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Genetic diversity of five Chinese goat breeds assessed by microsatellite markers

J.Y. Li, H. Chen, X.Y. Lan, X.J. Kong, L.J. Min

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The genetic diversity was studied using microsatellite DNA markers in Laoshan dairy goat (LS), Xinong Saanen dairy goat (SN), Guanzhong dairy goat (GZ), Banjiao goat (BJ) and Guizhou white goat (GW). Within the nine polymorphic loci, allele frequencies, number of effective alleles (Ne), heterozygosity (He), polymorphism information content (PIC), genetic identity (I) and Nei's standard genetic distance (D) were calculated, and UPGMA phylogenetic tree was constructed based on allele frequencies. The average number of alleles was 9.4, ranging from four to eleven at the nine assessed loci. The average values of Ne, He, PIC of all loci were 4.716, 0.765, 0.732, respectively. The GZ population showed the highest variability (PIC = 0.78, He = 0.80). There was a relatively high level of genetic diversity in these goat breeds. A UPGMA diagram, based on Nei's standard genetic distances, yielded relationships between populations that agreed with what is known about their origin, history and geographical distribution.

Keywords:

goat; microsatellites; biodiversity

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