Genetic evaluation of Spanish and Nigerian chickens using microsatellite markers

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Chickens are the most common and widespread domestic livestock species across the world. However, in recent times there has been a drastic reduction in genetic diversity among commercial and fancy breeds following selective breeding for specific production and phenotypic traits. The same possibly occurs among village chickens following extensive crossbreeding with commercial stocks. In this study, we evaluated, using 30 microsatellite markers, the genetic diversity and differentiation among three Spanish fancy breeds and 184 Nigerian free-range scavenging village chickens sampled from three different geo-political zones. On average 4.93 ± 0.23 alleles were detected for all microsatellites with mean polymorphic information content of 0.488. Nigerian chicken populations were more diverse than Spanish chickens in terms of mean number of alleles per locus (MNA = 7.6 ± 0.78 against 6.57 ± 0.54) but had lower average expected heterozygosity (He = 0.57 ± 0.04 against He = 0.61±0.03). The mean deficit of heterozygotes within populations (FIS) was higher in Spanish (FIS = 0.21 ± 0.03) than in Nigerian (FIS = 0.15 ± 0.06) village chickens. Phylogenetic neighbor joining analysis using Nei’s genetic distance, showed a clear separation between the different breeds, with Nigerian village chickens being clearly separated from their Spanish counterparts. Our results clearly suggest that while there has been a reduction in genetic diversity among chickens, a considerable level of diversity still occurs among village chickens and the panel of microsatellite markers employed in the current investigation are useful in studying the genetic diversity and divergence among both Spanish fancy chicken breeds and Nigerian village chicken.