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Genetic Analysis of Hybridisation Pattern in Goat Genotypes from East Africa

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Abstract

East Africa is home to an estimated 150,667,482 goats in different geographical regions which are exposed to diverse climatic, production and management conditions. This has shaped the goat genome due to adaptation or selection. This study aimed to investigate hybridisation pattern between distantly isolated goat populations in the East African community using Single Nucleotide Polymorphism (SNP) data genotyped using a 50K goat SNP chip. In Uganda, SNP data for 144 goats from six genotypes sampled from five agro-ecological zones was retrieved from the Zenodo genome archive. In Kenya, 94 goats from four genotypes sampled from three regions were used. Quality control procedures were performed in PLINK v 1.9. Data from Kenya (48,303 SNPs) and Uganda (46,105 SNPs) was then merged in Tassel software resulting in 94,408 SNPs available for joint downward analysis. Principle component and phylogenetic analysis was used to visualise relationships between the studied populations. Four well-defined clusters, two from each country were observed with some visible outliers. From the two clusters in each country, genetically mixed genotypes were identified in only one cluster. This might suggest inbreeding within the genotypes due to close proximity between them. The degree of genetic differentiation measured using F_{st} ranges from 0.191 to 0.324 indicating that all the genotypes within a country are to some extent isolated from each other. Only Boer genotype from Uganda was highly isolated from all genotypes in this study. The diversity shown between Kenya and Uganda goat genotypes might be due to uncommon ancestry, isolation distance or lack of capacity to use reproductive technologies. These results will be useful in the implementation of future genetic conservation, utilisation and improvement programs in the East African community.

Keywords: Genotypes, Inbreeding, Single Nucleotide Polymorphism (SNP)