



High polymorphism at microsatellite loci in the Chinese donkey

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ABSTRACT. To reveal the genetic diversity and phylogenetic relationships between Chinese donkey breeds, 415 individuals representing ten breeds were investigated using ten microsatellite markers. The observed number of alleles, mean effective number of alleles (N_E), mean expected heterozygosity (H_E), and polymorphic information content (PIC) of each breed and polymorphic locus were analyzed. The results showed that seven (HTG7, HTG10, AHT4, HTG6, HMS6, HMS3, and HMS7) of ten microsatellite loci were polymorphic. The mean PIC, H_E , and N_E of seven polymorphic loci for the ten donkey breeds were 0.7679, 0.8072, and 6.0275, respectively. These results suggest that domestic Chinese donkey breeds possess higher levels of genetic diversity and heterozygosity than foreign donkeys. A neighbor-joining tree based on Nei's standard genetic distance showed that there was close genetic distance among Xinjiang, Qingyang, Xiji,

and Guanzhong donkey breeds. In addition, Mongolia and Dezhou donkey breeds were placed in the same category. The phylogenetic tree revealed that the genetic relationships between Chinese donkey breeds are consistent with their geographic distribution and breeding history.

Key words: Chinese donkey; Microsatellite; Polymorphism; Phylogenetic relationship