Carcass traits, haematology and serum biochemical parameters of Nigerian indigenous chickens and their crosses with marshall

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Abstract

This study investigated the genetic variation in carcass traits and blood parameters of local naked neck and normal-feathered chickens and their crosses with Marshall broiler chickens. Two hundred and sixty three chickens consisting of 50 purebred Marshalls (M), 38 naked neck (Nk) and 48 normal-feathered (N), 61 Marshall x naked neck (MNk) and 66 Marshall x normal-feathered(MN) chickens were used for the study. Data were collected on carcass traits, haematology and serum biochemical parameters and were analysed using the General Linear Model procedure of Statistical Analysis System. Carcass traits such as eviscerated weight and weights of thigh, drumstick, breast, wings and organs were significantly ($P < 0.0001$) affected by genotype. Results showed that the purebred Marshall had the highest values in most of the traits followed by their crossbreds. In organs such as gizzard, liver and heart the local normal feathered ranked equal with its crossbred. Sex significantly ($P < 0.05$) affected carcass traits. Males consistently had higher values than females in all the parameters measured. Genotype significantly ($P < 0.05$) influenced blood parameters measured. The MNk had the highest value for PCV ($32.30 \pm 0.99\%$), Hb ($10.85 \pm 0.31 \text{ g/dL}$), Na ($148.58 \pm 3.94 \text{ mmol/L}$) and K ($7.88 \pm 1.07 \text{ mol/L}$). The Nk and N purebreds had the lowest values for Hb, WBC, RBC and highest values for globulin. The study revealed that the crossbreds obviously performed better than their local purebreds counterpart in carcass traits measured. Therefore, to obtain better cut-parts in the Nigerian local naked neck and normal feathered chickens, crossbreeding with the Marshall broiler breed is recommended.

Keywords: carcass traits, genetic variation, haematology, crossbreeding, genotype

Introduction

In Nigeria, indigenous chickens constitute about 80% of the 120 million poultry type raised in the rural areas (RIM, 1992). Their products are preferred by the majority of Nigerians because of the pigmentation, taste, leanness and suitability for special dishes (Horst, 1989). The indigenous poultry species represent valuable resources for livestock development because their extensive genetic diversity allows for rearing of poultry under varied environmental conditions, providing a range of products and functions. The demand for meat in the developing world has been increasing annually due to growing populations, rising income and urbanization. Theerachai (2006) reported

that their demand would grow from 111 million tonnes in 1997 to 213 million tonnes in 2020. According to FAO (2003), meat consumption per person in developing nations increased between 1964 – 1966 and 1997 – 1999, from 10.2kg per year to 25.5kg, respectively – a rise of 2.8 per cent per year which was particularly rapid for poultry with higher growth rates in developing countries. This has necessitated the need for increased livestock improvement in order to attain adequate provision of animal protein. Studies showed that the main problem of indigenous chickens in the tropics is that they are poor producers of meat and eggs (Alemu, 1995) compared to their modern counterpart. Consequently they are being

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replaced by commercial strains in many developing countries. Despite their low productivity, they are well adapted to the tropics, resistant to poor management, feed shortages and tolerant to some of the most common diseases and parasites in the environment. According to Mathur *et al.* (1989) crossbreeding improves the heterozygosity of non-additive genes causing heterosis, which is important in the adverse environmental conditions. Crossing constitutes one of the major tools for the exploitation of the genetic variation and the hybrid vigour through the combination of the different important characteristics of each breed (Willham and Pollack, 1985). The crossings between the adapted indigenous and the exotic breeds would allow exploitation of the rusticity of the first and the productive performances of the later at the same time in the tropical environment to produce adapted and more productive genetic types (Keambou *et al.*, 2010).

Materials and methods

The experimental birds

A total of two hundred and sixty-three (263) birds were used from five genetic groups. The genotypes were as follows; the parental genotypes – Marshall (M), Naked neck (Nk) and Normal feathered (N) while the crosses were, Marshall x Naked neck (MNk) and Marshall x Normal feathered (MN).

Carcass and organ evaluation

Carcass and organ evaluation were done simultaneously. This was obtained by starving the birds for about 10 hours before slaughtering. Ten birds (5 males and 5 females) from each genotype were used for the carcass evaluation. The birds were weighed before slaughtering by severing the carotid artery and the jugular vein and de-feathered before evisceration according to the method described by Hahn and

Spindler (2002). The cut parts (shank, thigh, drumstick, etc.) were weighed and recorded. While organs such gizzard, heart, lung etc. were excised and weighed.

Haematology and serum biochemistry

Blood samples were collected at 10 weeks of age. A total of 50 birds were randomly selected from 5 genetic groups, that is, 10 birds (5 males and 5 females) per genotype. Blood samples were collected from the wing vein of birds using 5ml disposable syringe. After collection, about 2ml of blood was transferred into a labelled EDTA bottle. The rest was allowed to clot and also labelled accordingly.

The non-coagulated blood was used to determine red blood cell (RBC) count and white Blood cell (WBC) count, packed cell volume (PCV), and haemoglobin (Hb) concentration using improved Neubauer haemocytometer, Wintrobe microhaematocrit, colorimetric cyano-methaemoglobin method, respectively (Swenson, 1977; Coles, 1986). Mean corpuscular volume (MCV), mean corpuscular haemoglobin (MCH) and mean corpuscular haemoglobin concentration (MCHC) was derived by calculation from the RBC, Hb, PCV values as described by Jain (1986). Serum was separated from the clotted blood following centrifugation where serum metabolites (total protein, albumin, globulin, sodium, potassium and chloride) were analyzed colorimetrically using diagnostic reagent kit (Reanal Diagnosztikai Reagents, Keszlet, Hungary).

Statistical analysis

Data were analysed using the General Linear Model procedure of SAS, (2005). Means were separated using Duncan's Multiple Range Test of the same software.

Statistical model

Carcass performance traits were analyzed using the model

$$Y_{ij} = \mu + A_i + B_j + (AB)_{ij} + e_{ijk}$$

where:

Y_{ijk} = observed performance of the j^{th} individual of the i^{th} genotype ($j = 1 - 5$); μ = overall mean; A_i = effect of i^{th} genotype (1, 2...5); B_j = effect of j^{th} sex (1, 2.); AB_{ij} = effect of interaction of i^{th} genotype and j^{th} sex (j = male, female); e_{ijk} = residual error

Results and discussion

The results of carcass traits are presented in Table 1. Genotype significantly ($P < 0.0001$) affected carcass yield. The purebred Marshall had the highest value for live weight, drumstick weight, and shank weight. This is in agreement with the findings of Karima and Fathy (2005) and Musa *et al.* (2006) who reported significant breed differences in live body weight and

other carcass parameters. Parameters such as eviscerated weight and weights of thigh, wings, back, breast, and organs such as empty gizzard, heart and lungs, were not statistically different in the pure Marshall genotype and their crosses. The values obtained for all the parameters in the pure Marshall and the Marshall crosses were higher and statistically different from those obtained for the purebred naked neck and normal feathered chickens. The pure indigenous normal feathered genotype ranked close to its crossbred in most organs such as liver weight, empty gizzard weight and lungs weight. This is in agreement with the report of Adebambo *et al.* (2010) that the normal feathered indigenous chickens performed better in most maintenance organs.

Table 1: Effect of genotype on carcass parameters

Gen	N	Live weight (g)	Eviscerated weight (g)	Thigh (g)	Drumstick (g)	Wings (g)	Breast (g)	Shank (g)	Neck (g)
<i>M</i>	10	1518.70±101.39 ^a	1086.60±71.94 ^a	165.10±10.79 ^a	157.70±11.74 ^a	132.60±9.33 ^a	223.30±19.23 ^a	76.10±4.50 ^a	64.10±5.97 ^a
<i>MNk</i>	10	1455.90±113.68 ^{ab}	983.50±81.12 ^a	156.10±14.46 ^a	131.70±13.78 ^b	126.90±9.34 ^a	215.10±16.10 ^a	53.90±5.18 ^b	57.10±3.38 ^{ab}
<i>MN</i>	10	1323.70±74.95 ^b	982.30±56.14 ^a	156.00±10.49 ^a	142.50±9.45 ^{ab}	122.70±6.80 ^a	214.10±12.56 ^a	58.80±3.92 ^b	59.10±3.39 ^a
<i>Nk</i>	10	965.00±55.30 ^c	678.90±38.96 ^b	97.90±5.73 ^b	91.70±6.56 ^c	91.20±4.64 ^b	146.10±8.88 ^b	35.00±2.40 ^c	38.60±2.54 ^c
<i>N</i>	10	983.80±56.20 ^c	655.90±54.76 ^b	106.30±7.34 ^b	96.30±6.89 ^c	90.60±5.90 ^b	142.90±8.48 ^b	35.60±2.88 ^c	48.10±3.45 ^b

^{a,b,c}Means within the same column with different superscripts are significantly different ($P < 0.0001 - P < 0.01$).

Gen – genotype; N – sample size; M- Marshall; MNk- Marshall X Naked neck; MN- Marshall X Normal feathered;

Nk- Naked neck, N- Normal feathered

Table 2: Effect of genotype on organ parameters

Gen	N	Full gizzard (g)	Empty gizzard (g)	Liver (g)	Heart (g)	Lungs (g)
<i>M</i>	10	71.00±4.02 ^a	44.70±3.48 ^a	42.00±3.71 ^a	6.80±0.39 ^a	10.10±1.10 ^a
<i>MNk</i>	10	66.90±5.85 ^{ab}	44.50±4.42 ^a	38.20±4.46 ^a	6.20±0.71 ^{ab}	10.70±1.12 ^a
<i>MN</i>	10	57.40±3.60 ^{bc}	41.10±2.26 ^{ab}	30.90±1.94 ^b	6.70±0.62 ^a	8.80±0.93 ^{ab}
<i>Nk</i>	10	47.30±2.80 ^d	33.40±1.96 ^c	20.50±0.99 ^c	5.40±0.45 ^b	7.70±0.73 ^b
<i>N</i>	10	50.00±2.86 ^{cd}	34.30±2.26 ^{bc}	25.70±1.69 ^{bc}	5.70±0.47 ^{ab}	7.30±0.50 ^b

^{a,b,c}Means within the same column with different superscripts are significantly different ($P < 0.0001 - P < 0.01$).

Gen – genotype; N – sample size; M- Marshall; MNk- Marshall X Naked neck; MN- Marshall X Normal feathered;

Nk- Naked neck, N- Normal feathered

Carcass and organ parameters as affected by sex are presented in Table 3 and 4. Effect of sex on carcass parameters was significant ($P < 0.05$). The values obtained for all the parameters showed that males

had consistently higher values than the females in all parameters measured. This result was in agreement with Marks (1990), Bartov and Plavnick (1998). Musa *et al.* (2006) observed further that males have

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higher live weight, carcass weight, eviscerated weight, breast muscle weight, liver weight and abdominal fat weight compared to females, in broiler breeds. The

superior average male performance among the traits measured was as a result of sexual dimorphism caused by faster growth and muscle-laying activity of the male hormone.

Table 3: Effect of sex on carcass parameters

Sex	N	Live weight (g)	Eviscerated weight (g)	Thigh (g)	Drumstick (g)	Wings (g)	Breast (g)	Shank (g)	Neck (g)
Male	25	1402.04±74.01 ^a	994.92±55.98 ^a	156.24±9.14 ^a	144.60±8.66 ^a	126.48±6.35 ^a	211.08±11.71 ^a	60.16±4.19 ^a	60.04±3.15 ^a
Female	25	1096.80±48.70 ^b	759.96±34.70 ^b	116.32±5.29 ^b	103.36±4.65 ^b	99.12±3.63 ^b	165.48±8.22 ^b	43.60±2.83 ^b	46.36±2.08 ^b

^{a,b} Means within the same column with different superscripts are significantly different (P < 0.0001 - P < 0.01); N – sample size

Table 4: Effect of sex on organs' parameters

Sex	N	Empty gizzard (g)	Liver (g)	Heart (g)	Lungs (g)
Male	25	44.68±1.98 ^a	35.96±2.50 ^a	7.08±0.36 ^a	10.32±0.67 ^a
Female	25	34.52±1.67 ^b	26.96±1.86 ^b	5.24±0.22 ^b	7.52±0.38 ^b

^{a,b} Means within the same column with different superscripts are significantly different (P < 0.0001 - P < 0.01)
N – sample size

Effect of genotype on blood parameters

Haematological parameters in birds have been found to be influenced by various factors such as age, sex, season, nutrition, breeds, climate, geographical location, and physiological factors (Sharmin and Myenuddin, 2004). The effect of genotype on blood parameters is presented in Table 6. The effect of genotype was significant (P<0.05) on blood parameters measured. The highest value (32.30%) for PCV was recorded for Marshall x naked neck crossbred. This was closely followed by the pure Marshall with 29.50% and the least value was 25.20% for naked neck purebred genotype. The values for the haemoglobin concentration followed a similar pattern with the Marshall x naked crossbred genotype having the highest value of 10.85g/dL, followed by the pure Marshall genotype and Marshall x normal crossbred genotype with values of 9.82g/dL and 9.41g/dL, respectively. The pure indigenous genotypes had the least value of 8.18g/dL and 8.21g/dL for naked and normal feathered respectively. For the White blood cells, Marshall x naked neck and Marshall x normal feathered

genotypes, had values that were significantly different (P<0.05) from their pure indigenous counterparts. The values recorded for the red blood cells showed that the crossbreds and the pure Marshall were similar but were significantly different (P<0.05) from the pure indigenous genotype. All the values obtained for the haematological indices were in consonance with the reference value of Jain (1993). The different values obtained amongst genotypes used in this experiment confirmed the conclusion drawn by several authors (Mushiet *al.*, 1999; Ihekumere and Herbert, 2003; Mmereole, 2009), that blood profiles varied among different breeds and the haemograms of these breeds remained unchanged. Within the indigenous genotypes, there were no significant differences for all the parameters measured. This might not be unconnected with the associated inherent resistance of the indigenous breeds to certain tropical diseases. The higher PCV, Hb and RBC values recorded for the Marshall x naked neck crossbred could be attributed to reduction in heat load. The biochemical profiles were significantly

affected by genotype. The result of serum biochemical parameters measured showed that total protein, albumin and globulin were significantly ($P < 0.05$) different amongst the genotypes. The least squares means of serum biochemical parameters as affected by genotype is presented in Table 7. For total protein, the Marshall x normal feathered crossbred had 4.05 g/dL which was lower and statistically different from the others which had 5.47 g/dL, 5.46 g/dL, 5.41 g/dL and 5.33 g/dL for Marshall, Marshall x naked neck, naked neck purebred, normal feathered purebred genotypes, respectively. The albumin content in the pure Marshall and Marshall-naked neck crossbred genotype were 3.32 and 3.04, respectively, which were significantly different ($P < 0.001$) from those of Marshall x normal-feathered crossbred, naked neck and normal feathered purebred genotypes which had values of 2.38, 1.82 and 2.28, respectively. The values recorded for the globulin content were 2.23, 2.45, 1.65, 3.59 and 3.05 for pure Marshall, Marshall x naked neck, Marshall x normal-feathered, naked neck and normalfeathered purebred, respectively. The result obtained for sodium (Na^+), were statistically different with Marshall x naked neck having 148.58 mmol/L which was the highest recorded, followed by 140.19 mmol/L, 139.14 mmol/L, 131.14 mmol/L and 129.75

mmol/L for naked x naked neck, purebred Marshall, Marshall x normal-feathered, normal x normal-feathered genotypes in that order. The values obtained for potassium (K^+) revealed that the Marshall x naked crossbred and the purebred Marshall were significantly different from the other genotypes. The pure Marshall and the Marshall x naked neck had lower values for chloride (Cl^-) (92.87 ± 3.26 mmol and 100.70 ± 4.45 mmol), respectively while Marshall x normal x feathered, naked x naked neck and normal x normal-feathered had significantly higher values. The corresponding values were 119.57 mmol/L, 119.92 mmol/L and 124.36 mmol/L, respectively. This result obtained from this study agrees with the report of Abuagla (2009) who reported significant differences for potassium and sodium among the three genotypes of chickens used in the experiment. The values obtained for sodium, potassium and chloride in this experiment were within the range and reference values given by Simaraks *et al.* (2004) and Clinical Diagnostic Division (1990) respectively. This is an indication that birds used for this experiment had proper acid-base balance which means that their metabolic pathway worked optimally. Although, the values obtained for the serum biochemical indices were higher than those reported by Kwari *et al.* (2011) for broilers. Variation in environment could have caused the differences.

Table 5: Effect of genotype on blood parameters

Gen	N	PCV (%)	Hb (g/dL)	WBC ($\times 10^6$)	RBC ($\times 10^{12}$)	MCV (fl)	MCH (Pg)	MCHC (g/dL)
M	10	29.50 $\pm$ 1.62 ^{ab}	9.82 $\pm$ 0.53 ^b	26.48 $\pm$ 2.16 ^{ab}	2.45 $\pm$ 0.15 ^b	121.07 $\pm$ 1.58	40.34 $\pm$ 0.60	33.32 $\pm$ 0.18 ^{ab}
MNk	10	32.30 $\pm$ 0.99 ^a	10.85 $\pm$ 0.31 ^a	30.16 $\pm$ 1.32 ^a	2.81 $\pm$ 0.09 ^b	115.18 $\pm$ 0.46	38.68 $\pm$ 0.16	33.61 $\pm$ 0.11 ^a
MN	10	27.90 $\pm$ 0.74 ^{bc}	9.41 $\pm$ 0.26 ^b	30.52 $\pm$ 1.07 ^a	2.37 $\pm$ 0.08 ^b	117.93 $\pm$ 1.05	40.47 $\pm$ 0.92	33.72 $\pm$ 0.14 ^a
Nk	10	25.20 $\pm$ 0.90 ^c	8.18 $\pm$ 0.32 ^c	21.50 $\pm$ 1.10 ^b	1.24 $\pm$ 0.59 ^a	120.20 $\pm$ 8.07	39.00 $\pm$ 2.62	32.50 $\pm$ 0.27 ^b
N	10	26.50 $\pm$ 0.75 ^{bc}	8.21 $\pm$ 0.27 ^c	23.70 $\pm$ 2.72 ^b	1.16 $\pm$ 0.53 ^a	126.50 $\pm$ 14.45	39.03 $\pm$ 4.45	31.00 $\pm$ 0.63 ^c

^{abc}Means within the same column with different superscripts are significantly different ($P < 0.05$).

Gen – genotype; N – sample size; M- Marshal; MNk- Marshal X Naked neck; MN- Marshal X Normal feathered; Nk- Naked neck; N- Normal feathered

PCV- Packed Cell Volume; Hb- Haemoglobin; WBC- White Blood Cell; RBC- Red Blood Cell; MCV- Mean Corpuscular Volume; MCH- Mean Corpuscular Haemoglobin; MCHC- Mean Corpuscular Haemoglobin Concentration

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Table 6: Effect of genotype on serum biochemical parameters

Gen	N	Total Prot. (g/dL)	ALB. (g/dL)	GLOBU (g/dL)	Na (mmol/L)	K (mmol/L)	Cl (mmol/L)
<i>M</i>	10	5.47±0.43 ^a	3.23±0.29 ^a	2.23±0.17 ^{cd}	139.14±4.27 ^{ab}	6.9±1.05 ^{ab}	92.87±3.26 ^b
<i>MNk</i>	10	5.46±0.50 ^a	3.04±0.34 ^a	2.45±0.23 ^{bc}	148.58±3.94 ^a	7.88±1.07 ^a	100.70±4.45 ^b
<i>MN</i>	10	4.05±0.24 ^b	2.38±0.12 ^b	1.65±0.14 ^d	131.46±1.93 ^b	4.54±0.19 ^c	119.57±5.32 ^a
<i>Nk</i>	10	5.41±0.16 ^a	1.82±0.11 ^b	3.59±0.23 ^a	140.19±6.67 ^{ab}	5.46±0.33 ^{bc}	119.92±3.99 ^a
<i>N</i>	10	5.33±0.24 ^a	2.28±0.19 ^b	3.05±0.26 ^{ab}	129.75±6.02 ^b	4.34±0.29 ^c	124.36±2.97 ^a

^{a,b,c,d}Means within the same column with different superscripts are significantly different (P < 0.05).

Gen – genotype; N – sample size; M- Marshal; MNk- Marshal X Naked neck; MN- Marshal X Normal feathered; Nk- Naked neck; N- Normal feathered
Total Prot. - Total protein; ALB. - Albumin; Globu.- Globulin; Na⁺- Sodium ion; K⁺- Potassium ion; Cl- Chloride

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