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## Use of Microsatellites and MtDNA to Assess Genetic Diversity Within and Between Zimbabwe Chicken Eco-types

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## Abstract

Village chickens play an integral role in meeting smallholder households social-economic and cultural needs. These local chickens are part of the total poultry biodiversity that is needed to cope with changing production environments, consumer preferences and market demands. The objective of the study was to test whether chickens reared under different climatic and socio-economic factors in geographically distant farming systems differ genetically. Twenty-nine microsatellite markers were typed for 238 individuals randomly selected from the five eco-zones of Zimbabwe. In addition 516bp of the D-loop region of mtDNA were sequenced for 53 chickens from the 5 eco-populations and 60 individuals from broiler and layer reference populations. A total of 238 alleles with an average of 8.41 (SD = 4.729) alleles per microsatellite locus were observed. Gene diversity averaged 0.66 (0.02) while observed heterozygosity was 0.60 (0.01). An average inbreeding coefficient ( $F_{IS}$ ) of 0.077 (SE = 0.012) was observed across the five eco-populations. Thirteen, 11, 12, 9 and 5 loci contributed to heterozygote deficiency in eco-zone 1-5 respectively. Overall population variation ( $F_{IT}$ ) was 0.084 (SE = 0.0129), 9% of which was due to among population variation  $(F_{ST})$ . Phylogenetic analysis indicated the Zimbabwe population clustered as one population surrounded by the commercial lines. Fourteen haplotypes were observed from the sequenced mtDNA fragment. Number of haplotypes per population ranged from 1 to 3. The major haplotype with an outgroup weight of 0.22 was found in three Zimbabwe eco-types and 3 commercial lines. The second widely distributed haplotype was unique to 52% of the Zimbabwe chickens across all the eco-zones. While commercial lines tend to be less polymorphic and do not share haplotypes with other populations, the Zimbabwe chicken eco-types shared some haplotypes among themselves and these reference populations. Results show that the Zimbabwe local chicken population although distributed over a broad geographic range is insignificantly sub-structured and might be sharing a considerable part of their genome with other commercial lines.

Keywords: Inbreeding coefficient, phylogenetic relationship, population structure, poultry diversity

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