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Assessing Genetic Diversity of Five Tanzanian Chicken Ecotypes Using Microsatellite Markers and Mitochondrial DNA D-loop Sequencing

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Abstract

The study aimed to evaluate the genetic diversity of Tanzanian chicken populations through phylogenetic relationship, and to trace the history of Tanzanian indigenous chickens. A total of 196 individuals of five ecotypes of Tanzanian local chicken (*Ching'wekwe*, *Kuchi*, *Morogoro Medium*, *Pemba* and *Unguja*) from eight different regions (Mwanza, Geita, Shinyanga, Tabora, Tanga, Morogoro, Unguja and Pemba) were used. The diversity study was based on morphological measurements, *i.e.* wing length, shank length, shank thickness, keel length and body weight, and 29 microsatellite markers proposed by ISAG/FAO advisory group for animal genetic diversity. Additionally, the degree of shared mtDNA haplotypes from the D-loop region was analysed to disclose likely maternal origin of Tanzanian indigenous chicken. A Principal Component Analysis of morphological measures distinguished individuals most by limb size and body weight. *Morogoro Medium*, *Pemba* and *Unguja* grouped together, while *Ching'wekwe* stood out due to their unproportional short shanks. *Kuchi* formed an independent group due to their comparably long limbs. Microsatellite analysis revealed three clusters of Tanzanian chicken populations: *Ching'wekwe* clustered together with *Morogoro medium*, *Unguja* and *Pemba* ecotypes made up a common cluster distinct from *Morogoro medium* and *Ching'wekwe* cluster, while *Kuchi* ecotype formed an independent cluster. According to reference mtDNA haplotypes, previously described in the literature by Liu and colleagues, the sampled Tanzanian chickens encompassed two haplogroups of different genealogical origins, *i.e.* the respective haplogroups D and E which originated from Southeast Asia and Indian subcontinent. The majority (95.2%) of *Kuchi* were found in haplogroup E, and in particular clustering with the E1 haplotype (76.2%). Latter is identical to haplotype A3 described by Oka and colleagues that contained Shamo game birds sampled from Shikoku Island of Japan in the Kōchi Prefecture. In all three analyses, *Kuchi* formed an outstanding group from the other four Tanzanian chicken ecotypes. The overlap with haplotypes from Shamo in Japan and the name “Kuchi” which is very similar to the Prefecture Kōchi implies that *Kuchi* might be imported to Tanzania from Japan. Haplotype network analysis of mtDNA suggests that Tanzanian chicken originated from the Indian subcontinent and Southeast Asia, respectively.

Keywords: Genetic diversity, indigenous chickens, East Africa