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MATRIX METALLOPROTEINASE-9 (MMP-9) GENE POLYMORPHISMS CONTRIBUTE TO CORONARY ARTERY DISEASE RISK IN A UIGHUR POPULATION OF CHINA

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Materials and methods 385 angiographically proven patients with coronary artery disease and 397 sex-matched and ethnically matched controls were genotyped for 2 MMP-9 polymorphisms by the PCR-restriction fragment length polymorphism (PCR-RFLP) technique. Genotype/allele frequencies were compared in patients and controls using the χ^2 test.

Results At MMP-9 -1562C>T locus, there were significant differences between patients and controls ($p<0.05$), leading to significant OR for TT genotype (OR 1.85, 95% CI 1.18 to 3.15) and *T allele (OR 1.41, 95% CI 1.09 to 2.03). These OR were higher in the subsample of smokers (3.04 and 1.87, respectively). Binary logistic regression analysis also confirmed that *R allele carriers (TT and CT) have a higher risk of CAD (OR 1.72, 95% CI 1.64 to 5.28). MMP-9 R279Q locus did not show significant differences between patients and controls, but QQ genotype and *Q allele were significant risk factors in the smoker group. TQ haplotype was also significantly associated with CAD risk (OR 1.79, 95% CI 1.04 to 1.99).

Conclusions MMP-9 -1562T allele and TT genotype are significantly associated with CAD patients in a Uighur population of China. This association was stronger in smokers,

supporting the conclusion that an interaction between MMP-9 activity and smoking augments CAD risk. Further studies with larger sample size are warranted to confirm these associations in different populations of China.