ABSTRACT

Population structure and relationship information among goats is critical for genetic improvement, utilization, and conservation. This study explored population structure and level of introgression among four goat breeds in Kenya: the indigenous Galla (n = 12) and three imported breeds, the Alpine (n = 29), Toggenburg (n = 31), and Saanen (n = 24). Genetic diversity was analyzed using four indices (polymorphic SNPs, mean allele frequency, observed and expected heterozygosity and inbreeding coefficient) within each breed. Population structure assessed using model-based clustering (ADMIXTURE) revealed four breeds according to their geographic regions in Kenya. Kenyan Alpine goats were the most admixed breed with about 10 % of its genome derived from Galla, 10 % and 6 % from Saanen and Toggenburg respectively. The association of Galla with other breeds was anticipated since the Galla breed was used as the founder population for crossbreeding with Saanen, Alpine and Toggenburg breeds. The relationship information evaluated by computing Reynolds genetic distance revealed five distinctive clusters: Alpine, Galla, Saanen, Toggenburg and some mixture of Alpine and Toggenburg. Saanen and Galla breeds seem to be the most genetically distinct among the sampled populations. The genetic variation among the goat populations observed will provide a good opportunity for sustainable utilization, conservation, and future genetic resource improvement programmes in goat breeds in Kenya.