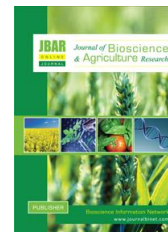




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Association between pituitary specific transcription factor 1 gene (pit 1) and some carcass traits in Sasso and Shika brown chickens

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ABSTRACT

This study was conducted to check the association between PIT 1 gene and some carcass traits in 30 Sasso and 30 Shika brown chickens. Growth data were collected for 12 weeks. DNA was extracted from the blood of the chickens using the Zymo spin column text kit by Zymo Research. Polymerase Chain Reaction (PCR) was done using PIT 1 primers and PCR products were digested with MSP1 restriction enzyme to generate the genotypes. Data generated were analyzed using SPSS Version 16, MEGA 6.0 and DNASP. The results showed allele frequency of A in Sasso was 0.4375 while in Shika, it was 0.5714. Allele frequency of B was 0.5625 in Sasso 0.4286 in Shika brown. The heterozygous frequency was 0.3750 in Sasso and 0.2857 in Shika brown. The highest expected frequency was in AB genotype both in Sasso (3.9375) and in Shika brown (3.4286). Hardy-Weinberg equilibrium was not significant ($p>0.05$) in Sasso chickens. In week 1, the highest body weight occurred in the genotype (BB) 83.42g. However, the highest value for body length was observed in the genotype (AA) 9.00cm in week 5, the highest body weight occurred in the genotype (AB) in Sasso $545.00\pm 121.74g$. The results exposed variation in the expression in PIT1 gene in carcass traits which could be exploited in chicken breeding programmes.

Key Words: PIT1, Association, Sasso, Shika brown and Carcass

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I. Introduction

More recently, different efforts by Nigerian geneticist have being directed towards characterization of the Nigerian local chicken breeds to improve their growth and carcass performances using molecular genetics. Agaviezor *et al.* (2018) worked on Single Nucleotide Polymorphism (SNPs) in chicken growth hormone gene and its association with growth performance in chicken and observed some significant associations. Adebambo *et al.* (2009) worked on the analysis of the Mitochondrial DNA D-Loop region in chickens in South Western Nigerian and observed a single multiple maternal origin among the populations studied. Haruna *et al.* (2003) have used Reverse Transcription-Polymerase Chain Reaction

(RT-PCR) to detect Infectious Bursal Disease Virus (IBDV) in naturally infected chickens in Nigeria. The importance of *PIT 1* gene and its association with economic traits in the poultry industry has been emphasized. Nie *et al.* (2008) emphasized that the *PIT1* gene in chicken is the most important candidate gene responsible for production traits. They also revealed that *PIT1* gene is associated with growth traits and not carcass traits in chicken. Also, *PIT1* gene has been reported to comprise 6 exons in mammals and 7 exons in birds and fishes. These are differences in precursor length (Tatsumi *et al.* 1992). Nei *et al.* (2008) observed a non-synonymous Single Nucleotide Polymorphism (SNP) (Asn299Ile) that was in exon 6 of the *PIT1* gene in chicken. This according to them was significantly associated with body weight of the chicken at week 8. They also observed that another Single Nucleotide Polymorphism (SNP) (SNP) in exon 6 was associated with Average Daily Gain from day old to 4 weeks of age, Body Weight at 21 days, 28 days, 35 days and Shank Diameter at 63 days as observed in this study. Allele frequencies have been observed to differ significantly between meat and egg type chickens (Jiang *et al.* 2004). This study was carried out to assess the association between Pituitary Specific Transcription Factor 1 gene (*PIT 1*) and some carcass traits in Sasso (exotic) and Shika brown (improved local) chickens

II. Materials and Methods

Sixty chickens that comprised 30 Sasso and 30 Shika brown chickens were randomly selected from a flock of about 100 chickens for this study. Carcass data (body weight, body length and breast girth) were collected from day old to 12 weeks. DNA was extracted from the blood of the chickens using the Zymo spin column text kit by Zymo Research. Polymerase Chain Reaction (PCR) was done using *PIT 1* primers with the following reaction: 2.5ul of 10xPCR buffer, 1.0ul of 25Mm Mgcl₂, 1.0ul of 5pMol forward primer (5" AGATTGCCAGATGGTTATGTC 3") and 1.0ul of 5pMol reverse primer (5" CTGCTGACACGTTTCCCGA - 3"). Also added were 1.0 ul DMSO, 2.0 ul of 2.5Mm DNTPs, 0.1 ul Taq 5u/ul, 3.0 ul of 10ng/ul DNA and 13.4 ul water. A touchdown PCR condition was used which involved initial denaturation at 94°C for 5minutes, 9 Cycles of Denaturation at 94°C for 15seconds, Annealing temperature at 62°C at 20seconds and extension at 72°C for 30seconds. This was followed by 35 cycles of Denaturation at 94°C for 15seconds, Annealing temperature at 55°C at 20seconds and extension at 72°C for 30seconds and a final extension at 72°C for 7 minutes. Polymerase Chain Reaction (PCR) Products of were sent out for sequencing at the International Institute for Tropical Agriculture (IITA) Ibadan, Nigeria. PCR products were digested with *MSP1* restriction enzyme to generate the genotypes. Data generated were analyzed using SPSS Version 16, MEGA 6.0 (Tamura *et al.* 2013), Tools for Population Genetic Analysis (TFPGA) 1.3 (Miller, 1997) and DNASP Version 5 (Librado and Rozas, 2009).

III. Results and Discussion

Table 01 shows the allele and heterozygous frequencies of *PIT 1* gene in Sasso and Shika brown chickens. Allele frequency of A in Sasso was 0.4375 while in Shika brown, it was 0.5714. Allele frequency of B was 0.5625 in Sasso 0.4286 in Shika brown. The heterozygous frequency was 0.3750 in Sasso and 0.2857 in Shika brown.

Table 01. Allele and heterozygous frequencies of *PIT 1* gene in Sasso and Shika brown chickens

Breed	Allele	Number of observations	Allele frequency	Heterozygous frequency
Sasso	A	7	0.4375	0.3750
	B	9	0.5625	
Shika brown	A	8	0.5714	0.2857
	B	6	0.4286	

Table 02 shows the test for Hard – Weinberg equilibrium of the genotypes of *PIT 1* gene in Sasso and Shika brown chickens. The highest expected frequency was in AB genotype both in Sasso (3.9375) and in Shika brown (3.4286). The least frequency was observed in BB genotype in Sasso (1.5313) and in Shika brown (1.2857). The Chi square test was not significant ($p>0.05$) in Sasso chickens but was significant ($p<0.05$) in Shika brown chickens.

Table 02. Test for Hard – Weinberg equilibrium of the genotypes of *PIT 1* gene in Sasso and Shika brown chickens

Breed	Genotype	Observed frequency	Expected frequency	Probability (p)
Sasso	AA	3.00	2.5313	0.5301
	AB	3.00	3.9375	
	BB	2.00	1.5313	
Shika brown	AA	3.00	2.2857	0.4406
	AB	2.00	3.4286	
	BB	2.00	1.2857	

Table 03 (see page 1942) shows the association of PIT-1 gene in carcass traits across breeds at week 1, week 5 and week 9. In week 1, the highest variation in body weight occurred in the genotype BB (83.42g). This was followed by genotype AA (77.00g) and AB genotype was the least (75.66g). For body length, the highest value was observed in the genotype AA (9.00cm) and was followed by genotype BB(8.75cm). The least was in genotype AB(8.50cm). Genotype BB gave the highest breast girth of 9.67cm. Next to it was genotype AA (9.42cm) and lastly genotype AB(9.17cm). At week 5, the highest body weight occurred in genotype AB (340.00g). This was followed by genotype AA (338.33g) and lastly, genotype BB (247.08g). The highest value for body length was observed in genotype AA (16.92cm) and was followed by genotype AB (15.17cm) and lastly, genotype BB (13.08cm). For breast girth, the highest value was observed in genotype AA (15.83cm) and the least in genotype BB (13.50cm). At week 9, the highest value of body weight occurred in the genotype AB (416.63g). This was followed by genotype AA (333.39g) and lastly genotype BB (285.81g). For body length, the highest value was observed in the genotype BB (23.50cm). This was followed by genotype AB (22.58cm) and lastly genotype AA (22.50cm). For breast girth at week 9, genotype BB recorded the highest value (23.50cm) and the least was in genotype AA (22.92cm).

Table 04 (see page 1942) shows the association between *PIT 1* gene and carcass traits across breeds for weeks 1, 5 and 9. In week 1, the highest value of body weight occurred in the genotype BB in Sasso chicken (90.33±6.05g). For the body length, the genotype (AA, AB and BB) in Sasso and genotype (AA) in Shika brown, gave the same breast girth of 9.00±0.41cm. Genotype BB in Sasso gave the highest breast girth of 10.33±0.49cm. In week 5, the highest value of body weight occurred in genotype AB in Sasso (545.00±121.74g). For the body length, genotype AA in Sasso (18.50±1.75cm) was the highest value. The genotype AA gave the highest breast girth (18.00±1.05cm). At week 9, the highest body weight occurred in the genotype AB in Sasso (3075.00±45.94). For body length, the highest value was observed in genotype AB in Sasso (24.67±0.70cm) while in breast girth, genotype AB in Sasso gave the highest value of 27.00±0.60cm.

Significant variations were observed between Sasso and Shika brown carcass traits. These could be as a result of different genetic improvement done on them over the years. Sasso (exotic) breed performed significantly better than the Shika brown chickens. Significant differences in the alleles and genotypes studied were observed. These findings of this study are supported by those reported by [Rodbari et al. \(2011\)](#) who observed that the frequency AA genotype was more than those of other genotypes and that the frequency of A allele was higher than that of B allele when they identified SNPs in PIT1 gene and its association with body composition traits in Iranian commercial broiler line. They also observed that the genotype distributions were not in Hardy–Weinberg equilibrium. However, [Nie et al. \(2008\)](#) in their research on polymorphism of *PIT 1* gene reported that the haplotypes of PIT1 gene generated were not associated with fatty and carcass traits but there was significant association with chicken growth traits. [Yan et al. \(2013\)](#) studied the effects of single as well as combined genotypes of MC4R and POU1F1 genes on two production traits in Langshan chicken and detected polymorphisms of the MC4R and POU1F1 genes by PCR-SSCP. There was association between genotype and carcass parameters across the different breeds studied. This is similar to the results of [Zhoa et al. \(2015\)](#) who reported association between IGFBP-2 gene and body weight in Jinghai yellow chicken. A similar report was also made by [Niknafs et al. \(2013\)](#) who studied SNPs in BMPR-1B and STAT5B genes and their association with growth and reproductive traits in chicken. [Rodbari et al. \(2011\)](#) also reported significant associations between

the genotypes of Pit1-Taq1 loci and body weight. These associations reported by these authors form the basis for the variation observed in the performances on chicken across breeds. There is an association between *PIT 1* gene and carcass traits in Sasso and Shika brown chickens. This association became more significant as the chickens increased in age.

IV. Conclusion

It is therefore concluded that *PIT 1* gene plays significant role in carcass traits in chicken and the variation in this gene in the breeds of chicken studied can be harnessed in the improvement and conservation of the Nigerian poultry breeds.

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Table 03. Association of pit-1 gene in growth traits across breeds at week 1, week 5 and week 9

Traits	Week1				Week 5				Week 9			
	AA	AB	BB	SEM	AA	AB	BB	SEM	AA	AB	BB	SEM
Body weight (g)	77.00	75.66	83.42	4.78	338.33 ^{ab}	340.00 ^a	247.08 ^b	96.24	333.39 ^{ab}	416.63 ^a	285.81 ^b	36.32
Body length (cm)	9.00	8.50	8.75	0.32	16.92	15.17	13.08	1.13	22.50	22.58	23.50	0.55
Breast girth (cm)	9.42	9.17	9.67	0.39	15.83	14.58	13.50	0.68	22.92 ^b	23.50 ^a	23.33 ^a	0.48

a, b: Means in the same row with different superscripts are significantly different (p<0.05).

Table 04. Association of breed and pit-1 gene and growth parameters in Sasso and Shika Brown

Breed	Genotype	Week 1			Week 5			Week 9		
		Body weight (g)	Body length (cm)	Breast girth (cm)	Body weight (g)	Body length (cm)	Breast girth (cm)	Body weight (g)	Body length (cm)	Breast girth (cm)
Sasso	AA	83.00±7.40 ^{ab}	9.00±0.50	9.50±0.60	360.00±149.00	18.50±1.75	18.00±1.05 ^a	1790.00±56.26 ^b	24.00±0.86 ^a	25.50±0.74 ^a
	AB	82.33±6.05 ^{ab}	9.00±0.41	9.33±0.49	545.00±121.74	16.33±1.43	15.67±0.86 ^b	3075.00±45.94 ^a	24.67±0.70 ^a	27.00±0.60 ^a
	BB	90.33±6.05 ^a	9.00±0.41	10.33±0.49	306.67±121.74	13.67±1.43	15.00±0.86 ^b	1620.00±45.94 ^b	24.00±0.70 ^a	25.67±0.60 ^a
Shika brown	AA	71.00±6.04 ^b	9.00±0.41	9.33±0.49	316.67±121.74	15.33±1.43	13.67±0.86 ^c	665.00±45.94 ^c	21.00±0.70 ^c	20.33±0.60 ^b
	AB	69.00±7.41 ^c	8.00±0.50	9.00±0.60	135.00±149.10	14.00±1.75	13.50±1.05 ^c	802.50±56.26 ^c	20.50±0.86 ^c	20.00±0.74 ^b
	BB	76.50±7.41 ^b	8.50±0.51	9.00±0.60	187.50±149.10	12.05±1.75	12.00±1.05 ^c	570.00±56.26 ^c	23.00±0.86 ^b	21.00±0.74 ^b

a, b, c: Means in the same row with different superscripts are significantly different (p<0.05).

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