ABSTRACT

Single nucleotide polymorphisms (SNPs) of Nigerian chickens; including the heavy ecotype (HE), light ecotype (LE), frizzle feathered (FF) and naked neck (NN) genotypes were investigated. A total of forty individual chickens were used for the DNA assay. Blood samples were collected in EDTA (ethylene diamine tetra acetic acid)- treated test tubes from the wing veins of chickens distributed among the four ecotypes as follows; 7 Frizzle feathered (FF) cocks, 7 Naked neck (NN) cocks, 13 Heavy ecotype (HE), and 13 Light ecotype (LE). Genomic DNA was extracted from blood tissues using the Zymobead® Extraction Kit following manufacturer's protocol. The genetic potentials of the ecotypes were evaluated by genotyping the SNPs of their prolactin gene. The PCR analysis of the DNA samples was done using a diluted working concentration of 10 nano-grams per micro-litre. Forward and reverse primers were designed based on the prolactin gene sequence in Genbank database. The PCR amplifications were carried out in a 25-ul buffered reaction solution. The quality of DNA obtained was assessed using a Nanodrop spectrophotometer. The PCR products were purified using Zymobead Research DNA Sequencing Clean-up Kit. Genomic DNA samples of the four ecotypes were sequenced using the BigDye® Terminator version 3.1 Cycle Sequencer of Applied BioSystems. DNA sequences' alignment and SNP sequence variation parameters such as Relative Synonymous Codon Usage (RSCU) were analyzed using (Molecular Evolutionary Genetics Analysis Version 6 (MEGA 6.0), PAST (Paleontological Statistics) version 3.14 and Tools for Population Genetic Analysis (TFPGA) Version 1.3, while GenePOP software was used to analyse SNP allelic frequencies. One-way analysis of variance of SNP effect on egg number and egg size was done and significant differences ($p < 0.05$) were separated using Duncan's New Multiple Range Test.

Three SNPs were identified in the Nigerian chicken ecotypes namely G-T, T-C and A-C having genotypic frequencies of 7 in NN, 10 in HE and 4 in both FF and LE chickens. The cPRL genomic sequence consisted of 130 base pair (bp) long. Comparison to other obtained chicken prolactin (cPRL) gene sequence gave 98% homology with White Leghorn (Accession No. AB013783.3). The Tajima "D" test of neutral molecular evolutionary rate was 2.7945. Phylogenetic relationship yielded two distinct clades or groupings of HE, LE and NN in Clade 1 and only FF in Clade 2. High RSCU values of 3.88, 3.65 and 3.43 were obtained for the codons UCU GCA and AGA respectively and RSCU value of zero was observed for the following 10 codons: CUA, CCG, GCU, GCC, GCG, UAC, UAG, CGC, CGA and GGU. Also, the T-C single base polymorphism showed significant ($p < 0.05$) negative association with egg number and egg size. A= Adenine, G= Guanine, C= Cytosine, T= Thymine and U= Uracil.