ABSTRACT

Indigenous chicken (IC) provides a viable enterprise to rural and peri-urban settings in Kenya. An analysis using microsatellite markers was carried out to determine the genetic variability and population structure between and within six IC ecotypes of Kenya. A total of 284 eggs were sourced, incubated and artificially hatched as follows: Elgeyo Marakwet (EM, n=68); Turkana (TR, n =51), Homa Bay (HB, n =33), Meru (MR n =45), Nandi (ND=38); (LM, n =49) and Lamu (LM, n =49). EM, n=68) ;(TR n =51) ;(HB, n =39) ;(MR, n =45) and (LM, n =49), respectively. Hatched birds were raised up to 14 weeks of age. Then 50 birds, each ecotype: n=10, had their feathers plucked for a PCR - DNA analysis. Results showed that alleles per primer ranged between 2 (MCW0097) and 8 (ADL0328). Allele frequency ranged between 0.25 and 0.81 with a mean of 0.49. All the markers used in the study were polymorphic, ADL0328 was the most polymorphic marker (PIC = 0.79) while MCW0097 was the least polymorphic (PIC = 0.25), the mean polymorphic content was 0.58. Expected heterozygosis ranged from 0.202 in TR to 0.453 in ND. Mean fixation index (FST) ranged between 0.003 and 0.057 for ND and TR; respectively. Mean fixation index for the whole population was 0.0296. The greatest variation in the study was between ecotypes (62.78%), while within the ecotypes was 37.22%. Both factorial and phylogenetic population analyses showed a mixed genetic background. PCA results did not segregate IC ecotypes into distinct geographical groups discerning a rich genetic diversity of Kenyan IC hence the need to protect the indigenous genotypes against genetic erosion.