

**GW26-e1803****Enhanced Expression of A-Disintegrin-and-Metalloproteinase-17 Promotes Extracellular Matrix Remodeling in Rats With Myocardial Infarction**

Miao Wang, Juan Zhao

Department of Cardiology Diseases, the First Affiliated Hospital, Harbin Medical University

**OBJECTIVES** This study aimed to investigate the effects of dynamic expression of cardiac tissue A-Disintegrin-and-Metalloproteinase-17 (ADAM-17) on myocardial remodeling after myocardial infarction (MI).

**METHODS** Forty adult male Wistar rats undergoing MI operation were divided into four subgroups based on survival time: MI1d (at the end of the first day), MI1w (at the end of the first week), MI4w (at the end of the fourth week) and MI12w (at the end of the 12th week). Hemodynamic characteristics were assessed by echocardiography and relative inflammation factors of left ventricular (LV) cavity were measured by ELISA. ADAM17 mRNA level was analyzed by quantitative reverse transcription-polymerase chain reaction (qRT-PCR). Protein expressions of tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), ADAM17 and tissue inhibitor of metalloproteinases-3 (TIMP-3) in ischemic cardiac tissue were analyzed by Western blot.

**RESULTS** One week after MI, left ventricular weight index (LVWI) was increased and systolic function examined by echocardiography was sharply worsened compared with that in Con1w subgroup ( $P < 0.05$ ). A reduced cell number and increased collagen accumulation were also displayed in the healing myocardium especially followed by a deteriorated MI-induced cardiac remodeling. TNF- $\alpha$  level was lower in the MI1w group compared with that in MI1d subgroup ( $P < 0.05$ ). However,  $\Delta$ TNF- $\alpha$  level, the net change of TNF- $\alpha$  concentration between the MI and Con groups, was significantly increased ( $P < 0.05$ ) from the MI1d to the MI1w. ADAM17 mRNA expression was significantly increased, especially at the end of the 1<sup>st</sup> week after MI ( $P < 0.05$ ). The results of Western blot also reveals that the protein expressions of ADAM17 and TNF- $\alpha$  were significantly up-regulated, and the expression of TIMP-3 was simultaneously sharply decreased in the MI1w subgroup ( $P < 0.05$ ).

**CONCLUSIONS** Enhanced ADAM17 expression may participate in myocardial remodeling, especially in the early stage after MI.

**GW26-e2144****Screening of Differentially Expressed MicroRNAs via MicroRNA Array Analysis Between Han and Uyghur Coronary Artery Disease Patients in Xinjiang**Ailifeire Maimaiti, Yining Yang, Bangdang Chen, Fen Liu, Yitong Ma  
Department of Cardiology, First Affiliated Hospital of Xinjiang Medical University, Urumqi, China

**OBJECTIVES** MicroRNAs (miRNAs) are approximately 22-nt-long noncoding RNAs which negatively regulate gene expression by binding to sites in the 3' untranslated regions (UTRs) of targeted messenger RNAs. Data shows that miRNAs are present in the circulation and could be used as potential prewarning biomarkers of cardiovascular diseases. In this study, we performed miRNA arrays analysis on Uyghur and Han stable angina pectoris patients and acute coronary syndrome (ACS) patients to obtain differential miRNAs expression profile between two ethnic groups under stable (stable angina pectoris) and unstable (ACS) status of coronary artery disease (CAD).

**METHODS** 18 CAD patients in total were selected after angiographic documentation of CAD, including 5 Han ACS (HA) patients, 5 Uyghur ACS (UA) patients, 5 Han stable angina pectoris patients (HS) and 3 Uyghur stable angina pectoris (US) patients. Patients with heart failure, leukopenia, thrombocytopenia, severe hepatic or renal dysfunction and inflammatory or malignant disease were excluded. Firstly, Patients' blood samples were drawn so as to isolate RNA from EDTA-plasma by using mirVana miRNA Isolation Kit (ABI), then we pre-amplified the products with Megaplex™ RT Primers Human Pool A v2.1 (ABI) to raise the RNA concentration. Subsequently, RNA products were reverse transcribed using the TaqMan microRNA Reverse Transcription (RT) kit (ABI) according to the instructions of the manufacturer. Finally, the RT products were used for detecting miRNA expression with TaqMan Human MicroRNA Array by quantitative PCR for the corresponding miRNAs. Comparisons were drawn between UA and HA groups as well as US and HS individuals. Significantly changed ( $RQ > 2.0$  or  $RQ \leq 0.5$ ,  $p < 0.05$ ) miRNAs were assessed for correlation with different ethnic groups.

**RESULTS** Three up-regulated miRNAs (hsa-miR-130a, hsa-miR-221, and hsa-miR-411) were identified in UA patients compared to HA patients (miR-130a,  $RQ = 3.3307$ ; miR-221,  $RQ = 2.6705$ ; miR-411,  $RQ = 2.5407$ ,  $p < 0.05$  for

all three miRNAs). Among stable angina pectoris subjects, we detected three up-regulated miRNAs (hsa-miR-219-1-3p, hsa-miR-551b, and hsa-miR-886-5p) and two down-regulated miRNAs (hsa-let-7a, hsa-miR-128) comparing US to HS subjects. (miR-219-1-3p,  $RQ = 2.1641$ ; miR-551b,  $RQ = 2.2171$ ; miR-886-5p,  $RQ = 2.2737$ ; let-7a,  $RQ = 0.1546$ ; miR-128,  $RQ = 0.4325$ ,  $p < 0.05$  for all).

**CONCLUSIONS** The differentially expressed miRNAs in different ethnic groups under different states of the same disease may represent different pathology processes, probably due to the heterogeneity of genetic susceptibility and miRNA regulatory system. The significance of these findings needs to be further determined.

**GW26-e2206****Phosphatidylinositol 4-Kinase  $\beta$  (PI4K $\beta$ ) and Phosphatidylinositol 4,5-Bisphosphate (PIP2) Modulated the Expression and Trafficking of BKCa Channels**Xiaoqi Tan,<sup>1,2</sup> Xiuli Cheng,<sup>2</sup> Li Yan,<sup>2</sup> Wengjun Huang,<sup>1</sup> Tao Li,<sup>1</sup> Yan Yang,<sup>1</sup> Xiaorong Zeng,<sup>2</sup> Jimin Cao<sup>2</sup><sup>1</sup>Key Laboratory of Medical Electrophysiology, Ministry of Education, Institute of Cardiovascular Diseases, Luzhou Medical College, Luzhou, China; <sup>2</sup>Department of Physiology, School of Basic Medicine, Peking Union Medical College, Beijing, China

**OBJECTIVES** Phosphatidylinositols (PI) play crucial roles in regulating cytoskeletal organization and trafficking of membrane protein. PI metabolism is controlled by phosphatidylinositol kinases. Phosphatidylinositol 4-kinase  $\beta$  (PI4K $\beta$ )-mediated phosphatidylinositol 4,5-bisphosphate (PIP2) production has been suggested to regulate biosynthetic traffic in yeast and mammalian cells. Here, we investigated the effect of PI4K $\beta$  and PIP2 on the expression and trafficking of large conductance calcium activated potassium (BK<sub>Ca</sub>) channels, the key modulator of the tone of vascular smooth muscles, expressing in HEK293 cells.

**METHODS** HEK293 cells with expressing BK<sub>Ca</sub> channels  $\alpha$  subunit (hSlo1) were constructed with transfection. BK<sub>Ca</sub> currents were recording by patch clamp technique under whole-cell and inside-out configuration. Western Blotting, flow cytometry (FCM), confocal were used to investigate the expression and trafficking of BK<sub>Ca</sub> channels. The direct interaction between phosphoinositides and BK<sub>Ca</sub> channels was investigated with PIP strips.

**RESULTS** PI4K $\beta$  increased the total and membrane expression of BK<sub>Ca</sub> channels expressing in HEK293 cells. The wild type PI4K $\beta$  (PI4K $\beta$ <sup>WT</sup>) increased the expression of BK<sub>Ca</sub> channels, while the dominant negative, kinase-dead PI4K $\beta$  (PI4K $\beta$ <sup>D656A</sup>, PI4K $\beta$ <sup>KD</sup>) decreased the expression of BK<sub>Ca</sub> comparing with the control group. Wortmannin and PAO, the inhibitors of PI4K $\beta$ , decreased the current density under whole-cell configuration. PIP2 increased total open probability (NPo) near three-fold from  $0.011 \pm 0.002$  to  $0.036 \pm 0.008$  ( $P < 0.05$ ,  $n = 6$ ) under inside-out configuration. PIP strips shown that BK<sub>Ca</sub> channels protein may bind with multiple PIs including P(3, 4)P2, P(3, 5)P2, P(4, 5)P2 and P(3, 4, 5)P3 directly. Wortmannin, PAO and the short hairpin interference RNA (shRNA) of PI4K $\beta$  significantly inhibited the trafficking of BK<sub>Ca</sub> channels protein to cell membrane with confocal and FCM ( $P < 0.05$  or  $P < 0.01$ ).

**CONCLUSIONS** these data above suggested that PI4K $\beta$  increased the expression and trafficking of BK<sub>Ca</sub> channels to membrane. PI4K $\beta$  may control the PI metabolism and the production of downstream PIs such as PIP2 in order to modulate the expression and trafficking of BK<sub>Ca</sub> channels indirectly.

**GW26-e2335****The Construction of Nano-Protein Complexes and Induce Human Bone Marrow-Mesenchymal Stem Cells (hBMSCs) Differentiate into Cardiac Progenitor Cells (CPCs) by Direct Reprogramming**Lin Jiang,<sup>1,2</sup> Xiaohong Li,<sup>1</sup> Yueheng Wu,<sup>1</sup> Yu Pan,<sup>1</sup> Xueyan Jiang,<sup>1</sup> Jing Xiao,<sup>1</sup> Xiangyu Yang,<sup>1</sup> Xiyong Yu<sup>1</sup><sup>1</sup>Guangdong General Hospital (Guangdong Academy of Medical Sciences); <sup>2</sup>Southern Medical University

**OBJECTIVES** To explore the best protein modified condition and influence factors to construct nano-protein complexes, and preliminarily analyze their process of entering into cells and intracellular metabolism. Then we try to induce hBMSCs to reprogram into CPCs by using this protein transfection technology, which shows high efficiency and low cytotoxicity to cells. It opens up new way for clinical cardiac reparations and regeneration treatment after myocardial infarction.

**METHODS** 4 kinds of cardiac specific transcription factors (Tbx5, Hand2, Mef2c, Gata4) are expressed and purified in an improved producing way, we've try to synthesis several compact and tightening