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KIR gene polymorphism study in the Uygur population in Xinjiang, China

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ABSTRACT. We analyzed killer cell immunoglobulin-like receptor (*KIR*) gene polymorphisms and genotype and haplotype characteristics in the Uygur population, a non-nomadic ethnic group found in Xinjiang, China, to provide a basis for studies on relationships between *KIR*s and diseases in this group. Sequence-specific primer PCR was used to detect the *KIR* gene in 84 Uygur individuals. A standard genotype and haplotype analysis was conducted using Hsu's standards. Sixteen *KIR* genes were detected; the 3DL3, 2DL4, 3DL2 genes were found in all individuals. The 2DL1, 3DP1, 2DP1, 2DL3 genes were relatively common, followed by 2DS4, 3DL1, 2DL5, 2DS2, 2DL2, 2DS1, 2DS5, and 3DS1. The 2DS3 gene had the lowest frequency. A total of 19 genotypes were detected, the AJ (2,2), AH (5,2) and M (2,8) genotypes were relatively common, with frequencies of 25, 10.7 and 10.7%, respectively; they were followed by P (2,17), AI (1,5), H (2,4), and C (5,3), with frequencies of 9.52, 5.95, 5.95, and 4.76%, respectively. The U (17,21), and T (8,8) genotypes, found in four individuals, had not been reported in the Han Chinese population. Eleven haplotypes were detected; the most common haplotype 2 (N = 74) was accounting for 48.7%, followed by haplotype 5 (N = 24), accounting for 15.8%. In addition, three new genotypes were found, for which haplotype analysis could not be performed based on existing standards. We conclude

that the Xinjiang Uygur population has unique *KIR* gene frequency, genotype frequency and haplotype frequency distributions; there also appears to be new genotypes and haplotypes in this population.

Key words: Killer cell immunoglobulin-like receptor; Uygur; Gene polymorphism; Polymerase chain reaction sequence-specific primers

