GW23-e1105

CLINICAL RESEARCH ON ASSOCIATION OF CD36 SINGLE NUCLEOTIDE POLYMORPHISMS WITH ESSENTIAL HYPERTENSION

doi:10.1136/heartjnl-2012-302920ah.5

Xueyan Liu, ping Yang. *China Japan Union Hospital, Jilin University*

Objectives Genetic mechanisms contribute to blood pressure regulation. This study investigated whether CD36 gene single nucleotide polymorphisms (SNPs) were associated with essential hypertension in Chinese Han population residing in Jilin province.

Methods SNPs were detected using PCR-sequencing. The genotype was determined by restriction fragment length polymorphism–PCR (RFLP-PCR) or signal strand conformation polymorphism–PCR (SSCP-PCR) in a total number of 589 unrelated participants including 272 EH cases and 317 controls.

Results +216T/C, +273A/G, +132C/T, +217T/C, +212T/G and +233T/C were identified. Distributions of genotypes AA, GA and GG of +273A/G were significantly different (EH: AA58%, GA36%, GG16%; the controls: AA70%, GA25%, GG5%, χ^2: 10.578, p<0.01), and G allelic frequency was higher in EHp<0.01, OR=1.629, 95% CI 1.224 to 2.168). No statistically associations were found in the other SNPs.

Conclusions +273A/G polymorphism in CD36 gene was associated with EH, and +273G could be an independent predictor.