[gw22-e1045]

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

Guoping HE, Jingjiao HUI, Dandan SHEN *Department of Cardiology, Affiliated Wujin Hospital of Jiangsu University, Changzhou, China*

10.1136/heartjnl-2011-300867.115

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.