

Expression of Ghrelin Gene in Chicken Using Semi-Quantitative Digital Analysis

Babatunde Moses ILORI¹ (✉)
Omotomiwa Abiodun OSIKOMAIYA¹
Babajide Samuel OBIMAKINDE¹
Samuel Olutunde DUROSARO¹
Mohammed Okanlawon ONAGBESAN²
Ayotunde Olutumininu ADEBAMBO¹

Summary

The study investigated Ghrelin gene (GHRL) expression patterns in improved Nigerian indigenous Normal feather and naked neck FUNAAB Alpha chicken. Data on body weight and weight gain were collected weekly for 24 weeks. Beginning from 12 weeks of age, two males and two females were slaughtered per genotype via cervical dislocation fortnightly until the birds reached the point of lay at 24 weeks. Tissue samples from the liver, ovary, and testes were removed aseptically, weighed, and RNA stored for analysis of gene expression. The total RNA of each tissue sample was extracted using the Quick RNA™ MicroPrep kit. Reverse transcription was also carried out using SensiFAST™ cDNA Synthesis Kit. A semi-quantitative analysis of reverse transcription was carried out by densitometric scanning. The collected data were analyzed through two-way analysis of variance (ANOVA) using the general linear SAS model. Genotype and sex were observed to have significant effect ($P < 0.05$) on body weight. Normal feather chickens and male chickens had a higher body weight. Semi-quantitative analysis of GHRL mRNA showed significant expression levels in the liver, ovary, and testes samples of both naked and normal feather chickens. Male and female naked neck chickens had significantly higher expression levels of the ghrelin gene at puberty. Normal feather chickens had significantly higher ghrelin mRNA expression levels throughout all weeks in the ovaries and testes. Our results suggest that chicken ghrelin expression may be related to tissue, age and chicken genotype.

Key words

ghrelin gene, growth, expression, indigenous chicken, polymerase chain reaction-electrophoresis

¹ Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria

² Department of Animal Physiology, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria

✉ Corresponding author: ilorim08@gmail.com; iloribm@funaab.edu.ng

Introduction

Ghrelin (GHRL) plays an important role in the regulation of energy metabolism due to its involvement in the hypothalamic melanocortin pathway (Jeong et al., 2014). Ghrelin stimulates food intake according to its orexigenic effect by activation of NPY/AgRP neurons (Chen et al., 2004). Ghrelin is usually a product of gastric tissue but its expression has been reported in a large array of tissues and cell types including the small intestine, pancreas, lymphocytes, placenta, kidney, lung, pituitary, brain, liver, and the gonads (Barreiro and Tena-Sempere, 2002; Gualillo et al., 2003; Van der Lely et al., 2004). One of the functional features of ghrelin that has attracted more attention is its ability to stimulate food intake and promote body weight gain. As an orexigenic signal, expression of ghrelin has been shown to increase after food deprivation and its plasma levels are (in most cases) negatively correlated with the body mass index. On this basis, ghrelin has been proposed as a unique circulating signal for energy insufficiency (the only known circulating orexigen), which may play a major role in the short- and long-term control of body weight (Cummings, 2006; Zigman and Elmquist, 2003). It is assumed that ghrelin plays an important role in feed efficiency because it is used to maintain energy balance (Wortley et al., 2004). Furthermore, the potential association between polymorphisms within the GHRL locus and economic traits have been investigated (e.g., feed intake, feed-gain ratio, body weight, the efficiency of growth) in different species of chicken (Jin et al., 2014). Ghrelin participates in the control of major areas of reproductive function (Arvat et al., 2001). It stimulates lactotroph and corticotroph functions, influences the pituitary–gonadal axis, inhibits pro-inflammatory cytokine expression, controls gastric motility and acid secretion and influences pancreatic exocrine and endocrine function (van der Lely et al., 2004; Otto et al., 2005). Ghrelin participates in the control of reproductive function both in male and females while sex differences may exist in the physiological extent of this control. Ghrelin has been found not only in the stomach and other parts of the gut but also in all the tissues (adrenal gland, atrium, breast, buccal mucosa, oesophagus, fallopian tube, fat tissue, gall bladder, human lymphocytes, ileum, kidney, left colon, liver, lung, lymph node, muscle, myocardium, ovary, pancreas, pituitary, prostate, right colon, skin, spleen, testes, thyroid and vein; (Gnanapavan et al., 2002).

The improved Nigerian indigenous chickens (FUNAAB Alpha) are bred as a dual-purpose chicken. It is newly registered and has been made commercially available for both meat and egg production in the rural and peri-urban areas of the country (Ilori et al., 2017; Yakubu et al., 2019). The traditional Nigerian indigenous chicken from which they were selected and improved for over many generations are found in large numbers distributed across different agroecological categories under a traditional family-based scavenging management system (Sonaiya and Olori, 1990; Ilori et al., 2017). Most of the birds are kept in small flocks in a scavenging system and the feed resources for the birds are household refuse, homestead pickings, crop residues, herbage, seeds, green grasses, earthworms, insects, and a small amount of supplemented feeds offered by the flock owner. They are well adapted to the adverse climatic conditions of the varied tropical

environmental and ecological conditions, stresses, and diseases, and characterized by low management inputs. They contain a highly conserved genetic system with high levels of heterozygosity and are highly important farm animals, kept for good sources of animal protein, income and socio-cultural roles (Ebozoje and Ikeobi, 1995; Wimmerset et al., 2000; Ajayi, 2010; Ilori et al., 2017). The Nigerian indigenous chickens are slow-growing and possess major genes that assist in early adaptation to the environment so that these genes cause a reduction in tropical heat stress (Peters, 2005). Genetic improvement of indigenous breed of livestock is very valuable because of high adaptability to harsh environmental conditions of climate and disease compared to exotic breeds (Ajayi and Agaviezor, 2016). Growth trait is a very important economic trait in chickens production and is controlled by complex genes. In poultry, growth rate and mature body weight are highly related to circulatory growth hormones level (Anthony et al., 1990), an example of which is the GHRL gene.

The semi-quantitative measurement of PCR amplicons using digital analysis of PCR-electrophoresis gels with ImageJ software is a semi-quantitation method of nucleic acids and immunoblot assays that allow laboratories with limited resources to empirically assess the relative amount of amplified PCR amplicons (Abramoff et al., 2004; Antiabong et al., 2016). It is a process that uses the agarose gel image analysis method for the semi-quantitation of PCR amplicons unlike the quantitative polymerase chain reaction (qPCR) also known as Real-Time PCR which uses different fluorescent reporters technologies in analyzing the relative amplicons of nucleic acid (Van Guilder, 2008). The semi-quantitative digital image endpoint analysis of PCR products is an easily accessible technology in laboratories in developing countries, cost-effective, and requires a less skilled manpower.

One of the most important applications of DNA arrays so far is the monitoring of gene expression (mRNA abundance). The collection of genes expressed or transcribed from genomic DNA sometimes referred to as the expression profile or the transcriptome, is a major determinant of cellular phenotype and function. The transcription of genomic DNA to produce mRNA is the first step in the process of protein synthesis, and differences in gene expression are responsible for both morphological and phenotypic differences as well as indicative of cellular responses to environmental stimuli and perturbations. In terms of understanding the function of genes, knowing when, where and to what extent a gene is expressed is central to understanding the activity and biological roles of its encoded protein. Also, changes in the multi-gene patterns of expression can provide clues about regulatory mechanisms and broader cellular functions and biochemical pathways (Lockhart and Winzeler, 2000).

This study established the temporal changes in expression levels of the ghrelin gene in different tissues of the liver, ovary, and testes during development in male and female improved Nigerian indigenous chickens of naked neck and normal feather chickens as a candidate gene for growth performance using the semi-quantitative digital analysis of PCR gel electrophoresis.

Materials and Methods

Experimental Location and Birds

This experiment was conducted at the Programme for Emerging Agricultural Research Leaders (PEARL) Unit of the Poultry Breeding Unit located at Teaching and Research Farms, Directorate of University Farms (DUFARMS) of the College of Animal Science and Livestock Production (COLANIM), Federal University of Agriculture, Abeokuta, Ogun State Nigeria. The experimental site was earlier described by Ilori et al. (2018). A total of 80 FUNAAB Alpha chicks comprising 16 males and 21 females naked neck, and 19 males and 24 females normal feather chickens were obtained from the FUNAAB hatchery. The birds were brooded from day-old to four weeks of age and reared on a deep litter floor in an open-sided poultry house from day old to six weeks of age and then transferred to the cage until they started laying at 24 weeks. They were fed *ad libitum* with a standard diet at the different phases. Cool and clean water was also provided without restriction. The experiment was conducted in April through September 2018 which is the period of rainfall in Southwest Nigeria. The study was conducted following the code of ethics for animal experimentation with prior approval from the Animal Care and Use Committee of the Federal University of Agriculture, Abeokuta, Nigeria Animal Ethics Committee.

Data and Tissue Collection

Body weight data were collected weekly and recorded in grams, and then weight gain was also estimated from weekly body weights. Four experimental birds for each genotype comprising of two males and two females were slaughtered fortnightly via cervical dislocation, commencing from 12 weeks of age until the birds started laying and the experiment terminated at 24 weeks (at 24th week the birds had reached 50% lay). The method of cervical dislocation was chosen as it quickly separates the spinal cord from the brain, provides fast and painless death of the bird, and also allows for easy extraction of organs. Tissues (liver, ovary, and testes) were removed aseptically, cleaned off, and weighed. The weight in grams of the organs was divided by the weight of the birds from which the organs were extracted and multiplied by 100% expressed as a percentage of the birds' weight at slaughter and then recorded as the relative weight of the organs. Each organ sample was preserved in a 1.5ml Eppendorf tube containing 500 μ l of RNA lysis buffer and stored in a -80 °C ultra freezer until the expression analysis.

RNA Extraction and Reverse Transcription (RT)-PCR Assay for GHRL Gene Expression

The total RNA of each tissue sample (0.5 g) of liver, testes, and ovaries were extracted using an animal tissue RNA purification kit according to the manufacturer's protocol (Quick RNATM MicroPrep ZYMO Research USA). The quantity and integrity of isolated RNA were determined for each sample using NanoDrop 2000 Spectrophotometer (Thermo Scientific Inc, Wilmington, Delaware, USA). Reverse transcription was performed with the SensiFASTTM cDNA Synthesis Kit according to the manufacturer's protocol in a Multigene Optimax thermocycler (Labnet International, Inc., U.S.A).

Amplification of cDNA by Polymerase Chain Reaction

This involves amplification of cDNA by polymerase chain reaction (PCR). RT products were used as a template DNA for the polymerase chain reaction (RT-PCR) of chicken Ghrelin gene fragment of 195 bp (Lu et al., 2008). Each PCR was performed in a 15 μ l reaction volume containing: 1.0 μ l of template with 10 ng cDNA, 3.0 μ l of PCR master mix (FIREPol[®]Solis Biodyne UK) which contains: *Taq* DNA polymerase, dNTPs, reaction buffer, MgCl₂, KCl, blue dye, yellow dye and PCR enhancer/stabilizer; 1.0 μ l of 0.4 μ M forward primer (5'-CTG AGA GAG CAA CGG AAG T-3'), 1.0 μ l of 0.4 μ M reverse primer (5'-GCA AAT AAA GAG TGA GGG G-3'), and 9.0 μ l nuclease-free water. Amplification for Ghrelin primer followed Lu et al. (2008) using annealing temperatures of 47.7 °C for 30 secs. PCR reactions were carried out in a Multigene Optimax thermocycler (Labnet International, Inc., U.S.A). Electrophoresis of the different PCR amplicons for the different tissue samples was carried out in 1% agarose using 5 μ l of amplicon and 100 bp molecular marker (NorgenBiotek Corporation, Canada) and using EtBr (Boi-rad, Australia) dye in tris-acetate ethylenediaminetetraacetic acid (TAE) buffer. Agarose gel electrophoresis was carried out at 120 Volt for 60 min. Fresh TAE buffer was prepared for each electrophoresis to prevent any additive effect of residual EtBr on the PCR band density. The band size and DNA concentration of each PCR amplicon was determined by comparison with the corresponding band in the molecular weight ladder that has been predetermined by the manufacturer. Images of the bands in the gel were captured under ultraviolet (UV) light and documented using a Digital Doc gel documentation system (Bio-rad; Australia) with constant UV exposure time with adjustable exposure time while all the experimental conditions and parameters used were kept constant in the study.

Digital Analysis of PCR Bands on Electrophoresis Gel

Semi-quantitative evaluation of RT signals was carried out by densitometric scanning as described (Antiabong et al., 2016) using image J Gel semi quantification software. A semi-quantitative method for conventional PCR amplicons uses digital image analysis of electrophoretic gel for quantitation of the relative amount of the amplified PCR amplicon. Digital analysis of agarose gel image method for the semi-quantitation of PCR amplicons (Abramoff et al., 2004) has been successfully applied in quantitative immunoblot assays and nucleic acid quantitation (Berchtold et al., 2007; Rai et al., 2010; Antiabong et al., 2016). Since ImageJ software measures the individual band densities by relative comparison of all the band characteristics in a single gel, samples were run on the same gel to ensure accuracy. The trends observed in different gel analyses was then compared. The size, thickness, density, picture format of the agarose gel, reagents, and other conditions was also kept constant. These were ensured to normalize the PCR reactions.

Statistical Analysis

The collected data were analyzed by two-way analysis of variance (ANOVA) using the General Linear Model (GLM) procedures of the SAS Institute (SAS 2001). The means comparison was performed using Duncan's Multiple Range Test at 5%

probability level. Preliminary analysis of the interaction between genotype and sex was not significant and therefore excluded from the analysis.

$$\text{Model is: } Y_{ijk} = \mu + G_i + S_j + E_{ijk}$$

where:

Y_{ijk} = Body weight and weight gains

μ = population mean

G_i = effect of i th genotype

S_j = effect of j th sex

E_{ijk} = residual error

Results

The performance of Nigerian indigenous chicken in terms of body weight and weight gain are presented in Table 1. The result of this study showed a significant effect ($P < 0.05$) of genotype on body weight from week 0 to week 20, except at week 24 where genotype was observed to have no significant effect ($P > 0.05$) on body weight. The mean body weight ranged from 43.91 ± 0.96 g and 48.74 ± 1.59 g at week 0 in the naked neck and normal feather respectively to 2228.0 ± 73.32 g and 2378.5 ± 197.16 g at twenty-four weeks. Genotype also had a significant effect ($P < 0.05$) on weight gain from week 4 to week 16 except at weeks 20 and 24 where there was no significant difference ($P > 0.05$). A steady increase in body weight was observed in the two genotypes with

an increase in age of the birds, and the normal feather genotype have a higher body weight and weight gain than the naked neck genotype in all ages.

The effect of sex on body weight and their weight gain of Nigerian Indigenous chicken are presented in Table 2. Sex had a significant effect ($P < 0.05$) on body weight and weekly weight gain of both sexes from week 8 to week 20, however a significant difference was not observed at weeks 0, 4, and 24 in body weight and weight gain of both sexes. The male birds had higher body weight and weight gain than the female birds at all weeks. The mean body weight ranged from 47.95 ± 1.85 g and 45.54 ± 1.08 g at week 0 in male and female chickens to 2391.40 ± 200.62 g and 2101.00 ± 100.01 g at twenty-four weeks respectively.

Table 3 shows the effect of the genotype on the liver weight of Nigerian indigenous chicken at different weeks. The effect of genotype was not significant effect ($P < 0.05$) on liver weight except at week 12 where the naked neck genotype had a higher liver weight than the normal feather genotype. There was no significant effect ($P < 0.05$) of sex on liver weight in all weeks, except at week 18, where males had significantly higher liver weight than the females (Table 4).

Table 5 shows the effect of genotype on testes weight of Nigerian indigenous chicken at different weeks. Genotype had no significant effect ($P < 0.05$) on testes weight from week 12 to week 18. However, a significant effect ($P < 0.05$) of genotype on testes weight was observed from week 20 to week 24 with a higher significant weight in the naked neck genotype.

Table 1. Least squares means of body weight and weight gain as affected by genotype in Nigerian indigenous chickens

Age (weeks)	Genotype	No of observation	Body weight	Weekly weight gain
0	Naked Neck	80	43.91 ± 0.96^b	-
	Normal Feather		48.74 ± 1.59^a	-
4	Naked Neck	80	272.96 ± 9.34^b	52.68 ± 3.64^b
	Normal Feather		364.56 ± 15.41^a	69.96 ± 5.55^a
8	Naked Neck	80	591.27 ± 22.76^b	104.14 ± 7.77^b
	Normal Feather		840.85 ± 38.66^a	143.41 ± 10.04^a
12	Naked Neck	72	883.29 ± 36.94^b	59.41 ± 6.00^b
	Normal Feather		1298.63 ± 66.67^a	93.26 ± 9.45^a
16	Naked Neck	64	1151.15 ± 46.67^b	60.15 ± 7.16^b
	Normal Feather		1652.40 ± 99.59^a	111.60 ± 10.42^a
20	Naked Neck	56	1524.13 ± 89.24^b	95.13 ± 16.18
	Normal Feather		2273.17 ± 181.20^a	106.00 ± 21.42
24	Naked Neck	48	2228.0 ± 73.32	71.5 ± 11.84
	Normal Feather		2378.5 ± 197.16	86.5 ± 9.52

Note: ^{ab} - means with different superscripts on the same row for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test

Table 2. Least squares means of body weight and weight gain as affected by sex in Nigerian indigenous chicken

Age (weeks)	Genotype	No of observation	Body weight	Weekly weight gain
0	Naked Neck	80	47.95 ± 1.85	-
	Normal Feather		45.54 ± 1.08	-
4	Naked Neck	80	341.00 ± 12.89	63.09 ± 4.12
	Normal Feather		310.25 ± 15.49	60.79 ± 1.86
8	Naked Neck	80	795.19 ± 40.30 ^a	146.67 ± 11.75 ^a
	Normal Feather		679.00 ± 34.41 ^b	110.11 ± 7.43 ^b
12	Naked Neck	72	1275.87 ± 80.67 ^a	106.73 ± 10.68 ^a
	Normal Feather		978.67 ± 46.17 ^b	56.24 ± 4.97 ^b
16	Naked Neck	64	1784.55 ± 119.65 ^a	123.64 ± 13.29 ^a
	Normal Feather		1191.53 ± 45.86 ^b	64.47 ± 5.68 ^b
20	Naked Neck	56	2370.40 ± 124.79 ^a	149.80 ± 22.34 ^a
	Normal Feather		1541.67 ± 77.31 ^b	72.60 ± 11.49 ^b
24	Naked Neck	48	2391.40 ± 200.62	74.67 ± 9.61
	Normal Feather		2101.00 ± 100.01	92.00 ± 8.01

Note: ^{ab} - means with different superscripts on the same row for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test

Table 3. Least squares means of liver weight as affected by genotype in Nigerian indigenous chickens

Age (weeks)	Number of observation	Liver weight (g)	
		Normal feather	Naked neck
12	8	1.84 ± 0.08 ^b	2.77 ± 0.05 ^a
14	8	2.25 ± 0.19	2.23 ± 0.12
16	8	2.46 ± 0.43	1.91 ± 0.23
18	8	2.11 ± 0.29	2.37 ± 0.16
20	8	1.83 ± 0.50	2.05 ± 0.29
22	8	2.87 ± 0.25	2.31 ± 0.11
24	8	1.62 ± 0.43	1.69 ± 0.22

Note: ^{ab} - means with different superscripts on the same row for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test

Table 4. Least squares means of liver weight as affected by sex in Nigerian indigenous chickens

Age (weeks)	Number of observation	Liver weight (g)	
		Male	Female
12	8	2.23 ± 0.27	2.24 ± 0.30
14	8	2.103 ± 0.14	2.43 ± 0.14
16	8	2.34 ± 0.49	2.07 ± 0.08
18	8	2.25 ± 0.06 ^a	1.39 ± 0.08 ^b
20	8	1.26 ± 0.30	2.08 ± 0.31
22	8	2.49 ± 0.23	2.68 ± 0.25
24	8	1.32 ± 0.14	1.97 ± 0.07

Note: ^{ab} - means with different superscripts on the same row for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test

Table 5. Least squares means of testes weight as affected by genotype at different weeks

Age (weeks)	Number of observation	Testes weight (g)	
		Naked neck	Normal feather
12	8	0.91 ± 0.02	0.73 ± 0.04
14	8	1.22 ± 0.32	0.94 ± 0.34
16	8	1.51 ± 0.43	1.00 ± 0.23
18	8	1.64 ± 0.29	1.35 ± 0.26
20	8	2.86 ± 0.68 ^a	1.96 ± 0.61 ^b
22	8	3.00 ± 0.55 ^a	2.04 ± 0.82 ^b
24	8	3.80 ± 0.98 ^a	2.85 ± 0.35 ^b

Note: ^{ab} - means with different superscripts on the same row for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test

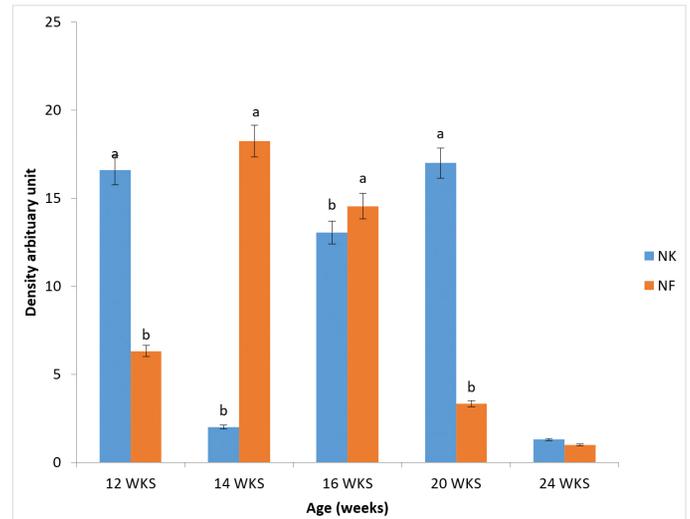
The effect of the genotype on the ovary weight of Nigerian indigenous chicken at different weeks is shown in Table 6. Genotype had no significant effect on ovary weight from week 12 to 18. However, a significantly higher ($P < 0.05$) ovary weight in the naked neck genotype was observed from week 20 to week 24.

Table 6. Least squares means of ovary weight as affected by genotype at different weeks

Age (weeks)	Number of observation	Ovary weight (g)	
		Naked neck	Normal feather
12	8	1.30 ± 0.68	1.15 ± 0.04
14	8	1.41 ± 0.52	1.29 ± 0.14
16	8	1.88 ± 0.55	1.35 ± 0.27
18	8	2.00 ± 0.29	1.38 ± 0.26
20	8	2.98 ± 0.44 ^a	1.56 ± 0.76 ^b
22	8	3.55 ± 0.55 ^a	2.04 ± 0.82 ^b
24	8	3.99 ± 0.78 ^a	2.22 ± 0.55 ^b

Note: ^{ab} - means with different superscripts on the same row for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test

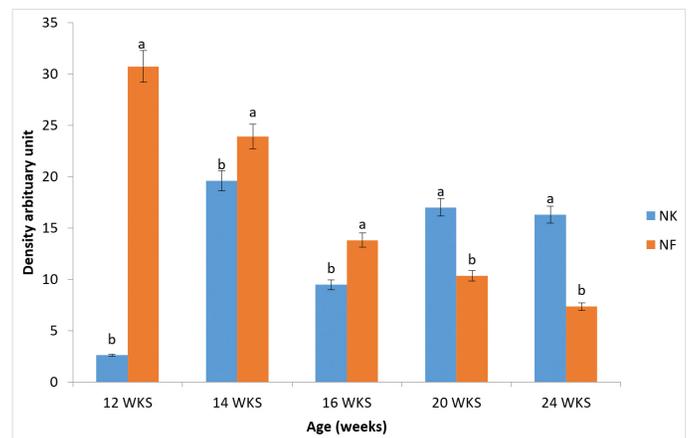
Fig. 1 shows the semi-quantitative analysis of ghrelin mRNA in the liver samples of the naked neck and normal feather male chickens. Significant differences ($P < 0.05$) were observed in the expression levels of ghrelin mRNA in the liver of the two genotypes except at week 24. The naked neck males had a higher expression level of ghrelin mRNA at weeks 12 and 20 while the normal feather males also had a higher level of GHRL mRNA at weeks 14 and 16.



Note: ab - bars with different superscripts for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test; NK = Naked neck chicken; NF = Normal feather chicken

Figure 1. Expression level of GHRL mRNA in liver samples of the naked neck males and normal feather males chickens at different weeks

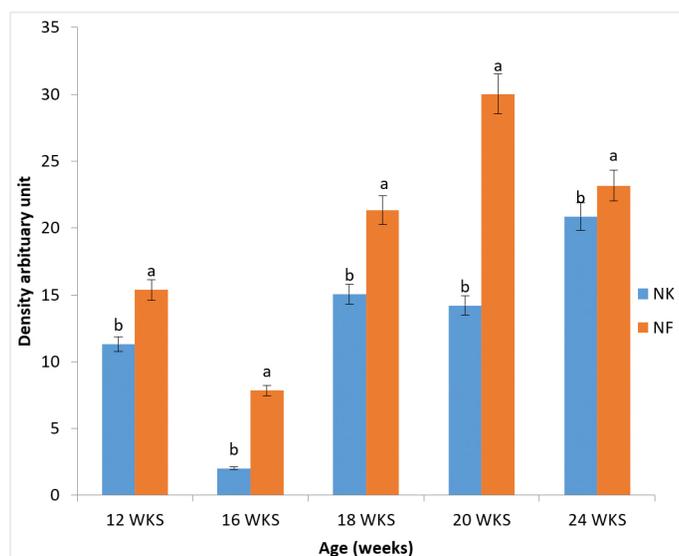
Semi-quantitative analysis of ghrelin mRNA in the liver samples of the naked neck and normal feather female chickens is shown in Fig. 2. Significant ($P < 0.05$) ghrelin mRNA expression levels were observed across all weeks considered, with a significantly higher expression level at weeks 12, 14, and 16 in the normal feather chicken while the naked neck was observed to have a higher expression level at weeks 20 and 24.



Note: ab - bars with different superscripts for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test; NK = Naked neck chicken; NF = Normal feather chicken

Figure 2. Expression level of GHRL mRNA in liver samples of the naked neck and normal feather female chickens at different weeks

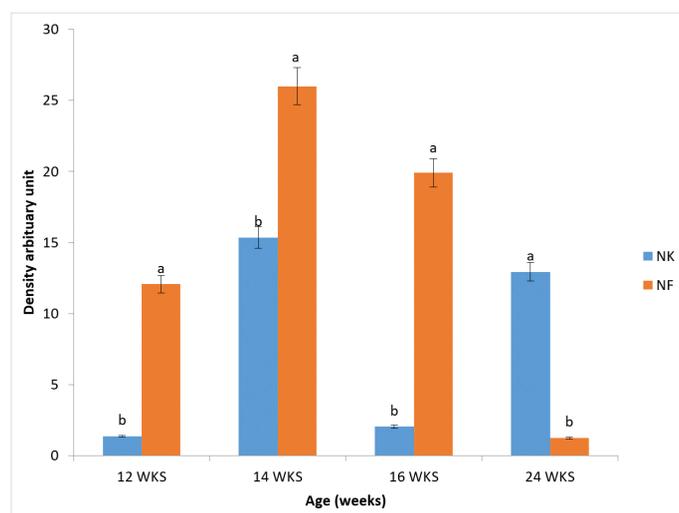
Fig. 3 shows the semi-quantitative analysis of ghrelin mRNA in the ovary samples of the naked neck and normal feather female chickens. Higher significant ($P < 0.05$) expression level of ghrelin mRNA was observed in the ovary of the normal feather chicken than the naked neck chickens across all the weeks.



Note: ab - Bars with different superscripts for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test ; NK = Naked neck chicken; NF = Normal feather chicken

Figure 3. Expression level of GHRL mRNA in ovary samples of the two chicken genotypes at different weeks

Semi-quantitative analysis of ghrelin mRNA in the testes samples of the naked neck female and normal feather male chicken is shown in Fig. 4. There were significant differences ($P < 0.05$) in levels of ghrelin mRNA expression in the testes of the two genotypes across all weeks. The normal feather males had higher expression levels of ghrelin mRNA at all weeks except at week 24.



Note: ab - bars with different superscripts for the same week are different significantly ($P < 0.05$) according to Duncan's Multiple Range Test ; NK = Naked neck chicken; NF = Normal feather chicken

Figure 4. Expression level of GHRL mRNA in testes samples of the two chicken genotypes

Discussion

The results from this study showed a higher body weight and weight gain in the normal feather genotype than the naked neck genotype. This is not in agreement with the results of Patra et al. (2002) and Adeleke et al. (2011) that reported a higher body weight in the naked neck chickens. According to their study, the higher body weight exhibited by the naked neck could be attributed to the possession of feather distribution genes (*Naked neck gene*) that had been reported to reduce feather mass by 20–40%. The reduction in feather mass improves heat dissipation through the naked area (Singh et al., 2001). In a similar study by Merat (1986), several mechanisms appear to be responsible for higher meat production of chickens with reduced plumage and stated that the more rapid dissipation of heat resulted in less appetite depression and consequently better growth, particularly at high ambient temperature. This research was conducted during April to September and in this period, which is the most abundant rainfall for the year and ambient temperature is quite low compared to other seasons of the year. Therefore, there is a high likelihood for the normal feather chicken to take advantage of this season of the year for more increased body weight than the naked neck chickens. In a similar study by Yalcin et al. (1997), naked neck chickens were observed to exhibit a highly significant advantage over the normal feather chicken in the hottest climate and they also reported that means were similar in both genotypes in the cool temperate climate.

The male chickens had a higher body weight than their female counterparts for both genotypes (Table 2). This is consistent with previous reports (Garcia et al., 1992; Ikeobi et al., 1995; Ilori et al., 2010) that sexual dimorphism was in favour of males in the performance of strains of birds studied. Also, the comparative advantage of males over females in most of the morphological traits examined in ducks (Yakubu, 2011) and turkey (Ilori et al., 2010) reported that the differences in the size of the birds could be attributed to sex differential hormonal effects on growth.

The significantly higher liver, ovary, and testes weight in the naked neck genotypes agree with the findings of Gunn (2008) who reported that naked neck birds had a higher weight of organs than the normal feather birds. Therefore it can be suggested that despite the lower body weight of the naked neck chicken as observed in this study, they performed better in terms of weight of reproductive organs and liver. This is also in agreement with the study of Oke and Ihemeson (2010) where the testes weight was significantly higher in the naked neck chickens than in the normal feather chickens.

The expression of the ghrelin gene in all the tissues sampled in this study suggests that ghrelin plays a role in all the tissues examined in this study. All tissues expressed the mRNA for the ghrelin gene suggesting that ghrelin protein was secreted by these tissues and with the presence of the receptors are utilized in these tissues. Ghrelin has been implicated in several metabolic (Saito et al., 2005; Chen et al., 2007) and reproductive functions (Tena-Sempere, 2005; Sirotkin et al., 2006) in avian species and also modulates secretion, food intake, and energy homeostasis (Van der Lely et al., 2004). From the results, ghrelin mRNA expression levels were observed to be significantly higher in normal feather chickens than in the naked neck chickens. The

significant expression level of ghrelin mRNA in the testes and ovaries of the normal feather chickens explains that this gene also plays a role in the male and female reproductive tract. The higher level of expression of ghrelin mRNA at maturity in naked neck chicken might not be unconnected with the consistently lower body weight and weekly weight gain compared to the normal feather chicken. One of the functional features of ghrelin that has attracted more attention is its ability to stimulate food intake and to promote body weight gain. As orexigenic signal, expression of ghrelin has been shown to increase after food deprivation, and its plasma levels are in most cases negatively correlated with the body mass index. On this basis, ghrelin has been proposed as a unique circulating signal for energy insufficiency (the only known circulating orexigen), which may play a major role in the short- and long-term control of body weight (Cummings, 2006; Zigman and Elmquist, 2003). The role of ghrelin in the ovary of the chicken has not been clearly defined but at the ovarian level, ghrelin has been implicated in the regulation of gonadotrophin-induced steroidogenesis and ovulation as several studies have reported ghrelin to promote granulosa cell proliferation, inhibit apoptosis, stimulate the release of all the steroid hormones in porcine species (Sirotkin et al., 2010) and also to regulate the ovarian cells secretory activities in chicken (Sirotkin and Grossmann, 2007). The higher expression of Ghrelin in the liver at puberty in the naked neck chicken may explain the low growth performance achieved in the chicken during this period as its plasma levels have been reported to be negatively correlated with the body mass index, proposed as a unique circulating signal for energy insufficiency and orexigenicity which may play a major role in the short- and long-term control of body weight (Cummings, 2006; Zigman and Elmquist, 2003). The results from this study confirm the result from a similar study by Montague et al. (1997) that the expression of these two genes is genotype-dependent.

Conclusion

From the result obtained from this study, it can be concluded that genotype and sex had a significant effect on the body weight of Nigerian indigenous chickens. The Naked neck chickens had higher mRNA expression in the liver at puberty, which may explain their low growth performance in that stage. This study further established the expression of ghrelin mRNA in the liver, ovary, and testes of Nigerian indigenous chicken suggesting and confirming that ghrelin protein is secreted by these tissues and with the presence of the receptors is utilized in these tissues. The method used in the study, although not performed at the exponential phase of the PCR amplification reaction as it is semi-quantitative optimization with ImageJ quantitation of PCR amplicons, allows the determination of the trend in expression of the target gene with useful information for candidate gene selection in genetic improvement programme.

CRedit authorship contribution statement

Ayotunde Olutumininu Adebambo: Conceived the project and supervised the work. **Babatunde Moses Ilori, Mohammed Okanlawon Onagbesan:** Supervised the work. **Omotomiwa Abiodun Osikomaiya:** Investigation, performed most of the experiments. **Omotomiwa Abiodun Osikomaiya, Babatunde Moses Ilori:** analysed the data and drafted the manuscript.

Babajide Samuel Obimakinde, Samuel Olutunde Durosaro: Performed some of the experiments, analysed some of the data. **Babatunde Moses Ilori:** edited the manuscript.

Declaration of Competing Interest

The authors declare that there are no conflicts of interest that could bias the integrity or objectivity of this work. There are no financial, personal, or professional relationships that could be perceived as influencing the research presented in this article. No external entity had any involvement in the study design, data collection, analysis, interpretation, or manuscript preparation.

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