MOLECULAR DIVERSITY IN SELECTED GROWTH-INFLUENCING GENES ASSOCIATED WITH GROWTH AND CARCASS TRAITS OF INDIGENOUS TURKEY IN SOUTHWESTERN NIGERIA

BY

KAYODE MUSLIM EWUOLA

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CERTIFICATION

I certify that this work was carried out by Mr. Muslim Kayode **EWUOLA** with Matriculation number 115188 in the Animal Breeding and Genetics unit, Department of Animal Science, Faculty of Agriculture, University of Ibadan, Ibadan, Nigeria, under my supervision.

…….……..…….

Supervisor

A.E. Salako

Professor of Animal Breeding and Genetics

B.Sc., M. Sc., Ph.D. (Ibadan)

Department of Animal Science

University of Ibadan, Ibadan, Nigeria

DEDICATION

To Almighty AlLah, the Lord of the World for completing His favour upon me and my family.

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ABBREVIATIONS AND ACRONYMS

AFLP	Amplified Fragment Length Polymorphism
AI	Artificial Insemination
AIC	Akaike Information Criterion
ANOVA	Analysis of variance
BIC	Bayessian Information Criterion
DFP	DNA fingerprint
DMRT	Duncan Multiple Range Test
DNA	Deoxyribonucleic acid
EAAP	European Association of Animal Production
EDTA	Ethylenediamine tetraacetic acid
EST	Express sequence tags
FAO	Food and Agriculture Organisation
FCR	Feed Conversion Ratio
FSH	Follicle Stimulating Hormone
GH	Growth Hormone
GHR	Growth Hormone Receptor
GLM	Generalised Linear Model
GSI	Genomic Sequence Information
GWAS	Genome-wide Association Studies
HWE	Hardy-Weinberg equilibrium
IGFs	Insulin-like Growth Factors
ISAG	International Society for Animal Genetics
LD	Linkage disequilibrium
MAS	Marker assisted selection
MoDAD	Measurement of Domestic Animal Diversity
mRNA	messenger Ribonucleic acid
MSE	Mean Square Error
NCBI	National Center for Biotechnology Information
PCR	Polymerase chain reaction
QTL	Quantitative Trait Loci
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction fragment length polymorphism
SNPs	Single nucleotide polymorphisms
SSRs	Simple Sequences Repeats
TDT	Transmission Diequilibrium Test
TGT	Transforming Growth Factor
bp	base pair
F_{IS}	within-breed fixation index
F_{ST}	across-breed fixation index
N_e	effective population size

ABSTRACT

Molecular diversity is critical for improvement of Economic Traits (ET) in Indigenous Turkeys (IT). Poor productive performance constitutes one of the main constraints to improvement of ET of IT which can be ameliorated by application of knowledge of variation in growth-influencing genes. Information on the variability in genes influencing growth traits of IT in Nigeria are inadequate. Therefore, diversity in selected growth-influencing genes in associations with growth traits of IT in Southwestern Nigeria were investigated.

Three hundred mature IT (124 Toms and 176 Hens) comprising 82 black, 114 spotted and 104 white strains were randomly sampled across southwestern states. Blood (2 mL) was collected from the IT to detect polymorphisms at Insulin-like Growth Factors 1 and 2 (IGF1, 1GF2), Growth Hormone (GH), GH Receptor (GHR) and myostatin genes using standard procedures. Poults hatched (n=300) from randomly purchased IT eggs were sorted (70 black, 140 spotted and 90 white strains) and managed for 21 weeks. Weekly Bodyweight (WB) was monitored for association of polymorphic variants and growth using standard method. At week 10, blood (2 mL) was sampled from each strain (n=60). The DNA was extracted, amplified, electrophoresed, sequenced and genotyped with restriction fragment length polymorphism. The WB and carcass traits at week 21 were associated with each of IGF1, 1GF2, GH, and myostatin genes. Allele and genotype frequencies, F-statistics, and test of Hardy-Weinberg's Equilibrum (HWE) were computed and phylogenetic tree constructed across genotypes. Parameter estimates were obtained from four non-linear growth models (Brody, Gompertz, Logistic and Von-Bertalanffy) that differ in goodness of fit, biological interpretation and ease of computation. The WB and carcass traits data were analysed using ANOVA at $\alpha_{0.05}$

Co-dominant alleles A and B corresponding to genotypes AA, AB and BB were detected across each of the five loci tested. Allele frequencies were between 0.73 (A) and 0.26 (B). Heterozygosity excess (*Fst*) ranged from -0.007 (IGF1) to -0.003 (myostatin) within strains. The closest genetic distance (0.001) was between spotted and white strains while farthest (0.005) was between black and white strains. Spotted (GHR and myostatin), white (GH and myostatin) and black (IGF1, IGF2 and GH) strains conformed with HWE. Bodyweight at week 21 had significant association with BB genotype for black (2731.2±44.7), spotted (2118.3±289.6) and white (2280.6±94.3) at myostatin locus. Genotype BB in IGF1 and GH loci were superior to AA and AB genotypes in breast weight for black and white strains.

Genotype BB of toms and hens had significant association with wing weight at IGF1 (241.1±12.3 and 190.7±8.7) and myostatin (233.6±14.1 and 190.2±12.1, respectively). Logistic and Brody models fitted best in black (AA), spotted (BB) and white (AB) at IGF1 locus. At IGF2 and GH loci, Von-Bertalanffy was the best on AB genotype across the strains while Gompertz fitted best in black (BB), spotted (AA) and white (BB) at myostatin locus.

Growth-influencing genes examined were polymorphic. Genotype BB was superior in growth at Insulin-like growth factors 1 and 2, growth hormone and myostatin loci and could be explored in marker-assisted selection for genetic improvement.

Keywords: Genetic diversity, Indigenous turkeys, Animal growth models, Genetic association

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CHAPTER ONE

INTRODUCTION

Genetic diversity of livestock breeds is mostly addressed by raising abundant quantity of breeds. Associating the patterns of biodiversity in existing populations is worthwhile for understanding the local adaptation of breeds (Chen *et al*., 2013). However, species-wide diversity is a key factor during selection within a breed. Selection is expected to safeguard breeds as biologically and traditionally diverse genetic resources and for better productivity whereas disregarding traits correlated to traits of preservation interest such as adaptation, specific genetic variants, and products quality which can lessen strain uniqueness as well as between-breed discrepancy (FAO, 2013). Genetic variation is the basis for improvement of economically important traits in livestock and accomplishment of genetic progress that enables a varied array of geographic environment for the production of farm animals. The genetic reserve base of the local turkey population in Nigeria is a promising one which should form the foundation for genetic improvement and variation to generate a strain well adapted to the particular environment for optimum performance. Genetic improvement is of high priority in indigenous turkey development plan due to its key role in the utilisation of genetic diversity of advantageous traits among individual within and between strains or breeds. Genetic improvement can take many forms but largely and reasonably a systematic pyramid of measures that originate from knowledge of production and population structures, choice of a suitable strains which can occasionally result to replacements of existing stock or strains, establishement of operational breeding systems and additional improvement by means of selective breeding of superior polymorphic variants within populations that best describe the production and marketing conditions.

Nigeria is endowed with diverse and dynamic arrays of local poultry genetic resources. Recent ranking of indigenous poultry species in Nigeria showed that domestic turkey is the smallest in population accounting for about 1.05 million in comparison to

their counterparts (FAOSTAT, 2011). Oluyemi and Oyenuga, 1971 described that, the potential of locally adapted poultry genetic resources is so imperative that particularly, when taken into account the enormous imported effect of the introduction of improved foreign stock and interaction between genotype and environment leading to significant loss of fitness of the foreign stock. Production of turkey is together a vital and a profitable agrarian enterprise, with an expanding universal plea to its eggs and meat (Case *et al*., 2010). Indigenous turkeys in Nigeria play a pivotal role in social-economic wellbeing of rural people and are distributed all over the agro-ecological zones of the country. They are adaptable; survive on low quality feed, less vulnerable to diseases than their indigenous couterparts and somewhat promising amongst indigenous poultry species owing to its fast growth rate and the improved carcass yield of toms. Inspite all these positive attributes, little or no consideration has been given to the genomic characterisation, conservation, diversity and development of these valuable genetic resources at DNA level.

Genomic tools have been largely used to estimate and characterise the genetic diversity and population structures of farm animals. Also, the detecting loci influencing advantageous traits are of primary concern in the genome of farm animals. These eventually do lead to better selective breeding programmes, improved accuracy of selection schemes and finally do lead to effective genetic progress. Developments in genomics have endorsed the identification of genomic similarities and variances in the species of livestock. Several of these genomic marks possibly will uncover loci inducing beneficial qualities in farm animals. Based on these marks, there is every tendency to detect loci which are conceivable targets of progressive selection.

Development of molecular techniques are promising ways to unveil enormous amount of DNA sequence level of polymorphism serving as indicators in genomic origin estimation for the detected morphostructural variation. The applications of molecular markers play a pivotal role in breeding of livestock species which describe and determine polymorphic variants and their productive characteristics. They are potent materials in the valuation of genomic diversity and in revelation of genetic associations within and among species.

Classification of Quantitative Trait Loci (QTL) to enable selection of genotype is one of the ultimate uses of DNA marker. In recent years, applications of different

molecular markers have been advanced towards detection of QTL in livestock. To be able to analyse genetic diversity between and within breeds for improvement purposes, the determination of the genetic variability, population based association studies of selected growth influencing genes with growth and carcass traits, population structure and phylogenetic relationships using PCR-RFLP marker becomes imperative. PCR-RFLP method is a simple and sensitive marker, applicable to SNP analysis, reliable method and require minimum investment in instrumentation.

The traits of production importance in farm animals which are affected by many genes are mainly growth and carcass traits. Unique approach to detect molecular markers linked affecting the advantegeus traits is by mapping quantitative trait loci (QTL) in order to perform marker assisted selection and equally correlate the markers with advantageous traits so as to select based on the information from the markers (Lande and Thomson, 1990). However, molecular markers for genes of known biological function that perform imperative roles in improvement of farm animals should as well play identical function in marker assisted selection. Also, analysis of genetic markers for candidate genes associated with production traits in different breeds of livestock is expected to illuminate the genetic regulation of the advantageous traits (Zhao, 2002).

The Nigeria locally adapted turkey consists of three main strains classified according to their plumage colour. These are spotted, black and white. Although recent work has reported phenotypic and biochemical characterisations (Yakubu *et al*., 2013), the information on genetic variation of growth and carcass traits of Nigerian local turkey at DNA level using candidate gene approach is limited and implies that the study of the local turkey genome is still at infancy compared to that of chickens and other farm animals.

However, candidate gene method is a potent technique to examine the ralationships between polymorphic variants of genes with beneficial traits in livestock species (Rothschild *et al*., 1997). In this study, five genes such as insulin-like growth factor 1(IGF-1), insulin-like growth factor11 (IGF-11), growth hormone (GH), growth hormone receptor (GHR) and myostatin (MSTN) were preferred as candidate genes. These are the genes of somatotropic axis which play crucial roles in animal growth and development. Variation in genes influencing growth may perhaps play an essential role in the evaluation of their effects on turkey growth and carcass traits. Amills *et al*., 2003

reported that polymorphisms of these genes influence growth traits significantly. Therefore, associating polymorphisms of these genes with the growth and carcass traits is imperative which would probably be beneficial to marker assisted selection of livestock species. Therefore, the focus of the current research is to reveal the polymorphisms of selected growth influencing genes (IGF-I, IGF-II, GH, GHR and MSTN) to characterise population structure in locally turkey and associate these genes with growth parameters.

1.1 Objectives of the Study

Main Objective

Estimating molecular diversity of indigenous turkeys in Nigeria with respect to growth influencing genes for the basis of genetic improvement

Specific Objectives

1 To estimate allelic and genotypic frequencies of various polymorphic variants in some growth influencing genes in three strains of turkey in Nigeria
2 To determine phylogenetic relationship among three strains of turkey in Nigeria at IGF1, IGF2, GH, GHR and MSTN loci
3 To describe growth patterns of three strains of turkey in Nigeria at IGF1, IGF2, GH, GHR and MSTN loci using four non-linear mathematical models
4 To determine associations among the variants of some growth-influencing genes with growth and carcass traits in three strains of turkey in Nigeria

1.2 Research Hypothesis

1. H_O: There are no polymorphic variants in selected growth influencing genes in three strains of indigenous turkeys in Nigeria

2. H_A: There are polymorphic variants in selected growth influencing genes in three strains of indigenous turkeys in Nigeria

3. H_O: Phylogenetic relationship among three strains of indigenous turkeys in Nigeria at IGF1, IGF2, GH, GHR and myostatin loci do not exist

4. H_A: Phylogenetic relationship among three strains of indigenous turkeys in Nigeria at IGF1, IGF2, GH, GHR and myostatin loci do exist

5. H_O: Gene products of IGF1, IGF2, GH, GHR and myostatin do not have effect on growth and carcass traits of three strains indigenous turkeys in Nigeria

6. H_A: Gene products of IGF1, IGF2, GH, GHR and myostatin do have effect on growth and carcass traits of three strains of indigenous turkeys in Nigeria

7. H_O: The selected non-linear growth models will not describe the growth patterns of three strains of indigenous turkeys in Nigeria at IGF1, IGF2, GH, GHR and myostatin loci

8. H_O: The tested non-linear growth models will describe the growth patterns of three strains of indigenous turkeys in Nigeria at IGF1, IGF2, GH, GHR and myostatin loci

1.3 Justification

Conservation, management and improvement of indigenous poultry genetic resources have been a great global concern particularly in developing countries like Nigeria so as to improve on food production and economic provisions for the masses. This is in line with the Food and Agricultural Organisation global strategy. Turkey is an important poultry genetic resource which plays a pivotal role in the socio-economic lives of people in the world, Nigerians inclusive. Genetic improvement of economic traits of indigenous turkeys in Nigeria is a promising approach which can offers lasting solution to their poor productive performance. Indigenous poultry (turkey inclusive) diversity primarily in the care of the rural farmers are utilised for food as well as income source, all in accondance with the global action strategy of livestock genetic assets. Increase loss of genetic diversity of indigenous poultry species (turkey inclusive) has been observed particularly in Nigeria. Genetic diversity is the basis of animal breeding and selection. The amount of genetic improvement achievable in livestock species is largely dependent on the genetic selection. Indigenous turkeys in Nigeria are genetically unimproved and the improvement of this valuable stock for optimum productivity by genetic selection requires that strategies are in place to increase muscle growth. However, growth and carcass traits need to be predicted and selected in indigenous turkeys as this will permit early selection of desirable breeding stock thereby increasing genetic gain for traits of interest. Advances in molecular genetics have led to identification of variation in genes that influence growth and

carcass composition in farm animals. The genes of somatotropic axis play a crucial role in turkey growth and development. These genes include growth hormone (GH), growth hormone receptor (GHR), insulin-like-growth factor-1(IGF1), insulin-like-growth factor-2(IGF2) and myostatin. Different polymorphisms have been identified in the sequence of these genes that have significant association with growth and carcass traits. The genetic variation in the selected growth-influencing genes associated with growth and carcass composition of indigenous turkey strains in Nigeria would be addressed and information provided here could be replicated in other livestock species.

CHAPTER TWO

LITRATURE REVIEW

2.1 Turkey Domestication

Domesticated turkey (*Meleagris gallopavo*) (Agina *et al*., 2015) which originated from North America from the native wild turkey has been domesticated worldwide including Nigeria, and functions as a vital source of poultry protein.

Crawford, 1992 reported that *Meleagris gallopavo* was the first progenitor of the domesticated turkey and this is universally accepted. The wild turkey crossbred with domestic turkey of Mexico generated the commercial turkey. The wild turkey of Merriam called *M.g. Merriami* which was domesticated to present day commercial turkeys and their poults have the ability to run fast.

Some strains of wild turkey were identified in the North America which is genetically distant from contemporary commercial lines. Conceivably, when turkeys were initially presented to Europe, the taught was that they originated and the word was said to be from Turkey because it was somewhat alien and the word eventually was later attached to the species name. However, selection for fast, better growth rate and improved body mass of modern strains of domesticated turkeys has been in existence since their domestication. Artificial insemination (AI) is a means of fertilisation because the weight of the mature toms are heavy and bulky enough to cause injury to reproductive hen thus, the need to safeguard the welfare of the hens. Therefore, natural mating is always avoided. Generally, domesticated birds preserve many of the features of their feral behaviour; however, some of the fundamental variations still exist. The enormous preponderance of domesticated turkeys are limited in number of strains with dominant white plumage, nevertheless some have reserved the feral nature spotted external feature. Indigenous turkeys are conventionally raised on farms and their growths are not as fast as the exotic breeds. According to Williams 1981, exotic toms at week 20 are heavier than a feral male turkey of 156 weeks old. Apparentlly, the distinction in flight performance in the feral type and domesticated turkey is that

domesticated turkey is incapacitated to fly due to alteration in body texture over time after domestication.

2.2 Turkey production in Nigeria

Turkey production in Nigeria has largely persisted at the small holder level due to innumerable causes ranging from management difficulties to dearth of motivations by Government. There is apparent dearth of information on explicit requirements for turkey production in Nigeria and this could be ascribed to low level of investigation in Nigeria. Nigeria is endowed with an impressive array of domestic livestock. Status of poultry species in Nigeria showed that domesticated turkey is the least populated and about 40% are locally adapted turkey. This bountiful animal resource base reflects the availability of unconstrained supply of poultry to bridge the dietary protein gap. The development of turkey enterprise in Nigeria has increased to thousands of tonnes annually. Turkey industry grew fast due to the escalation of production and development of enormous strains with average bodyweights of 16kg and 8kg for both tom and hen respectively and several of these emanated from farmstead (Ojewola, 1993). However, the privation of attention on turkey production was mainly due to the government course of action that liberalised turkey importation since 32 years ago. Domestic turkey accounts for about 1.5 g of animal protein consume by Nigerians on daily basis and turkey has an unlimited possibilities to supply good excellence animal protein with great degree of revenue of venture (Ojewola *et al*., 2002). The potential of indigenous poultry species cannot be underestimated bearing in mind the giant external exchange concern of the importation of improved foreign stock and also genotype environment interaction which leads to considerable loss of adaptability of the foreign stock (Oluyemi and Oyenuga, 1971). Currently, no recognised taboos are stigmatised to the breeding, production and consumption of turkeys as about 55-60% of Nigerians are active consumers hitherto they are infrequent to find. Scarceness of this valuable genetic variant could be partly connected to the acquaintance with exotic chickens which grow rapidly that melt down the recognition of other poultry species and partly due to introduction and acceptance of improved modern turkeys that have been recognised for commercial production.

Indigenous turkeys are functionally and genetically valuable since they contain innate constituents, which possibly will have been nowhere to be found in the improved gene

pool. They have genetic variants that are moreover absent in modern improved stocks or existing in their rare ancestors. Such traits may be of commercial value (Adebambo, 2003).

2.3 Description of Indigenous Turkey in Nigeria

Indigenous farm animals are important genetic resources containig irreplaceable gene pool which needs to be conserved for impending use. Indigenous turkeys in Nigeria are unimproved type of poultry species with variegated plumage which may equally appear as distinct black or white (Adebambo, 2003). The common plumage types in Nigeria are black, white, spotted and their crosses. The crosses between black and black, white and white, spotted and spotted provided black, white and spotted respectively in their F1 generation. Dominance and co-dominance effect of black gene to white and spotted gene were resulted from the crosses among numerous plumage as well as the interaction of spotted and white. Toms have a bare, greatly rough head which remains usually perky red in colour then changes to white covered with perky blue once the thrilled. Additional distinctive phenotypic appearance of the toms are a elongated snood that develops from the forehead above the bill; a fat wattle developing from the esophagus; a tassel of rough, a protruding beard developed from the breast; and supplementary or fewer protuberant leg spurs. The length of the body of tom is 100 cm with bodyweight of 7kg on the average while the bodyweight of hens is usually ranged between 2-4.5kg with commonly fewer warty heads in comparison with toms (Adewumi, 2011).

Plate 2.1: Black strain of indigenous turkey in Nigeria

Plate 2.2: Spotted strain of indigenous turkey in Nigeria

Plate 2.3: White strain of indigenous turkey in Nigeria

2.4 Economic Importance of Turkey Production

Conservation of indigenous livestock resources is the main objective of the farm animal genetic resources in Nigeria so as to boost food safety and economic provisions of the masses (Yakubu *et al*., 2011). Biodiversity of indigenous livestock species in Nigeria is mainly in the care of the traditional producers which are utilised for farm work, transportation and food, all in accordance with the FAO global strategy.

Turkeys (*Meleagris gallopavo*) play considerable economic and social significance in Nigeria, as they are used as gifts in the festive period like Christmas as an emblem of thankfulness and manifestation of generosity. So far, there is no known taboo towards producing and eating of turkeys (Nwagu, 2002). Globally, among poultry species, domesticated turkey is the next to chicken regarding production of meat. The domesticated turkey is simple to keep, require less devotion, resistant to infections unlike chickens. In many European as well as African countries, roasted turkey has long been a customary Christmas dish (Bland, 2009). In America, turkey is specifically associated with thanksgiving. Farming of turkey is periodic, though in countries of the world such America, ready-to-cook, meaty, filleted turkey is obtainable in rolls all year round. Turkeys are genetic resources for breeding.

2.5 Characterisation of Poultry Genetic Resources

Poultry diversity plays a critical input in biological diversity of farm animals. Many species of poultry have immence contribution to solving the problem food scarcity and agriculture at large, providing meat and eggs for consumption of mankind. In recent time, the process of domestication of different livestock species that occured many years back has led to the array of diversity of farm animal genetic resources which is an extensive and complex history. Ever since domestication, farm animals have diversed with migrations of mankind and trading to all inhabited regions. Several factors such as local adaptation, selection, sudden change in genetic makeup, migrations and genetic drift have resulted into the genetic variation netted with the process of domestication into a massive pattern of phenotypic alterations, physiology and economically advantageous traits. Genetic variation which was emphasised by the occurrence of strains and additional quarantined livestock species were accorded by effective selective breeding process. The rate of genomic segregation and improvement

were best noticeable in the advance worlds where the demand and supply of foodstuff resulted in validation of farming. For instance, improvement and development of Holstein Friesian cattle which is an exceedingly productive dairy breed of cattle.

The universal distribution of the improved breeds, which typically indigenous to Europe, is exposing the numerous well locally adapted breeds to endanger as well as extinction. Several studies (Rege and Gibson, 2003; Köhler-Rollefson *et al*., 2009) have reported the evidence of such trend that is predominant in marginal areas particularly where local farming practices are being neglected. Genetic erosion of farm animal genetic resources is a major concern in FAO global strategy (FAO, 2007a). According to Taberlet *et al*., 2008, the implication of lost of diversity and inbreeding depression have been adequately reported as this may be expressed in erosion of viability, fertility as well as resistance to diseases and the regular incidence of recessive genetic diseases. Approximately 0.1 and 0.15 of livestock breeds became extinct and endangered consequently as reported by FAO, 2007b in the book of the "State of the World's livestock Genetic Resources for Food and Agriculture". Furthermore, the status quo is currently unidentified for 0.34 of the breeds, majority of which are raised in developing nations.

Global Plan of Action has it that characterisation, record and watching of trends of farm animal genetic resources diversity for effective and accurate measures breeds value and guide decision making in farm animal improvement and breeding scheme is their strategic primacy.

The breed entails clusters of faunas with similar genomic features dependent on ecological zones and species is the functional unit in preservation of genomic materials. Majority of the breeds patenting from developed nations are well-defined and morphometrically distinctive and were genetically quarantined all through the course of their improvement at all time. Furthermore, Asian and African breeds regularly relate to indigenous stocks are at difference steadily according to ecological departure. Additionally, breeds with diverse identity may occasionally have a current common ancestorial background, and in other circumstances their distinctiveness had been lost through crossing. Moreover, the genomic features of every strain accessible for a breeding scheme and improvement of locally adapted breeds is repeatedly disregarded due to lack of information favouring the introduction of germplasm from

foreign breeds with more detailed information. Hence, characterisation of breeds at the level of livestock morphology associated with the systems of production and at the genomic level is highly indispensable.

2.6 Molecular Characterisation of Animal Diversity

Molecular data have been applied to the characterisation of livestock genetic diversity three decades ago (Groeneveld *et al*., 2010). In the past, an international scheme for characterisation of livestock genetic materials such molecular genetic characterisation, and articulated the ancillary procedures was proposed by food and agricultural organisation (FAO) working group in which amount of Domestic livestock Diversity with approvals for the DNA assay of livestock diversity on a large measure through a research program was to be harmonised via the FAO (1993). Monitoring of livestock genetic resources diversity and creation of a standard method for molecular characterisation were necessitated by FAO of MoDAD when the MoDAD program endorsed formerly by the working group was not achieved.

Globally, researchers have conducted independent trials to characterise locally obtainable livestock species, however universal efforts on a large scale on characterisation of breed have generated broad DNA database for majority of the farm animal species. Farm animal genetic diversity at DNA level had advanced into a major dynamic aspect of study, which for instance receives substantial consideration in scientific media and at symposiums of societies like International Society for Animal Genetics (ISAG) and the European Association of Animal Production (EAAP).

Furthermore, majority of the genomic research pinpointed the application of neutral genetic marker data, serving as an alternative or probability evaluation of significant practical genomic diversity among strains which has accomplished identification of the wild progenitor of most farm animals together with a place of domestication. It has equally provided insight on procreation and homogeneity of breed as well as evaluation of the genetic composition of breeds through numerical measures of the variation, admixture, subdivision, inbreeding, introgression and assortative mating. Phylogeny restoration of livestock breeds at random and untying the ancestral relationship among livestock breeds are possibility. Molecular data enable search of procedures that develop prioritising of the species for preservation which would pose direct relevant for conservation and utilisation of farm animal genetic resources.

2.7 Detection of genes of interest in livestock

Examination of the genetic design of production traits, estimating the amount of genes as well as their impact on morphological manifestation are the central objective of DNA investigation in farm animals. However, the objective is hard to achieve because the production traits are polygenic in nature with each of the gene contributing a percentage to the morphology. Detection of genes of interest is based on three main approaches, namely; mapping of quantitative trait loci, sequencing of DNA and mRNA, and analysis of candidate genes.

2.7.1 Quantitative Traits Loci

Detection of Correlation of regions of chromosome with the single nucleotide polymorphisms of production trait is determined by the mapping of quantitative traits loci. This detection is impossible without the improvement of genomic records inundated with variant DNA markers and population structure expressing separation for the advantageous traits. The Improvement of markers in the genomic region emerged as a result of detection of single nucleotide polymorphism (Collins *et al*., 1998) as well as short tandem repeats. In recent time, evaluation of advantageous traits in farm animals in addition to the detection of regions of chromosome encoding genes that regulate growth and improvement of muscle mass, meat yield and quality are enabled via advances in statistical procedures and genetic maps.

Mapping of quantitative trait loci has been clearified by the application of experimental crosses and analysis of segregation in informative families. In a meta-analysis conducted by Khatkar *et al*., 2004, twenty consensus genomic regions of cows were shown which were analogous to regions containing quantitative trait loci coincidence and mapped in a random populations for the similar traits. The percentages of the genomic variance of milk trait were explained by seventeen consensus regions which were located on chromosome 87, one was found on chromosome 49 and the remaining two were located on chromosome 6. Amnio acid yield and percentage, fat yield and percentage, milk yield had significant correlation with the first of consensus genomic regions. In *Ovis aris*, some phenotypic traits both antemortem and post-mortem, dairy production and resistance to parasites (Davies *et*

al., 2006) were associated with the mapping of quantitative trait loci. Also, phenotypic, health and physiological traits were mapped on 2,284 quantitative trait loci in domestic birds. According to Du *et al.*, 2007, in an independent population of 6,000 pigs in Monsanto more than 4,000 autosomal single nucleotide polymorphism were genotyped for the examination of the amount and variation of linkage disequilibrium (LD) in the genomic region of pig there enabling the correlation of the production with polymorphic variants. However, quantitative traits loci permit detection of the regions of the genome covering genes of interest. However, mapping of quantitative traits loci was crucial to the detection of genes influencing production traits in livestock species. For instance, myostatin gene which regulates muscle growth in Bovine and *Ovis aris*.

2.7.2 Sequencing of DNA and mRNA

Understanding the impact of genomic variation on advantageous trait by mapping the trait on particular chromosome is aided by Genomic sequence information (GSI) (Schmutz and Grimwood, 2004). Genetic maps having copious short tandem repeats (SSR) and single nucleotide polymorphism together with haplotype maps comprising mapped quantitative trait loci will have straight correspondence with the sequence of genome in any populations. Body and target tissue are good sources of detecting candidate genes and facilitate re-sequencing of quantitative trait loci intervals enabling the detection of affecting causal mutations.

For tissues of economic importance in numerous livestock species, express sequence tags (EST) collections are being established. A typical example is the chicken databank containing over 599,000 EST according to Fadiel *et al* ., 2005. The express sequence tags assembly acquired Bovine on the Genbank deposited is more than 1,315,093 and over 641,896 for swine.

Analysis of the pattern of gene expression could be improved through collections of DNA and mRNA sequences in order to obtain sequence of gene and its genomic position. The principle depends on the assumption that animals having variance of morphological traits display distinction manifestation of gene correlated to those traits. To comprehend sequential and longitudinal variations in gene action through cell growth in addition to differentiaton that gives rise to detection of a particular and differential gene expression in diverse populations of livestock species, the outline of

gene expression is imperative. Andersson and George, 2004 asserted that microarrays are critical to evaluating the biological roles of genes through tissue-specific expression pattern together with augmenting the genetic data acquired by recording and sequencing of quantitave plans so as to stimulate the detection of gene's association with production traits of economic importance.

One of the limiting factors to sequencing of DNA and mRNA is that microarrays entail erstwhile information of the gene sequence dotted against the stand that limit the accessibility of collections for all farm animals of importance. Whole genome sequencing gives a large-scale detection of single nucleotide polymorphism which permit the development of innovative techniques for mapping genes of interest in as much as they are remarkably useful gene-markers to stimulate fine mapping, with the aim of defining the least region of genome comprising a quantitative trait loci (Glover *et al* ., 2004).

Genetic map was made up of an enormous catalog comprising thousands of DNA sequences and thousands of markers. The first farm animal to have its entire genome sequenced and published was chicken as reported by Wallis *et al* ., 2004. The DNA of a single female of *Gallus gallus*, the progenitor of the domesticated chicken has sequence of 1.05Gbp in its genome and Elsik and his co-wokers, 2009 were the first reseachers to publish whole genome sequence bovine of female Hereford. Conversely, improvements have been accomplished in genotyping of livestock species using single nucleotide polymorphism (SNP) chips for the concurrent revealing of numerous SNP that have been made readily available. With the scanning of the genome of a population trial for numerous SNP concurrently, at lesser rates and lesser time in comparison to what is being done currently with the use of microsatellites, single nucleotide polymorphism (SNP) chips is expected to lead to better genetic progress in livestock genomics..

2.7.3 Candidate Gene Approach

One of the strategic ways of associating polymorphic variant of a gene with advantageous traits in farm animals is the use of candidate gene approach. This approach involves the use of candidate genes, genes whose biological roles are known to improve production traits in farm animals. They are commonly called genes with

identified biological function ultimately regulating the developmental practices of the investigated traits, which could be inveterated by evaluating the effects of the causative gene variants in an association analysis. Genetic disease research, genetic association studies, biomarker and drug target selection in living organisms are largely dependent on this approach. Many of these genes of advantageous traits or disease resistance/susceptibility were primarily detected, although the total number of the publicly accepted genes is still absolutely insignificant (Zhu *et al*., 2007). The use of Insulin-like Growth Factors (IGFs) genes correlated with growth, FCR, skeletal traits, growth of adipose tissue and fat deposition in chickens (Zhou *et al .,* 2005) is a typical illustration of this approach. Also, Baron *et al*., 2002 and Dunner *et al*., 2003 have reported the effect polymorphic variants of *myostatin* gene with production traits in farm animals. Selection for better meat tenderness had been applied in animal production using the mutations detected in calpain and calpastatin genes. One of the most limiting factors to this approach is that only a infinitesimal region of genes regulating traits of economic importance are identified.

2.8 Insulin-like Growth Factor 1 Gene (IGF1)

IGF1 plays a pivotal role in mammals such as intervening the growth-promoting actions of growth hormone and equally functions as a locally controlled autocrine or paracrine growth stimulator. The Insulin-like Growth Factor (IGF1) is a gene with known biological function that is responsible for growth, anabolism, catabolism, body composition, growth of adipose tissue and bone as well as fat deposition in chickens (Zhou *et al .,* 2005). Siddiqui and his co-workers (1992) described superior correlation in the polymorphic variant of IGF1 and live weight in chickens. Reseraches have shown that polymorphic variants at IGF1 locus affect variability in some production traits such as feeding, growth, carcass, milk production and fat deposition. Ge *et al*., 2001 also reported IGF1 gene products correlation with growth and carcass traits in Cattle of Angus. Nagaraja *et al* . (2000) reported the effect of gene products of IGF-1 on feed conversion ratio (FCR) and egg production traits and further stated that, the possibility of improving the advantageous traits by IGF-1 variants in random population is enabled. Average daily gain at 107 days was associated with single nucleotide polymorphisms at IGF1 locus (Amills *et al.,* 2003). Zhou *et al.,* (2005) reported superior association between polymorphic variants of IGF1 gene and average daily gains of meat type chicken. Gouda and Essawy (2010) examined the

polymorphisms at IGF1 locus amongst locally adapted chicken breeds in Egypt and specified superior association with the growth traits. In recent times, broad distribution of single nucleotide polymorphism (SNP) in the genomic region of chicken has gained interest.

The physiological role of Insulin-like growth factor 1 (IGF-1) in controlling growth and development, catabolism and anabolism as well as lactation in dairy cattle have been reported (Lucy, 2008) and it equally plays a vital role in the preservation of discerned purpose in various organ and in explicit types of cell. Laron, 2001 reported the stimulative role of IGF1 in the process of anabolic and mitogenic of growth hormone in numerous tissues. Liver and target tissues are the main site of production of IGF1.

Velazquez, (2008) reported associations of IGF1 with fertility and reproductive performance measurements in Bovine. Davis and Simmen, 1997 recorded repeatability estimates of 0.48 of Serum IGF-1 for Angus in the post-weaning period and this is an indication that IGF1 is very heritable. This recommends superior additive genetic control at the locus and this locus is being controlled at both transcriptional and translational level as reported by Wang *et al*., (2003). Wang *et al*., (2003) stated that, single nucleotide polymorphisms at IGF1 locus and its associative effect on advantageous traits as for instance, bodyweight, carcass fatness and weight, daily weight gain, food conversion efficiency, milk poduction, deposition of fat in farm animals. Sahana and her co-workers (2010) described quantitative trait loci (QTL) intersecting the *IGF1* section. Conversely, regardless of the significance physiological roles of IGF-1 gene, studies involving the analyses of the relationship between *IGF-1* gene products and productive performance of farm animals are not adequate. Beccavin *et al*., (2001) reported significant higher IGF1 mRNA levels in the high growth rate broiler line as compared to low growth rate line chickens.

2.9 Insulin-like Growth Factor 11 Gene (IGF-11)

Insulin-like growth factor 2 (IGF2) is one of the growth-influencing genes which plays a pivotal function in the differentiation and proliferation of livestock development (Kaneda *et al*., 2007), together with reproduction and the regulation of ovarian follicle growth. The *IGF2* is greatly articulated in the dominant follicle supporting crucial roles for follicular growth in animals. It poses significant effect on prolificacy in pigs

and bovine (Stinckens *et al.*, 2010) and may also improve ovarian growth via follicle-stimulating hormone (FSH) (Baumgarten *et al* , 2015).

Insulin-like growth factor II (IGF-II) is responsible for the growth of cell, survival, locomotion and distinctin through the IGF1 receptor tyrosine kinase (Chao *et al* .,2008). Furthermore, it enhances mitogenic reactions through approach of insulin receptor isoform-A in addition, it plays essential role in growth of foetal and development. According to Gicquel and Le, 2006, the locus of IGF2 knockout results in substantial decrease in mice bodymass. Constância *et al*., (2002) described that, hormonal influence of fetal growth and placental precise knockout indicated an imperative function in development of organ and uses. Mainly, placental-specific IGF-II modulates placental and fetal growth. McMurtry, 1998 reported the functional role of IGFII in controlling rate of growth, body conformation together with fat and oil absorption in avian. Implantation of osmotic miniature pumps having both saline and recombinant mammalian IGF2 into 30-day mature broiler hen such that the administered birds received 0.5mg IGF2/kg bodyweight daily revealed the influences of IGF2 on the comparative mass of the intestinal fat of bird (Spencer *et al* ., 1996).

High absorptions of IGF2 peptide and mRNA in uterus show the essential role of IGF2 in the fetus. O'Dell and Day, 1998 reported the pivotal role of IGF11 in growth and development, influencing fetal cell division, differentiation and possibly catabolic together with anabolic control of living organisms. Gene products of IGF-II gene in mouse through restriction fragment length polymorphism were said to have effect on 21-day weight in cocks and 42-day weight in hens. Winkelman and Hodgetts, 1992 reported that interaction of variants of IGF2 and sexes, could help develop the genetic model for growth.

IGF2 is imperative in regulating the growth of animals. Mice with hypoabsorbtion of IGF2 are possible 40% runt in comparison to their counterparts. These IGF2 knockouts were said to have influenced fetal growth reduction significantly, especially in the first trimestal. In the same vein, scientific confirmation proposes that augmented intensities of IGF2 pose an optimistic consequence on growth and enlargement in vivo (Engström *et al*., 1998). Hypermanifestation of IGF2 is a pssible reason for sporadic genomic disorders, such as Wiedemann Beckwith disorder (Ward, 1997), which leads to abnormal growth and disturbances, and augmented incidences of neoplasia. Transgenic

mice with hypermanifestation of IGF2 had anomalous organ growth and tumor development (Ward *et al*., 1994).

2.10 Growth Hormone Gene

Growth hormone (GH) is a growth-influencing hormone secreated through the exocytosis of somatotrophs in the anterior pituitary via a sequences of biological stimuli involving the activities of GH releasing hormone (GHRH) and somatostatin, and fluctuations in the blood concentrations of glucagon, insulin, IGFs, estrogen hormones and thyrotrophin releasing hormone (Yaylali *et al* ., 2010). Growth hormone is crucial to growth and development, body composition, lactation, reproduction, anabolic and catabolic processes in farm animals. (Breier, 1999). Growth is an increase in mass and size that is characteristically influence by many factors which bring about by the interaction of genetics and molecular by which the GH plays a foremost part in living organism (Goldstein *et al*., 2011). Moreover, it intricate in numerous other biological actions influencing fat and oils metabolic rate (Davidson, 1987), saccharides and amino acids absorption according to Moller *et al*., 2003 as well as maintenance of immune system. Growth hormone gene; a product of growth hormone is a typical growth-influencing gene for identifying polymorphisms that are correlated with the growth and carcass traits in farm animals (Thakur *et al*., 2006). The growth hormone (GH) axis has a main impact on a varied array of biological activities, from the cellular level to whole-body morphostructural alterations. The research conducted on genetic conditions of transgenic animals comprising genes of the GH axis, the in vivo and in vitro administration of GH are proofs of effects of the critical role of GH. Growth hormone of domesticated turkey is a peptide hormone produced and secreted by hypophsis. This hormone performs numerous physiological roles, for example, growth and development, body morphology, egg production, aging, and reproduction. Shaw *et al* ., 1991 reported that, the GH gene had remained apportioned to G-band region of chromosome. This gene contains 5 and 4 coding and non-coding regions respectively, as it exists in other GH genes of living organism**.** Conversely, the GH gene is considerably larger in comparison to the corresponding genes of living organism, due to the size on non-coding region, which magnifies it to 3.5 kb according to Tanaka *et al* ., 1992. Researches conducted on egg-type and meat-type chickens with the applications of restriction endonusleases revealed that, the GH gene was greatly polymorphic in the non-coding region. Additionally, alleles detected were convoluted

in the selection of a chain of hens for egg production and in the selection of the size of the abdominal fat pad in meat-type chickens (Fotouhi *et al* ., 1993). Mou *et al* . (1995) described the incidence of 2 MspI sites in birds intron 1, with 1 MspI RFLP being formed. Kuhnlein *et al* . (1997) examined 12 non-inbred strains of egg-type chickens by PCR-RFLP at respective 3 MspI sites (PM1, PM2, and PM3) and 1 SacI site (PS1). The resistance-associated GH alleles were also dominant for the inception of ovulation and recessive for the persistency of egg production. On the other hand, no significant effect of the GH genotype was detected on juvenile bodyweight, egg weight, or egg specific gravity (Kuhnlein *et al*., 1997). A moment ago, a unique endonuclease *Msp*I site on non-coding region 1 of the GH gene has been reported.

2.12 Growth Hormone Receptor Gene (GHR)

GHR is a member of the cytokine/hematopoietin receptor superfamily comprising three efficient domains of the extracellular (ligandbinding) domain, the transmembrane domain and the cytoplasmic domain (signal transducing). Moreover, it stimulates amino acid uptake and protein production in muscle and other tissues (Armstrong and Hogg, 1994). The gene products of GHR gene may affect the binding capacity of growth hormone; a candidate gene said to influence growth and development in domesticated animals. The homozygous genotype GG at chromosome 4 of GHR locus was projected to have better productive performance in caprine according to An *et al*., 2011. Single nucleotide polymorphism detected in non-coding region 4 of the GHR gene had superior association with bodyweight and feed conversion ratio in bovine meat type. The F297Y polymorphism found on chromosome 8 at coding region had significant effect on milk yield (Waters *et al*., 2011). Correlation between gene products at this locus in on chromosome 10 in the coding region and carcass traits in buck was also reported. Furthermore, mutation on chromosome 3 in the coding region at the locus of GHR in animals have been observed and reported to pose significant effect on augmented reaction to high dosage recombinant mammalian GH as this is a recommendation that chromosome 3 in the coding region could be an important binding site to growth hormone.

Conversely, hormone signaling of GH desires growth hormone receptor (GHR) as GH is not a steroid hormone (Carter-Su *et al* ., 2016), and its core role is linked to signaling of GHR into a cell. GHR deficit is associated with obesity, diabetes and

cancer risk is possible to occure. Consequently, deficient GHR might influence GH function to be less modulation signals. It could express a type of reduced pituitary hormone condition, leading to greater threat of metabolic disorder (Khang *et al* ., 2016), because the findings recommend that the role of GH is interrelated to GHR function. GHR deficiency is connected with adiposity such as, GHR-null in mice (Sackmann-Sala *et al* ., 2014), which exhibited insulin sensitivity and amplified adiposity.

2.13 Myostatin Gene (MSTN)

Myostatin is a key gene for growth and function as an inhibitor factor on muscles growth. Several gene products have been recognised in the sequence of this gene that has a significant effect on growth and carcass traits. These gene products are used as proficient marker in livestock species in order to upturn quality and quantity of meat.

Myostatin belongs to the group of transforming growth factor-beta (TGF-beta) super family (Mc Croskery *et al*., 2003). The sequence of myostatin gene is known in farm animals such as cattle, sheep, goat, swine, etc. It was initially revealed in mice (Marchitelli *et al*., 2003) and was then detected in bovine as the gene controlling double muscling. Myostatin is principally manifested in muscular tissues, and Mc Croskery *et al*., (2003) had stated the negative role of myostatin in controlling growth of skeletal muscle. Karim *et al*., (2000) reported that, mutations in myostatin controlling regions were correlated with abdominal fat weight, abdominal fat percentage, hatch weight, and breast muscle percentage and weight in poultry. In chicken, the locus of myostatin comprised of three exons and two introns. Baron *et al* . 2002 recorded 373 bp, 374 bp and 1567 bp for the exons 1, 2, and 3 correspondingly. The gene products of myostatin locus had strong associations with survivability and growth rates, feed conversion efficiency, breast depth and percentage, eviscerated carcass weight, leg deformity, blood oxygen level, and hen antibody titer to the Gomboro disease virus in three selected commercial broiler chicken lines as reported by Ye *et al* . 2007. He also detected five polymorphic variants at myostatin locus which had significant effect on bodyweight at day 7 and day 40 in one of the broiler lines. Studies have shown that 13 gene products were detected in the coding regions (exons) 1, 2 and 3 and the two non-coding regions (introns) at myostatin locus, where myostatin (2100, 2109, 2244, 2283, 2346, 2373, 2416, 4842, 7434, 7435 and 7436)

were in the coding regions and myostatin (4405 and 4954) were in non-coding regions. Baron *et al.,* (2002) detected seven polymorphic variants and one deletion in the coding region 2 at myostatin locus in meat-type and egg-type chicken lines. Zhiliang *et al*., (2004) detected three and two single nucleotide polymorphisms in the 5' and 3'regulatory regions in the chicken, and the variants varied in the frequencies of allele between breeds and they also discovered that in a second fillia generation from a cross of meat-type and silky chickens, homozygous individuals AA and BB at a locus in the 5' regulatory region have a greater intestinal fat weight and intestinal fat proportion than heterozygous AB individuals.

Conclusively, previous research reported that myostatin gene activity knocked-out the production of early and late myoblasts (Cusella-De Angelis *et al*., 1994) together with foetal and postnatal satellite cells (Hathaway *et al*., 1994).

2.14 Genomic selection of growth and carcass parameters in Turkey production

Growth is beyond live weight but carcass parameters are inclusive in domestic turkey as they are mostly sold based on weight of carcass. Meat is a derivative of muscles and the growth of those muscles are largely dependent on numerous factors such as sex, genetics, physiological responses and plane of nutrition. With the realisation of the full promise of molecular genetics, use of genetic assessment tools like breeding values would be useful to describing genetic merit which would has a great impact on the turkey industry in Nigeria. The amount of genomic improvement achievable in livestock species is largely dependent on the genomic selection. Genomic selection is the key for genetic improvement in farm animals. Enormous genetic improvement in productivity and performance of poultry species in advance world has been achieved through genomic selection. The improvement of farm animals for better carcass composition by genomic selection requires that policies are in place to increase muscle growth and sustain meat quality at slaughter. Significantly, carcass yield and meat quality need to be projected and selected in live animal as this will allow early selection of required breeding stock and thus increase genetic gain for desirable traits. The use of gene-markers to detect turkey carrying traits of production is a vital approach to achieve genomic selection. The group of genes that have been applied as gene-markers are growth-influencing genes. The Product of these genes regulates muscle growth and development.

2.15 Growth Modeling

Several studies have been conducted to determine the fittest non-linear regression models among the models used for describing growth in farm animals. Application of growth sigmoid curve is essential to study the animal growth and development, make comparison among livestock of the same species. Considering the livestock production and economic importance of some characteristics like bodyweight, weight gain, mature age and highest weight, numerous models that express growth can be found. Several number of mathematical functions known as growth models have been explored to describe growth pattern of livestock species. These include Brody, Von Bertallanffy, Gompertz, Richards and Logistic,

The most used three-parameter models to analyze growth of broilers are Von Bertallanffy, Gompertz, and Logistic growth curves (Topal and Bolukasi, 2008). One of the models of choice to examine the growth pattern of poultry species is Gompertz model due to its effectiveness or fittness and the simplicity of its biological interpretation of the model parameters. A moment ago, many findings have been conducted with reference to growth study in dawdling developing meat type chicken. Santos *et al*., 2005, conducted growth study using the Gompertz model to examine pattern of growth in two dawdling developing meat type chicken lines raised intensively and semi-intensively respectively. N'Dri *et al*., 2006 estimated heritability and repeatability for Gompertz model parameters in dawdling developing meat type chicken raised in intensive system. Gompertz model had been equally applied to examine the growth curve of dawdling developing meat type chicken on free range system. Yang *et al*., 2006 applied Logistic, Gompertz and Bertalanffy respectively to evaluate growth curve of Jinghai yellow mixed-sex fowls and compare the fitting ability of the three non-linear models. Gompertz, Logistic and Richards were fitted by Norris *et al*., 2007 to assess and compare the growth curve parameters for bodyweight of inidigenous, Venda and Naked Neck fowls and some examination were conducted to test the presence of variations in the growth pattern in these breeds. Significantly, many a non-linear growth functions are applicable in the determination of age-bodyweight correlations of the living organisms and the growth curves obtainable are expected to have variations in model characteristics together with different functional restrictions. It is assumed from previous finding (Norris *et al*., 2007) that it is essential to cautiously examine the choice of a fitting model that best describes a specific

growth pattern. (Ersoy *et al*., 2005) reported that the most appropriate function to estimate in the poultry growth prototype that three growth biological growth aspects have been described: 1) size, higher limit or asymptote; 2) the index, a measure to specify the time requested of the growth increase; and 3) shape, a quantitative measure that describe the path of the growth process. The Richards and Gompertz models have been shown to give good descriptions of growth in species such as cattle, elks, chicken, ostrich, turkey and emus (Ersoy *et al*., 2005). The Gompertz growth model has been cited as the model of chpice for chicken data based on its overall fit and biological meaning of model parameters (Aggrey, 2002). The Gompertz model was then used as the standard to which the logistic model was compared. The rationality behind the use of the models lies in the fact that these models have some important parameters enabling one to comment on the biological growth processs.

2.16 Genetic association Analysis

Association analysis in its pretentious practice relates the frequency of marker alleles of the affected and unaffected unrelated farm animals. Genetic association is classically carried-out when genetic markers are genotyped in the region of chromosome detected by genome-wide linkage analysis, or in prospective candidate genes of known biological function based on their physiological role. Ewens and Spielman (2001) reported that, allele that is more or less expressed amongst affected living organisms is reflected to be correlated with the infection. This is commonly tested with the use of a chi-square analysis. Conversely, due to the linkage disequilibrum configuration in the genomic region, the linking marker can be in linkage disequilibrum by the real causal variant. However, this is not in favoure of direct correlation study, in which the variant itself is assumed to be affected by syndrome, this occurrence has been applied to indirect correlation analysis, targeted to constricting down the genes accommodating the vulnerable locus. The tenacity of this linkage disequilibrum founded mapping is much greater than in traditional linkage study. Association study can equally be accomplished for morphological traits. The t-test or analysis of variance (ANOVA) is a typical method to execute this type of study, in which a measurable morphostructure is serves as dependent variables and gene products as independent variables.

Population stratification that may result in negative associations concerning a marker and external appearance is a known difficulty in association analysis. Incidences of negative associations are likely probability due to differences between the frequencies allele and syndrome of subpopulations. One resolution to this challenge is the application of base populations, populations that are derivative of a imperfect quantity of characters. Application of these genomic isolates also decreases the genomic distinction, and is thus beneficial to linkage and association analysis in streamlining the genomic basis of a trait of interest (Varilo and Peltonen 2004). Additionally, one of the frequently used resolutions for the population stratification challenge is the transmission disequilibrium test (TDT), in which the gene products of parentages of infected individuals are used (Spielman *et al*., 1993). Conversely, it is much more strenuous and lengthy to harvest DNA of parentages of pretentious individuals than from genetically distant individuals. Hence, traditional case control examinations with genetically distant individuals are quiet desirable as well as essentially applicable.

The selection preference, in which cases and controls are not copiously similar, can also be circumvented by by means of a potential group analysis. In this study scheme, individuals have been carefully chosen prior to disease inception and are monitored in anticipation of the incidence of a particular effect. The potential group study is irreplaceable due to its permissibility to threat evaluations to be made at a population level and ecological factors to be examined. Conversely, time constraint and enormous samples sizes have limited the usage of this apparently beneficial study design as reported by Manolio *et al*., (2006). Irrespective of the used study design and sample size, the association studies should be repeated in an independent population.

2.17 Restriction Enzymes

Restriction enzymes are molecular scissors that cut DNA into fragments at or near specific recognition sites within the molecule called restriction sites. These enzymes are structurally different from one another and they cut the DNA substrate at their recognition site and cleavage sites are distinct from one another. To cut DNA, all restriction enzymes make two incisions, once through each sugar-phosphate backbone of the DNA double helix (Pingoud *et al*., 1993).

These enzymes are found in bacteria and archaea and provide a defense mechanism against invading viruses. In prokaryotes, the restriction enzymes cut up foreign DNA

by selection in a reaction process known as restriction; however, host DNA is secured by a methyltransferase that modifies the prokaryotic DNA and blocks cleavage. Together, these two processes form the restriction modification system.

More than 3000 restriction enzymes have been extensively examined, and over 600 of the endonucleases are accessible commercially (Roberts *et al;* 2007*)*. These enzymes are habitually applied to modify DNA in laboratories, and they are vital materials in molecular cloning (Massey *et al.,* 2001*)*.

Insertion of genes into plasmid vectors during gene cloning and synthesis of protein are achieved through restriction enzymes. For optimum usage, plasmids that are regularly used for gene cloning are altered to include a multiple cloning site, rich in restriction enzyme recognition sequences. This permits flexibility during insertion of gene fragments into the plasmid vector; restriction sites contained naturally within genes influence the choice of endonuclease for digesting the DNA, then it is important to circumvent restriction of desired DNA however purposefully cutting the ends of the DNA. To clone a gene fragment into a vector, both plasmid DNA and gene insert are classically cut with the same restriction enzymes, and then bonded together with the assistance of an enzyme called a DNA ligase (Nettleship *et al*., 2008*)*. These enzymes are applied to distinguish gene alleles by explicitly recognising single base alterations in DNA known as single nucleotide polymorphisms (SNPs) (Zhang *et al.,* 2005*)*. This is conversely only probable if a SNP changes the restriction site existing in the allele. In this method, the DNA samples are genotyped by avoiding high rate of gene sequencing. The sample is first digested with the restriction enzyme to make DNA fragments, and then the distinct sized fragments separated by gel electrophoresis. Commonly, alleles with correct restriction sites will generate two visible bands of DNA on the gel, and those with different restriction sites will not be cut and will produce only a single band. A DNA map by restriction digest is also probably generated which provide the relative positions of the genes. The different lengths of DNA produced by restriction digest also generate a precise pattern of bands after gel electrophoresis, and could be applied to DNA fingerprinting.

2.18 Molecular markers and their applications in livestock improvement

Increased food insecurity and a worldwide food production crisis loom in the future as the most significant scientific challenge facing us in the next 30 years. Expectations that human population growth will soon go from 7.3 billion to 9.6 billion by 2050, and food production must double despite evidence of climate change and limited land and water resources. There is a significant increased demand for animal source foods especially in the power countries of the developing world where most livestock are produced by small holders (Rothschild and Plastow, 2014). Many researchers have touted that the genomic revolution offers solutions to increasing food in the developing world (Ajmone-Marsan *et al*., 2014).

The detected genetic diversity of the population is affected by factors like migration, population size and selection. Therefore, selection of appropriate genetic markers are both used to characterised breeds conservation purposes; selection depends on the availability, applicability and objectives of the study, as markers are highly variable in their information content (Talle *et al*. 2005). The application of DNA based markers in diversity studies is valuable for filling gaps in documentation and confirming its accuracy. Recent developments in DNA technologies have made it possible to uncover a large number genetic polymorphisms at the DNA sequence level, and to use them as markers for evaluation of the genetic basis for the observed phenotypic variations at DNA level are referred to as the molecular markers as published in Yakubu *et al*. (2013). The progress in development of molecular markers suggests their potential use for genetic improvement in livestock species.

2.19 Properties of Molecular Marker

The molecular markers, capable of detecting the genetic variation at the DNA sequence level possess unique genetic properties that make them more useful than other genetic markers. The properties of an ideal molecular marker are as follows on table 2.1

Table 2.1: Properties of Molecular Markers

Properties	RAPD	AFLP	RFLP	SSRs	SNP
Polymorphism	High	High	Low	High	High
Co-dominance	Yes	Yes	Yes	No	Yes
Genomic occurrence	Broad	Broad	Restricted	Broad	Broad
Detection technique	PCR	PCR	PCR	PCR	PCR
Availability	Yes	Yes	Yes	Yes	Yes

2.21 Polymerase Chain Reaction (PCR)

The PCR procedure was established almost four decades ago by Kary Mullis in California. PCR embroils multiplication of minute hereditary material known as DNA to spawn billions of duplicate fragments in shortest while. Actually, the reaction is very easy to perform which involve a PCR machine called thermocycler. The primary element of PCR is a heat constant DNA polymerase known as enzyme, principally *Taq* and *Vent* polymerases.These enzymes perform efficiently even at excessive heats to separate the two DNA strands in the *Watson-Crick* DNA double helix structure.

It is a simple and novel method in molecular genetics to augment a small or few replicas of a piece of DNA across numerous orders of enormousness, in order to generate billions of copies of a precise order of nucleotide of DNA. The process depends on thermal-cycling, comprising of series of repetitive heating and cooling of the reaction for DNA melting and enzymatic copying of the DNA. The fundamental constituents of this reaction are the primers or short DNA fragments containing order of nucleotides complementary to the target region and a DNA polymerase or replicating enzymes in cells and these key constituents of the reaction permit occurrence of selective and repeated amplification. As the reaction advances, the DNA generated functions as a prototype for replication, setting in motion a chain reaction in which the DNA prototype is exponentially augmented.

2.22 Marker Assisted Selection

The addition of genomic information to phenotypic information to increase the selection response to the traditional method is known as Marker-Assisted Selection (MAS). The concept of Marker Assisted Selection (MAS) utilizing the information of polymorphic loci as an aid to selection was introduced as early as in 1900 (Wakchaure *et al.*, 2015). The method where marker genes used to indicate the presence of desirable genes is called as marker assisted selection (Well *et al*., 1998). Marker assisted selection (MAS) is indirect selection process where a trait of interest is selected not based on the trait itself but on a marker linked to it (Ribaut *et al*., 2007). The purpose is to combine all genetic information at markers and QTL with the phenotypic information to improve genetic evaluation and selection. The advantage of using MAS is that the effect of genes on production is directly measured on the genetic

makeup of the animal and not estimated from the phenotype. The use of Marker Assisted Selection (MAS) has the potential if the markers are highly correlated with the desired phenotype to enhance the power of the present-day breeding strategy.

2.23 Electrophoresis

Electrophoresis is a technique which involves migration and separation of charged particles in an electric field applied. The charged particles are macromolecules such as nucleic acids (DNA and RNA) and proteins which are loaded into a gel matrix. This technique involves separation of macromolecules based on mass thereby revealing polymorphism through the use of detection agent. By loading the particules into the gel matrix and applying an electric field, the molecules migrate via the matrix at changed rates. The negatively charged particle migrates toward the positive pole and the positively charged particle migrates toward the negative pole. Since DNA is negatively charged, the samples are loaded near the negative pole, and they migrate toward the positive pole.

The polymeric gel is inert, uncharged and does not cause retardation by binding the molecule. Instead it, forms pores of different size (depending on the concentration of polymer) and sample pass through these pore and as a result their electrophoretic mobility. Hence, electrophoretic mobility is directly proportional to the charge and inversely proportional to the viscosity of the medium, size and shape of the molecule. The gel is positioned in a Submarine Agarose Chamber, which is then connected to a direct current. Once the electric current is applied, the superior particles are set in motion more slowly via the gel while the smaller molecules are faster in motion (i.e. sieving) and the distinct sized particles form distinctive bands on the gel.

Electrophoresis is a post PCR and digestion procedure which is used to validate the presence or absence of DNA. It offers the basis for several analytical techniques used for separating molecules by size, charge, or binding affinity. Gel matrix used mainly is polyacrylamide and agarose. DNA Gel electrophoresis is regularly performed for analytical purposes, often after amplification of DNA via PCR, but may be used as a preparative technique prior to use of other methods such as mass spectrometry, RFLP, PCR, cloning, DNA sequencing, or Southern blotting for further characterisation.

2.24 Phylogenetic Tress Construction

The word "phylogeny" is coined from two Greek words, phyle (tribe – in – particular, the largest political subdivision in the ancient Athenian state and another word from this is "phylum") and geneia (origin and another word from this is "gene"). It was created by the developmental scientist Ernst Haeckel in 1866 and then championed by Darwin in his famous work, on the origin of species. Both biologists tied the idea of "phylogeny" – the origin of groups to evolution. A phylogenetic tree, also called a phylogeny, which is a diagramatic representation of the lines of evolutionary trend of different species of farm animals or genes from a common progenitor. Baum, (2008) opined that, Intervention of biodiversity, structural identifications, and events that happened in the course of evolution requires adequate knowledge of phylogeny. Additionally, phylogenetic tree (generally called tree of life) indicates descent from a common progenitor, and because much of the strongest proof for evolution comes in the form of common ancestry, researchers must have adequate comprehensive knowledge of phylogenies so as to completely appreciate the awesome proof supporting the evolution theory. Various systems of tree diagrams have been used in the past particularly in evolutionary biology since the time of Charles Darwin. Most phylogenetic trees are rooted, meaning that one branch corresponds to the common progenitor of all the livestock species involved in the phylogeny. A clade is a piece of a phylogeny that include an ancestral lineage and all the descendants of that ancestor. This group of organisms has the property of monophyly (from the Greek for "single clan"), so it may also be referred to as a monophyletic group. A clade or monophyletic group is easy to identify visually: it is simply a piece of a larger tree that can be cut away from the root with a single cut. Consequently, if a tree needs to be cut in two places to extract a given set of taxa, then those taxa are non- monophyletic (Baum, 2008). One of the approaches used by scientists to measure the quality of their phylogeny estimates is the bootstrap support of particular nodes in the phylogenetic tree.

2.25 Hardy-Weinberg Equilibrium (HWE)

In an infinite random breeding population, where there are no natural forces such as mutation, selection, migration or genetic drift, the allele and genotype frequencies remain the same from generation to generation. A population is said to be in Hardy-Weinberg Equilibrium when there is no alteration in the allele and genotype

frequencies (Falconer and Mackay, 1996). Other factors that might lead to the change of gene and genotype frequencies in any population or DNA loci are; differential selection pressure, sampling error, misclassification of genotypes, failure to detect rare alleles and the inclusion of non-existing alleles, or if inbreeding has occurred in the population or loci examined. However, to test likely nonconformities from Hardy-Weinberg equilibrium, the precise p-values for distinct strains must be assembled and all examined strains would be in Hardy-Weinberg equilibrium.

In a study of the genetic diversity of prolactin gene in Japanese quail as affected by location in Nigeria using restriction fragment length polymorphism technique, Eichie *et al*., (2016) reported that, all the population utilised in their study showed significant deviation from Hardy-Weinberg Equilibrium. Farrag *et al*., 2013 observed in their study of genetic variation analysis of Sinai chicken and Japanese quail populations using three microsatellite markers that none of the loci or studied sites of chicken population differed significantly from the Hardy-Weinberg proportions whereas the entire population of quail for the three microsatellite loci reflected statistical significant departure from Hardy-Weinberg equilibrium

2.26 Assessment of Farm Animal Genetic Variation

Genetic variation refers to genetic differences both within and among populations. There may be multiple variants of any given gene (alleles), leading to polymorphism. High genetic variability within populations and significant genetic differentiation between populations indicate rich genetic resources of a species. The knowledge of the distribution of genetic variation within and among populations is essential for an evolutionary interpretation of interactions and for the management of endangered or commercially important taxa. Proper utilisation of gene pool of an organism requires utilization of biochemical genetic markers to monitor stock purity i.e., to quantify the genetic variability, to identify parents and progeny in single pairs or complex crosses (Sharma *et al.,* 2000).

Adaptation of the livestock species to changing production environments and in respond to artificial selection is largely affected by the measure of genetic variation, however, conservation and genetic improvement strategies require adequate knowledge of the state of genetic variation in any population. Genetic variation or diversity is the basis of selective breeding and improvement that describe and observe

range of alleles and polymorphic variants. Occasionally, such as for plumage colour in poultry species, it results in distinctive phenotypes. Moreover, variation of allele is expressed as detectable continuous variation. Traits such as production, reproductive, milk and egg are the most important form of genetic diversity as they determine the ability to evolve or to be genetically improved (Toro *et al*., 2011) in order to record effective genetic progress.

In a random population with no mutation and selection, variation in frequencies of allele remain constant as oppose changes in the frequencies of allele when the population is disturbed or the number of individuals permitted for breeding is legitimately small which results in greater homozygosity and losses of effective number of alleles. The accretion of genetic differentiation between breeds and population through isolation and selection of breeds has been forced by human for advantageous traits in the course of breeding farm animals. Hence, consistent information about genetic variances between individuals, populations and strains are prerequisite to setting up effective conservation and utilisation measures. The DNA sequences, distinct genes, chromosomes or continuous genetic distinction are called Genetic information. Quantitative evaluation of genetic variation within and among breeds or population plays a vital role in making decision for genetic conservation, utilisation plans and effective breeding programme. The most commonly used technique to quantify genetic diversity or variation are by utilisation of morphological and biochemical traits as well as molecular markers.

Genetic variability and relatedness is commonly detected through polymorphic markers generated by isozymes, protein electrophoresis pattern, and restriction enzymes. Restriction fragment length polymorphism (RFLP) and southern hybridization based DNA fingerprints (DFP) has been extensively used to detect polymorphism. The advent of molecular technology has greatly enhanced genetic studies in poultry. By detecting genetic variation, genetic markers may provide useful information at different levels: population structure, level of gene flow, phylogenetic relationships, pattern of historical biogeography and the analysis of parentage and relatedness (Feral, 2002)

CHAPTER THREE

STUDY ONE

POLYMORPHISMS OF IGF1, IGF2, GH, GHR AND MYOSTATIN GENES OF THREE STRAINS OF NIGERIAN INDIGENOUS TURKEY

MATERIALS AND METHODS

3.1.1. Study Area and Experimental Animals

Three hundred indigenous turkeys comprising both sexes were sampled from fifty five farmers across three southwestern states of Nigeria (Figure 3.1) as summarised in the table (3.1);

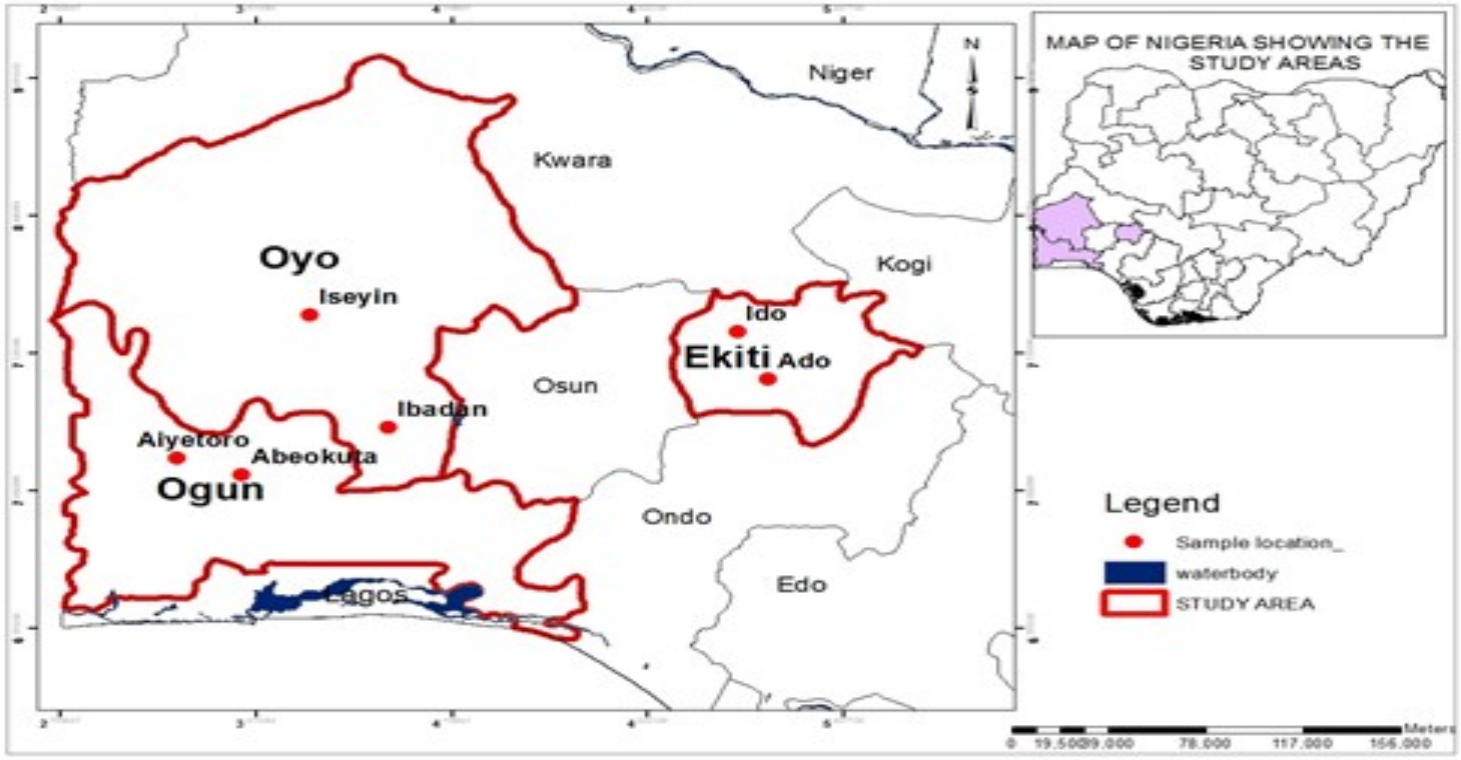

Figure 3.1: Map of Nigeria showing the sampling areas

Table 3.1: Number of Turkey Sampled in each Southwestern States of Nigeria

States	Number of Towns	Number of Farmers	Total number of Turkey Sampled
Oyo	4	25	140
Ogun	4	20	90
Ekiti	4	10	70
Total	12	55	300

3.1.2. Sampling: Location, Procedure and Sample size

Birds were sampled from fifty five (55) different flocks in twelve towns across three different states in Southwestern Nigeria as described in table 3.1.1. These towns where the birds were sampled were purposively chosen because of the availability of pure locally adapted strains of turkey in them. A multi-stage purposive sampling technique was used first to select the states, towns and then to select the turkey farmers in South-West Nigeria.

A total of three hundred turkeys of both sexes comprising 82 black, 114 spotted and 104 white strains were sampled. All the birds sampled were toms and hens.

3.1.3. Blood Sample Collection

Two (2) millilitres (ml) of whole blood were sampled via the wing vein of each of the turkey and stored in 5mls tubes containing Ethylenediamine Tetra Acetic Acid (EDTA) as anti-coagulant. All blood samples were kept cold by placing them into ice box containing ice packs and were carefully handled to prevent exposure to high temperature. The samples were stored in the laboratory at -20 °C until DNA extraction.

3.1.4. DNA extraction

Genomic DNA was extracted from the blood samples using Quick-gDNA Miniprep extraction kits following the manufacturer protocol with little modifications. The laboratory procedures were carried out at Biotechnology laboratory affiliated with the Animal Production department FUTA, Akure, Ondo State, Nigeria. The extraction procedure is as follow:

1. To obtain optimum result, beta-mercaptoethanol was added to the genomic lysis buffer to a final dilution of 0.5% (v/v) i.e 250 µl per 50 ml or 500 µl per 100ml.
2. 400µl of genomic lysis buffer was added to 20µl of whole blood, (20:1).
3. It was mixed completely by vortexing 4-6 secs, then incubated 5-10 minutes at room temperature.
4. The mixture was transferred to a Zymo-Spin^{TM} column in a collection tube and centrifuged at 1000xg for 1 minute. The collection tube was discarded with the flow through.
5. The Zymo-Spin^{TM} column was transfered to a new collection tube.

6 200µl of DNA pre-Wash Buffer was added to the spin column and centrifuged at 10000g for one minute.

7 The spin column was added to a clean microcentrifuge tube.

8 ≥ 50µl DNA Elution Buffer or water was added to the spin column and incubated 2-5 minutes at room temperature and then centrifuged at top speed for 30 secs to elute the DNA.

9 The Eluted DNA was used immediately for PCR amplification

3.1.5. PCR Amplification

The different base pair sizes of DNA fragment was amplified in a Mastercycler Gradient 5331 thermal cycler (Eppendorf) in a total reaction volume of 25µL containing 50ng genomic DNA, 12.5pmol of forward primer and the same amount of reverse primer, dNTPs, $MgCl_2$, Taq DNA polymerase, reaction buffer, PCR stabilizer and enhancer at optimal concentrations. Amplicons were detected on 1.5% agarose. The Gels were stained with ethidium bromide (EtBr) and photographed under Transilluminator (an ultraviolet light box) or a gel documentation system. PCR amplification was performed using five primers of GH, GHR, IGF1, IGF2 and myostatin as shown in Table 3.2. The thermal conditions for the five primers at 35cycles for each reaction are shown in the tables 3.3, 3.4, 3.5, 3.6 and 3.7 respectively.

Table 3.2: Designed Primers Used in this study

Primers	Product Size (bp)	Primer sequence (5'-3')	Annealing Temp (^{0}C)
GH	300	F:AACATCCTCCCCAACCTTTCC R: CCCTGTCAAGGTTAGGCTCA	57
GHR	500	F: AACATCTGCATTTCCCATAC R: CATGGGCATCCCAGTTTGAC	60
IGF1	450	F:TGTTCTGCATTTCCCATACTT R:GGCTTCTTGGCTAGTTGCAGT	58
IGF2	550	F:CTCCATGTGGCTTCCCTGTACC R:GGCTTCTTGGCTAGTTGCAGT	57
MSTN	700	F: AACCAATCGTCGGTTTTGACA R: GAAAAGCAGCAGGGTTGTTA	62

Table 3.3: PCR protocol of 300bp DNA fragment at GH locus

Reaction Steps	Thermal conditions (^{0}C)	Running Time (seconds)
Initial Denaturation	94	300
Denaturation	94	45
Annealing	57	45
Extension	72	50
Final Extension	72	120

Table 3.4: PCR protocol of 500bp DNA fragment at GHR locus

Reaction Steps	Thermal conditions (^{0}C)	Running Time (seconds)
Initial Denaturation	94	300
Denaturation	94	45
Annealing	60	45
Extension	72	60
Final Extension	72	180

Table 3.5: PCR protocol of 450bp DNA fragment at IGF1 locus

Reaction Steps	Thermal conditions (^{0}C)	Running Time (seconds)
Initial Denaturation	97	120
Denaturation	94	58
Annealing	58	45
Extension	70	60
Final Extension	72	120

Table 3.6: PCR protocol of 550bp DNA fragment at IGF2 locus

Reaction Steps	Thermal conditions (^{0}C)	Running Time (seconds)
Initial Denaturation	95	240
Denaturation	94	45
Annealing	57	45
Extension	72	50
Final Extension	72	120

Table 3.7: PCR protocol of 700bp DNA fragment at myostatin locus

Reaction Steps	Thermal conditions (^{0}C)	Running Time (seconds)
Initial Denaturation	94	300
Denaturation	94	45
Annealing	62	45
Extension	72	50
Final Extension	72	120

3.1.6. Restriction Fragment Length Polymorphism Analysis

The PCR products of primers GH, GHR, IGF1, IGF2 and MSTN were digested with restriction enzymes *AluI, MnI and EcoR1* respectively. 20µl of molecular graded water, 2µl of 10X FastDigest Green Buffer, 20µl of concentrated PCR products and 1µl of FastDigest enzyme were subjected to digestion for 20 minutes at 65°C the manufacturers' instructions. The restriction digests were separated on 1.5 agarose gel in 1xTBE at a constant current of 100v for 1hour. The gels were stained with ethidium bromide and the fragments were visualized under UV transilluminator. Band scorring was carried out manually.

3.1.7. Statistical Analysis

Genotype Analysis: Genotype and allele frequencies of GH, GHR, IGF1, IGF2 and myostatin were determined by direct counting method according to the method of Falconer and Mackay (1996). Allele and genotype frequencies of each gene in each turkey strain were examined for Hardy-Weinberg equilibrium (HWE) and the variances between the observed and expected numbers of each allele and genotype were compared using a goodness of fit chi-square test. HWE was assumed for >0.05 using GENEPOP statistical software (Kuhner and Felsenstein 1994).

3.1.8. Phylogenetic Analysis

A dendrogram depicting phylogenetic relationship among three strains of Nigerian turkey was constructed on the basis of genetic distance indices using computer software MEGA 7 (Tamura *et al*., 2011)

3.1.9. Estimation of Genetic Distance and Wright's F-statistics

The amount of inbreeding within population (*f*), and the amount of differentiation among populations (Theta) per locus were estimated according to Weir and Cockerham (1984) and using the software GENPOP (Kuhner and Felsenstein 1994), with corresponding P-values obtained based on 1000 randomisations. The within-breed inbreeding coefficient (FIS) was calculated, with a 95% confidence interval,

determined by 1000 permutations and 10000 bootstraps, using the software GENEPOP (Kuhner and Felsenstein 1994).

STUDY TWO

GROWTH MODELLING OF THREE STRAINS OF NIGERIAN TURKEY AT 1GF1, IGF2, GH AND MYOSTATIN LOCI

MATERIALS AND METHODS

3.2.1. Collection of Hatchable Eggs

Four hundred and fifty hatchable eggs were procured randomly from turkey farmers rearing the three strains sampled in study one and stored for seven days at room temperature. The eggs were taken to reputable hatchery in Ibadan for incubation.

3.2.2. Sourcing of Experimental Birds

At 28 day, three hundred 1 day-old poults hatched from 450 eggs procured were collected from the hatchery and used for the experiment

3.2.3. Experimental Site

The experiment was conducted at Duke Poultry Farm, Omoluabi Street, Orogun, Ibadan, Oyo State, Nigeria.

3.2.4. Housing and Management of Experimental Poults

Prior to the arrival of the experimental poults, the brooding house as well as equipment was thoroughly cleaned and disinfected. A total of 300 one day-old poults collected from reputable hatchery were kept on deep litter system. Poults hatching weight were considered as bodyweight at week 0. Each poult was tagged with numbered tags using tagging gun subcutaneously at the neck region for easy identification and the tagged birds were properly monitored throughout the experiment. Afterwards, individual poult's bodyweights were measured on weekly basis for 21 weeks and recorded on a 5kg sensitive scale. All measurements were taken at 7am before feed administration. Poults were fed commercial diet according to their nutrient requirement based on the following schedule: 0 to 4 weeks (21% CP and 2800kcal/kg/ME) then 5 to 21 weeks (17%CP and 2600kcal/kg/ME). Birds were supplied fresh feed and water *ad libitum* during the period of the experiment which lasted 21 weeks.

3.2.5. Blood Sample Collection

At 10 weeks, two (2) millilitres (ml) of blood were sampled via the wing vein of 250 growers as earlier described in study one.

3.2.6. Laboratory Analysis

DNA extraction, DNA yield and quality assessment, PCR amplification of 150 samples, PCR-RFLP analysis and agarose gel elecrophoresis were done as earlier described in study one.

3.2.7. Sequencing of The Selected Genes

Forty quality amplicons were selected and sent for sequencing at Inqaba Biotec, South Africa

3.2.8. Sequence Analysis

BioEdit version 6.5 was used to open the sequence results and Blastn search was applied to blast the sequences on National Center Biotechnlogy Information (NCBI) database to unveil regions amplified by each of the genes.

3.2.9. Data Collected

Body weights on weekly basis from week 1 to week 21 were purposefully fitted into four non-linear growth equations according to polymorphic variants.

3.2.10 Statistical Analysis

The weekly bodyweights obtained were analysed using descriptive statistics with statistical package of SPSS version 23.0 and growth curve graphics were elaborated by Excel software. Parameters A, B and k were determined as a result of Levenberg Marquardt iteration techinique using similar software while iteration was done, 1.0E-8 was used as convergence criteria. The four models (table 3.4) used were tested for goodness of fit in order to select the most effective model for individual genotype at specific locus.

Table 3.8: Non linear growth models and their mathematical functions

S/N	Model	Mathematical Functions
1	Brody	$W_t = A*(1-B* \exp(-k*t)$
2	Gompertz	$W_t = A * \exp(-B*\exp(-k*t))$
3	Logistics	$W_t = A/(1+B* \exp(-k*t))$
4	Von bertalanffy	$W_t = A*(1-B* \exp(-k*t))**3$

W_t = weight of individual animal at age t(weeks); A= asymptotic weight(mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)t = age in weeks. (Salako, 2014)

STUDY THREE

ASSOCIATION OF IGF1, IGF2, GH AND MYOSTATIN GENES WITH GROWTH AND CARCASS TRAITS IN THREE STRAINS OF NIGERIAN INDIGENOUS TURKEY

MATERIALS AND METHODS

3.3.1. Experimental Animals

Ninety turkeys of equal strains and sexes were purposefully selected according to polymorphic variants obtained and used for this study.

3.3.2. Parameters collected

Bodyweights of ninety turkeys consist of both strains and sexes from week 1 to week 21 were selected for this study. A total of ninety turkeys were sacrificed for carcass analysis at 21 week according to the standard procedure. The 16 carcass traits collected were defeathered weight, dressed weight, eviscerated weight, head weight, back weight, breast weight, drumstick weight, neck weight, shank weight, thigh weight, wing weight, empty gizzard weight, full gizzard weight, heart weight, liver weight and spleen weight respectively. Weekly bodyweights and carcass parameters obtained were associated with each of the polymorphic variants of the sequenced genes.

3.3.3. Statistical Analysis

Data collected were subjected to analysis of variance (ANOVA) in a completely randomised design following generalized linear mixed model (GLM) procedure of SAS (2012) statistical software to test the fixed effects of polymorphic variants, strain and their interactions. Significant differences between polymorphic variants and traits measured were determined using Duncan Multiple Range Test (DMRT) at 95% confidence interval of the same software. The general linear mixed model used is as follow:

$Y_{ijkl}=\mu+G_i + S_j + X_k + GS_{ij} + GX + GSX + e_{ijkl}$

Y_{ijkl} = individual observation

μ= the overall mean

G_i= fixed effect of ith genotype

S_j= fixed effect of jth strain

x_k= fixed effect of kth sex

GS_{jk}= interaction effect of ith genotype and jth strain

GX=interaction effect of ith genotype and kth sex

GSX=interaction effect of ith genotype, jth strain and kth sex

e_{ijkl}= random error associated with each record.

CHAPTER FOUR

4.0 RESULTS

STUDY ONE

4.1.1. Restriction fragment length patterns of IGF1, IGF2, GH, GHR and myostatin genes

Gel images of the IGF1, IGF2, GH, GHR and myostatin genes of indigenous turkey in Nigeria are presented in Plates 4.1, 4.2, 4.3, 4.4 and 4.5.

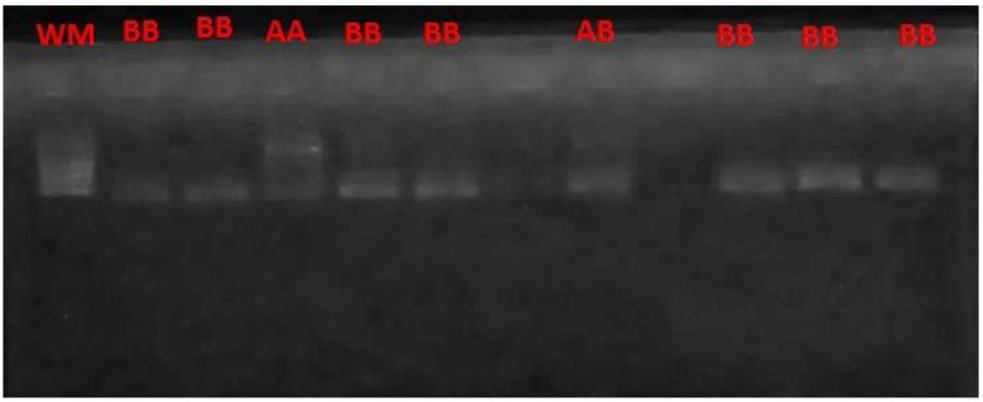

Plate **4.1**: PCR-RFLP fragment of Insulin-like growth factor-1 gene of Nigerian indigenous turkey.

WM: weight of marker
BB: homozygote
AA: homozygote
AB: heterozygote

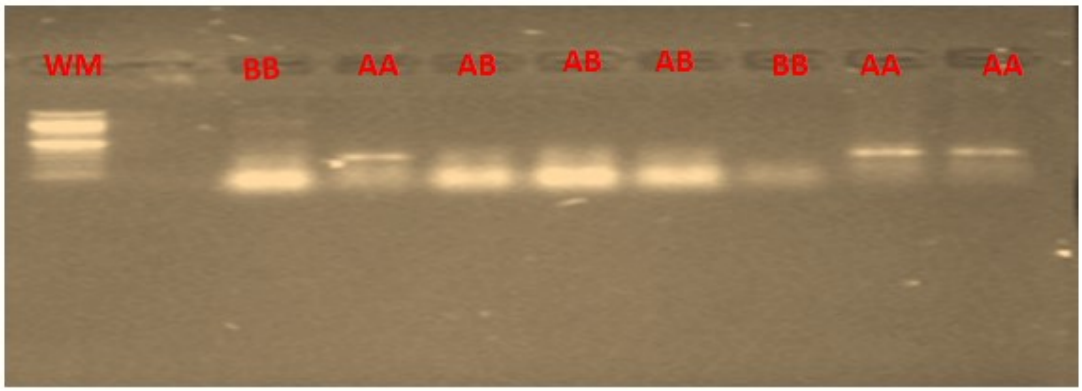

Plate **4.2**: PCR-RFLP fragment of Insulin-like growth factor-2 gene of Nigerian indigenous turkey.

WM: weight of marker
BB: homozygote
AA: homozygote
AB: heterozygote

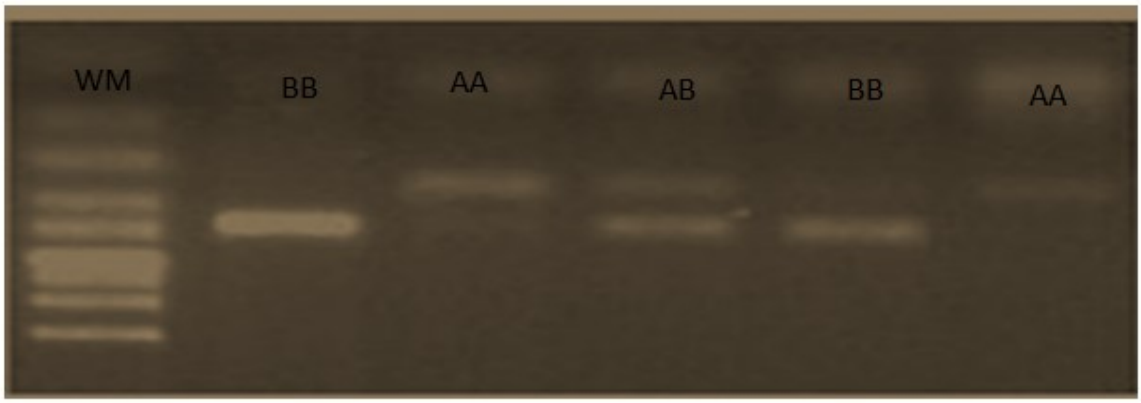

Plate **4.3**: PCR-RFLP fragment of Growth hormone gene of Nigerian indigenous turkey.

WM: weight of marker
BB: homozygote
AA: homozygote
AB: heterozygote

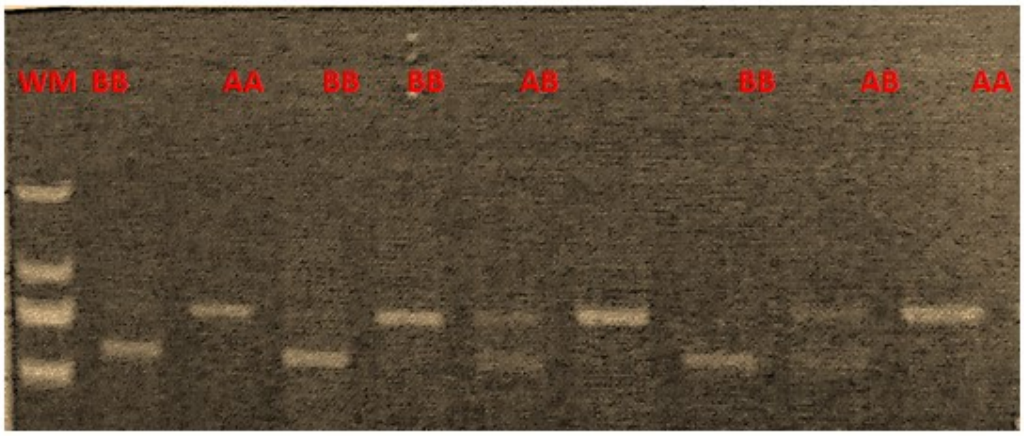

Plate **4.4**: PCR-RFLP fragment of Growth hormone receptor gene of Nigerian indigenous turkey.

WM: weight of marker
BB: homozygote
AA: homozygote
AB: heterozygote

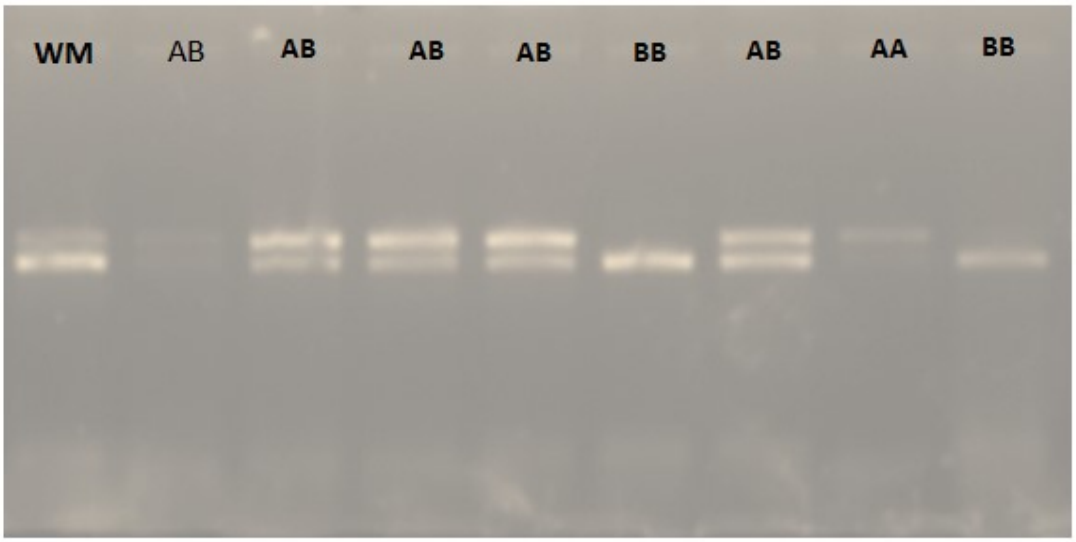

Plate 4.5: PCR-RFLP fragment of Myostatin gene of Nigerian indigenous turkey.

WM: weight of marker
BB: homozygote
AA: homozygote
AB: heterozygote

4.1.2. Allele and genotype distribution of Insuin-like Growth Factor 1 (IGF1) gene

Table 4.1 shows distribution of alleles and genotypes frequencies observed at IGF1 locus. At this locus, genotypes AA, AB and BB with alleles A and B were identified at this locus. The AA, AB and BB genotype frequencies were 0.40, 0.34 and 0.25 (Black), 0.29, 0.48 and 0.22 (Spotted) and 0.29, 0.52 and 0.18 (White). The respective allele frequencies of A and B were 0.57 and 0.42 (Black), 0.53 and 0.46 (Spotted) and 0.55 and 0.44 (White). Allele A is preponderant allele across the three strains genotyped. At this locus, black strain was not conformed to Hardy–Weinberg equilibrium (P>0.05) except spotted and white strains of turkey.

4.1.3. Allele and genotype distribution of Insuin-like Growth Factor 2 (IGF2) gene

At IGF2 locus, three genotypes were found namely: AA, AB and BB which show fragments at different base pair (bp) using *EcoR1* for PCR-RFLP. The AA, AB and BB genotype frequencies were 0.36, 0.47 and 0.16 (Black), 0.46, 0.36 and 0.17 (Spotted) and 0.34, 0.49 and 0.16 (White) respectively and the corresponding allele frequencies of A and B were 0.60 and 0.40 (Black), 0.64 and 0.35 (Spotted) and 0.59 and 0.40 (White) respectively as shown in Table 4.2. The frequencies of allele A were significantly higher than of the B allele. The frequency of the genotype of black strain differed significantly from the expectation of Hardy-Weinberg equilibrum.

4.1.4 Allele and genotype distribution of Growth hormone (GH) gene

For GH gene, genotypes AA, AB and BB were observed in black, spotted and white strains of turkey with frequencies of 0.47, 0.32 and 0.20 (Black), 0.53, 0.39 and 0.68 (Spotted) and 0.50, 0.44 and 0.72 (White) respectively while its allele frequencies for A and B were 0.63 and 0.36 (Black), 0.73 and 0.26 (Spotted) and 0.72 and 0.27 (White) respectively as shown in Table 4.3. Allele frequencies of A were found to be significantly higher than those of B allele across the populations studied. At this locus, black and white populations were not in Hardy–Weinberg equilibrium (P>0.05) except spotted strain.

4.1.5 Allele and genotype distribution of Growth Hormone Receptor (GHR) gene

In GHR gene, genotypes AA, AB and BB have the frequencies of 0.30, 0.45 and 0.23 (Black), 0.35, 0.43 and 0.21(Spotted) and 0.33, 0.48 and 0.18 (White) respectively with allele A and B having frequencies of 0.53 and 0.46 (Black), 0.56 and 0.43 (Spotted) and 0.57 and 0.42 (White) respectively as shown in Table 4.4. At this locus, allele A is dominant allele in the three populations utilised. The observed genotype frequencies of AA and AB were significantly higher than that of BB genotype and Chi-square value (1.48) of the spotted strain showed significant difference which shows that the population of the spotted turkey was not in conformity with Hardy–Weinberg equilibrium ($P>0.05$)

4.1.6 Allele and genotype distribution of Myostatin gene

At myostatin locus, the AA, AB and BB genotype frequencies were 0.32, 0.47 and 0.20 (Black), 0.37, 0.41 and 0.21(Spotted) and 0.38, 0.35 and 0.25 (White) while the corresponding allele frequencies were 0.56 and 0.43 (Black), 0.57 and 0.42 (Spotted) and 0.56 and 0.43 (White) for A and B respectively as shown in Table 4.5. The Chi-square distribution table showed significant difference ($Pr<0.05$) at myostatin locus for spotted and white populations in the three strains of indigenous turkey studied. However, the significant Chi-square values were not conformed to Hardy–Weinberg equilibrium ($P>0.05$).

Table 4.1**: Alleles and genotypes frequency for IGF1 gene of three strains of indigenous turkey in Nigeria**

Strains		Genotype	Frequency		Allele	Frequency		HWE	
	N	AA	AB	BB	A	B	χ^2	Pr<0.05	Sig
Black	55	0.40	0.34	0.25	0.57	0.42	4.75	0.032	*
Spotted	102	0.29	0.48	0.22	0.53	0.46	0.12	0.686	NS
White	93	0.29	0.52	0.18	0.55	0.44	0.40	0.678	NS

Chi-square (χ^2)* Significant at P<0.05; ^{ns} not significant (P>0.05) HWE=Hardy Weinberg equilibrum, N=sample size

Table 4.2: Alleles and genotypes frequency for IGF2 gene of three strains of indigenous turkey in Nigeria

Strains		Genotype	Frequency		Allele	Frequency		HWE	
	N	AA	AB	BB	A	B	χ^2	Pr<0.05	Sig
Black	55	0.36	0.47	0.16	0.60	0.40	0.01	0.910	*
Spotted	102	0.46	0.36	0.17	0.64	0.35	4.52	0.033	NS
White	93	0.34	0.49	0.16	0.59	0.40	0.08	0.821	NS

Chi-square (χ^2)* Significant at P<0.05; ^{ns} not significant (P>0.05) HWE=Hardy Weinberg equilibrum, N=sample size

Table 4.3: Alleles and genotypes frequencies for GH gene of three strains of indigenous turkey in Nigeria

Strains		Genotype	Frequency		Allele	Frequency		HWE	
	N	AA	AB	BB	A	B	χ^2	Pr<0.05	Sig
Black	55	0.47	0.32	0.20	0.63	0.36	4.71	0.042	*
Spotted	102	0.53	0.39	0.68	0.73	0.26	0.01	0.940	NS
White	93	0.50	0.44	0.05	0.72	0.27	1.07	0.469	*

Chi-square (χ^2)* Significant at P<0.05; ^{ns} not significant (P>0.05) HWE=Hardy Weinberg equilibrum, N=sample

Table 4.4: Alleles and genotypes frequencies for GHR gene of three strains of indigenous turkey in Nigeria

Strains		Genotype	Frequency		Allele	Frequency		HWE	
	N	AA	AB	BB	A	B	χ^2	Pr<0.05	Sig
Black	55	0.30	0.45	0.23	0.53	0.46	0.40	0.566	NS
Spotted	102	0.35	0.43	0.21	0.56	0.43	1.48	0.249	*
White	93	0.33	0.48	0.18	0.57	0.42	0.01	0.924	NS

Chi-square (χ^2)* Significant at P<0.05; ^{ns} not significant (P>0.05) HWE=Hardy Weinberg equilibrum, N=sample size

Table 4.5: Alleles and genotypes frequencies for MSTN gene of three strains of indigenous turkey in Nigeria

Strains		Genotype	Frequency		Allele	Frequency		HWE	
	N	AA	AB	BB	A	B	χ^2	Pr<0.05	Sig
Black	55	0.32	0.47	0.20	0.56	0.43	0.08	0.778	NS
Spotted	102	0.37	0.41	0.21	0.57	0.42	2.47	0.144	*
White	93	0.38	0.35	0.25	0.56	0.43	7.20	0.009	*

Chi-square (χ^2)* Significant at P<0.05; ^{ns} not significant (P>0.05) HWE=Hardy Weinberg equilibrum, N=sample size

4.1.7 F-Statistics and Gene Flow

Fixation indices Fis, Fit and Fst are primary measures of estimating and testing the magnitude of genetic divergence among populations as shown in Table 4.6. When all populations were analysed for the 5 loci, the global heterozygosity deficit (Fit) varied from 0.042 (GH) to 0.081 (myostatin) and within breed deficit in heterozygote (Fis) ranged from 0.037 (GH) to 0.084 (myostatin) for all loci. The fixation coefficients of subpopulations within total population (Fst) across the 5 loci were estimated with a range of -0.007 (IGF1) to -0.003 (myostatin). The gene flow values for all loci ranged from 0.008 (GHR) to 7.203 (IGF1). The IGF1 gene recorded the highest value of global heterozygosity deficit (Fit) (0.175), within breed deficit in heterozygote (Fis) (0.181) and gene flow (Nm) (7.203) but lowest value of subpopulations within total population (Fst) (-0.007). The inbreeding is at lowest level at IGF1 locus.

Table 4.6: F-Statistics and estimates of gene flow for five loci of three strains of indigenous turkey in Nigeria

Loci	Fit	Fis	Fst	Nm
GH	0.042	0.037	-0.005	1.077
GHR	0.073	0.077	-0.005	0.008
IGF1	0.175	0.181	-0.007	7.203
IGF2	0.054	0.059	-0.005	0.406
MSTN	0.081	0.084	-0.003	0.051

N_m:Gene flow from Fst=[1/Fst-1]/4, Fit= inbreeding coefficient of individual within total population, Fis= inbreeding coefficient of individual within sub-population and Fst= inbreeding coefficient of sub-population within total population

4.1.8 Heterozygosity

Heterozygosity values were calculated to determine the level of genetic variation within the populations as shown in table 4.7. The Nei expected heterozygosity values observed were 0.48(48.0%) for black population, 0.46(46.0%) for spotted population and 0.47(47.0%) for white population respectively. The most diverse population observed was the black with highest Nei expected heterozygosity value of 48.0%. The Shannon-Wiener Indices recorded ranged from 3.77 for black population to 4.16 for white population.

Table 4.7: Heterozygosity estimates of all loci for each strain

Strain	N	H	Hexp
Black	55	3.77	0.48
Spotted	102	4.10	0.46
White	93	4.16	0.47

N:Sample size, H:Shannon-Wiener Index, H_{exp}: Nei expected heterozygosity

4.1.9 Phylogenetic relationship

A dendrogram depicting phylogenetic relationships among indigenous turkey in Nigeria was constructed in figure 4.1.The estimated distance among the three populations ranged between 0.001 to 0.005. The smallest genetic distance was observed between spotted and white strains while farthest genetic distance was observed between black strain and white strain respectively. However, the spotted and white turkey strains appeared to be more related than their black counterparts at the selected loci.

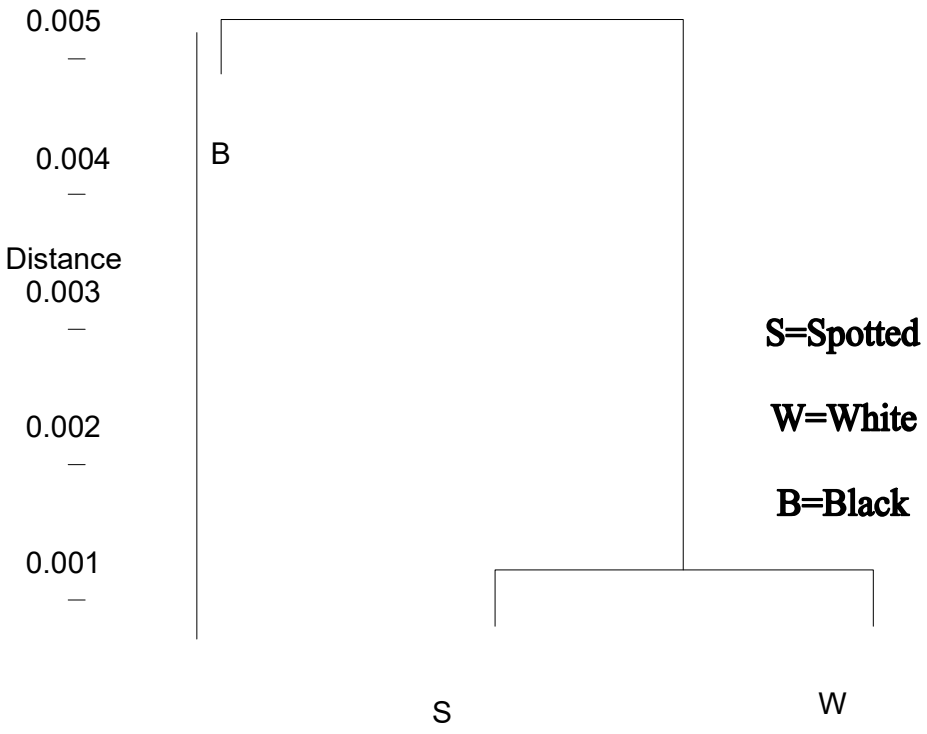

Figure 4.1:Dendrogram depicting phylogenetic relationships among indigenous turkey in Nigeria

STUDY TWO

4.2.1 Descriptive Statistics of Bodyweight of Three Strains of Nigerian Indigenous Turkey

Table 4.8 shows the descriptive destributions of bodyweights of Nigerian indigenous turkey separated by strains. The results showed that variation existed in weekly bodyweights among the populations with spotted strain recorded the highest mean values across the production weeks compared to black and white populations respectively except at weeks 4, 6 and 7 when white population recorded highest mean values (304.08±7.82, 454.12±11.16 and 515.08±15.01, respectively).

Table 4.8: Descriptive Statistics of Bodyweigth of Three Strains of Nigerian Indigenous Turkey

Age(week)	Black (n=42)	Spotted (n=58)	White (n=50)
1	72.43±1.57	74.93±1.66	74.68±1.36
2	137.76±3.26	140.38±3.31	139.44±3.16
3	204.10±5.64	209.57±4.70	207.06±5.21
4	292.62±7.65	301.81±6.78	304.08±7.82
5	381.14±10.96	393.93±8.89	392.60±10.26
6	447.07±12.36	451.10±11.11	454.12±11.16
7	511.36±14.93	514.41±14.74	515.08±15.01
8	597.17±14.77	594.59±15.81	586.96±15.15
9	683.21±14.01	670.98±15.97	660.54±17.37
10	777.36±15.08	761.05±15.45	734.50±17.86
11	876.38±15.78	845.66±17.42	820.52±18.19
12	987.52±18.49	939.34±19.72	913.90±19.10
13	1154.02±24.10	1068.57±24.12	1042.74±21.85
14	1318.88±29.87	1221.90±28.21	1185.08±28.15
15	1510.10±30.81	1395.09±31.07	1365.76±30.68
16	1726.69±33.71	1563.83±36.54	1536.64±31.14
17	1930.00±31.92	1741.19±38.73	1732.96±32.76
18	2077.88±44.79	1935.31±40.72	1901.14±35.97
19	2262.38±47.08	2091.64±40.45	2053.30±35.75
20	2452.02±50.33	2242.19±44.37	2190.34±34.85
21	2607.88±50.65	2411.74±50.45	2340.14±38.78

n= sample size

4.2.2 Estimates of growth curve parameters of three strains of Nigerian indigenous turkey of 5' Flanking region at IGF1 locus

Table 4.9 shows the estimates of growth parameters under different genotypes of 5' Flanking region at IGF1 locus. Asymptotic weight (A) for Logistic model ranged from 3702.90g to 4472.00g for AA and BB genotypes (black), 3564g to 4029.30g for BB and AB genotypes (spotted) and 3536.30g to 4265g for AB and BB genotypes. Brody model asymptotic weight were 485779g to 732870g for AA and BB genotypes (black), 390244g to 452281g for BB and AA genotypes (spotted) and 26213.60g to 462088g for AB and BB genotypes (white). In Von-Batalanfy model, asymptotic weight ranges from 28927g to 253323g for AA and BB genotypes (black), 34492g and 252995 for BB and AB genotypes (spotted) and 7702g and 375529g for AB and BB (white). For Gompertz model, asymptotic weight were 8079.40g, 11362.30g and 13714.10 for AA, AB and BB genotypes (black),10354.70g, 12901.30 and 8298.50 for AA, AB, and BB genotypes (spotted) and 11540.40, 7702.30 and 14073.80g for AA, AB and BB genotypes (white) respectively. Brody model recorded the highest asymptotic weight of 732870g for homozygote BB genotype while Logistic model recorded the lowest asymptotic weight of 3536.30g for heterozygote AB genotype. The constant of integration (B) of the growth functions for Logistic ranged from 21.10 to 26.39 for AA and BB genotypes (black), 19.04 to 21.68 for BB and AA genotypes (spotted) and 18.60 to 22.10 for AB and BB genotypes (white).

In Brody, constant of integration (B) of 1.0 was observed across the three strains studied for AA, AB and BB genotypes except heterozygotes AB that recorded 0.82 under white strain. Von-Batalanfy, constant of integration (B) ranged from 0.84 to 0.92 for AA and BB genotypes (black), 0.84 to 0.91 for BB and AB genotypes (spotted) and 0.89 to 3.96 for AA and AB genotypes (white). In Gompertz, constant of integration (B) ranged from 4.14 to 4.63 for AA and BB genotypes (black), 4.02 to 4.37 for BB and AB genotypes (spotted) and 3.96 to 4.48 for AB and BB genotypes (white) correspondingly. Growth rate (k) for Logistic model ranged from 0.18 to 0.19 for BB and AA genotypes (black), 0.16 to 0.18 for AB and BB genotypes (spotted) and 0.16 to 0.18 for BB and AB genotypes (white). For Brody model, 0.00 growth rate was

observed for all the genotypes across the three strains except for heterozygote AB that recorded 0.02 growth rate for white strain.

Table 4.9: Estimates of growth curve parameters of three strains of Nigerian indigenous turkey of 5' Flanking region at IGF1 locus

	Black			Spotted			White		
	A	B	k	A	B	K	A	B	k
Log									
AA	3702.90	21.10	0.19	3807.80	21.68	0.18	4003.40	21.78	0.17
AB	4159.10	23.50	0.18	4029.30	20.56	0.16	3536.30	18.60	0.18
BB	4472.00	26.39	0.18	3564.00	19.04	0.18	4265.00	22.10	0.16
Brody									
AA	485779.00	1.00	0.01	452281.00	1.00	0.01	457833.00	1.00	0.01
AB	586643.00	1.00	0.01	408797.00	1.00	0.01	26213.60	0.82	0.02
BB	732870.00	1.00	0.01	390244.00	1.00	0.01	462088.00	1.00	0.01
Batalanffy									
AA	28927.00	0.84	0.02	83674.20	0.88	0.01	125035.00	0.89	0.01
AB	98409.90	0.89	0.12	252995.00	0.91	0.01	7702.30	3.96	0.06
BB	253323.00	0.92	0.00	34492.00	0.84	0.01	375529.00	0.92	0.00
Gomp									
AA	8079.40	4.14	0.06	10354.70	4.29	0.05	11540.40	4.35	0.05
AB	11362.3	4.42	0.05	12901.30	4.37	0.04	7702.30	3.96	0.06
BB	13714.10	4.63	0.05	8298.50	4.02	0.05	14073.80	4.48	0.04

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.3 Estimates of growth curve parameters of three strains of indigenous turkey in Nigeria of exon 3 at IGF2 locus

Estimates of growth parameters under different genotypes of exon 3 at IGF2 locus are presented in Table 4.10. Asymptotic weight (A) for Logistic model ranged from 3614.30g to 4443.50g for BB and AB genotypes (black), 3247g to 4360.20g for BB and AB genotypes (spotted) and 3676.80g to 4094.20g for BB and AA genotypes. Brody model asymptotic weights were 32442.40g to 593144.00g for BB and AB genotypes (black), 415954g to 447744g for AA and BB genotypes (spotted) and 416124.00g to 447592g for BB and AA genotypes (white). In Von-Batalanfy model, asymptotic weight ranges from 32442.40g to 115158g for BB and AA genotypes (black), 11232.50g and 611253g for BB and AB genotypes (spotted) and 38402.20g and 124459g for BB and AA (white). For Gompertz model, asymptotic weight were 8163.50g, 12337.80g and 9385.80G for BB, AB and AA genotypes (black),10489.30g, 17268.50g and 5579g for AA, AB, and BB genotypes (spotted) and 11795.70g, 10550.80g and 11795.70g for AA, AB and BB genotypes (white) respectively. Brody model recorded the highest asymptotic weight of 593144g for heterozygote AB while Logistic model recorded the lowest asymptotic weight of 3614.30g for homozygote BB for black population. Constant of integration (B) of Brody model observed across the three strains studied for AA, AB and BB genotypes were 1.00 except homozygotes BB that recorded 0.84 under black strain. Von-Batalanfy, constant of integration (B) ranged from 0.84 to 0.89 for BB and AB genotypes (black), 0.80 to 0.93 for AB and BB genotypes (spotted) and 0.85 to 0.89 for BB and AB genotypes (white). In Gompertz, constant of integration (B) ranged from 4.16 to 4.43 for BB and AB genotypes (black), 3.96 to 4.70 for BB and AB genotypes (spotted) and 4.10 to 4.32 for BB and AA genotypes (white) respectively. The constant of integration (B) of the growth functions for Logistic ranged from 21.10 to 26.39 for AA and BB genotypes (black), 19.04 to 21.68 for BB and AA genotypes (spotted) and 18.60 to 22.10 for AB and BB genotypes (white). Constant of integration (B) and growth rate (k) of Logistic model were significantly higher than the rest of the models for the different genotypes detected.

Table 4.10: Estimates of growth curve parameters of three strains of indigenous turkey in Nigeria of exon 3 at IGF2 locus

	Black			Spotted			White		
	A	B	k	A	B	K	A	B	k
Log									
AA	3910.20	23.29	0.19	3809.60	20.44	0.17	4094.20	21.12	0.17
AB	4443.50	23.75	0.18	4360.20	23.36	0.16	3789.80	21.55	0.17
BB	3614.30	21.73	0.19	3247.0	21.86	0.22	3676.80	20.09	0.18
Brody									
AA	561048.00	1.00	0.01	415954	1.00	0.01	447592.00	1.00	0.01
AB	593144.00	1.00	0.01	495285	1.00	0.01	432022.00	1.00	0.01
BB	32442.40	0.84	0.01	447744.00	1.00	0.01	416124.00	1.00	0.01
Batalanffy									
AA	46941.70	0.86	0.01	86340.30	0.88	0.01	124459.00	0.89	0.01
AB	115158.00	0.89	0.01	611253.00	0.93	0.00	95909.20	0.89	0.01
BB	32442.40	0.84	0.01	11232.50	0.80	0.03	38402.2	0.85	0.01
Gomp									
AA	9385.80	4.29	0.06	10489.30	4.24	0.05	11795.70	4.32	0.05
AB	12337.80	4.43	0.05	17268.50	4.70	0.04	10550.80	4.31	0.05
BB	8163.50	4.16	0.06	5579.00	3.96	0.08	8669.60	4.10	0.05

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.4 Estimates of growth curve parameters of three strains of indigenous turkey in Nigeria of 5' flanking region at GH locus

Estimates of growth parameters under different genotypes of 5' flanking region at GH locus are presented in Table 4.11. Asymptotic weight (A) for Logistic model ranged from 3586.00g to 4121.00g for BB and AB genotypes (black), 3086.50g to 470807.00g for AB and BB genotypes (spotted) and 4329.00g to 4118.20g for BB and AB genotypes. In Von-Batalanfy model, asymptotic weight ranges from 31452g to 139608g for BB and AB genotypes (black), 14480g and 174760g for BB and AB genotypes (spotted) and 61659.30g and 470343g for homozygotes AA and BB genotypes (white). For Gompertz model, asymptotic weight were 9377.60g, 11878.20g and 8056.70g for AA, AB and BB genotypes (black),12145.70g, 11910.40g and 5918.70g for AA, AB, and BB genotypes (spotted) and 9722.10g, 11098.50g and 14746.00g for AA, AB and BB genotypes (white) correspondingly. Brody model asymptotic weights ranged from 32442.40g to 593144.00g for BB and AB genotypes (black), 415954g to 447744g for AA and BB genotypes (spotted) and 416124.00g to 447592g for BB and AA genotypes (white) populations respectively and was recorded to be significantly higher than the asymptotic values recorded for other models considered. Brody model recorded the highest asymptotic weight of 597531.00g for heterozygote AB genotype while Logistic model recorded the lowest asymptotic weight of 3086.50g for homozygote BB genotype. The constant of integration (B) of the growth functions for Logistic ranged from 20.67 to 24.53 for BB and AB genotypes (black), 1.00 to 21.22 for AB and AA genotypes (spotted) and 20.97 to 21.05 for AA, AB and AB genotypes (white). In Brody model, constant of integration (B) of 1.0 was observed across the three strains studied for AA, AB and BB genotypes except homozygote AA that recorded 21.17 under white strain. Von-Batalanfy model constant of integration (B) ranged from 0.84 to 0.90 for BB and AB genotypes (black), 0.80 to 0.90 for BB and AB genotypes (spotted) and 0.87 to 0.93 for AA and BB genotypes (white). In Gompertz, constant of integration (B) ranged from 4.10 to 4.48 for BB and AB genotypes (black), 3.82 to 4.39 for BB and AB genotypes (spotted) and 4.23 to 4.45 for AB and BB genotypes (white) correspondingly. Constant of integration (B) and growth rate (k) of Logistic model were significantly higher than the rest of the models for the different genotypes detected.

Table 4.11: Estimates of growth curve parameters of three strains of Nigerian indigenous turkey 5' flanking region at GH locus

	Black			Spotted			White		
	A	B	K	A	B	K	A	B	K
Log									
AA	3966.20	23.20	0.19	4010.90	21.22	0.17	4329.00	20.97	0.16
AB	4121.50	24.53	0.18	470807.00	1.00	0.00	4118.20	21.05	0.17
BB	3586.00	20.67	0.18	3086.50	18.02	0.19	4329.00	20.97	0.16
Brody									
AA	561119.00	1.00	0.01	439572.00	1.00	0.01	3771.10	21.17	0.18
AB	597531.00	1.00	0.01	470807.00	1.00	0.01	458635.00	1.00	0.01
BB	439291.00	1.00	0.01	312641.00	1.00	0.01	2338152.00	1.00	0.01
Batalanffy									
AA	44175.10	0.86	0.01	170544.00	0.90	0.01	61659.30	0.87	0.01
AB	139608	0.90	0.01	174760.00	0.90	0.01	84355.40	0.88	0.01
BB	31452.00	0.84	0.01	14480.9	0.80	0.02	470343.00	0.93	0.01
Gomp									
AA	9377.60	4.28	0.06	12145.70	4.36	0.04	9722.10	4.23	0.05
AB	11878.20	4.48	0.05	11910.40	4.39	0.05	11098.50	4.26	0.05
BB	8056.70	4.10	0.06	5918.70	3.82	0.06	14746.00	4.45	0.04

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.5 Estimates of growth curve parameters of three strains of indigenous turkey in Nigeria of exon 3 at myostatin locus

Estimates of growth parameters under different genotypes of exon 3 at myostatin locus are presented in Table 4.12. Asymptotic weight (A) for Logistic model ranged from 3929.90g to 3999.70g for AA and AB genotypes (black), 3341.20g to 4094.00g for AB and BB genotypes (spotted) and 3504.50g to 4642g for AB and BB genotypes. Brody model asymptotic weights ranged from 505128g to 565973g for BB and AB genotypes (black), 400069g to 435297g for AB and AA genotypes (spotted) and 403325.00g to 579539g for AA and BB genotypes (white) populations respectively. In Von-Batalanfy model, asymptotic weight ranges from 47146.20g to 63245.90g for BB and AB genotypes (black), 25567.90g and 411183.00g for AB and BB genotypes (spotted) and 40678.80g and 779982.00g for AB and BB (white). For Gompertz model, asymptotic weights were 9499.50g, 10149.80g and 9468.40 for AA, AB and BB genotypes (black),11037.80g, 7302.90g and 13790.00g for AA, AB, and BB genotypes (spotted) and 9685.30g, 8412.30g and 20243.00g for AA, AB and BB genotypes (white) respectively. Von-Batalanfy model recorded the highest asymptotic weight of 779982g on homozygote BB genotype for white strain while Logistic model recorded the lowest asymptotic weight of 3341.20g on heterozygote AB genotype for spotted strain. The constant of integration (B) of the growth functions for Logistic ranged from 22.63 to 24.25 for BB and AB genotypes (black), 20.25 to 21.28 for AB and BB genotypes (spotted) and 19.61 to 26.31 for AA and BB genotypes (white).

In Brody, constant of integration (B) of 1.0 was observed across the three strains studied for AA, AB and BB genotypes except heterozygotes AB that recorded 0.03 under spotted strain. Von-Batalanfy constant of integration (B) were 0.86, 0.88 and 0.86 AA, AB and BB genotypes (black), 0.88, 0.83 and 0.92 for AA, AB and BB genotypes (spotted) and 0.86, 0.85 and 0.94 for AA, AB and BB genotypes (white). In Gompertz, constant of integration (B) ranged from 4.26 to 4.39 for BB and AB genotypes (black), 4.05 to 4.45 for AB and BB genotypes (spotted) and 4.12 to 4.92 for AA, AB and BB genotypes (white) correspondingly. Growth rate (k) for Logistic model ranged from 0.18 to 0.19 for AB and AA genotypes (black), 0.16 to 0.18 for BB and AB genotypes (spotted) and 0.17 to 0.18 for BB and AB genotypes (white). Gompertz model, recorded the significant highest rate of growth across the three single nucleotide polymorphisms for all strains of turkey examined.

Table 4.12: Estimates of growth curve parameters of three strains of indigenous turkey in Nigeria of Exon 3 at myostatin locus

	Black			Spotted			White		
	A	B	K	A	B	K	A	B	K
Log									
AA	3929.90	22.96	0.19	3910.80	20.81	0.17	3879.60	19.61	0.17
AB	3999.70	24.25	0.18	3341.20	20.25	0.18	3504.50	20.40	0.18
BB	3941.60	22.63	0.19	4094.0	21.28	0.16	4642.10	26.31	0.17
Brody									
AA	556189.00	1.00	0.01	435297.00	1.00	0.01	403325	1.00	0.01
AB	565973.00	1.00	0.02	400069.00	1.00	0.03	426828	1.00	0.03
BB	505128.00	1.00	0.04	421306.00	1.00	0.01	579539	1.00	0.01
Batalanffy									
AA	48443.80	0.86	0.01	104149.00	0.88	0.01	51713.70	0.86	0.01
AB	63245.90	0.88	0.01	25567.90	0.83	0.02	40678.80	0.85	0.01
BB	47146.20	0.86	0.01	411183.00	0.92	0.01	779982.00	0.94	0.01
Gomp									
AA	9499.50	4.28	0.06	11037.80	4.28	0.05	9685.30	4.12	0.05
AB	10149.80	4.39	0.05	7302.90	4.05	0.06	8412.30	4.12	0.05
BB	9468.40	4.26	0.06	13790.00	4.45	0.04	20243.00	4.92	0.04

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.6 Correlation estimates of growth parameters of three strains of indigenous turkey of 5' Flanking region at IGF1 locus

Table 4.13 shows approximate correlation of growth parameter estimates of the indigenous turkey strains. Correlation estimates of the mature weight and the hatch weight AB for the Logistic, Von-Bertallanfy and Gompertz were positive for all the three strains across the three genotypes (AA, AB and BB) detected while Brody models were negatively correlated across the three strains of different genotype. The highest positive correlation was obtained from Von-Bertallanfy model and Brody model recorded the strongest negative correlation for parameters AB. Correlation between mature weight and the maturing rate Ak: Parametrs Ak were all negative for the models examined. The strongest negative correlation of individual genotype was observed in Brody model for parameter Ak across the three strains. Also, correlation between Bk of some of the genotype for all the models in the three strains of turkey except in Brody model where it was positive for all genotypes. The Bk correlations for Logistic model were positive for individual AA and AB genotype for black strain and for heterozygote AB in white strain. Homozygote BB of Von-Bertallanfy model recorded positive correlation of Bk (0.998) for white population and it was the highest positive correlation of parameter Bk.

Table 4.13: Correlation estimates of growth parameters of three strains of indigenous turkey of 5' Flanking region at IGF1 locus

	Black			Spotted			White		
	AB	Ak	Bk	AB	Ak	Bk	AB	Ak	Bk
Log									
AA	0.088	-0.915	0.302	0.451	-0.925	-0.095	0.558	-0.928	-0.223
AB	0.321	-0.922	0.054	0.732	-0.934	-0.451	0.362	-0.923	0.006
BB	0.405	-0.924	-0.040	0.372	-0.923	-0.004	0.699	-0.932	-0.405
Brody									
AA	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
AB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
BB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
Batalanffy									
AA	0.982	-0.998	-0.971	0.997	-0.999	-0.995	0.998	-0.999	-0.996
AB	0.997	-0.999	-0.994	0.999	-0.999	-0.998	0.988	-0.998	-0.979
BB	0.998	-0.999	-0.997	0.993	-0.998	-0.986	0.999	-0.999	0.998
Gomp									
AA	0.798	-0.987	-0.697	0.946	-0.990	-0.895	0.960	-0.991	-0.918
AB	0.927	-0.990	-0.869	0.979	-0.992	-0.949	0.890	-0.988	-0.815
BB	0.947	-0.991	-0.899	0.915	-0.989	-0.849	0.977	-0.992	-0.947

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.7 Correlation estimates of growth parameters of three strains of indigenous turkey of exon 2 at IGF2 locus

Approximate correlation of growth parameter estimates of the indigenous turkey strains are presented in Table 4.14. Correlation estimates of the mature weight and the hatch weight AB for the Logistic, Von-Bertallanfy and Gompertz were positive for all the three strains across the three genotypes (AA, AB and BB) detected except on individuals BB of Logistic model in spotted strain population while Brody models were negatively correlated across the three strains of different genotype. The highest positive correlation was obtained from Von-Bertallanfy model and Brody model recorded the strongest negative correlation for parameters AB. Correlation between mature weight and the maturing rate Ak: Parametrs Ak were all negative for all the models examined. The strongest negative correlation of individual genotype was observed in Brody model for parameter Ak across the three strains. Also, correlation between Bk of some of the genotype for all the models in the three strains of turkey were all negative except in Brody model where it was positive for all genotypes. The Bk correlations for Von-Bertallanfy and Gompertz models were negative for the different genotypes obtained for the three populations while Logistic and Brody models recorded positive correlation for parameter except negative correlation of parameter Bk on heterozygote AB across the three populations.

Table 4.14: Correlation estimates of growth parameters of three strains of indigenous turkey of Exon 3 at IGF-2 locus

	Black			Spotted			White		
	AB	Ak	Bk	AB	Ak	Bk	AB	Ak	Bk
Log									
AA	0.158	-0.918	0.229	0.566	-0.928	0.234	0.609	-0.930	0.287
AB	0.442	-0.925	-0.083	0.774	-0.935	-0.509	0.544	-0.928	-0.206
BB	0.138	-0.917	0.250	-0.332	-0.891	0.703	0.362	-0.923	0.006
Brody									
AA	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
AB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
BB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
Batalanffy									
AA	0.991	-0.999	-0.985	0.998	-0.999	-0.995	0.998	-0.999	-0.997
AB	0.997	-0.999	-0.995	0.999	-0.999	-0.999	0.998	-0.999	-0.996
BB	0.987	-0.998	-0.978	0.707	-0.995	-0.641	0.993	-0.998	-0.987
Gomp									
AA	0.862	-0.988	-0.780	0.959	-0.991	-0.915	0.964	-0.991	-0.924
AB	0.941	-0.990	-0.888	0.986	-0.993	-0.963	0.955	-0.991	-0.910
BB	0.839	-0.987	-0.749	0.031	-0.979	-0.158	0.910	-0.989	-0.843

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.8 Correlation estimates of growth parameters of three strains of indigenous turkey of 5' Flanking region at GH locus

Approximate correlation of growth parameter estimates of the indigenous turkey strains are presented in Table 4.15. Correlation estimates of the mature weight and the hatch weight AB for the Logistic, Brody and Von-Bertallanfy were positive for all the three strains across the three genotypes (AA, AB and BB) detected while Gompertz model were negatively correlated across the three strains of different genotype. The highest positive correlation was obtained from Von-Bertallanfy model and Brody model recorded the strongest negative correlation for parameters AB. Correlation between mature weight and the maturing rate Ak: Parametrs Ak were all negative for the models examined. The strongest negative correlation of individual genotype was observed in Brody model for parameter Ak across the three strains. Also, correlation between Bk of some of the genotype for all the models in the three strains of turkey except in Brody model where it was positive for all genotypes. The Bk correlations for Logistic model were positive for individual AA and AB genotype for black strain and for heterozygote AB in white strain. Homozygote BB of Von-Bertallanfy model recorded positive correlation of Bk (0.997) for black population and it was the highest positive correlation of parameter Bk.

Table 4.15: Correlation estimates of growth parameters of three strains of indigenous turkey of 5' Flanking region at GH locus

	Black			Spotted			White		
	AB	Ak	Bk	AB	Ak	Bk	AB	Ak	Bk
Log									
AA	-0.078	-0.515	-0.313	-0.151	-0.875	-0.095	-0.648	-0.938	-0.312
AB	-0.213	-0.910	-0.054	-0.532	-0.955	-0.451	-0.362	-0.925	0.018
BB	-0.421	-0.624	-0.040	-0.412	-0.723	-0.004	-0.699	-0.913	-0.512
Brody									
AA	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
AB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
BB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
Batalanffy									
AA	-0.982	-0.968	-0.971	-0.997	-0.999	-0.995	-0.998	-0.987	-0.949
AB	-0.997	-0.959	-0.994	-0.999	-0.999	-0.898	-0.988	-0.997	-0.978
BB	-0.998	-0.999	-0.997	-0.993	-0.998	-0.986	-0.999	-0.989	0.979
Gomp									
AA	-0.798	-0.998	-0.698	0.897	-0.990	-0.898	0.890	-0.880	-0.858
AB	-0.927	-0.963	-0.878	0.899	-0.987	-0.899	0.895	-0.968	-0.815
BB	-0.947	-0.975	-0.997	0.920	-0.899	-0.965	0.897	-0.977	-0.977

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.9: Correlation estimates of growth parameters of three strains of indigenous turkey Exon 3 at Myostatin locus

Approximate correlation of growth parameter estimates of the indigenous turkey strains are presented in Table 4.16. Correlation of the mature weight and the hatch weight AB for the Logistic, Von-Bertallanfy and Gompertz were positive for all the three strains across the three genotypes (AA, AB and BB) detected while Brody models were negatively correlated across the three strains of different genotype. The highest positive correlation was obtained from Von-Bertallanfy model and Brody model recorded the strongest negative correlation for parameters AB. Correlation between mature weight and the maturing rate Ak: Negative parameters Ak of different genotypes were observed for all models examined. The strongest negative correlation of individual genotype was observed in Brody model for parameter Ak across the three strains. Also, correlation between Bk of all the genotypes for the Logistic and Brody models in the three strains of turkey were all positive except in Von-Bertallanfy and Gompertz models where positive correlation of parameters Bk were obtained.

Table 4.16: Correlation estimates of growth parameters of three strains of indigenous turkey of Exon 3 at Myostatin locus

	Black			Spotted			White		
	AB	Ak	Bk	AB	Ak	Bk	AB	Ak	Bk
Log									
AA	0.183	-0.918	0.203	0.563	-0.928	0.231	0.548	-0.928	0.211
AB	0.266	-0.921	0.115	0.164	-0.917	0.223	0.268	-0.920	0.111
BB	0.221	-0.919	0.163	0.744	-0.934	0.468	0.758	-0.934	0.485
Brody									
AA	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
AB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
BB	-0.999	-0.999	0.999	-0.999	-0.999	0.999	-0.999	-0.999	0.999
Batalanffy									
AA	0.992	-0.999	-0.986	0.998	-0.999	-0.996	0.996	-0.999	-0.992
AB	0.994	-0.999	-0.990	0.985	-0.998	-0.975	0.993	-0.999	-0.988
BB	0.992	-0.999	-0.986	0.999	-0.999	-0999	0.999	-0.999	-0.999
Gomp									
AA	0.873	-0.988	-0.795	0.961	-0.991	-0.918	0.945	-0.990	-0.893
AB	0.896	-0.989	-0.826	0.842	-0.987	-0.751	0.904	-0.989	-0.835
BB	0.879	-0.988	-0.801	0.981	-0.993	-0.953	0.987	-0.994	-0.964

A= asymptotic weight (mature weight) of the animal; B = constant of integration; k = growth rate (maturation rate)

4.2.10 Goodness of fit criteria of 5' flanking region at IGF1 locus for three strains of indigenous turkey in Nigeria

The results of goodness of fit for different genotypes of IGF1 gene for three strains of indigenous turkey in Nigeria are presented in Table 4.17. At IGF1 locus, the mean square error (MSE) values for Logistic model were 1537.60, 2027.20 and 1248.00 on AA, AB and BB genotypes for black strain while spotted strain has mean square error (MSE) values of 1962.50, 2599.00 and 2717.90 on AA, AB and BB genotypes respectively and white strain recorded mean square error (MSE) values of 1824.70, 1855.30 and 2031.50 respectively across the three genotypes. The mean square error (MSE) values for Brody model were 24866.60, 32831.70 and 38240.00 on AA, AB and BB genotypes for black strain while spotted strain has mean square error (MSE) values of 19010.10, 20657.90 and 23792.80 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 23989.30, 1048.00 and 24864.10 respectively across the three genotypes. The mean square error (MSE) values for Von-Batalanfy model were 1632.10, 2357.60 and 1346.10 on AA, AB and BB genotypes for black strain while spotted strain has mean square error (MSE) values of 2058.60, 2202.90 and 2600.60 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 1608.80, 1226.20 and 1729.40 respectively across the three genotypes. Gompertz model recorded mean square values of 1515.10, 2225.10 and 1253.20 on AA, AB and BB genotypes for black strain, 2015.40, 2316.00 and 2619.70 on AA, AB and BB genotypes for spotted strain and 1650.90, 1226.20 and 1810.80 on AA, AB and BB genotypes respectively for white strain. The coefficient of determination (R^2) ranged from 0.910 to 0.999 for the different individual genotype across the three populations utilised. Logistic equation provided the best fit having recorded greatest R^2 (0.999) for black and spotted strains respectively on homozygotes AA and BB individuals while Brody model was the model of best fit for white population with R^2 value of 0.999 on heterozygote AB individuals. At this locus, Logistic model recorded the lowest values of MSE, AIC and BIC for black and spotted strains on individuals with genotype AA and BB while Brody model reported the lowest values of MSE, AIC and BIC respectively on individuals with AB for white population.

Table 4.17: Goodness of fit criteria of 5' flanking region at IGF1 locus for the three strains of Nigerian indigenous turkey

	Black			Spotted			White		
	MSE	R^2	AIC	MSE	R^2	AIC	MSE	R^2	AIC
Logistics									
AA	1537.60	0.998	360.519	1962.50	0.999	520.137	1824.70	0.995	406.550
AB	2027.20	0.994	320.928	2599.00	0.930	590.165	1855.30	0.980	421.025
BB	1248.00	0.999	250.620	2717.90	0.910	680.655	2031.50	0.950	485.140
Brody									
AA	24866.60	0.997	990.319	19010.10	0.995	910.665	23989.30	0.955	1335.540
AB	32831.70	0.960	1320.820	20657.90	0.960	1090.425	1048.00	0.999	208.744
BB	38240.00	0.935	2390.510	23792.80	0.925	1520.250	24864.10	0.925	1535.125
Batalanffy									
AA	1632.10	0.985	285.122	2058.60	0.980	600.287	1608.80	0.950	385.235
AB	2357.60	0.925	336.420	2202.90	0.950	690.555	1226.20	0.980	262.120
BB	1346.10	0.997	256.120	2600.60	0.927	810.238	1729.40	0.937	415.450
Gompertz									
AA	1515.10	0.990	300.219	2015.40	0.990	575.457	1650.90	0.970	310.235
AB	2225.10	0.970	320.118	2316.00	0.950	670.556	1226.20	0.990	258.550
BB	1253.2	0.998	298.150	2619.70	0.928	920.410	1810.80	0.958	406.430

MSE= Mean Square Error; R^2= Coefficient of determination; AIC= Akaike's Information Criteria

4.2.11 Goodness of fit criteria of exon 2 at IGF2 locus for three strains of indigenous turkey in Nigeria

The results of goodness of fit statistics for different genotypes of IGF2 gene for three strains of indigenous turkey in Nigeria are reported in Table 4.18. At IGF2 locus, the mean square error (MSE) values for Logistic model were 1587.00, 1736.10 and 1678.80 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 2054.20, 2271.50 and 5160.20 on AA, AB and BB genotypes respectively and white strain recorded mean square error (MSE) values of 1984.10, 1471.10 and 1865.30 respectively across the three genotypes. The mean square error (MSE) values for Brody model were 29589.90, 32466.70 and 1979.30 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 20507.00, 26014.10 and 29383.40 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 23139.50, 21063.60 and 19911.00 respectively across the three genotypes. The mean square error (MSE) values for Von-Batalanfy model were 1854.40, 1275.00 and 1979.30 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 2176.20, 1807.50 and 8584.50 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 1565.30, 1168.60 and 1532.60 respectively across the three genotypes. Gompertz model recorded mean square values of 1699.30, 1348.10 and 1834.10 on AA, AB and BB genotypes for black strain, 1868.70, 2195.80 and 7503.80 on AA, AB and BB genotypes for spotted strain and 1667.20, 1225.80 and 1592.00 on AA, AB and BB genotypes respectively for white strain. The coefficient of determination (R^2) ranged from 0.925 to 0.999 for the different individual genotype across the three populations utilised. Bertalanfy equation provided the best fit having recorded greatest R^2 (0.999) for black, spotted and white strains respectively on the heterozygote AB individuals detected. At this locus, Bertalanfy model recorded the lowest values of MSE and AIC for black and spotted strains on different genotypes obtained across the three populations studied.

Table 4.18: Goodness of fit criteria of Exon 2 at IGF 2 locus for the three strains of indigenous turkeys in Nigeria

	Black			Spotted			White		
	MSE	R^2	AIC	MSE	R^2	AIC	MSE	R^2	AIC
Logistics									
AA	1587.00	0.995	385.510	2054.20	0.988	720.135	1984.10	0.985	655.320
AB	1736.10	0.940	402.528	2271.50	0.968	910.165	1471.10	0.996	530.125
BB	1678.80	0.955	350.110	5160.20	0.950	1015.105	1865.30	0.980	605.250
Brody									
AA	29589.90	0.985	1190.119	20507.00	0.998	1010.220	23139.50	0.925	1295.250
AB	32466.70	0.955	1220.530	26014.10	0.955	1285.555	21063.60	0.950	928.524
BB	1979.30	0.998	495.230	29383.40	0.950	1615.320	19911.00	0.985	855.125
Batalanffy									
AA	1854.40	0.980	435.342	2176.20	0.958	590.555	1565.30	0.985	555.523
AB	1275.00	0.999	266.420	1807.50	0.999	520.250	1168.60	0.999	455.120
BB	1979.30	0.957	486.110	8584.50	0.925	930.252	1532.60	0.988	550.125
Gompertz									
AA	1699.30	0.950	365.109	1868.70	0.990	555.327	1667.20	0.950	720.530
AB	1348.10	0.995	280.110	2195.80	0.970	650.525	1225.80	0.998	502.425
BB	1834.10	0.935	398.532	7503.80	0.928	950.585	1592.00	0.958	595.220

MSE= Mean Square Error; R^2= Coefficient of determination; AIC= Akaike's Information

4.2.12 Goodness of fit criteria of 5' flanking region at GH locus for three strains of indigenous turkey in Nigeria

The results of goodness of fit statistics for different genotypes of GH gene of three strains of indigenous turkey in Nigeria are reported in Table 4.19. At GH locus, the mean square error (MSE) values for Logistic model were 1587.00, 1736.10 and 1678.80 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 2054.20, 2271.50 and 5160.20 on AA, AB and BB genotypes respectively and white strain recorded mean square error (MSE) values of 1984.10, 1471.10 and 1865.30 respectively across the three genotypes. The mean square error (MSE) values for Brody model were 29589.90, 32466.70 and 1979.30 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 20507.00, 26014.10 and 29383.40 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 23139.50, 21063.60 and 19911.00 respectively across the three genotypes. The mean square error (MSE) values for Von-Batalanfy model were 1854.40, 1275.00 and 1979.30 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 2176.20, 1807.50 and 8584.50 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 1565.30, 1168.60 and 1532.60 respectively across the three genotypes. Gompertz model recorded mean square values of 1699.30, 1348.10 and 1834.10 on AA, AB and BB genotypes for black strain, 1868.70, 2195.80 and 7503.80 on AA, AB and BB genotypes for spotted strain and 1667.20, 1225.80 and 1592.00 on AA, AB and BB genotypes respectively for white strain.The coefficient of determination (R^2) ranged from 80% to 99% for the different individual genotype across the three populations utilised. Bertalanfy equation provided the best fit having recorded greatest R^2 (0.999) for the three populations on the heterozygote AB individuals detected. At this locus, Bertalanfy model recorded the lowest values of MSE and AIC for black and spotted strains on different genotypes obtained across the three populations studied.

Table 4.19: Goodness of fit criteria of Exon 3 at GH locus for the three strains of Nigerian indigenous turkeys

	Black			Spotted			White		
	MSE	R^2	AIC	MSE	R^2	AIC	MSE	R^2	AIC
Logistics									
AA	1587.00	0.998	385.510	2054.20	0.997	520.137	1984.10	0.985	516.550
AB	1736.10	0.995	402.528	2271.50	0.995	590.165	1471.10	0.995	320.025
BB	1678.80	0.997	350.110	5160.20	0.989	675.755	1865.30	0.989	405.220
Brody									
AA	29589.90	0.889	1190.119	20507.00	0.955	950.620	23139.50	0.925	995.510
AB	32466.70	0.885	1220.530	26014.10	0.935	1290.335	21063.60	0.950	908.374
BB	1979.30	0.980	495.230	29383.40	0.899	1710.250	19911.00	0.955	835.505
Batalanffy									
AA	1854.40	0.990	435.342	2176.20	0.988	540.135	1565.30	0.985	385.235
AB	1275.00	0.999	266.420	1807.50	0.999	490.237	1168.60	0.999	258.550
BB	1979.30	0.957	486.110	8584.50	0.989	930.232	1532.60	0.988	360.520
Gompertz									
AA	1699.30	0.950	365.109	1868.70	0.998	505.217	1667.20	0.950	310.235
AB	1348.10	0.999	280.110	2195.80	0.979	530.355	1225.80	0.998	262.535
BB	1834.10	0.935	398.532	7503.80	0.988	720.550	1592.00	0.958	346.520

MSE= Mean Square Error; R^2= Coefficient of determination; AIC= Akaike's Information

4.2.13 Goodness of fit criteria of 5' flanking region at myostatin locus for three strains of indigenous turkey in Nigeria

The results of goodness of fit statistics for different genotypes of myostatin gene of three strains of indigenous turkey in Nigeria are presented in Table 4.20. At myostatin locus, the mean square error (MSE) values for Logistic model were 1700.10, 1706.90 and 1328.70 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 2039.50, 2134.20 and 2919.10 on AA, AB and BB genotypes respectively and white strain recorded mean square error (MSE) values of 2215.50, 2022.30 and 1523.80 respectively across the three genotypes. The mean square error (MSE) values for Brody model were 29319.50, 29566.00 and 27749.80 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 22364.00, 19321.00 and 22095.20 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 18797.40, 22128.00 and 31890.00 respectively across the three genotypes. The mean square error (MSE) values for Von-Batalanfy model were 1956.80, 1550.10 and 1323.10 on AA, AB and BB genotypes for black strain while spotted strain had mean square error (MSE) values of 1935.30, 2396.00 and 2567.10 on AA, AB and BB genotypes and white strain recorded mean square error (MSE) values of 1437.60, 2623.90 and 1486.90 respectively across the three genotypes. Gompertz model recorded mean square values of 1812.20, 1530.90 and 1245.40 on AA, AB and BB genotypes for black strain, 1907.40, 2292.30 and 2670.50 on AA, AB and BB genotypes for spotted strain and 1577.60, 2427.00 and 1361.30 on AA, AB and BB genotypes respectively for white strain. The coefficient of determination (R^2) ranged from 0.920 to 0.999 for the different individual genotype across the three populations utilised. Gompertz equation was the most effective model having recorded greatest R^2 (0.999) for black, R^2 (0.998) for spotted and R^2 (0.999) for white populations on BB, AA and BB genotypes respectively. At this locus, Gompertz model recorded the lowest values of MSE and AIC for black, spotted and white strains on different genotypes obtained across the three populations studied.

Table 4.20: Goodness of fit criteria of Exon 2 at MSTN locus for the three strains of Nigerian indigenous turkeys

	Black			Spotted			White		
	MSE	R^2	AIC	MSE	R^2	AIC	MSE	R^2	AIC
Logistics									
AA	1700.10	0.980	430.550	2039.50	0.988	870.555	2215.50	0.976	855.356
AB	1706.90	0.955	402.228	2134.20	0.955	710.105	2022.30	0.980	830.255
BB	1328.70	0.988	355.520	2919.10	0.925	955.105	1523.80	0.985	675.230
Brody									
AA	29319.50	0.920	1890.239	22364.00	0.940	1410.250	18797.40	0.969	995.570
AB	29566.00	0.925	1960.240	19321.00	0.980	1166.235	22128.00	0.950	1228.304
BB	27749.80	0.955	1477.220	22095.20	0.930	1205.170	31890.00	0.945	1805.525
Batalanffy									
AA	1956.80	0.950	605.222	1935.30	0.988	555.310	1437.60	0.969	505.550
AB	1550.10	0.980	406.550	2396.00	0.965	528.555	2623.90	0.975	645.310
BB	1323.10	0.987	346.540	2567.10	0.950	630.252	1486.90	0.988	530.555
Gompertz									
AA	1812.20	0.970	550.559	1907.40	0.998	520.550	1577.60	0.968	720.530
AB	1530.90	0.990	430.235	2292.30	0.980	633.224	2427.00	0.950	632.258
BB	1245.40	0.999	298.532	2670.50	0.958	760.505	1361.30	0.999	455.120

MSE= Mean Square Error; R^2= Coefficient of determination; AIC= Akaike's Information

4.2.14 Growth curve describing weight-age relationships

The weight-age growth curve of both sexes and those of the different genotypes for all models of the three strains of indigenous turkey in Nigeria are presented in figures 4.2-4.40. From the growth curve, the weight of the male turkey was significantly higher than the weight of the female (figure 4.40). Also, the black strain of turkey grew faster and significantly bigger in size than the spotted and white populations (figure 4.39). From figures 4.2-4.38, it was observed that, fit lines of the predicted of all the models are very close to the observed values for all the individual genotype.

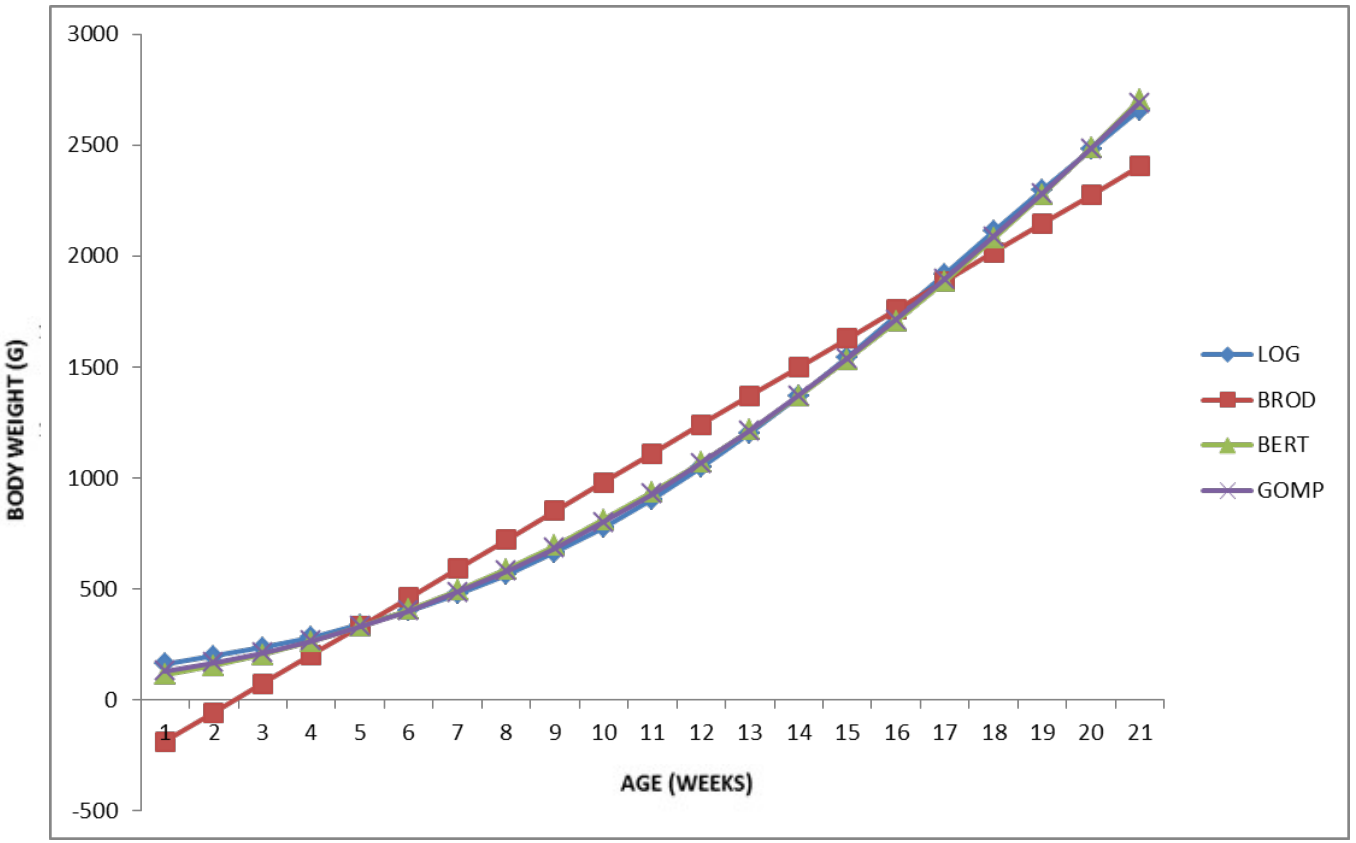

Figure 4.2: Growth curve describing weight-age relationship of black strain of indigenous turkey for AA genotype of Exon 3 at GH locus

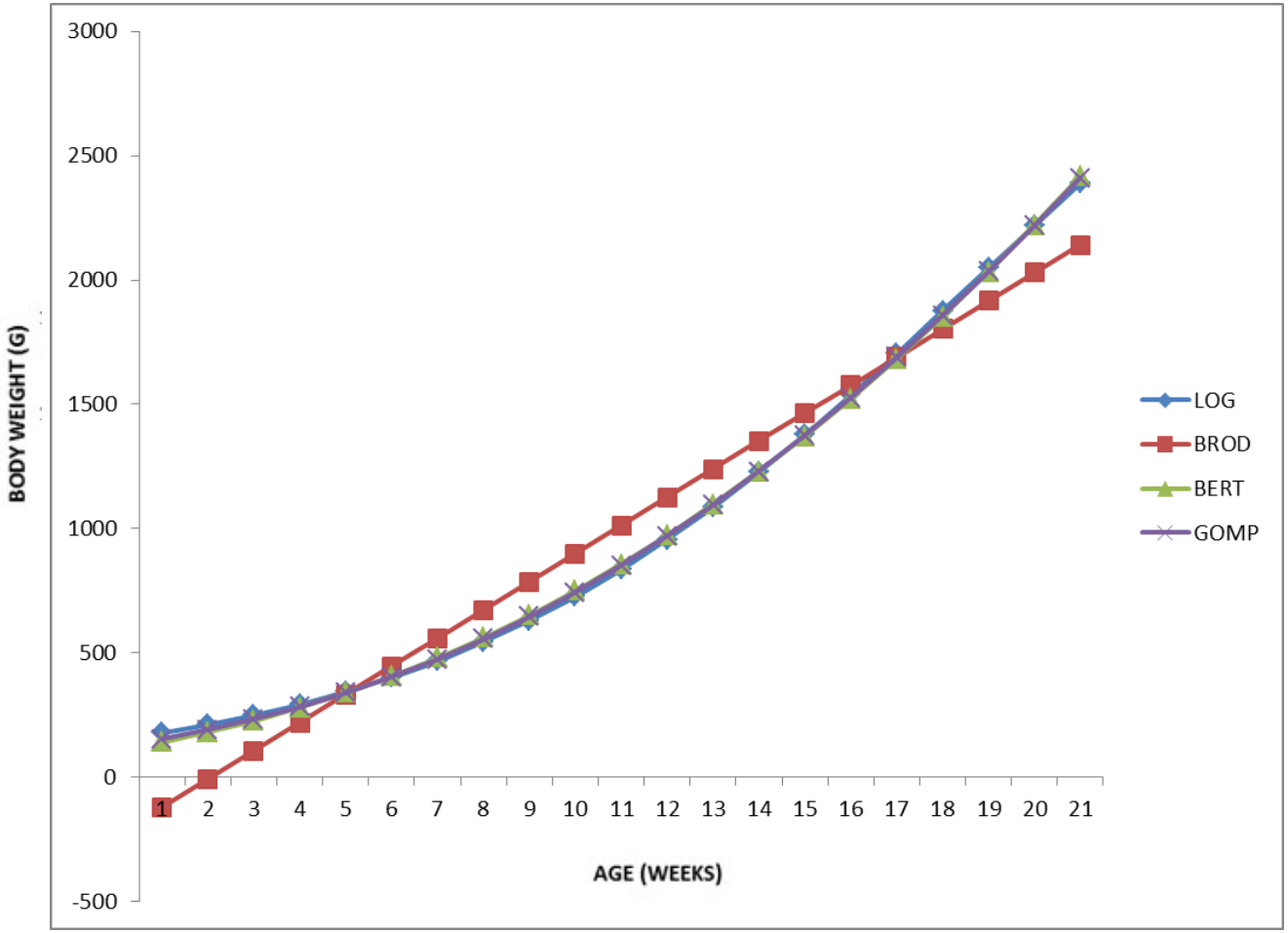

Figure 4.3: Growth curve describing weight-age relationship of black strain of indigenous turkey for AB genotype of Exon 3 at GH locus

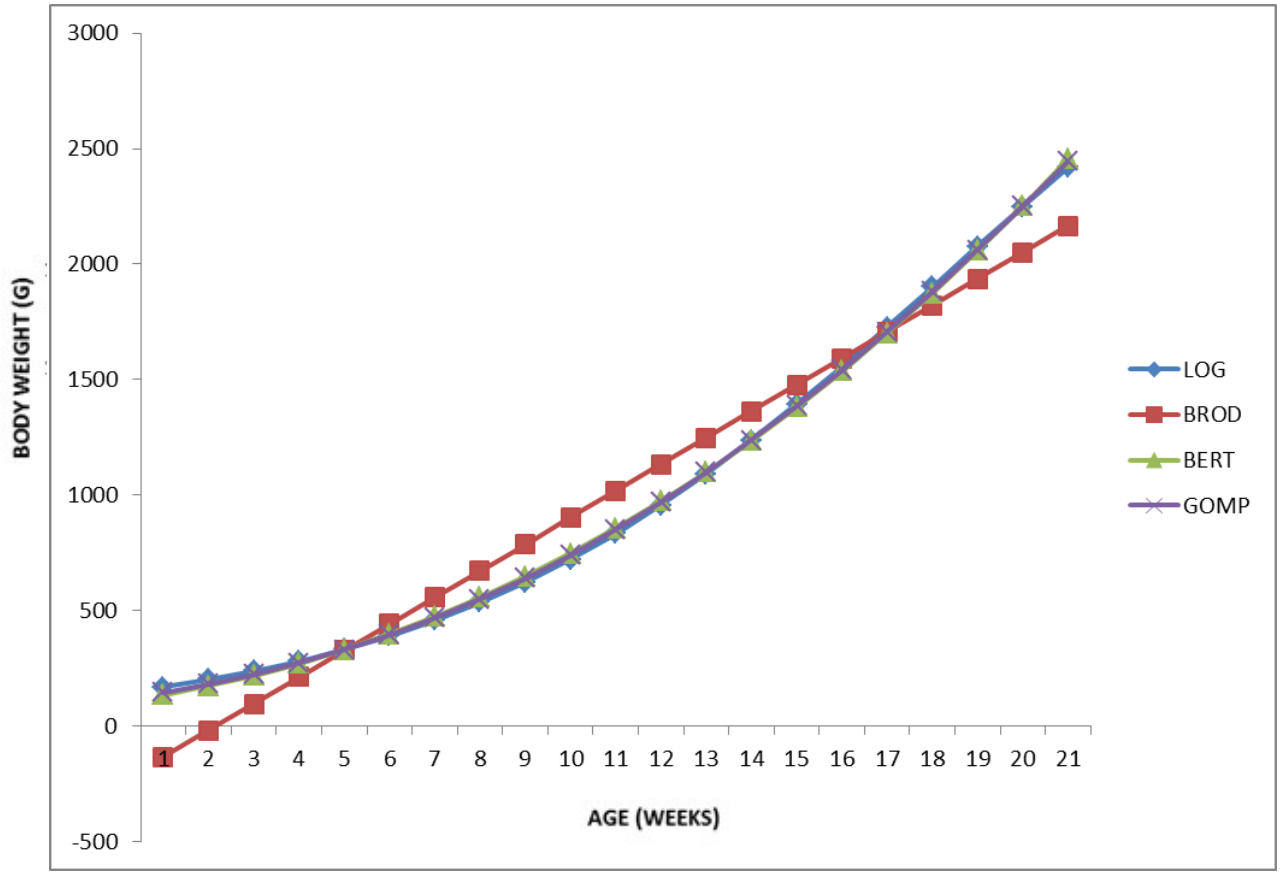

Figure 4.4: Growth curve describing weight-age relationship of black strain of indigenous turkey for BB genotype of Exon 3 at GH locus

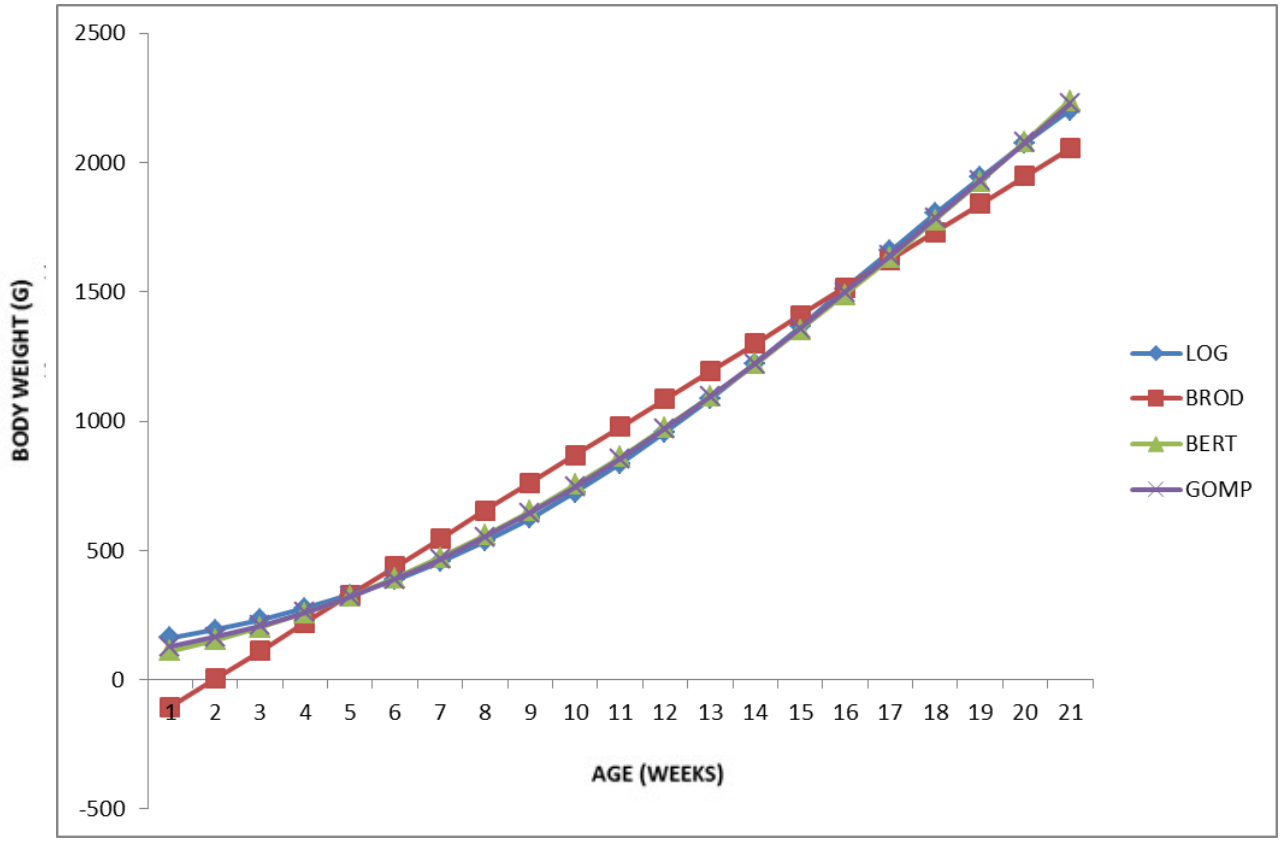

Figure 4.5: Growth curve describing weight-age relationship of spotted strain of indigenous turkey for AA genotype of Exon 3 at GH locus

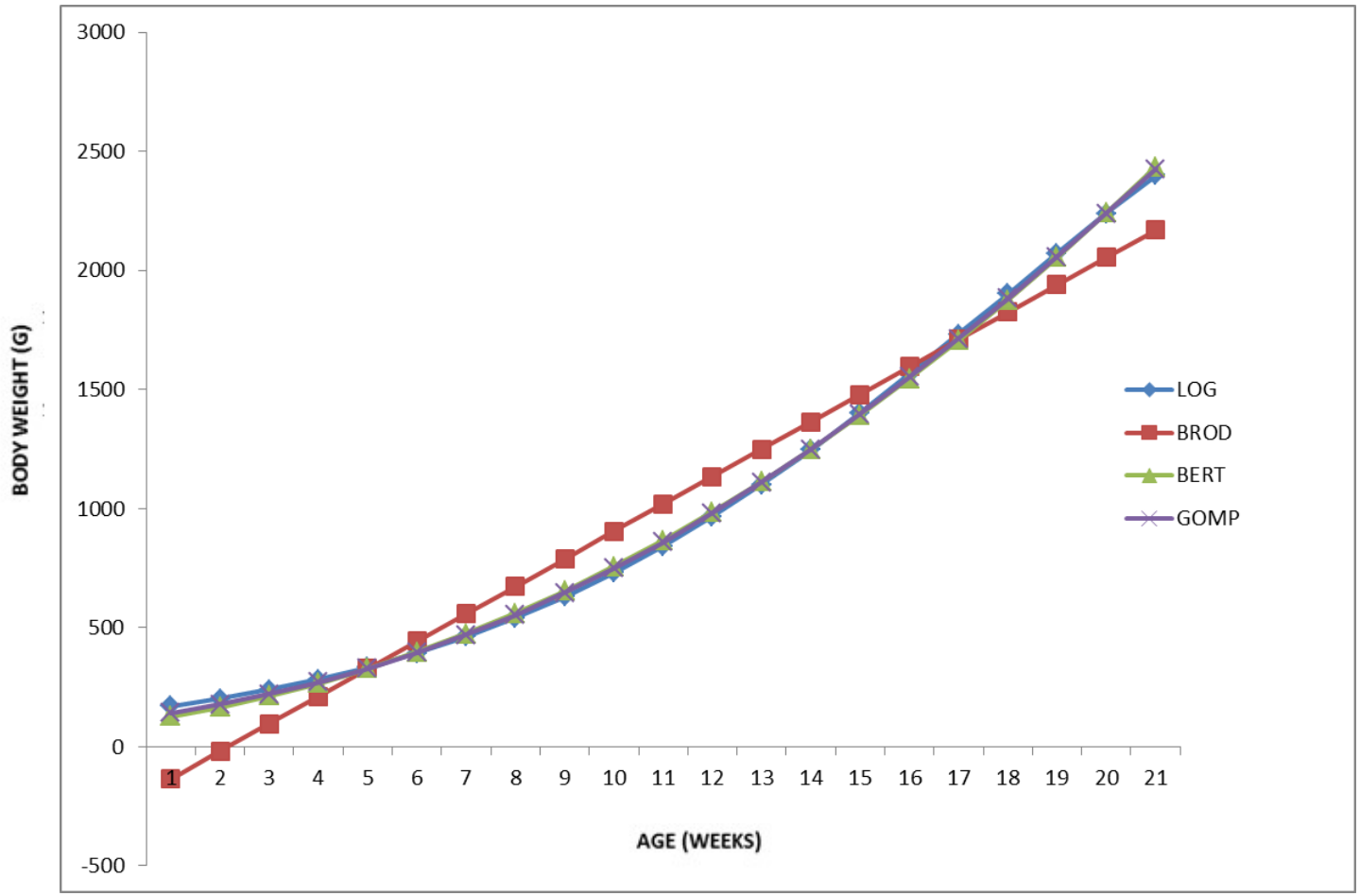

Figure 4.6: Growth curve describing weight-age relationship of spotted strain of indigenous turkey for AB genotype of Exon 3 at GH locus

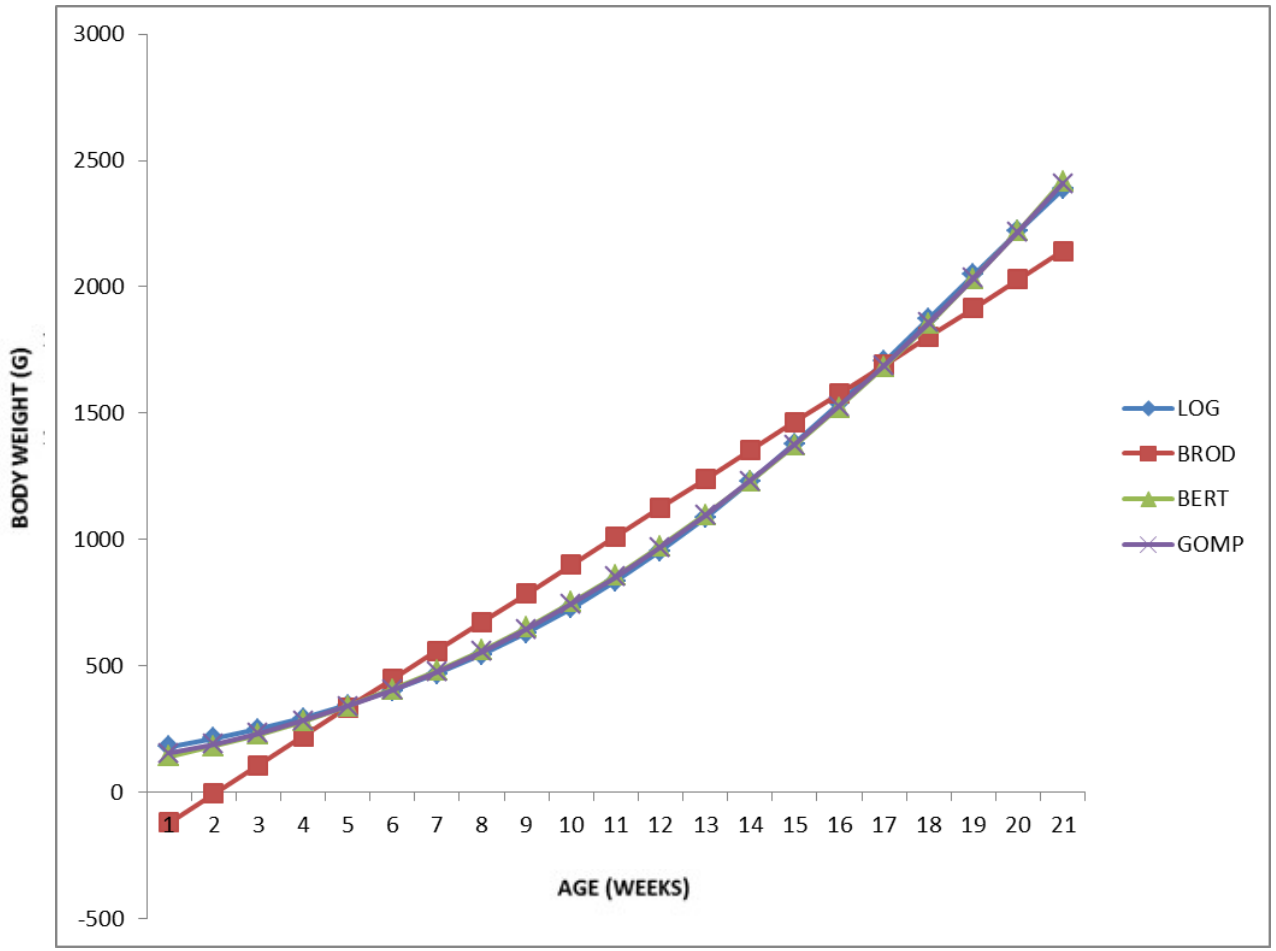

Figure 4.7: Growth curve describing weight-age relationship of spotted strain of indigenous turkey for BB genotype of Exon 3 at GH locus

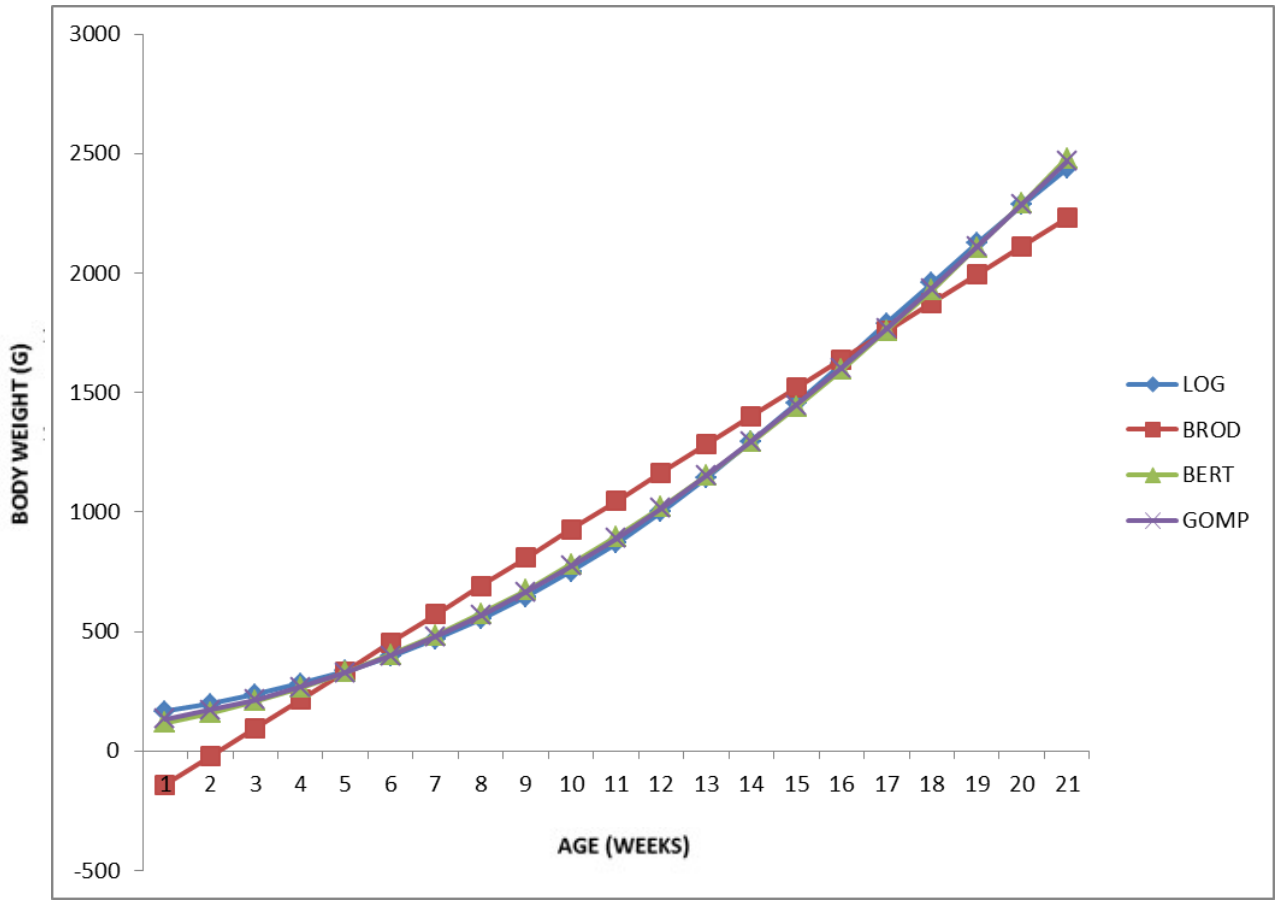

Figure 4.8: Growth curve describing weight-age relationship of white strain of indigenous turkey for AA genotype of Exon 3 at GH locus

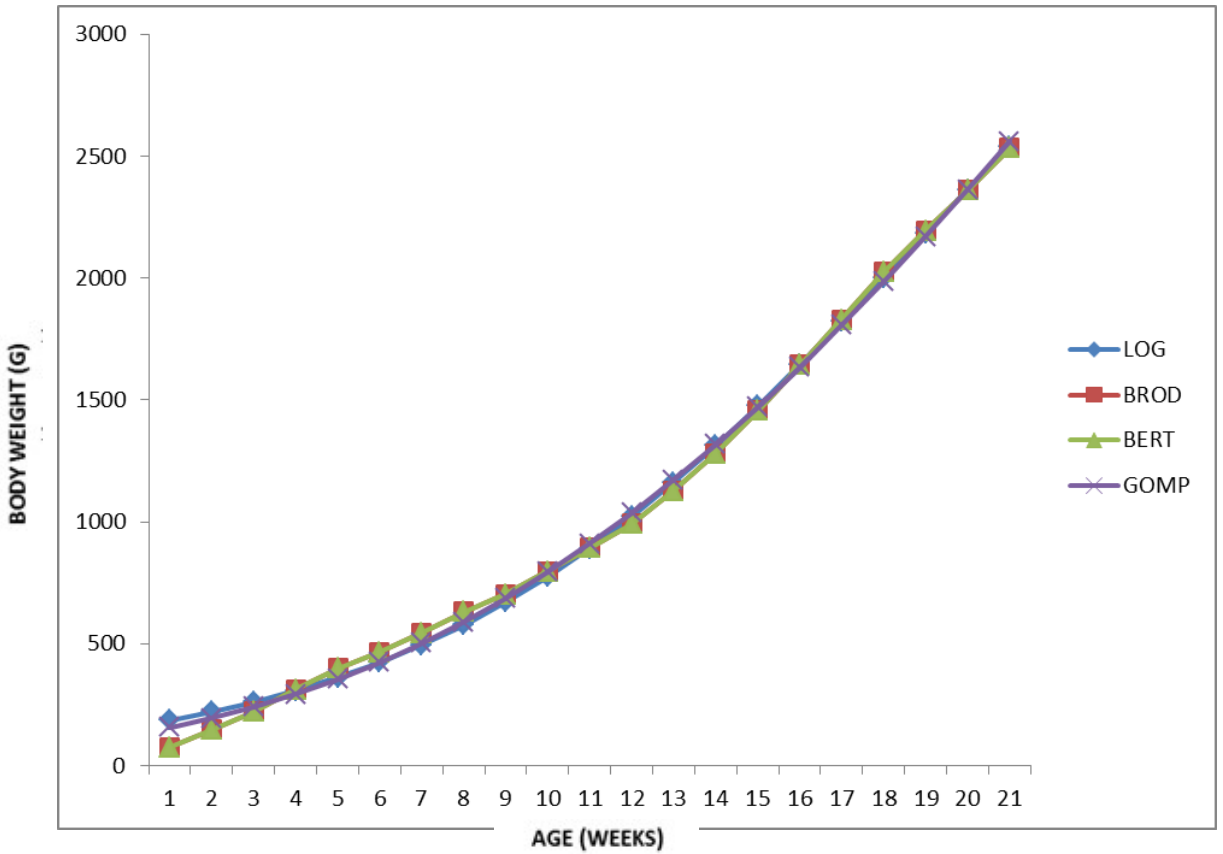

Figure 4.9: Growth curve describing weight-age relationship of white strain of indigenous turkey for AB genotype of Exon 3 at GH locus

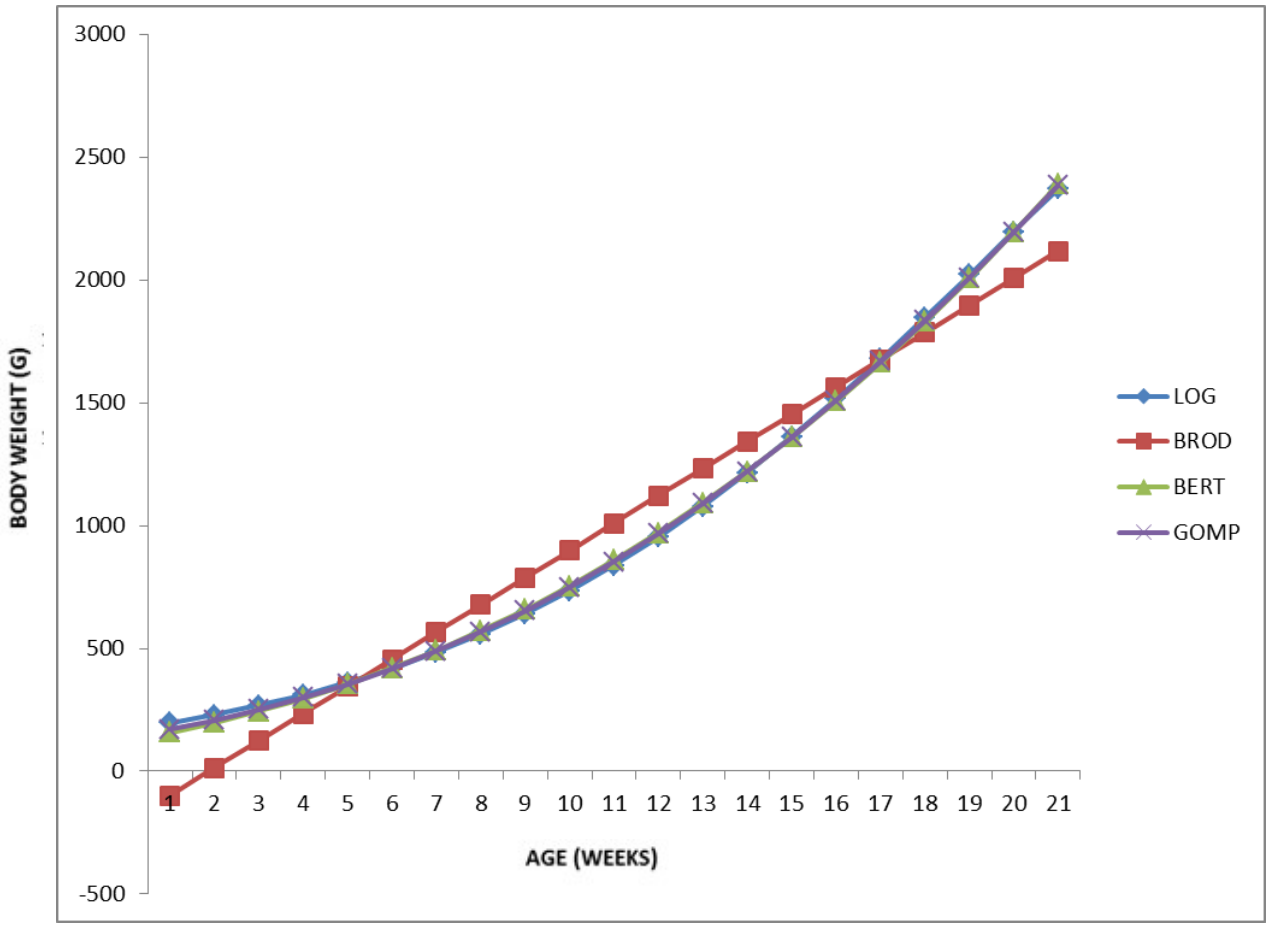

Figure 4.10: Growth curve describing weight-age relationship of white strain of indigenous turkey for BB genotype of Exon 3 at GH locus

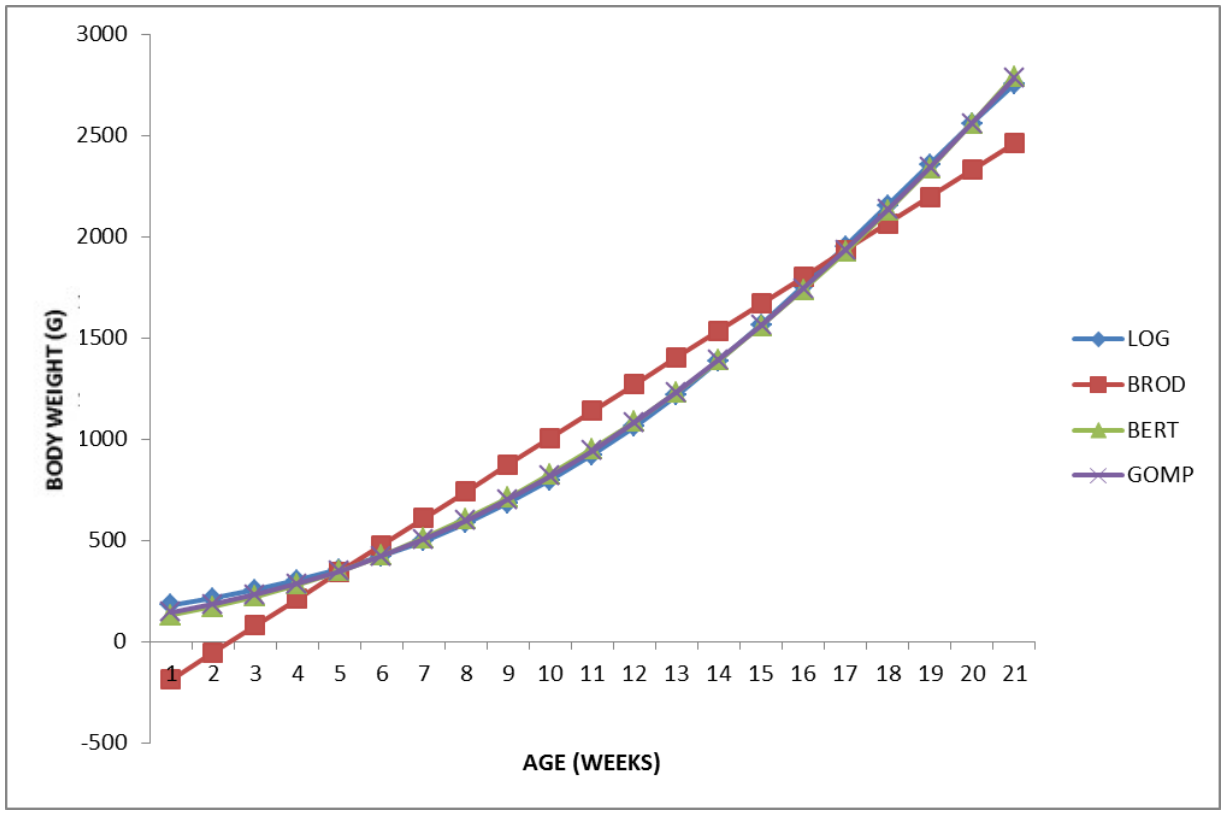

Figure 4.11: Growth curve describing weight-age relationship of black strain of indigenous turkey for AA genotype of 5' Flanking region at IGF2 locus

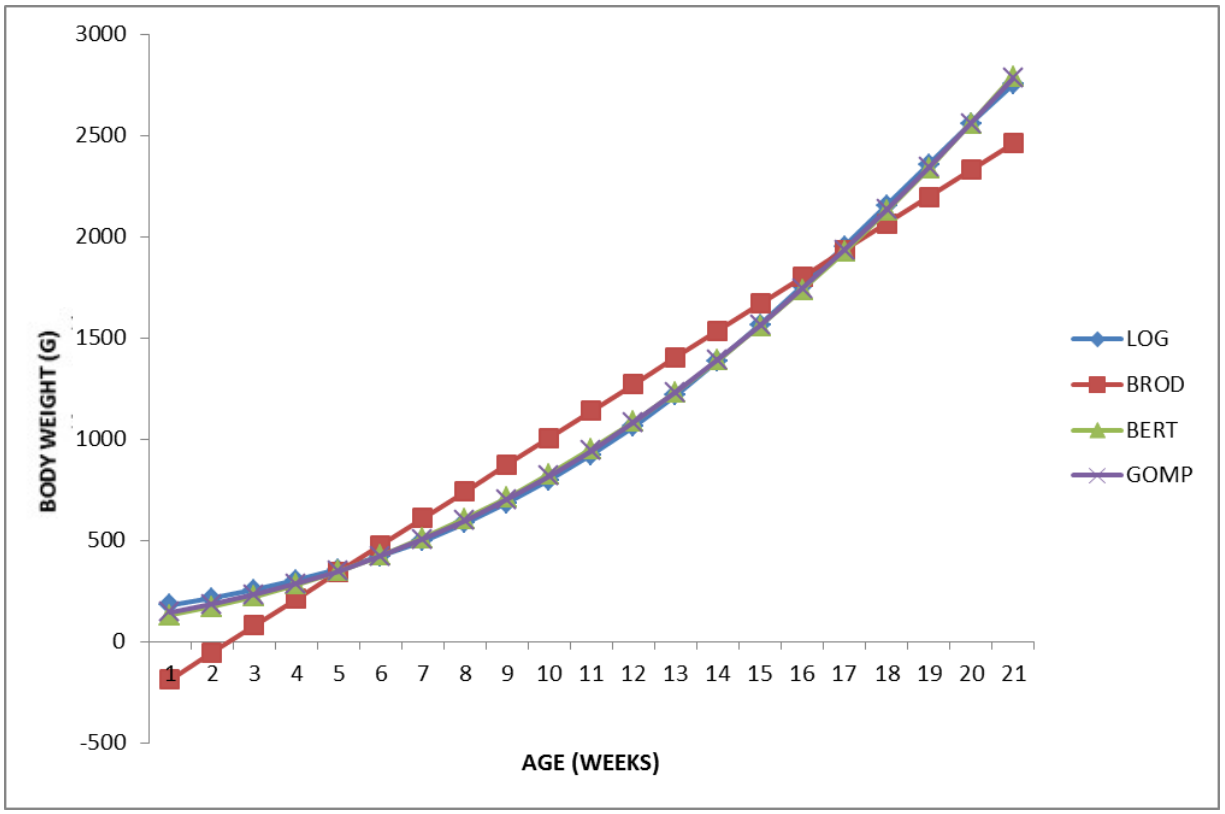

Figure 4.12: Growth curve describing weight-age relationship of black strain of indigenous turkey for AB genotype of 5' Flanking region at IGF2 locus

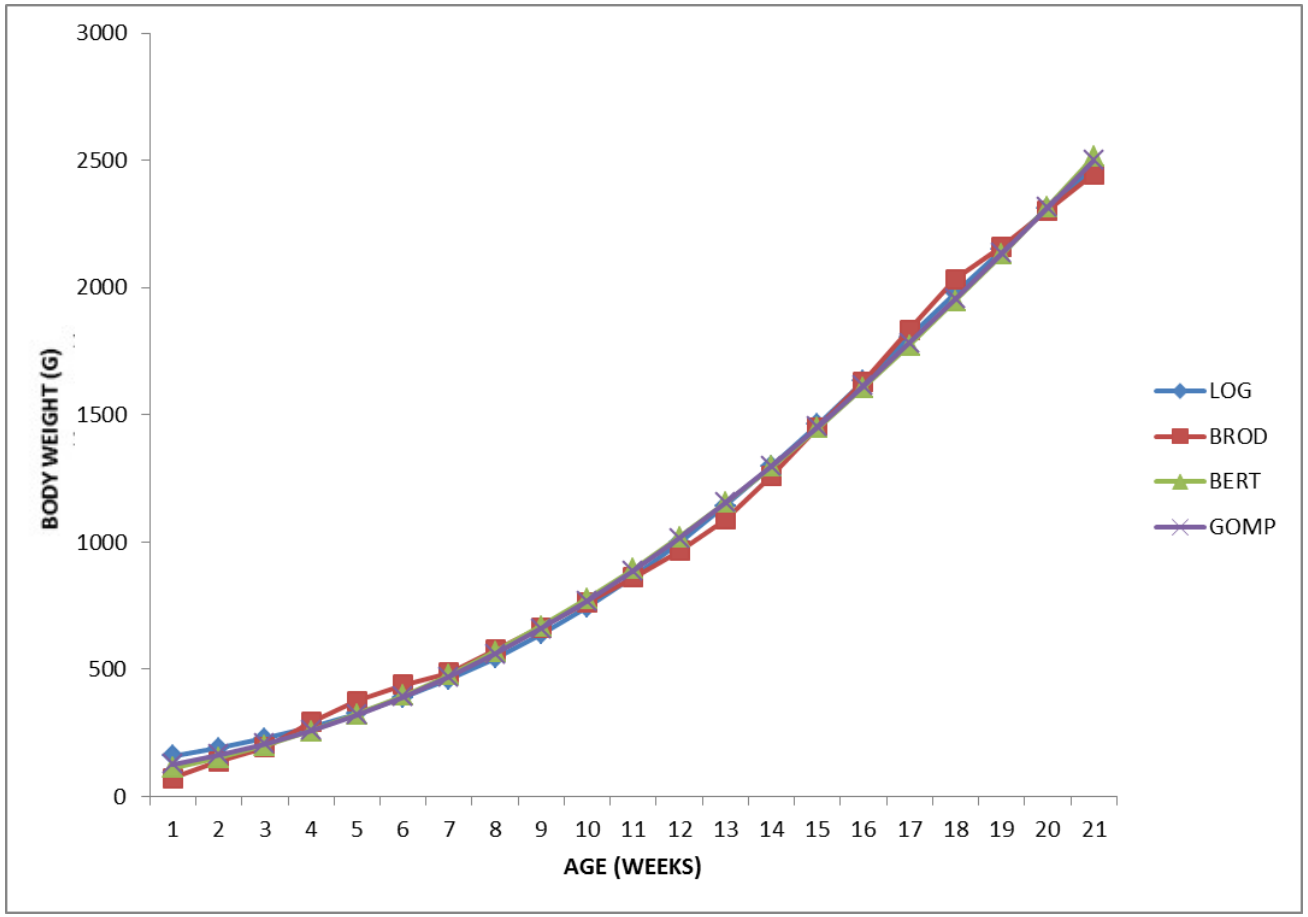

Figure 4.13: Growth curve describing weight-age relationship of black strain of indigenous turkey for BB genotype of 5' Flanking region at IGF2 locus

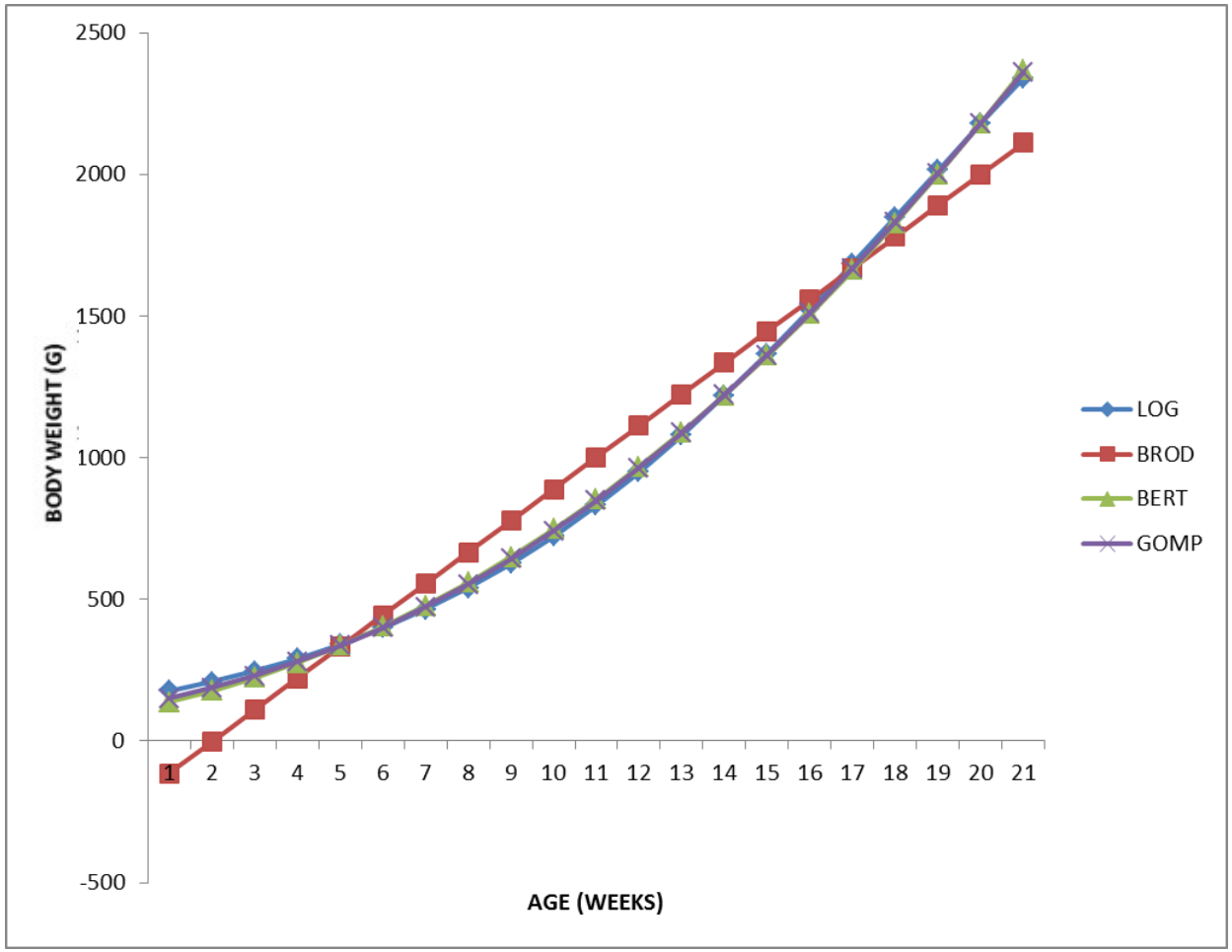

Figure 4.14: Growth curve describing weight-age relationship of spotted strain of indigenous turkey for AA genotype of 5' Flanking region at IGF2 locus

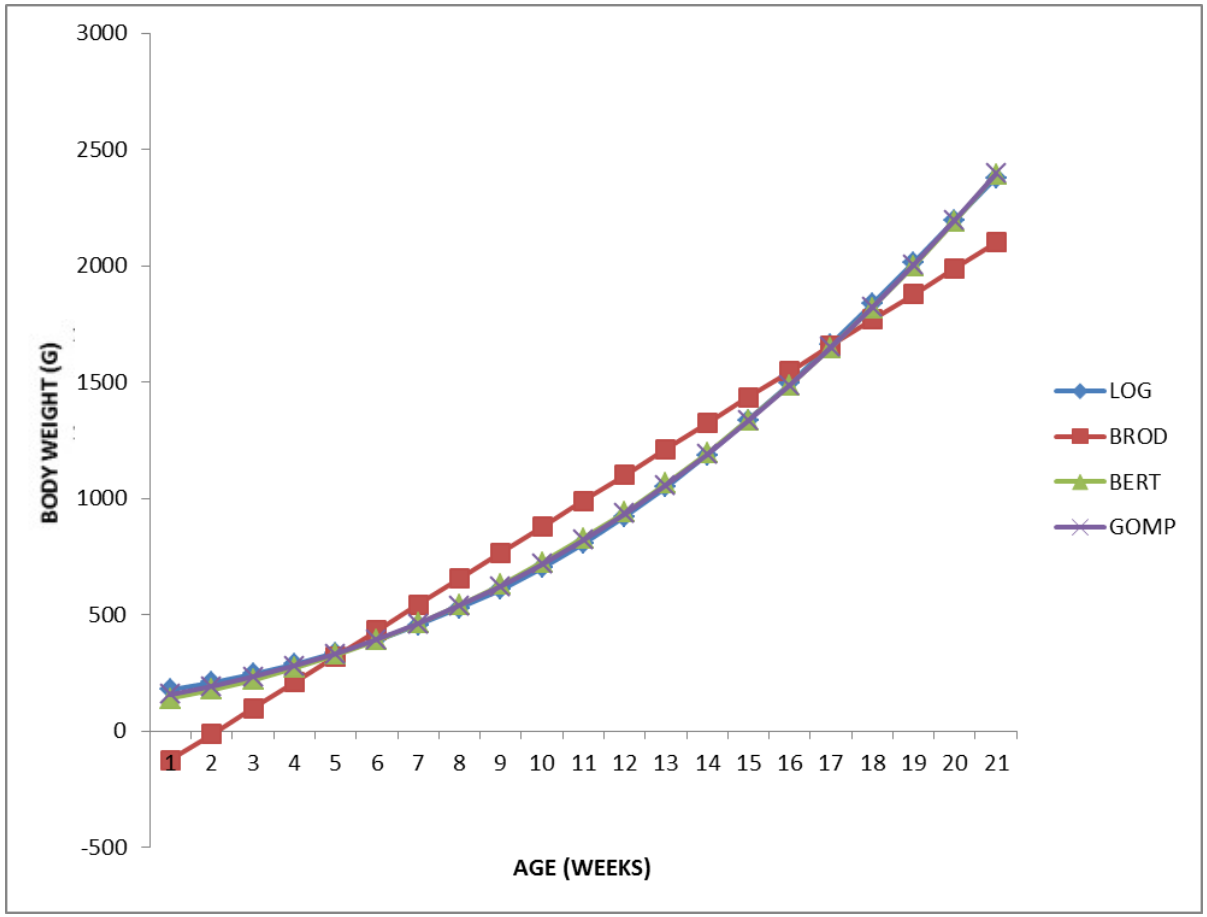

Figure 4.15: Growth curve describing weight-age relationship of spotted strain of indigenous turkey for AB genotype of 5' Flanking region at IGF2 locus

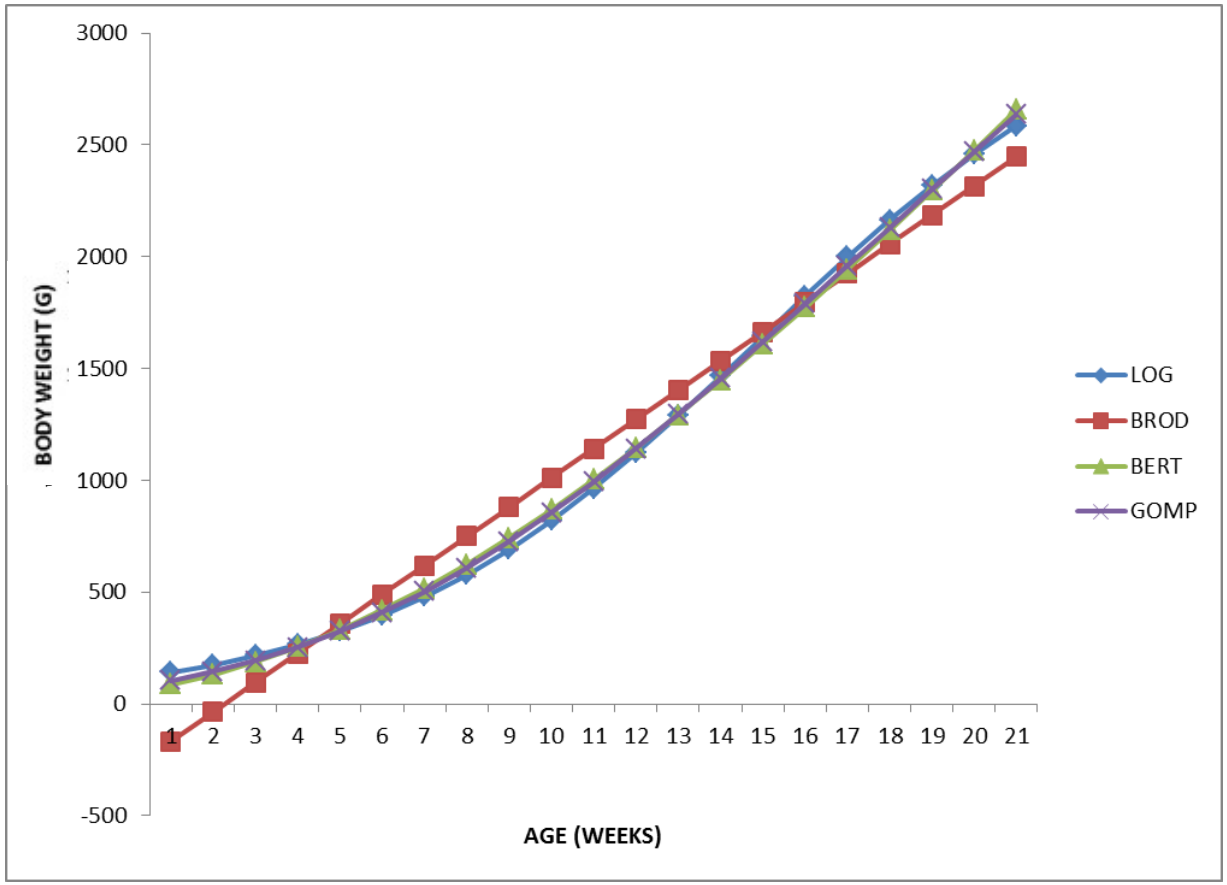

Figure 4.16: Growth curve describing weight-age relationship of spotted strain of indigenous turkey for BB genotype of 5' Flanking region at IGF2 locus

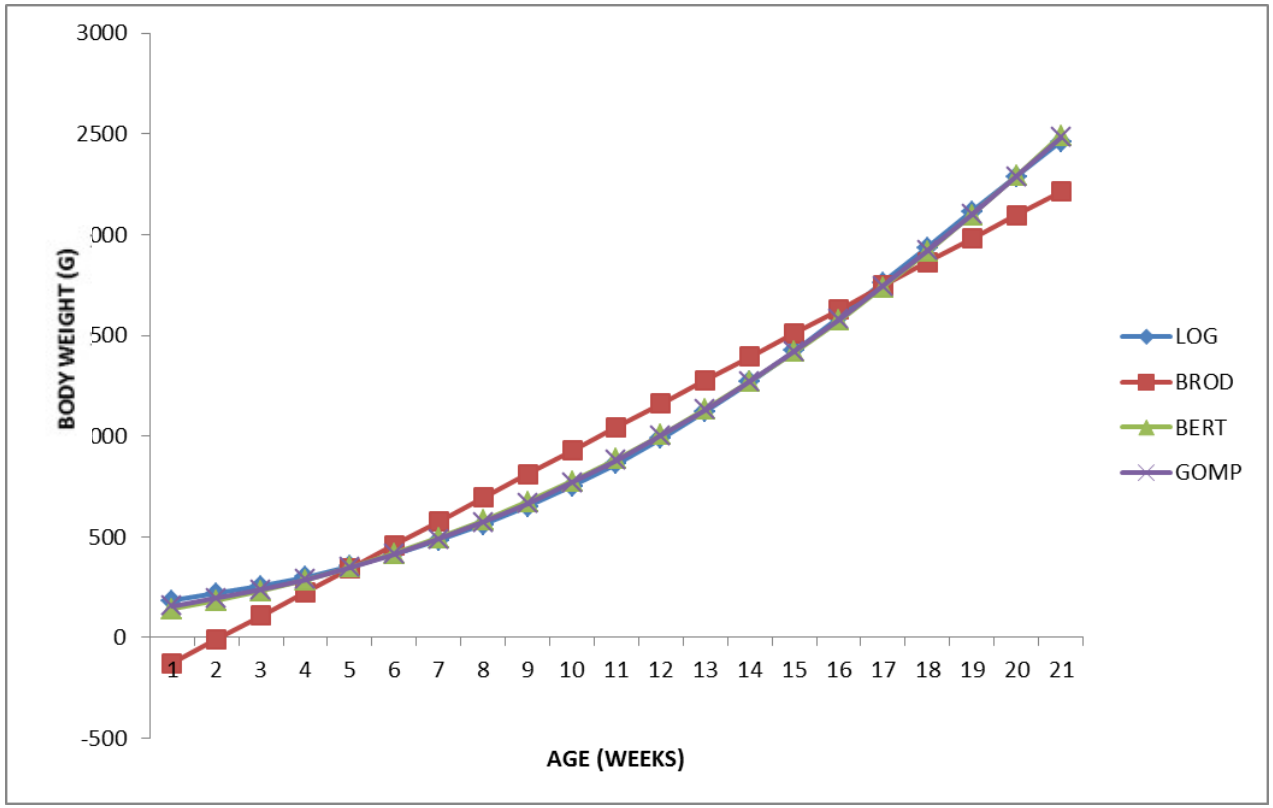

Figure 4.17: Growth curve describing weight-age relationship of white strain of indigenous turkey for AA genotype of 5' Flanking region at IGF2 locus

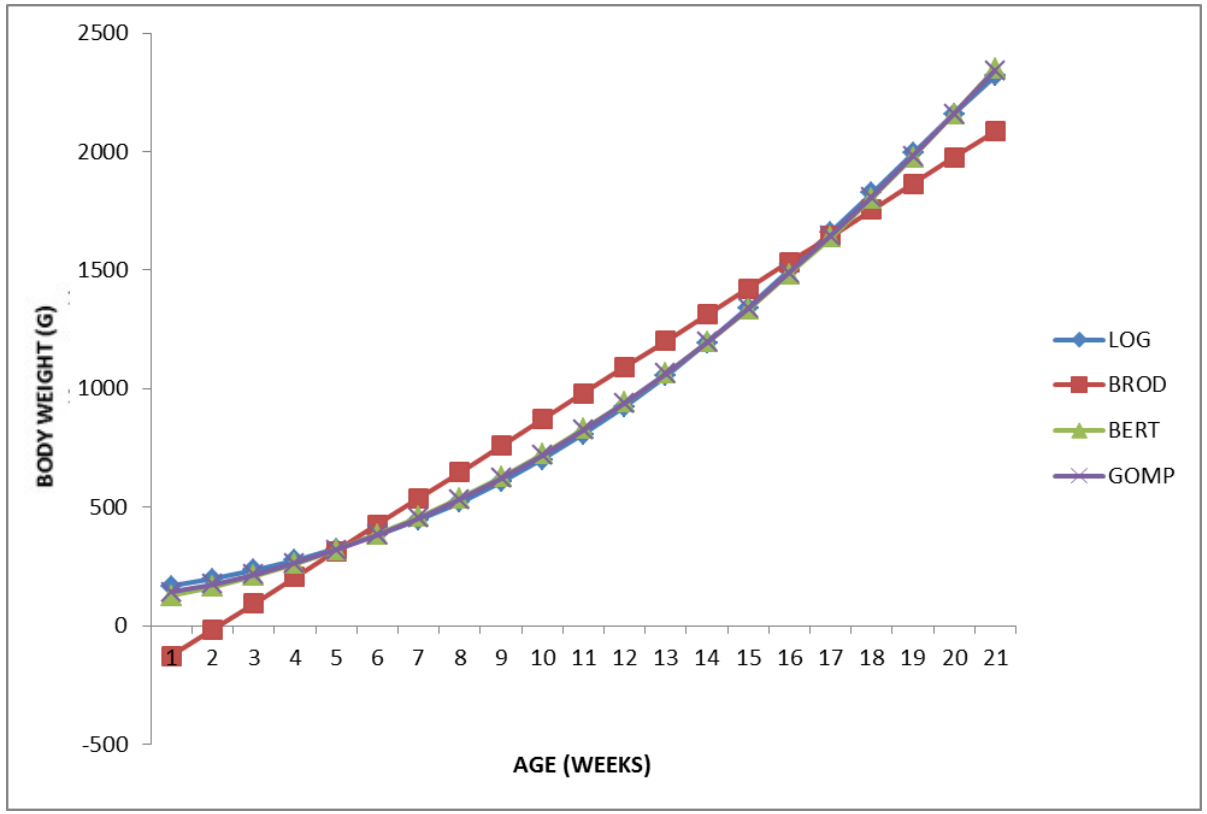

Figure 4.18: Growth curve describing weight-age relationship of white strain of indigenous turkey for AB genotype of 5' Flanking region at IGF2 locus

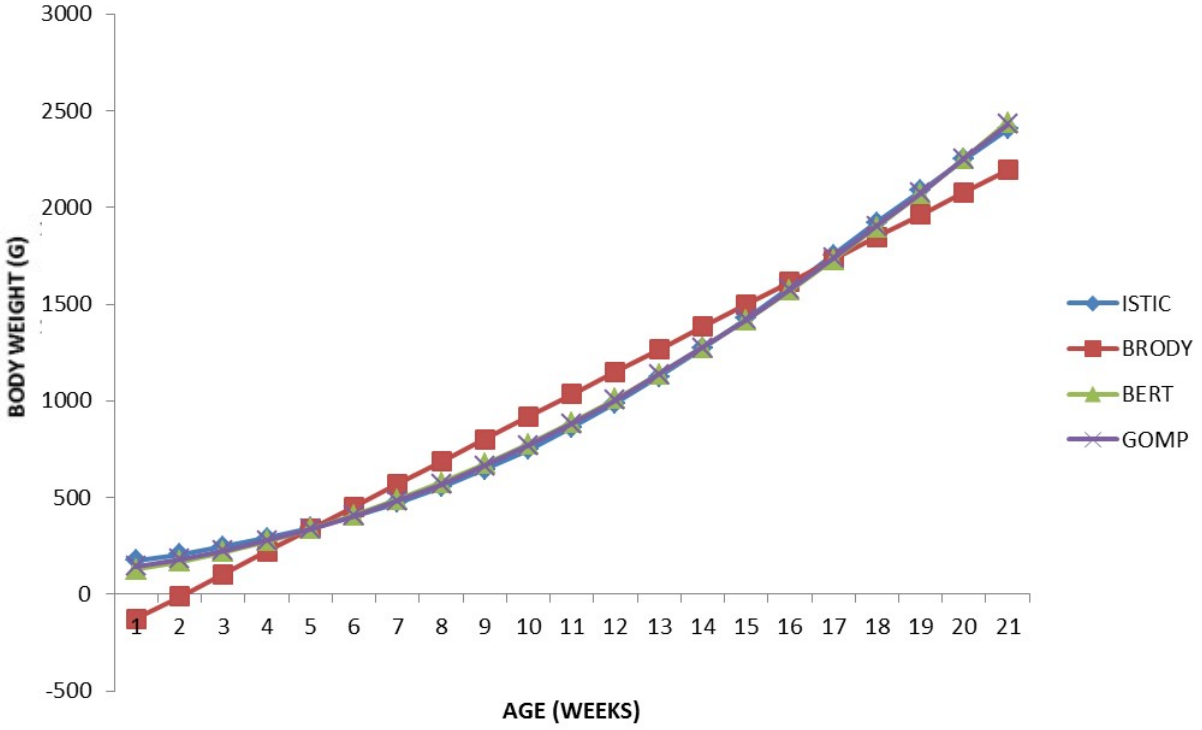

Figure 4.19: Growth curve describing weight-age relationship of white strain of indigenous turkey for BB genotype of 5' Flanking region at IGF2 locus

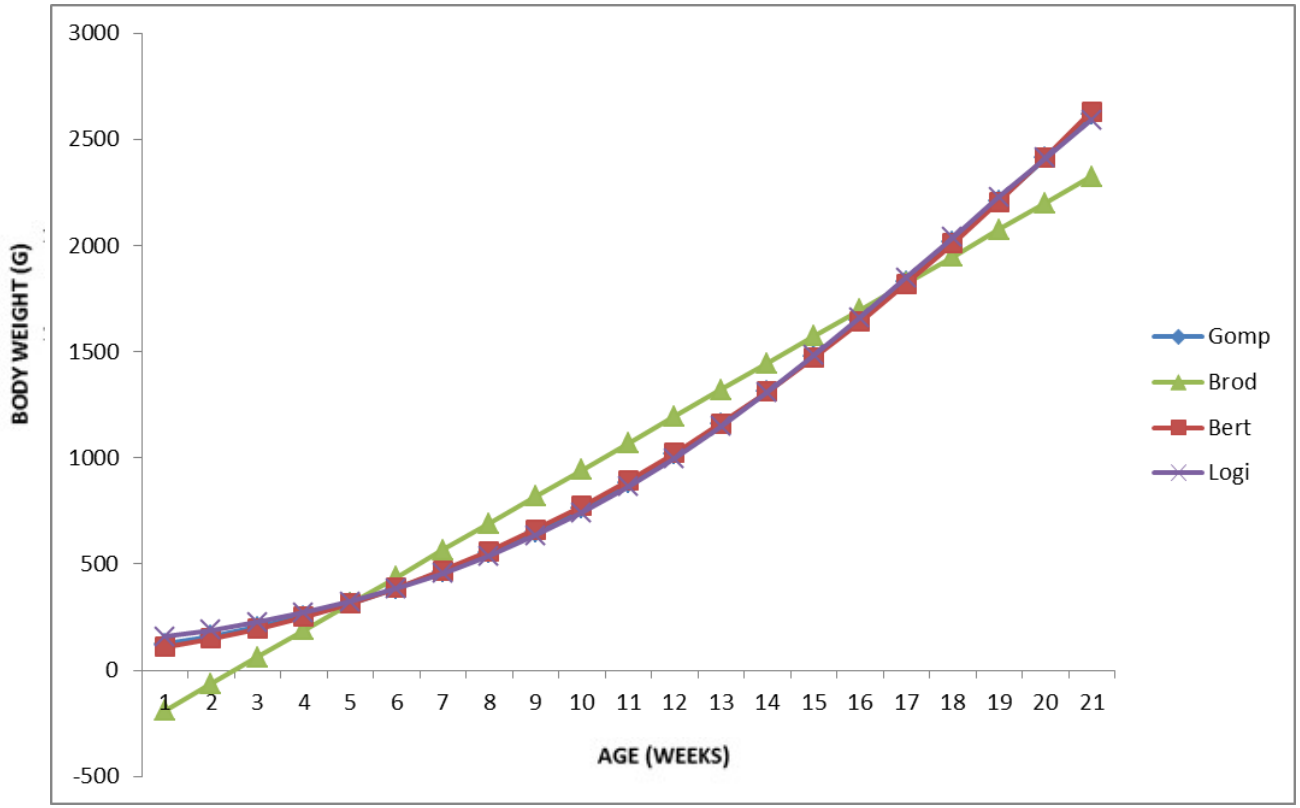

Figure 4.20: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of black strain indigenous turkey for AA genotype of Exon 2 at myostatin locus

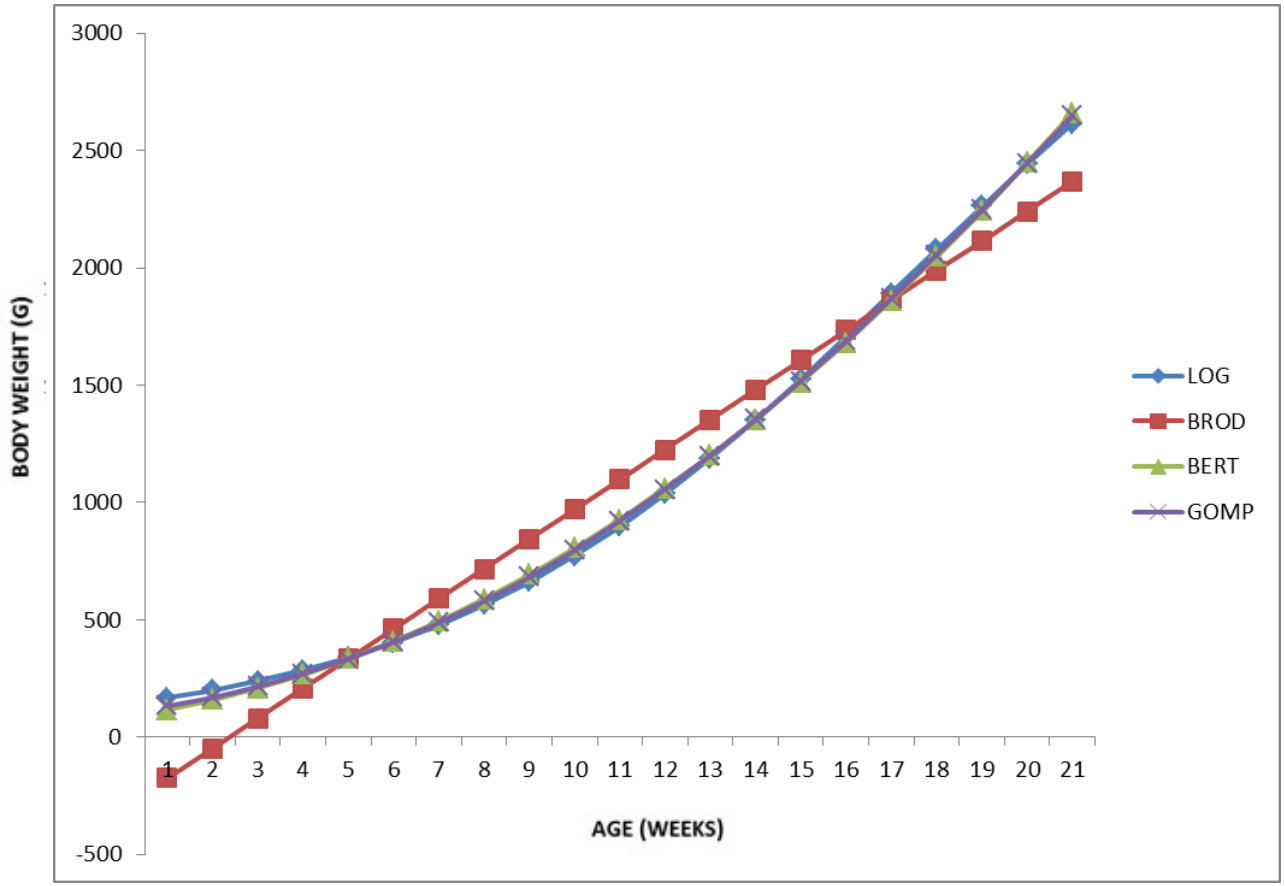

Figure 4.21: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of black strain indigenous turkey for AB genotype of Exon 2 at myostatin locus

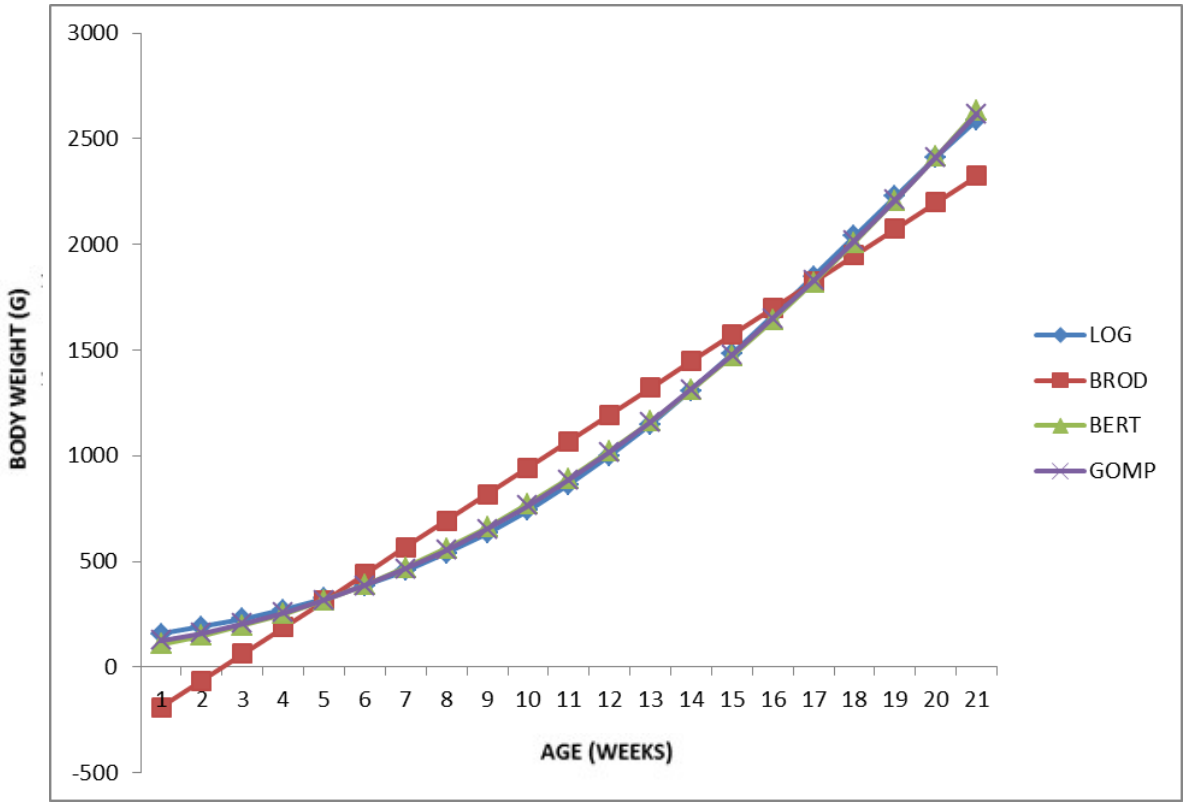

Figure 4.23: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of black strain indigenous turkey for BB genotype of Exon 2 at myostatin locus

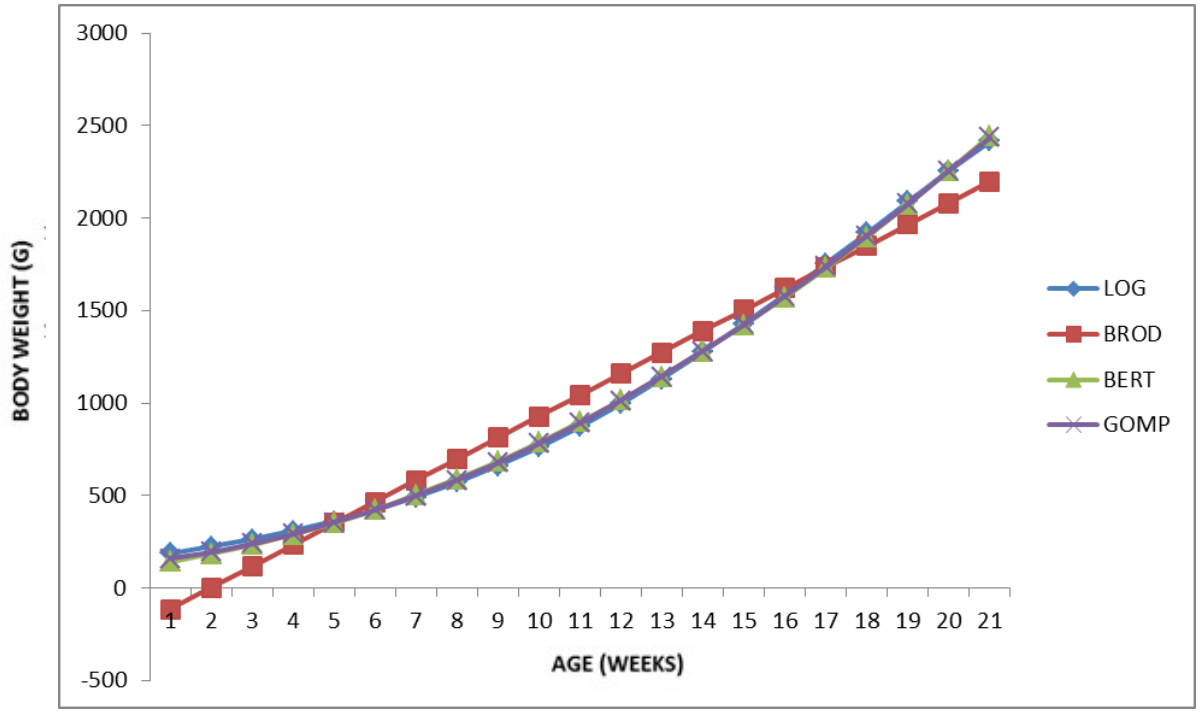

Figure 4.24: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of spotted strain indigenous turkey for AA genotype of Exon 2 at myostatin locus

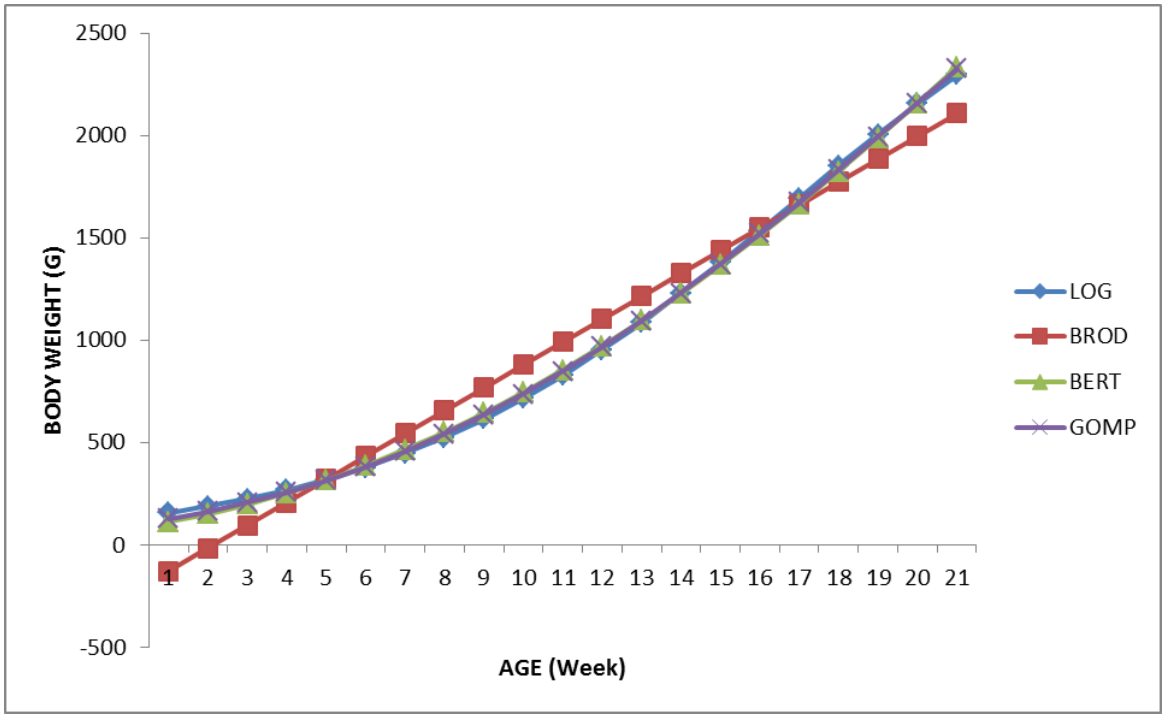

Figure 4.25: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of spotted strain indigenous turkey for AB genotype of Exon 2 at myostatin locus

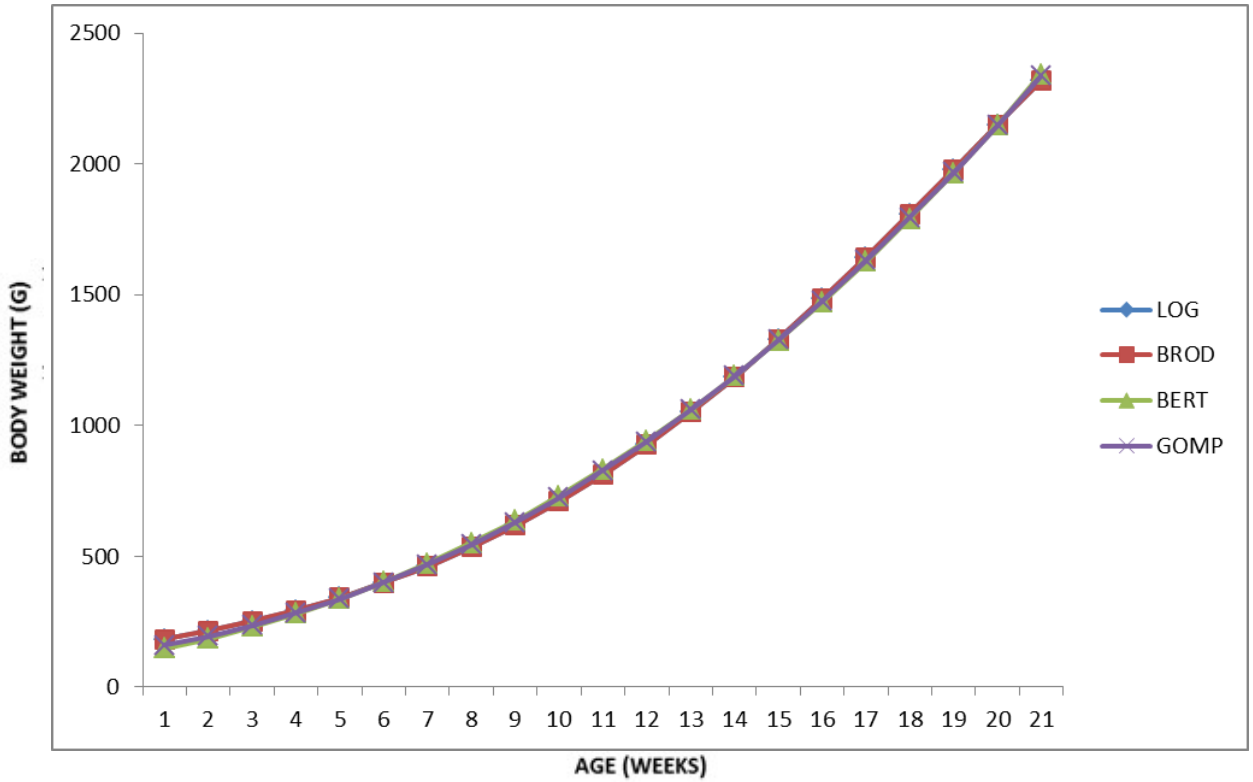

Figure 4.26: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of spotted strain indigenous turkey for BB genotype of Exon 2 at myostatin locus

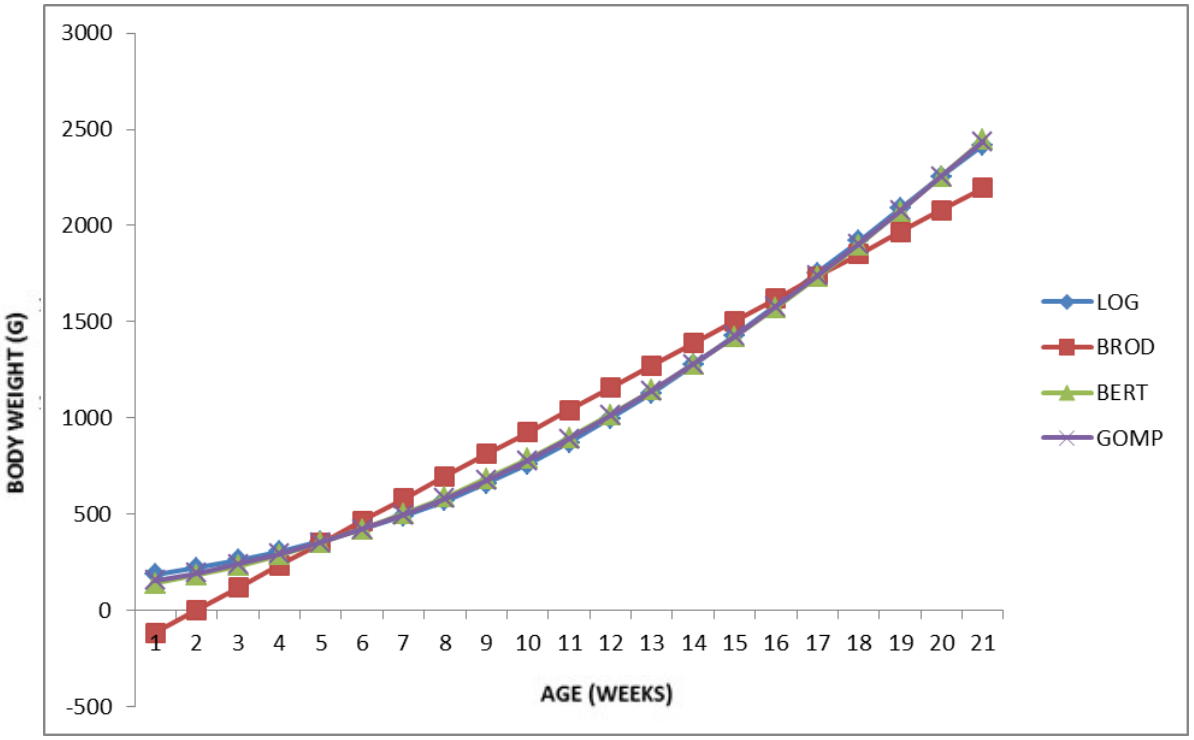

Figure 4.27: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of white strain indigenous turkey for AA genotype of Exon 2 at mystatin locus

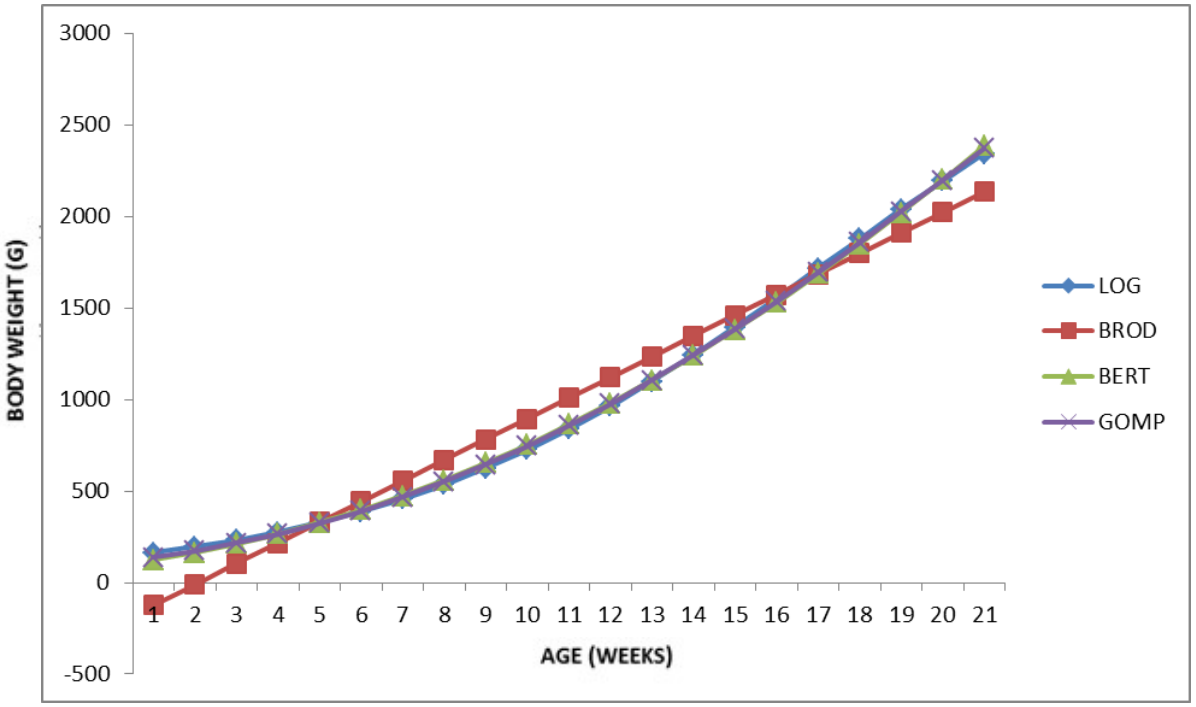

Figure 4.28: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of white strain indigenous turkey for AB genotype of Exon 2 at myostatin locus

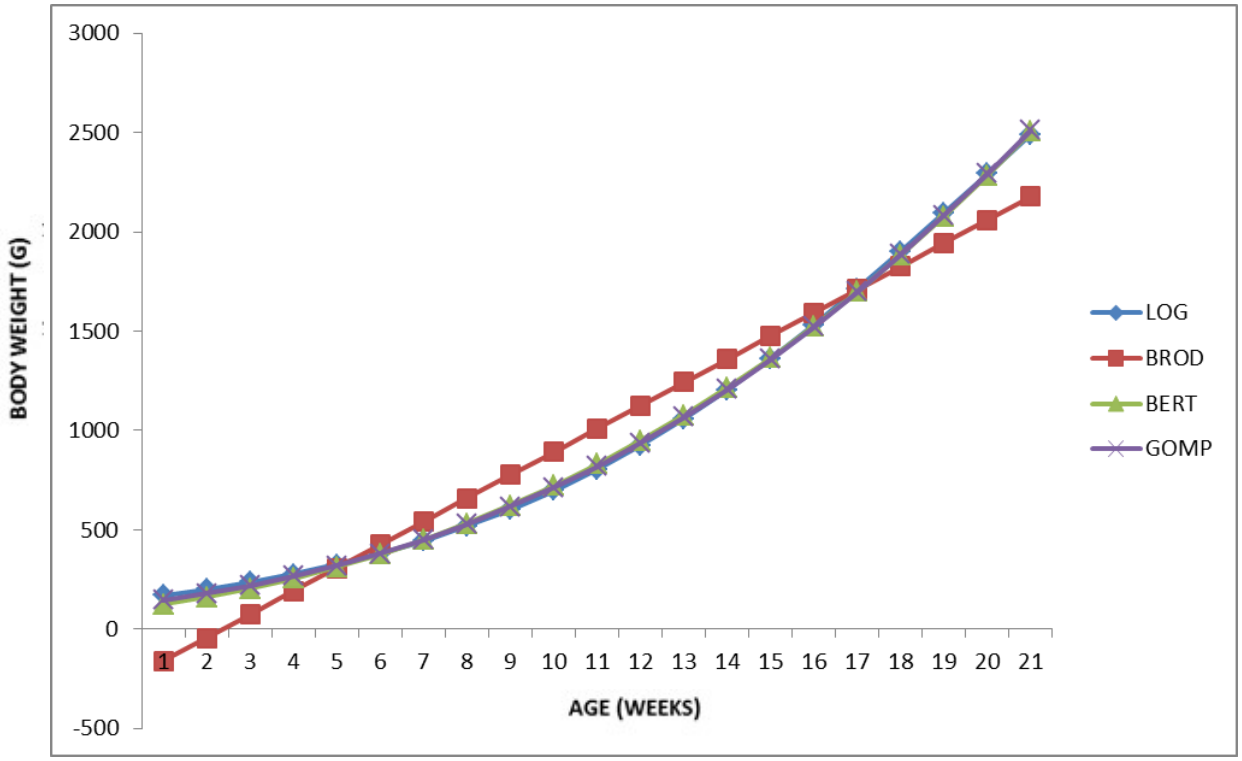

Figure 4.29: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of white strain indigenous turkey for BB genotype of Exon 2 at myostatin locus

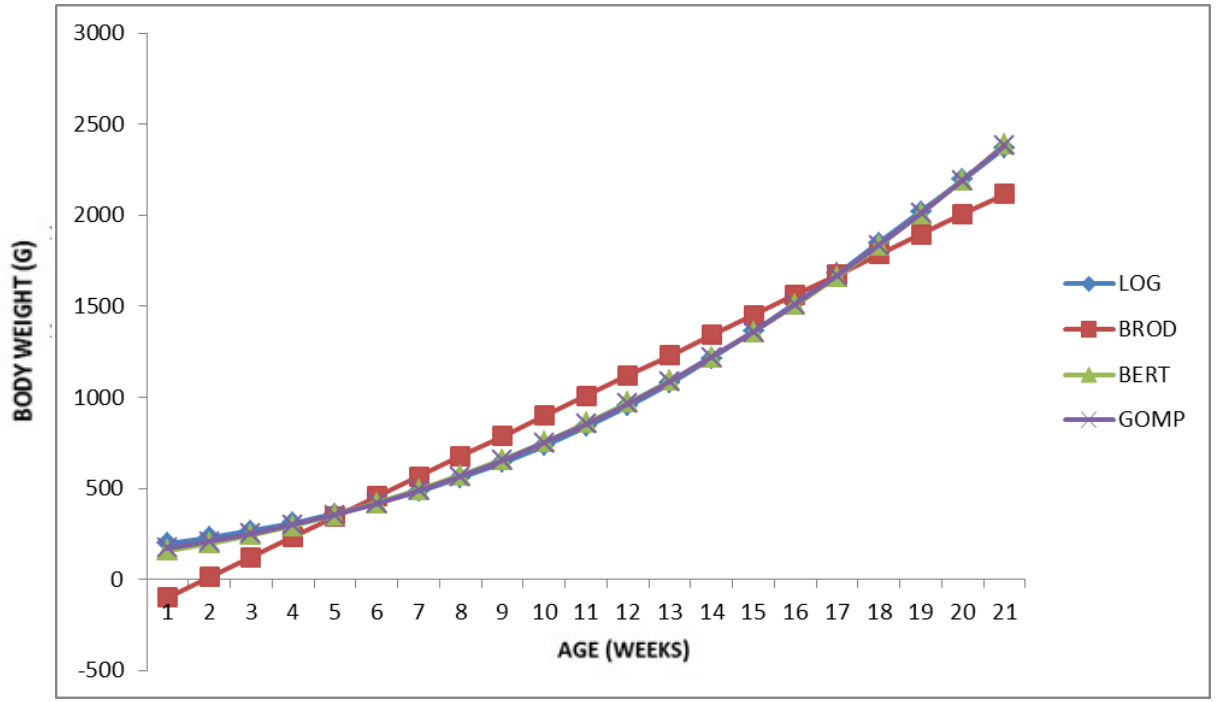

Figure 4.30: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of black strain indigenous turkey for AA genotype of Exon 2 at IGF1 locus

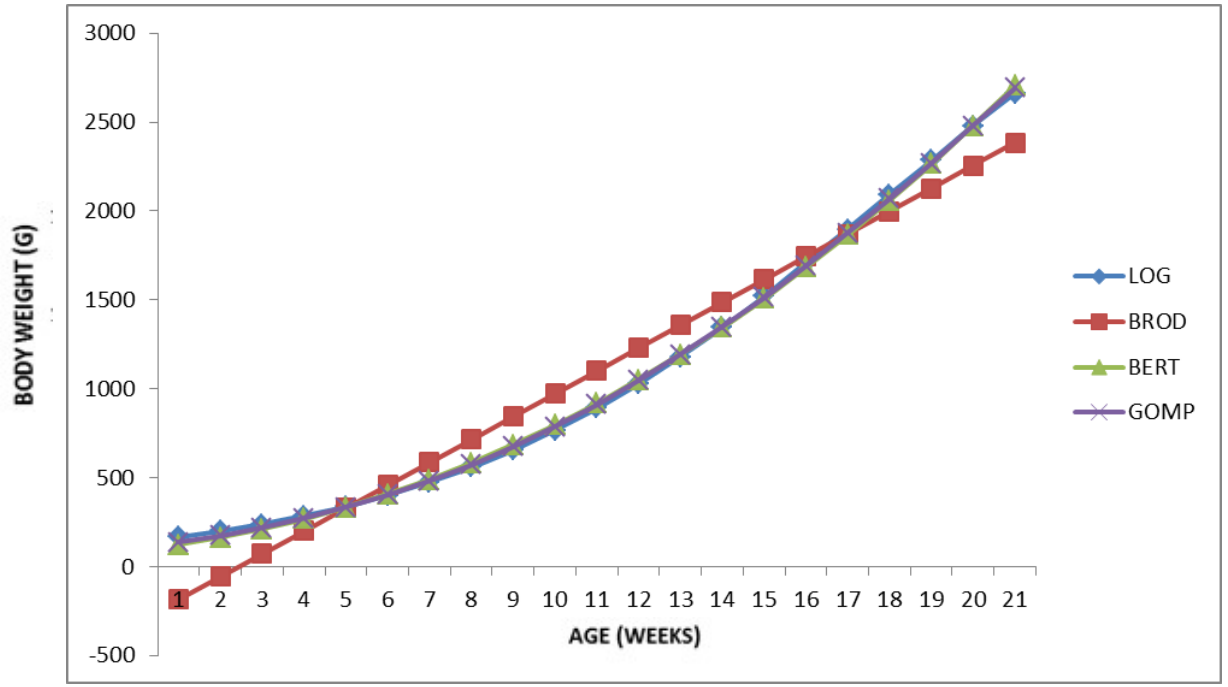

Figure 4.31: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of black strain indigenous turkey for AB genotype of Exon 2 at IGF1 locus

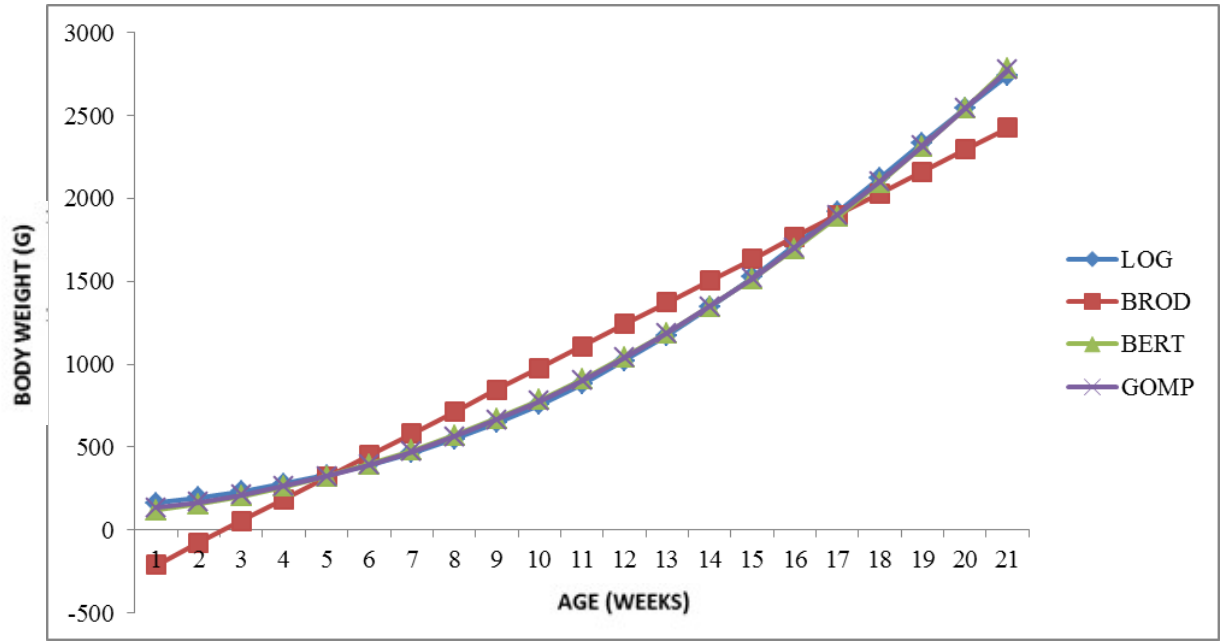

Figure 4.32: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of black strain indigenous turkey for BB genotype of Exon 2 at IGF1 locus

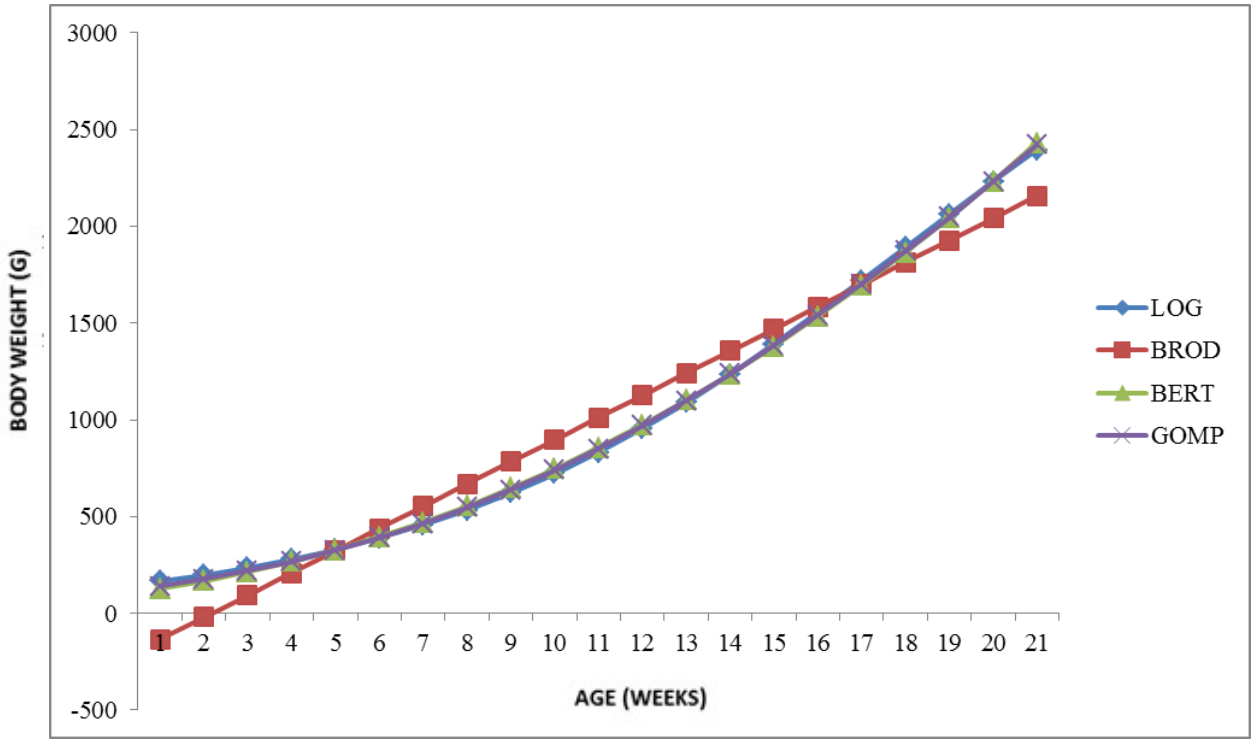

Figure 4.33: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of spotted strain indigenous turkey for AA genotype of Exon 2 at IGF1 locus

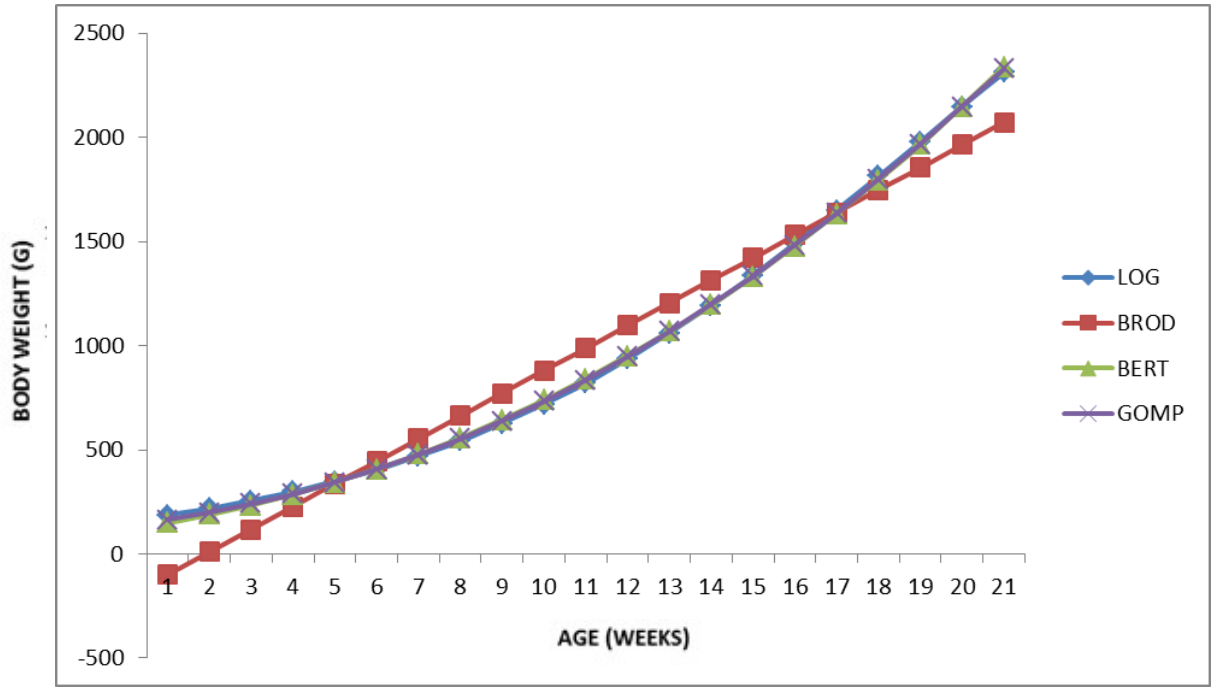

Figure 4.34: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of spotted strain indigenous turkey for AB genotype of Exon 2 at IGF1 locus

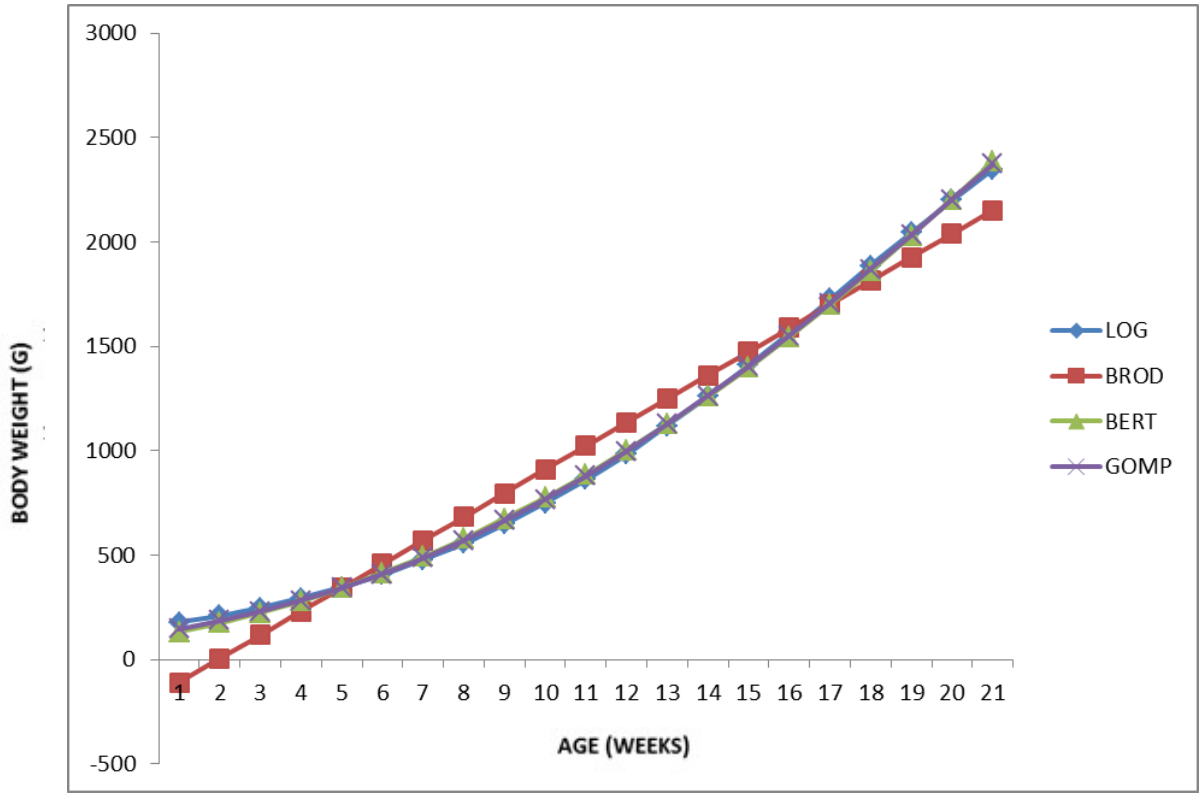

Figure 4.35: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of spotted strain indigenous turkey for BB genotype of Exon 2 at IGF1 locus

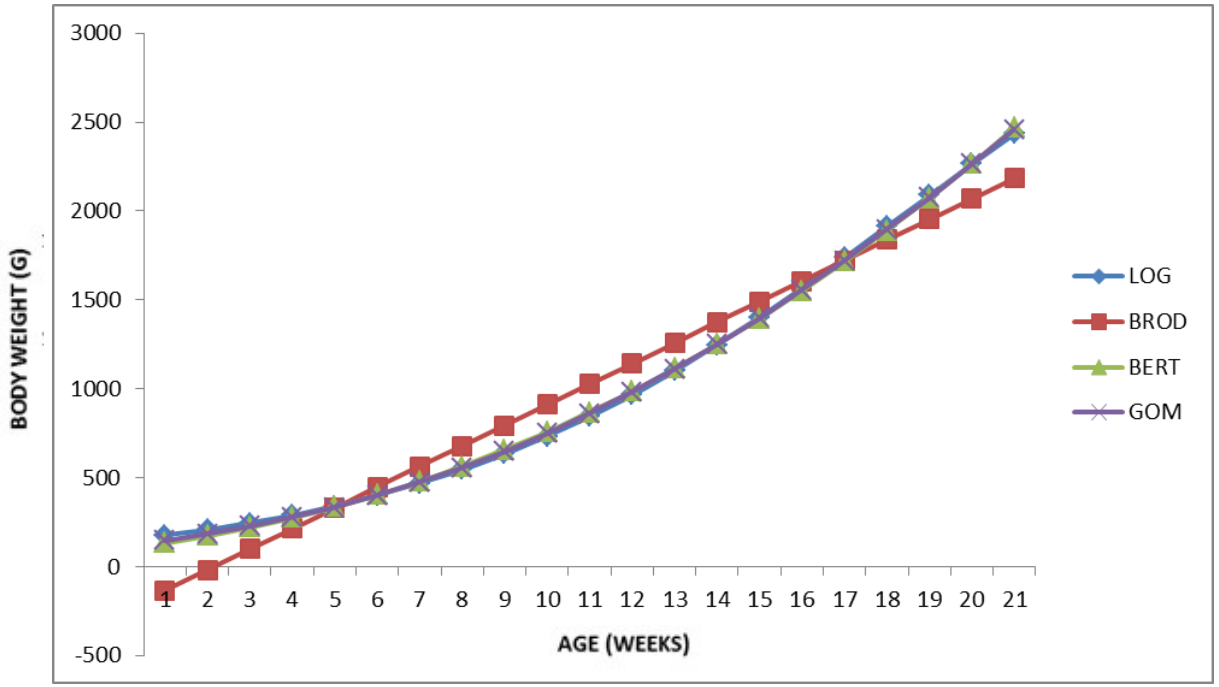

Figure 4.36: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of white strain indigenous turkey for AA genotype of Exon 2 at IGF1 locus

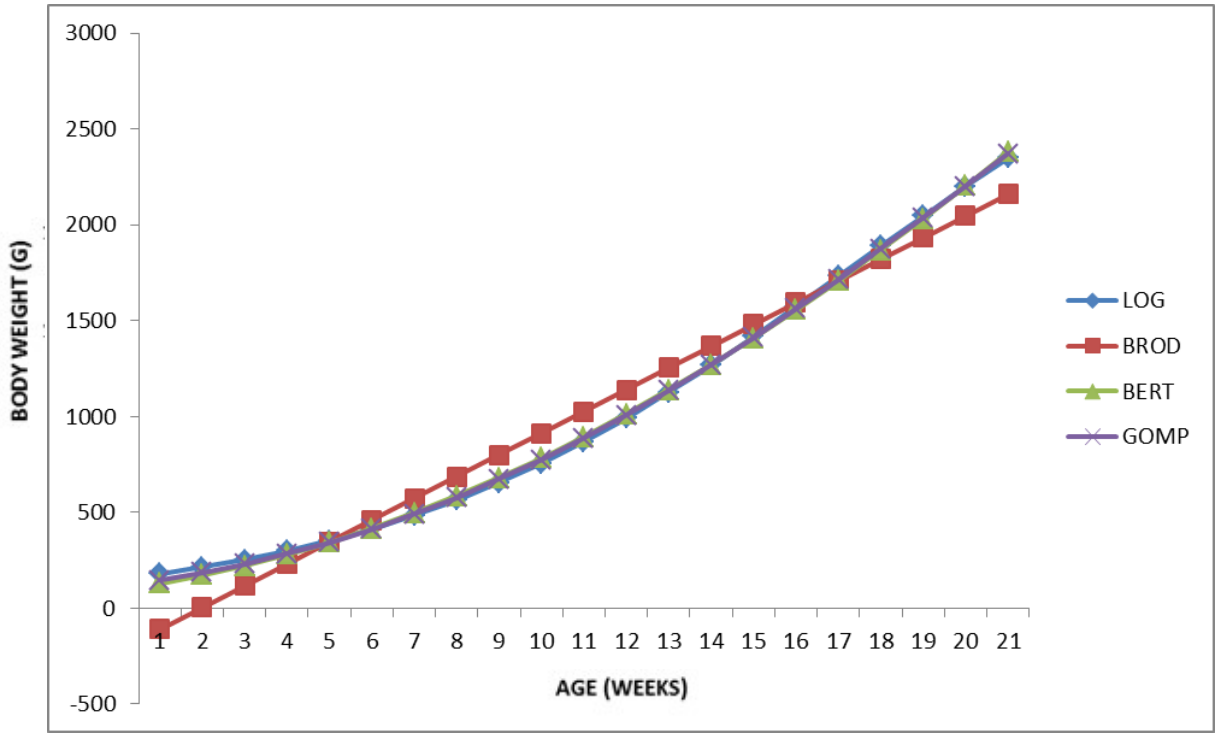

Figure 4.37: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of white strain indigenous turkey for AB genotype of Exon 2 at IGF1 locus

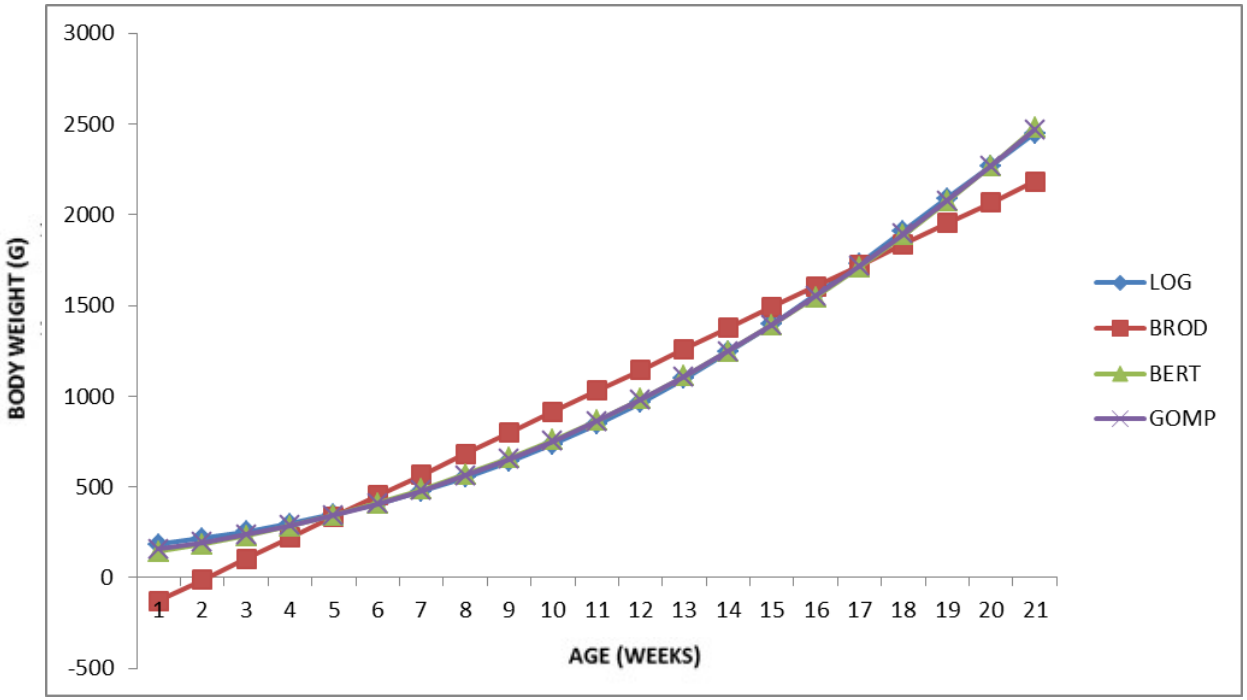

Figure 4.38: Body weight (g) prediction in relation to age (weeks) obtained with different growth models of white strain indigenous turkey for BB genotype of Exon 2 at IGF1 locus

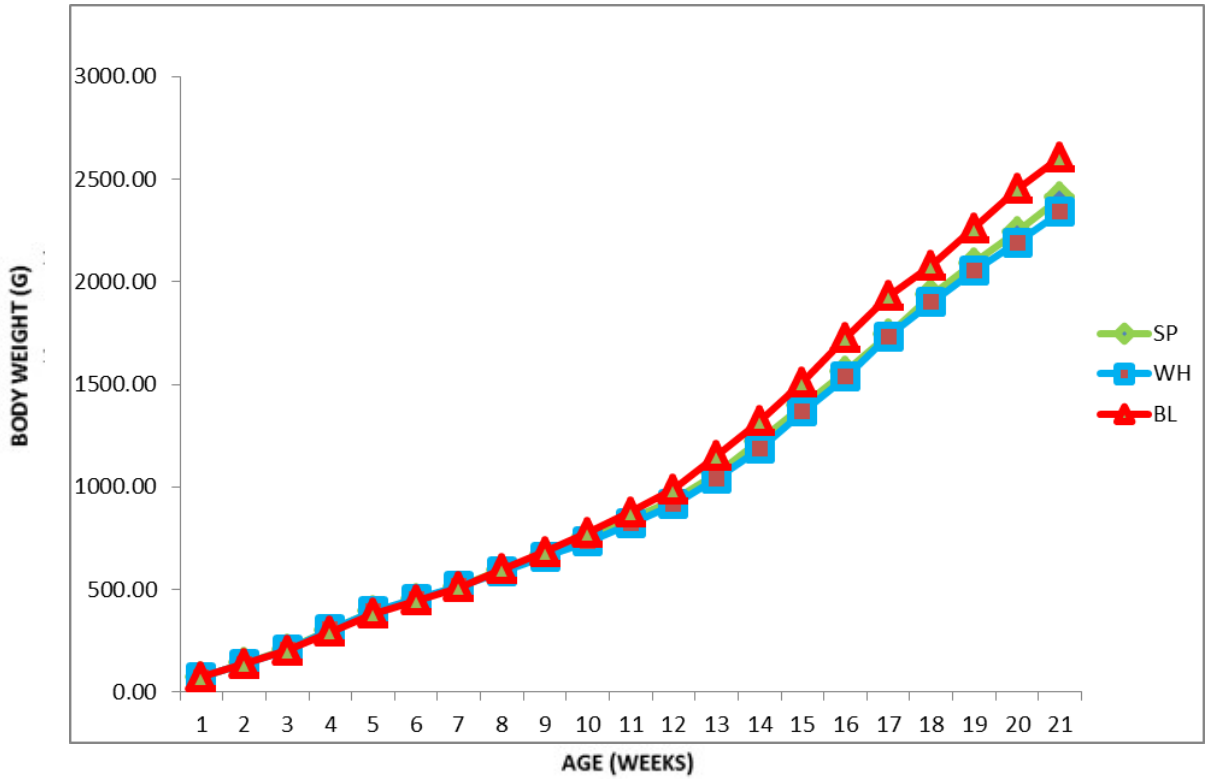

Figure 4.39 : Weight-age growth curve of three strains of indigenous turkey in Nigeria SP:Spotted; WH: White; BL; Black35

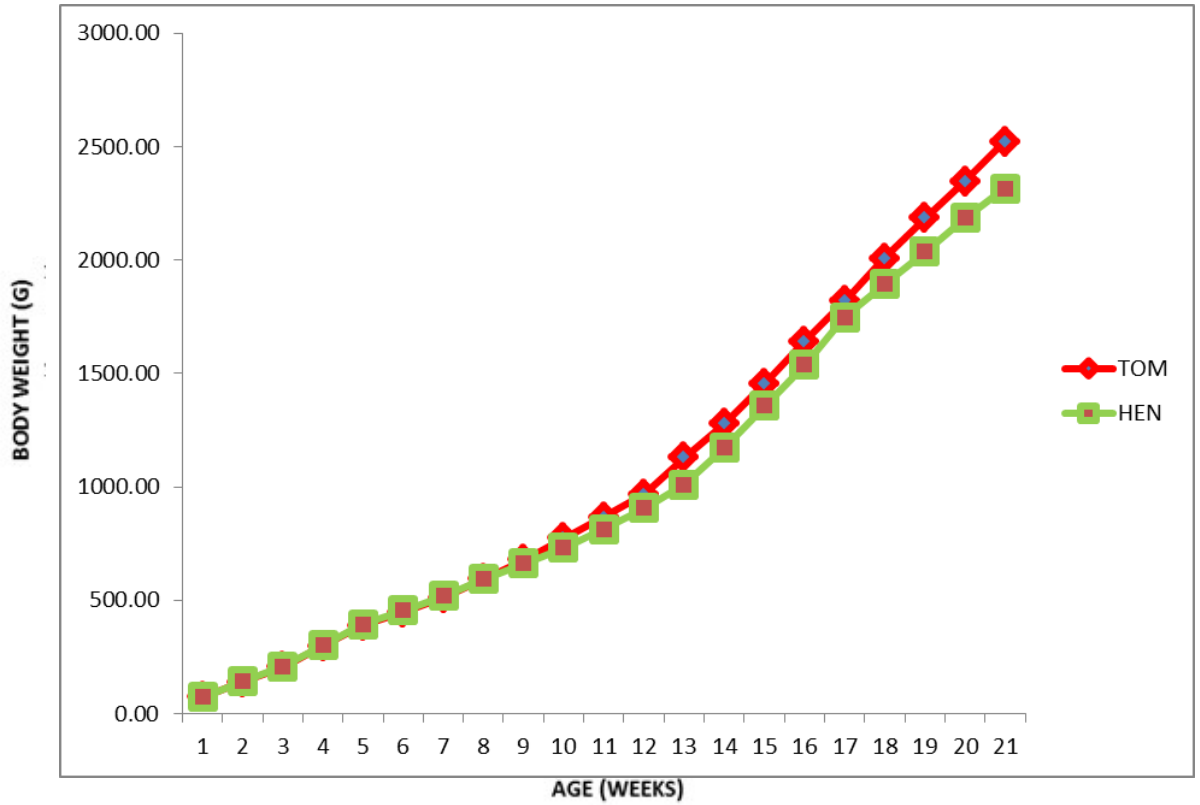

Figure 4.40 : Weight-age growth curve for tom and hen of three strains of indigenous turkey in Nigeria

STUDY THREE

4.3.1 Association of polymorphism of 5' flanking region of IGF1 gene with growth and carcass traits of three strains of indigenous turkey in Nigeria

Table 4.21 and 4.22 show the results of association analysis between different genotypes and growth and carcass. Across the three strains of turkey, there were no significant differences among genotype AA, AB and BB for bodyweight from ages of week 1 to week 17. Genotypes AB and BB for black and spotted strains were significantly associated with bodyweight at week 19, significant differences occurred between individuals with BB genotype and bodyweight at week 21 in black, spotted and white strains of turkey respectively. Genotype BB of both spotted and white populations showed significant correlation with empty gizzard weight. Individuals with genotype AB and BB of black and spotted strains were significantly associated with neck weight and breast muscle. There were significant differences between homozygotes AA and BB for back muscles in black and spotted populations. Furthermore, no significant associations were recorded between the three genotypes and carcass weghts such as liver, full gizzard, spleen, heart, head, shank, breast, wing, thigh, drumstick, defeathered, eviscerated anddressed respectively at ($P < 0.05$).

Table 4.21: Association of 5' Flanking region at locus of IGF1 gene with strain on weekly body weight of Nigerian indigenous turkey

	Spotted			White			Black		
Weeks	AA	AB	BB	AA	AB	BB	AA	AB	BB
1	74.58±1.93	74.25±2.81	75.60±2.63	75.97±2.12	70.50±3.56	77.33±3.91	70.83±2.16	73.85±2.88	75.5±3.74
3	205.21±8.42	212.56±6.99	202.71±12.91	208.59±6.14	207.32±12.74	215.17±7.52	205.71±8.24	202.6±10.13	201.13±11.86
5	379.04±15.90	414.69±15.35	389.80±23.43	389.22±12.89	398.71±17.94	400.92±16.67	382.38±14.43	385.9±23.39	371.5±27.31
7	498.58±21.99	535.56±26.09	521.92±34.66	504.47±19.42	531.42±34.77	521.58±29.78	507.63±21.03	523.1±18	507.88±44.13
9	652.79±25.85	673.19±32.54	658.91±35.42	670.94±18.51	667.64±44.59	675.42±32.76	687.92±19.82	684.9±22.47	667.23±36.22
11	818.58±29.45	821.38±29.66	823.80±36.76	836.66±21.80	874.43±41.24	836.08±39.59	884.46±21.43	864.2±27.78	867.38±42.72
13	1044.58±32.67	1032.56±36.95	1054.62±52.78	1050.66±30.21	1107.31±47.26	1071.53±66.39	1165.04±32.4	1126.2±41.69	1155.75±67.34
15	1380.88±52.41	1345.19±42.46	1362.42±61.96	1384.28±40.34	1436.43±55.83	1375.67±86.05	1505.38±38.43	1510.7±61.1	1523.52±92.80
17	1733.04±52.16	1712.12±54.98	1766.30±65.41	1750.06±45.02	1725.64±95.13	1735.67±99.08	1926.75±37.95	1931.9±63.7	1937.38±103.03
19	2105.00±53.23^{abc}	1963.06±66.18^{c}	2073.61±59.58^{abc}	2103.81±47.32^{abc}	2046.64±98.09^{bc}	2111.67±103.32^{abc}	2228.38±70.78^{ab}	2289.5±64.12^{ab}	2330.50±104.32^{a}
21	2253.17±111.02^{c}	2337.56±51.02^{bc}	2328.21±68.11^{bc}	2423.00±63.88^{bc}	2371.43±117.59^{bc}	2428.75±117.43^{bc}	2556.83±72.59^{abc}	2633.5±70.07^{ab}	2728.75±125.53^{a}

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different.

Table 4.22: Association of 5' Flanking region at locus of IGF1 gene with strains on carcass traits of Nigeria indigenous turkey

Carcass traits	Spotted			White			Black		
	AA	AB	BB	AA	AB	BB	AA	AB	BB
LIVER	49.38±2.64^{ab}	52.36±4.20^{ab}	53±4.81^{ab}	51.06±2.49^{ab}	45.43±4.57^{ab}	42.67±5.70^{b}	48.3±2.84^{ab}	52.8±3.72^{ab}	60.00±5.8^{ab}
FLGZ	90.00±4.74	91.82±7.13	102.33±8.75	87.76±2.40	87.43±6.21	84.67±5.86	96.85±5.81	95.6±14.25	97.60±7.68
EMGZ	58.92±3.58^{ab}	58.09±4.35^{ab}	70.33±5.38^{a}	54.59±1.49^{ab}	56.57±3.08^{ab}	52.33±4.48^{b}	63.4±4.14^{ab}	57.2±9.67^{ab}	62.40±5.46^{ab}
SPLEEN	3.77±0.85	3.64±0.74	3.00±0.68	4.18±1.02	1.71±0.18	2.67±0.42	3.15±0.45	4.80±1.74	3.80±1.62
HEART	8.92±0.49	9.09±0.78	9.00±0.86	9.18±0.73	8.29±1.11	10.33±1.31	9.70±0.60	10.00±1.26	9.60±0.4
HEAD	63.85±3.77	67.55±4.36	68.67±3.50	87.94±23.65	65.00±5.31	65.17±4.76	65.90±2.60	67.20±4.19	70.20±3.77
NECK	142.92±9.12^{ab}	148.18±14.85^{ab}	127.50±12.00^{b}	127.65±5.89^{b}	119.43±11.13^{b}	117±8.87^{b}	146.65±10.19^{ab}	175.20±7.77^{a}	141.60±18.69^{ab}
SHANK	80.85±5.82	80.91±5.42	81.33±8.35	69.65±3.32	62.43±6.39	65.17±7.44	78.80±4.89	70.80±7.33	65.80±3.07
BRST	264.23±24.19^{b}	275.64±32.64^{b}	333.83±15.63^{ab}	269.53±19.54^{b}	288.29±32.4^{b}	252.33±30.92^{b}	321.4±24.49^{ab}	288.80±57.19^{b}	392.60±39.97^{a}
WING	193.77±15.03	193.00±15.02	212.83±14.55	199.82±10.05	185.29±17.31	195±17.66	219.50±9.88	215.00±21.76	219.60±16.29
THGH	183.00±14.63	181.82±14.86	207.5±10.95	189.76±10.39	184.29±17.20	193.00±17.00	218.15±9.92	210.40±19.7	224.20±17.45
DRST	217.54±13.47	227.36±16.77	248.67±12.84	236.29±11.02	226.71±14.18	254.33±11.84	252.50±7.36	242.20±16.75	256.40±10.91
BACK	270.08±25.18^{b}	283.55±26.27^{ab}	347.5±14.16^{ab}	309.59±15.49^{ab}	303.71±17.93^{ab}	330±12.91^{ab}	347.1±11.98^{ab}	323.2±17.67^{ab}	350.20±12.30^{a}
DFWT	1.88±0.15	1.83±0.15	1.88±0.17	1.71±0.06	1.58±0.09	1.58±0.18	1.97±0.10	1.59±0.21	1.9±0.21
EVWT	1.61±0.12	1.56±0.14	1.61±0.12	1.48±0.05	1.37±0.09	1.33±0.14	1.77±0.08	1.43±0.16	1.69±0.19
DRWT	1.26±0.09	1.27±0.1	1.27±0.08	1.17±0.04	1.07±0.07	1.05±0.13	1.37±0.06	1.14±0.12	1.31±0.12

$^{ab:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weight

4.3.2 Association of polymorphism of 5' flanking region of IGF1 gene with growth and carcass traits of both sexes of indigenous turkey in Nigeria

The results of association analysis between different genotypes and growth and carcass traits of both sexes were presented in Table 4.23 and 4.24.There were significant associations of homozygotes BB with bodyweight from week 1, 13, 15, 17, 19 and 21 for male and female turkeys. No significant association of different genotypes with bodyweight at weeks 3, 5, 7, 9 and 11 were observed ($P < 0.05$). Genotype BB interaction with both sexes were significantly associated with liver weight, wing and thigh muscles. The significant associations between homozygote BB genotype and carcass weghts of liver, wing and thigh for male turkey were superior to female turkey. There were no significant associations of different genotypes with carcass weghts like full gizzard, empty gizzard, spleen, heart, head, neck, shank, breast, drumstick, back, defeathered, eviscerated and dressed of both sexes.

Table 4.23: Association of 5' Flanking region at locus of IGF1 gene with sex on weekly body weight of Nigeria indigenous turkey

Weeks	Female			Male		
	AA	AB	BB	AA	AB	BB
1	73.84±1.97^{b}	71.93±2.54^{b}	82.14±5.61^{a}	74.16±1.54^{b}	73.31±2.44^{b}	74.48±1.88^{b}
3	209.22±6.50	203.43±9.20	220.00±12.17	204.56±5.56	210.65±7.37	203.39±6.87
5	392.38±13.19	393.93±20.23	393.71±26.63	377.00±10.11	406.19±12.02	388.04±14.20
7	519.68±17.76	533.29±35.00	494.00±52.26	489.86±15.75	529.54±17.12	525.35±20.63
9	662.70±18.94	672.36±42.48	627.57±55.85	677.37±15.93	675.15±22.69	679.65±19.06
11	822.41±20.93^{a}	836.79±39.00^{a}	721.14±31.07^{b}	865.51±18.82^{a}	858.12±22.62^{a}	876.61±23.05^{a}
13	1023.27±24.16^{b}	1033.57±46.91^{ab}	900.43±36.92^{c}	1134.67±26.63^{ab}	1108.12±27.93^{ab}	1145.52±38.7^{a}
15	1382.30±37.99^{a}	1378.14±52.97^{a}	1177.14±44.67^{b}	1451.67±34.75^{a}	1440.23±38.54^{a}	1481.74±51.91^{a}
17	1799.00±35.43^{a}	1726.07±79.80^{a}	1519.71±61.11^{b}	1797.07±42.15^{a}	1796.35±53.74^{a}	1884.87±56.49^{a}
19	2098.19±46.25^{ab}	1937.50±98.68^{c}	1903.71±37.55^{c}	2178.84±46.06^{a}	2147.38±50.7^{a}	2234.52±63.15^{a}
21	2341.32±54.56^{abc}	2302.21±98.97^{bc}	2210.00±68.31^{c}	2473.19±76.47^{ab}	2488.65±56.59^{ab}	2555.87±77.50^{a}

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different

Table 4.24: Association of 5' Flanking region of IGF1 gene with sex on carcass traits of Nigerian indigenous turkey

Carcass traits	Male			Female		
	AA	AB	BB	AA	AB	BB
LIVER	48.44±1.93[b]	53.67±3.82[ab]	60.00±4.16[a]	50.78±2.53[ab]	46.73±3.22[b]	46.73±4.24[b]
FLGZ	87.04±2.04	93.50±7.51	101.33±2.51	97.78±5.33	88.91±5.96	91.09±6.68
EMGZ	55.78±1.54	59.08±4.75	65.00±4.46	63.30±3.84	55.64±3.44	59.82±4.61
SPLEEN	4.00±0.66	3.42±0.80	3.00±0.68	3.26±0.59	3.18±0.78	3.18±0.75
HEART	9.56±0.46	8.83±0.83	9.33±0.99	9.04±0.59	9.27±0.78	9.82±0.69
HEAD	65.19±2.43[b]	68.17±3.34[b]	69.67±4.35[b]	81.87±17.52[a]	65.09±4.39[b]	66.91±2.72[b]
NECK	135.48±6.54	149.17±13.62	126.5±11.46	143.61±8.26	141.09±11.7	128.73±10.16
SHANK	75.63±3.60	76.75±5.51	74.33±9.09	76.91±4.31	69.09±5.38	69.27±4.62
BRST	266.3±18.67[b]	267.67±31.68[b]	349±38.94[a]	315.43±19.06[ab]	298.36±28.58[ab]	307.82±25.36[ab]
WING	207.19±10.02[ab]	206.75±13.29[ab]	241.17±12.31[a]	204.87±8.38[b]	183.09±14.47[b]	190.73±8.75[b]
THGH	192.67±9.90[b]	194.00±13.42[b]	234.33±10.01[a]	207.22±8.99[ab]	183.09±14.47[b]	192.55±10.11[b]
DRST	231.15±10.02[ab]	233.00±15.63[ab]	262.67±13.07[a]	245.83±6.03[ab]	227.55±11.07[b]	247.64±7.21[ab]
BACK	295.89±16.47	297.00±24.60	328.33±16.39	335.96±10.49	299.73±13.95	349.64±7.13
DFWT	1.86±0.08	1.69±0.13	1.94±0.21	1.86±0.09	1.72±0.13	1.7±0.12
EVWT	1.63±0.07	1.49±0.10	1.67±0.14	1.61±0.07	1.45±0.12	1.46±0.11
DRWT	1.28±0.05	1.22±0.08	1.32±0.09	1.26±0.06	1.14±0.09	1.14±0.09

[Ab]Means with different superscripts along the same row are significantly ($p<0.05$) different FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weight

4.3.3 Association of polymorphism of exon 3 of IGF2 gene with growth and carcass traits of three strains of indigenous turkey in Nigeria

The results of association analysis between different genotypes with growth and carcass traits are given in Table 4.25 and 4.26. In the three strains of turkey, there were significant associations of genotypes AB and BB with bodyweight at week 1 and week 5 of the spotted strain. Animals with genotype BB for black and spotted strains were significantly associated with bodyweight from week 13 to week 19. No significant associations were recorded for all the genotypes detected with bodyweights of the population utilised at weeks 3, 7, 9, 11 and 21 respectively but bodyweights of homozygote BB genotypes across the three strains were higher than those of AA and AB genotypes respectively. Genotype AA and AB of black and white populations showed significant correlation with head weight. Individuals with genotype AB of black and white strains were significantly associated with breast, wing and thigh muscles respectively. There were significant no significant associations of the different genotypes detected with the weights of the liver, full gizzard, empty gizzard, spleen, heart, neck, shank, drumstick, back, defeathered, eviscerated and dressed in the populations observed.

Table 4.25: Association of exon 3 at locus of IGF2 gene with strain on weekly body weight of Nigerian indigenous turkey

	Spotted			White			Black		
Weeks	AA	AB	BB	AA	AB	BB	AA	AB	BB
1	75.13±1.41^{ab}	66.86±4.79^{b}	82.22±2.13^{a}	74.67±2.22^{ab}	74.41±3.23^{ab}	77.13±4.38^{ab}	71.24±1.99^{ab}	74.60±5.01^{ab}	75.38±2.65^{ab}
3	208.89±6.05	184.86±13.50	224.23±10.86	206.36±5.47	216.35±11.16	208.38±10.84	205.31±6.90	209.80±15.03	196.13±13.92
5	395.79±12.16^{ab}	356.14±24.55^{b}	419.4±23.95^{a}	379.70±11.65^{ab}	422.82±16.23^{ab}	391.25±21.49^{ab}	385.66±13.51^{ab}	358.00±32.16^{ab}	379.25±24.92^{ab}
7	509.71±18.28^{ab}	493.57±27.32^{ab}	586.00±32.73^{a}	518.76±20.42^{ab}	536.29±25.08^{ab}	450.00±34.22^{b}	518.45±17.48^{ab}	482.20±38.9^{ab}	503.88±42.23^{ab}
9	661.58±20.15	656.71±50.65	658.00±55.26	688.12±22.11	659.82±27.78	624.00±39.63	683.45±17.45	689.80±35.27	678.25±34.30
11	824.18±20.53	829.29±49.95	780.40±72.33	850.33±24.06	835.00±34.26	849.00±35.29	873.24±19.97	878.40±24.66	886.50±40.50
13	1049.5±24.3^{ab}	1063.57±66.37^{ab}	962.20±76.85^{b}	1073.12±34.78^{ab}	1059.41±44.86^{ab}	1069.25±41.71^{ab}	1146.21±29.13^{a}	1147.20±29.14^{a}	1186.63±71.20^{a}
15	1378.55±35.93^{ab}	1391.71±79.98^{ab}	1232.20±78.38^{b}	1416.70±42.72^{ab}	1366.53±63.96^{ab}	1366.63±45.46^{ab}	1500.14±38.20^{a}	1537.40±62.06^{a}	1529.13±80.60^{a}
17	1747.92±39.13^{ab}	1700.14±90.43^{b}	1665.20±68.93^{b}	1771.21±48.58^{ab}	1700.06±83.03^{b}	1704.75±96.63^{b}	1908.38±39.23^{ab}	1978.40±79.43^{a}	1978.13±77.44^{a}
19	2078.95±37.85^{abcd}	2053.57±86.38^{bcd}	1858.00±171.76^{d}	2122.85±44.59^{abcd}	2062.18±99.78^{abcd}	2025.50±96.52^{cd}	2220.31±62.77^{abc}	2340.00±83.61^{ab}	2366.38±74.50^{a}
21	2347.05±44.49^{a}	1971.43±309.47^{b}	2353.8±116.06^{a}	2441.33±61.82^{a}	2372.35±115.17^{a}	2373.38±112.11^{a}	2575.69±67.55^{a}	2672±101.45^{a}	2684.25±85.61^{a}

Table 4.26: Association of Exon 3 at locus of IGF2 gene with strains on carcass traits of Nigerian indigenous turkey

Carcass traits	Spotted			White			Black		
	AA	AB	BB	AA	AB	BB	AA	AB	BB
LIVER	51.55±2.82	51.33±0.67	49.60±2.32	49.22±2.54	46.00±5.45	47.00±4.20	50.48±2.79	50.00±1.83	54.00±7.77
FLGZ	93.18±4.79	100±8.08	88.80±6.34	87.67±2.41	84.75±6.22	89.00±4.65	97.95±5.60	95.50±6.7	92.80±14.61
EMGZ	60.68±3.12	64.67±7.06	59.60±6.21	54.67±1.27	54.00±4.44	55.50±2.22	61.90±4.09	61.00±3.87	64.40±9.74
SPLEEN	3.77±0.52	1.67±0.33	3.80±1.62	2.67±0.68	5.13±1.60	2.50±0.50	3.57±0.63	4.5.00±1.26	2.60±0.6
HEART	9.09±0.41^{ab}	10.00±1.15^{ab}	8.00±1.26^{b}	8.56±0.48^{ab}	10.25±1.53^{ab}	10.00±1.83^{ab}	9.33±0.48^{ab}	11.50±1.71^{a}	10.00±1.10^{ab}
HEAD	64.77±2.67^{ab}	82.00±5.77^{ab}	62.80±4.84^{ab}	84.39±22.45^{b}	69.25±5.01^{ab}	67.00±6.14^{ab}	65.57±2.49^{ab}	74.25±3.01^{a}	66.20±3.93^{ab}
NECK	136.32±7.88	168.00±26.23	150.00±19.2	121.28±6.37	127.13±9.29	127.00±3.70	141.52±9.82	180.50±15.95	164.60±8.69
SHANK	81.09±4.33	83.33±11.10	79.00±7.65	68.67±2.99	65.00±7.74	64.00±6.06	76.14±4.56	78.25±8.45	69.40±8.17
BRST	279.59±17.78^{b}	391.33±56.64^{a}	229.00±32.49^{b}	283.50±19.11^{b}	253.50±31.66^{b}	245.75±20.68^{b}	323.43±26.52^{ab}	392.75±17.74^{a}	294.40±40.46^{ab}
WING	194.32±10.37^{ab}	234.00±18.9^{ab}	188.40±24.23^{b}	201.11±8.48^{ab}	182.75±19.15^{b}	195.50±22.43^{ab}	213.81±9.78^{ab}	245.75±13.09^{a}	218.00±17.79^{ab}
THGH	183.27±9.73^{bc}	232.00±19.43^{b}	179.20±24.04^{bc}	195.00±8.23^{bc}	176.75±19.27^{c}	187.50±24.74^{bc}	210.9±9.55^{abc}	258.75±4.50^{a}	214.40±16.51^{abc}
DRST	224.36±9.54^{ab}	268.67±10.73^{a}	215.80±31.19^{b}	242.61±7.95^{ab}	230.88±18.76^{ab}	229.00±25.9^{ab}	248.95±6.94^{ab}	248.25±12.11^{ab}	264.40±17.53^{ab}
BACK	281.05±16.48	358.67±8.67	291.20±56.76	314.61±13.42	298.75±21.33	329.00±15.84	341.48±11.08	365.00±13.08	335.60±22.85
DFWT	1.79±0.10	2.15±0.23	1.99±0.31	1.67±0.07	1.63±0.12	1.63±0.07	1.90±0.11	2.13±0.12	1.71±0.18
EVWT	1.54±0.08	1.83±0.22	1.68±0.25	1.43±0.05	1.42±0.11	1.41±0.08	1.70±0.09	1.91±0.12	1.52±0.13
DRWT	1.21±0.06	1.45±0.19	1.42±0.17	1.13±0.05	1.12±0.09	1.13±0.08	1.32±0.06	1.47±0.08	1.22±0.09

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different

FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weight

4.3.4 Association of polymorphism of exon 2 of IGF2 gene with growth and carcass traits of both sexes of indigenous turkey in Nigeria

In both sexes, there were significant associations of homozygote BB with bodyweight from at week 11and 13 respectively as shown in Tables 4.27 and 4.28. Significant differences also occured for male and female turkeys at weeks 15 and 19 respectively. No significant association of different genotypes with bodyweight at other weeks were observed ($P < 0.05$). Genotypes AB and BB interaction with both sexes were significantly associated with spleen and head weights respectively while breast muscle is strongly associated with breast muscle. There were no significant associations of three genotypes observed with other traits in both sexes

Table 4.27: Association of Exon 3 at locus of IGF2 gene with sex on weekly body weight of Nigerian indigenous turkey

Weeks	Female			Male		
	AA	AB	BB	AA	AB	BB
1	72.70±1.94	74.88±4.86	80.70±2.30	74.62±1.25	71.76±2.78	74.91±3.10
3	204.23±5.93	229.13±10.75	212.70±12.30	208.88±4.34	199.43±9.69	202.73±8.58
5	382.85±12.13	429.88±32.92	403.60±18.13	390.67±8.78	382.48±13.32	384.09±20.34
7	522.35±18.41	520.88±44.23	509.10±37.36	510.48±13.32	515.05±18.2	497.27±32.67
9	674.78±21.50	633.88±42.16	626.40±33.49	677.95±13.32	675.81±23.74	676.73±32
11	827.45±21.24^{ab}	787.13±43.25^{b}	779.70±39.14^{b}	860.10±15.39^{ab}	861.67±27.07^{ab}	908.09±26.41^{a}
13	1028.38±25.11^{bc}	964.00±48.01^{c}	978.70±44.77^{c}	1123.32±22.29^{ab}	1118.05±34.98^{ab}	1188.27±47.55^{a}
15	1388.48±36.82^{ab}	1260.50±60.48^{b}	1305.60±59.00^{ab}	1451.68±28.94^{a}	1456±52.23^{a}	1479.18±61.36^{a}
17	1777.48±37.07^{ab}	1613.63±116.23^{b}	1735.80±64.52^{ab}	1818.58±34.37^{a}	1799.29±63.79^{ab}	1857.36±91.40^{a}
19	2059.23±43.40^{ab}	1933.13±133.63^{b}	2025.00±107.29^{ab}	2184.57±34.98^{a}	2174.62±71.53^{a}	2197.73±101.36^{a}
21	2327.15±48.24^{ab}	2128.75±169.55^{b}	2421.40±67.67^{a}	2522.68±43.95^{a}	2402.86±131.89^{a}	2546.91±112.51^{a}

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different

Table 4.28: Association of Exon 3 at locus of IGF2 gene with sex on carcass traits of Nigerian indigenous turkey

Carcass traits	Male			Female		
	AA	AB	BB	AA	AB	BB
LIVER	51.33±2.06	53.2±5.28	50.60±4.09	49.68±2.37	45.60±3.40	50.00±3.37
FLGZ	91.93±2.68	84.80±3.20	89.80±7.44	94.42±4.66	93.60±6.03	91.50±5.68
EMGZ	57.97±1.81	55.20±3.44	59.00±5.33	60.65±3.22	59.40±4.20	63.00±5.07
SPLEEN	3.33±0.47^{b}	6.80±2.24^{a}	3.30±0.82^{b}	3.42±0.52^{b}	3.00±0.67^{b}	2.25±0.63^{b}
HEART	9.20±0.37	10.40±1.94	9.20±0.90	8.84±0.38	10.60±1.08	9.50±1.71
HEAD	65.33±2.16^{ab}	75.80±6.05^{a}	65.70±3.42^{ab}	76.16±13.07^{a}	71.80±3.79^{ab}	64.00±4.24^{b}
NECK	132.17±7.00	147.00±15.34	150.70±10.85	135.13±6.81	150.80±13.39	143.50±11.00
SHANK	78.47±3.34	72.20±11.27	69.40±5.46	73.06±3.52	72.20±6.10	76.00±7.44
BRST	292.5±20.14^{ab}	268.60±42.68^{ab}	237.80±22.46^{b}	299.06±15.52^{ab}	343.00±32.67^{a}	305.50±31.49^{ab}
WING	212.63±8.81	223.40±25.75	202.60±15.65	193.74±6.8	203.00±15.95	197.00±19.02
THGH	198.23±8.56	211.80±28.33	193.00±16.10	194.32±7.11	208.60±17.33	197.00±19.02
DRST	236.00±8.43	242.80±26.66	231.90±20.14	240.35±5.34	243.20±11.16	249.50±14.50
BACK	299.03±14.57	300.00±34.06	305.20±28.96	324.06±9.12	342.60±12.42	349.50±14.20
DFWT	1.85±0.08	1.79±0.09	1.78±0.17	1.74±0.07	1.9±0.15	1.81±0.17
EVWT	1.61±0.06	1.62±0.09	1.55±0.13	1.5±0.06	1.64±0.14	1.54±0.16
DRWT	1.27±0.05	1.3±0.07	1.28±0.09	1.18±0.05	1.27±0.11	1.22±0.13

^{Ab} Means with different superscripts along the same row are significantly ($p<0.05$) different

FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weight

4.3.5 Association of polymorphism of 5' flanking region of GH gene with growth and carcass traits of three strains of indigenous turkey in Nigeria

The results of association analysis between different genotypes with growth and carcass traits are given in Table 4.29 and 4.30. In the three strains of turkey, there were no significant associations of different genotypes obtained with bodyweight from week 1 to week 11. Animals with genotype BB for black and spotted strains were significantly associated with bodyweight from at 13 while heterozygote AB was strongly associated with bodyweight at from week 15 to week 21. Genotype BB of spotted and white populations showed significant correlation with liver weight. Individuals with homozygote BB of black and white strains were significantly associated with full gizzard weight, spleen weight and breast muscle respectively. Animals with genotype AB were significantly different from each other across the three strains in head weight. There were significant no significant associations of the different genotypes with other carcass traits in the populations observed.

Table 4.29: Association of 5' flanking region at GH locus with strain on weekly body weight of Nigeria indigenous turkey

	Spotted			White			Black		
Weeks	AA	AB	BB	AA	AB	BB	AA	AB	BB
1	74.86±22.00	77.73±1.49	71.18±3.11	74.39±2.03	73.75±4.53	78.44±3.95	72.35±2.18	74.25±3.21	70.88±3.07
3	207.25±7.94	215.91±8.37	197.73±9.27	209.15±5.55	204.25±14.73	216.22±11.66	208.15±8.16	202.50±10.46	192.50±8.23
5	398.00±16.79	400.64±12.11	370.82±14.10	396.37±9.96	381.25±25.20	394.11±29.34	388.08±14.91	374.50±23.15	365.25±22.70
7	538.61±20.76	519.45±32.85	450.82±20.55	529.22±17.58	471.75±25.05	484.89±44.94	516.88±20.64	526.13±30.64	478.63±27.96
9	699.29±23.46^{a}	639.45±35.28^{ab}	583.00±25.90^{b}	678.39±19.55^{ab}	634.75±32.45^{ab}	669.44±44.92^{ab}	690.35±19.99^{a}	684.13±21.73^{ab}	659.13±28.77^{ab}
11	845.32±28.18	794.27±32.91	783.64±21.77	864.76±20.99	791.25±27.68	807.00±50.77	888.58±23.46	857.75±18.72	855.38±27.15
13	1067.54±33.93^{ab}	1014.55±36.87^{b}	1007.82±31.80^{b}	1086.15±29.28^{ab}	1005.38±36.95^{b}	1044.67±73.87^{ab}	1146.46±34.26^{ab}	1157.88±35.01^{ab}	1174.75±54.10^{a}
15	1395.64±44.72^{abc}	1283.55±54.81^{c}	1371.91±57.59^{abc}	1420.71±35.84^{abc}	1305.25±37.85^{bc}	1358.22±111.88^{abc}	1491.19±42.11^{ab}	1562.25±65.71^{a}	1519.38±61.10^{a}
17	1763.00±47.02^{abc}	1618.91±70.8^{c}	1770.55±45.11^{abc}	1758.93±48.64^{abc}	1705.13±55.60^{bc}	1692.44±109.45^{bc}	1913.23±43.20^{ab}	1970.25±78.94^{a}	1944.25±55.29^{a}
19	2071.18±55.65^{ab}	1981.82±59.13^{b}	2079.27±55.19^{ab}	2102.73±52.43^{ab}	2060.88±45.97^{ab}	2068.44±103.19^{ab}	2244.88±59.24^{ab}	2331.88±79.46^{a}	2249.75±142.36^{ab}
21	2334.18±91.07^{bcd}	2202.18±83.91^{d}	2288.73±82.35^{cd}	2449.49±58.95^{abcd}	2243.75±157.42^{cd}	2389.11±120.15^{abcd}	2573.42±61.69^{abc}	2701.25±91.39^{a}	2626.25±156.64^{ab}

^{Ab} Means with different superscripts along the same row are significantly ($p<0.05$) different

Table 4.30: Association of 5' Flanking region of GH gene with strains on carcass traits of Nigerian indigenous turkey

Carcass traits	Spotted			White			Black		
	AA	AB	BB	AA	AB	BB	AA	AB	BB
LIVER	48.13±1.97^{ab}	53.50±4.81^{ab}	56.33±6.40^{a}	48.96±2.31^{ab}	50.00±6.58^{ab}	38.67±8.11^{b}	49.37±3.15^{ab}	59.60±4.62^{a}	49.00±3.21^{ab}
FLGZ	89.75±3.69^{b}	89.25±8.48^{b}	107.33±10.39^{ab}	88.17±2.41^{b}	83.00±3.87^{b}	84.00±13.01^{b}	91.26±5.39^{b}	90.20±7.38^{b}	119.67±10.22^{a}
EMGZ	56.94±2.76^{ab}	60.50±5.05^{ab}	72.00±6.77^{a}	55.74±1.45^{ab}	53.00±1.73^{b}	48.00±8.08^{b}	58.63±3.58^{ab}	64.40±7.22^{ab}	71.67±9.83^{a}
SPLEEN	3.25±0.57^{ab}	4.00±1.13^{ab}	3.83±1.11^{ab}	3.09±0.63^{ab}	5.00±3.00^{ab}	2.67±0.67^{b}	3.37±0.59^{ab}	4.00±1.55^{ab}	3.67±1.09^{a}
HEART	8.75±0.48	9.25±0.92	9.33±0.84	9.22±0.70	9.50±0.96	8.67±0.67	9.37±0.53	9.20±1.02	11.33±1.12
HEAD	62.38±3.34^{b}	67.38±4.04^{b}	74.67±4.25^{b}	65.13±2.40^{b}	169.50±98.36^{a}	55.00±1.73^{b}	67.42±1.83^{b}	69.80±6.12^{b}	62.50±6.39^{b}
NECK	150.00±10.03	132.25±8.56	132.50±20.56	125.30±4.90	116.50±17.68	120.00±15.53	142.89±9.77	159.60±20.25	167.33±15.57
SHANK	80.81±4.56^{ab}	68.25±5.44^{b}	98.33±5.40^{a}	64.48±3.25^{b}	73.50±3.50^{b}	78.33±8.69^{ab}	76.42±4.46^{b}	67.60±7.70^{b}	78.17±9.66^{ab}
BRST	291.75±24.14^{ab}	265.13±29.85^{b}	280.17±37.79^{ab}	274.35±15.48^{b}	281.00±62.37^{ab}	226.67±32.26^{b}	323.58±25.12^{ab}	283.80±52.22^{ab}	378.00±44.39^{a}
WING	195.25±11.72^{ab}	186.50±15.28^{b}	217.17±25.03^{ab}	194.70±8.8^{ab}	203.50±27.37^{ab}	190.67±17.98^{ab}	220.05±9.23^{ab}	187.20±15.97^{ab}	241.00±18.06^{a}
THGH	187.44±11.27^{ab}	181.75±15.12^{b}	195.17±26.05^{ab}	190.35±9.26^{ab}	183.50±21.88^{ab}	187.33±15.38^{ab}	219.53±9.38^{ab}	190.60±20.40^{ab}	235.33±16.07^{a}
DRST	224.81±12.03	222.25±15.26	241.00±25.16	240.00±8.51	220.00±28.58	243.33±6.67	256.11±7.40	234.60±8.07	250.67±15.58
BACK	293.75±22.33	292.63±31.03	279.00±32.49	314.91±10.99	296.50±43.15	313.33±16.67	339.32±11.31	348.40±19.53	353.33±21.53
DFWT	1.88±0.13	1.7±0.18	2.02±0.17	1.66±0.05	1.66±0.23	1.60±0.34	1.81±0.10	2.09±0.19	2.03±0.24
EVWT	1.62±0.10	1.44±0.15	1.72±0.12	1.43±0.04	1.45±0.15	1.32±0.25	1.63±0.07	1.86±0.19	1.78±0.18
DRWT	1.30±0.08	1.14±0.12	1.35±0.09	1.13±0.04	1.14±0.13	1.05±0.23	1.28±0.06	1.41±0.13	1.35±0.15

^{Ab} Means with different superscripts along the same row are significantly ($p<0.05$) different.

FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weight

4.3.6 Association of polymorphism of 5' flanking region of GH gene with growth and carcass traits of both sexes of indigenous turkey in Nigeria

In both sexes, there were significant associations of homozygotes AA and BB with bodyweight from at week 11in both male and female respectively as shown in Table 4.31 and 4.32. Significant differences occured for male and female turkeys at weeks 13 between homozygote AA of male and other different genotypes of female while significant association occurred in homozygote BB bodyweight at week 19 and homozygote BB of female at week 21 differ significantly from different genotypes of male. No significant association of different genotypes with bodyweight at other weeks observed ($P < 0.05$). Genotype BB interaction with both sexes were significantly associated with full gizzard weight. Genotypes AB and BB were significantly different from each other in both sexes for shank weight and breast muscle respectively while homozygote BB was significantly associated with thigh and back muscles respectively. There were no significant associations of three genotypes observed with other traits in both sexes

Table 4.31: Association of 5' Flanking region of GH gene with sex on weekly body weight of Nigerian indigenous turkey

Weeks	Female			Male		
	AA	AB	BB	AA	AB	BB
1	75.13±1.91	72.6±2.66	73.11±5.36	73.16±1.56	77.24±2.18	73.58±1.69
3	208.08±6.46	215.00±9.0	207.11±11.52	208.48±5.09	204.65±8.37	199.84±6.82
5	387.41±13.31	405.00±17.49	403.33±24.26	399.57±9.12	376.65±13.92	364.11±13.80
7	525.92±19.48	521.50±30.51	491.78±39.16	530.48±13.40	498.94±22.19	459.26±19.15
9	669.41±20.94	661.50±32.00	622.67±51.22	700.64±14.39	645.29±22.76	637.21±18.75
11	822.95±22.86^{ab}	806.60±26.55^{ab}	781.22±40.84^{b}	895.21±16.23^{a}	815.47±22.80^{ab}	826.05±22.34^{ab}
13	1012.9±25.24^{b}	1014.30±36.22^{b}	998.67±61.19^{b}	1155.86±23.62^{a}	1077.82±31.71^{ab}	1099.89±37.14^{ab}
15	1362.64±36.15	1332.10±52.08	1357.22±90.13	1481.34±29.30	1396.35±54.02	1434.47±53.79
17	1757.08±42.64	1727.40±52.16	1729.56±83.78	1833.89±37.68	1761.00±72.12	1826.11±53.39
19	2040.51±51.74^{ab}	2073.80±45.03^{ab}	1974.00±110.75^{b}	2196.29±40.59^{a}	2129.65±67.74^{ab}	2195.79±59.95^{a}
21	2359.15±51.78^{ab}	2294.90±99.20^{ab}	2152.67±110.07^{b}	2512.29±58.94^{a}	2402.06±104.77^{a}	2542.84±74.45^{a}

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different

Table 4.32: Association of 5' Flanking region of GH gene with sex on carcass traits of Nigerian indigenous turkey

Carcass traits	Male			Female		
	AA	AB	BB	AA	AB	BB
LIVER	51.52±2.13	52±4.28	50.25±4.38	46.21±1.91	56.67±4.32	49.43±5.95
FLGZ	86.9±2.53^{bc}	95.25±6.71^{bc}	99.75±6.97^{b}	92.34±3.61^{bc}	81.67±5.45^{c}	116.57±12.1^{a}
EMGZ	55±1.59^{b}	63.25±4.02^{ab}	63±6.02^{ab}	59.03±2.5^{b}	56.89±4.9^{b}	71.71±9.41^{a}
SPLEEN	3.79±0.61	3.00±1.00	4.13±0.85	2.66±0.3	5.33±1.45	2.86±0.86
HEART	9.03±0.45^{ab}	10.25±0.96^{ab}	9.5±0.91^{ab}	9.24±0.54^{ab}	8.44±0.44^{b}	10.57±0.84^{a}
HEAD	66.76±2.11^{b}	71.25±4.76^{b}	61.25±4.33^{b}	63.48±1.98^{b}	110.67±44.29^{a}	71.14±5.47^{b}
NECK	141.52±7	134.75±11.56	128.13±14.93	134.24±6.56	138.22±13.4	162±15.76
SHANK	75.28±3.56^{ab}	71.25±5.3^{b}	82±7.64^{ab}	70.52±3.4^{b}	67.56±4.49^{b}	91.14±6.9^{a}
BRST	283.1±18.67^{ab}	248.13±36.66^{b}	287.63±40.3^{ab}	307.45±16.12^{ab}	297.67±30.45^{ab}	332.57±38.91^{a}
WING	216.03±8.58^{ab}	192.75±18.58^{ab}	214.38±19.76^{ab}	190.28±7.02^{b}	188.89±10.95^{b}	229.43±17.63^{a}
THGH	205.93±8.87^{ab}	177.63±16.28^{b}	192.88±19.05^{b}	192.28±7.79^{b}	191.11±12.65^{b}	228.86±16.25^{a}
DRST	243.24±9.27^{ab}	209.88±16.1^{b}	235±19.65^{ab}	238.93±5.94^{ab}	239.11±9.59^{ab}	257.14±8.97^{a}
BACK	306.48±14.5^{ab}	296.88±35.21^{ab}	282.5±26.69^{b}	327.66±8.98^{ab}	321.56±17.65^{ab}	353.43±11.08^{a}
DFWT	1.79±0.08^{ab}	1.95±0.21^{ab}	1.83±0.17^{ab}	1.75±0.07^{ab}	1.68±0.12^{b}	2.07±0.21^{a}
EVWT	1.58±0.06	1.69±0.17	1.59±0.11	1.51±0.06	1.45±0.13	1.75±0.19
DRWT	1.27±0.04	1.31±0.13	1.24±0.09	1.18±0.05	1.14±0.09	1.35±0.15

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) differen FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weight

4.3.7 Association of polymorphism of exon 2 of myostatin gene with growth and carcass traits of three strains of indigenous turkey in Nigeria

The results of association analysis between different genotypes and growth and carcass traits are given in Tables 4.33 and 4.34. Genotypes AA and BB were significantly different from each other at week 1 for black strain. At weeks 5, 13, 15, 17 and 19 individuals with homozygote BB were significantly associated with bodyweights in black and white strains respectively while BB genotypes of black and spotted strains were also associated with bodyweight at 21 week. Animals with homozygote BB of both black and white populations showed significant correlation with spleen and heart weights respectively. Genotypes AB and BB showed significant differences and were found to associated with shank weight. Significant associations were also recorded for heterozygote AB of black and spotted populations with breast, wing, thigh, drumstick and back muscles. Moreover, no significant association of different genotypes with other traits were recorded ($P < 0.05$).

Table 4.33: Association of Exon 2 at locus of MSTN gene with strain on weekly body weight of Nigeria indigenous turkey

	Spotted			White			Black		
Weeks	AA	AB	BB	AA	AB	BB	AA	AB	BB
1	73.73±1.73^{ab}	75.22±2.91^{ab}	78±3.51^{ab}	73.33±2.36^{ab}	78.8±3.06^{ab}	75.87±3.22^{ab}	69.96±1.93^{b}	71.80±2.95^{ab}	80.63±3.61^{a}
3	206.03±6.34	202.22±12.93	216.75±14.09	209.52±6.82	218.30±8.87	203.87±8.66	197.21±8.58	204.30±5.47	224.50±11.14
5	385.91±11.47^{bc}	381.22±28.64^{bc}	433±28.13^{ab}	395.48±12.77^{abc}	426.40±20.59^{bc}	368.87±12.23^{c}	357.46±14.58^{c}	388.1±13.88^{abc}	443.50±22.09^{a}
7	503.82±16.50^{ab}	512.67±41.47^{ab}	564.25±45.76^{a}	538.79±18.85^{ab}	515.60±42.82^{ab}	460.00±23.37^{b}	493.50±22.16^{ab}	528.20±28.48^{ab}	543.88±19.49^{ab}
9	651.15±19.16	646.89±33.58	714.63±65.91	685.73±20.05	683.60±48.01	630.13±29.11	669.25±19.18	694.60±32.27	710.88±22.98
11	817.06±19.03^{ab}	791.11±28.38^{b}	867.88±78.44^{ab}	848.82±21.98^{ab}	886.30±53.13^{ab}	811.60±31.22^{ab}	866.08±20.62^{ab}	878.70±42.14^{ab}	904.38±21.34^{a}
13	1039.55±24.52^{b}	1019.67±35.16^{b}	1081.88±87.57^{ab}	1060.36±31.84^{ab}	1140.30±76.42^{ab}	1038.80±35.31^{b}	1136.63±32.18^{ab}	1155.60±63.78^{ab}	1204.25±25.16^{a}
15	1361.88±34.91^{b}	1309.00±36.42^{b}	1445.63±122.77^{ab}	1395.27±40.85^{b}	1457.20±97.96^{ab}	1353.27±48.81^{b}	1494.96±42.76^{ab}	1465.10±71.61^{ab}	1611.75±31.71^{a}
17	1728.94±36.48^{bc}	1653.44±57.09^{c}	1839±122.68^{abc}	1763.15±52.53^{bc}	1670.30±121.63^{c}	1740.13±55.55^{bc}	1920.54±44.22^{ab}	1878.70±75.03^{abc}	2022.50±35.9^{a}
19	2030.61±42.89^{c}	2057.44±74.40^{bc}	2142.25±112.70^{abc}	2122.33±53.35^{abc}	2036.90±140.16^{c}	2060.60±51.71^{bc}	2312.92±45.21^{ab}	2065.60±151.43^{bc}	2356.75±43.42^{a}
21	2315.76±47.73^{bcd}	2376.67±83.26^{bcd}	2118.38±289.68^{d}	2452.91±64.93^{abc}	2472.50±139.65^{abc}	2280.67±94.03^{cd}	2641.21±53.55^{ab}	2429±158.3^{abcd}	2731.25±44.78^{a}

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different

Table 4.34: Association of Exon 2 at locus of MSTN gene with strains on carcass traits of Nigerian indigenous turkey

Carcass traits	Spotted			White			Black		
	AA	AB	BB	AA	AB	BB	AA	AB	BB
LIVER	50.84±2.69	46.80±3.72	56.00±5.19	49.75±2.99	45.43±4.55	46.86±4.34	50.78±3.54	55.00±2.17	44.00±3.56
FLGZ	94.00±5.38	81.60±4.66	100.00±4.95	87.63±2.91	85.71±5.76	87.14±4.40	94.22±6.34	100.13±9.74	101.50±4.03
EMGZ	62.21±3.44	51.6±3.97	64.50±4.88	55.00±1.66	53.14±3.88	55.14±2.89	60.89±4.41	66.00±6.21	60.50±8.46
SPLEEN	3.79±0.68^{ab}	3.00±0.89^{ab}	3.33±0.67^{ab}	4.25±1.03^{ab}	2.71±0.89^{ab}	1.71±0.18^{b}	3.11±0.63^{ab}	3.25±0.75^{ab}	6.00±1.41^{a}
HEART	9.47±0.50^{ab}	8.80±0.80^{ab}	7.67±0.61^{b}	9.00±0.66^{ab}	11.14±1.30^{a}	7.71±1.02^{b}	9.33±0.49^{ab}	10.00±1.00^{ab}	11.00±1.73^{a}
HEAD	71.00±2.96.00	56.80±3.67	58.67±3.29	90.75±25.00	70.86±5.65	56.14±2.31	68.44±2.42	67.25±3.75	58.75±5.74
NECK	143.95±9.14	132.60±11.75	142.50±19.52	121.50±5.14	135.00±10.25	117±11.58	157.11±9.65	129.75±16.79	162.75±13.65
SHANK	81.58±4.25^{ab}	74.80±8.35^{abc}	84.17±9.65^{ab}	66.88±3.69^{bc}	75.43±6.92^{abc}	59.14±3.24^{c}	72.06±4.12^{abc}	88.50±7.14^{a}	63.50±9.00^{bc}
BRST	287.84±21.09^{abcd}	215.60±36.37^{d}	320.50±29.66^{abc}	257.31±17.03^{bcd}	252.43±29.74^{cd}	318.57±35.44^{abc}	306.28±27.08^{abcd}	365.88±35.99^{a}	348.75±54.76^{ab}
WING	200.42±10.58^{ab}	157.40±15.45^{b}	220.67±21.37^{a}	194.69±10.41^{ab}	192.86±18.08^{ab}	199.86±15.82^{ab}	216.28±10.35^{a}	221.00±16.18^{a}	225.50±18.71^{a}
THGH	189±10.47^{ab}	154.00±19.43^{b}	210.50±18.65^{a}	189.31±10.54^{ab}	181.71±17.6^{ab}	196.14±15.66^{ab}	213.83±10.25^{a}	224.38±15.39^{a}	223.00±21.58^{a}
DRST	233.42±10.63^{a}	185.00±20.31^{b}	243.50±18.28^{a}	233.75±11.82^{a}	232.29±15.6^{a}	252.00±7.87^{a}	250.50±7.79^{a}	260.13±10.89^{a}	238.25±14.76^{a}
BACK	311.58±18.33^{a}	214.40±41.23^{b}	287.17±25.75^{a}	308.75±14.17^{a}	298.00±22.81^{a}	334.71±16.25^{a}	335.50±12.74^{a}	355.63±15.05^{a}	356.25±8.98^{a}
DFWT	1.87±0.11	1.84±0.29	1.84±0.23	1.68±0.07	1.66±0.15	1.59±0.09	1.82±0.11	2.00±0.14	2.06±0.26
EVWT	1.58±0.09	1.61±0.23	1.6±0.17	1.47±0.05	1.39±0.11	1.34±0.09	1.65±0.09	1.76±0.13	1.77±0.18
DRWT	1.28±0.07	1.23±0.17	1.27±0.11	1.16±0.05	1.11±0.10	1.07±0.08	1.3±0.07	1.36±0.09	1.34±0.17

$^{abcd:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weight

4.3.8 Association of polymorphism of exon 2 of myostatin gene with growth and carcass traits of both sexes of indigenous turkey in Nigeria

The results of association analysis between different genotypes with growth and carcass traits for male and female turkeys are presented in Table 4.35 and 4.36. In both sexes, there were significant associations of heterozygotes AB with bodyweight from at weeks 11, 13 15 and 21 respectively. At week 17, homozygote AA of male was significantly higher than heterozygote AB of female and both genotypes were found to be associated with bodyweight of both sexes while at week 19 of age, heterozygote AB of female was significantly correlated with the different genotypes obtained for male turkey. There were no significant associations of three genotypes observed with bodyweights from week 1 to week 9 in both sexes. Significant associations were observed with head weight for homozygote AA of female and other different genotypes of male. Homozygote BB individuals of male were significantly higher than heterozygote AB of the same sex and were significantly associated with thigh and back muscles in male and female respectively. Genotypes AB and BB were significantly associated with shank weight in both male and female respectively while heterozygote AB individuals also showed strong relationship with breast muscle in both sexes. Significant associations were recorded between wing muscle and genotype BB individuals of male and other different genotypes of female turkey. There were significant differences between AB and BB genotypes of both male and female respectively and were found to be associated with heart weight. There were no significant associations of three genotypes observed with other carcass traits in both sexes.

Table 4.35: Association of Exon 2 of MSTN gene with sex on weekly body weight of Nigerian indigenous turkey

Weeks	Female			Male		
	AA	AB	BB	AA	AB	BB
1	74.14±1.99	75.1±3.29	74.55±4.18	71.49±1.46	75.37±2.10	79.35±2.07
3	206.54±6.42	218.40±7.41	209.36±12.86	203.85±5.36	203.26±7.02	214.25±6.85
5	384.51±12.93	411.80±14.88	404.00±27.94	379.96±9.06	392.53±17.42	405.05±12.02
7	521.46±19.02	521.10±33.42	513.36±40.67	508.60±13.22	517.95±27.71	505.90±19.26
9	662.30±19.81	653.60±30.25	662.27±55.69	673.09±13.60	687.79±29.81	678.55±20.56
11	818.38±18.31^{ab}	780.70±33.92^{b}	827.73±60.82^{ab}	858.11±15.73^{ab}	892.79±31.44^{a}	862.35±23.38^{ab}
13	1008.73±20.93^{bc}	968.60±41.03^{c}	1056.82±71.14^{bc}	1117.98±23.88^{ab}	1181.58±43.1^{a}	1112.30±27.73^{ab}
15	1360.73±31.93^{ab}	1260.10±32.68^{b}	1430.09±102.95^{a}	1443.74±31.91^{a}	1494.89±56.90^{a}	1451.35±39.08^{a}
17	1751.78±39.03^{ab}	1639.10±39.45^{b}	1832.64±99.47^{a}	1821.06±37.23^{a}	1788.42±78.26^{ab}	1841.75±48.40^{a}
19	2059.95±45.58^{a}	1811.80±96.21^{b}	2158.91±84.86^{a}	2195.08±38.26^{a}	2180.21±85.71^{a}	2157.65±52.48^{a}
21	2345.43±54.60^{bc}	2122.50±91.43^{c}	2393.09±88.09^{ab}	2527.81±43.51^{ab}	2588.42±83.39^{a}	2334.15±140.05^{bc}

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different

Table 4.36: Association of Exon 2 at locus of MSTN gene with sex on carcass traits of Nigerian indigenous turkey

Carcass traits	Male			Female		
	AA	AB	BB	AA	AB	BB
LIVER	51.08±2.40	51.40±2.44	52.22±4.59	49.93±2.60	47.80±3.66	46.25±3.01
FLGZ	88.54±3.80	89.00±2.72	98.67±3.54	95.63±4.57	91.90±9.27	91.00±4.90
EMGZ	57.31±2.49	55.40±1.30	62.33±4.15	61.78±3.13	60.40±6.42	56.75±3.87
SPLEEN	4.15±0.69	3.10±0.82	3.11±0.59	3.26±0.56	2.90±0.48	3.50±1.04
HEART	9.08±0.47^{ab}	10.40±0.88^{a}	8.89±0.75^{ab}	9.48±0.41^{ab}	9.80±0.96^{ab}	8.00±1.20^{b}
HEAD	69.19±1.98^{b}	68.70±4.86^{b}	56.67±2.75^{c}	82.74±14.85^{a}	63.10±2.82^{bc}	58.75±2.70^{c}
NECK	141.85±6.93	131.20±9.97	134.11±16.59	141.44±7.84	133.40±12.52	139.75±9.43
SHANK	73.92±3.26^{ab}	80.80±6.71^{a}	75.44±7.76^{ab}	73.89±3.72^{ab}	80.20±5.83^{a}	61.75±4.74^{b}
BRST	268.96±18.73^{ab}	246.70±32.99^{b}	337.33±35.02^{a}	300.22±17.93^{ab}	330.50±31.03^{a}	314.00±22.03^{ab}
WING	211.46±8.73^{ab}	192.10±18.91^{b}	233.67±14.16^{a}	196.96±8.36^{b}	198.40±12.16^{b}	190.25±12.09^{b}
THGH	198.12±8.92^{ab}	179.30±18.1^{b}	221.33±14.34^{a}	196.96±8.59^{ab}	204.40±13.97^{ab}	192.00±13.22^{ab}
DRST	235.15±9.77	221.60±19.82	253.67±12.14	243.33±6.67	241.60±7.55	236.88±8.42
BACK	305.15±14.71^{ab}	264.80±31.05^{b}	326.78±22.57^{a}	332.04±9.99^{a}	335.50±14.21^{a}	318.75±12.02^{a}
DFWT	1.79±0.08	1.92±0.17	1.80±0.19	1.80±0.09	1.76±0.13	1.77±0.12
EVWT	1.58±0.06	1.67±0.14	1.57±0.14	1.56±0.08	1.51±0.11	1.49±0.11
DRWT	1.28±0.04	1.3±0.1	1.22±0.11	1.21±0.06	1.17±0.09	1.19±0.08

$^{abc:}$ Means with different superscripts along the same row are significantly ($p<0.05$) different FLGZ: Full gizzard, EMGZ: Empty gizzard, BRST: Breast, THGH: Thigh, DRST: Drumstick, DFWT: Defeathered weight, EVWT: Eviscerated weight, DRWT: Dressed weigh

CHAPTER FIVE

DISCUSSION

5.1.1 Distribution of Allele and Genotype Frequencies for IGF1, IGF2, GH, GHR and Myostatin Genes

At the selected loci, three genotypes (AA, AB and BB) and two co-dominant allele (A and B) were detected across the three strains of indigenous turkey. This is signal of high genetic polymorphisms at the examined loci. Frequencies of genotypes and alleles obtained in the present study were dispersed and distributed among the strains. The differences observed for both co-dominant allele in the present study regarding their frequencies is an indication of their genetic distribution among the indigenous turkey strains studied. This might be ascribed to the difference in geographical locations where the turkeys were sampled. This result is in consistent with the work of Eichie *et al*., 2016 who obtained similar result on genetic diversity of prolactin gene in two strains of Japanese Quail sampled from different regions in Nigeria. Ali *et al*., 2013 also obtained similar findings at IGF1 locus in native Aseel chicken breed of Pakistan using PCR-RFLP as molecular marker. The highest genotype frequencies were observed in homozygote AA and heterozygote AB across the three strains for all loci studied except spotted strain of turkey at GH locus. This might be due to sharing of common allele A to AA and AB genotype. Allele frequencies obtained in this study were higher than frequencies obtained of B allele across the three strains of indigenous turkey at the studied loci. This is an indication of dominant effect of allele A over B allele. Results obtained in the current findings were in conformity to the findings of Wang and his co-workers (2004) who recorded greater frequency of allele A and genotype AB in Chinese locally adapted breeds and similar findings was also reported for frequency of allele A in Korean native ogol chicken (Seo *et al*., 2001). The report obtained in the present study showed that the

highest frequencies of A allele were in black strain at IGF1 locus, spotted strain at IGF2, GH and MSTN loci and white at GHR locus. This might be vindicated with the discoveries of Tang and his coworkers, (2010) who indicated that the individual carrying greater frequency of allele A exhibited superior weight gain in comparison with the ones conceded lesser frequency of allele A as is the case of Aseel chicken known for better meat production in comparison with Naked neck and Desi native chickens carrying lesser frequencies and are also low producers. Nehra and Singh, (2006) reported that up to 60% of the variance of IGF1 serum level has a genetic basis, therefore, the productivity of allele A at the studied loci is an indication of fast moving band which may be superior as a target candidate gene for selection and breeding of indigenous turkey in Nigeria.

At IGF1 & IGF2 loci, the chi-square test confirmed that the genetic frequencies of black strain was not in coordination with Hardy-Weinberg Equilibrium while those of spotted and white strains were in Hardy-Weinberg Equilibrium. At GH locus, black and white strains were confirmed to be deviated from HWE and spotted strain was in support of HWE concurrently.

At GHR and myostatin loci, spotted and white were not in conformity with HWE. The deviations of some of the strains of turkey from HWE at the studied loci might not be unconnected to the undetected insignificant alleles, superfluous of heterozygote population than homozygote population, migration, rapid rate of mutation and artificial selection in the population. Significant nonconformities of allele frequencies might also occur due to differential selection pressure, sampling, error, misclassification of genotypes, inability to identify rare alleles and the insertion of non-existing alleles, or if inbreeding has ensued in the population studied. The statistical significant deviation or conformity of some of the loci from Hardy-Weinberg proportions are in agreement with the findings of Farrag and his co-workers, 2013 who observed in their study that, none of the loci or studied sites of chicken population differed significantly from the Hardy-Weinberg proportions whereas the entire population of quail for the three microsatellite loci examined reflected statistical significant departure from Hardy-Weinberg equilibrium.

Obvious variations were observed in the distribution of IGF1, GH, GHR as well as myostatin generated genotypes in the current study across the three strains of indigenous

turkey in Nigeria. The difference among the three turkey strains at the studied loci might be connected to differential breeding antiquities. This conforms to the findings of Li *et al*., 2010 that studied the association at the locus DRB with Hydatidosis resistance in Chinese sheep.

5.1.2 Gene Flow and F-Statistics

The F-Statistics value Fit and Fst are measure of derivation from HWE proportion and total population. In the present study, positive values specify a deficit of heterozygotes while negative value indicates heterozygotes excess. The Fis reads indices of inbreeding. The values of Fis across the studied loci which indicate the degree of departure from random mating and a reflection of heterozygosity excess were significantly negative in the current findings. This is consistent with the finding of Tadano *et al*., 2012 who obtained similar result on commercial and 2 Nagoya lines of Japanese native chickens. This result contrasts result obtained by Zanetti *et al*., (2011) who obtained positive value of 0.042 for Fis in Italian chicken breeds signifying heterozygosity deficit and deviation from random mating due to inbreeding in the populations. It can be observed that at IGF1 locus negative values of Fit, Fis and Fst were higher compare to the rest of the loci. This might be connected to excess of heterozygotes, non-random mating and genomic altercation of individuals appearing more pronounce at this locus. This could be justified by Eichie *et al*., (2016) who suggested that nonexistence of any substantial inbreeding effects might be a reflection of great gene flow of individuals sustained by high gene flow value, the large population from which the sample were drawn and the fact that related individuals were purposively avoided. The negative values of Fit, Fis and Fst obtained at the five loci in the three strains studied showed deficit of homozygotes in the population and that male were less correlated in contrast with the average association of the individuals. Current result indicates that genetic diversity quantified by the studied loci as molecular markers shows genetic sustainability and differentiation among the strains of indigenous turkey in Nigeria. According to Slatkin 1987, genomic diversity will lead to substantial discrepancy where gene flow value is less than 1 but not where gene flow value greater than 1. In the present study, the estimated number of migrants or gene flow obtained at GHR, IGF2 and MSTN loci across the three strains of indigenous turkey in Nigeria were less than 1 which

implies that substantial flow of gene between the populations utilised leading to low measures of genetic disparity and inbreeding.

5.1.3 Heterozygosity

Heterozygosity coefficients which are measures of genetic diversity were similar in the populatins utilised. Nei expected heterozygsity obtained in this study ranged between 0.46 and 0.48 across the three strains of indigenous turkey studied which indicates diminutive genomic variation among the populations. Takezaki and Nie, 1996 recommended that marker should be in the range of 0.3- 0.8 in a population so as to to be expedient for measuring genetic diversity. The range of values recorded in the current findings is useful for measuring genetic variation of the candidate gene in the three strains of indigenous turkey in Nigeria. The relative higher value (0.48) of heterozygosity observed for black strain might be connected to low level of inbreeding, sampling error. This is justified by the work of Dalirsefat *et al*., 2015 who observed greater genomic diversity in Yimeng Blue population and Lindian among Chinese native blue-shells chickens recorded from whole genomic region of the SLCO1B3 red in the present study were lower than the range of values reported by Kowalska and Zatoń-Dobrowolska (2008) who reported heterozygosity coefficients in the range of 0.591 and 0.703 with an overall value of 0.655. However, all strains showed numerically close heterozygosities.

5.1.4 Genetic Distance and Dendrogram

The range of value (0.001-0.005) of genetic distance obtained in the current findings fall in the range of values of genetic distance reccommended for local breeds which is between 0.000 and 0.058. Elgendy *et al*., 2005 reported genetic distance values of 0.405 in Cairina species and 0.264 to 0.383 genetic distance values in Anas species using RAPD-PCR analysis of molecular charactisation of genetic biodiversity in ducks which were higher than the range of genetic distance values obtained in this result. However, spotted and white strains were genetically more distant from black strain. This result confirm the result of Nagamine and Higuchi (2001) who stated the expediency of genetic distances to categorise and explicate the ancestral relationship of individuals, level of genomic variation and antiquity of faunas. The importance of expending genetic distance estimates

to measure biodiversity, structural population and genetic alterations in white Pekin Muscovy ducks was also described by Maak *et al*., 2003.

The dendrogram conducted on the basis of genetics distance separated black strain from the other two populations of indigenous turkey in Nigeria indicating either early pre-historic separation of the black turkey strains or separate historical origin at their respective loci. The phylogenetic analysis has the protection of better genetic diversity, characteristics population structure and specie-specific genomic differentiation at the studied loci among indigenous turkey in Nigeria. The emphasis on severe breeding activities focused primarily into preservation and the potential progressive effect that might have been played by viable natural breeding activities in modeling the genomic variation of DRB gene as reported by Das *et al*., (2012). The interrelationships surrounded by the turkey strains in the present study are indications of continuous evolutionary patterns of the studied genes. This corroborates the assertion of Singh *et al*., 2012 that constant evolutionary array of DRB genes over various genera of mammals were assured through interrelationships between the spotted and white strains of turkey might be ascribed to potential interbreeding between the two individuals to form an identical population parted by physical geographic boundaries. Furthermore, the close genomic relationship between spotted and white strains may also be due to similarity in geographical location and production system in such populations. This confirms the work of El-Gendy *et al*., 2005 who obtain similar result between Sudani breed and Muscovy duck. The black strain of turkey in the present study appeared to be genetically distant from spotted and white strain. This might be connected to the different production trend in the studied population. Also, the closer level of relatedness between spotted and white strains as well as the standing out of black strain obtained in the current discoveries could be attributed to distinct plumage discrepancy which was possibly affected by measure of genetic distance. Due to the greatest value of Nei genetic distance (0.005) obtained in this result, cross breeding program between black and either of the two other populations is endorsed since the crosses between breeds which are homogenous but conspicuously dissimilar in their relationship is expected to provide hybrid vigour. In the present study, the dendrograms effectively revealed the original genetic history of indigenous turkey populations in Nigeria.

5.1.5 Biological interpretation of model parameter on growth of indigenous strain of turkey at IGF1, IGF2, GH and MSTN loci

Maturing rate, rate of gain and size at maturity are directly linked to economic of production and as such are essential traits which have engrossed consideration of breeders and poultry scientists particularly, the broiler enterprise. The utilisation of these parameters in growth models via curve fitting using weight-age data might change economic returns in a progressive way. Parameter A an estimate of mature weight. Larger estimate of parameter A is in some of the models in the present findings at their respective loci or variants is an indication that faunas are as weighty as adults and may be reported slow growing as these turkeys need more period to get to maturity in comparison to other poultry species. Malhado *et al*., 2009 opined that the definition of an optimum mature weight is controversial as its dependent on the species, breed, selection method, management system as well as environment. The parameter denotes rate of maturing translating to growth rate to reach asymptotic (mature) weight. However, parameter K is an important feature to be considered. Small value of K is an indication that the animal is late maturing. In the 5' flanking region of IGF1, Brody model predicted highest values of asymptotic weight for black and spotted strains BB and AA genotypes while the Batallanffy had highest asymptotic limit for white strains (BB) genotype of turkey. In the present study, logistic and Gompertz models had the lowest values for all the genotypes (AA, AB, and BB) across the three strains of indigenous turkey considered. This is consistent with Sengul and Kiraz (2005) who obtained lower values of A with the logistic model in comparison with the Gompertz model on a study conducted using non-linear

models for growth curves in large white turkey. Lower values of A obtained in the present study indicates different models predict different mature body weight in turkeys.

At exon 2 of IGF2, Brody model gives a highest asymptotic weight for black and white strains at AB and AA genotypes and Batalanffy gives the highest symptotic weight for spotted strain at AB genotype. The highest symptotic weights obtained for AA and AB genotypes in the exon 2 of IGF2 locus in the study could be ascribed to sharing of allele A that is common to both AA and AB genotypes. Highest asymptotic weight recorded for Brody and Batallanffy models in the current study is at variance to the work of Aggrey, (2002) who obtained higher value of asymptotic weight for Gompertz model for guinea fowl genotypes raised on the organic system.

In the 5' flanking region of GH, Brody model recorded the highest value of asymptotic weight for both black and spotted strains for heterozygote AB genotype and Batallanffy recorded highest value for white strains for BB genotype. The results obtained in this study is in contrast with the findings of Aggrey 2002 who reported that Richard and Gompertz models recorded highest asymptotic weight in a study conducted on comparison of three non-linear and spline regression models for describing chicken growth curves.

In the Exon 2 of MSTN, Brody model gives the highest estimates of asymptotic weight across the three strains with their respective individual genotypes AA and AB.

Generally, the larger estimates of asymptotic weight (A) were associated with smaller estimate of K and these were found for the Brody and Batallanffy models across the loci studied at their respective genotypes of the strains of indigenous turkey considered.

The discrepancies and high estimates of constant of integration (B) obtained in the current findings for all the strains in the logistic, Gompertz, Batallanffy and Brody models across the studied loci at their respective genotypes (AA, AB and BB) could be connected to dependence of parameter B on the ratio between weight at hatch (week 0) and mature weight in each model rather than the difference among strains and genotypes obtained. Maturing rate (k) equally connotes the constant rate of growth sustained till the animal reached the table size or adult weight. In the present study, the logistic model recorded the

highest k. The maturing rate (k) values which range from 0.01 to 0.22 across the three strains at the studied loci seem to be close to 0.096 and 0.105 stated for Dual-purpose sasso birds at all parameter for the black (AA) strain loci studied except BB genotype at IGF2 locus for spotted train. This implies that individual animal with genotype AA for black strain at IGF1, GH and MSTN loci and genotype BB at IGF2 locus for spotted strain got to maturity faster compared to the counterparts at reduced weight.

5.1.6 Ease of Computation

In the present study, Brody model had the highest number of iterations and more accurately fit the data but was computationally more difficult than the Gompertz, Logistic and Batallanffy models. The difficulty encountered in computing the Brody model in the current study is a possibility due to high starting values of its parameters or as a result of poorly conditioned matrices which may prevent convergence to a reasonable solution and increase number of iterations. This is consistent with the report of Brown *et al*., (1976) who mentioned particular difficulties faced at fitting the form of Richards function. The other three models converge with ease and were computationally simple. Non orthogonality of the fitted parameters may lead to estimates which are mathematically feasible but biologically impossible.

5.1.7 Correlation of the parameter estimates

The most imperative biologically correlation for a growth curve is between A and K parameters. In the current study, the greater k and the smaller A from the models but negatively correlated to k is an indication that the earliest animals are less likely to reveal great adult mass. da Silva *et al*. (2012) reached similar conclusions about the relationships between maturing rate mature weight of sheep. This is consistent with the findings of Adeyemi *et al*., (2018) in a related study on quails where females with lower maturity rate had higher mature weights. The negative correlation between Ak at the respective genotypes in relation the animals generally recorded in this study could be attributed to the variations in genes or differences among the strains considered.

5.1.8 Good of fit comparison for three strains of indigenous turkey at IGF1, IGF2, GH and MSTN loci

Coefficient of determination (R^2) and other goodness of fit criteria such as mean square error (MSE), Akaike Information Criteria (AIC) and Bayessian Information Criterian (BIC) have been used to evaluate model of best fit in some growth studies (Behzadi *et al*., 2014). The models that recorded highest R^2 value and lowest MSE and AIC values have been accepted as the best fitting for the data set.

At GF1 locus of 5' flanking region, logistic models was the most appropriate models that best described the data on the black and spotted strains of indigenous turkey on individuals homozygote AA and BB genotypes followed by Brody model that fitted best for white strain on heterozygote AB individual. The result of the current findings agree with the report of Adeyemi *et al*., 2018 who reported that logistic was the best model of fit for describing the growth of Japanese quail raised under different nutritional environments. Aggrey, (2002) also reported Brody model as the bet model of fit in the comparison of non-linear growth models to describe the growth curve of chicken.

At IGF2 and GH locus, Von-Batallanffy model resulted in the best fit model across the three strains of indigenous turkeys on individuals' heterozygote AB genotype. At myostatin locus, Gompertz model fitted best in black and white strains on homozygote BB individuals and in white spotted strain on homozyzgote AA genotype. The result of this study is consistent with the result of Yakubu and Madaki, (2017) who reported Gompertz model as the most effective non-linear growth model on modeling growth of dual-purpose sasso hens in the tropics using various algorithms. Several studies have reported Richards and Gompertz models as the most fitted models among for competing models. Individuals' genotype AB and BB that occur more frequent than individual AA genotype in the current findings might be attributed to sharing of allele B that is common to individuals AB and BB genotypes for the competing models studied across the three strains of indigenous turkey in Nigeria.

5.1.9 Growth curve describing weight-age relationship

In the present study, sigmoid patterns of growth curve were obtained. At 1-20 weeks old, the male body weight was about 25% higher than that of female bodyweight at the same age, this agrees with the findings of Yakubu and Madaki, (2017) due to the sexual dimorphism in duck that is considerable where mature male weight is 15% to 50% more than the one in female. The shape of the growth curve revealed that toms were generally heavier than its hen counterparts. The growth variance and dominance demonstrated by the tom submitted that it had a higher propensity for growth than the female turkey. This could be connected to hormonal and physiological differences which resulted in sexual dimorphism which was in favour of male. This conforms to the result of Gbangboche and his co-workers (2008) who obtained similar result in dwarf sheep in West Africa. This could also be ascribed to the difference in genomic influence of sex emanated from the male biological actions. It was equally described by Ibe and Nwosu (1999) that sex variances were frequently attributed to varied hormonal influence, ferociousness and dominance traits displayed by males particularly when both sexes are collectively raised. The lower bodyweight of the female turkeys could be as a result of lower hatching weight. Generally, male appeared to be heavier and bigger than female. This result was in consistent with report of Aggrey, (2002) in which males of the pearl grey variety of guinea fowl exhibited higher body weight than their female counterparts.

The result of the present study also showed that bodyweight increased in all three strains but values were slightly higher for black strain of the turkey than the either strains considered. This could be due to genetics and inherent variability in environment since all the strains were raised in the same pen and served similar feed and management. This is an indication that strains of turkeys utilised in the current findings are genomically varied from each other and the observed differences could be illuminated by the diverse geographical origin of the flocks. In the entire growth curve models case studied, the rate of growth increased with the increase age for all the three strains considered across the loci examined and the growth pattern of the three strains of individuals genotypes AA, AB and bb were similar for all the models except on AB and BB, BB individuals for the three strains at GH, IGF2 and myostatin loci where the four models cases considered were very

close. Looking closely at the four model curves, Von-Batallanffy model had the best fitting lines for all the three strains across the loci tested. This might be connected to the fact that, the observed and the predicted curves almost fall on the same line in comparison to the other model curves. Therefore under optimum growing conditions, the rate of maturing was the best in Von-Batallanffy equation that described the turkey growth.

5.1.10 Association of 5' flanking region at locus IGF1 with growth traits of indigenous turkey in Nigeria

The candidate gene approach has been an important tool to determine associations of gene polymorphism with production traits in livestock. In the present study, the IGF1 gene was one of the growth influencing genes selected to investigate association of gene polymorphisms with growth and carcass traits in the populations utilized. The effect of IGF1 gene polymorphism showed no genetic correlation from week 1 to week 17 with genotypes AA, AB and BB cross the three strains of indigenous turkey studied. This is an indication that black strain of indigenous turkey of BB individuals mature faster and bigger than its counterparts. The negative genetic correlation of the polymorphic variants (AA, AB and BB) obtained in the present study at IGF1 locus corroborate the work of Davis and Simmen 1997, who obtained similar result of IGF1 concentration with posthatch weights and gains. Genotype BB individuals of black strain of indigenous turkey had the lowest poult weight and highest bodyweight at week 21. This finding was in accordance with the report of Nagaraja *et al*., 2010 who obtained higher bodyweight for genotype BB individuals than AA and AB genotypes in domestic fowl. Nagaraja *et al*., 2010 also obtained no significant differences between genotypes of IGF1 gene polymorphism and bodyweight of chicken aged 140, 265 and 365days. Effects of IGF1 gene polymorphism on carcass traits were also studied in the present study. Polymorphism of IGF1 shows that it is a potential candidate gene associated with growth, body composition and caracass traits in chicken (Zhou *et al*., 2005). Study have shown that, IGF1 gene polymorphism is significantly related to the breasts and leg muscles of the chickens but this study shows that there were no significant relationship of the IGF1 gene with some of the turkey carcass traits, although higher mean value were observed in eviscerated weight, and internal organs weight, breast, wing, drumstick, back, thigh

muscles with genotype BB individuals than AB and AA genotypes across the three strains of indigenous turkey A significant difference was recorded on individuals with genotype BB with empty gizzard weight between spotted and white strains , with spotted strains having the higher mean value. Animals with genotype AB with black strain had selective advantage for neck weight than animals with AB genotype under white strain. Genotype BB individuals of black strain turkey had superior association with breast and back muscles in comparison with their counterparts under white and spotted strains. The superiority of B allele with bodyweight at certain age and some important carcass traits might be attributed to natural selection favoring animals carrying the B allele or variants having B allele may be artificially selected with other traits favored by artificial selection.

Association of IGF1 genotypes with sex did not follow a definite pattern as there were varying responses to growth indices by both sexes. Under SNP and sex interaction, individuals with BB genotypes stand to be more selected because they appeared to be more associated with bodyweight at weeks 1, 12, 14, 16, 18 and 21 as well as with wing and thigh muscles of both sexes having superior association with male turkeys. This is an indication that IGF1 gene and sex would help developing the genetic model for growth thereby improving performance of the animal and increase productivity.

5.1.11 Association of *IGF2* genotypes with growth and carcass traits of indigenous turkey

Insulin-like growth factor 2 (IGF2) is an imprinted gene expressed in most tissues affecting muscle content in farm animals and plays a vital role in livestock growth, influencing cell division and differentiation. Therefore, the coding region (exon 3) of IGF-II was examined for genetic markers. The alteration in variation in the exons was expedient for estimation of association with advantageous traits. The variation of IGF2 gene exon 3 could be connected to alternative variation in the IGF2 gene resulting in the alteration amino acid sequence.

The result of the present findings revealed the influence of IGF2 on posthatch growth and carcass traits. In the present study, no significant associations were recorded for all the IGF2 genotypes AA, AB and BB with bodyweight at weeks 1, 3, 5, 7, 9, 11 and 21 across

the three strains studied. This might be due to production of linkage disequilibrum (LD) with another mutation located in the IGF2 locus or another linked gene. However, genotype BB had significantly greater means for growth traits than the genotypes AA and AB in black and spotted strains at weeks 13, 15, 17 and 19 respectively. Though, the chief role of IGF2 gene is to regulate early growth in mammals but the present study showed it has an effect on chick stage of turkey. Individuals with genotype BB showed superior growth rate with black and spotted strains of turkey from week 13 to week 19. This might be attributed to dominant effect of B allele which might be associated with greater growth rate. The results of this study were consistent with the findings of Nagaraja *et al.,* 2010 who studied gene effect on bodyweight, carcass yield and meat quality of locally adapted chicken. The results of the current study corroborates with those of previous finding of Darling and Brickell, (1996) which confirm that IGF2 plays a pivotal role in chicken growth and development by stimulating myogenic cell lines proliferation, differentiation, and metabolism (Chao *et al*., 2008). However, the results are in divergence with the findings of Amills and his co-workers (2003), who reported similar coding region of the gene (exon 3). The significant influence may be ascribed to allele A to B substitution; the present outcomes infer that this substitution might lead to alterations in peptide sequence, which could change the action of the hormone. Therefore, variances in the genetic structure among the strains of indigenous turkey used in this study with those studied by Amills *et al*., (2003) and Zhang *et al*., (2008) might explain the inconsistent results. Polymorphic effects of 1GF2 were also examined on carcass traits in the current findings. In the present study, no results revealed significant associations of genetic variation in the exon 3 of IGF2 gene with carcass traits like liver, full gizzard weight, empty gizzard weight, spleen, heart weight, neck weight, shank weight, drumstick weight, back muscle, defeathered weight, eviscerated weight and dressed weight. This is an indication that, the aforementioned carcass traits showed no linkage disequilibrum (LD) with any of the polymorphic variants of IGF2 gene in the coding region. For head weight, Individuals with genotype AB showed superior association than homozygotes AA and BB. Therefore, this polymorphism may have overdominant effects on head weight. Animals with genotype AB had better carcass composition with breast, wing and thigh muscles in white and black strains of the populations utilised and it did not show significant relationship

with all carcass traits in spotted strain. However, allele B might be dominant and might be associated with better carcass composition and higher growth rate.

Association of IGF2 genotypes with sex did not follow a regular array as there were changing reactions to growth and carcass triats by both sexes. In the present study, there were no correlations in the coding region (Exon 3) with bodyweight at 1, 3, 5, 7, 9, and 17 weeks respectively. There were no significant relationship with of IGF2 variants (AA, AB and BB) with liver weight, full gizzard weight, empty gizzard weight, heart weight, defeathered weight, eviscerated weight, dressed weight, back weight, drumstick weight, thigh muscle, wing weight, shank weight as well as neck weight of both sexes. Animals with BB genotype stand to confer more selective advantage than AA and AB genotypes as they superior association with bodyweight at weeks 11, 13, 15, 19 and 21 as well as with breast weight, head weight and spleen weight. This is an indication that IGF2 gene and sex would help developing the genetic model for growth thereby improving performance of the animal and better carcass composition thereby increase productivity.

5.1.12 Association of 5' flanking region at the locus of Growth Hormone with growth traits of indigenous turkey in Nigeria

Study has shown that GH gene was a candidate gene associated with the growth and carcass traits in farm animals (Kuhnlein *et al*., 1997). In the current findings, the GH gene was chosen as a gene of interest to examine association of gene polymorphisms with growth and carcass traits in indigenous turkey populations. The findings of the current study detected novel variants of the 5' flanking region of the GH gene by genotyping. The results of the present study assessed association between various products of GH gene with growth and carcass traits including posthatch weight: 1-, 3-, 5- , 7-, 9-, 11-, 13-, 15-, 17-, 19- and 21-week weight and carcass weights: breast weight, back weight, drumstick weight, thigh weight, wing weight, shank weight, neck weight, head weight, heart weight, spleen weight, empty gizzard weight, full gizzard weight, live weight, eviscerated weight, defeathered weight and dressed weight respectively. The results showed that BB genotype was associated with bodyweight of black and spotted strains at week 13 of age and AB genotype was associated with bodyweight of both black and spotted strains from week 15 to 21 week of age. This is an indication that GH gene of AB and BB genotypes affect

mostly the growers' stage of turkey. AB and BB genotypes showed superior association with most of the carcass traits except drumstick, back, defeatehred, eviscerated, dressed, heart, neck and shank weights respectively. This might be due to allele B sheared by both genotype that conferred comparative advantage over allele A which did not show association with carcass traits. However, the strong associations of allele B with some of the carcass traits was assumed that to have a quantitative trait locus (QTL) regulating growth in the 5' flanking region and allele B was dominant to A and associated with growth and carcass traits. Research conducted by Breier, 1999 revealed that variants of GH gene had effect on growth, reproduction, skeletal integrity and metabolic absorption. In the current findings, the indigenous turkey strains examined provided an opportunity to identify the interface between the GH gene and the genetic history of three strains of turkey populations for growth and carcass traits. Interactions between the GH gene and the genetic background were identified for the associations between the polymorphic variants, growth and carcass traits across the strains of turkey populations, and this clarifies the significance of describing gene effects in particular populations for impending use like marker-assisted selection. In the present study, polymorphism of GH gene, and its effects on growth and carcass traits in black, spotted and white strains of indigenous turkey populations was reported. Based on the outcomes found from this study, it could be construed that variation in the 5' flanking region of GH gene influenced growth and carcass traits in the three turkey populations including hens and toms. Animals with genotypes AB and BB had comparative and selective advantage with growth traits at ages 18 and 20 weeks. AB and BB genotypes also showed superior association with some of the carcass traits. This is consistent with the findings of Shaw *et al*., 1991 who reported SNPs of intron 2 and 3 of GH genotypes relationship with specific economically important traits in domestic duck. This is an indication that the AB and BB genotypes might perhaps served as a molecular marker for better growth traits and better carcass composition.

5.1.13 Association of exon 2 at the locus of myostatin gene with growth traits of indigenous turkey in Nigeria

Myostatin is autocrine signal protein secreted by muscle and acts as a negative regulator of muscle growth. The high polymorphic tendency of the DNA sequence of the myostatin gene, which has been detected in earlier works (Baron *et al*., 2002; Dunner *et al*., 2003) was further obtained in the current findings in the three strains of indigenous turkey in Nigeria. In the current study, three genotypes AA, AB and BB were detected with corresponding alleles A and B were identified.

Homozygote BB conferred comparative advantage on bodyweights at weeks 5, 13, 15, 17 and 19 in black and white strains and in black and spotted strains at 21 week. The results of this study also showed that, AA and AB genotypes had higher significant effect on bodyweights of male turkey than female. Associations of some of the genotypes with bodyweights at this locus in the population studied may be due to the alteration in amino-acid sequence in exon 2 at myostatin locus, although functional analysis will be needed to verify this. This indicates that, because the key role of myostatin gene is regulation of skeletal muscle growth, therefore, alterations in its protein sequence is a possibility which can transform growth function. In this study, the identified associations of the different genotypes with bodyweights at different ages might be connected to their linkage disequilibrium (LD) with other polymorphisms that occur in exon 2 of myostatin or to quantitative trait loci (QTL) beyond the myostatin gene. The results of this findings is in agreement with the work of Gu *et al*., (2004) who reported a polymorphic site in the 5'regulatory region of myostatin, which was associated with hatch weight in F2 chickens from a broiler by Silky cross.

Polymorphic effects of myostatin gene were also examined on carcass traits of turkey in the present study which showed no significant associations with carcass traits like liver, full gizzard weight, empty gizzard weight, spleen, heart weight, neck weight, defeathered weight, eviscerated weight and dressed weight. This is an indication that, the aforementioned carcass traits showed no linkage disequilibrum (LD) with any of the polymorphic variants of myostatin gene in the exon 2. Individuals with homozygote BB showed superior association with spleen and heart weights. Therefore, this polymorphism may have overdominant effects on spleen and heart weights. Animals with genotype AB

had better carcass composition with breast, wing, drumstick and back muscles in black and spotted strains of the populations utilised and it did not show significant relationship with all carcass traits in spotted strain. Associations of some of the genotypes with two or more carcass traits might be due to the pleiotropic effect of the myostatin gene in the populations utilised. The results of this study corroborates the report of Gu *et al*. (2004) who found homozygous genotypes AA and BB at a locus in the 5'regulatory region to be associated with higher abdominal fat weight and abdominal fat percentage than AB in the F2 chickens from a cross of broiler and Silky chickens.

CHAPTER SIX

6.1 CONCLUSIONS AND RECOMMENDATIONS

Findings reported from this research represent the first molecular documentation of IGF1, IGF2, GH, GHR and myostatin genes in the three strains (black, spotted and white) of indigenous turkey in Nigeria. The presence of SNPs in the specified exon and flanking regions obtained from the studied genes is an indication that the genes were polymorphic. Allele A showed dominant effect on B across the five growth-influencing genes examined. For all loci studied across the three stains such as black, spotted and white indigenous turkey populations utilised, homozygote AA and heterozygote BB recorded highest genotype frequencies except in spotted strain of turkey at IGF1 locus. The black strain of indigenous turkey population conformed with Hardy-Weinberg Equilibrum (HWE) at IGF1 and IGF2 consequently. At GHR and myostatin loci, spotted and white populations were deviated from HWE and at GH locus, black and white populations were conformed with HWE. The deviations from HWE of some of the studied populations at varying loci are reflection of selection pressure differential. The estimates of heterozygosity and fixation indices obtained using information from the growth-influencing genes examined were within the recommended range for measuring genetic diversity among turkey populations and as such, the estimates were useful in the study of three strains of indigenous turkey in Nigeria. The fixation indices estimate in this study indicated to some extent the degree of departure from random mating. The genetic distance across the entire loci examined showed that, the spotted and white populations of indigenous turkey were the most genetically related. Phylogenetic tree constructed revealed great diversity and interrelatedness among the different strains of indigenous turkey in Nigeria.

The high coefficient of determination (R^2) for the four models, namely Brody, Gompertz, Logistic and Von-Batallanffy indicate that the models were adequate in describing the

growth pattern of indigenous turkey in Nigeria at different gene loci examined. On the basis of goodness of fit criteria; R^2, MSE, AIC and BIC values, the Logistic was the best model of fit for black and spotted strains of indigenous turkey on individuals with homozygote AA and BB genotypes and Brody model for white strain on heterozygote AB individual at IGF locus. Von-Batallanfy model fitted best across the three strains of indigenous turkey on heterozygote AB genotype at IGF2 and GH loci. Gompertz model fitted best in black, white and spotted strains of indigenous turkey on AB and AA individual genotypes at myostatin locus. The shape of the growth curve reflected that toms were generally heavier than hens. Bodyweight of the indigenous turkey increased across the three strains utilised but values were higher for black strain than its counterparts. Individuals with genotypes AB and BB across the loci examined had higher proclivity for growth and better carcass composition than AA genotype. At the myostatin locus, genotype BB significantly influenced the bodyweight in toms.

Variations at the IGF1, IGF2, GH, and myostatin loci associated with some of the growth and carcass traits obtained in this study are indications that the studied loci are potential molecular markers for improvement of growth rate and better carcass composition of indigenous turkey in Nigeria and this may help breeders and researchers to develop new characteristics in response to changes in environment and maintain genetic diversity as well as improve productivity. The results of this study support significant diversity at the selected loci which may have functional impact on growth performance and productivity in different indigenous turkey strains in Nigeria.

Based on the highest result of Nei genetic distance obtained in this result, cross breeding program between black and either of the two other populations is suggested in the meantime the crosses between strains which are similar but conspicuously varied in their relationship is expected to breed heterosis. Future conservation and effective management policies are recommended for optimum growth and productive performance of the three turkey strains. The result of the growth modeling indicated that weight gain of indigenous turkey was highest in black strain and this could be considered additional information for use in selective breeding programs. Future studies regarding growth modelling on indigenous turkey should span the period of the experiment beyond 21weeks before

terminating the experiment so as to attain point of inflection in growth curve and to allow turkey full maturity. The genetic markers obtained in this research may be supported with genome-wide association studies (GWAS) so as to explore the whole genome with the possibility of obtaining all the genes responsible for growth and carcass traits. To validate the associations between growth influencing genes with economically important traits, additional study should be repeated in bigger independent populations from numerous locations and several traits like meat yield and quality, disease and heat resistance should be applied in the selection objective.

CONTRIBUTION TO KNOWLEDGE

- Findings reported in this study represent the first molecular documentation of Insulin-Like Growth Factors 1 and 2 (IGF1, 1GF2), Growth Hormone (GH), Growth Hormone Receptor (GHR) and myostatin genes of indigenous turkey in Nigeria.

- Individuals with genotype BB across the loci had higher propensity for growth and better carcass composition than AA and AB genotypes.

- Von-Batalanffy was the best model of fit on AB genotype across the populations of indigenous turkey in Nigeria at Insulin-Like Growth Factors 2 (IGF2) and Growth Hormone (GH) loci.

- Black strain of indigenous turkey in Nigeria was the most superior in growth rate in comparison with spotted and white strains.

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