

Genetic Diversity and Population Structure of the Indigenous Sheep in Kenya
Based on Microsatellite Analysis

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ABSTRACT

The knowledge of the genetic relationship and admixture among neighbouring populations is crucial for conservation efforts. The aim of this study was to analyze the genetic diversity and population structure of the indigenous sheep in Kenya using 15 microsatellite markers. Blood samples from 582 individuals were obtained and genotyped across 15 microsatellite markers. Values of expected heterozygosity and Mean number of alleles ranged from 0.596 to 0.807 and 6.67 to 9.33 respectively depending on the population. Most of the investigated populations showed a significant heterozygote deficiency caused by a moderately high level of inbreeding indicated by f_{IS} (0.109). The observed genetic diversity was found to be high in the nucleus flocks as opposed to those kept by the famers. Genetic differentiation between breeds was moderate ($\theta_{ST} = 0.101$) but significant. The genetic distances obtained reflect the historical knowledge of these breeds and some patterns of ancestral and recent gene flow between neighbour populations arise. According to genetic relationships, multivariate and structure analyses four population clusters were detected which were majorly based on geographical proximity and interbreeding among the populations. These results indicate that the levels of admixture observed warrant the institution of conservation measures if the genetic purity and integrity of the indigenous sheep in Kenya is to be maintained. However, a more encompassing study that includes all the regions in the country known to harbor the indigenous sheep, as well as a larger sample size with more microsatellite markers genotyped is necessary to enable a comprehensive understanding of the dynamics of genetic introgression in the country.