

ABSTRACT

In this study, indigenous chickens were collected from eight different regions in Kenya and kept at InCIP-Egerton University. These were studied using eighteen microsatellite markers to determine genetic variation. Statistics related to genetic variation were estimated using GenALEx6. Mean percentage polymorphic loci (PPL) was 96.71% and 4% genetic variance ($p = 0.003$) was seen between the eight populations. MCW0123 marker had the highest genetic variance of 13% among populations ($p = 0.003$) at 95% CI. Mean H_e ranged from 0.351 ± 0.031 (SIB) to 0.434 ± 0.022 (BM) with a grand mean H_e of 0.399 ± 0.011 across the populations using the microsatellite markers. Nei's genetic distance ranged from 0.016 (SIB and WP) to 0.126 (NR and SIB). DARwin6.501 analysis software was used to draw the population dendrogram and two major population clusters were observed, also seen with PCoA. This study found a lot of genetic variation and relatedness within and among populations. Based on the phylogenetic tree result, it is concluded that the clustering of the chicken populations in the present study is not based on geographical proximity. The microsatellite markers used in this study were suitable for the measurement of the genetic biodiversity and relationship of Kenyan chicken populations. These results can therefore serve as an initial step to plan the conservation of indigenous chickens in Kenya. 2017 Production and hosting by Elsevier B.V. on behalf of Academy of Scientific Research & Technology. This is an open access article under the CC BY-NC-ND license