as a result of differences in environmental influences.

Expected genetic gain: The genetic progress expected as a result of selection applied.

Generation interval: The period from birth to reproduction of first progeny.

Genetic variance (V_G or σ_G): The value of the genetic variation.

Genetic variation: The differences among individuals in a population in a trait as a result of the genes they carry (i.e. their genotype).

Index score (I): An aggregate value. The combination of the values of two or more attributes into one (aggregate) score or value.

Major genes: Single genes controlling whole traits.

Minor genes: Genes contributing small effects to the manifestation of a character.

Phenotypic variance (V_p or σ_p^2): The value of the total (observable) variation.

Phenotypic variation: The observable (measurable) total variation between individuals in a population due to genetic and environmental effect.

Polygenes: a group of genes, each contributing small effects to the manifestation of a trait.

Predicted response: The response expected in a trait based on the selection differential and heritability values.

Quantitative trait loci: Chromosomal regions containing one or more genes that influence a multifactorial trait.

Realized genetic gain: The superiority of the progeny of the selected parents over the parental population.

Selection differential: Superior of selected group over their contemporaries.

Selection intensity: The strength of selection applied on a trait.

Variance: A measure of variation

Variation: The differences among individuals in a population in a trait (characteristic) or a number of traits.

TABLE OF CONTENTS

LIST OF TABLES

CHAPTER ONE

1.0 INTRODUCTION

The report of the FAO expert consultation on animal genetic resources (FAO 1973) recommended the improvement and conservation of animal genetic resources indigenous to countries. However, two major constraints delayed its implementation until the 1980s. These constraints include the lack of funds on the one hand, and the delay caused by the disagreement between scientists concerning the genetic merits of these indigenous breeds on the other hand. Most scientists were at this time locked in the paradigm of economic progress as the only value.

Consequently, the prevailing animal production policy then (1960s and 1970s) was to try to improve tropical breeds by introducing temperate breeds with high genetic merits (AGRI, 2002). Indigenous breeds were considered obsolete. Improving and conserving indigenous breeds were regarded as uneconomic and, therefore, should be allowed to disappear. But Payne and Hodges (1997) had noted that the philosophy of improving animal production in the tropics with temperate breeds did not only fail but also damaged indigenous breed resources.

Humanity shapes biodiversity, knowingly or unknowingly. This biodiversity results both from natural selection for adaptation and artificial selection through human choices for use and/or aesthetic value. The preferential selection of distinct genetic traits is reflected in the breed types and races that are adapted to specific uses or environments. Nigeria is blessed with a vast array of animal biodiversity (Nwosu, 1990). This array of breeds is a human heritage worthy of improvement and conservation. Their loss is bound to deplete the quality of human life (Hodges, 2002).

The population of Nigeria was estimated to be about 144 million people (National Population Commission, 2006). With an estimated population growth rate of 2.9% per annum, the population is currently about 160 million. The provision of adequate food for this teaming population is the mandate of the agricultural sector.

Animal agriculture must also provide the animal protein needs of Nigerians. This is an enormous responsibility. The British Medical Association recommends a minimum animal protein intake of 34g per caput per day (Okuneye, 2002). Also, the food and Agriculture Organization (FAO) of the United Nations (1989), recommends 20g of animal protein per caput per day as the minimum for consumption for developing countries (Okuneye and Banwo, 1990) but 75g as the optimum for normal growth and development (Food and Agriculture

Organization, FAO, 1992). This translates to a minimum demand of about 3.4 million kiogrammes and a maximum of 7.5 million kilogrammes of animal protein per day for a population of about a 100 million people. But according to Oluyemi (1979), the average animal protein intake per caput per day in Nigeria was a mere 7.6g or 38% of the FAO minimum recommendation for developing countries and a mere 10% of the requirement for excellent growth and development. The Central Bank of Nigeria, CBN (2000) while analyzing the economic sub-sectors noted that the Gross Domestic Product (GDP) has been on a downward trend. And since the nature of GDP reflects the standard of living of the citizens it means that the standard of living of Nigerians has been on the decline. By extension this also implies that the animal protein intake of the average Nigerian has continued to fall far below the recommended levels.

The Federal Ministry of agriculture and Rural Development (FMARD)(2008) gave the estimated number of indigenous chicken in Nigeria as 166 million. The exotic breeds were believed to number about 5 million. Akinwumi et al. (1979) gave an estimate of about 123.0 million for indigenous fowls and 9.6 million for exotic birds. In addition to the above are thousands of horses, camels and pigs as well as millions of donkeys, cattle, goats and sheep.

The above statistics are impressive but where are the products? In 1998, out of a total of 101 million metric tones of poultry meat projected for production, only 77 million metric tones were realized. In 1999, 109 million metric tones were projected but only 82 million metric tones were supplied by the poultry sector. The figure for the year 2000 was similar as only 88 million metric tones were supplied out of a total projection of 116 million metric tones (CBN, 2002).

Livestock value is not measured in numbers but in terms of amount of useable animal products harvested for human consumption (Nwosu,1990). A reliable yardstick for measuring productivity of animal products is hence the total production and the production per person per year. Thus, it is significant to note that in 1994, 1996, and 2000 the total meat products (of various types) produced per person in Nigeria was 8.224kg, 8.694kg, and 8.772kg, respectively (Okuneye,2002). These figures reveal serious shortages from the recommended 75g per caput daily animal protein intake or its equivalent 25.375kg per person per annum intake (FAO,1989).

To make up for these shortages, Nigeria must import animal milk and meat products from other countries. Thus in spite of the enormous number of indigenous livestock resources, Nigeria remains a net importer of livestock products since the 1980s (Okuneye, 2002). Von Mason

(1989) stated that Nigeria was the biggest importer of dairy products in West Africa. The 2,428 metric tones of beef and 198,000 metric tones of milk imported by Nigeria in 1987 cost the nation a whopping sum of US$3.27 million and US$69.00 million, respectively (ILCA, 1991). This trend has not abated till date (Okuneye, 2002). To bridge the animal protein demand and supply gap the Nigerian government in the 1970s and 1980s attempted to improve local breeds of cattle by importing temperate breeds. These efforts failed principally because the exotic breeds could not adapt to the tropical Nigerian environment as the challenges of tropical climate, pests and diseases were unbearable to them. The problem of streptothricosis in crossbred cattle was quite devastating. The importation and rearing of exotic poultry species have not also been able to bridge this gap. The reasons also include the challenges of stressful environment and diseases which reduce performance added to the high cost of inputs (genetic and feed materials, drugs and bio-organics) which discourage so many investors from investing in the industry.

Locally adapted breeds (indigenous species) are better able to survive and produce valuable products in low input and variable environments (AGRI, 2002). A strategy to develop these breeds is, therefore, likely to be more sustainable over the long term than reliance on external genetic resources. Nwosu (1979) had deplored the lack of a co-ordinated effort to preserve, harness, and improve the genetic potentials of Nigeria's indigenous livestock breeds.

1.1 Research Objectives

The general objective of this study is to improve the performance of the Nigerian heavy ecotype local chickens with respect to their body weight and egg production (egg number and egg weight).

The specific objectives are to:

1. Evaluate the Nigerian Heavy Local Chicken Ecotype (NHLCE) for growth (body weight) from 0 – 20 weeks of age and for short term (16 weeks) egg production.
2. Estimate the genetic parameters, namely heritabilities (h^2) and genetic correlations (r_g) as well as phenotypic and environmental correlations (r_p and r_E, respectively) of body weight, egg weight and short-term egg production (egg number) in this population in the Nsukka environment.
3. Estimate the relative economic weight of egg number, egg weight and body weight at first egg in the NHLCE.

4. Undertake selection in the NHLCE using mass selection for body weight in males and a selection index for body weight, egg weight and short–term egg production (egg number) in females with a view to improving its performance.

1.2 Problem Statement

There has been a total neglect of the indigenous species of livestock. The raw materials have remained undeveloped. The few poultry farms and hatcheries in the country are stock multipliers rather than primary breeders. They depend on foreign sources for hatchable eggs, commercial day-old chicks, and grand parent stocks, hence the high cost of these inputs and the low returns of commercial poultry ventures.

The neglect of the local breeds is mostly due to poor product yield resulting from non improvement as well as from poor and stressful environment. The local chicken for instance is unattractive to investors because of its small body size (hence poor carcass yield) as well as poor egg production performance both in total number of eggs laid and the sizes of eggs produced (mostly pee wees).

It is, therefore, imperative that efforts be channeled towards the improvement of the Nigerian indigenous chickens. Improvement in body weight performance will increase its carcass yield and enhance its acceptance as a meat bird while improvement in her egg production performance (egg number and egg weight) will enhance its acceptance as a source of commercial egg production. A scientific proof that the local chicken responds positively to genetic improvement strategies could stimulate public/private sector investment to improve the local chicken. In this way the value of the native chicken can be enhanced to provide a buffer against the recurrent shortages and prohibitive cost of animal protein materials in Nigeria.

1.3 Justification

Nigeria is endowed with numerous livestock species which are indigenous to her. These animals have lived, adapted and produced for centuries in the Nigerian environment (Nwosu, 1990). They, therefore, constitute genetic resources and raw materials capable of being developed into modern improved breeds and strains. The application of basic principles of animal breeding and genetics, as well as, improved management practices could significantly enhance the productive performance of the Nigerian indigenous species of livestock including the local chicken.

The improvement of the indigenous livestock resources hence requires a more methodical, sustained and painstaking approach. Selection provides the basic tool. Selection and purposeful mating, therefore, are the foundations of a serious effort towards the improvement of the local chicken. In this era of harsh economic conditions and dwindling national resources, sustainability becomes the watch word of every endevour. A poultry industry built on imported inputs (fertile eggs, F_1 day – old chicks, feed raw materials, bio-organics, drugs etc) cannot be sustained. Improving the indigenous stock hence remains the only way of building a strong and viable poultry industry (Nwosu, 1990, Ikeme, 1990).

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Characterization of the Nigerian Indigenous Chicken

The term indigenous or local chicken is used interchangeably to denote a group of unimproved, unpedigreed and unselected population of random breeding native chickens (Nwosu, 1979; Kitayi, 1998). They are spread throughout the rural areas of Nigeria and may occur as two ecotypes namely the light ecotype found mostly in the Swamp, rainforest and derived savannah areas of southern Nigeria, and the heavy ecotype found mainly in the montane areas of southeastern (and western) Nigeria, middle belt and northern Nigeria. The heavy ecotype birds in the middle belt zone are commonly called 'Tiv' chicken.

The local chickens vary in body weight, egg weight and egg production and have various shades of plumage colours (Nwosu, 1979, 1987; Omeje and Nwosu 1983). Mature body weight varies between 450g to 1350g for females and 680g to 1710g for males (Hill, 1954). The hens lay an average of 40-80 eggs per year, each weighing 28.3g to 35.4g under extensive husbandry and 128 eggs per annum under intensive deep litter system. Age at first egg is about 135 days (Nwosu, 1979). Other early characterization of the indigenous chicken of Nigeria include the work by Hill and Modebe (1961) who showed that the indigenous chicken responded well to improved husbandry methods with mean annual egg production of 124 eggs in intensive battery cage system. Mean body weight at day–old, 4^{th} week, 12^{th} week and 20^{th} week of age were 27.22g, 62.50g, 396.89g and 1079.28g, respectively, while egg weight was in the range of 29.0g to 36.0g. Oluyemi and Oyenuga (1971) reported a mean value of 25.15g, 78.85g, 484.33g and 1047.92g, respectively, for the above age periods for indigenous chickens from Ondo, Ogun, Lagos and Kwara States. Akinokun and Dettmers (1977) reported mean body weight of 179.20g, 644.60g and 1037.60g for 4^{th}, 12^{th} and 20^{th} week of age, respectively, for local chickens from Oyo State. Nwosu and Asuquo (1985) reported mean body weight of 92.0 ± 2.1g, 289.0 ± 2.2g, 581.0 ± 4.4g, 744.0 ± 0.01g and 980.0 ± 4.1g for 4^{th}, 8^{th}, 12^{th}, 16^{th} and 20^{th} week of age, respectively, for indigenous chickens of south eastern Nigeria. Mean egg weight was reported as 38.6 ± 0.8g (Nwosu, 1990). Atteh (1990) reported body weight range of 980g to 1420g (Average 1290g) and 1460g to 2210g (Average 1760g) for hens and cocks, respectively, above 24 weeks of age. Nwosu *et al.* (1984) found body weight at sexual maturity and at the end of annual egg production to be 1140g and 1270g, respectively. More recent reports by Adedokun and Sonaiya

(2001) working with local chickens from derived savannah, guinea savannah and rainforest zones of Nigeria gave body weight at hatch, 4th, 8th, 12th, 16th and 20th week of age as 23.0 ± 1.6g, 104.0 ± 14.5g, 262.0 ± 4.9g, 605.0 ± 67.5g, 765.0 ± 103.4g and 948.0 ± 130.6g, respectively, for hens while cocks averaged 311.0 ± 36.4g, 702.0 ± 55.3g, 914.0 ± 65.4g and 1096.0 ± 84.1g for 8th, 12th, 16th and 20th weeks, respectively. The same authors reported average egg weights of 39.0 ± 1.0g, 37.9 ± 1.0g and 37.1 ± 1.0g, respectively, for local chickens from the three ecological zones. Okpeku *et al.* (2003) reported similar values for local chickens of Edo State with average body weight of 1530g for males and 1490g for females. Momoh (2005) classified the local chicken of Nigeria into two ecotypes namely heavy and light ecotypes based on body weight characteristics. The heavy ecotype averaged 30.223 ± 0.06g at day – old, 157.16 ± 0.45g at 4th week, 349.88 ± 3.01g at 8th week, 719.72 ± 9.47g at 12th week, 840.43 ± 9.35g at 16th week and 976.08±3.01g at 20th week. The corresponding mean body weights of the light ecotype were 24.27 ± 0.05g, 139.35 ± 2.24g, 299.48 ± 3.01g, 560.20 ± 4.31g, 707.08 ± 4.80g and 830.55 ± 5.52g, respectively. Mean egg weight was 40.34 ± 0.24g, and 37.32 ± 0.23g for heavy and light ecotypes, respectively. The same author reported weight of first egg of 38.06g for heavy ecotype hens and 30.42g for light ecotype hens.

Elsewhere in the world chickens indigenous to countries are also identified into ecotypes or lines based on body weight characteristics and/or distinct plumage colour lines. Lawrence (1998) working in Tanzania reported mature body weight of 2708g and 1827g for male and female Kuchi ecotype, 2915g and 2020g for Singamagazi ecotype, 1612g and 1394g for Foembeya ecotype and 1850g and 1107g for Morogoro ecotype. Cresswell and Gunawan (1982) reported average 20 week body weight of five distinct groups (ecotypes) of indigenous chicken of Indonesia as 1408g, 1480g, 1320g, 1203g and 1669g for black Kedu, white Kedu, Pelung, Minukan and Sayur ecotypes, respectively. AL-Rawi and Al-Athari (2002) described five genetic lines of purified/selected population of Iraqi indigenous chickens based on plumage colours. Body weight at sexual maturity was between 1333.4g and 1457.6g for males and females. Average egg weight was 54.2g while annual egg production ranged between 147.9 to 175.10 eggs.

2.2 Variation among the Indigenous Chickens

Characterization studies using indigenous chickens from various ecological zones of Nigeria (Oluyemi and Roberts 1979; Sonaiya *et al., 1998; Okpeku et al., 2003*) indicate that there is much similarity among local chickens within and across zones. They cannot, therefore, be classified as distinct strains or breeds. Even the heavy ecotype local chicken does not exist as a distinct isolated population but has to be sorted out from the normally mixed population of local chickens using body weight differences. Specifically, Oluyemi and Roberts (1979) characterized indigenous chickens from south-western Nigeria and found no significant variation in body weight, egg weight, egg production and other external characteristics. Sonaiya *et al.* (1998) studied genetic variation in immunological competence and egg production within a local chicken population assembled from Ogun, Osun, Kwara, Kaduna, Jos, Makurdi, Ilorin and Nsukka areas of Nigeria and found no significant differences between these populations. Okpeku *et al.* (2003) investigated the phenotypic and genetic variation among the local chickens of Edo State, Nigeria and found no significant variation among the chickens in body weight and other biometrical body measurements studied. These authors hence concluded that the birds cannot be classed as separate strains rather the individuals and groups adapted to various ecological regions can be exploited by inbreeding and selection in order to develop Nigerian breeds for different purposes. Sonaiya *et al.* (1998) hence proposed the term ecotypes to identify the group adaptations to various ecological zones.

2.3 Egg Production in Chickens

The egg production of a chicken is the result of many genes acting on a large number of biochemical processes, which in turn control a range of anatomical and physiological traits. For the chicken to express fully its genetic potentials appropriate environmental conditions which include nutrition, ambient temperature, water, freedom from disease, light etc must be ensured. It is only then can the many genes controlling all the processes associated with egg production act to allow the chicken express its full genetic potentials (Fairfull and Gowe, 1990).

Egg production is the major index of performance of the commercial layer. It accounts for about 90% of the income of a layer enterprise. This is followed by egg size (egg weight), feed efficiency and mortality (Oluyemi and Roberts, 2000).

2.4 Genetic Factors Influencing Egg Production

2.4.1 Age at sexual maturity (ASM)

Hens come into lay 20 to 22 weeks of age (140-154 days) and continue in lay for a period of approximately one year or when the hens are 72 weeks old (Nordskog, 1981). Age influences egg production within the first laying cycle and over subsequent laying cycles. In each cycle, egg production per hen housed or per live hen quickly rises to a peak (6-8 weeks after coming into lay) and declines slowly thereafter to the end of the cycle usually terminating with a natural or induced moult (Oluyemi and Roberts 2000). In successive cycles of egg production, the peak is usually lower and the rate of lay is more rapid (Fairfull, 1982; Gowe and Fairfull, 1982a; Oluyemi and Roberts, 2000). The quick sigmoid rise to peak egg production arises mainly due to differences in age at first egg of individual hens in the production. When egg production records are synchronized for sexual maturity the 'hook' at the start of the production record largely disappears (Gavora et al., 1982; McMillan et al., 1986). The decline of the egg production curve results from reduced rate of lay and, in the case of hen-housed egg production, from mortality. Changes in heritability estimates of egg production traits with age are very small. These small changes occur because environmental variation and thus phenotypic variation, experiences relatively large increases with age. Thus changes in the variation of egg production with changes in the age of the bird are much larger than would be predicted from heritabilities (genetics).

Additive genetic variation, as estimated from sire component, increases during the first laying cycle by about 1.5 to 2 times for egg production traits (Liljedahl *et al*., 1984; Liljedahl and Engstrom, 1986). Increases of similar order also occur with respect to non-additive genetic variation. In summary, within egg production cycles, egg production declines with increasing age while its variation increases. Over successive cycles, egg production peaks at a lower rate and declines more rapidly. ASM influences egg yield by influencing the length of the biological year (Nordskog, 1981). It also influences the speed at which a pullet reaches mature egg size(Morris, 1980; Koutoulis *et al.,* 1997).

2.4.2 Body weight at sexual maturity(BWSM)

This has a direct effect on egg weight. BWSM influences size of first egg which is usually about 75% of the maximum reached when the pullet is mature (Nordskog, 1981). The ultimate or mature egg size, however, is a function of the genetic size measured by bone size (e.g. shank length). A breeder can change average egg weight appreciably (2 to 3g) by altering the ASM and BWSM (Joly, 2003).

2.4.3 Single Gene Effects

Single genes can affect several traits of the phenotype due to pleiotropy or linkage. Pleiotropic effects are permanent over time while linkage effects disappear over time. Except linkage is very close, it breaks up because of crossing over at meiosis. Genes that reduce body weight/size such as sex-linked dwarf gene (dw) were reported to cause reduced egg number and rate of egg production in many breeds (Hutt, 1959; Telloni *et al.,* 1973; Coquerelle and Mérat, 1979).

The major histocompatibility complex (MHC), also known as the B blood type locus (E_G-B), is known to be associated with varied effects on egg production. While at least two alleles in this locus are known to enhance egg production, one allele has been reported to be consistently associated with reduced egg production (Nordskog, *et al.,* 1973; Gebriel *et al.,* 1984). As a result of these varied effects, linkages or exposure to a pathogen seems to be involved in the association of egg production and the E_G-B alleles.

The blue eggshell gene (O) present in native South American breed is known to be autosomal dominant and is reported to depress egg production (Sadjadi *et al.,* 1983).

The slow feathering gene (K) has sometimes been found to be associated with reduced egg production and this was assumed to be due to pleiotropic effects. Further research, however, suggested that morbidity and mortality may be the indirect cause of the lower production. It is believed that the negative effects of the K gene are likely due to close linkage between the endogenous viral gene (en-21) and the k allele (Bacon *et al*., 1988). Birds carrying the k gene are immunotolerant to both endogenous and exogenous leucosis virus. The exogenous viruses have been shown to reduce egg production in clinically normal hens as well as increasing mortality from other causes.

2.4.4 Other genetic components of egg production

In addition to ASM and BWSM there are other genetic factors that influence egg production. These include persistency, intensity of egg production, rate of pauses and broodiness (Nordskog, 1981; Flock, 1994). Emphasis on these traits differ widely but intensity, rate of pauses and broodiness are still widely regarded by most commercial breeders as important traits (Flock, 1994).

2.5 Environmental Factors influencing egg production

2.5.1 Nutritional Factor

Major productive traits in chickens are influenced to a great extent by plane of nutrition. Inadequate dietary energy lowers body weight, egg weight and egg production (Whitehead, 1981). Addition of oil improves palatability and feed intake leading to improvement in these traits (Whitehead, 1981; Halle, 1996; Meluzzi *et al.* 2001). A deficiency in any of the essential amino acids leads to a reduction in performance of which 60 to 65% is due to a lowering of rate of lay and 35 to 40% to a reduction in egg weight (Huyghebaert and Butter 1991; Jais *et al.,* 1995; Joly, 1995; Joly *et al.,* 1997; Joly, 2001; 2003).

2.5.2 Disease

Mortality reduces the number of hens available to lay while morbidity reduces the laying ability of affected hens. The effects of mortality and morbidity on egg production record depend on the age of the hen when affected. Mortality and morbidity also significantly affect genetic and environmental variations, heritabilities and accuracy of selection.

2.5.3 Temperature (Heat)

Temperature affects all productive traits in the chicken. Rate of lay is generally only affected at temperatures above 30^{o}C. Egg weight falls by 0.4% per ^{o}C between 23 and 27^{o}C; above 27^{o}C the reduction is about 0.8% per ^{o}C. Growth at start of lay is reduced above 24^{o}C and is extremely low above 28^{o}C. The feed conversion ratio is minimum at a temperature around 28^{o}C, above 28^{o}C it increases due to the lowering of production (Peguri and Coon 1993; Zollitsch *et al.,* 1996). These figures are, however, only indicative, because air movement speed and relative humidity affect thermoregulation (Joly, 2003).

2.5.4 Lighting

The oviposition interval in the chicken is hormonally controlled, mediated by a circadian rhythm resulting at least in part from a 24 hour light-dark cycle. The ovulation interval is normally slightly longer than the oviposition interval (Fairfull and Gowe, 1990). The hen starts a clutch by laying early in the day, and usually lays at a slightly later time each day until she skips a day and lays early in the next day again to start a new clutch. The hen has a potential limit of

one egg per day or an annual maximum of 365 eggs. This potential is never attained because of the reduction in rate of lay with age. Under good environment and optimum management commercial flocks frequently average 300 eggs per year (Fairfull and Gowe, 1990) but 200-250 eggs per year is most common in the tropics (Oluyemi and Roberts 2000).

The threshold of light intensity for the stimulation of the pituitary gland is 0.04 foot candles but adequate light intensity is above 0.5 foot candles (Oluyemi and Roberts 2000). The pattern of light is however more important than the intensity of light. Day-length should be increased by 15-30 minutes per week starting from the 31st week of age until an optimum of 14 hours or a maximum of 17 hours is reached. Whichever level that is attained should be maintained because a decrease in photoperiod may depress production, while further increase may adversely affect the eyes, induce nervousness and either depress production or over stimulate oviposition, causing a depression in egg qualities (small eggs, thin shells and yolkless eggs).

2.6 Genetic Improvement in Chicken

The ultimate goal of a breeding programme for an animal population is the genetic improvement of the traits defined in the breeding objective. The major tool to achieve this is to select the best animals as parents to produce the next generation and among those parents decide which ones should have the largest number of progenies (Strandberg and Malmfors, 2006). Selection is, therefore, a directional choice, a discriminatory process which allows the possessors of certain genes and/or genotypes to have more offsprings than those that lack such genes or gene combinations – a non-random differential reproduction of genotypes (Lerner, 1958; Strandberg and Malmfors, 2006) whose ultimate aim is the maximization of progeny performance. With successful selection, the progeny generation will on average be better than the average of the population from which their parents were selected – genetic progress is obtained.

2.7 Selection Strategies

The trait(s) to be improved in a population are usually defined in the breeding plan. A few of the productive traits are controlled by one or a few pairs of genes (alleles) so that the true genotype of the trait can be determined (mostly by DNA test) and individuals exhibiting them can be accurately selected. Most productive traits are, however, quantitative in nature hence they

are controlled by many gene pairs at different loci and by the environment in which the animal exists. Such traits are often normally distributed and selection is commonly based on predicting breeding values.

Individuals can be selected based on their performance on one trait only (mass selection) or a combination of traits (multiple trait selection). Multiple trait selection could be by tandem, independent culling level or selection index method. The concept of multiple – trait index selection dates back to Fisher's discriminant function (Fisher, 1936). Smith (1936) applied Fisher's concept to develop an index for the selection of plant lines while Hazel (1943) extended the index procedure for the selection of individuals in animal populations. Since then the classical Smith – Hazel index or discriminant function (1936; 1943) has undergone much modification and extension leading to various types of indices developed to meet diverse needs of breeders and breeding objectives as well as circumvent certain limitations inherent in the classical index (Lin, 1978; Sato *et al*., 1985).

When improvement is desired for several traits that may differ in variability, heritability, economic importance and in the correlations among their phenotypes and genotypes, simultaneous multiple trait index selection was found to be more effective than independent culling levels which in turn was better than tandem or sequential selection (Hazel and Lush, 1942; Young, 1961; Finney 1962; Yamada et al., 1975; Sato et al., 1985; Hazel et al., 1994). Young (1961) demonstrated that relative efficiency depends upon number of traits selected, relative economic values of the traits, heritability, phenotypic and genetic correlations between traits as well as selection intensity.

2.8 Genetic Relationship between Traits

When two traits are related in such a way that one varies with the other directly (positively), or inversely (negatively), both traits are said to be correlated. There are three kinds of correlation namely phenotypic, genetic and environmental correlations. Phenotypic correlation is the observable (net) effect of all genetic and environmental factors that influence the two traits together. Genetic correlation (correlation of breeding values) is the correlation of additive effect of genes affecting the traits (Ibe, 1998). The causes of genetic correlation are pleiotropy, linkage disequilibrium and different breeding objectives in a population (Nordskog, 1981). Pleiotropy is

a permanent cause of genetic correlation while linkage disequilibrium and different breeding objectives are, transient or temporary causes of genetic correlation.

. Correlation be it phenotypic, genetic or environmental is an important concept in animal genetic improvement through multiple quantitative trait selection and the magnitude and nature of the phenotypic and genetic correlations between two traits are of critical importance in the simultaneous selection of the traits. Positive genetic correlation means that both traits can be improved in the same direction whereas negative genetic correlation calls for carefulness in designing the selection programme to avoid a selection effort that is self defeating (Lerner, 1950). Erroneous values of genetic and phenotypic correlations also reduce the efficiency of multiple – trait index selection (Cochran, 1951; Tallis, 1960; Williams, 1962a; Harris, 1964; Vandepitte and Hazel, 1977; Sato *et al*., 1985).

Experimental values of genetic, phenotypic and environmental correlations abound in literature. Falconer (1964) reported genetic correlation coefficients of –0.16 and 0.18 for genetic and environmental correlations, respectively, for body weight at 18 weeks of age and egg production up to 72 weeks of age; 0.50 and –0.05 for that between body weight at 18 weeks and egg weight; 0.29 and –0.50 for that between body weight at 18 weeks and age at first egg- all in a leghorn population. Mark (1985) summarized the genetic correlation between female reproductive traits in chickens. The values are –0.11 for sexual maturity and egg production; 0.07 for sexual maturity and egg weight and
–0.20 for egg production and egg weight. Fairfull and Gowe (1990) summarized genetic correlation values between body weight at 18 to 22 weeks with various part record egg production. Values were generally positive, ranging from 0.13 to 0.29 for early part-record production but became increasingly lower and negative (0.13 to -0.16) with later part-records. The genetic correlation for mature body weights with egg production followed two distinct trends in leghorn stocks. In unselected strains, the values were positive ranging from 0.38 to 0.45 while in selected strains, the values were negative, ranging from –0.01 to –0.54. Genetic correlation for egg weight with egg production was reported to be mostly negative for all part-records ranging from –0.2 to –0.6 with no apparent trend with regard to age nor systematic differences between selected and unselected populations (Fairfull and Gowe, 1990; Kinney, 1969). Kinney (1969) also reported genetic correlations between egg weight and mature body weight to be mostly positive (0.15 to 0.40).

2.9 Economic weights (values) of Quantitative Traits in Farm Animals

The economic weight (value) of a trait measures the average amount which a given variation in that trait actually raises or lowers the net phenotypic merit of the animal (Lerner, 1958). Hazel (1943) defined relative economic importance of a trait as the net increase in profit of the production enterprise for a unit of change in one trait, independent of effects from genetic change in other traits included in the definition of aggregate breeding value. Relative economic weight also reflects changes in production costs and hence cost to consumers of animal products. Defined in this way, it is the expected reduction in cost per unit of equivalent output value (Hazel *et al*., 1994). This definition recognizes the effect of genetic change in performance traits which is more meaningful and stable as a proportion of production cost than of profit (Hazel *et al.,* 1994). Smith *et al.* (1986), however, showed that both definitions lead to essentially the same relative economic weights if price per unit output was assumed constant.

The actual economic weights are usually calculated in an *ad hoc* way (Hazel 1943, Syrstad, 1966). In countries where farm products are graded and market prices (values) are standardized, economic values are easily determined from market costs. Where suitable data are available and many traits, genetically correlated, are defined in the breeding objective, relative economic weights are computed as partial regression coefficients of the net value of the individual on the separate component traits (Moen, 1968; Cunningham, 1969). Thus, the relative economic values reflect the direct or partial regression of net economic return (H) on genetic value (G_i) for each trait when the genetic values (G_j) for other traits are unchanged (Hazel *et al*., 1994).

More precise estimation of relative economic importance of traits can also be obtained through production and marketing system simulation (Moav and Moav 1966; Cartwright, 1970; Cartwright *et al*., 1975). Harris (1970) and Harris and Newman (1992) defined relative economic weights in terms of simulated profit functions that include the non-linear economic effects of genetic change in component traits on the net merit (H) for individual candidate breeders.

Most times, multiple trait selection indexes include traits which cannot be measured directly on the animal. Such traits like feed efficiency, carcass conformation etc are hence improved by selecting on a correlated trait. Hazel (1951) examined this problem for cattle while Nordskog (1986) considered the case in poultry. Both authors suggested assigning economic

weights only to the minimum number of (primary) traits most directly controlling efficiency of production and then using the genetic and phenotypic parameters of other (secondary) traits and their genetic correlations with the primary traits to derive the optimal weighting for the traits to be included in a composite selection index.

The relative importance of each trait in an animal is established separately for each kind of animal, each region, each type of farming (production system), marketing system and almost for each breeder (Lerner, 1958). Economic weights are, therefore, not permanent but varies within and among these entities and are reviewed whenever the market demands and premiums make large and presumably permanent change.

Hazel *et al*. (1994) suggested that economic values must of necessity be based upon conditions likely to exist some time in the future, since several generations are required for appreciable genetic change. Selection indexes are well – adapted to such situations because they provide a logical method of changing goals gradually as developing situations indicate the need and the direction of change. Production system simulation is also highly useful to estimate the independent effects of unit changes in each component trait on cost per unit output over ranges of performance and for differing breed roles, production and marketing systems.

Values of relative economic weights for primary economic traits in livestock abound in literature but none exists for the indigenous livestock species (cattle, sheep, goat and chicken) in Nigeria. Table (1) contains statistical information (arbitrary values) required for selection index for cattle (Hazel 1951). Table (2) contains likely economic values (early form) per unit product per genetic standard deviation of change for egg production traits as used in Kimber farms (Emsley and Dickerson, 1974; Bennet *et al*., 1981). Hazel and Terrill (1946) estimated relative economic importance of traits included in a multiple – trait index for selection of range Rambouillet lambs as standard partial regression on each component as 0.40 for face covering, 0.39 for neck fold, 0.38 for body weight, 0.16 for body condition, 0.14 for staple length and 0.01 for body type. In a selection index for weaning traits in spring lambs, Givens *et al*. (1960) assigned 22 cents as economic value for the increase of one pound of live weight at 120 days and 3.02 pounds as the economic value of a unit increase of full market grade. In a similar index for selecting yearling Rahmani sheep, Karam (1959) estimated the economic value for yearling weight, twin lamb and fleece weight to be 4.90, 1.34 and 15.06 pounds, respectively. Becker (1992) calculated the economic value of feed efficiency for a swine index to be – 0.50 pence

based on income over feed cost and 12.0 pence for eye muscle area based on income per unit increase in the trait. Nordskog (1981) assigned economic weights (values) of 10 cents, – 25 cents and 8.75 cents for egg weight, body weight and egg rate, respectively. The corresponding relative economic weights were 1.14 for egg weight, – 2.86 for body weight and 1.00 for egg rate.

Table (1): Statistical information required (arbitrary values) for example of selection index for beef cattle

No	Character	Economic value	Standard deviation	Heritability	r_P				r_g			
1	Weaning weight	0.30	40.0	0.25	2	3	4	5	2	3	4	5
2	Weaning score	2.00	1.0	0.35	0.4	0.1	0.0	0.2	0.2	0.2	–0.1	0.3
3	Feed efficiency	– 15.00	0.5	0.50		0.0	0.2	0.0		0.0	0.6	–0.2
4	Slaughter grade	10.00	1.0	0.40			0.0	-0.3			0.3	–0.5
5	Rate of gain	16.00	0.3	0.65				–0.2				–0.3

Source: Hazel, 1951.

r_p = phenotypic correlation

r_g = genetic correlation

Table (2): Example of economic value per unit and per genetic standard deviation of change for egg production traits

Character	Genetic variation (σ_G)	Economic value per unit	Economic value per σ_G
Fertility, %	0.95	0.008	0.008
Hatch, %	1.60	0.008	0.013
Normal, %	1.70	0.008	0.014
Early viability, %	4.0	0.012	0.05
Adult viability, %	7.0	0.025	0.18
Egg production to 72wk, %	3.84	0.110	0.42
Age at first egg, day	7.9	0.023	0.18
Calmness score, 0 to 1	0.128	0.500	0.06
At 32 week			
Body weight, kg	0.133	0.772	0.10
Egg weight, g	2.41	0.085	0.21
Specific gravity score (0.004)	0.75	0.080	0.06
Shape 10L/w, 0 + 01	0.26	0.050	0.013
Albumen, Haugh unit	3.35	0.020	0.07
No. blood, 1%	1.28	0.040	0.05
No. colour	0.20	0.50	0.10
Shell smoothness	0.056	0.50	0.03

Source: Bennet *et al.* (1981)

2.10 Genetic Parameters for Body Weights, Egg number and Egg weight in chicken

2.10.1 Heritability

This is a measure of the relative contribution of genes to the phenotypic value of a trait. It is therefore, the proportion of total phenotypic variance due to average gene effect (Falconer, 1964, Stanfield, 1969, Dalton, 1981).

Reliable estimates of heritabilities are important in the design and execution of animal breeding plans and in making accurate predictions of direct and correlated responses to selection. Heritability estimates for growth and egg traits in chickens abound in literature. Values for growth traits – body weight, body weight gain and linear body measurements – from various studies and reviews (Kinney, 1969; Smith and Goodman, 1971; Gowe *et al.,* 1973; Chambers *et al.,*1984; Leenstra *et al.,* 1986; Crawford, 1990; Segura *et al.,* 1990, Ikeobi and Peters, 1996; Kiani – Manesh *et al*., 2002) using various variance components (sire, dam, sire + dam) and mating designs indicate that growth traits have mostly moderate to high heritabilities (≥ 0.2). Estimates based on variance components (sire, dam and sire + dam) or additive genetic effects from factorial or diallel mating designs were generally less varied because of the partitioning of the various variance components and the consequent estimation and removal of the compounding effects of maternal, non-additive and sex – linked variance components (Crawford, 1990).

Generally, heritability estimates involving different populations of a species vary greatly. Estimates involving samples drawn from a population also differ as a result of sampling variation, differing sample size or, differences among genetic groups and environment, relative size of sires and dams as well as persistent variation deviation from average variation among dams mated to each sire (Chambers *et al.,* 1984). Heritability estimates based on regression of offspring performance on parent performance seem to resemble those based on sire variance component but realized heritability estimates based on regression are higher approaching those based on sire + dam variance components.

Estimation of heritabilities of growth traits in local chickens was pioneered by Oluyemi and Oyenuga (1974), Oluyemi (1979a), and Nwosu (1979). Nwosu and Asuquo (1985) reported values of 0.33 ± 0.5, 0.43 ± 0.07 and 0.38 ± 0.07 for body weight between the ages of 4 weeks to 20 weeks. Asuquo and Nwosu (1987) using sire, dam and sire + dam variance components

obtained a range of 0.27 to 0.49 as heritability values in a local chicken population. More recently Momoh (2005) reported heritability values of between 0.19 and 0.43 for 4^{th} to 20^{th} week body weights in the Nigerian heavy local chicken ecotype using sire component of variance. Ndofor *et al*. (2006) estimated heritability of body weight of local chicken ecotypes reared in Nsukka in the derived savanna zone of Nigeria and reported a range of 0.23 to 0.56 for 4^{th} to 16^{th} week body weights in the light ecotype, 0.25 to 0.46 for the heavy ecotype and 0.12 to 0.46 for the main cross population. All estimates were based on paternal half – sib variance component.

Early estimates of heritability and realized heritability for hen housed egg production to 39, 55 and 71 weeks of age based on sire, dam and sire + dam as well as parent – offspring regression were summarized by Kinney (1969) and by Fairfull and Gowe (1990) for selected and unselected populations. Kinney (1969) reported mean heritability values of 0.11 for sire, 0.45 for dam and 0.18 for sire + dam variance components for short term egg production, 0.15 for sire, 0.64 for dam and 0.31 for sire + dam for annual egg production. Fairfull and Gowe (1990) gave a range of 0.18 to 0.29 for unselected and 0.11 to 0.20 for selected populations using sire component of variance. For sire + dam variance components, the same authors reported a range of 0.26 to 0.28 for unselected and 0.17 to 0.23 for selected populations. Using parent – offspring regression a range of 0.10 to 0.28 and 0.25 to 0.27 were reported for unselected and selected populations, respectively. Other estimates pertaining to survivor egg production and hen-day rate of production fall within the range 0.13 to 0.32 for selected and unselected populations. Generally, estimates based on sire + dam variance components were higher than the sire component heritability estimates although there were frequent exceptions.

For the indigenous chicken of Nigeria, Omeje *et al*. (1987) reported a value of 0.46 ± 0.24 for egg number while Momoh (2005) reported 0.23 ± 0.43 for short term egg production.

Heritability estimates for egg weight were summarized by Kinney (1969) for various variance components. For sire, dam and sire + dam variance components mean heritability values were 0.57, 0.65 and 0.67, respectively, for early egg weight and 0.58, 0.54 and 0.58, respectively, for mature egg weight. Momoh (2005) reported a value of 0.12 ± 0.38 for egg weight based on sire component of variance.

Generally, heritability values of egg production traits are low to moderate, an indication that non-additive genetic and environmental variation (effects) may be very important in their

expression. Nordskog and Hardiman (1980) explained that low heritability is the lot of all reproductive and fitness traits such as hatchability, fertility and viability.

2.10.2 Genetic Relationships

2.10.2.1 Relationship between growth and reproduction

Increased growth rate has a negative genetic effect on reproductive traits of cockerels. There is negative genetic correlation between body weight and motility of spermatozoa. Ejaculates from cockerels of high body weight line are higher in volume but has lesser concentration of spermatozoa. They also contain spermatozoa with lower metabolic rate and higher percentages of dead and abnormal members (Crawford 1990). Males from high body weight lines also exhibit reduced libido and mating frequency.

The net effects of genetic increases in growth rate or juvenile body weight on female reproduction are negative (Fairfull and Gowe, 1990). Some of these effects appear to be positive (e.g. ova production), however, it appears that physiological imbalances nullify any beneficial influences. There is positive genetic correlation between body weight and egg weight. Kinney (1969) reported genetic correlation of 0.26 between body weight at 8 weeks and egg weight and a range of 0.15 to 0.40 between adult body weight and mature egg weight. Estimates of genetic correlations and responses to selection indicate that in meat type chickens a negative genetic correlation exists between juvenile body weight and egg production. The apparent discrepancy between increased ova production and reduced egg production is accounted for by increased incidence of abnormal eggs (double yolks, extra calcified shells, compressed-sided eggs- collectively called erratic oviposition and defective egg syndrome or EODES); internal laying (manifested as Pengium stance) and progressive regression of developing follicles.

2.10.2.2 Relationship between egg production and other productive traits

Estimates of genetic correlation between egg production and rearing body weight (8 – 12 weeks of age) are generally positive while those between mature body weights and egg production are mostly negative (Fairfull and Gowe, 1990). All valid egg production records and hen day rate traits appear to be negatively correlated with viability traits although a few estimates in unselected lines in Fairfull and Gowe (1990) were positive. The standard errors of the estimates were, however, large indicating that the estimates were extremely variable, probably

due to the low heritability of viability (Fairfull and Gowe, 1990). This also indicates that selection should proceed under environments with low level of mortality.

2.11 Effect of Selection

2.11.1 Effect of selection on genetic variance and Heritability

The simple theoretical expectation is that selection should lead to fixation with the consequent loss of genetic variance (Falconer, 1964). A reduction in genetic variance will be reflected in a reduction of the phenotypic variance. A number of researchers (Yamada *et al.,* 1958; Lin, 1978; Gowe and Fairfull, 1985) reported that selection reduces genetic variation especially in the first few generations. Experimental evidence (Falconer, 1964), however, suggest no loss of phenotypic variance and a lack of experimental support for the widely held idea of selection plateau on account of exhaustion of useable variation. Lush (1945) reported that selection of parents altered the variability of the next generation in two principal ways namely changes in gene frequency and increases in the proportion of parental gametes having intermediate combinations of both desirable and undesirable genes. The same author argued that the effect of these two pathways on variance (which could be an increase or a decrease) is very small. There is much experimental evidence in support of persistent availability of genetic variation in populations undergoing selection. With a limited population of white leghorns (4- 20 sires, 45 – 132 dams, 255 – 877 hens per generation), Yamada *et al.* (1958) selected for part-period rate of lay as the primary trait along with viability, hatchability and egg size for over ten generations. Even though viability tended to decrease, there was considerable genetic variation at the end of the study. Heritability did not change from the third to the tenth generation. Friars *et al*. (1962) selected for five traits simultaneously for nine generations (5 – 18 sires, 32 – 125 dams, 106 – 543 adult progeny) in a population synthesized from several breeds. There was no change in heritability of egg production. Goher *et al*. (1978a) reported no significant change in sire variance component during eleven (11) generations of selection. In the California selection study in which Lerner (1958) used White Leghorns, the heritability of egg production remained constant over about 15 generations of selection. Chen and Michele (2003) estimated genetic variability and selection response for clutch length in two lines of dwarf brown egg layers for 16 generations. Heritability estimates obtained using an additive genetic model and a model allowing for dam's environment were mostly constant with a range of 0.42 to 0.57 across the

sixteen generations indicating no significant reduction of genetic variability. Realized heritabilities were also constant in one of the lines but fluctuated (rise and fall) more in the second line. Also Marks (1983) selected for body weight at 8 weeks for five (5) generations in normal (line 1) and dwarf (line 2) meat – type chickens. Realized heritabilities were high and constant (0.78 to 1.17) for line 1 and (0.43 to 0.77) for line 2 across the 5 generations.

2.11.2 Genetic and Phenotypic Correlations

The genetic relationship among important traits can and do change with selection in an unpredictable manner. Evidence of changes in genetic correlation values is fairly common (Fairfull and Gowe, 1990). Ibe *et al*. (1982) reported significant curvilinear trends in correlated responses to selection for whole record egg number and rate; egg weight and body weight. Morris (1963) had reported changes in genetic correlation of early and late egg production due to selection. Liljedahl and Weyde (1980) reported that genetic correlation between part-record egg production and egg weight became negative as a result of selection on part-record egg production. Gowe and Fairfull (1985) published different correlation values between part-record egg production and body weight and between part-record egg production and age at first egg for selected and unselected populations.

In spite of the above reports it is still generally believed that genetic correlation values remain relatively constant in a population either without much change or after an initial change (Gowe and Fairfull, 1985).

2.12 Response to Selection (R)

Experimental report/data on response to selection for productive traits in farm animals abound in literature but little is known about responses in productive traits of the Nigerian local chicken to selection. Apart from Oluyemi (1979b) who reported responses in 12 week body weight to 7 generations of mass selection in Nigerian indigenous chicken, no other estimate exists in the Nigerian literature of selection studies involving the Nigerian local chicken ecotypes. Oluyemi (1979b) using mass selection obtained responses of 40.1 ± 0.37g, 36.9 ± 0.37g and 39.4 ± 0.37g per generation for males, females, and the sexes combined, respectively. Elsewhere, Boukila *et al.* (1985) selected for increased egg production based on annual records in three strains of white leghorns and reported that selecting on part-record egg production between 21 and 42 weeks of age increased residual egg production to 71 week of age in the three

strains. Marks (1983) selected for body weight at 8 weeks of age in dwarf and normal meat – type chickens for 3 generations and reported significant responses in 8 week body weight which resulted in correlated improvement in 22 and 40 week body weights in the flock. Cheng *et al.* (1996) predicted genetic gains in body weight, egg production and shell quality traits in the Brown Tsaiya laying duck (Anas platyrhynchos) and reported per generation responses of +0.177g for egg weight at 40 weeks, +8.029g for body weight at 40 weeks, +0.935 eggs for number of eggs laid to 52 weeks, and + 0.017kg/cm^2 for egg shell strength at 30 to 40 weeks of age. Chen and Michele (2003) estimated genetic variability and selection response for clutch length in dwarf brown – egg layers for 16 generations. The annual genetic gain in average clutch length was estimated to be between 0.33 and 0.37 for the classical analytical method (deviation of mean of selected population from the mean of the control line) and 0.43 and 0.46 for the animal model (mixed model methodology). Nwagu *et al.* (2007) studied response of egg number to 280 days (egg 280D); age at sexual maturity (ASM); average egg weight (AEW) and body weight at 40 weeks (BWT 40) to selection on part-period egg production in Rhode Island chickens. They reported among others an average phenotypic response of 1.67 eggs per generation in the female line and a genotypic average gain of 0.42 eggs in the male line. A correlated response of 3.4g/year was realized for body weight in the male line.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 The Study Site

This research was carried out at the local chicken research unit of the poultry farm of the Department of Animal Science, University of Nigeria, Nsukka, latitude 05^0 22^1 North and longitude $07^0 24^1$ East. Annual rainfall ranges from 1567.05mm to 1846.98mm. The natural day length is 12 – 13 hours and average minimum and maximum daily temperatures are 20.99^0C and 30.33^0C, respectively. Relative humidity ranges from 48.68% to 76.20% (Metrological center, crop science dept., UNN, 2009. unpublished). Nsukka belongs to the humid derived savannah of the South – eastern Nigeria.

3.2 The Reference Population

The reference population refers to the population of heavy ecotype local chickens from which the base population or foundation stock for this study was derived. It consists of a population of random breeding heavy local chicken ecotype (cocks and hens) maintained in the Department of Animal Science Farm for Teaching and Research purposes. The birds were randomly assembled from rural areas in Obudu (Cross River State), a montane region of South–South Nigeria and the adjourning towns of Vandeikiya, Katsina–Ala and Wannune in Benue State.

3.2.1 The Foundation Stock or Base Population

Fifty (50) heavy local chicken ecotype hens and five (5) cocks were randomly selected from the reference population and randomly assigned to five (5) pens in the breeding house in a mating ratio of one (1) cock to ten (10) hens. The cocks (sires) were identified with sire and pen number using wing tags. These fifty-five birds formed the foundation stock or base population from which birds subjected to selection (G_o generation) were generated. Two conical feeders and one 6 litre metal drinker were used to serve feed and water, respectively, to the birds in each breeding group. The birds were fed layers mash containing 16.5% crude protein and 2600kcal/kg ME at the rate of 100g per bird per day. Water was provided *ad libitum*.

The birds were de-wormed, given a five-day antibiotic regime and vaccinated against Newcastle disease and fowl pox.

3.2.2 Generation of the Starting Stock (Go Generation)

Random mating within each breeding group of the base population (foundation stock) produced fertile eggs which were collected twice a day at 12.00 noon and at 6.00 p.m., identified with pen and sire number and stored in crates in a well ventilated room for seven days before incubation. Eggs were sorted to remove unwholesome eggs before incubation. Two still–air, hand–turned, 100 egg capacity locally fabricated incubators were used for the hatching operation. A total of 302 day old chicks were produced. These birds formed the G_0 generation to which selection was applied.

3.3 Management of the G_0 generation

On hatching, chicks were identified with sire (genetic) group using colour makers. They were weighed and then transferred into brooding cages constructed to house the chicks for the first three weeks of life. At three weeks the chicks were transferred to the deep litter brooding house with wood shaving as litter material. Heat was provided to the birds throughout the brooding period by means of electric bulbs but kerosene lanterns and mini-stoves were employed during power outages. The brooding period was from day–old to 8 weeks. The chicks were fed chicks starter containing 18% cp and 2800 Kcal/kg of metabolisable energy. Feed and water were provided *ad libitum* during the brooding period.

After 8 weeks the birds were transferred to the deep litter rearing pens in the open sided rearing (grower) house. A growers mash containing 15% Cp and 2670Kcal/kg ME were fed to the birds from the 8^{th} week to the 20^{th} week of life. Males and females were reared together from 0 to the 12^{th} week of life. Thereafter, males were separated from females.

At 20 weeks of age, all pullets were moved into individual laying cages for egg production. The cocks were left on deep litter. From the 20^{th} week, pullets were fed a layer mash containing 16.5% CP and 2,600Kcal/kg ME at the rate of 100g per bird per day. Feed was provided once a day in the morning while water was provided *ad libitum*. Table 3 (a, b, and c) contain the percentage composition of the chicks mash, growers mash, and layers mash used in the experiment.

Table 3: Experimental Ratio

(a) Chick Mash

Feed ingredients (DM Basis)	Percentage composition (%)
Maize	53.0
Wheat offal	13.0
Soya bean cake	18.0
Palm kernel cake	9.0
Fish meal	3.0
Bone meal	3.0
Lysine	0.25
Methionine	0.25
Vitamin premix	0.25
Salt	0.25
Total	100
Calculated:	
Crude protein (%)	18%
Energy (Kcal ME/kg)	2,800

(b) Growers Mash	
Ingredients (DM Basis)	Percentage composition (%)
Maize	43.5
Wheat offal	30.0
Soya bean cake	10.0
Palm kernel cake	10.0
Fish meal	2.5
Lysine	0.25
Methionine	0.25
Vitamin premix	0.25
Salt	0.25
Bone meal	3.0
Total	100
Calculated:	
Crude protein (%)	15%
Energy (Kcal ME/kg)	2,670

(c) Layers Mash)	
Ingredients	Percentage composition (%)

Maize	43.0
Wheat offal	18.0
Soya bean cake	17.5
Palm kernel cake	9.0
Fish meal	2.5
Bone meal	3.0
Lysine	0.25
Methionine	0.25
Vitamin premix	0.25
Salt	0.25
Oyster shell	6.0
Total	100
Calculated:	
Crude protein (%)	16.5%
Energy (Kcal ME/kg)	2,600

Proximate composition of feed major ingredient	**Percentage crude protein**	**Kcal ME/kg**
Maize	9.0	3430
Wheat offal	17.0	1870
Soya bean cake	44.0	2400
Palm kernel cake	18.0	2800
Fish waste	50.0	2700

Legend: ME = Metabolizable energy
Kcal = Kilo calories

Hens were monitored for short term egg production from point of first egg drop to 16 weeks of lay. Eggs were collected and recorded twice daily between 10 am and 12.00 noon and by 6.00 p.m. Eggs were recorded in a daily egg chart identified with sire, hen and generation numbers. Eggs were also identified with sire and hen numbers for purposes of weighing.

Regular medication and routine vaccination against prevalent poultry diseases were employed to ensure good health, optimal performance and reduced mortality in the flocks. The routine vaccination schedule followed are as outlined in table 4.

Table 4: Vaccination Schedule

Age	Disease	Vaccine	Route
Day – old	Newcastle disease	NDV	1/0
Week 2	Gumboro disease	IBDV	1/0
Week 3	Newcastle disease	NDV – Lasota	1/0
Week 4	Gumboro disease	IBDV – booster	1/0
Week 6	Fowl pox	Pox vaccine	Wing-Web
Week 8	Newcastle disease	NDV – Komarov	1/M
Week 12	Newcastle disease	NDV-K booster	1/M
Bi-monthly	Newcastle disease	NDV-L booster	1/0

Source: National Veterinary Research Institute, Vom

3.4 Establishment of Control Population

15 males and 15 females were randomly selected from the G_0 population at 12 weeks of age and housed together in a deep litter rearing pen to form a random breeding control population for the G_0 generation. At 20 weeks of age the females were transferred into individual laying cages and monitored for short term egg production along with the population undergoing selection. Cocks were left on deep litter. After the short term egg production in cages, the hens were returned to the cocks on deep litter. Fertile eggs were collected and hatched to produce the control population for the next generation.

Similar management procedures used for the population undergoing selection were also applied to the control population.

3.5 Generation and Management of G_1 and G_2 Generations

After selection in the G_0 generation, the selected sires (No = 8) and the selected dams (No = 47) were randomly assigned to 8 pens to form eight sire families. Fertile eggs were collected and hatched to produce the G_1 generation.

The G_2 generation was likewise generated from selected sires and dams from the G_1 generation. Management of the breeding groups and generated populations were as stated in paragraph 3.3 for G_0 generation.

The control populations were used to correct for environmental changes in each generation and enabled the estimation of expected direct genetic response due to selection in each generation as the difference between the mean for the selected population and the mean for the control population for each trait.

3.6 Measurement of Traits

3.6.1 (i) Growth trait

Individual body weights at hatch, 4^{th}, 8^{th}, 12^{th} and 20^{th} week of age were measured. Hatch and 4^{th} week body weights were measured by means of a sensitive 250g capacity Salter scale spring balance. Subsequent body weights (8^{th} to 20^{th} week) were measured using a 5kg capacity kitchen scale.

(ii) Body weight at first egg (BWFE): Each hen was weighed on the day she laid her first egg. This is the body weight at first egg. BWFE along with total egg number and average egg weight were combined in an index as criteria for selection of dams.

(iii) Final body weight of cocks: At the end of the 16 weeks egg production (39 weeks of age) of all hens in a generation, the surviving cocks were weighed to obtain their 39^{th} week body weights. Selection of cocks as sires was based on their 39^{th} week body weights.

3.6.2 Egg Production Traits

(i) Total egg number: Total egg number (TEN) was recorded as the total number of eggs laid by each hen from the date of first egg to the end of the 16 weeks (short term) egg production. Eggs were collected and recorded against the hen that laid it in a daily egg chart. All eggs laid by each hen and which could be weighed were recorded for the hen.

(ii) Average egg weight: Eggs were weighed singly using a 250g capacity Salter scale spring balance. Egg weights were recorded to the nearest gram. The mean egg weight for each

hen was the sum of the weight of all eggs laid within the 16 weeks laying period divided by the total number of eggs recorded for the hen.

3.7 Selection in the G_0 Generation

3.7.1 Selection within the male population

Males that served as sires for the next generation (G_1) were selected using mass selection based on individual (own) body weight performance at 39 weeks of age when their female (dam) counterparts were selected. Selection intensity values for sires were 2.11, 1.75 and 1.16 for G_0, G_1 and G_2 generations, respectively. Males were more intensely selected than females.

3.7.2 Selection within the female population

At the end of the 16 weeks (short term) egg production, all hens belonging to the G_0 generation, were subjected to selection using a selection index incorporating total egg number (TEN), average egg weight (AEW) and body weight at first egg (BWFE). Females were on the average 39 weeks old (mean age at first egg = 23 weeks (161 days) + 16 weeks egg production) when they were selected. The phenotypic performances of each hen in these traits were represented in the index as x_1, x_2 and x_3 for TEN, AEW and BWFE, respectively. The index score (I) for each hen became a univariate character (trait) subjectable to selection. The index score (I) thus enabled the ranking of the hens for purposes of selection.

3.7.3 Construction of Selection Index

A simple linear selection index in which the relative economic weights and the heritabilities of the traits were used as weighting factors for the phenotypic values was constructed. This is the heritability index (Heidhues and Henderson, 1962) or index of weighted breeding values – an extension of the base index by Williams (1962b) in which the only weighting factor is the relative economic weights of the traits. The index has the general form:

$$I = \sum b_i x_i$$

$$= \sum a_i h_i^2 x_i^1 = a_1 h_1^2 x_1^1 + a_2 h_2^2 x_2^1 + \ldots + a_i h_i^2 x_i^1$$

where,

$b_i = a_i h_i^2$

a_i = relative economic weight of the ith trait in the index.

h_i^2 = additive genetic heritability of the ith trait in the index.

x_i^1 = standardized phenotypic value of the ith trait in the index

The standardized variable x_i^1 was obtained by using the following expression:

$$x_i^1 = \frac{x_i - \bar{x}_i}{\sigma_{xi}}$$ (Stanfield, 1969).

Where,

x_i = record performance of an individual in the ith trait of the index.

$\bar{x}_i$ = mean performance of the whole population in the ith trait of the index.

σ_{xi} = population phenotypic standard deviation for the ith trait.

The standardization of the phenotypic values of the different traits makes them pure numbers. Thus, the standardized variable (x^1) is a pure number (independent of the unit of measure) based on the mean and standard deviation of the trait. A constant, K was added to each calculated index value. The value of K was chosen so that the value of the index (1) was always positive.

For the indexes used in this experiment, K = 10 was used.

The use of the heritabilities of the different traits to weight their phenotypic values was to obtain the best estimate of each individual's breeding value for the traits (Ibe, 1998). The relative economic weights weight the breeding values to yield an economic breeding value for each trait.

The summation of the different economic breeding values yielded an aggregate economic breeding value for each individual represented by the index score (I). The index score thus represented an estimate of the true aggregate economic breeding value (A) for each candidate for selection. The ranking of the candidates according to their index score thus enable the selection of the best candidates in the aggregate economic breeding value.

3.7.4 Determination of Relative Economic weights

The relative economic weights (values) of egg number and egg weight were determined based on the additional gain derived from an increase of one unit in laying performance and egg weight, respectively, over the 16 weeks production period (Nordskog, 1981) while that for body

weight was determined based on income over feed cost, that is, the additional gain or loss incurred as a result of a unit increase in body weight after deducting the cost of feed required to attain the unit increase in body weight (Nordskog, 1981; Becker, 1992). Thereafter, the least economic value was used to divide through (disregarding positive or negative signs) to obtain the relative economic weights for the three traits (Nordskog, 1981). The step by step procedure for the determination of the relative economic weights for the three traits in G_0 generation are as outlined below.

3.7.4 (i) Body Weight

The economic weight for body weight is the additional gain or loss incurred by a unit (1g) gain in the body weight of the chickens over the 16 weeks production period taking into consideration the cost of feed required to attain the additional unit gain.

Average body weight at first egg of G_0 generation chickens (females) = 1330.44g. Average body weight at end of the 16weeks egg production = 1474. 44g.

Body weight gain over the production period = 1474.44 – 1330.44 = 144g.

Average daily feed consumption per chicken = 100g.

Cumulative feed consumption per chicken for 16 weeks = 11200g

Feed efficiency given as feed conversion ratio is:

$$\text{F.C.R.} = \frac{Feed\ consummed\ (g)}{Body\ weight\ gain\ (g)}$$

$$= \frac{11200}{144} \quad = \quad \underline{\underline{77.78}}$$

Therefore, 1g gain in body weight required 77.78g feed.

25000g (25kg) of layers mash (formulated ration) was ₦850.00

$$\text{Therefore, 77.78g feed cost } \frac{77.78\ x\ 850}{25{,}000}$$

= ₦2.64

Cost of mature local chicken (about 1.5kg body weight) = ₦400

$$\text{Therefore, revenue from 1g local chicken carcass} = \frac{400}{1500} \quad = \quad 0.27K$$

Since the income accruing to 1g of local chicken carcass is negligible compared to the cost in feed required to attain it (₦0.27 Vs ₦2.64), the value of ₦2.64 is considered a loss and

assumes a negative value (Nordskog, 1981). The economic weight of body weight is therefore – 2.64.

(ii) Egg Number: The economic weight of egg number is the additional income from a 1% increase in the laying performance of the local chicken flock over the 16 week production period.

At a laying percentage of 50 over the 16 week laying period each hen will produce 56 eggs.

An increase of 1% over the 16 week period yielded 57.12 eggs per hen or an additional 1.12 eggs per hen. A crate of eggs (30 eggs) sold at ₦200.00 hence each egg costs ₦6.67.

1.12 additional eggs gave additional income (gain) of 1.12 x 6.67 = ₦7.47.

Therefore economic weight of egg number is ₦7.47.

(iii) Egg Weight: The economic value of egg weight is the additional profit derived from an increase of 1g in the egg weight of the local chickens over the 16 weeks egg production period.

At 50% laying performance, each hen produced 56 eggs. A 1g increase in the weight of these eggs yields additional 56g egg.

Average weight of local chicken eggs for G_0 generation was 41.27.

56g egg is equivalent to

$$\frac{56}{41.27} = 1.35 = 1.4 \text{ eggs.}$$

At ₦6.67 per egg, 1.4 eggs gave additional income of

1.4 x 6.67 = ₦9.34.

Therefore economic weight of egg weight = ₦9.34.

The relative economic weights of the traits are obtained by dividing the economic weights by the least value disregarding the negative or positive signs.

Thus:

$$\text{Body weight} = \frac{-2.64}{2.64} = -1.00$$

$$\text{Egg number} = \frac{7.47}{2.64} = 2.83$$

$$\text{Egg weight} = \frac{9.34}{2.64} = 3.54$$

The relative economic weights for the traits for the G_1 and G_2 generations were determined by similar reasoning with appropriate adjustments in prices of products and cost of input (feed) as occasioned by the prevailing production and marketing situation. Thus, prices of eggs and feed were reviewed upwards.

3.7.5 Selection in Subsequent Generations (G_1 and G_2)

A new selection index was constructed for purposes of selection in each subsequent generation. This is to correct for changes in relative economic weights and in heritability estimates from one generation to another.

3.8 Data Analysis

3.8.1 Performance Statistics

Data on total egg number, egg weight, and body weight at first egg for dams as well as body weight for sires were subjected to statistical analysis using the SPSS (2001) computer programme to obtain means, standard error and coefficient of variation for all populations namely: whole, selected and control populations across the three generations. All survivor hens were included in the analysis.

3.8.2 Estimation of Genetic Parameters

A sire model was used to generate data for estimation of genetic parameters. The model is as given below:

$$Y_{ij} = \mu + S_i + e_{ij}$$

Where,

Y_{ij} = performance of the jth progeny of the ith sire in the trait being considered

μ = overall population mean for the trait

S_i = the random effect of sire

e_{ij} = residual

This is the paternal half – sib analysis which assumes all effects to be random, normal and independent with expectation zero. Also maternal, dominance, epistasis and sex linkage effects are assumed to be zero and all experimental subjects share a common environment.

3.8.2.1 Heritability (h^2)

Analysis of variance using the SPSS package (SPSS, 2001) yielded estimates of sire component of variance from which the additive genetic heritabilities of the individual traits were calculated using the formular:

$$\therefore h^2 = \frac{4\sigma_s^2}{\sigma_s^2 + \sigma_w^2}$$

where

σ_s^2 = sire variance component

σ_w^2 = residual variance

3.8.2.2 Genetic Correlation (r_g)

The genetic correlation between any two of the traits being considered was obtained using the following relationship by Becker (1992).

$$r_g = \frac{4COVs_{x1x2}}{\sqrt{4\sigma^2_{s_{(x1)}}} \bullet \sqrt{4\sigma^2_{s_{(x2)}}}} = \frac{COVs_{x1x2}}{\sqrt{\sigma^2_{s_{(x1)}} \bullet \sigma^2_{s_{(x2)}}}}$$

$$= \frac{COVs_{x1x2}}{\sigma_{s_{(x1)}} \bullet \sigma_{s_{(x2)}}}$$

where,

r_g = genetic correlation between traits x_1 and x_2

$COVs_{x1x2}$ = additive genetic (sire component) covariance between traits x_1 and x_2

$\sigma_{s_{(x1)}}$ and $\sigma_{s_{(x2)}}$ = additive genetic standard deviation for traits x_1 and x_2 respectively.

The sire component of covariance (COVs) is obtained from:

$$COVs = \frac{MCPs - MCPw}{K}$$

where,

MCPs = Mean cross product of sire

MCPw = Mean cross product within sire or error mean cross product

K = Number of progeny per sire (for unbalanced data).

K is given by:

$$K = \frac{1}{S-1}\left(n. - \frac{\sum n_i^2}{n_i}\right)$$

Where,

S – 1 = Degree of freedom sire

n. = total number of progeny

$\sum n_i^2$ = Sum of the square of number of progeny per sire.

n_i = Number of progeny per sire.

The mean cross product values (MCPs and MCPw) were obtained by analysis of covariance.

3.8.2.3 Phenotypic Correlation (r_p)

The phenotypic correlation (r_p) between any two of the traits was obtained by correlation analysis using the SPSS (2001) computer programme. The computational formula is however given by Becker (1992) as:

$$r_p = \frac{COVw + COVs}{\sqrt{\left(\sigma^2_{w_{(x1)}} + \sigma^2_{s_{(x1)}}\right)\left(\sigma^2_{w_{(x2)}} + \sigma^2_{s_{(x2)}}\right)}}$$

Where, $cov_{w(x1\ x2)} + Cov_{s(x1\ x2)} = Cov_{P(x1\ x2)}$ = phenotypic covariance between traits x_1 and x_2.

$\sigma^2_{w_{(x0)}} + \sigma^2_{s_{(x1)}} = \sigma^2_{P_{(x1)}}$ = phenotypic variance of trait x_1

$\sigma^2_{w_{(x2)}} + \sigma^2_{s_{(x2)}} = \sigma^2_{P_{(x2)}}$ = phenotypic variance of trait x_2

3.8.2.4 Environmental Correlation (r_E)

The environmental correlation (r_E) between pairs of traits was calculated using the relationship:

$$r_E = \frac{COV_{w(x1,x2)} - 3COV_{s(x1,x2)}}{\sqrt{\left(\sigma^2_{w(x1)} - 3\sigma^2_{s(x1)}\right)} \bullet \sqrt{\left(\sigma^2_{w(x2)} - 3\sigma^2_{s(x2)}\right)}}$$

Where, $COV_{w(x1,\ x2)}$ = error covariance between traits x_1 and x_2

$COV_{s(x1,\ x2)}$ = sire (additive genetic) covariance between traits x_1 and x_2.

$\sigma^2_{w(x1)}; \sigma^2_{w(x2)}$ = errors variances of traits x_1 and x_2, respectively

$\sigma^2_{s(x1)}; \sigma^2_{s(x2)}$ = sire variances of traits x_1 and x_2, respectively.

3.8.3 Measurement of Selection Applied

3.8.3.1 Selection differential (ΔS)

The selection differential (ΔS) which expresses the superiority of the selected individuals over the population from which they were chosen was calculated as the mean difference between the selected population and the whole population before selection in the trait considered.

That is,

$\Delta S = \overline{X}_S - \overline{X}_W$ (Falconer, 1964; Stanfield, 1969; Pirchner, 1983; Becker, 1992)

Where,

ΔS = selection differential

$\overline{X}_S$ = mean of selected group

$\overline{X}_W$ = mean of population before selection.

3.8.3.2 Selection Intensity (i)

The selection intensity (i) is a measure of the selection applied. It was calculated using the following expression:

$$i = \frac{\Delta S}{\sigma_P}$$ (Falconer, 1964; Becker, 1992).

Where,

ΔS = selection differential

σ_P = phenotypic standard deviation of the trait being considered.

The selection intensity is therefore the selection differential expressed in units of standard deviations.

3.8.3.3 Cumulative Selection differential

This is the sum of the expected selection differential in the current generation and the expected selection differential in the previous generation(s).

That is,

$$\text{Cum}\Delta s_i = \sum_{i=1}^{n} \Delta s_i \quad \text{(Nordskog, 1981; Marks, 1983; Ibe, 1998)}$$

where,

$\text{Cum}\Delta s_i$ = cumulative selection differential up to (and including) the ith generation i = 0, ---, n.

$\sum$ = summation

Δs_i = expected selection differential in the ith generation

3.8.4 Measurement of Response to selection

3.8.4.1 Expected direct response (R_i)

The expected direct response to selection (R_i) for each trait was calculated as the difference between the means of selected and control populations in the trait concerned.

That is,

$R_i = \overline{X}_{iS} - \overline{X}_{iC}$ (Cheng *et al.,* 1996)

Where,

R_i = expected direct genetic response in the ith trait

$\overline{X}_{iS}$ = mean of the selected population in the ith trait

$\overline{X}_{iC}$ = mean of the control population in the ith trait.

3.8.4.2 Cumulative direct response (CumR)

This was calculated as the sum of the expected direct response in the current generation and the cumulated response in the previous generation(s) thus,

$\text{Cum}R_i = R_i + \text{Cum}R_i - 1$ (Oluyemi, 1979b; Marks, 1983)

Where,

$\text{Cum}R_i$ = cumulative direct response in the ith (current) generation

R_i = expected direct response in the ith generation

$\text{Cum}R_i - 1$ = cumulative direct response in the (i -1)th generation.

3.8.4.3 Average direct genetic response per generation

The expected average direct response per generation $\left(\overline{R}_i\right)$ was obtained by regressing the cumulative direct genetic responses on generation number (N). The average direct response per generation $\left(\overline{R}_i\right)$ being equal to the regression coefficient, b, (slope) of the regression line.

Thus,

$\overline{R}_i = b_{\mathbf{cumR,N}}$

where,

$\overline{R}_i$ = average direct genetic response per ith generation. i= 0, 1 or 2

$b_{cumR,N}$ = regression of cumulative responses (cumR) on generation number (N).

3.8.4.4 Expected direct genetic gain per year

The expected annual direct genetic gain (ΔG_x/yr) was calculated using the following expression

$$\Delta G_x/yr = \frac{\Delta G_i}{t.} = \frac{R_i}{t.} \qquad \text{(Ibe, 1998)}$$

Where,

ΔG_x/yr = expected annual direct genetic gain

$\Delta G_i = R_i$ = expected direct genetic gain for the ith generation

t = generation interval

Thus for a generation interval of one (1) year, the annual genetic gain becomes:

$$\Delta G_x/yr = \frac{\Delta G_i}{1} = \Delta G_i \text{ OR } \frac{R_i}{1} = R_i$$

3.8.4.5 Predicted direct genetic response (R_p)

The predicted or estimated direct genetic response in each trait was calculated using the fundamental equation for gain thus:

$R_{Pi} = h_i^2 . \Delta S_i = i\sigma_{Pi} \quad h_i^2 = ih_i\sigma_A$ (Nordskog, 1981; Falconer, 1964; Pirchner, 1983)

Where,

R_{Pi} = estimated (predicted) direct genetic response in the ith trait

h_i^2 = additive genetic heritability of the ith trait

ΔS_i = selection differential of the ith trait.

σ_{Pi} = phenotypic standard deviation of the ith trait

$\sigma_A = \sqrt{V_A} = \sqrt{\sigma_A^2}$ = additive genetic standard deviation

$h_i = \sqrt{h_i^2}$ = square root of additive genetic heritability

3.8.4.6 Realized (observed) genetic response (ΔG_R)

The observed (realized) genetic response (ΔG_R) which is the response realized in the progeny as a result of selection in the parental generation was calculated as the difference between the mean of the progeny of the selected parents and the mean of the parental population before selection

That is,

$\Delta G_R = \bar{X}ip - \bar{X}iw$

where,

ΔG_R = realized genetic response or gain

$\bar{X}ip$ = mean of progeny in the ith trait

$\bar{X}iw$ = mean of parental population before selection

3.8.4.7 Expected genetic gain (response) in the index value due to selection on the index score (I)

This was calculated using the expression

$\Delta G_I = i_I \sigma_{GI} h_I \sqrt{K}$ (Pirchner, 1983)

where,

ΔG_I = expected genetic gain in index value

i_I = selection intensity factor for index

σ_{GI} = additive genetic standard deviation of index

$h_I = \sqrt{h_I^2}$ = square root of heritability of index

K = number of traits included in the index

3.8.4.8 Expected genetic gain in the component traits of the index due to selection on the index score (I)

This was calculated using the expression,

$$\Delta gi = \frac{\Delta S_I}{\sigma_I^2}\sigma_{G(xi,I)} \quad \text{(Yamada, 1977)}$$

where,

ΔS_I = selection differential for index

σ_I^2 = variance of index

$\sigma_{Gxi,I}$ = $Cov_{G(xi,I)}$ = covariance between genotype of ith trait and index

Δg_i = expected genetic gain

3.8.4.9 Effectiveness of Selection

The effectiveness of (selection) was tested by the ratio of observed (realized) to expected genetic response for each trait.

That is,

$$\text{Effectiveness of selection} = \frac{\text{Realised genetic gain}}{\text{Expected genetic gain}}$$

$$= \frac{\Delta G_R}{\Delta gi} \quad \text{(Fairfull and Gowe, 1990)}$$

CHAPTER FOUR

4.0 RESULT AND DISCUSSION

4.1 Body weight

The descriptive statistics (mean ± S.E, coefficient of variation, C.V.) for body weight (g) at various ages (0 to 20 weeks) for Go, G_1, and G_2 generations (sexes combined) are presented in Table 5. The Table shows that there were significant differences ($P \leq 0.05$;) in body weight of birds belonging to Go, G_1 and G_2 generations at the various ages, except at 20 weeks, with G2 birds having highest body weights, followed by G1 and G0. The body weight performances as obtained for G_0 at various ages were higher than those reported by Hill and Modebe (1961), Oluyemi and Oyenuga (1971), Akinokun and Dettmers (1977), Oluyemi (1979a), Nwosu and Asuquo (1985), Adedokun and Sonaiya (2001) and Okpeku *et al.* (2003) for indigenous chickens

from the derived savannah, Guinea savannah and rainforest zones of South-Eastern and Western Nigeria. These birds containing variable numbers of the heavy and light ecotypes were expectedly lower in body weight than the 'pure' heavy ecotype chicken that made up the G_0 generation in this study. The results were thus very similar to values reported for heavy ecotype local chickens by Momoh (2005) and Ndofor-Foleng *et al.* (2006).

The superiority of the G_1 generation over the G_0 generation in body weight at hatch, 4^{th} and 8^{th} weeks of age is expected. G_1 birds being progenies of selected parents from the G_0 population manifested realized selection responses in body weight due to selection in the G_0 population of males superior in body weight at 39 weeks and females superior in egg weight. These favourable responses, manifested as increased body weight at these age periods. The effect of these favourable responses on body weight at these age periods, however, waned towards the mature age periods and the body weight of birds of G_1 generation though still higher was no longer significantly different ($P \geq 0.05$) from those of G_0 generation. The body weight performance of the G_2 birds as obtained in this study also reflect the cumulative effects of realized genetic gain as a result of positive responses to selection at 39 weeks of males of superior body weight and females of superior egg weight in G_0 and G_1 generations. Expectedly, there were highly significant differences ($P \leq 0.01$) between the body weights of G_2 birds and those of G_0 birds at hatch, 4, 8, 12, and 16 weeks of age. G_2 birds were also significantly ($P \leq 0.05$) higher in body weight than those of G_1 generation at hatch, 4, 12 and 16 weeks of age.

The table also shows increasing values of the standard error of means from hatch to 20 weeks of age. Both the standard error of means and the coefficient of variation, however, appeared similar across the three generations for each age group. The increasing values observed for the standard error of means (SEM) indicate increasing values of phenotypic variance with concurrent increases in body weight. It does appear that means and variances for growth are correlated. Gowe and fairfull (1985) had shown that environmental variation and thus phenotypic variation, experiences relatively large increases with age. The between generation similarity among SEM and C.V values across generations for each age group indicate homogeneity of variances across generations.

Table 6 presents the mean ± standard error for body weight (g) at different ages (12, 16 and 20 weeks) for G_0, G_1 and G_2 generations (sexes separated). The Table indicate that males of G_1 and G_2 generations consistently surpassed those of G_0 generation across the age periods. In

particular, at weeks 12 and 20, males of G_1 and G_2 generations were similar in body weight performance but exceeded significantly ($P \leq 0.01$) those of G_0 generation while at week 16 males of G_2 generation were significantly higher ($P \leq 0.05$) in body weight than those of G_1 generation which were in turn significantly superior ($P \leq 0.05$) to those of G_0 generation. For the female population, the Table shows statistically significant differences ($P \leq 0.05$) between body weight of females across the ages. Evidently, females belonging to G_2 generation numerically surpassed those of G_1 and G_0 generations in body weight values across the ages.

Table 5: Descriptive statistics for body weight (g) from hatch to 20 weeks of age for G_0, G_1 and G_2 generations (sexes combined)

		Generation		
Age	Statistics	G_0	G_1	G_2
0	Mean ± S.E	30.30±0.167[a]	31.65±0.148[b]	33.48±0.168[c]
	C.V	0.096	0.094	0.076
4 week	Mean ± S.E	151.41±1.743[a]	160.78±1.158[b]	166.86±1.664[c]
	C.V	0.190	0.139	0.145
8 week	Mean ± S.E	344.19±4.139[a]	391.72±3.0903[b]	399.63±4.877[b]
	C.V	0.186	0.148	0.170
12 week	Mean ± S.E	705.05±7.218[a]	712.85±6.148[a]	747.15±7.365[b]
	C.V	0.152	0.158	0.132
16 week	Mean ± S.E	847.92±8.009[a]	853.45±7.349[a]	914.44±10.664[b]
	C.V	0.131	0.155	0.152
20 week	Mean ± S.E	1002.72±9.920	1023.51±8.917	1019.57±11.305
	C.V	0.134	0.154	0.142

[abc]: Means within the same row with different superscripts are significantly different ($P \leq 0.05$).
Legend: G_0, G_1, G_2: Generation zero, one and two, respectively. C.V Coefficient of variation

Table 6: Mean ± S.E. for body weight (g) for 12 to 20 weeks of age for G_0, G_1 and G_2 generations (sexes separated)

			Generation		
Age	Sex	Statistics	G_0	G_1	G_2
12 weeks	M	Mean ± S.E	791.40±8.76[a]	835.82±7.09[b]	825.28±7.54[b]
	F	Mean ± S.E	667.98±6.30[a]	650.19±5.41[b]	673.98±6.48[a]
16 week	M	Mean ± S.E	932.25±7.83[a]	961.24±9.19[b]	1027.83±9.90[c]
	F	Mean ± S.E	791.52±6.24[a]	779.97±5.27[a]	812.54±7.72[b]
20 week	M	Mean ± S.E	1112.60±11.98[a]	1144.68±10.05[b]	1156.69±11.74[b]
	F	Mean ± S.E	911.59±6.33[a]	926.87±5.01[ab]	939.64±7.28[b]

[abc]: Means within the same row with different superscripts are significantly different ($P \leq 0.05$).

Legend: M = male; F = Female.

G_0, G_1, G_2 = Generation zero, one and two, respectively.

The above results reveal the superiority of males of G_1 and G_2 generations over those of G_0 generation. The results indicate positive realized responses to selection for body weight in males which was cumulative over the generations. The females were, however, more uniform in body weight over the age periods and across the three generations. There was therefore, weaker impact of selection on body weight of females. This result is not surprising considering that females were selected based on an index incorporating egg number, egg weight and body weight at first egg with body weight at first egg negatively weighted in the index. Again, selection in females did not target improvement in body weight within the accelerating growth phase (0 to 20 weeks). Furthermore, the selection intensity for body weight at first egg (in females) was very low across the generations (mean, -0.277) compared to that applied for selection of males at 39 weeks (mean, 1.67).

Generally, the generational differences in body weights within the accelerating growth phase (0 – 20 weeks) both for sexes combined and sexes separated were not as striking as would be expected from mass selection. The selection of females based on an index incorporating body weight at first egg, egg number and egg weight reduced the gain in body weight below what it would have been if it was the sole trait under selection. The marginal increases in body weight values obtained within the accelerating phase of growth (0 – 20 weeks) in subsequent generations (G_1 and G_2) therefore, represent net positive responses to selection across the generations. Though males were selected on the basis of their body weight performance, body weight at 39 weeks of age was the criterion. Thus much of the genetic potentials for growth had been exhausted and additive genetic differences (variation) among individuals in each generation had waned. Selection for body weight improvement in chicken populations has been shown to be most effective at juvenile age periods (4 to 8 weeks) in meat type birds (Marks, 1983) and at 4^{th} , 8^{th} , 12^{th} and 20^{th} week in local chickens and egg – type chickens (Oluyemi 1979b; Momoh, 2005). Momoh (2005) had shown that additive genetic heritability- a reflection of additive genetic variance- was 0.18 at 4^{th} week, 0.43 at 8^{th} week, 0.29 at 12^{th} week, 0.16 at 16^{th} week and 0.30 at 20^{th} week. Momoh (2005) hence advised that for maximum progress, selection for body weight improvement in the heavy local chicken ecotype should be based on 8 weeks, 12 weeks or 20 weeks body weights. The additive genetic heritabilities obtained in this study for body weights from hatch to 20 weeks (for sires and for sexes combined) across the three generations also followed a similar trend. Generally, heritability estimates for 39 week body weight for sires were

low (0.132) to moderate (0.247) as against the moderate (0.242) to high (0.593) obtained for the same population for body weights from 12 to 20 weeks. Marks (1983) reported an apparent plateau of body weight at 40 weeks of age in a population of meat type birds selected for 4 and 8 weeks body weights due to exhaustion of genetic variability and wondered if this could be a definite trend.

Table 7 Presents the between sex comparison for body weight at 12, 16 and 20 weeks for G_0, G_1 and G_2 generations. The Table shows consistent, highly significant between sex differences ($P \leq 0.01$) in body weight across the age periods and for the three generations. In general, males were highly significantly superior ($P \leq 0.01$) to females in body weight at the different age periods. The superiority of males over females in body weight is expected and confirms the well established differential growth between male and female chickens (Marks, 1983; Oluyemi, 1979a, 1979b; Atteh, 1990; Adedokun and Sonaiya, 2001; Momoh, 2005).

Table 8 presents the between population comparison of mean body weight (g) values for the males at selection (39 weeks) for selected, whole and control populations across the G_0, G_1 and G_2 generations. The Table shows that the selected population of sires were, highly significantly ($P \leq 0.01$) higher in body weight than the whole and control populations across the three generations. The whole and control populations were similar in G_0 and G_1 generations but differed significantly ($P \leq 0.01$) in G_2 generation. Table 9 compares the generational mean values for body weight at 39 weeks for the males (selected, whole and control populations). From the Table it can be observed that the selected populations for G_1 and G_2 generations were similar but highly significantly superior ($P \leq 0.01$) to that of G_0 generation with that for G_2 generation having the highest body weight. For the whole population, body weight differed significantly across the three generations while for the control population G_0 and G_2 were similar in body weight but significantly ($P \leq 0.01$) inferior to G_1.

Table 7: Between sex comparison for body weight (g) (Mean ± S.E) for 12 to 20 weeks of age for G_0, G_1 and G_2 generations

Age	Gen.	Male	$(G_j - G_i)$	Female	$(G_j - G_i)$
12 weeks	G_0	791.40±8.76[a]		667.98±6.30[b]	
			(44.42)		(-17.79)
	G_1	835.82±7.09[a]		650.19±5.41[b]	
			(-10.54)		(23.75)
	G_2	825.28±7.54[a]		673.94±6.48[b]	
16 week	G_0	932.25±7.83[a]		791.52±6.24[b]	
			(28.99)		(-11.55)
	G_1	961.24±9.19[a]		779.97±5.27[b]	
			(66.59)		(32.57)
	G_2	1027.831±9.90[a]		812.54±7.72[b]	
20 week	G_0	1112.60±11.98[a]		911.59±6.33[b]	
			(32.08)		(15.28)
	G_1	1144.68±10.05[a]		926.87±5.01[b]	
			(12.01)		(12.77)
	G_2	1156.69±11.74[a]		939.64±7.28[b]	

[abc]: Means within the same row with different superscripts are significantly different ($P \leq 0.01$).
Legend: G_0, G_1, G_2: Generation zero, one and two respectively.
G_j: The mean value for jth generation (j = 1, 2).
G_i: The mean value for the ith generation (i = 0, 1).

Table 8: Between population mean comparison for 39 week body weight (g) for G_0, G_1 and G_2 generations (males)

Gen.	Selected	$(G_j - G_i)$	Whole	$(G_j - G_i)$	Control	$(G_j - G_i)$
G_0	1693.75±19.91[a]		1372.66±16.48[b]		1396.67±26.49[b]	
		(336.25)		(284.22)		(196.33)
G_1	2030.00±39.85[a]		1656.88±27.45[b]		1593.00±44.54[b]	
		(-30.00)		(111.87)		(-173.00)
G_2	2000.00±31.34[a]		1768.75±33.15[b]		1420.00±31.55[c]	

[abc]: Means within the same row with different superscripts are significantly different ($P \leq 0.01$).
Legend: G_0, G_1, G_2: Generation zero, one and two respectively.
G_j = the mean of the jth generation (j = 1, 2)
G_i = the mean of the ith generation (i = 0, 1)

Table 9: Between generation mean comparison for 39 week body weight (g) for selected, whole and control populations (males)

Population	G_0	$(P_i - P_j)$	G_1	$(P_i - P_j)$	G_2	$(P_i - P_j)$
Selected	1693.75±19.91[a]	(321.09)	2030.00±39.85[b]	(373.42)	2000.00±31.34[b]	(231.25)
Whole	1372.66±16.46[a]	(-24.01)	1656.58±27.45[b]	(63.58)	1768.75±33.15[c]	(348.75)
Control	1396.67±26.49[a]		1593.00±44.54[b]		1420.00±31.55[a]	

[abc]: Means within the same row with different superscripts are significantly different ($P \leq 0.05$).
Legend: G_0, G_1, G_2: Generations zero, one and two respectively.
P_i = The mean of the ith population (i = selected, whole populations).
P_j = The mean of the jth population (j = whole, control).

The highly significant heavier body weight of selected population of sires was in response to the selection of superior individuals (phenotypes and genotypes) within each generation to become parents of the next generation. The mean difference between the selected and whole populations yielded the well known selection differential (ΔS) which is the observable (phenotypic) result or outcome of the selection effort (Falconer, 1964; Stanfield, 1969; Nordskog, 1981; Pirchner, 1983; Cheng *et al*., 1996; Ibe, 1998). The predominant similarity between the whole and control populations in body weight values over G_0 and G_1 generations was in high accord with the report by Nwagu *et al.* (2007) who reported mean body weight at 40 weeks of 1623.8g and 1633.6g for whole and control populations, respectively, over five generations of selection in Rhode Island chickens. The superiority of the G_2 whole population over the control population could be as a result of accumulated realized selection response due to selection in G_0 and G_1 generations.

The consistently significant increases in body weight from G_0 to G_2 generations observed for the whole population confirms positive realized genetic gains in 39 week body weight of the sires as a result of selection in G_0 and G_1 generations. Marks (1983) reported such linear increases in body weight in a broiler population selected for 8 weeks body weight. Oluyemi (1979b) reported similar trends in a population of Nigerian indigenous fowl selected for 12 weeks body weight. Also Nwagu *et al.* (2007) reported increases in 40 weeks body weight (in the male line) over four (4) out of five (5) generations of selection in a population of Rhode Island chicken selected for part period egg production. The control populations being random bred populations expectedly remained essentially the same for G_0 and G_2 generations.

4.2 Heritability Estimates for Body Weight at Various Age Periods

Table 10 presents the heritability estimates (h^2_s) for body weight using sire components of variance at various ages (sexes combined) for the Nigerian heavy local chicken ecotype. The Table shows that for G_0 generation heritability values for hatch, 4^{th} week and 16^{th} week body weights were low (0.169, 0.149, and 0.152, respectively). The heritability values rose to 0.422 and 0.426, respectively, for week 8 and week 12 body weights while it was moderate 0.298 for week 20 body weight. For G_1 generation, heritability values were low (0.165 and 0.180) at 4^{th} and 16^{th} week body weight. It was moderate (0.230, 0.232 and 0.320) at hatch, 20^{th} and 12^{th} weeks, respectively. The value was high for week 8 body weight (0.436). For the G_2 generation,

low heritability values were observed at weeks 4, and 16 (0.151 and 0.129, respectively) while it was moderate (0.291, 0.349 and 0.379) for hatch, 8 weeks and 20 weeks body weights, respectively. High heritability value of 0.517 was recorded for body weight at 12 weeks.

Table 10: Heritability estimates $\left(h_s^2\right)$ for body weight (g) from hatch to 20 weeks for G_0, G_1 and G_2 generations (sexes combined)

	Generation		
Age	G_0	G_1	G_2
Hatch	0.169 ± 0.15	0.230 ± 0.14	0.291 ± 0.24
4 week	0.144 ± 0.16	0.165 ± 0.13	0.151 ± 0.17
8 week	0.422 ± 0.33	0.436 ± 0.25	0.349 ± 0.30
12 week	0.426 ± 0.33	0.320 ± 0.17	0.517 ± 0.38
16 week	0.152 ± 0.18	0.180 ± 0.15	0.127 ± 0.16
20 week	0.298 ± 0.26	0.232 ± 0.13	0.379 ± 0.31

G_0, G_1 and G_2 = Generations zero, one and two, respectively.

Table 11 presents the estimates of heritability (h^2_s) values for 12; 16; 20 and 39 week body weights for males across the three generations. High heritability values were obtained for 12, 16 and 20 weeks body weights (0.440, 0.435 and 0.512 respectively) and a moderate value of 0.247 for 39 week body weight for G_0 generation. For G_1 generation heritability values were generally moderate namely 0.386, 0.361, 0.290 and 0.215 for 12, 16, 20 and 39 weeks body weights, respectively. For G_2 generation, heritability value was high for 12 weeks body weight (0.593), moderate for 16 and 20 weeks body weights (0.336 and 0.242 respectively) and low for 39 weeks body weight (0.132). Thus for sexes combined, body weights at hatch, 4^{th} and 16^{th} weeks had the least heritability values while body weights at 8^{th}, 12^{th} and 20^{th} weeks had the highest heritability values across the three generations. For the males, heritability values were least for 39 weeks body weight across the three generations and it showed a downward trend from G_0 to G_2 generations.

Table 11: Heritability estimates $\left(h_s^2\right)$ for body weight (g) for 12 to 20 weeks of age for G_0, G_1 and G_2 generations (males)

	Generation		
Age	G_0	G_1	G_2
12 week	0.440 ± 0.39	0.386 ± 0.26	0.593 ± 0.45
16 week	0.435 ± 0.39	0.361 ± 0.26	0.336 ± 0.31
20 week	0.512 ± 0.31	0.290 ± 0.23	0.242 ± 0.27
39 week	0.247 ± 0.31	0.215 ± 0.39	0.132 ± 0.49

G_0, G_1 and G_2 = Generations zero, one and two respectively.

The heritability estimates obtained in this study for body weights at hatch to 20 weeks (sexes combined) and 12 weeks to 39 weeks (sires only) fall within the range commonly reported in literature (Falconer, 1964; Marks, 1983; Oluyemi 1979b; Gowe and Fairfull, 1990, Nwosu and Asuquo, 1985, Omeje and Nwosu 1983, Momoh, 2005). The moderate to high heritability values for body weight in males in the accelerating phase of growth indicate the availability of high additive genetic variance in the heavy local chicken ecotype and that body weight at these age periods will respond favourably to selection.

4.3 Selection Differentials, phenotypic standard deviation(σ_P), and Selection Intensity for Males

Table 12 presents the selection differential (ΔS), cumulative selection differential (CumΔS), phenotypic standard deviation(σ_P), and selection intensity (i) of 39 weeks body weight for male for G_0, G_1 and G_2 generations. The Table shows positive selection differentials for body weight namely 321.07g, 373.12g and 231.25g respectively for G_0, G_1 and G_2 generations. Cumulative selection differentials were equally positive amounting to 925.46g in G_2 generation. The phenotypic standard deviation increased from 152.054 in G_0 to 212.630 in G_1 and reduced slightly to 198.870 in G_2 with an average of 187.851 for the three generations. The selection intensity (i) which measures the strength of selection applied decreased from 2.11 in G_0 generation to 1.75 in G_1 and 1.16 in G_2 generation.

The positive selection differentials observed, followed from the superiority of selected population over the whole population of sires in 39 weeks body weight. The cumulative selection differentials were correspondingly positive and increasing in value. The phenotypic standard deviation – a measure of total variance in the population indicate persistence of usable variation across the generations. The selection intensity values, show that on the average a selection intensity of 1.67 standard deviations was applied across the generations for the selection of sires. The low selection pressure after G_0 generation resulted from the declining additive genetic variability among individuals of G_1 and G_2, generations in their 39 week body weight. This declining additive genetic variance was further reflected in the heritability estimates of 39 weeks body weight which expectedly declined to 0.132 in G_2 generation from 0.247 in G_0 generation. The selection intensity values reported in this study are higher than the values reported by Marks (1983) who reported average selection intensities of 0.70 and 0.91 in two populations of broilers

selected for 8 weeks body weight (males and females separated) for four (4) generations. The values are, however, in high accord with selection intensities calculated from data reported by Oluyemi (1979b) which ranged from 0.996 to 2.40 over seven (7) generations of selection for 12 weeks body weight in the Nigerian indigenous fowl.

Table 12: Selection differential (Δs); cumulative selection differential (CumΔs); phenotypic standard deviation (σ_P); and selection intensity (i) of 39 week body weight (g) (males)

Generation	Δs(g)	CumΔs(g)	σ_P	i
G_0	321.07	321.07	152.054	2.11
G_1	373.12	694.19	212.630	1.75
G_2	231.25	925.44	198.870	1.16
Average	302.19		187.851	1.67

Legend: G_0, G_1, G_2: Generation zero, one and two, respectively.
Δs = Selection differential.
CumΔs = Cumulative selection differential.
σ_P = phenotypic standard deviation.
i = selection intensity.

4.4 Response to selection in the Male population

Table 13 presents the expected genetic response (R), predicted genetic response (R_P), realized genetic gain (ΔG_R), ratio of realized to expected genetic response and ratio of realized to predicted genetic response for 39 week body weight for males across G_0, G_1 and G_2 generations. From the Table, the expected genetic response based on the selection applied were 297.06g for G_0, 437.00g for G_1 and 580.00g for G_2 generations. The predicted response on the other hand increased from 79.30g in G_0 to 80.22g in G_1 but dropped to 30.53g in G_2 generation. The realized genetic gain was 284.22 for G_0 and 111.87 for G_1. The ratio of realized to expected genetic gain was 0.96 for G_0, and 0.28 for G_1 generation (mean 0.61) while the ratio of realized to predicted was 3.58 for G_0 and 1.39 for G_1 generations (mean 2.49).

The expected genetic responses, predicted responses and realized genetic gains obtained in this study followed naturally from the positive selection differentials observed. The increasing values of expected responses to selection were indicative of favourable responses to selection for body weight trait in chickens. The predicted responses were, however, very low compared to the expected responses. This was not surprising since the 39 week body weight was associated with low additive genetic variability reflected in the low to moderate heritability values obtained in this study. The predicted responses being proportional to the selection differential and the additive genetic heritability were therefore, comparatively low relative to the corresponding expected genetic responses. The realized response was very close to the expected response in the G_0 generation, lower than expected response but higher than predicted response in G_1 generation. The generational differences among expected, predicted and realized responses, as well as, the non-correspondence in values of these responses per generation for each trait are not out of place. Generational mean values are neither constant nor linear but fluctuate rather erratically (Falconer, 1964) and so do responses derived from them (Falconer, 1964; Fairfull and Gowe, 1990). Observed (realized) selection response per generation was usually lower than expected response as obtained in the present study (Fairfull and Gowe, 1990). Reasons adduced for the variable responses include genotype by environment interaction or correlated responses among traits (Srivastava, 1985). Sampling error and variation in environmental effects across generations account for variations in generational mean values. The mean ratio of 0.61 or 61% obtained for realized to expected responses in this study shows that selection was effective to improve the 39 week body weight of males of the heavy local chicken ecotype. The ratio of

realized to predicted responses were generally very high (3.58 and 1.39). The values were therefore, higher than those by Oluyemi (1979b) who reported a range of 0.57 to 1.08 (57% to 108%) as ratio of realized to predicted responses for 12 week body weight in the Nigerian indigenous fowl.

Table 13: Expected, cumulative response, predicted, realized genetic gain, ratio of realized to expected response and ratio of realized to predicted response in 39 week body weight (Males)

Generation	R	CumR	R_P	ΔG_R	$\frac{\Delta G_R}{R}$	$\frac{\Delta G_R}{R_P}$
G_0	297.06	297.06	79.30	284.22	0.96	3.58
G_1	437.00	734.06	80.22	111.87	0.26	1.39
G_2	580.00	1314.06	30.53	---*[1]	----	----
Average/Gen	508.50				0.61	2.49

Legend: G_0, G_1, G_2: Generation zero, one and two, respectively.
R = expected genetic response.
R_P = predicted genetic response.
ΔG_R = realized genetic response.
*[1] = values not available because G_2 progeny (G_3 generation) were not generated.
CumR = cumulative response.

4.5 Total Egg Number, Average egg weight and body weight at first egg

Table 14 presents the mean values for total egg number (TEN), average egg weight (AEW) and body weight at first egg (BWFE) of the Nigerian heavy local chicken ecotype for selected, whole and control populations across the three generations. The Table expresses the superiority of the selected populations over the whole and control populations in total egg number across the three generations and in average egg weight for G0 and G1 generations. For BWFE, the whole population had the highest value in G0 and G1 generations while in G_2 generation, both the selected and whole populations significantly ($P \leq 0.05$) surpassed the control population. The between generation comparison for total egg number, average egg weight and body weight at first egg for selected, whole and control populations are presented in table 15. The table reveals significant ($P \leq 0.05$) between generation differences in total egg number, average egg weight and body weight at first egg for the selected and whole populations across the three generations. Specifically, selected G_1 population was significantly higher than selected G_2 population ($P \leq 0.05$), which was in turn highly significantly superior ($P \leq 0.01$) to the G_0 selected population for total egg number. For the whole population, G_2 birds highly significantly ($P \leq 0.01$) surpassed those of G_1 which in turn highly significantly ($P \leq 0.01$) exceeded G_0 whole population in the same trails. The control populations were more similar in egg production across the three generations with G_0 and G_1 control populations being similar but highly significantly different ($P \leq 0.01$) from the G_2 control population in total egg number. For average egg weight, G_1 selected population differed significantly ($P \leq 0.05$) from selected G_2 population which was in turn highly significantly different ($P \leq 0.01$) from selected G_0 population. G_0 whole population was highly significantly inferior ($P \leq 0.01$) to G_1 and G_2 whole populations with G_2 whole population having the highest average egg weight value. The control populations showed some degree of similarity in their average egg weight across the three generations. Average egg weight value for the G_0 control population was not significantly different ($P \geq 0.05$) from that of G_2 generation but both differed significantly ($P \leq 0.05$) from that of G_1 control population. For body weight at first egg, table 14 reveals highly significant differences ($P \leq 0.01$) between the body weight at first egg of G_2 selected population and those of G_1 and G_0 generations. Selected G_1 population was the least in body weight at first egg being significantly inferior ($P \leq 0.05$) to that of G_0 generation. For the whole populations, G_2 generation highly significantly ($P \leq 0.01$) exceeded those of other generations with G_1 whole population recording the least value and

being significantly inferior ($P \leq 0.05$) to that of G_0 generation. The control populations also differed significantly across generations. G_2 control population exceeded highly significantly ($P \leq 0.01$) those of G_1 and G_0 generations with the G_1 control population having the least value and being significantly inferior ($P \leq 0.05$) to that of G_0 population.

Table 14: Between population comparison for index traits across G_0, G_1 and G_2 generations

Trait	Gen	Selected	$(G_j - G_i)$	Whole	$(G_j - G_i)$	Control	$(G_j - G_i)$
TEN	G_0	82.92±0.146[a]		75.60±0.177[b]		78.66±0.323[c]	
			(6.81)		(2.19)		(-0.72)
	G_1	89.73±0.089[a]		77.79±0.136[b]		77.94±0.227[b]	
			(-0.82)		(1.59)		(-2.40)
	G_2	88.91±0.112[a]		79.38±0.194[b]		75.54±0.237[c]	
AEW	G_0	41.94±0.071[a]		41.27±0.058[b]		40.11±0.102[c]	
			(1.90)		(1.65)		(0.90)
	G_1	43.84±0.081[a]		42.92±0.053[b]		41.01±0.069[c]	
			(-0.65)		(0.26)		(-0.94)
	G_2	43.19±0.120[a]		43.18±0.070[a]		40.07±0.064[b]	
BWFE	G_0	1301.18±2.459[a]		1330.44±2.141[b]		1301.89±3.793[a]	
			(-12.88)		(-25.60)		(-18.74)
	G_1	1288.30±2.080[a]		1304.84±1.579[b]		1283.15±3.023[a]	
			(145.90)		(123.64)		(106.12)
	G_2	1434.20±5.520[a]		1428.48±3.051[a]		1389.27±3.372[b]	

[abc]: Means within the same row with different superscripts are significantly different ($P \leq 0.05$).

Legend: TEN = Total egg number.

AEW = Average egg weight.

BWFE = Body weight at first egg.

G_j = the mean observation for jth generation.

G_i = the mean observation for ith generation.

$(G_j - G_i)$ = mean difference (increase (+) or decrease (-)) between jth and ith generations (i = 0, 1, and j = 1, 2).

Table 15: Between generation comparison of the performances of selected, whole and control populations in index traits

Trait	Population	G_0	$(P_i - P_j)$	G_1	$(P_i - P_j)$	G_2	$(P_i - P_j)$
TEN	Selected	82.92±0.149[a]		89.73±0.089[b]		88.91±0.112[c]	
			(7.32)		(11.94)		(9.53)
	Whole	75.60±0.177[a]		77.79±0.136[b]		79.38±0.194[c]	
			(-3.06)		(-0.15)		(3.84)
	Control	78.66±0.323[a]		77.94±0.227[a]		75.54±0.237[b]	
AEW	Selected	41.94±0.071[a]		43.84±0.081[b]		43.19±0.120[c]	
			(0.67)		(0.92)		(0.01)
	Whole	41.27±0.058[a]		42.92±0.053[b]		43.18±0.070[c]	
			(1-16)		(1.91)		(3.11)
	Control	40.11±0.102[a]		41.01±0.069[b]		40.07±0.064[a]	
BWFE	Selected	1301.18±2.429[a]		1288.30±2.080[b]		1434.20±5.520[c]	
			(-34.44)		(-59.1)		(5.72)
	Whole	1330.44±2.141[a]		1347.40±1.579[b]		1428.48±3.051[c]	
			(28.55)		(64.25)		(39.21)
	Control	1301.89±3.793[a]		1283.15±3.023[b]		1389.27±3.372[c]	

[abc]: Means within the same row with different superscripts are significantly different ($P \leq 0.05$)

Legend: TEN = Total egg number.
AEW = Average egg weight.
BWFE = Body weight at first egg.
G_0, G_1, G_2 = Generation zero, one and two, respectively.
P_i = the mean of the ith population (i = selected, whole).
P_j = the mean of the jth population (j = whole or control).
$(P_i - P_j)$ = mean difference between ith population mean and jth population mean.

4.6 Response to Selection in the female population

Table 16 presents the expected selection differentials, cumulative selection differential, phenotypic standard deviation and selection intensity for total egg number, average egg weight and body weight at first egg for G_0, G_1 and G_2 generations. There were positive selection differentials for egg number and egg weight across the generations leading to progressive increases in cumulative selection differentials in these traits. The selection differential for body weight at first egg was negative for G_0 and G_1 but positive for G_2 generation. The cumulative selection differentials were correspondingly negative across the three generations. The phenotypic standard deviation remained relatively stable and positive for each trait across the three generations. The selection intensity factor for egg number increased from 0.530 in G_0 to 0.852 in G_1. It was 0.806 in G_2 averaging 0.729 for the three generations. For egg weight the selection intensity was 0.149 in G_0, 0.167 in G_1 but very low (0.002) in G_2. For body weight at first egg there were negative selection intensities in G_0 and G_1 generations. It became positive but very low (0.031) in G_2 generation.

The positive selection differentials (Δs) obtained for total egg number and average egg weight across the three generations followed from the superiority of the selected populations over the whole populations in mean values for these traits. The selection differential values for body weight at first egg were also understandably negative for G_0 and G_1 generations but positive for G_2 generation. The per generation selection differential values for total egg number and average egg weight as obtained in the present study are higher than the values of 1.67 eggs and -1.21g for egg number and average egg weight to 40 weeks, respectively, reported by Nwagu *et al.* (2007) in a population of Rhode Island chickens selected for 5 generations. The values are, however, lower than 15.28 eggs and 1.54g for egg number to 52 weeks and egg weight to 40 weeks, respectively, reported by Cheng *et al.* (1996) in a population of *Anas platyrhnchos*. The values for body weight at first egg are similarly lower than that reported by Cheng *et al.* (1996) for body weight at 40 weeks (-5.41g Vs 11.0g) for *Anas platyrhnchos* but higher than that by Nwagu *et al.* (2007) for body weight at 40 weeks in Rhode Island chickens (-5.41 Vs -28.60).

The increasing values of cumulative selection differentials for total egg number and average egg weight across the G_0, G_1 and G_2 generations was as a result of persistent positive phenotypic responses (selection differentials) observed for these traits over the generations. The cumulative selection differential values for body weight at first egg were correspondingly

negative. The values for phenotypic standard deviation (σ_P) for all traits were positive indicating persistent availability of variation among individuals of each generation in these traits. The fractional (ith) selection intensity factor for each trait in each generation was highest for egg number but least for body weight at first egg. This shows that the multiple trait selection index employed in this study differentially applied greater selection pressure on egg production, than egg weight and least pressure on body weight at first egg. The low (indeed negative) fractional selection intensity values accruing to body weight at first egg in G_0 and G_1 generations may have been responsible for the very low (indeed negative) selection differentials obtained in G_0 and G_1 generations for this trait. This reflects the scaling effect of multiple trait economic selection index which weight traits according to their relative economic values.

Table 16: Selection differentials, cumulative selection differential, phenotypic standard deviation and selection intensity for index traits

Trait	Generation	Δs(g)	Cum Δs(g)	σ_P	i
TEN	G_0	7.32	7.32	13.815	0.530
	G_1	11.94	19.26	14.007	0.852
	G_2	9.53	28.79	11.821	0.806
Average/Gen		10.74			
AEW	G_0	0.67	0.67	4.494	0.149
	G_1	0.92	1.59	5.500	0.167
	G_2	0.01	1.60	4.254	0.002
Average/Gen		0.47			
BWFE	G_0	-29.26	-29.26	167.012	-0.206
	G_1	-16.54	-45.80	162.409	-0.102
	G_2	5.72	-40.08	185.799	0.031
Average/Gen		- 5.41			

Legend: TEN = Total egg number.
AEW = Average egg weight.
BWFE = Body weight at first egg.
G_0, G_1, G_2 = Generation zero, one and two, respectively.
Δs = selection differential.
Cum Δs = cumulative selection differential.
σ_P = phenotypic standard deviation.
i = standardized selection differential (selection intensity).

4.7 Genetic, Phenotypic and Environmental Correlations (r_g, r_p and r_E)

Table 17 contains the genetic parameters (genetic correlation, r_g, phenotypic correlations, r_p and environmental correlations, r_E) between pairs of traits across the three generations (G_0, G_1 and G_2). Generally genetic correlations between egg number and egg weight were low ranging from -0.01 to 0.01 for unselected population and -0.03 to 0.02 for selected populations across G_0, G_1 and G_2 generations. Similar trends were observed for genetic correlations between egg number and body weight at first egg and for egg weight and body weight at first egg.

The values obtained for the different correlation coefficients reflect the strength of association or joint response to common causal effects by the traits concerned. Genetic correlations between egg production and egg weight and between egg production and body weight are generally negative (Falconer, 1964; Fairfull and Gowe, 1990). In Leghorns, however, the picture is not as definite. Genetic correlations between egg production and body weight at sexual maturity (18 to 22 weeks), equivalent to body weight at first egg, were positive (0.13 to 0.29) for early part – record but became increasingly lower and negative (0.07 to -0.11) with later parts. Thus, for Leghorns, the picture is mixed. Generally, positive and negative, moderate and low values were found (Fairfull and Gowe, 1990). For egg production and mature body weights (39 to 55 weeks), a definite trend was reported by the same authors. Genetic correlations between egg production and body weight were generally negative (-0.12 to -0.08) for selected populations but positive (0.38 to 0.45) for unselected (random bred) populations. Such definite trends were not the case in the present study and the results tend to correspond with the values reported for 18 – 22 weeks of age as stated above. Cheng *et al*. (1996) reported the genetic and phenotypic correlations between egg number and body weight at 40 weeks as 0.006 and 0.063, respectively. For egg weight and body weight, a value of 0.617 and 0.424 were reported for genetic and phenotypic correlations, respectively. Francesch *et al*. (1997) gave a range of -0.22 to 0.19 and -0.18 to 0.14, respectively, as genetic and phenotypic correlations between egg number and egg weight in three catalan poultry breeds. The low genetic and phenotypic correlation values observed in this study suggest that at present the antagonism associated with strong negative genetic correlations between egg production and egg weight and egg production and body weight may not be a serious limitation in combining these traits in a multiple trait selection index for the improvement of egg production traits in the Nigerian heavy local chicken ecotype. The results also seem to suggest that the productive genes in the Nigerian local chicken

are not yet ‘properly aligned’ or ‘definitely linked’ in relation to one another and having been under the influence of adverse environmental effects these genes are still masked by genes for survival which at present seem preponderant in the local chicken population (Ibe, 1998).

Table 17: Estimates of Genetic, Phenotypic and Environmental correlations for pairs of traits in the index

		Generation								
		G_0			G_1			G_2		
Trait	**Population**	$\mathbf{r_g}$	$\mathbf{r_P}$	$\mathbf{r_E}$	$\mathbf{r_g}$	$\mathbf{r_P}$	$\mathbf{r_E}$	$\mathbf{r_g}$	$\mathbf{r_P}$	$\mathbf{r_E}$
EN-EW	Whole	0.01	0.09	0.83	0.0002	0.014	0.55	-0.01	-0.12	1.31
EN-BWFE	Whole	0.01	0.08	0.52	-0.06	0.011	0.56	-0.001	-0.04	0.69
EW-BWFE	Whole	0.02	0.22	0.52	0.002	0.23	0.38	0.01	0.21	0.85

Legend: EN x EW = Correlation between egg number and egg weight
EN x BWFE = Correlation between egg number and body weight at first egg
EW x BWFE = Correlation between egg weight and body weight at first egg
r_g = genetic correlation
r_P = phenotypic correlation
r_E = environmental correlation

4.8 Estimates of Additive genetic heritability (h_s^2) for egg number, egg weight and body weight at first egg

Table 18 presents estimates of additive genetic heritability (h_s^2) for egg number, egg weight and body weight at first egg for G_0, G_1 and G_2 generations. The heritability estimates were low to moderate (0.124 to 0.236) for egg number, moderate to high (0.340 to 0.432) for egg weight and high (>0.50) for body weight at first egg.

Table 18: Estimates of additive genetic heritability (h_s^2) for index traits

	Trait		
Generation	TEN	AEW	BWFE
G_0	0.124 ±0.08	0.340 ± 0.21	0.636 ± 0.38
G_1	0.135 ± 0.06	0.432 ± 0.21	0.566 ± 0.26
G_2	0.236 ± 0.16	0.344 ± 0.24	0.694 ± 0.48

Legend: TEN = Total egg number.

AEW = Average egg weight.

BWFE = Body weight at first egg.

G_0, G_1, G_2 = Generation zero, one and two, respectively.

h_s^2 = additive genetic heritability.

4.9 Relative economic weights for egg number, egg weight and body weight at first egg

Table 19 contains the relative economic weights (a_i) for index traits. The relative economic weights were 2.83, 3.50 and 2.83 for egg number for G_0, G_1 and G_2 generations, respectively. For egg weight, the corresponding values were 3.54, 4.07 and 3.28 while for body weight at first egg the relative economic weight was -1.00 across the three generations.

The relative economic weights (a_{is}) calculated for egg number, egg weight and body weight at first egg reflect the relative economic importance of the three traits, that is, their relative contribution to the overall economic (Naira) value (worth) of the heavy local chicken ecotype. Egg production (egg number and egg weight) is the major index of performance of the commercial layer (Oluyemi and Roberts, 2000). Other indices include feed efficiency and mortality. Egg production, therefore, accounts for over 90% of the revenue or income accruable from an egg production enterprise. These traits (egg number and egg weight) were, therefore, more heavily weighted (mean 3.05 and 3.63, respectively) than body weight at first egg, which major contribution to the performance index of an egg production enterprise seems to be its correlated effect on egg weight. Body weight had negative economic value because of the negative relationship between revenue from a unit gain in body weight and the cost of feed consumed to attain such a gain in the local chicken. Relative economic values for productive traits in the indigenous chickens of Nigeria are absent in literature but the values reported here are similar in direction to those reported by Nordskog (1981). Relative economic values per genetic standard deviation calculated from data reported by Bennet *et al*. (1981) were 4.20, 2.10 and 1.00 for egg number, egg weight and body weight, respectively.

Table 19: Estimate of relative economic weights for index traits

Relative economic weights			
	Trait		
Generation	TEN	AEW	BWFE
G_0	2.83	3.54	-1.00
G_1	3.50	4.07	-1.00
G_2	2.83	3.28	-1.00

Legend: G_0, G_1, G_2: Generations zero, one and two, respectively.

4.10 Selection response in egg number, egg weight and body weight at first egg

Table 20 presents the expected direct genetic response (R_i), cumulative direct response (CumR), expected (average) direct response per generation $\left(\overline{R}_i\right)$ and expected annual direct genetic response (R_i/yr) for egg number, egg weight and body weight at first egg across the three generations of selection. The table shows that expected direct response increased progressively for the three traits selected from G_0 to G_2 generations leading to similar trends in cumulative selection response for all the traits. Specifically expected direct genetic response for total egg number increased from 4.26 eggs for G_0 generation to 11.79 eggs and 13.37 eggs for G_1 and G_2 generations, respectively. The expected average direct response per generation was 12.58 eggs for egg number, 2.98g for egg weight and 25.04g for body weight at first egg.

Table 21 contains the predicted genetic response (gain) (R_p) and realized genetic gain (ΔG_R) for egg number, egg weight and body weight at first egg. For egg number, predicted genetic gain was positive and increased progressively from 0.91 eggs for G_0 to 2.25 eggs for G_2. The realized response was 2.19 eggs (51% of expected) for G_0 and 1.59 eggs (13% of expected) for G_1 generation. For egg weight, predicted response increased initially from 0.23g in G_0 to 0.40g in G_1 but dropped drastically to 0.003g in G_2 generation. The realized genetic response on its part decreased from 1.65g (90% of expected) in G_0 to 0.26g (9% of expected) in G_1 generation. Predicted responses were negative for G_0 and G_1 generations for body weight at first egg but became positive though low (3.97g) for G_2 generation. Realized response was also negative in G_0 generation but became positive (123.64g) in G_2 generation.

Table 20: Expected direct, cumulative, and average genetic responses for index traits across G_0, G_1 and G_2 generations

Trait	Generation	R_i	CumR_i	$\overline{R}_i$	R_i/yr
TEN	G_0	4.26	4.26		4.26
	G_1	11.79	16.05		11.79
	G_2	13.37	29.42	12.58	13.37
AEW	G_0	1.83	1.83		1.83
	G_1	2.83	4.66		2.83
	G_2	3.12	7.78	2.98	3.12
BWFE	G_0	-0.71	-0.71		-0.71
	G_1	5.15	4.44		5.15
	G_2	44.93	49.37	25.04	44.93

Legend: TEN = Total egg number.
AEW = Average egg weight.
BWFE = Body weight at first egg.
G_0, G_1, G_2 = Generation zero, one and two, respectively.
R_i = expected direct genetic response in ith trait.
CumR = cumulative response.
R_i = expected average direct response in the ith trait per generation.

Table 21: Predicted and realized genetic responses for index traits

Trait	Generation	R_P	ΔG_R
TEN	G_0	0.91	2.19
	G_1	1.61	1.59
	G_2	2.25	---*[1]
AEW	G_0	0.23	1.65
	G_1	0.40	0.26
	G_2	0.003	---*[1]
BWFE	G_0	-21.90	-25.60
	G_1	-33.45	123.64
	G_2	3.97	---*[1]

Legend: TEN = Total egg number, AEW = Average egg weight.
BWFE = Body weight at first egg.
G_0, G_1, G_2 = Generation zero, one and two, respectively.
R_p = Predicted direct genetic response.
ΔG_R = realized genetic gain.
*[1] = values not available because G_2 progeny (G_3 generation) were not generated.

The values obtained for expected direct genetic response, cumulative direct response, average direct genetic response per generation and expected annual direct response in the present study indicate a net positive selection response expected in the progeny of the selected parents across the generations. Comparison of the observed values and published reports of similar studies show, that the values reported in this study are higher. Nwagu *et al*. (2007) reported genetic and phenotypic change per generation of 3.14 eggs and 1.67 eggs, respectively, for egg number, -0.89g and -1.21g, respectively, for egg weight and 6.12g and -28.60g, respectively, for body weight at 40 weeks. Cheng *et al*. (1996) observed per generation expected genetic response of 0.119g for egg weight, -6.463g for body weight at 40 weeks and 1.432 eggs for egg number using an index incorporating these traits. The higher values obtained in this study could be attributed to the fact that the population that was the material for this study has not undergone artificial selection previously and showed an initial surge in response to this initial stimulus due to availability of raw genetic variability.

Expectedly, the values obtained for realized genetic gain in total egg number and average egg weight for G_0 and G_1 generations were positive corresponding to the positive predicted values and indicate improvement in these traits across the generations. Though realized response was negative for body weight at first egg in G_0 generation it equally became positive in G_1 generation probably due to favourable genotype by environment interaction favouring the progenies of selected parents from G_0 generation. Cheng *et al*. (1996) reported a value of 0.177g for egg weight; 0.937 eggs for egg number and 8.029g for body weight to 40 weeks of age. Nwagu *et al*. (2007) reported predicted values of 5.14, 6.17 and 3.77 eggs, respectively, for the first three (3) generations of selection in Rhode Island chickens.

4.11 Mean values, Selection Differential, Phenotypic Standard Deviation, Selection Intensity, Heritability and Expected Response for Index Score.

Table 22 contains the mean index value for selected (Is) and whole (Iμ) populations; selection differential for index score (ΔS_I); phenotypic standard deviation for index (σ_I), selection intensity for index (i_I), heritability of index $\left(h_I^2\right)$ and expected genetic gain in index score (ΔG_I) for G_0, G_1 and G_2 generations. The table shows that mean index value, selection differential for index, phenotypic standard deviation, heritability of index and expected genetic response in index values increased progressively across the three generations. For instance, the additive genetic heritability for index increased from a value of 0.08 in G_0 to 0.09 in G_1 and 0.133 in G_2 generation. The selection intensity for index remained relatively stable with a value of 0.703 in G_0, 0.989 in G_1 and 0.890 in G_2 generation.

The increasing values obtained for selection differential for index indicate that selection was effective in improving phenotypic responses in index value. Progressive increases in values of phenotypic standard deviation of index point to persistent availability of variation in index score of individuals within each generation which also means availability of additive genetic variability as evident in the increasing values obtained for heritability of index. The values obtained for expected genetic response in index score were therefore, in line with the above positive results.

Table 22: Mean index values, selection differential, phenotypic standard deviation, selection intensity, heritability, and expected genetic gain for index score for G_0, G_1 and G_2 generations

Generation	$\bar{I}s$	$\bar{I}\mu$	Δs_I	σ_I	i_I	h_I^2	ΔG_I
G_0	11.071	9.932	1.139	1.621	0.703	0.08 ± 0.23	0.156
G_1	12.177	9.893	2.284	2.309	0.989	0.09 ± 0.16	0.356
G_2	12.372	9.982	2.390	2.686	0.890	0.133 ± 0.38	0.554

Legend: $\bar{I}s$ = mean index score for selected population.
$\bar{I}\mu$ = mean index score for whole population.
Δs_I = expected selection differential for index.
σ_I = phenotypic standard deviation for index.
i_I = selection intensity factor for index.
h_I^2 = heritability estimate for index.
ΔG_I = expected genetic gain in index.

4.12 Response in the Component Traits of the Index due to Selection on the Index Score

Table 23 presents the expected genetic gain in index traits due to selection on index score and the ratio of realized to expected genetic gain in index traits for G_0, G_1 and G_2 generations. From the table it is observed that expected genetic response in the index traits as a result of selection on the index score was positive for the three traits selected across the three generations. For total egg number, the value increased from 0.964 eggs in G_0 to 1.531 eggs in G_1 and 1.878 eggs in G_2 generation (mean, 1.705 eggs). For egg weight, expected genetic gain was 0.523g for G_0, 1.081g for G_1 and 0.817g for G_2 (mean, 0.949g) while for body weight at first egg it increased from 26.85g for G_0, to 36.63g for G_1 and 51.22g for G_2 (mean, 43.93g). The ratio of realized direct genetic gain in index traits (table 21) to expected genetic gain in index traits (table 23) was positive and high for all the traits and across the three generations. It was 2.27 and1.22 (mean, 1.75) for egg number; 3.15 and 0.24 (mean, 1.70) for egg weight; and 0.95 and 2.21 (mean, 1.58) for body weight at first egg.

The values obtained for expected genetic responses in the index traits across the generations as a result of selection on index score are sequel to the positive and increasing selection differentials in index values, as well as, persistence of additive genetic variability in the index traits across the generations.

The ratio of observed (realized) to expected genetic gains in index traits ($\Delta G_R/\Delta gi$) as observed in this study are higher than the values reported by Fairfull and Gowe, (1990) which gave a range of 0.77 to 1.47 (mean, 1.12) as ratio of observe to expected responses and that of Nwagu *et al*. (2007) which gave a range of 0.38 to 1.46 (mean, 1.08) for ratio of observed to expected genetic gain for egg production in Rhode Island chickens. The higher ratios indicate higher realized genetic gain in the Nigerian heavy local chicken ecotype probably due to favourable genotype by environment interaction as well as a surge in response to this initial selection stimulus.

Table 23: Expected genetic gain in index traits as a result of selection on index score

Trait	Generation	Δg_i	CumΔg_i	$\Delta G_R/\Delta g_i$
TEN	G_0	0.964	0.964	2.27
	G_1	1.531	2.495	1.22
	G_2	1.878	4.373	*---
Av/Gen.		1.705		
AEW	G_0	0.523	0.523	3.15
	G_1	1.081	1.604	0.24
	G_2	0.817	2.421	*---
Av/Gen.		0.949		
BWFE	G_0	26.85	26.85	0.95
	G_1	36.63	63.48	2.21
	G_2	51.22	114.70	*---
Av/Gen.		43.93		

Legend: Δg_i = expected genetic gain.
ΔG_R = realized direct genetic gain (table 18).

***--- =** value not available because G2 progeny were not generated.

CHAPTER FIVE

5.0 CONCLUSION AND RECOMMENDATION

5.1 Conclusion

From the foregoing it can be concluded as follows:

1. Mass selection for body weight at 39 weeks of age in the male line was effective in improving the 39 week body weight of males as well as the body weight performances of the birds within the accelerating phase of growth (0 – 20 weeks). Greater improvement will however be expected if in future selection for body weight improvement in the Nigerian heavy local chicken ecotype is based on 8, 12 or 20 weeks body weight as recommended.
2. The multiple trait selection index employed for the simultaneous selection of total egg number, average egg weight and body weight at first egg brought about improvement in these traits and the efficiency factors reported in this study were positive and high. Body weight at first egg was not, however, a good selection criterion for improvement in the growth performance of hens within the accelerating phase of growth (0 – 20 weeks).
3. The selection pressure applied brought about modest improvement in the traits concerned and significant genetic variation was still present to ensure positive selection responses in subsequent generations.
4. The relative economic weights determined for the traits in this study appropriately weighted the traits according to their relatively contribution to the economic worth of the Nigeria heavy local chicken ecotype. While the values for egg number and egg weight ensured that individuals with good performances in these traits were selected in each generation, the negative weighting of body weight at first egg ensured that hens with high body weight values without corresponding high values in egg number and/or egg weight were rejected as it costs much more to maintain local chickens of high body weights than would be realized from sale of local chicken carcass.
5. The final mean phenotypic values of 79.38 eggs in 16 weeks (112 days) for unselected population (expected annual mean, 258.69 eggs) and 88.91 eggs for the same period for selected population (expected annual mean, 289.75 eggs) is quite impressive. Commercial flocks (exotic breeds) commonly average 200 to 250 eggs per year within the tropics. The performance of the Nigerian heavy local chicken ecotype in egg

production as obtained in this study hence compares favourably with any exotic breed in Nigeria. This in addition to attaining a body weight of above 1kg at sexual maturity makes the Nigerian heavy local chicken ecotype a potential dual purpose bird.

5.2 Recommendations

The recommendations sequel to the above empirical observations are hence:

1. That co-ordinated effort at industrial and governmental levels be made to improve the Nigerian heavy local chicken ecotype.
2. That the ultimate improvement through selection could see the “creation” of a new breed of the Nigerian heavy local chicken ecotype.
3. That researches similar to the one under consideration should be instituted for other indigenous livestock species (cattle, sheep and goat) to determine their true genetic potentials.

REFERENCES

Adedokun, S.A., and Sonaiya, E.B. (2001): Comparison of the performance of Nigerian indigenous chickens from three agro ecological zones. Livestock research for rural development 3(2). 34 – 39.

AGRI. (2002): The global strategy for the management of farm animal genetic resources – an update. AGRI (2002), 32: 1- 12.

Akinokun, O., and Dettmers, A. (1977a): Comparison of the Ife breeds of the indigenous chicken of Nigeria with improved exotic strains. 2: body weight at sexual maturity. Nig. J. Anim. Production 4 (1): 269 – 270 (Abstract).

Akinwumi, J.A., Adegeye, A.J., Ikpi, A.E., and Olayide, S.O. (1979): Economic analysis of the Nigerian poultry industry. Fed. Livestock Dept. Lagos.

AL-Rawi, A.A., and AL-Athari, A.K. (2002): Characteristics of indigenous chicken in Iraq. AGRI, 2002, 32: 87 – 93.

Asuquo, B.O., and Nwosu, C.C. (1987): Heritability and correlation estimates of body weight in the local chicken and their crosses. E. Afr. Agric. For J. 52 (4): 267 – 271.

Atteh, J.O. (1990): Rural poultry p roduction in western middle-belt region of nigeria. In rural poultry production in Africa. Ed. Sonaiya, E.B. Proceedings of an international workshop on rural poultry in Africa. Ile-Ife Nigeria 13-16 Nov. 1989. 211 – 217.

Bacon, L.B., Smith, E.J., Crittenden, L.B., and Havenstein, G.B. (1988): Association of the slow feathering (K) and endogenous viral (en – 21) gene on the z-chromosome of chickens. Part 1. Evaluation of short term response to selection. In Crawford, R.D. Poultry breeding and genetics. Elsevier science publishing company inc. 1990.

Becker, W. A. (1992): Manual of Quantitative genetics. 5th Edition USE; Academic Enterpise Pullman, 189pp.

Bennett, G.L., Dickerson, G.E., and Kashyap, T.S., (1981): Effectiveness of multiple-trait index progeny test selection for field performance of strain-cross layers. Poult. Sci. 60:22.

Boukila, B., Desmarais, M., Pare, J.P., and Bolamba, D. (1985): Selection for increased egg production based on annual record in three strains of white leghorns. I. comparison of different partial records to improve annual egg production. Poultry sci. 66: 1077 – 1084.

Cartwright, T.C. (1970): Selection criteria for beef cattle for the future. J. Anim. Sci. 30:706.

Cartwright, T.C., Fitzhugh, H.A., and Long, C.R. (1975): Systems analysis of sources of genetic and environmental variation in efficiency of beef production and mating plans. J. Anim. Sci. 40:433.

Central Bank of Nigeria, C.B.N. (2000): Annual reports and statement of account, 2000. C.B.N. Abuja.

Central Bank of Nigeria, C.B.N. (2002): Annual reports and statement of account, 2002. C.B.N. Abuja.

Chambers, J.R., Bernon, D.E., and Gavora, J.S. (1984): Synthesis and parameters of new populations of meat-type chickens. Theor Appl. Genetics 69: 23 – 30.

Chen, C– F., and Michele, T– B. (2003): Estimation of genetic variability and selection response for clutch length in dwarf brown – egg layers carrying or not the naked neck gene. Genet. Sel. Evol. 32 (2003) 219 – 238.

Cheng, Y.S, Poivey, J.P., Rouvier, R. and Tai, C. (1996): Prediction of genetic gains in body weight, egg production and shell quality traits in the brown Tsaiya laying duck (Anas platyrhgnchos). Genet. Sel. Evol. (1996) 28: 443 – 455.

Cochran, W.G. (1951): Improvement by means of selection. Page 449 in proc. 2nd Berkeley symp. Math. Stat. prob., Univ. California Press, Berkeley.

Coquerelle, A., and Mérat, P. (1979): Gène de reduction de taille lié an sexe chez la poule (dw^B): effet sur la ponte et la consommation d'aliment. In: Crawford, R.D., editor poultry breeding and genetics. Elsevier science publishing company Inc. N.Y. USA.

Crawford, R.D. (1990): Poultry breeding and genetics. Elsevier science company Inc. N. Y. USA.

Cresswell and Gunawan (1982): Genetic progress in broiler traits: Implication for welfare. Proc. Brit. Soc. Anim. Sci. 50p. In: Lohman information vol. 43 (1) April, 2008, 43pp www.fao.org/docrep/009/toz84e.

Cunningham, E.P. (1969): Animal breeding theory. Intronordic licenciat course in quantitative genetics. Pg. 199 – 236.

Dalton, D. C. (1981): An introduction to practical animal breeding (ELBS Ed.). Granada publishing co. Ltd, Great Britain. Pp 89 – 94.

Emsley, A. and Dickerson, G.C. (1974): Predicting 12-trait aggregate breeding value from indexes composed of fewer than 12 traits in egg production chickens. Page 157 in Proc. XV World Poultry Congr. New Orleans,

Fairfull, R.W. (1982): Combining ability, heterosis and reciprocal effects for first and second year performance in six selected leghorn strains crossed in a complete diallel. Proc. 31st Nat. Breeders Round table 1st hours: 119 – 137.

Fairfull, R.W., and Gowe, R. S. (1990): Genetics of egg production in chicken. In: Crawford, R. D. poultry breeding and genetics. Elsevier science publishing company Inc. pp 705 – 760.

Falconer, D.S. (1964): Introduction to Quantitative genetics. Robert Máclehose and co. Ltd. Glasgow.

Federal Ministry of Agriculture and Rural Development (FMARD) (2008): National of livestock survey. In: Livestock module National programme for food security (NPFS).

Finney, D.J. (1962): Genetic gains under three methods of selection. Genet. Res. 3: 417 – 423.

Fisher, R.A. (1936): The use of multiple measurements in taxonomic problems. Ann. Eugen. (London) 7, 179 – 189.

Flock, D. (1994): Proc. 9th European poultry conference, Glasgow, U.K.

Food and Agriculture Organization (FAO) (1973): Report of the 4th expert consultation on animal genetic resources (poultry breeding), Houxilly, France, March, 1973.

Food and Agriculture Organization (FAO) (1989): Protein requirement in developing countries. In: Okeneye and Banwo (1990): Blood meal, livestock feed and investment opportunities in Nigeria and elsewhere. J. Biol. Wastes. 31(2) 85 – 95.

Food and Agriculture Organization, F.A.O. (1992): F.A.O. Production year book. Vol. 45: F.A.O. Rome.

Francesch, A., Estany, J., Alfonso, L. and Iglesias, M. (1997): Genetic parameters for egg number, egg weight and egg shell color in three catalan poultry breeds. Poultry science 76. 1627 – 1631.

Friars, G.W., Bohren, B.B., and Mckean, H.E. (1962): Time trends in estimates of genetic parameters in a population of chickens subjected to multiple objective selection. Poultry sci. 41: 1773 – 1784.

Gavora, J.S., Liljedahl, L.E., McMillan, I. and Aheln, K. (1982): Comparison of three mathematical models of egg production. Brit. Poultry Sci. 23: 339 – 348.

Gebriel, G.M., Abdou, F.H. and EL-Nadi, M.M. (1984): Effects of the B-blood group genotypes on some egg production traits in two outbred leghorn chickens. Egypt. J. Anim. Prod. 24: 151 – 158.

Givens, C.S. Jr., Carter, R.C. and Gaines, J.A. (1960): Selection indexes for weaming traits in spring lambs. J. Anim. Sci. 19: 134 – 139.

Goher, N.E., McGibbon, W. H., Rotledge, J.J. and Chapman, A.B. (1978a): Evaluation of selection methods in poultry breeding programme. I. selection for rate of egg production on the basis of part year record with and without full-sibbing. Egypt. J. Genet. Cytol. 7: 79 – 90.

Gowe, R.S, and Fairfull, R. W. (1985): The direct response to long-term selection for multiple traits in egg stocks and changes in genetic parameters with selection. In: Hill, W.G., J.M. Manson, and D. Hweitt, editors. Poultry genetics and breeding. Brit. Poultry sci. symp. 18.

Gowe, R.S., and Fairfull, R.W. (1982a): Heterosis in egg type chickens. Proc. 2nd World Cong. Genet. Appl. Livestock Prod. (Madrid) 6: 228-242.

Gowe, R.S., Lentz, W.E., and Strain, J.H. (1973): Long-term selection for egg production in several strains of white leghorns: Performance of selected and control strains including genetic parameters of two control strains. Proc. 4th Ecer. Poultry Conf. (London), 225 – 245.

Halle, I. (1996): Untersuchungen zum einfluss untershiedlicher Nahrungsfette auf leistungsparameter und Dotterfettsaures pektrum bei Legehennen. Arch. Geflugelk., 60: 65 – 72.

Harris, D.L. (1964): Expected and predicted progress from index selection involving estimated population parameters. Biometrics 20:46.

Harris, D.L. (1970): Breeding for efficiency in livestock production: defining the economic objectives. J. Anim. Sci. 30: 860.

Harris, D.L., and Newman, S. (1992): How does genetic evaluation become economic improvement? Paper presented symp. Appli. Expected Progeny Differences lives. Improve. Am. Soc. Anim. Sci. Pittshurgh, PA.

Hazel, L. N. (1943): The genetic basis for constructing selection indexes. Genetics 28:476 – 490.

Hazel, L.N. (1951): Construction and use of selection indexes in beef cattle. Page 34 in Annu. Rep. NC-1 Reg. Coop. Res. Project Improvement of Beef cattle through breeding. Univ. Nebraska, Lincoln.

Hazel, L.N., and Lush, J.L. (1942): The efficiency of three methods of selection. J. Hered. 33: 393 – 399.

Hazel, L.N., and Terrill, C.E. (1946): The construction and use of a selection index for range Rambouillet Lambs. J. Anim. Sci. 5: 412.

Hazel, L.N., Dickerson, G.E., and Freeman, A.E. (1994): The selection index – then, now, and for the future. Symposium, Selection index theory. J. Diary Sci. 77: 3236 – 3251.

Heidhues, T., and Henderson, C.R. (1962): Beitrag zum problem des basis index. 2 Tierzuchig. Zurhtgsbiol 77: 297 – 311.

Hill, D.H. (1954): Poultry production in Nigeria. Sectional paper 67. 10th world poultry congress (Edinburgh) pp 318 – 321.

Hill, D.H. and Modebe, A.N.A. (1961): Poultry production at university college, Ibadan (1950 – 1958). Univ. of Ibadan, Fac. Agric. Tech. Bull. No. 2.

Hodges, J. (2002): Conservation of farm animal biodiversity. History and prospects. In: Animal genetic resources information 32: 1 – 12.

Hutt, F.B. (1959): Sex-Linked dwarfism in the fowl. J. Hered. 50: 209 – 221.

Huyguebaert, G. and Butter, E.A. (1991): Optimum threonine requirement of laying hens. Br. Poult. Sci. 32: 575 – 582.

Ibe, S.N. (1998): An introduction to genetics and animal breeding. BENCOD press limited Iganum, Lagos, Nigeria.

Ibe, S.N., Rutledge, J.J. and McGibbon, W.H. (1982): Curvillnear trends in direct and correlated responses to nineteen generations of selection for part record rate of egg production in a randombred line of chickens. Poultry sci. 61: 821 – 828.

Ikeme, A.I. (1990): The poultry industry in Nigeria: prospects and problems. In: Challenges of agriculture in National Development. Fac. Agric. Univ. of Nig. Nsukka (1990).

Ikeobi, C.O.N and Peters, S.O. (1996): Strain differences in genetic parameter estimates for growth traits in meat-type chicken. Nig. J. Anim. Prod. 23 (2): 103 – 106.

ILCA. (1991): A handbook of African livestock statistics. International livestock research centre for Africa, Addis – Ababa.

Jais, C., Roth, F.X. and Kirchgebner, M. (1995): Die Bestimmung des optimalen verhaltnisses zwischen den essentiellen aminosauren im futter von legehennen. Arch. Geflugelk., 59, 292 – 302.

Joly, P. (1995): 10th European sump. on poultry nutrition. WPSA Proceedings. Antalya. P. 294 – 299.

Joly, P. (2001): Evaluation des besoins en Isoleucine et valine de la pondeuse. In Quatriemes journees de la Recherce Avicole. 23 – 25 Mars 1999, p. 153 – 156.

Joly, P. (2003): Factors that influence egg weight: How to change it to meet market requirements? ISA-Hendrix Genetics 5 Rue Buffon, 22000 SAINT BRIEUC, FRANCE.

Joly, P., Bougon, M., Barrier-Guillot, B. (1997): Besoins en tryptophane de la pondeuse. In Deuxiemes Journees.

Karam, H.A. (1959): Selecting Yearhing Rahmani sheep. J. Anim. Sci. 18:1452 – 1459.

Kiani – Manesh, A., Nejati – Javaremi, A. and Saneei, D. (2002): Estimation of co-variance component of economically important traits in Iranian native fowls. Proc. 17th world congress on genetics applied to livestock production. Montpellier France, August 19 – 23. Abstract.

Kinney, T.B., Jr. (1969): A summary of reported estimates of heritabilities and genetic and phenotypic correlations for traits of chickens. Agric. Res. Services, United States Dept. Agric.

Kitayi, A.J. (1998): Village chicken production system in rural Africa: Household food security and gender focus. FAO animal production and health papers 142: 101 pp.

Koutoulis, K.C., Perry, G.C. and Lewis, P.O. (1997): Effect of lighting regimen, calcium supply and age at first egg on tibia stiffness and breaking strength, and shell quality in laying hens. Br. Poult. Sci. 39 (suppl)., 59 – 510.

Lawrence, P. (1998): Ecotypes and natural resistance among scavenging local chickens in Tanzania. M.Sc. Thesis. The royal veterinary and agricultural university, Copenhagen. 198pp.

Leenstra, F.R., Vereijken, P.F.G., Pit, R. (1986): Fat deposition in a broiler sire strain. I. Phenotypic and genetic variation in, and correlations between, abdominal fat, body weight, and feed convention. Poultry sci. 65: 1225 – 1235.

Lerner, I.M. (1958): The genetic basis of selection. Weiley and Sons, Inc. London/new York.

Liljedahl, L.E., and Engstrom, G. (1986): Effects of age on the expression of genetic variation in relation to the environmental variation in laying hens. Pro. 3rd world cong. Genet. Appl. Livestock prod. (Lincoln) 11: 514 – 519.

Liljedahl, L.E., and Weyde, C. (1980): Scandinavian selection and crossbreeding experiment with laying hens. 11. Results from the Swedish part of the experiment Acta Agric. Scand. 30: 237 – 260.

Liljedahl, L.E., Gavora, J.S., Fairfull, R.W. and Gowe, R.S. (1984): Age changes in genetic and environmental variation in laying hens. Theor. Appl. Genet. 67: 391 – 401.

Lin, C.Y. (1978): Index selection for genetic improvement of quantitative characters. Theor. Appl. Genet. 52: 49 – 56.

Lush, J.L. (1945): Animal breeding plan. Ames. Iowa State College Press. 3rd ed.

Mark, H.L. (1985): Direct and correlated responses to selection for growth. In. Hill, W.G., J.M. Manson, and D. Hewitt, editors. Poultry genetics and breeding. Brit. Poultry sci. Symp. 18.

Marks, H.L. (1983): Selection for body weight at eight weeks of age in Dwarf and Normal meat-type chickens originating from a common control population Background. Poult. Sci. 62: 227 – 234.

McMillan, I., Gowe, R.S., Gavora, J.S., Fairfull, R.W. (1986): Prediction of annual production from part record egg production in chickens by three mathematical models. Poultry Sci. 65: 817 – 822.

Meluzzi, A., Sirri, F., Tallarico, N. and Franchini, A. (2001): Effect of different vegetable lipid sources on the fatty acid composition of egg yolk and on hen performance. Arch. Geflugelk 65:207 – 213.

Moav, R., and Moav, J. (1966): Profit in a broiler enterprise as a function of egg production of parent stock and growth rate of their progeny. Br. Poultry Sc. 7:5.

Moen, R. (1968). Selection index for performance tested boars. In: Cunningham, E.P. Animal breeding theory. Pp. 222.

Momoh, O.M. (2005): Genetic and phenotypic evaluation of the Nigerian Heavy chicken ecotype and its crossbred with the light ecotype. Ph.D. Thesis Dept. Anim. Breeding and physiology, University of Markurdi.

Moris, T.R. (1980): Recent developments in lighting patterns for poultry in light-proof housing.

Morris, J.A. (1963): Continuous selection for egg production using short – term records. Aust. J. Agric. Res. 14: 909 – 925.

National Population Commission, NPC, (2006):Census figures by state and local governments. Government Press Enugu.

Ndofor – Floeng, H.M., Uberu, N.P., Nwosu, C.C. (2006): Estimation of heritability of body weight of the local chicken ecotypes reared in Nsukka in the derived savannah zone of Nigeria. Proc. 11th Ann. Conf. Anim. Sci, assoc. of Nigeria (ASAN). Sept. 18 – 21, 2006. I. S.R. & T. Ibadan, Nig.

Nordskog, A.W. (!981): Notes on poultry breeding and genetics 2nd ed. Pp 123 – 134.

Nordskog, A.W. (1986): Economic evaluation of breeding objectives in layer-type chickens. Proc. 3rd World Congr. Genet. Appl. Livest. Prod., Lincoln, NE XII: 207.

Nordskog, A.W., and Hardiman, J. (1980): Inbreeding depression and natural selection as factors limiting progress from selection in poultry. In: Nordskog, A.W., editor, Notes on poultry breeding and genetics 2nd edition.

Nordskog, A.W., Rishell, W.A., and Briggs, D.M. (1973): Influence of B. Locus blood group on adult mortality and egg production in the white leghorn chickens. Genetics 75: 181 – 189.

Nwagu, B.I., Olorunju, S.A.S., Oni, O.O., Eduvie, L.O., Adeyinka, I.A, Sekoni, A.A. and Abeke, F.O. (2007): Response of egg number to selection in Rhode Island chickens selected for part period egg production. Int. J. poultry sci. 6 (1): 18 – 22.

Nwosu, C.C. (1979): Characterization of the local chicken of Nigeria and its potential for egg and meat production. In: Poultry Production in Nigeria. Proc. 1st National Seminar on poultry production. Zaria. Pp 187. 210.

Nwosu, C.C. (1987): The local chicken as a genetic raw material for layer chicken breeding in Nigeria. Invited paper presented at the 5th seminar of the Agricultural session of the Professors of World Peace Academy held in Kaduna on 5th June, 1987.

Nwosu, C.C. (1990): Review of indigenous poultry research in South-Eastern Nigeria. In: Rural poultry production in Africa. Ed. Sonaiya, E. B. proceeding of an international workshop on rural poultry in Africa. Ile-Ife, Nigeria. 13 – 16 Nov. pp. 62 – 77.

Nwosu, C.C. and Asuquo, B.O. (1985): Heritability and correlation estimates of body weight in the local chicken. In: Self-sufficiency in animal protein supply under changing economic fortunes. Ed. Olomu, J.M., Ikhatua, U.J., Taiwo, A.A. and Jagun, A.G. Proc. 9th Annual Conf. Nig. Soc. Anim. Prod. 49 – 56.

Nwosu, C.C., Gowen, F., Obioha, F.C., Omeje, S.S. I., Bellonwu, C.T., and Onuora, G.I. (1984): Growth performance of local and Shaver Star Cross chickens under deep litter system of management. World. Rev. Anim. Prod. Vol xx No. 2: 17 – 26.

Okpeku, M., Orheruata, M., and Imumorin, I.G. (2003): Phenotypic and genetic variation among local chicken in Edo State Nigeria. Proc. 25th Annual conf. Nig. Soc. Anim. Prod. 28: 119 – 121.

Okuneye, B.A. (2002): Livestock sub-sector in Nigeria: Challenges and prospects. In: Bullion-bulletin of the Central Bank of Nigeria. July/September 2002. 16 – 22.

Okuneye, B.A., and Banwo, P.A. (1990): Blood meal, livestock feed and investment opportunities in Nigeria and elsewhere. J. Biol. Wastes. 31 (2) 85 – 95.

Oluyemi, J.A. (1979a): Potentialities of the indigenous species of poultry for meat and egg production in Nigeria. In: Poultry production in Nigeria. Proc. 1st National seminar on poultry production. Zaria. 163 – 186.

Oluyemi, J.A. (1979b): Selection of the Nigerian indigenous fowl for 12 – week body weight. Nig. J. Anim. Prod. 6 (1 and 2), 1979 15 – 20.

Oluyemi, J.A. and Roberts, F.A. (2000): Poultry production in Warm Wet Climates (revised ed.). spectrum Books limited Ibadan.

Oluyemi, J.A., and Oyenuga, V. A. (1974): Evaluation of Nigeria indigenous fowls. 1st world congress on genetic appl. to livestock production (Madrid) 1187 – 1189.

Oluyemi, J.A., and Oyenuga, V.A. (1971): A preliminary evaluation of the Nigerian indigenous fowl as table birds. Proc. Agric. Sci. Nig. 3: 22 – 25.

Oluyemi, J.A., and Roberts, F.A. (1979): Poultry production in warm wet climate 1st edition. London. Macmillan Ltd. 244pp.

Omeje, S.S.I., Nwosu, C.C., and Umunna, C.U. (1987): Heritability and components of variance estimates of egg weight and shell thickness in local and Yaffa x Gold – link crossbred chickens. Nig. Agric. J. 22: 110 – 117.

Omeje. S.S.I. and Nwosu, C.C. (1983): Egg production patterns in local chickens and their crosses in the short-term. Nig. J. Anim. Prod. 10 (1 and 2): 91 – 96.

Payne, W.J.A., and Hodges, J. (1997): Tropical cattle: Origin, Breed and Breeding policies. Blackwell Science Co., Oxford, U.K. 328.

Peguri, A. and Coon, C. (1993): Effect of feather coverage and temperature on layer performance. Poult. Sci. 72: 1318 – 1329.

Pirchner, F. (1983): Population genetics in animal breeding (3rd ed.) Plunum press, New York.

Sadjadi, M., Renden, K.A., Benoff, F.H., and Harper, J.A. (1983). Effects of the blue egg shell allele (0) on egg quality and other economic traits in the chicken. Poultry sci. 62: 1717 – 1720.

Sato, M., Bockholt, A.J., and Kokubu, T. (1985): Evaluation of the efficiencies of selection indices with erroneous parameters. Mem. Fac. Agr. Kogoshima Univ, 21: 67 – 75.

Segura, J.C., Gavora, J.S., Fairfull, R. W., Gowe, R.S., and Bucklend, R.B. (1990): Heritability estimates of male reproductive and morphological traits and their genetic correlations with female egg production and other related traits in chickens. Poultry sci. 69: 2217 – 2220.

Smith, C., James, J.W. and Brascamp, E.W. (1996): On the derivation of economic weights in livestock improvement. Anim. Prod. 43: 545.

Smith, F. (1936): A discriminant function for plant selection. Ann. Eug. 7: 240 – 250.

Smith, J.L., and Goodman, B.L. (1971): Heritability and correlation estimates for serum alkaline phosphase and growth in chickens. Poultry sci. 50: 1728 – 1729.

Sonaiya, E.B., Otubole, I.K. Baelman, R., Demey, F., Wimmers, K., Valle Zarate, A., and Horst (1998): Evaluation of Nigerian local poultry ecotypes for genetic variation, disease resistance and productivity. Proc. Silver Aniv. Conf. Nig. Soc. Anim. Prod. Pp 316.

SPSS (2001): Statistical package for social sciences version (13.0). SPSS Inc., Chicago, U.S.A.

Stanfield, W.O. (1969): Schaum's outline of theory and problems of genetics. Schaum's outline series. McGraw-Hill book Co. New York.

Strandberg, E., and Malmfors, B. (2006): Compendum selection and genetic change version 2006 – 06-14. Dept. Anim. Breeding and genetics, Swedish Univ. of Agric. Scs., Uppsala, Sweden.

Syrastad, O. (1966): Studies in diary herd records. IV. Estimates of phenotypic and genetic parameters. Acta. Agr. Scand. 16: 79 – 96.

Tallis, G.M. (1960): The sampling errors of estimated genetic regression coefficients and errors of predicted gains. Aust. J. Stat. 2: 66.

Telloni, R..V, Custoclio, R.W.S. and Jaap, R.G. (1973): Body weight and egg production in small egg-type pullets. Poultry sci. 52: 2093 (Abstract).

Vandepitte, W.M., and Hazel, L.N. (1977): The effect of errors in economic weights on accuracy of selection indexes. Ann. Genet. Sci. Anim. 9: 87.

Von Mason, V.A. (1989): Diary imports into sub-Sahara Africa: Problems, Promises and prospects. I.L.C.A Research Report. No. 17. Addis-Ababa.

Whitehead, C.C. (1981): The response of egg weight to the inclusion of different amount of vegetable oil and linoleic acid in the diet of laying hens. Br. Poult. Sci. 22: 525 – 532.

Williams, J.S. (1962a): The evaluation of a selection index. Biometrics 18: 375 – 393.

Williams, J.S. (1962b): Some statistical properties of a genetic selection index. Biometrika 49, 325 – 337.

Yamada, Y. (1977): Evaluation of the culling variation used by breeders in actual selection. Genetics 86: 885 – 899.

Yamada, Y., Bohren, B.B., and Crittenden, L.B. (1958): Genetic analysis of white leghorn closed flock apparently Plateaued for egg production. Poultry sci. 37: 565 – 580.

Yamada, Y., Yokouchi, K., and Nishida, A. (1975): Selection index when genetic gain in individual traits are of primary importance. Jpn. J. Genet. 50, No 1: 33 – 41.

Young, S.S.Y. (1961): A further examination of the relative efficiency of three methods of selection for genetic gains under less restricted conditions. Genet. Res. Camb. 2: 106 – 121.

Zollitsch, W., Cao, Z., Peguri, A., Zhang, B., Cheng, T. and Coon, C. (1996): Nutrient requirements of laying hens. In Simposio internacional sobre exigencies nutricionais de avec e suinos. Edifor: Horacio Santiago Rostagno.

APPENDICES

Appendix 1: Sire component of variance and mean square values for body weight (g) (0 – 20 wks) for G_0 generation

	Df																	
	1	2	3	4	5	6												
	Age																	
SV	0	4	8	12	16	20	MS_1	MS_2	MS_3	MS_4	MS_5	MS_6	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$	$\sigma^2_{s_4}$	$\sigma^2_{s_5}$	$\sigma^2_{s_6}$
Sire	4	4	4	4	4	4	29.758**	2424.241*	24579.648***	65261.535***	29964.635*	65931.827**	0.359	29.860	439.008	1248.828	471.649	1356.531
Error	297	267	233	215	187	177	8.128	802.348	3725.854	10460.714	11938.814	16,858.200						
C.V.%	-	-	-	-	-	-	9.57	18.98	18.55	15.18	13.09	13.36						

Legend: *** = sig. level 0.000; ** = sig. level 0.01; * = sig level 0.05; SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square
C.V = coefficient of variation; df = degree of freedom

Appendix 2: Sire component of variance and mean square values for body weight(g) (0 – 20 wks) for G_1 generation

	Df																	
	1	2	3	4	5	6												
	Age																	
SV	0	4	8	12	16	20	MS_1	MS_2	MS_3	MS_4	MS_5	MS_6	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$	$\sigma^2_{s_4}$	$\sigma^2_{s_5}$	$\sigma^2_{s_6}$
Sire	7	7	7	7	7	7	33.877***	1430.871***	19214.843***	55083.412***	48289.658***	67203.661***	0.511	20.628	370.499	1030.444	787.211	1110.112
Error	394	363	343	329	314	305	8.369	479.359	3027.779	11835.354	16700.624	23917.897						
C.V.%	-	-	-	-	-	-	9.38	13.87	14.78	15.83	15.45	15.41						

Legend: *** = sig. level 0.000; SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square
C.V = coefficient of variation; df = degree of freedom

Appendix 3: Sire component of variance and mean square values for body weight (g) (0 – 20 wks) for G_2 generation

	Df																	
	1	2	3	4	5	6												
	Age																	
SV	0	4	8	12	16	20	MS_1	MS_2	MS_3	MS_4	MS_5	MS_6	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$	$\sigma^2_{s_4}$	$\sigma^2_{s_5}$	$\sigma^2_{s_6}$
Sire	4	4	4	4	4	4	27.739***	1514.099*	20163.911***	54655.529***	40724.054NS	85576.886***	0.476	22.298	409.706	1286.199	625.980	2024.688
Error	223	207	189	174	164	159	6.059	569.431	4285.706	8675.717	18694.667	19336.243						
C.V.%	-	-	-	-	-	-	7.58	14.52	17.00	13.19	15.16	14.20						

Legend: *** = sig. level 0.000; * = sig. level 0.05; NS = Not sig.; SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square; C.V = coefficient of variation ; df = degree of freedom

Appendix 4: Mean square values for body weight(g) (0 – 20 wks) for G_o, G_1 and G_2 generations

	Df											
	1	2	3	4	5	6						
	Age											
	0	4	8	12	16	20	MS_1	MS_2	MS_3	MS_4	MS_5	MS_6
Gen	2	2	2	2	2	2	656.032***	14929.350***	213862.936***	98714.775***	254687.478***	25727.043NS
Error	929	852	780	733	680	656	8.105	624.267	3884.781	11620.343	16416.562	21996.620
C.V.%	-	-	-	-	-	-	9.74	16.10	17.53	15.15	15.09	14.59

Legend: *** = highly significance; C.V.% = Coefficient of variation; MS_1 = mean square values; df = degree of freedom

Appendix 5: Sire component of variance and mean square values for body weight (g) of males (12 – 20 weeks and 39 weeks) G_0 generation)

	Df											
	1	2	3	4								
	Age											
SV	12	16	20	39	MS_1	MS_2	MS_3	MS_4	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$	$\sigma^2_{s_4}$
Sire	4	4	4	4	29867.183**	22357.531**	49987.165**	48347.619*	989.635	759.152	1975.500	1449.089
Error	109	106	91	89	7969.328	6213.498	13460.992	21986.540				
C.V.%	-	-	-	-	11.82	8.85	11.01	10.62				

Legend: ** = sig. level 0.01; * = sig. level 0.5;. SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square; C.V = coefficient of variation; df = degree of freedom

Appendix 6: Sire component of variance and mean square values for body weight(g) of males (12 – 20 weeks and 39 weeks); G_1 generation

	Df											
	1	2	3	4								
	Age											
SV	12	16	20	39	MS_1	MS_2	MS_3	MS_4	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$	$\sigma^2_{s_4}$
Sire	7	7	7	7	31935.676***	47659.909***	43024.769**	61216.777NS	953.002	1434.044	1262.978	2444.599
Error	186	178	163	52	8909.238	14465.428	16171.987	43056.899				
C.V.%	-	-	-	-	11.81	13.04	11.48	12.83				

Legend: *** = sig. level 0.000; ** = sig. level 0.01; NS = Not sig.; SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square; C.V = coefficient of variation; df = degree of freedom

Appendix 7: Sire component of variance and mean square values for body weight (g) of males (12 – 20 weeks and 39 weeks); G_2 generation

	Df											
	1	2	3	4								
	Age											
SV	12	16	20	39	MS_1	MS_2	MS_3	MS_4	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$	$\sigma^2_{s_4}$
Sire	4	4	4	4	34106.693***	35670.864*	3868.025*	47826.265NS	1103.670	1015.070	993.793	1316.737
Error	122	117	113	31	6336.792	11155.264	15466.539	38481.087				
C.V.%	-	-	-	-	10.29	10.64	11.00	11.24				

Legend: *** = sig. level 0.000; * = sig. level 0.05; NS = Not sig.; SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square; C.V = coefficient of variation; df = degree of freedom

Appendix 8: Between generation comparison for mean square values for body weight(g) of males at 39 weeks for G_0, G_1, and G_2 generations (whole population)

	Df							
	1	2	3	4				
	Age							
SV	12	16	20	39	MS_1	MS_2	MS_3	MS_4
Gen	2	2	2	2	72405.755***	288391.466***	56218.246*	2667250.601***
Error	432	416	387	187	8746.085	12272.961	16250.342	34363.262
C.V.%	-	-	-	-	11.58	11.98	11.25	16.22

Legend: *** = sig. level 0.000; * = sig. level 0.05; SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square; C.V = coefficient of variation; df = degree of freedom

Appendix 9: Sire component of variance and mean square values for egg number (no.), egg weight(g) and body weight at first egg(g) for G_0 generation (females)

	Df								
	1	2	3						
	Trait								
SV	EN	EW	BWFE	MS_1	MS_2	MS_3	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$
Sire	4	4	4	7092.517***	2051.634***	5376687.603***	5.956	1.740	4608.304
Error	6080	6080	6080	186.302	18.855	24374.110			
C.V.%	-	-	-	18.27	10.89	12.55			

Legend: *** = sig. level 0.000. SV = source of variation; σ^2_S = sire variance; MS_1 = Mean square; C.V = coefficient of variation; df = degree of freedom

Appendix 10: Sire component of variance and mean square values for egg number (no.), egg weight(g) and body weight at first egg(g) for G_1 generation (females)

	Df								
	1	2	3						
	Trait								
SV	EN	EW	BWFE	MS_1	MS_2	MS_3	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$
Sire	7	7	7	8905.864***	4369.601***	5013490.375***	6.649	3.313	3807.007
Error	10574	10574	10574	190.430	27.377	23075.256			
C.V.%	-	-	-	18.01	12.81	12.42			

Legend: *** = sig. level 0.000. SV = source of variation. EN = Egg number, σ^2_S = sire variance, EW = egg weight. WFE = Body weight at first egg. MS_1 = Mean square for trait 1 = egg no.; df degree of freeom

Appendix 11: Sire component of variance and mean square values for egg number (no.), egg weight(g) and body weight at first egg(g) for G_2 generation (females)

	Df								
	1	2	3						
	Trait								
SV	EN	EW	BWFE	MS_1	MS_2	MS_3	$\sigma^2_{s_1}$	$\sigma^2_{s_2}$	$\sigma^2_{s_3}$
Sire	4	4	4	6257.311***	1176.813***	4584171.761***	8.363	1.584	6219.921
Error	3704	3704	3704	133.126	16.845	29607.870			
C.V.%	-	-	-	14.89	9.84	13.01			

Legend: *** = sig. level 0.000. SV = source of variation. EN = Egg number, σ^2_S = sire variance, EW = egg weight. WFE = Body weight at first egg. MS_1 = Mean square for trait 1 = egg no.; df = degree of freedom

Appendix 12: Mean square values for egg number (no.), egg weight(g) and body weight at first egg(g) for G_0, G_1 and G_2 generation (females)

	Df					
	1	2	3			
	Trait					
SV	EN	EW	BWFE	MS_1	MS_2	MS_3
Gen.	2	2	2	17910.325***	6396.726***	21079943.62***
Error	20373	20373	20373	184.321	25.034	28311.872
C.V.%	-	-	-	17.62	11.93	13.06

Legend: *** = sig. level 0.000. SV = source of variation. EN = Egg number, EW = egg weight. BWFE = Body weight at first egg. MS_1 = Mean square for trait 1 = egg no.; df = degree of freedom

Appendix 13: Sire component of variance and mean square values for egg number (no.), egg weight(g) and body weight at first egg(g) for G_0, G_1 and G_2 generations

	df								
	Gen								
SV	0	1	2	MS_0	MS_1	MS_2	$\sigma^2_{S_0}$	$\sigma^2_{s_1}$	σ^2_{s2}
Sire	4	7	4	3.525^{NS}	7.319^{NS}	9.258^{NS}	0.052	0.120	0.240
Error	79	134	43	2.559	5.212	6.973			
C.V.%	-	-	-	0.163	0.233	0.268			

Legend: NS = Not significant (P≥ 0.05); df = degree of freedom; SV = source of variation. MS_1 mean square of ith index score σ^2_S = sire variance component for ith index score; C.V. % = Coefficient of variation in percentages