

[gw22-e0538]

INFLUENCE OF 144 CANDIDATE GENETIC POLYMORPHISMS ON STATIN TREATMENT IN HAN CHINESE

Yue Qi¹, Jing Liu¹, Chang-sheng Ma², Xiao-hui Liu², Qiang Lv², Yan Li¹, Jie Ren¹, Hai-hang Liu¹, Dong Zhao¹ ¹*Department of Epidemiology, Beijing IHLBVD, Capital Medical University Beijing Anzhen Hospital, Beijing, China;* ²*Department of Cardiology, Capital Medical University Beijing Anzhen Hospital, Beijing, China*

10.1136/heartjnl-2011-300867.200

Objective We aimed to assess the influence of candidate genetic variation on statin efficacy in a cardiovascular disease (CVD)-high-risk Chinese population to elucidate the inherited genetic underpinnings, which would further direct the statin therapy and thus the CVD prevention.

Methods This study included 318 patients aged 20 to 70 years based on the standards of statin administration. All patients were treated with atorvastatin at a dosage of 20 mg daily for four weeks. Lipid-relevant indexes were measured before/after administration. Total 144 common polymorphisms harbouring 17 candidate genes related to statin or lipids metabolism were genotyped by the Illumina gene microarray method.

Results Four polymorphisms were individually and significantly associated with the percentage reduction in low-density lipoprotein cholesterol (LDL-C), including rs2235013 G>A, rs1128503 T>C, rs10276036 G>A in ATP-binding cassette, subfamily B, member1 (ABCB1) gene and rs717620 C>T in ATP-binding cassette subfamily C member2 (ABCC2) gene. Moreover, the strength of associations between ABCC2 gene rs717620 and ABCB1 rs1128053 polymorphisms with LDL-C reduction remained even after adjustment for other CVD-relevant risk factors. Under the dominant genetic mode, carriers of rs717620 T allele conferred 1.85-times higher LDL-C response (odds ratio (OR)=1.85; 95% CI: 1.11 to 3.08; p=0.019], with respect to those with homozygote CC genotype, and the strength exhibited statistical significance even after multivariate adjustment. While under the recessive model, rs1128053 CC genotype had 60% lower LDL-C response (OR=0.40; 95% CI=0.17 to 0.95; p=0.037) than T allele. Haplotype rs717620 T and rs1128503 T alleles had remarkable predominance in increasing LDL-C response (OR=2.00; 95% CI: 1.22 to 3.32; p=0.006). Multivariate logistic regression analysis showed that rs717620 and rs1128503 together explained 23% of percentage change in LDL-C in response to atorvastatin.

Conclusions This study lent some credence to the fact that statin excretion relevant genes ABCB1 and ABCC2 might be

potential candidates for atorvastatin lowering lipids in CVD-high-risk Chinese, which was further strengthened by our conjoint analysis of these two genes.