

GW23-e1022

A META ANALYSIS ON THE CORRELATION BETWEEN GENE POLYMORPHISM

doi:10.1136/heartjnl-2012-302920d.14

Tian Ke-jun, Zhong Yi-ming. *The First Affiliated Hospital of Ganzhou Medical University***Objectives** To evaluate the association of gene Polymorphism of inflammatory

Cytokines (IL-6-174G/C, ICAM-1K46/E, PECAM-1+125C/G, MHC2TA-168A/G) and Coronary Heart Disease.

Methods The studies according to the correlation between gene Polymorphism of inflammatory cytokines (IL-6-174G/C, ICAM-1 E469/K, PECAM-1+125C/G) and the risk for CHD were comprehensively searched. All the related studies were further strictly selected according to the inclusion criteria. Then relevant data were extracted for methodological eligible and heterogeneity analysis. Hierarchies analysis according to the regional distribution, The statistical packages Statal 10.0 and Reman5.0 were applied for investigating heterogeneity among individual studies and summarising overall effects across studies by proper effect mathematical model, calculating the Pooled OR and its 95% CI, and testing the overall effects, Egger'S test were performed for evaluating the publication bias. The sensitivity analysis by different effect model and sample size was employed for the reliability of meta-analysis.**Results** All the included studies about IL-6-174G/C polymorphism and the association with the Susceptibility of CHD exist heterogeneity, With the random effect mathematical model to analysis the overall effect, OR=1.22, 95% CI 1.05 to 1.43, p=0.01, Hierarchies analysis according to the regional distribution show all the included studies of Chinese population exist heterogeneity, but all the studies about the European and the USA' population exist heterogeneity, all the studies about the Chinese population with the Mantel-Haenszel fix effect mathematical model, OR=0.38, 95% CI 0.10 to 1.44, p=0.15 use the random effects model analysis the European and the USA' population, OR=1.24, 95% CI 1.06 to 1.46, p = 0.07. All the included studies of the Correlation between Polymorphism of ICAM-1 Gene E469K and CHD in Chinese population exist heterogeneity, use the random effects model analysis the overall effect, OR=2.09, 95% CI 1.40-3 to 12, p=0.0003. a significant heterogeneity was found about the Correlation between Polymorphism of PECAM-1+125L/V and CHD. With the random effect mathematical model, the OR for the V allele was 1.17, 95% CI 0.94 to 1.46. Hierarchies analysis according to the regional distribution, No statistical publication bias and heterogeneity was found between 4 studies about the Caucasian population. with the Mantel-Haenszel fix effect mathematical model, the OR for the overall effect of V allele was 1.09, 95% CI 0.91 to 1.30, p=0.008. To analysis the overall effect of the Mongolia studies, the OR for the overall effect of V allele was 1.39, 95% CI 1.14 to 1.68.**Conclusions** No association between the polymorphism of IL-6-174G/C and coronary heart disease in Chinese population, but associated with the European and the USA'population, people who carries the C allele had a higher risk to be subject to coronary heart disease. The ICAM-1E469K polymorphism Was associated with coronary heart disease in Chinese population, people who carries the K allele had a higher risk to be subjected to coronary heart disease. PECAM-1+125L/V were not associated with

coronary heart disease in Caucasian population, but associated with the Chinese population, people who carries the V allele had a higher risk to be subject to coronary heart disease.