ABSTRACT

The Kenyan indigenous Maasai goats (*Capra hircus*) have been very scantily characterized, which has resulted in poor efforts to fully exploit and conserve these genetic resources. Genetic characterization is necessary because it would be a guide in prioritizing the efforts of conservation and production. It will also help in developing genomic tools to be used in selective breeding programs. This study aimed at characterizing and comparing the gene pools of the indigenous Maasai goats in Narok and Kajiado counties using the mitochondrial DNA (MtDNA) control region. Fifty goat blood samples were obtained from both counties (25 from each county) but only thirty samples were used in the analysis; fifteen from each county. Extraction of DNA from whole blood was done using the standard phenol: chloroform method and amplified successfully to the expected size of 880 base pairs. Phylogenetic and haplogroup analysis using 22 MtDNA reference sequences showed that these goats clustered into two haplogroups A and G. Haplogroup A was the most common and internally varied as compared to haplogroup G. Seventy four (74) polymorphic sites and 26 haplotypes were determined in an 880-bp sequence. This study also found a very high haplotype diversity of 0.98 ± 0.013 and a low nucleotide diversity of 0.02252 ± 0.0016 between these two indigenous goat populations. There were no fixed differences between the two populations. Genetic diversity showed a slightly positive Tajima’s D value (0.231463) which may indicate that the population may have undergone a recent bottleneck or there is over-dominant selection of a trait that is linked to the analysed locus. A Chi-square analysis of genetic differentiation gave a p-value of 0.4236 (df:37) which was statistically non-significant at p<0.05, indicating a lack of statistical difference between the two populations. This is an indication that a strong gene flow exists between the goat populations in Narok and Kajiado counties and may further suggest that the two populations share a single gene pool. This study shows the presence of high genetic diversity and variation within the two goat populations. It also shows that there is positive selection of a trait that is linked to the mitochondrial DNA control region. These results can serve as an initial step to plan for the conservation of indigenous Maasai goats in Narok and Kajiado counties. However, further research should be carried out using other molecular markers and also including indigenous goat populations from other counties in Kenya.