Gene flow in three broiler chicken populations in Abeokuta using jackknife procedure

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Abstract

Jackknife procedure (JP) is a less biased and fascinating method of obtaining gene flow among populations. The purpose of this study was to use JP to eliminate bias associated with indirect estimators of gene flow. With microsatellite markers, it has been possible to estimate gene flow (Nm_e) in natural populations. To quantify Nm_e in chicken populations, we used five polymorphic microsatellite markers with 115 genomic deoxyribonucleic acid (DNA) obtained from (dihybrid (DH = 37), trihybrid (TH = 32) and Anak White (AW = 46) broiler chicken populations, respectively. Through polymerase chain reaction, we amplified DNA from the broiler chicken populations, subjected amplicons to electrophoresis, fragment sizes determined and analysed across populations considering selected markers through which standardized genetic variance among sub-populations in total sample depicted as (F_{ST}) was obtained per marker for chicken population pairs. Its average across markers/population pairs was used to infer Nm_e in the chicken population pairs. We used JP which is a mathematical approach that utilizes mean F_{ST} across markers to obtain Nm_e in the chicken population pairs. Gene flow based on JP in chicken population pairs designated as (Nm_e)_{JP} were 3.4267 (DH vs. TH), 7.0127 (TH vs. AW) and 11.7405 (DH vs. AW) and among chicken populations, (Nm_e)_{JP} was 7.1969. Considering these estimates, we concluded that there was gene flow among the three broiler chicken populations examined in Abeokuta, Nigeria.

Keywords: Estimates, fragment sizes, genetic exchange, markers.

Introduction

Recently in Nigeria, there have been efforts on the production of broiler chickens because of its production, which does not require much capital and there are also quick returns on investment. There are different broiler chicken strains reared by poultry farmers in the six geo-political zones of Nigeria. Some ubiquitous strains include Anak White, Anak Titan, Marshall, Hubbard, Arbor Acre, Ross, Obi Marshall, Dihybrid, Trihybrid, etc.

Productive performance of some of these broiler chicken strains have been examined

under intensive management (Olowofeso, 2009; Olawumi and Fagbua, 2011; Sanda *et al.*, 2014a). Genetic parameter estimates of some quantitative traits have also been determined when some of these broiler chickens were used as experimental models (Adeleke *et al.*, 2011; Sanda *et al.*, 2014b). As a result of mating and different breeding activities involving these chicken strains, there has been intermixing of populations and this has resulted in profound genetic exchange. Level of this genetic exchange most especially in broiler chickens in Nigeria remained undetermined. Gene flow

is the alteration of the frequencies of alleles of any genes in a population, and it results from interbreeding with organisms from another population having different frequencies. Gene flow among populations of species is an essential factor in maintaining species integrity. Direct estimation of this parameter is a herculean task (Neigel, 1997), hence why its estimation in natural populations are carried out using indirect approaches such as use of F-statistics and conditional average frequency generated when unique (rare) allele frequencies in a population were averaged across markers (Singh and Rhoberg, 1987; Slatkin and Barton, 1989; Whitlock and McCauley, 1999). However, and based on our literature search, a simple, straightforward, less biased and fascinating method of obtaining gene flow among populations is to use the jackknife procedure suggested by Mosteller and Tukey (1977). Jackknife procedure is a ready tool that can be used to solve myriads of problems, but particularly useful for variance and bias estimation.

In literature, extensive information about level of inbreeding, genetic diversity, genetic relationships, genetic variability and divergence time among common chicken populations including broilers abound, but surprisingly, levels of gene flow quantified through appropriate procedure among chicken populations are limited. There is need to infer levels of gene flow in natural populations according to Hudson *et al.* (1992), and such populations include broiler chicken populations so as to concentrate efforts on chicken strains possessing desirable genes.

To estimate this gene flow in broiler chicken populations reared in Abeokuta, Nigeria, important tools need to be employed and readily available tools for this is the microsatellites (tandem DNA repeats of a 2

to 5 basepair units, or STRs (simple tandem repeats) or SSRs (simple sequence repeats), which is capable of revealing all information that are abundant in any genetic resource. According to Reed *et al.* (2002), microsatellite markers are important tools in genetic analysis of populations and experimental families. Potentials of microsatellite markers have been reiterated by several researchers such as Hillel *et al.* (2003; 2007), Groeneveld *et al.* (2010); Mwacharo *et al.* (2013). Microsatellite markers can be used with animal genetic resources including chickens to obtain measures of genetic diversity; it can detect rare or population-specific alleles, can be used to infer level of relationships and genetic distances among populations and can be used to obtain F-statistics or fixation indices such as inbreeding coefficient within population (F_{is}), inbreeding coefficient of individual within total population (F_{it}) and inbreeding coefficient of sub-populations within total population (F_{st}). Among the F-statistics, one most relevant to gene flow in any natural population is F_{st} , and the actual meanings have been given by Neigel (1997), but can be regarded as the standardized genetic variance among sub-populations in the total sample (Wright, 1965).

Using molecular markers especially microsatellite markers with genetic resource populations, genetic data can be obtained with ease and when such data are analysed, produce this important component of F-statistics called F_{st} , which can be used to infer levels of gene flow in natural populations. In achieving this, we have used five polymorphic microsatellite markers with genetic material (DNA) isolated from three broiler chicken populations (Dihybrid, Trihybrid and Anak White). These three broiler chicken strains were considered because genetic

information on them has not been documented. The objective of this study was to quantify gene flow among three broiler chicken populations in Abeokuta, Ogun State, Nigeria using a more fascinating method called jackknife procedure.

Materials and Methods

Broiler chicken populations

Dihybrid (DH), Trihybrid (TH) and Anak White (AW) broiler chickens were sampled for this study. The dihybrid is a crossbreed between pure indigenous normal feathered Nigerian chicken and broiler breeder, Anak Titan. The indigenous normal feathered chicken is a purebred following seven generations of breeding and selection. Phenotypically, the indigenous chicken has blue-black plumage colour with black beak and shank colour. Plumage of the dihybrid is white with blue-black patches. It is a dual purpose strain with 50% indigenous blood composition. The eggshell colour is light brown. The trihybrid from which blood samples were collected was generated through crossing of dihybrid with broiler breeder, Arbor Acre. Phenotypic features of Arbor Acre have been detailed in Sanda *et al.* (2014b). The trihybrid has 25% indigenous chicken blood composition with white plumage. It lays light brown eggs. Anak White is one of the commonest broiler strains found virtually everywhere in Nigeria. It has entirely white plumage with prominent yellow shank. At 8-10 weeks, they attained average market weight of 2.50 kg.

Blood collection

The Animal Research study protocol approved by the College of Animal Science and Livestock Production, Federal University of Agriculture, Abeokuta, Nigeria were adhered to and basic protocol for sampling of blood for DNA

recommended by FAO (2011) was followed. Total of one hundred and fifteen blood samples made up of DH = 37, TH = 32 were collected. Samples of DH and TH were collected from the Directorate of University Farms (DUFARMS) located within Federal University of Agriculture, and the remaining forty six (AW = 46) samples were obtained from reputable commercial poultry farm in Camp, Alabata Road. Sampling locations are within Alabata, Abeokuta, Nigeria and the geographical location of Alabata is as reported elsewhere by Jegede *et al.* (2015). Blood samples collected were transferred to Central Biotechnology Laboratory, Federal University of Agriculture, Abeokuta, Nigeria for DNA isolation.

DNA isolation

Norgen Genomic DNA Isolation Kit was used. The Norgen proteinase K was re-suspended through vortexing and 20 μ L of proteinase K was transferred into centrifuge tube and 100 μ L chicken blood sample added, followed by addition of 300 μ L Lysis solution and vortexing of the mixture was done for 10 s. Tube containing the mixture was spin to collect drop of liquid from inside the lid and was incubated at 55°C for 600 s. Thereafter, 250 μ L of 100% ethanol (C₂H₅OH) was added to sample, mixed and vortexed for 10 s and tube was spin to collect drops of liquid from inside the lid. A column with one of the collection tube was assembled and lysate applied to the column, centrifuged for 60 s at 6,000 x g, before the flow through was discarded. When the lysate had passed, samples were centrifuged for 120 s. Column wash was done with addition of 500 μ L Wash solution I to the column and centrifuged for 60 s at 6,000 x g, and flow through was then discarded. Spin column was reassembled with its collection tube and 500 μ L Wash solution II was added to the column,

centrifuged for 60 s at 14,000 x g and the flow through was again discarded and spin column reassembled with its collection tube. Addition of Wash solution II was carried out twice and column was spin for 120 s to dry column at 14,000 x g, before collection tube was discarded. Column was placed into a 1.70 ml Elution tube and 200 µL Elution buffer added to column, incubated at room temperature for 60 s and centrifuged for 60 s at 6,000 x g. DNA was collected and stored at -20°C before polymerase chain reaction amplification. DNA stock was diluted 1:10 in sterile water to a concentration of 50 ng/ µL. Isolated DNA was quality-tested on agarose gel electrophoresis carried out in a horizontal Submarine Agarose Chamber.

Microsatellite markers used and polymerase chain reaction programme

Five microsatellite markers (ADL136, ADL0268, MCW0085, MCW0206 and LEI0166) were used in this study and were selected based on their degree of polymorphisms and high heterozygosity values as evidenced by literature searched. For example, ADL136, LEI0166 and MCW0085 have been used by Olowofeso (2005), ADL136 by Nahashon *et al.* (2008), ADL0268, MCW0206 by Hillel *et al.* (2003) and FAO (2004; 2011) recommended ADL0268, LEI0166 and MCW0206 as informative markers for biodiversity studies in chickens. Sequences of the selected markers, their annealing temperatures and fragment sizes are presented in Table 1.

Table 1: Sequences, annealing temperature and fragment size range (in basepair) of markers used across broiler chicken populations

Marker	Sequences (Forward and Reverse)		Anneal. temp. (°C)	Fragment size range
ADL136	TGTCAGGCCATCGTATCAC	CCACCTCTCTCTCTGTTCA	52	148-166
ADL0268	CTCCACCCCTCTCAGAACTA	CAACITCCCATCTACTACT	58	110-118
MCW0085	CTGCAAGTATATGGAAGTCTC	GGTATACAGGGCTTCTGAAA	56	294-332
	TC	CA		
MCW0206	CTTGACAGTGATGCATTAAT	ACATCTAGAATTGACTGTTT	60	225-241
	TC	AC		
LEI0166	CTCCCTGCCCTTAGCTACUCA	TATCCCTGGCTGGGAGTTT	60	342-360

Polymerase chain reaction (PCR) mixture with total volume of 12.50 µL contained 1.00 µL DNA, 1.50 µL (i.e. 0.75 µL each of forward and reverse primers), 5.00 µL Master Mix (made up of PCR buffer, Taq DNA polymerase, dNTP, Mg²⁺) and 5.00 µL nuclease free water. PCR amplification carried out in 9600 Perkin Elmer thermal cycler series was (94°C, 300 s) of initial denaturation, 35 cycles of denaturation at (94°C, 60 s), annealing temperatures of the five microsatellite markers ranged from 52°C to 60°C (Table 1) and extension at (72°C, 60 s), followed by final extension at (72°C, 600 s).

Electrophoresis and fragment size determination

Electrophoresis of PCR products was performed on a 12% denaturing polyacrylamide gel. Re-suspended products were run on an ABI 377 DNA Sequencer with pBR322 DNA/MspI used as internal ladder for precise on gel size determination and gels were stained with a drop of ethidium bromide. Amplification was carried out with a pair of primer at a time and this was observed for all the markers. Gels were visualised and photographed on ultraviolet (UV) trans-illuminator. Fragment sizes were determined with

reference to ladder incorporated in each gel using GeneScan 3.7 software (Applied Biosystems).

Statistical analysis

Fragment sizes (in basepair) obtained in each chicken population and markers were prepared into Excel Worksheet. Allele frequencies for each marker and across broiler chicken populations and standardized genetic variance among sub-populations in the total sample (also known as global F_{ST}) were generated with Microsatellite Analyser (MSA) version 4.05 (Dieringer and Schlotterer, 2003). F_{ST} and p-values among broiler chicken populations and markers were derived. Similarly, with number of permutations equal 10,000, global F-statistic and p-values for each marker and across chicken populations were obtained from MSA data file. F_{ST} values were taken as F_{ST} per marker across broiler chicken populations. F_{ST} per marker for chicken population pairs was generated through a re-run of same software and mean F_{ST} across markers for each population pairs generated was used to compute gene flow in the chicken population pairs. We examined the accuracy of mean F_{ST} across markers and across chicken populations with Olowofeso (2005) relation depicted as:

$$\bar{F}_{ST(1+2+3)} = \frac{\sum [\bar{F}_{ST(1+2)} + \bar{F}_{ST(1+3)} + \bar{F}_{ST(2+3)}]}{3}$$

where 1, 2 and 3 were the three chicken populations (DH, TH and AW) and 1 vs. 2, 1 vs. 3 and 2 vs. 3 represents chicken population pairs (DH vs. TH, DH vs. AW and TH vs. AW), respectively. However, our main objective of this study was to get less biased estimator of gene flow. To achieve that, we analysed our data further using jackknife procedure suggested by Mosteller and Tukey (1977); Slatkin

(1985). The formula used was of the form:

$$(Nm)_{JP} = [n(Nm_i)] - \left[\frac{n-1}{n} \left(\sum Nm_i \right) \right]$$

where $(Nm)_{JP}$ is gene flow quantified through jackknife procedure, n = number of microsatellite markers used, Nm_i is actually Nm_i based on markers used excluding marker i , and Nm_i is gene flow inferred using mean F_{ST} across markers and populations earlier defined by both Slatkin (1985) and Johnson *et al.* (1988) as:

$$Nm_i = \frac{\left[\frac{1}{\bar{F}_{ST}} - 1 \right]}{4}$$

Results and Discussion

Fragment sizes (in basepair) of the five microsatellite markers are summarised in Table 1. Allele frequencies generated per marker in the three broiler chicken populations are represented in Figures 1 through 5. There were variations in the number and frequencies of alleles in each marker and chicken populations. Some rare (unique) alleles (i.e. alleles seen in one population, but completely absent in the other populations) were detected by the markers in the chicken populations. Total of 10 rare alleles were detected by four of the markers across chicken populations (i.e. one by ADL136 seen in AW chicken, 3 (2 rare alleles in DH and 1 rare allele in TH chickens) by MCW0085, 1 by MCW0206 detected in AW and 5 (2 rare alleles in TH and 3 rare alleles in AW) by LEI0166, while ADL0268 do not detect any rare allele in the chicken populations.

Five rare alleles were detected in AW chicken produced by four of the markers, followed by three rare alleles detected in TH chicken by (LEI0166 which detected 2 rare alleles and MCW0085 detected one rare allele), and the only two rare alleles detected

in DH chicken were produced by MCW0085. LEI0166 produced the highest number of rare alleles (5), followed by MCW0085 (3), while ADL136 and MCW0206 produced one rare allele each. The five microsatellite markers used were polymorphic as there was no allele detected that has frequency beyond 0.99, meaning

that the markers were effective for genetic characterisation and can also be used to obtain F-statistic particularly F_{ST} , which can be used to infer gene flow in natural populations including broiler chicken populations. In this study, F_{ST} and p-values among broiler chicken populations and markers are summarised in Table 2.

Table 2: Standardized genetic variance (F_{ST}) values and p-values (in parentheses) among broiler chicken populations examined with five polymorphic microsatellite markers^a

Population	Population		
	DH	TH	AW
DH	0 (0)	0.0480 (0.0001)	0.0214 (0.0461)
TH	0.0480 (0.0003)	0 (0)	0.0387 (0.0030)
AW	0.0214 (n.s.)	0.0387 (0.0090)	0 (0)

^aAbbreviations were as defined within text and n.s. = not significant.

F_{ST} values ranged from 0.0214 (DH vs. AW) to 0.0480 (DH vs. TH) and p-values ranged from 0.0001 (DH vs. TH) to 0.0461 (DH vs. AW), but not significant in DH vs. AW broiler chicken populations. When number of permutations was set at 10,000, global F_{ST}

over markers used was 0.0362 and p-value was 0.0002. Genetic differentiation (G_{ST}) over markers was 0.0490 with p-value of 0.0006. Global F_{IT} and F_{IS} were 0.4693 and 0.4494, respectively (Table 3).

Table 3: Global F-statistic over markers, p-values and global F-statistic and p-values of each marker used across broiler chicken populations^a

Global F-statistic	Values	p-values	p-values
Global F_{ST} over markers	0.0362	0.0002	
Global F_{IT} over markers	0.4693		
Global F_{IS} over markers	0.4494		
G_{ST} over markers	0.0490	0.0006	
Marker	Values	p-values	
	ADL136	Global F_{ST}	0.0087
		Global F_{IT}	0.6836
		Global F_{IS}	0.6857
ADL0266		G_{ST}	0.0238
		Global F_{ST}	0.0122
		Global F_{IT}	0.6061
		Global F_{IS}	0.6408
MCW0085		G_{ST}	0.0200
		Global F_{ST}	0.0583
		Global F_{IT}	0.1188
		Global F_{IS}	0.2797
MCW0206		G_{ST}	0.0597
		Global F_{ST}	0.0243
		Global F_{IT}	0.3905
		Global F_{IS}	0.3753
LEI0166		G_{ST}	0.0387
		Global F_{ST}	0.1435
		Global F_{IT}	0.3821
		Global F_{IS}	0.3041
	G_{ST}	0.0893	0.0001

^a F_{ST} = inbreeding coefficient of sub-population within total population, F_{IT} = inbreeding coefficient of individual within total population, F_{IS} = inbreeding coefficient of individual within sub-population and G_{ST} = genetic differentiation among populations.

Table 3 also present global F_{ST} and p -values of each marker used across broiler chicken populations. F_{ST} value per marker for chicken population pairs, mean of this

F_{ST} , gene flow (Nm_{ij}) quantified using this F_{ST} and gene flow inferred using jackknife procedure (Nm_{ij}) are summarised in Table 4.

Table 4: Estimates of gene flow (Nm_{ij}) based on F_{ST} and jackknife procedure (Nm_{ij}) of each marker for chicken population pairs and across broiler chicken populations^c

(A) In chicken population pairs									
Marker	DH vs. TH			DH vs. AW			TH vs. AW		
	F_{ST}	Nm_{ij}	$(Nm_{ij})_{jk}$	F_{ST}	Nm_{ij}	$(Nm_{ij})_{jk}$	F_{ST}	Nm_{ij}	$(Nm_{ij})_{jk}$
ADL136	-0.0074	5.2519	5.4267	-0.0133	11.6681	11.7405	-0.0055	6.8780	7.0127
ADL0268	-0.0176	5.3621		-0.0172	11.6720		-0.0016	6.8741	
MCW0085	0.0710	5.1735		0.0284	11.6264		0.0622	6.8103	
MCW0206	0.0550	5.1895		0.0256	11.6292		-0.0092	6.8817	
LEI0166	0.1267	5.1178		0.0814	11.5734		0.1294	6.7431	
		Σ			Σ			Σ	
	$\bar{F}_{ST} =$			$\bar{F}_{ST} =$			$\bar{F}_{ST} =$		
	0.0455			0.0210			0.0351		
	$Nm_{ij} =$			$Nm_{ij} =$			$Nm_{ij} =$		
	5.2445			11.6548			6.8725		
(B) Across chicken populations									
Marker	F_{ST}	Nm_{ij}	$(Nm_{ij})_{jk}$						
ADL136	-0.0087	7.0686	7.1969						
ADL0268	-0.0122	7.0721							
MCW0085	0.0543	7.0056							
MCW0206	0.0243	7.0356							
LEI0166	0.1135	6.9464							
		Σ							
	$\bar{F}_{ST} =$								
	0.0342								
	$Nm_{ij} =$								
	7.0599								

^c Values in bold form are levels of gene flow in chicken population pairs and among chicken populations based on jackknife procedure.

Across chicken populations and for each of microsatellite marker used, F_{ST} value per marker, mean of this F_{ST} , gene flow (Nm_{ij}) quantified using this F_{ST} and gene flow inferred using jackknife procedure (Nm_{ij}) are also presented in Table 4. Gene flows quantified were 5.2445, 6.8725 and 11.6548 in DH vs. TH, TH vs. AW and DH vs. AW chicken population pairs, respectively. Similarly, gene flows quantified between chicken population pairs using jackknife procedure were 5.4267, 7.0127 and 11.7405 for DH vs. TH, TH vs. AW and DH vs. AW.

Across chicken populations and markers, mean F_{ST} was 0.0342 and gene flow (Nm_{ij}) quantified using this value was 7.0599, and when jackknife procedure was used, it was 7.1969 (Table 4). Results also showed that in the three chicken population pairs as well as across three chicken populations, gene flow inferred (Nm_{ij}) was lower than the one obtained through jackknife procedure (i.e. $(Nm_{ij}) < (Nm_{ij})_{jk}$). Overall, gene flow across chicken populations quantified through jackknife procedure was higher than gene flow in chicken population pairs (DH vs. TH

Figure 1: Allele sizes (bp) and their frequencies produced by ADL136 across the three broiler chicken populations.

Figure 2: Allele sizes (bp) and their frequencies produced by ADL0268 across the three broiler chicken populations.

Figure 3: Allele sizes (bp) and their frequencies produced by MCW0085 across the three broiler chicken populations.

Figure 4: Allele sizes (bp) and their frequencies produced by MCW0206 across the three broiler chicken populations.

Figure 5: Allele sizes (bp) and their frequencies produced by LEI0166 across the three broiler chicken populations.

and TH vs. AW), but lower than gene flow in DH vs. AW chicken population pair.

Numbers of alleles produced were 5 in ADL0268, 9 in MCW0206, and 10 each were produced by ADL136, MCW0085 and LEI0166, which culminated into 44 alleles detected across markers and across broiler chicken populations. Proportion of rare alleles in these total alleles was 22.70%, while the rest (fixed) alleles (34) or 77.30% were found in two or three chicken populations. Figures 1 to 5 clearly represents allele sizes together with allele frequencies generated across the three broiler chicken populations examined with each marker used. Allele numbers range limits were 5-10 considering the five markers used across broiler chicken populations.

The observed numbers of alleles in this study were consistent with numbers of alleles observed by Nahashon *et al.* (2008), Ayang *et al.* (2016) and Seilsuth *et al.* (2016) when microsatellite markers were used with common animal genetic resources. Considering allele numbers range limits in this study, it means that the lower limit was greater than 4, the minimum number of alleles suggested by Wimmers *et al.* (2000) and FAO (2004; 2011) for microsatellite markers to be used with any genetic resource. This therefore means that the five markers used in this study were suitable for further analysis of chicken

populations including quantifying gene flow in populations.

F_{ST} considered all alleles in populations and reduces risk of misinterpreting just few, hence why it is more relevant and reliable in quantifying gene flow according to Johnson *et al.* (1988), Wolf and Soltis (1992). Mean F_{ST} in the three chicken population pairs, when further averaged over number of chicken population pairs was equal to mean F_{ST} of markers across chicken populations and this further confirmed the validity of relation suggested by Olowofeso (2007) in generating mean F_{ST} across markers and populations (See Table 4).

In this study, indirect estimator of gene flow (Nm_j) in chicken population pairs and among the three chicken populations were generally lower than gene flow quantified through jackknife procedure and these results were consistent with estimates of gene flow reported by Johnson *et al.* (1988), Wolf and Soltis (1992), Yamanishi and Innan (2017). Our results also indicated that jackknife procedure eliminate bias associated with indirect estimators of gene flow.

Gene flows estimated in the chicken population pairs and among chicken populations were relatively high, this might be due to the fact that the populations considered were closely related or

sampling areas too close. Gene flow may be overestimated if number of populations involved is minimal or less than 10 (Wolf and Soltis, 1992), hence this might be another factor responsible for the high gene flow quantified using mean F_{ST} and jackknife procedure in this study. Relatively high estimates of gene flow as seen in this study may also be due to hidden alleles in the populations. In this study, our indirect estimator of gene flow based on mean F_{ST} and jackknife procedure were greater than one (i.e. $Nm_e > 1$), meaning that gene flow is high and significant, which further substantiates the earlier assertion of Gasperi *et al.* (1991).

Conclusion

The degree of polymorphism of the microsatellite markers used was high as there was no allele frequencies that exceeds 0.99, thus justifying the suitability of the markers for genetic characterisation and for easy generation of F-statistic particularly F_{ST} which can be used to infer gene flow in chicken populations. Novel information of this study could be summarised thus: Anak White broiler chicken has more rare alleles than the other two broiler chicken populations examined and using the rare allele detected in the chicken populations as selection criterion, the order of selection of the broiler chicken populations for increased meat production should be AW, TH and DH chickens, respectively. Secondly, the jackknife procedure of quantifying gene flow in populations is less biased and more fascinating than the indirect estimator of gene flow. Estimated gene flow in chicken population pairs and among chicken populations were relatively high and hidden alleles in the chicken populations might not be excluded from being responsible for the high values observed. Based on the values generated,

we concluded that there was gene flow among the three broiler chicken populations examined in Abeokuta, Nigeria.

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