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ASSOCIATION OF ALOX5AP GENE SG13S114T/A POLYMORPHISM WITH ACUTE CORONARY SYNDROME

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Objective To investigate the distribution of ALOX5AP gene SG13S114T/A polymorphism and the association of the ALOX5AP gene SG13S114T/A polymorphism with acute coronary syndrome (ACS) in the Chinese Han population of Sunan region.

Methods This study was conducted with a case-control design including 545 patients with ACS (ACS group) and 567 control subjects who were free from coronary artery disease (control group). ALOX5AP gene SG13S114T/A polymorphism was determined by polymerase chain reaction and restriction fragment length polymorphism analysis.

Results There were AA, AT and TT genotypes of the ALOX5AP gene SG13S114T/A polymorphism both in ACS group and control group. The genotype distribution of the ACS group and control group conformed to the Hardy-Weinberg balance via χ^2 test ($p>0.05$), which suggested that the selected sample was representative. As compared with those in the control group, the genotype frequency of AT (37.57% vs 48.99%, $p=0.015$) was higher, the genotype frequency of TT (48.15% vs 38.17%, $p=0.034$) was lower, and the frequencies of AA genotype (14.28% vs 12.84%, $p=0.054$) and T allele (66.93% vs 62.66%, $p=0.330$) were not significantly different (all $p>0.05$) in ACS group. Subgroup analysis showed that as compared with those in control group respectively: (1) the genotype frequency of AT (30.30% vs 56.41%, $p=0.003$) was higher, the genotype frequency of TT (53.30% vs 32.50%, $p=0.017$) was lower, and the frequencies of AA genotype (16.67% vs 13.54%, $p=0.263$) and T allele (68.33% vs 60.26%, $p=0.331$) were not significantly different (all $p>0.05$) in AMI group; (2) the genotype frequency of AT (30.30% vs 47.14%, $p=0.045$) was higher, the frequencies of AA (16.67% vs 10.00%, $p=0.146$) and TT (53.33% vs 42.86%, $p=0.291$) genotypes and T allele (68.33% vs 60.26%, $p=0.727$) were not significantly different (all $p>0.05$) in UAP group; (3) the frequency of T allele (68.06% vs 82.42%, $p=0.046$) was higher in male ACS group and not significantly different ($p>0.05$) in female ACS group, there were no significant statistical difference of the genotype frequencies of AA ((13.19% vs 8.02%) and (5.41% vs 14.04%)), AT ((37.50% vs 33.69%) and (37.99% vs 45.03%)) and TT ((49.31% vs 58.29%) and (46.59% vs 40.94%)) in male ACS group and female ACS group (all p value >0.05); (4) the genotype frequency of AT (38.58% vs 50.93%, $p=0.041$) was higher, the genotype frequency of TT (48.66% vs 35.28%, $p=0.020$) was lower, the frequencies of AA (12.76% vs 13.79%, $p=0.722$) genotype and T (61.22% vs 60.74%, $p=0.931$) allele were not significantly different in elderly ACS group; (5) the frequencies of AA (16.96% vs 10.11%, $p=0.127$), AT (36.09% vs 50.00%, $p=0.078$) and TT (46.96% vs 39.39%, ($p=0.338$) genotypes and T allele (65.00% vs 64.29%, $p=0.932$) were not significantly different in premature ACS group. Multivariate logistic regression analysis showed that there was statistically significant correlation of AT and TT genotype, and T allele with ACS (P was 0.001, 0.001 and 0.031, respectively). Furthermore, subgroups analysis showed that AT and TT genotype were correlated with AMI (all $p<0.001$); AT genotype was correlated with UAP ($p=0.007$); AT and TT genotypes, and T allele were correlated

with male ACS ($p < 0.001$, was 0.001 and 0.016, respectively); AT and TT genotypes, and T allele were correlated with the elderly ACS (p was 0.004, 0.001 and 0.013, respectively).

Conclusion Three genotypes including AA, AT and TT genotypes exist in the ALOX5AP gene SG13S114T/A both in ACS group including its subgroups and control group. There was statistically significant association of the SG13S114T/A polymorphism of ALOX5AP gene with risk of ACS, AMI, UAP, male ACS and the elderly ACS in the Chinese Han population of Sunan region, which suggest ALOX5AP gene SG13S114T/A polymorphism play a potential role in the origin and development of ACS.