

GENETIC DIVERSITY OF CHICKEN POPULATIONS IN SOUTH-SOUTH REGION OF NIGERIA USING MICROSATELLITE MARKERS

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ABSTRACT: Eighty genomic DNA were isolated from three indigenous chicken populations-Normal feathered (NF), Frizzle feathered (FF) and Naked Neck (NN) maintained in South-South region of Nigeria. Samples were used in a polymerase chain reaction (PCR) with eight microsatellite markers. PCR products obtained were separated on a 12% polyacrylamide gel electrophoresis using double cassette glass plates. Genetic diversity measures considered were allele numbers (No) and their frequencies, effective number of allele (Ne), observed and expected heterozygosity (H_o , H_e) and polymorphism information content (PIC). Genetic similarity between populations and genetic distance among chicken populations were obtained using the allele frequencies considering all loci and the three chicken populations. Dendrogram was generated from estimates of genetic distance among chicken populations. Mean allele number (No) for all loci ranged from 5.6250 (NN) to 9.8750 (NF) and mean effective number of allele (Ne) ranged from 5.0133 (NN) to 7.1637 (NF). Mean PIC was between 0.7588 (NN) and 0.8282 (NF). Averages of observed heterozygosity among loci were 0.5068, 0.5236 and 0.5755 for NN, NF and FF chicken populations, respectively. Genetic distance estimates revealed that the NF and FF chicken populations are closely related with genetic distance value of 0.5183. Genetic distance value (0.6177) intermediate and (0.6306) farthest were obtained for NF vs. NN, and FF vs. NN, respectively. The study revealed the existence of moderate genetic diversity in chicken populations studied and also showed that the markers used were highly informative and can be used in future studies involving chicken populations.