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MKL1-184C>T gene polymorphism is associated with coronary artery disease in the Chinese Han population

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ABSTRACT. We investigated genetic susceptibility to coronary artery disease (CAD) by studying the association of MKL1 gene polymorphisms with CAD in the Chinese Han population. We performed a case-control study with 476 unrelated CAD patients and 325 non-CAD controls. All SNPs were genotyped with a TaqMan SNP genotyping assay. The distribution of MKL1-184C>T gene polymorphism in each group was in Hardy-Weinberg equilibrium. The frequency of the MKL1 T allele in the CAD group was significantly higher than in the control group (38.6 *vs* 30.8%). After logistic regression models adjusted for CAD risk factors, the risk of CAD among CT genotypes was 1.765 times higher than among the CC genotypes [odds ration (OR) = 1.765, 95% confidence interval (CI) = 1.246-2.5], and for TT genotypes it was 1.806 times higher than for the CC genotypes (OR = 1.806, 95%CI = 1.203-2.71).

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In summary, genotypes with at least one T allele (CT or TT genotypes) had a significantly increased CAD risk than the CC genotypes, with a ratio of 1.78 to 1 (OR = 1.780, 95%CI = 1.311-2.418). There was a close association between -184 T allele and 3VD (OR = 1.614, 95%CI = 1.259-2.07, $P < 0.05$). We conclude that the -184C>T of MKL1 is an important susceptibility factor for CAD in the Han Chinese in Henan Province. Homozygosity for the T allele is not only associated with an increased risk for CAD, it is also correlated with severity of stenosis in the Chinese Han population.

Key words: MKL1; Gene polymorphism; Coronary artery disease

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