



Analysis of geographic and pairwise distances among sheep populations

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ABSTRACT. This study investigated geographic and pairwise distances among seven Chinese local and four introduced sheep populations via analysis of 26 microsatellite DNA markers. Genetic polymorphism was rich, and the following was discovered: 348 alleles in total were detected, the average allele number was 13.38, the polymorphism information content (PIC) of loci ranged from 0.717 to 0.788, the number of effective alleles ranged from 7.046 to 7.489, and the observed heterozygosity ranged from 0.700 to 0.768 for the practical sample, and from 0.712 to 0.794 for expected heterozygosity. The Wright's F -statistic of subpopulations within the total (F_{ST}) was 0.128, the genetic differentiation coefficient (G_{ST}) was 0.115, and the average gene flow (N_m) was 1.703. The phylogenetic trees based on the neighbor-joining method by Nei's genetic distance (D_A) and Nei's standard genetic distance (D_S) were similar. Sheep populations clustered

into group 1 (Ta, M, L, H, O, G, and Q breeds) and group 2 (PD, WS, B, and T breeds). These results will have an important value applied and directive significance for sheep breeding in the future.

Key words: Sheep; Geographic distance; Pairwise distance; Genetic diversity