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<AT>Genetic diversity, population structure and phylogeography of Myanmar goats

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<ABS-HEAD>Abstract

<ABS-P>The diversity of goats in Myanmar is represented by three indigenous breeds, Jade Ni, Nyaung Oo and Waithar Li. This study aimed at characterizing the genetic diversity and relationship of Myanmar goat breeds using microsatellite and mitochondrial DNA variations. A total of 147 goats from all three indigenous breeds were genotyped at 27 microsatellite loci. Genetic diversity in terms of allelic polymorphisms, observed and expected heterozygosities were moderately high. The mean observed heterozygosity within breeds varied between 0.566 ± 0.183 (Nyaung Oo) and 0.595 ± 0.182 (Waithar Li) while the expected heterozygosity varied from 0.605 ± 0.181 (Jade Ni) to 0.647 ± 0.176 (Waithar Li). Considerable heterozygosity deficit ranging from 5.5% to 8.2 % was observed in Myanmar goat breeds. Wright's F statistics revealed most of the variations within breeds and only 1.9% of the total observed variation was explained by between breed differences. Principal components and Bayesian clustering analyses showed complete admixture of Nyaung Oo and Waithar Li goats indicating high rate of gene flow among these populations.

<ABS-P><ST>Population</ST> stratification was observed in Jade Ni with a subset of individuals clustering distinctly. Variations in mitochondrial DNA control region revealed 22 distinct haplotypes belonging to two major haplogroups A and B. Haplogroup A was found to predominate Myanmar goats similar to other goat populations in Asia. Comparative analysis of mtDNA variations indicated possible Chinese origin of the maternal haplotypic lineages of Myanmar goats.

<KWD>Keywords: Myanmar goats; microsatellite; genetic structure; phylogeny; mitochondrial DNA

Introduction

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