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Genetic polymorphism at the *KIR* gene locus: determination of gene, genotype, and haplotype frequencies in the Xinjiang Han population

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ABSTRACT. The aim of this study was to explore the genetic polymorphism, genotype, and haplotype characteristics of the *KIR* locus in the Xinjiang Han population in order to establish a foundation for future analysis of the relationship between *KIR* genes and disease. *KIR* genes were detected by sequence-specific primer-polymerase chain reaction in 184 randomly selected, healthy individuals from the Han population in Xinjiang, China. Standard genotype and haplotype analyses were conducted using Hsu's standards classified for analysis. Sixteen *KIR* genes were detected: *3DL3*, *2DL4*, *3DL2*, and *3DL2* (100%); *2DL1* and *2DP1* (99.46%); *2DL3* (98.91%); and so on. The *2DS2* gene frequency was the lowest at 21.74%. Twenty-one genotypes were detected: AJ (2, 2) was relatively common (42.39%), followed by AH (5, 2), AE (2, 8) and H (2, 4), with frequencies of 17.39, 11.96, and 8.15%, respectively. In addition, six novel genotypes were identified in 11 Han individuals as well as in other populations in China, which could not be classified for analysis. These results indicated that the Xinjiang Han population shares *KIR* gene,

genotype, and haplotype frequency distributions with the Chinese Han population, but also has unique genotypes and haplotypes.

Key words: Killer cell immunoglobulin-like receptor (KIR); Polymerase chain reaction-sequence specific primers; Genetic polymorphism; Genotype; Haplotype

