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MICRORNA EXPRESSION AND IDENTIFICATION OF CD4 +T LYMPHOCYTES IN PATIENTS WITH ACUTE CORONARY SYSDROME

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Objectives To screen differential microRNA expression profiles of CD4+T lymphocyte from the patients with acute coronary syndrome (ACS) and the healthy controls by microarray analysis technique. To elucidate the mechanism responsible for modulation of CD4+T lymphocyte and provide insights into the effects of miRNA on ACS.

Methods Ten patients with ACS were enrolled in the study, and 10 patients with normal coronary artery angiogram were served as a control group. Blood samples were taken from peripheral vein and the CD4+T lymphocytes were isolated from mononuclear cells prepared with Ficoll-Hypaque density-gradients centrifugation from human peripheral blood by magnetic cell sorting system (MACS). The purity of CD4+T lymphocytes was measured by flow cytometry analysis. The viable count was detected by the rejection experiment of trypanblau. Total RNA was abstracted from CD4+T lymphocyte with Trizol reagent. McroiRNA was isolated and enriched of by use of Polyethylene Glycol from 40 μg total RNA. The microRNA extracted from CD4+T lymphocytes was hybridised and microRNA expressions profiles of CD4+T lymphocyte were screened with the Affymetrix GeneChip microRNA array. The image signal was scanned by Affymetrix GeneChip Scanner 3000 and analysed by Affymetrix GeneChip Command Console™ 1.1 software. Then the image signal was transformed into digital information, which was analysed with SAM software. The differentially expressed microRNA were identified between the two groups. Real-time quantitative PCR (qRT-PCR) was used to confirm the result of selected genes from microarray analysis.

Results The results showed that the expression of mcroiRNA-155, microRNA-21, microRNA-424 and microRNA-127-3p were over 1.5 folds up-regulated, and the expression of microRNA-30b and microRNA-181a were over 0.5 folds down-regulated in ACS group compared to the control group. The qRT-PCR results were in accordance with those obtained using microarray analysis.

Conclusions The differentially expressed microRNA of CD4+T lymphocyte may participate in the occurring and developing of ACS.