

incidences of dyslipidemia, smoking and the early onset group had stronger family history of coronary arteries diseases were high risk groups, The patients taking Anajia may also the high risk groups in our area. (3) Morbidity: accounted for 9.7% in all patients with coronary artery disease in the same time (the cases ( $\leq 40$ ) accounted for 4.6%). (4) (4) The coronary angiography characteristics about half is the single vessel diseases, especially left anterior descending branch diseases; coronary angiography in some patients has no significant lesions, and mainly to myocardial infarction; there were differences about two and three-vessel diseases, right coronary artery and circumflex diseases, collateral circulation between young ( $\leq 45$ ) and old ( $> 60$ ); there were not differences about the left main coronary arteries diseases, left anterior descending branch diseases and the degree of narrowed coronary arteries between young ( $\leq 45$ ) and old ( $> 60$ ).

## Clinical and Research Medicine: Acute Coronary Syndrome

### e0426 PROTEOMIC ANALYSIS OF PLASMA FROM PATIENTS WITH ACUTE CORONARY SYNDROME

doi:10.1136/hrt.2010.208967.426

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**Background** Proteomics is the new system biological approach to the study of proteins and protein variation on a large scale as a result of biological processes which can identify several proteins at a given time in a sample. Proteomic analysis has provided important insights into ischaemic heart disease, heart failure, and cardiovascular pathophysiology. Blood represents one of the most accessible sources for biomarkers and has broad clinical significance. Serum or plasma samples provide an excellent source of materials for proteomic analysis.

**Objectives** The aim of this study was to seek the special plasma molecule in the plasma protein map from the patient with acute coronary syndrome (ACS) using proteomics.

**Methods** Plasma from 60 patients, 20 with acute myocardial infarction (AMI) and 20 with unstable angina (UA), was investigated. The control group included 20 age-matched volunteers. 2-DE-DIGE/MALDI-TOF-MS analysis was performed during the procedure. The optimal abundant proteins in plasma were removed with the polyclonal antibody affinity column.

**Results** With 2DE-DIGE/MALDI-TOF-MS analysis, 14 different expression proteins were found in plasma of patients with ACS. (1) As compared with the control, serum amyloid A2, CP20 kDa protein, alpha-1 antitrypsin, haptoglobin beta and alpha-2 chain, C6 precursor and C4, fibrinogen gamma chain and fibrin beta were up-regulated in plasma from UA and AMI patients. (2) Meanwhile, apolipoprotein A-I, A-IV and A-IV precursor, TF 11 and 7 kDa protein, transthyretin, gelsolin and gelsolin precursor isoform 1, myosin-11, HBB Truncated beta-globin were down-regulated in plasma from ACS patients. (3) Moreover, ELISA analysis showed that SAA was up-regulated and gelsolin was down-regulated in the plasma of UAP and AMI.

**Conclusions** Various proteins involving in acute phase protein, complement system, and cytoskeleton, apolipoprotein, energy metabolism were participated in the procession of ACS. The newly discovered different proteins, serum amyloid A2 and gelsolin might be the special molecules for ACS. But further investigation should be carrying out in the future.

### e0427 NO ASSOCIATION OF MCP-1 GENE POLYMORPHISMS WITH MYOCARDIAL INFARCTION IN A HAN CHINESE COHORT

doi:10.1136/hrt.2010.208967.427

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**Objective** To explore the association of MCP-1 gene polymorphisms with myocardial infarction in a Han Chinese cohort.

**Methods** The study comprised 330 patients with MI (MI group) and 156 healthy controls (control group). This polymorphism was determined by using the PCR-restriction fragment length polymorphism method.

**Results** Our data showed that frequencies distribution of the genotypes (AA: 17.27%, AG: 48.48% and GG: 32.24% in MI group; AA: 12.82%, AG: 56.41% and GG: 30.77% in control group;  $p$  was 0.237, 0.126, and 0.472, respectively;) and the G allele genotype (58.48% in MI group; 58.97% in control group;  $p$  was 0.871) were not significantly different between the cases and the controls. Multivariate logistic regression analysis confirmed the lack of association of MCP-1 gene A-2518 G single nucleotide polymorphism with MI ( $p > 0.05$ ).

**Conclusion** No significant association of A-2518G polymorphism of MCP-1 gene with MI is found in the Han Chinese population.

### e0428 NO ASSOCIATION OF THE THROMBOSPONDIN-4 A387P POLYMORPHISM WITH ACUTE CORONARY SYNDROME IN THE CHINESE HAN POPULATION

doi:10.1136/hrt.2010.208967.428

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**Objective** The aim of this study was to explore the possible association of the thrombospondin-4 (TSP-4) gene G29926C (A387P) polymorphism with acute coronary syndrome (ACS) in a Chinese Han population.

**Methods** The TSP-4 A387P polymorphism was determined by PCR and restriction fragment length polymorphism (RFLP) analysis. A total of 749 unrelated subjects were included in the study, consisted of two groups: the ACS group and control group. The ACS group was composed of 412 patients with ACS (298 men and 114 women) recruited from hospitalised patients at four participating hospitals between November 2003 and May 2006. The diagnosis of ACS was based on the diagnostic criteria of 2002. AHA/ACC guideline. The control group consisted of 337 age- and sex- match subjects (232 men and 105 women) who were judged to be free of CAD by history, clinical examination, electrocardiography, exercise test and angiography, which were selected from inpatients at the same hospitals. Subjects with cardiomyopathy, tumour, and renal or hepatic disease were excluded from the study.

**Results** Slightly decreased frequency of GC genotype was observed in patients with ACS, compared with controls (5.3% vs 7.1%), but the difference did not reach statistical significance ( $p = 0.31$ ). Similarly, the prevalences of the C allele were 2.7% and 3.6% for ACS and control groups, respectively ( $p = 0.32$ ). None of the homozygote was detected for the C allele. Further analyses in subjects subgrouped according to sex and age also showed no association of TSP-4 A387P polymorphism with ACS. Furthermore, after adjustment for conventional risk factors by multiple logistic regression analysis, the carrier prevalence of the C allele did not differ significantly between the ACS and control groups (OR=0.85; 95% CI 0.45 to 1.59;  $p = 0.60$ ).

**Conclusion** The present study suggested that the TSP-4 A387P variant showed a low prevalence compared with western populations and failed to associate with an altered risk of ACS in the Chinese Han population. The findings further supplement experimental data for TSP-4 gene study of the coronary disease.