GW23-e1343 — SCREENING RELATED GENES BY GENECHIP ON PERIPHERAL BLOOD MONONUCLEAR CELLS IN PATIENTS WITH ACUTE MYOCARDIAL INFARCTION (STEMI) AND EXPRESSIONS OF TNFSF6 AND CYP1A1

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Objectives Patients admitted to our ER and CCU from November 2007 to February 2008. Consisting of 11 patients, 7 males and 4 females, mean age 61.44 ± 13.70 years with a range from 33 to 75 years. All cases are diagnosed based on the AMI diagnosis criteria under Chinese Medical Association in 1999, For patients with normal controls with age, sex matching healthy volunteers 10 people, 7 male and 3 female, the average age 53.00 ± 6.55 (32–61). Acute onset in STEMI group hospital diagnosed after extracting cubits 10 ml 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 10 ml; The comparison group: morning, fasting extraction method 10 ml were cubits under the same approach as that for the patients group. PBMCs 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 CYP1A1 TNFSF6 by Real time PCR. All data to differences with mean$\pm$SD, Value of patients and controls were compared by ANOVA analysis. And correlation analysis method, the related to $p < 0.05$ to was statistically significant differences.

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Results

1. Of the STEMI group, general average STEMI genes that significant changes in 14, 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 (HSPD1, DNAJB1, DNAJB2), and repair DNA damage related gene 1 (RAD50), and apoptosis signal related gene 2 (TNFSF6 TRADD,) Significant down regulated of those genes: the cell proliferation/cancer related gene 1 (CCNG1), oxidation or metabolic stress related gene gene 2 (CAT, CYP1A1), DNA damage and restoration related gene 1 (ATM).
2. The expression of TNFSF6 in STEMI group is higher than of the healthy group and CYP1A1 was lower than the normal value.

Conclusions

1. The moderation 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 TNFSF6 and CYP1A1 genes after myocardial IRI in AMI at various stage. They may be involved in the myocardial ischaemia/reperfusion injury physiopathological process.