

Mitochondrial DNA D-loop sequence variability reveals high haplotype diversity and multiple maternal origins in twelve indigenous goat populations from Tanzania.

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Abstract

The Small East African (SEA) goat (*Capra hircus*) breeds are widely distributed in different agro-ecological zones of Tanzania. We report the genetic diversity, maternal origin, and phylogenetic relationship among the 12 Tanzanian indigenous goats populations, namely Fipa (n = 44), Songwe (n = 34), Tanga (n = 33), Pwani (n = 40), Newala (n = 49), Lindi (n = 46), Gogo (n = 73), Pare (n = 67), Maasai (n = 72), Sukuma (n = 67), and Ujiji (n = 67), based on the mitochondrial DNA (mtDNA) D-loop. High haplotype ($H_d = 0.9619-0.9945$) and nucleotide ($\pi = 0.0120-0.0162$) diversities were revealed from a total of 389 haplotypes. The majority of the haplotypes (h = 334) drawn from all the goat populations belonged to Haplogroup A which was consistent with the global scenario on the genetic pattern of maternal origin of all goat breeds in the world. Haplogroup G comprised of 45 haplotypes drawn from all populations except the Ujiji goat population while Haplogroup B with 10 haplotypes was dominated by Ujiji goats (41%). Tanzanian goats shared four haplotypes with the Kenyan goats and two with goats from South Africa, Namibia, and Mozambique. There was no sharing of haplotypes observed between individuals from Tanzanian goat populations with individuals from North or West Africa. The indigenous goats in Tanzania have high genetic diversity defined by 389 haplotypes and multiple maternal origins of haplogroup A, B and G. There is a lot of intermixing and high genetic variation within populations which represent an abundant resource for selective breeding in the different agro-ecological regions of the country.

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