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THE INFLUENCE OF GENE MUTATION TO STATIN RESPONSIVENESS ON HIGH-RISK CVD POPULATION IN CHINESE

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Objectives To study the influence of gene mutation to statin responsiveness on high-risk cardiovascular disease (CVD) population in Chinese.

Methods This study collected 318 subjects of Chinese Han aged 20–70 years, who need statins treatment according to 'Chinese guidelines on prevention and treatment of dyslipidemia in adults' in 2007. Atorvastatin was taken 20 mg every night from first day of taken drugs to the end of 4 weeks. Statin responsiveness related to gene mutation was analysed.

Results

(1) The relationship between genotypes of 144 SNP with LDL-C change% was analysed, 5 SNP were found to have significantly difference, which is rs2235013, rs2235033, rs1128503, rs10276036 of ABCB1 gene and rs717620 of ABCC2 gene.
(2) The correlation between SNP and statin responsiveness were analysed in three genetic models, the results showed that the significant difference can be seen in the additive and dominant models of rs717620 and additive model of rs2235033 after adjusted for age, sex, BMI and baseline LDL-C levels.
(3) Multivariable analysis on the correlation between rs1128503 and rs717620 with LDL-C change% indicated that striking differences were observed for LDL-C change% across two genotypes of two SNPs. Compared with the wild genotypes, carriers of mutant genotypes had 78% increased risk or 59% decreased risk. Statin response was compared under the joint effects of two SNPs under study involving the same pathway. Our results indicated that the joint effects of these two SNPs were significantly higher than that of respective one, LDL-C change% increased one times in group of rs1128503 wild +rs717620 mutant compared with group carried two wild genotypes.

Conclusions Genes encoding ABCB1 and ABCC2 may be logical candidates for statin response among Chinese with high CVD risk.

The joint effect of two SNPs within these two genes was more obvious than any single SNP.