ISSN 1682-8356
ansinet.org/ijps

INTERNATIONAL JOURNAL OF

POULTRY SCIENCE

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International Journal of Poultry Science 9 (8): 731-737, 2010
ISSN 1682-8356

Genotype and Sex Effect on Gastrointestinal Nutrient Content, Microflora and Carcass Traits in Nigerian Native Chickens

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Abstract: The nutrient concentration of crop and gizzard contents of three genotypes of indigenous scavenging chickens under rural conditions were investigated along-side with the micro-flora community of the Gastrointestinal Tract (GIT), body dimensions and carcass traits. Genotype significantly ($p<0.01$) affected the Crude Protein (CP) and Dry Matter (DM) values while Ether Extract (EE) value was significantly ($p<0.05$) influenced by sex of bird. The interaction between genotype and sex significantly ($p<0.01$) affected only CP and EE values while Crude Fibre (CF), ash and Gross Energy (GE) values were statistically similar across both genotype and sex of the bird. The genotype significantly ($p<0.01$) affected Live Weight (LWT), Bled Weight (BDWT), Plucked Weight (PLWT), Dressed Weight (DRWT), Breast Girth (BRG), liver weight, lung weight, heart weight, GIT weight and GIT length. The sex of bird also significantly ($p<0.01$) influenced Body Length (BLT), LWT, BDWT, PLWT, BRG, shank length, keel length, heart weight, gizzard weight, lung weight and GIT length while the interaction between genotype and sex significantly ($p<0.05$) affected LWT, BDWT, PLWT, DRWT, BRG, heart weight, gizzard weight and lung weight. Both genotype and sex significantly ($p<0.01$) influenced bacteria population of the chickens caeca. *Salmonella sp.*, *Escherichia coli* and *Staphylococcus aureus* were prevalent in the caeca of all the scavenging birds. It was concluded that there are genotype and sex effects on crop and gizzard content, linear body measurements and presence or absence of bacteria in the caeca of the Nigerian native chickens raised under rural extensive system This findings further corroborates the abundance of genetic variation that can be exploited in developing any stock improvement programme for growth, carcass or disease resistance traits involving the Nigerian local chickens.

Key words: Genotype, sex effect, indigenous, native chickens, Nigeria

INTRODUCTION

The Nigerian indigenous chicken is a dual purposed bird which is used both for meat and egg production in the rural and peri-urban areas of the country. They are found in large numbers distributed across different agro-ecological categories under a traditional family based scavenging management system (Sonaiya and Olori, 1990). Most of the birds are kept in small flocks under a scavenging system and the feed resources for the birds are household refuse, homestead pickings, crop residues, herbage, seeds, green grasses, earthworms, insects and small amount of supplemented feeds offered by the flock owner. They are well adapted to the adverse climatic conditions of the tropical environment and low management inputs. They contain a highly conserved genetic system with high levels of heterozygosity (Wimmers *et al*., 2000). These indicates that they are highly important farm animals, kept for good source of animal protein, for income and socio-cultural roles. Ebozoje and Ikeobi (1995) reported the adaptive potentials of the Nigerian indigenous chicken to varied ecological conditions, stresses and diseases. There have been some efforts at characterizing the Nigerian indigenous chickens. These efforts includes; classification based on ecotypes(Sonaiya and Olori, 1990), based on plumage and shank color (Ebozoje and Ikeobi, 1995; Ikeobi *et al*., 1996), possession of the major genes of feather distribution and feather structure (Ibe, 1993; Ebozoje and Ikeobi, 1995; Peters *et al*., 2002; 2005, 2007, 2008a and 2008b). Major genes effect on growth, fertility, hatchability and semen quality characteristics have also been reported (Peters *et al*., 2002, 2005, 2008a 2008b). Wekhe (1992) earlier reported that Nigerian indigenous chicken are more resistant to infectious disease agents than their exotic counterparts. While there are reports in the literature about growth, fertility, hatchability, reproductive performance and semen quality of the indigenous

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chicken, there are few or no reports on genotype/strain differences on carcass, nutritional content of some organs and micro flora community of the gastro-intestinal community of the Nigerian indigenous chicken. In this present report, we present the genotype and sex effect on carcass, nutritional content of the crop and gizzard and also a survey of the microflora community of the gastroinstestinal tract of the Nigerian scavenging indigenous chicken.

MATERIALS AND METHODS

The indigenous scavenging chickens that was used for this investigation were purchased from owners in ten villages located in Odeda local government area of Ogun State, Nigeria. Ogun State, in located in the South-Western part of Nigeria, having ambient temperature ranging from 28°C in December to 36°C in February with relative humidity of 82% while the vegetative site represents an inter-phase between the tropical rainforest and the derived savannah.

A total of one hundred and twenty (120) Local Scavenging Chickens (LSC) randomly selected from a population of about one hundred and fifty (150) (LSC) were used for this research. The chickens comprised of three (3) genotypes (frizzle feathered, naked neck and normal feathered). Forty (40) birds per genotype made up of 20 males and 20 females were used for this investigation. Matured males and females that had undergone at least one breeding cycle were collected from the households in the evening period at the end of the day's scavenging, (around 6 pm) wing-tagged and moved to the Animal Nutrition Laboratory of the College of Animal Science and Livestock Production, University of Agriculture, Abeokuta for Slaughtering and Analysis on the same day.

Morphometric trait measurements: The live weight of the birds were taken with the use of kitchen weighing balance with a capacity of up to 3 kg and recorded. Other body parameters measured before slaughter were linear body dimensions which include body length, breast girth, shank length and keel length.

Live weight (LWT): Weight of each bird was taken with the use of weighing balance.

Body length (BLT): This was taken as the distance between the last cervical vertebrae before the thoracic vertebrae and the caudal vertebrae, i.e. the length of the synsacrum which is fused with the pelvic girdle. This was measured with the use of flexible tape graduated on a centimeter scale.

Breast girth (BRG): This parameter was taken as the circumference of the breast around the deepest region of the breast. A flexible tape was used for this measurement.

Shank length (SHLT): This was taken as the length of the tarso-metatarsus from the anterior end joining the tibia bone to the first digit (hallux) of the digits (the foot). This measurement was taken through the use of a flexible tape.

Keel length (KLT): This was taken as the distance of the region of the sternum; a flexible tape was used for this measurement.

After measurements were taken, the birds were killed by exsanguination, de-feathered and weighed again. After then the plucked weight was taken and recorded. Each of the bird was eviscerated and the organs separated. Then the dressed weight, liver weight, lung weight and GIT weight were measured. All these were taken with the aid of electric sensitive scale. Also, the GIT length was measured with tape rule.

The crop and gizzard were separated from the GIT and weighed separately. The contents of the crops and gizzards were removed and weighed frozen at -20°C. The crop and gizzard contents were dried and weighed again to obtain the dry matter content and stored until chemical analysis (Mwalusanya *et al*., 2002).

Contents of dried crops and gizzards were and after the grits have been removed from the samples, they were analyzed for proximate components of Dry Matter (DM), Crude Protein (CP), Ether Extract (EE), Crude Fibre (CF), ash and Gross Energy (GE), according to AOAC (1990) procedures.

Micro-flora community in the chicken GIT

Collection of samples: After killing and evisceration of the chickens the caeca were separated from the intestine with sterilized scissors. The caeca were then cut open and the content scraped out under aseptic condition into separate Petri dishes for each bird genotype by sex.

Preparation of media for bacteria growth: Nutrient agar powder was weighed according to manufacturer specification (28 g/L). It was soaked in distilled water for 15 min and sterilized at 126°C for 11 min. After cooling to room temperature, it was used for inoculation of samples.

Dilution and isolation: The samples were serially diluted to different decimal dilutions under aseptic condition and 1.0 ml of the dilutions were aseptically inoculated on the freshly prepared nutrient agar plates using the pour plates method. The samples were inoculated in duplicates. Incubation was carried out at 37°C for 48 h. The number of colonies was counted after the incubation period. The bacteria colony on the plates were further sub-cultured on nutrient agar plates until the pure culture were obtained. The pure cultures were stored on a slant of nutrient agar for further characterization.

Preparation of media for fungi growth: Potato Dextrose Agar (PDA) was weighed according to manufacturer's specification (39 g/L). It was heated to dissolve the constituent properly and sterilized at 126°C for 11 min. After cooling to room temperature, the media was used for inoculation of samples. PDA supports the growth of fungi.

Dilution and isolation for fungi: The samples were serially diluted to different decimal dilutions under aseptic condition and 1.0 ml of the dilutions were aseptically inoculated on the freshly prepared potato dextrose agar plates using the pour plate method. The samples were inoculated in duplicates. Incubation was carried out at 30°C for five (5) days and after five days there was no fungal growth.

Biochemical tests for bacteria

Gram staining: A loopful of each organism was placed on a grease-free clean glass slides. It was allowed to air-dry and was fixed over Bunsen-burner flame. The slide was flooded with crystal violet for 30 sec, washed off and flooded with gram's iodine for another 30 sec, washed off and flooded with 95% ethanol before counter staining with safrania solution. The slide was air-dry and observed under the microscope using the oil-immersion lens (x100).

Catalase test: A loopful of the organism was aseptically transferred into 3% hydrogen peroxide on a glass slide. It was observed for effervescence where for positive (+) or no air bubbles for negative(-) result.

Coagulase test: A drop of rabbit plasma was placed on a clean grease-free glass slide and a loopful of the organism was added aseptically. The mixture was observed for coagulation or not.

Starch hydrolysis test: The organism was inoculated on a 1% starch nutrient agar plate and incubated at 30°C for 48 h. After the incubation period the plate was flooded with iodine solution and observed under microscope. A transparent region around the colony indicated a zone of hydrolysis of the starch while colonies with blue-black region around it show no hydrolysis.

Sugar fermentation test: Nutrient broth containing 0.5% of different sugars (glucose, lactose, maltose and sucrose) were prepared. Phenol red indicator (0.01%) was incorporated in the broth. The broth was inoculated with the different organisms and incubated at 30°C for 48 h. It was then observed for colour change, that is, from red (active fermentation) to yellow (no fermentation).

Gelatine liquefaction test: Fraziers gelatine medium in petri dishes was dried and the organism was streaked across the plate and then incubated at 30°C for 72 h. After the incubation period, Mercury chloride solution was poured into the plates to test for the gelatine liquefaction, that is, appearance of clear zone around the colony which shows positive test and white opaque precipitate which shows un-hydrolyzed gelatine around the colony.

Data management and statistical analysis: All data generated were subjected to a two-way Analysis of Variance (ANOVA) to determine the effects of genotype and sex on the parameters of interest using SAS (2001; version 8.2 for windows) Comparison among means were made using Duncan Multiple Range Test.

RESULTS

The results obtained from this investigation were as presented in Table 1-4. Table 1 shows the effects of genotype on proximate composition of gut ingesta (Dry Matter (DM)), Crude Protein (CP), Ether Extract (EE), Crude Fibre (CF), ash and Gross Energy (GE). The results obtained indicated that genotype significantly ($p<0.01$) affected the CP and DM values, while the values for CP, EE, ash and GE were significantly ($p<0.01$) influenced by GIT part (crop and gizzard) as indicated by the p-values. In addition, the CP in gizzard contents was lower than CP in crop contents, The percentage decrease in CP values between the crop and gizzard were: normal feather (76.11%), naked-neck (30.46%) and frizzle feather (47.31%). The interaction between genotype and GIT parts significantly ($p<0.05$) affected only CP and GE values (Table 1). As presented in Table 1 the chickens with at naked-neck gene had the highest mean values for CP both in crop and gizzard contents while the normal feathered genotype had the lowest, both in the crop and gizzard respectively. EE, CF, ash and DM values were statistically similar ($p>0.05$) across both genotype and GIT part.

There were significant ($p<0.01$) differences between the GE of the crop contents and that of the gizzard contents across all the genotypes with the normal feathered genotypes having the highest mean values.

The effects of genotype and sex on proximate composition of GIT contents were presented in Table 2. The results indicated that genotype significantly ($p<0.01$) influenced DM and CP values, while EE value was significantly ($p<0.05$) affected by sex of the birds. The CP values in male chickens as presented in Table 2 was higher than the obtained value from their female counterparts. The interaction between genotype and sex significantly ($p<0.01$) affected CP and EE values only. CF, ash and GE values were statistically similar ($p>0.05$) across both genotype and sex of the bird.

Table 1: Means and SE of crop and gizzard proximate contents as affected by genotype

	Normal feather		Naked-neck		Frizzle feather		P-values	
Composition	Crop	Gizzard	Crop	Gizzard	Crop	Gizzard	Genotype	GITPRT
Dry matter (DM) %	89.50±0.02	89.66±0.15	89.70±0.11	89.91±0.10	89.62±0.11	89.36±0.06	0.0039**	0.5852
Crude protein (CP) %	19.47±0.66^{a}	4.65±1.22^{d}	20.22±1.57^{a}	14.06±1.68^{b}	19.51±1.65^{a}	10.28±2.52^{c}	0.0011**	<0.0001**
Ether extract (EE) %	4.18±0.13	1.97±0.26	3.55±0.40	1.95±0.10	3.85±0.19	2.58±0.53	0.134	<0.0001**
Crude fibre (CF) %	6.57±0.69	5.76±0.65	4.54±0.42	4.96±2.40	5.24±0.59	8.90±2.08	0.2399	0.3276
Ash %	10.18±0.88	13.24±1.11	9.09±1.45	18.93±1.82	9.53±1.74	15.08±1.68	0.235	<0.0001**
Gross energy (Kcal/g)	3.06±0.01^{a}	1.02±0.01^{d}	2.84±0.36^{b}	1.07±0.01^{d}	2.76±0.33^{b}	1.80±0.36^{c}	0.2836	<0.0001**

$^{a, b, c, d}$Means on the same row with different superscript are significantly different p<0.05. **Significant at p<0.01

Table 2: Means and S.E of proximate composition of GIT contents as affected by genotype and sex

	Normal feather		Naked-neck		Frizzle feather		P-values		
Composition	Male	Female	Male	Female	Male	Female	Genotype	Sex	G*S
Dry matter (%)	89.69±0.11	89.47±0.09	89.83±0.10	89.79±0.13	89.56±0.14	89.45±0.04	0.0039	0.0795	0.275
Crude protein (%)	13.02±3.23^{c}	11.11±3.62^{c}	14.99±2.27^{bc}	19.29±1.45^{a}	16.72±1.46^{b}	13.07±3.76^{c}	0.0011**	0.669	0.0071**
Ether extract (%)	3.26±0.42^{a}	2.89±0.62^{b}	2.50±0.50^{c}	2.97±0.40^{b}	3.85±0.25^{a}	2.58±0.53^{c}	0.134	0.041*	0.0043**
Crude fibre (%)	6.76±0.73	5.55±0.54	6.44±2.11	3.06±0.60	7.05±0.58	7.10±2.38	0.2399	0.1802	0.449
Ash (%)	10.76±1.00	12.66±1.26	13.19±2.03	14.83±3.27	13.38±1.65	11.22±2.40	0.2350	0.6816	0.2671
Gross energy (Kcal/g)	2.05±0.45	2.03±0.46	1.82±0.48	2.08±0.46	2.77±0.31	2.07±0.46	0.2836	0.7183	0.275

$^{a, b, c}$Means on the same row with different superscript are significantly different. **Significant at p<0.01. *Significant at p<0.05.
G*S = interaction between genotype and sex

Table 3: Means and SE of morphological and carcass parameters of scavenging chickens

	Genotype			Sex		P-values		
Measurements	Normal feathered	Naked neck	Frizzled feathered	Male	Female	Genotype	Sex	G*S
Body dimensions (cm)								
Body length	29.25±0.62	29.00±0.58	28.95±0.71	30.67±0.43^{a}	27.47±0.61^{b}	0.7785	<0.0001**	0.2446
Shank length	6.83±0.22	6.89±0.20	6.22±0.25	7.80±0.37^{a}	5.70±0.34^{b}	0.2759	<0.0001**	0.7628
Keel length	8.87±0.34^{a}	8.15±0.36^{b}	8.43±0.31^{ab}	9.03±0.24^{a}	7.94±0.22^{b}	0.0230*	<0.0001**	0.2137
Breast girth	23.10±0.27^{a}	23.40±0.26^{a}	22.05±0.28^{b}	24.00±0.26^{a}	21.70±0.33^{b}	0.0048**	<0.0001**	0.0015**
Carcass traits (g)								
Live weight	1003.50±25.01	898.00±20.11^{b}	908.00±31.41^{b}	1046.00±34.21^{a}	827.00±32.52^{b}	0.0018**	<0.0001**	0.0083**
Bled weight	967.20±23.44^{a}	866.20±24.98^{b}	873.70±20.60^{b}	1008.07±30.01^{a}	795.67±26.34^{b}	0.0019**	<0.0001**	0.0070**
Plucked weight	847.90±23.00^{a}	757.60±23.31^{b}	751.10±21.92^{b}	880.33±27.92^{a}	690.73±25.41^{b}	0.0007**	<0.0001**	0.0011**
Dressed weight	657.29±16.40^{a}	604.41±17.32^{b}	595.00±17.10^{b}	709.52±26.31^{a}	528.35±20.92^{b}	0.0150*	<0.0001**	0.0006**
Organ weight (g)								
Liver	24.05±1.71^{a}	24.50±1.79^{a}	18.52±1.66^{b}	23.26±1.42	21.44±1.74	0.002**	0.1097	0.1384
Heart	5.15±0.31^{a}	4.62±0.34^{b}	4.38±0.29^{b}	5.34±0.93^{a}	4.09±0.88^{b}	0.0118**	<0.0001**	0.0211*
Lung	14.85±1.11^{a}	7.22±1.01^{b}	5.62±1.03^{c}	12.07±1.01^{a}	6.39±1.32^{b}	<0.0001**	<0.0001**	<0.0001**
GIT	144.52±8.92^{a}	114.26±7.66^{b}	126.97±7.99^{c}	128.68±5.77	128.61±6.48	<0.0001**	0.0032**	0.0804
Crop	12.59±1.21	13.21±1.51	9.32±1.44	10.77±2.53	12.64±0.99	0.2206	0.3336	0.5215
Gizzard	42.17±2.43^{a}	34.81±1.64^{b}	38.63±1.34^{a}	40.50±1.35^{a}	36.47±1.24^{b}	0.0016**	0.0090**	0.0198*
GIT contents (g)								
Gizzard	14.56±0.62	14.12±0.64	15.42±0.60	15.00±2.41	14.00±2.31	0.3332	0.4111	0.6194
Crop	8.16±0.58^{ab}	10.13±0.66^{a}	6.85±0.63^{b}	7.98±1.40	8.79±1.25	0.0572	0.4513	0.1991
GIT length (cm)	178.50±8.31^{a}	163.00±7.13^{b}	159.00±6.42^{b}	173.07±4.64^{a}	160.67±3.35^{b}	0.0007**	0.0032**	0.0804

$^{a, b, c}$Means on the same row with different superscript are significantly different. **Significant at p<0.01. *Significant at p<0.05

Table 3 showed the individual and the interactive effects of genotype and sex on the body dimensions (Body Length (BLT), Shank Length (SHLT), Keel Length (KLT) and Breast Girth (BRG)); carcass traits (Live Weight (LWT), Bled Weight (BDWT), Plucked Weight (PLWT) and Dressed Weight (DRWT)); organ weight (liver, heart, lung, GIT, crop and gizzard); GIT content (crop and gizzard) and the GIT length. The genotype significantly (p<0.01) affected LWT, BDWT, PLWT, BRG, DRWT, liver, lung, heart and GIT weights and GIT length. The sex of birds also significantly (p<0.01) influenced BLT, BDWT, PLWT, BRG, LWT, SHLT, KLT, GITLT, heart, gizzard and lung weights while the interaction between genotype and sex significantly (p<0.05) affected LWT, DRWT, BDWT, PLWT, BRG, heart, gizzard and lung weights. In this study there were significant (p<0.05) difference between values obtained for male and female birds in relation to all body dimensions, carcass traits, organ weights, GIT length, with the exception of crop weight and GIT weight (Table 3) Sex had no significant (p>0.05) influence on liver weight, crop weight, gizzard content weight and crop content weight.

At the end of the incubation period for micro-flora determination (precisely fungi and bacteria), there was no fungal growth after five (5) days of incubation while bacterial growth was observed in all the genotypes and sexes after 48 h. The bacteria species present in the caecum of different scavenging chickens was based on

Table 4: Bacteria species present in the caecum of scavenging chickens

	Normal feather		Naked-neck		Frizzle feather	
Species	Male	Female	Male	Female	Male	Female
Salmonella sp.	+	+	+	+	+	+
Escherichia coli	+	+	+	+	-	+
Bacillus sp.	+	+	-	-	-	-
Staphylococcus aureus	+	+	+	+	+	-
Streptobacillus sp.	-	-	-	+	+	+
Brucella sp.	-	+	-	-	+	-

+ = Present; - = Absent

microbiological analysis. The results (Table 4) showed that genotype significantly ($p<0.01$) influenced the bacteria population in the chicken caeca. Sex also significantly ($p<0.01$) affected the caeca bacteria population (Table 4). *Salmonella sp*. were present in all the genotype and sexes while *Escherichia coli* were also present in all the genotype and sexes except in frizzle feather male (Table 4). *Bacillus sp*. was present only in the normal feather birds. All caeca contained *Staphylococcus aureus* except frizzle feathered-female. Normal feather chicken and naked-neck males caeca did contain *Streptobacillus sp*. but the organism was present in all others. *Brucella sp*. was the least common and was present only in the normal feather female and frizzle feather male scavenging chickens.

DISCUSSION

The values of the DM contents of the chickens evaluated in this study (89.61%) are slightly lower when compared to the values (91.1-92.5%) reported by Mekonnen *et al*. (2010). It is however higher than 34.4% and 45.5- 48.9% reported by Gunaratne *et al*. (1993) and Rashid *et al*. (2004) respectively. The CP content of the crop across the genotypes were comparable and it is important to note that the value reported in this study is higher than reports from similar studies in literature (Tadele and Ogle, 2000; Mwalusanya *et al*., 2002; Rashid *et al*., 2004; Rashid *et al*., 2005; Mekonnen *et al*., 2010). This value is even higher than the NRC (1994) recommended level of CP. The higher CP found can be attributed to possible access to insect, worms, maggots and developing larvae. Furthermore, the CP in the gizzard contents was lower than CP in the crop contents, this results might probably be due to the digestion process of CP in the proventriculus on the way from the crop to the gizzard. This argument is consistent with the views of Smith (1990). Results obtained in this study regarding the contents of CF and ash in the chickens' crops and gizzards were lower than 10.2% reported by Tadele and Ogle (2000) but were within the range reported by Rashid *et al*. (2004) and Mekonnen *et al*. (2010). The maximum recommended CF content for commercial layers ration is 5% as the digestibility of the diet is reduced due to the presence of lignin and hemicelluloses by endogenous enzymes of monogastrics such as poultry. The Naked neck birds had values that were within the acceptable range for CF in this study. The difference in the GE as presented in the results above is contrary to expectation in the tropics where heat stress is one of the limiting factors for Poultry production. The possession of higher GE by fully feathered genotype in comparison to Naked neck and frizzled feather genotype may also be attributed to the Possession of Major genes of feather distribution and feather structure gene by the Naked and frizzled feather genotypes. These genes were reported by Ibe (1993) as having thermoregulatory roles. The CP values in male chickens as presented in Table 2 was higher than those in the females and this is consistent with the higher requirement for CP by male birds compared to their female counterparts. Payne (1990) reported that male chickens has higher CP requirement than their female counterparts. Generally, it was observed from the results of the mean values of the nutrients from the crop and gizzard across the genotypes and sexes were lower than the recommended values in Payne (1990) and NRC (1994). The mean live weight for Males and females across the genotypes reported in this study is lower than values reported by Mekonnen *et al*. (2010) but was within the range reported by Gueye (1998) and Aini (1999). The sex effects on carcass traits observed in this study is consistent with the reports of Garcia *et al*. (1993). They reported sexual dimorphism at slaughter and carcass yield of the chicken used for their investigation. Males had higher carcass yield than females. They further reported that male chickens had significantly higher body weight and carcass weight, a better feed conversion and less carcass fat than female counterparts in their study. The mean weight of GIT contents, most especially crop in this study was found to be lower than values 27.2 g reported by Mekonnen *et al*. (2010) for indigenous scavenging chickens in Ethiopia. The difference in the result may be attributed to the availability of grains to the scavenging chicken in Ethiopia. Mekonnen *et al*. (2010) reported that grain represented about 47-49% of the mean weight of the crop contents of the chicken studied. The results of the consistency of the presence of bacteria in the GIT of the chickens used for this investigation when compared to no fungal growth is very similar to observations reported by Fuller (1992). He reported consistent presence of bacteria in the GIT of adult broilers used for his

investigation. The variability in the presence or absence of bacteria in each bird genotype and sex may be genotype specific and sex specific. A probable reason why fungi did not grow in the media could be attributed to the fact that fungi are more selective in the environment they live when compared to bacteria that have been widely reported to adapt and survive in a wide range of environmental conditions.

Conclusion: From the results reported in this study, it is concluded that genotype of the Nigerian indigenous chicken significantly affected nutrient composition of the crop and gizzard content of the scavenging chickens. The CP and other nutrients available to the indigenous scavenging chicken can vary widely. In this study there were found to be higher than the recommended rate. Genotype effect was also significant on linear body measurements, carcass traits and organ weights. Genotype differences were also observed in the presence or absence bacteria microflora in the caeca of the scavenging chicken. Sexual dimorphism also existed for linear body measurements and presence and absence of bacteria in the caeca of the Nigeria indigenous scavenging chickens. It appears there will be a need to carry out an expanded study across seasons and geographical zones to validate results.

REFERENCES

Aini, I., 1999. Diseases in rural family chickens in South East Asia. In: The First International Network for Family Poultry Development (INFPD), Electronic Conferences on the Scope and Effect of Family Poultry Research and Development, FA.

AOAC, 1990. Official Methods of Analysis. 15th Edn., Association of Official Analytical Chemists. Washington DC.

Ebozoje, M.O. and C.O.N. Ikeobi, 1995. Productive performance and occurrence of Major genes in the Nigerian local chicken. Nig. J. Genet., 10: 67-77.

Fuller, R., 1992. Probiotics, the scientific basis. The University Press, Cambridge.

Garcia, E.A., A.A. Mendes and P.R. Curi, 1993. Effect of line on growth of broilers. Anim. Breeding Abstract, Vol. 9361.

Gueye, E.F., 1998. Village egg and fowl meat production in Africa. World's Poult. Sci. J., 54: 73-86.

Gunaratne, S.P., D.N. Chandrasiri, W.A.P. Mangalika Hemalatha and J.A. Roberts, 1993. Feed resource base for scavenging chickens in Sri Lanka. Trop. Anim. Health Prod., 25: 249-257.

Ibe, S.N., 1993. Growth performance of normal, frizzle feather and naked-neck chickens in a tropical environment. Nig. J. Anim. Prod., 20: 25-29.

Ikeobi, C.O.N., M.O. Ozoje, O.A. Adebambo, J.A. Adenowo and O.A. Osinowo, 1996. Genetic differences in the performance of local chicken in South-Western Nigeria. Nig. J. Genet., 11: 33-39.

Mekonnen, H., B. Kelay, T. Berhan and D. Mulatu, 2010. Assessment of nutritional status of indigenous scavenging chickens in Ada'a district, Ethiopia. Trop. Anim. Health Prod., 42: 123-130.

Mwalusanya, N.A., A.M. Katule, S.K. Mutayoba, M.M.A. Mtambo, J.E. Olsen and U.M. Minga, 2002. Productivity of the local chickens under village management conditions. Trop. Anim. Health Prod., 34: 405-416.

Mwalusanya, N.A., A.M. Katule, S.K. Mutayoba, U.M. Minga, M.A. Mtabo and J.E. Olsen, 2002. Nutrient status of crop contents of rural scavenging local chickens in Tanzania. Br. Poult. Sci., 43: 64-69.

National Research Council, 1994. Nutrient requirements of poultry. 9th Revised Edition, National Academy Press, Washington DC, USA, pp: 19-34.

Payne, W.J.A., 1990. An introduction to Animal Husbandry in the Tropics, 4th edition, (Essex and New York, Longman Scientific and Technical), pp: 684-744.

Peters, S.O., B.M. Ilori, M.O. Ozoje, C.O.N. Ikeobi and O.A. Adebambo, 2008b. Gene segregation effects on fertility and hatchability of pure and crossbred chicken genotypes in the humid tropics. Int. J. Poult. Sci., 7: 954-958.

Peters, S.O., O.O. Shoyebo, B.M. Ilori, M.O. Ozoje, C.O.N. Ikeobi and O.A. Adebambo, 2008a. Semen quality traits of seven strains of chickens raised in the humid tropics. Int. J. Poult. Sci., 7: 949-953.

Peters, S.O., C.O.N. Ikeobi, M.O. Ozoje and O.A. Adebambo, 2002. Genetic variation in the reproductive performance of the Nigerian indigenous chicken. Trop. Anim. Prod. Invest., 5: 37-46.

Peters, S.O., C.O.N. Ikeobi, M.O. Ozoje and O.A. Adebambo, 2005. Modellling Growth in Seven chicken genotypes. Nig. J. Anim. Prod., 32: 28-38.

Peters, S.O, C.O.N. Ikeobi, M.O. Ozoje, O.A. Famakinwa, Y.S. Oshodi and O.A. Adebambo, 2007. Egg quality of the Nigerian local chicken as influence by some major genes. Nig. J. Anim. Prod., 34: 25-31.

Rashid, M.M., M.N. Islam, B.C. Roy, K. Jakobsen and C. Lauridsen, 2005. Nutrient concentration of crops and gizzard contents of indigenous scavenging chickens under rural conditions of Bangladesh. Livestock Research for Rural Development 17(2): http://www.cipav.org.co/lrrd/lrrd17/2/rash17016.htm.

Rashid, M., B.C. Roy and V. Asaduzzaman, 2004. Chemical composition of crop contents of local scavenging chickens. Pak. J. Nutr., 3: 26-28.

SAS Institute, 2001. SAS Statistics Users Guide, Statistical Analysis System, 8th edition, 8.2 version, (Carry, NC, SAS Institute Inc.).

Smith, A.J., 1990. Poultry-Tropical Agriculturist Series, CTA, Macmillan Publishers, London, pp: 179-184.

Sonaiya, E.B. and V.E. Olori, 1990. Village Poultry Production in South Western Nigeria. In: Sonaiya E.B. (Ed) Rural Poultry in Africa: Proceedings of an International Workshop held in Ile-Ife, Nigeria, November 13-16, 1989. Thelia house, Ile-Ife, pp: 243-247.

Tadele, D. and B. Ogle, 2000. Nutritional status of village poultry in the central highlands of Ethiopia as assessed by analysis of crop contents. Ethiopian J. Agric. Sci., 17: 47-56.

Wekhe, S.N., 1992. Susceptibility of indigenous (Nigerian) and exotic (Harco) chickens to fowl typhoid infection. Trop. Vet., 10: 1-2.

Wimmers, K., S. Ponsuksili, T. Hardge, A. Valle-Zarate, P.K. Mathur and P. Horst, 2000. Genetic distinctness of African, Asian and South American local chickens. Anim. Genet., 31: 159-165.