GW23-e1551 **RELATIONSHIP BETWEEN NOVEL POLYMORPHISMS OF THE C5L2 GENE AND CORONARY ARTERY DISEASE**

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Objectives C5L2, a G protein-coupled 7-transmembrane domain complement, has been demonstrated to be a functional receptor of acylation-stimulating protein (ASP), which is a stimulator of triglyceride synthesis or glucose transport. In this study, we will investigate the variations in the coding region of the C5L2 gene (C698T and G901A) and their association with coronary artery disease (CAD).

Methods We identified novel single nucleotide polymorphisms (SNPs), (C698T and G901A) in exon 2 using a PCR direct-sequencing method. We examined the role of this SNP for CAD using two independent case–control studies: one was in the Han population (492 CAD patients and 577 control subjects) and the other was in the Uygur population (319 CAD patients and 554 control subjects).

Results Using a PCR direct-sequencing method. We identified novel single nucleotide polymorphisms (SNP), 698C>T (P233L), and G901A (A300H) in exon 2. C698T causes the amino-acid order from proline to leucine at codon 233. G901A causes the amino-acid order from Arginine to glutaminate at codon 300. We examined the role of C698T for CAD using two independent case–control studies: one was in the Han population (492 CAD patients and 577 control subjects) and the other was in the Uygur population (319 CAD patients and 554 control subjects). Heterozygote carriers of the 698CT genotype were more frequent among CAD patients than among controls not only in the Han population (7.3% vs 1.7%) but also in the Uygur population (4.7% vs 1.6%). The OR for carriers of the 698CT genotype for CAD was 4.484 (95% CI 2.197 to 9.174) in the Han group and 2.989 (95% CI 1.292 to 6.909) in the Uygur population. After adjustment of confounding factors such as sex, age, smoking, alcohol consumption, hypertension, diabetes, as well as serum levels of triglyceride, total cholesterol, high-density lipoprotein, the difference remained significant in the Han group ($p<0.001$, OR=6.604, 95% CI 2.776 to 15.711) and in the Uygur group ($p=0.047$, OR=2.602, 95% CI 1.015 to 6.671). We also examined the role of G901A for CAD using two independent case-control studies: one was in the Han population (492 CAD patients and 577 control subjects) and the other was in the Uygur population (319 CAD patients and 554 control subjects). Heterozygote carriers of the 698CT genotype were more frequent among CAD patients than among controls not only in the Han population (8.3% vs 1.8%) but also in the Uygur population (5.2% vs 0.9%). The OR 0.172 (OR) for carriers of the 698CT genotype for CAD in the Han group in the Uygur population. After adjustment of confounding factors such as sex, age, smoking, alcohol consumption, hypertension, diabetes, as well as serum levels of triglyceride, total cholesterol, high-density lipoprotein, the difference remained significant in the Han group $p<0.001$, 0.172) and in the Uygur group 0.172 (OR=0.172, 95% CI 0.052 to 0.569). Two haplotypes in the Han population in the result analysis, which the C-A haplotype frequencies in the CHD group was significantly lower than the control group, a statistically significant difference ($\chi^2=22.713$, $p<0.001$), the T-A haplotype distribution in the CHD group was significantly higher, the difference was statistically significant ($\chi^2=19.022$, $p<0.001$). In Uighur population three haplotype in the analysis results. Analysis of the T-A haplotypes frequency (0.025) was significantly higher than that of the control group (0.008) difference was statistically significant ($p=0.004$); C-G haplotype (0.005) frequency in CAD group was significantly lower than the control group (0.026), the difference statistically significant ($p=0.001$).

Conclusions

(1) two mutations of C5L2 gene (C698T and the G901A) in Han and Uygur population are association with coronary heart disease;
(2) C5L2 gene C698T heterozygous genotype may be a risk factors of coronary heart disease in Xinjiang Han and Uighurs population; G901A heterozygous genotype may be protective factors of coronary heart disease in Han and Uigur population;
(3) the C5L2 genes C-G haplotype may be protective factors of coronary heart disease in Han population in Xinjiang, a single T-G ploidy may be risk factors for coronary heart disease in Han population in Xinjiang;
(4) the C5L2 genes C-A haplotype may be protective factors of coronary heart disease in Xinjiang Uygur population, T-G haploid may be risk factors of coronary heart disease in Xinjiang Uygur population.