GW25-e3246

**Expressions of tnf66 and cyp1a1 and screening related genes by GeneChip on peripheral blood mononuclear cells in patients with Acute Myocardial Infarction**

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**Objectives:** Understand the changes in the genes of oxidative stress and the process of cell toxic with myocardial IRI due to before and after operative of PCI in STEMI patients. Observe in a dynamic environment the changes in the mRNA expression of TNSF6 and CYPIA1 resulting from myocardial IRI and clinical significance.

**Methods:** Patients admitted to our ER and CCU from November 2011 to February 2012. Consisting of 22 patients, 14 males and 8 females, mean age 63.32±12.40 years with a range from 37 to 91 years. All cases are diagnosed based on the AMI diagnosis criteria under Chinese Medical Association in 2003. For patients with normal controls with age, sex matching healthy volunteers 12 people, 8 male and 4 female, the average age 63.13±7.57 (35-82). Acute onset in STEMI group hospital diagnosed after extracting cubits 10ml were immediately into containing 0.05 ml of heparin without bacteria. After acute onset of emergency PCI and conventional treatment, the third day and the seventh day each pump once again were cubits 10ml; The comparison group: morning, fasting extraction method 10ml were cubits under the same approach as that for the patients group. PMBCs separation adopts the lymphocyte separate liquid density gradient centrifugation. Using Human Stress & Toxicity Pathway Finder PCR Array screening method of myocardial IRI related gene changes. The validation of expression of CYPIA1 TNSF6 by Real time PCR. All data to differences with mean±standard deviation (x±s), Value of patients and controls were compared by ANOVA analysis. And correlation analysis method, the related to P<0.05 was statistically significant differences.

**Results:** (1) Of the STEMI group, general average STEMI genes that significant changes in 16, which were up regulated the gene expression of significant for 8, were significant down regulated for four genes. The genes expression were up regulated which are cell growth/aging related genes1 (GADD45A), oxidation stress and metabolic related gene 1 (PRDX2), Heat shock related gene 3 (HSPP1, DABJ1B, DABJ1B), and repair DNA damage related gene 1 (RAD50) and apoptosis signal related gene 2 (TNSF6 TRADD, ). Significant down regulated of those genes: the cell proliferation/cancer related gene 1 (CCNG1), oxidation or metabolic stress related gene 2 (CAT, CYPIA1), DNA damage and restoration related gene 1 (ATM). (2) The expression of TNSF6 in STEMI group is higher than of the healthy group and CYPIA1 was lower than the normal value.

**Conclusions:** (1) The modulation of multiple genes resulting from myocardial IRI due to After PCI with Acute myocardial infarction. It provides a more complete view in the complication and complexity of myocardial IRI gene regulation. (2) The quantitative analysis of TNSF6 and CYPIA1 genes after myocardial IRI in AMI at various stage. They may be involved in the myocardial ischemia/reperfusion injury physio-pathological process.

GW25-e6118

**Analysis of Bacteroides and Bifidobacterium diversity in fecal samples from patients with coronary artery disease by using PCR-denaturing gradient gel electrophoresis fingerprinting**

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**Objectives:** The investigation provides molecular analyses of the faecal microbiota in coronary artery disease (CAD). This study aimed to clarify the relationship between CAD and gut predominant microbiota by analyzing the diversity of Bacteroides and Bifidobacterium.

**Methods:** In order to assess whether there are changes in the diversity and similarity of gut microbiota in CAD patients when compared with healthy individuals, bacterial DNAs from 30 CAD and 30 healthy individuals were extracted from faecal samples and characterised by PCR-denaturing gradient gel electrophoresis (DGGE) with primers specifically targeting V3 region of the 16S rRNA gene. After DGGE profiles was obtained, the diversity and similarity analyses were carried out by the number of band, Shannon-Weaver (Hp), cluster analysis and the cumulative distribution curve of similarity.

**Results:** The range of Shannon-Weaver (Hp) in diabetes group and healthy group was 0.88 (0.74-0.94) and 0.94 (0.88-0.96) for Bacteroides; 0.84 (0.74-0.93) and 0.87 (0.73-0.93) for Bifidobacterium. The cumulative distribution curve of intra-group similarity showed that the Dice similarity coefficient (Cs) lower than (or equal to) 0.5 took up 85.83% of the total Cs for Bacteroides in diabetes group and 35.71% in healthy group; the Cs lower than (or equal to) 0.4 constituted 90% of the total Cs for Bifidobacterium in CAD group and 60.7% in healthy group. It was showed that the composition of gut microbiota in CAD group might be changed due to atherosclerosis status.

**Conclusions:** Sequencing results also revealed that bacterial composition of CAD group was different from that of the healthy group. DGGE profiling has shown individual specificity in CAD group and healthy group for Bacteroides and Bifidobacterium. The intra-group similarity of Bacteroides and Bifidobacterium is lower in CAD group than in healthy group. Taken together, in this work we observed the characterisation of gut microbiota in CAD patients, which suggests that the gut microbiota of CAD patients have some changes associated with occurrence and development of CAD.

GW25-e3093

**Predictive value of serum uric acid level for left atrial thrombus or spontaneous echo contrast in patients with atrial fibrillation**

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**Objectives:** To investigate the predictive value of serum uric acid (SUA) levels for left atrial thrombus (LATH)/spontaneous echo contrast (SEC) in patients with atrial fibrillation (AF).

**Methods:** The study enrolled 525 patients (Male 357, Female 188, mean age of 66.6±2.2 years old. 83% with paroxysmal AF) with AF who underwent transthoracic echocardiography (TEE) in Guangdong province cardiovascular institute from July 2007 to January 2013. Patients were categorized into LATH/SEC group (n=57) and non-LATH/SEC group (n=468), according to the TEE results. The clinical baseline of both group including age, gender, AF types, SUA levels, indices of echocardiography and complications were collected and analyzed. The relationships between the potential risk factors and LATH/SEC were performed using Logistic regression analysis.

**Results:** SUA level (391.5±98.45μmol/L vs 349.27±83.93 μmol/L, P<0.01), left atrial diameter (LAD) (41.95±6.06mm vs 37.44±5.17mm, P<0.01), proportion of patients with persistent AF (50.9% vs 13.7%, P<0.01) were significantly increased in patients of LATH/SEC group compared with patients of non-LATH/SEC group. ROC curve were presented by SUA level, which indicated area under curve was 0.612 (P=0.006) and the best SUA cut-point was 448.5μmol/L. Logistic regression analysis indicated that female (OR=2.344, 95% CI 1.228-4.755, P=0.011), persistent AF (OR=5.993, 95% CI 3.127-11.486, P<0.001), SUA level (OR=2.890, 95% CI 1.380-6.051, P=0.005), LAD>40mm (OR=4.845, 95% CI 2.528-9.284, P<0.001). CHA2DS2-VASc score (OR=1.422, 95% CI 1.051-1.829, P=0.006) were indepen-dent risk factors of LATH/SEC in patients with AF.

**Conclusions:** SUA level is independent risk factor and predictive index for LATH/SEC in patients with AF.

GW25-e3529

**Traditional Chinese Medicine Qiliqiangxin attenuates cardiac remodeling after acute myocardial infarction in mice**

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**Objectives:** Qiliqiangxin (QL), a traditional Chinese medicine, has been approved by China Food and Drug Administration for the treatment of chronic heart failure since 2004. Recently, a multicenter randomized double-blind study from our group has proved that QL reduced the levels of B-type natriuretic peptide (BNP) and N-terminal pro-B-type natriuretic peptide (NT-proBNP) during 12 weeks of treatment in 512 chronic heart failure patients, suggesting that QL may have a protective effect on injury heart. However, whether QL can improve cardiac remodeling and the underlying mechanism are still unclear.

**Methods:** Four groups of C57BL/6 adult male mice (saline plus sham, saline plus AMI remodeling, QL 0.5g/kg/d plus sham, and QL 0.5g/kg/d plus AMI remodeling) were randomly divided in this study. Echocardiography and histopathology were detected to evaluate cardiac function and morphological changes. TTC staining and immunofluorescence were used to test myocardial necrosis and apoptosis. Quantitative reverse transcription polymerase chain reactions (RT-PCR)s and western blotting were also used to determine expression levels of peroxisome proliferator-activated receptor-α (PPAR-α), β, γ.

**Results:** QL significantly prevented AMI-induced decreases in ejection fraction (% EF; MI with saline 38%, MI with QL 48%) and fractional shortening (%FS; MI with saline 18%, MI with QL 22%) after AMI. In addition, QL decreased myocardial infarct size by 49% and myocardial apoptosis by 40%. Most importantly, PPARγ, a key regulator for cardiac energy metabolism after myocardial infarction, was found to be down-regulated in AMI remodeling and was up-regulated after QL administration.

**Conclusions:** QL may attenuate cardiac remodeling after AMI remodeling. Compared with the administration of QL alone, combination of PPARα activator with QL did not have significant difference on cardiac function.