



Association between polymorphisms of fat mass and obesity-associated gene and metabolic syndrome in Kazakh adults of Xinjiang, China

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ABSTRACT. The aim of this study was to assess the association between three FTO polymorphisms (rs9939609, rs8057044, and rs1421085) and metabolic syndrome (MS)-related outcomes in the low-income, rural, nomadic minority Khazakh population in far western China. A total of 489 subjects (245 MS patients, 244 controls) were included in the study and DNA samples were genotyped for the three polymorphisms by matrix-assisted laser desorption/ionization time of flight mass spectrometry. The frequencies of the rs1421085 and rs9939609 genotypes and alleles did not differ significantly between MS patients and control, while the frequencies of rs8057044 G alleles and GG genotypes were higher in MS patients ($P < 0.05$) than in control subjects (G: 61.16 vs 53.53%, GG: 39.07 vs 29.05%) and the frequencies of rs8057044 A genotypes and alleles were lower ($P < 0.05$) in MS patients compared with controls (AA: 17.36 vs 21.99%, A:

38.84 vs 46.47%). Risk analysis of the rs8057044 polymorphism revealed individuals with GA and GG genotypes to have 1.112 and 1.731 times higher risks of developing MS than those with the AA genotype, respectively, while the G allele was found to be associated with a 1.367 times higher risk of developing MS compared with the A allele. These apparent correlations, however, did not hold true when adjusted for BMI. Weight, WC, HC, and BMI differed significantly between rs8057044 GG and AA+GA genotypes ($P < 0.05$).

Key words: FTO gene; Metabolic syndrome; Polymorphisms; Kazakh