



Association between polymorphisms in *ADAM33*, *CD14*, and *TLR4* with asthma in the Uygur population in China

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ABSTRACT. We evaluated the associations between single nucleotide polymorphisms (SNPs) and haplotypes of the genes encoding a disintegrin and metalloproteinase 33 (*ADAM33*), cluster of differentiation 14 (*CD14*), and Toll-like receptor 4 (*TLR4*) and the susceptibility of developing specific adult phenotypes of bronchial asthma in a Chinese Uygur population. Five SNPs of *ADAM33* (T1, T2, and V4), 3 SNPs of *CD14* (-1359G/T, -1145G/A, and -159T/C), and 2 SNPs of *TLR4* (-896A/G and -1196C/T) were genotyped in a Chinese Uygur sample of 126 adult asthmatic patients and

126 control subjects. Gene polymorphisms were detected by polymerase chain reaction-restriction fragment length polymorphism analysis. The genotyping results were confirmed in a random subgroup of our samples using direct DNA sequencing. The allele frequencies of *ADAM33* T1 (TC), T2 (AG), and V4 (GG) were significantly higher in patients than in controls ($P < 0.05$). The genotypes T1 (TC+CC), T2 (AG+AA), and V4 (CG+GG) significantly increased the risk of asthma. After adjusting for confounding factors, these associations were stronger and remained significant. The T1 (TC) and V4 (GG) genotypes in the *ADAM33* gene were associated with significantly decreased FEV1 levels in patients with asthma. The haplotype frequencies of Hap3 (CAC) and Hap4 (CAG) were significantly higher in patients than in controls ($P < 0.05$). Our results suggest that polymorphisms T1, T2, and V4 in *ADAM33* may contribute to the susceptibility to asthma. Specific haplotypes of *ADAM33* may contribute to a higher susceptibility to asthma in the Chinese Uyghur population.

Key words: ADAM33, CD14, TLR4, Asthma, Polymorphisms, Uyghur population