underwent heart transplantation in China and the effects of these mutations on protein localization and expression in myocardial tissue for the sake of clarifying the potential molecular genetics of ARVC.

**Methods:** (1) DNA extracted from myocardial tissue of ARVC patients who received heart transplantation and sequenced by targeted sequencing, then verified by Sanger sequencing. (2) Diseased tissue samples with desmosomal gene mutations studied for desmosomal protein distribution and expression using immunohistochemistry and western blot, respectively.

**Results:** We identified 2 mutations in DSG2 in 3 of 26 ARVC patients (11%), 2 mutations in PKP2 in 1 of 26 patients (3.8%) and 1 mutation in DSP in 1 of 26 patients (3.8%). The results of immunohistochemistry showed that compared to normal control, the location of desmosomal protein in intercalated disc in mutation carriers was similar; in contrast, the staining for DSG2 and PKP2 was decreased in those carriers who carried DSG2 and PKP2 mutations. And the results of western blot exhibited reduced expression level of these two proteins in mutation carriers. However, the expression level of desmplakin in DSP mutation carriers was similar when compared to normal control.

**Conclusions:** Five disease-causing mutations of desmosomal genes in ARVC patients were described in this study, two of them were the reported and three of them are newly found. Our results implied that mutations of desmosomal genes causing ARVC via decreasing expression levels of desmosomal proteins, and suggested a dominant-negative effect of the mutated desmosomal proteins because they were incorporated into the desmosomes.

**GW25-e3531**
Quantitative proteomics of changes in cardiac cytoprotection-related proteins in atrial tissue from valvular disease patients with permanent atrial fibrillation
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**Objectives:** There is convincing evidence demonstrating a close association between cardiac cytoprotection-related proteins and atrial fibrillation (AF). The aim of the present study was to identify the underlying mechanisms via profiling of the expression of cardiac cytoprotection-related proteins in the left atrial appendage (LAA) of patients with AF.

**Methods:** Label-free relative and absolute quantification-coupled 2-D liquid chromatography-tandem mass spectrometry (iTRAQ-coupled 2-D LC-MS/MS) was used to profile the expression of the LAA from valvular disease patients with sinus rhythm (SR, n=6) and AF (n=8). Specimens were pulverised and homogenised in a lysis buffer, then digested by trypsin and labelled with different iTRAQ tags. The pooled labelled peptides were analysed by liquid chromatography tandem mass spectrometry (LC-MS/MS). Protein identification and relative iTRAQ quantification were performed with the ProteinPilot Software 4.0. Protein differentially expression were validated by Western blot analysis to verify the results obtained by iTRAQ proteomic studies.

**Results:** 1023 unique proteins from the cardiac tissues were identified. Among these proteins, we identified 16 cardiac cytoprotection-related proteins, consisting of 12 heat shock proteins, 4 peroxisome enzyme related proteins. 7 proteins of them were expressed downregulated in the atrial appendage of patients with AF when compared with SR patients. 4 proteins like 10 kDa heat shock protein, heat shock protein 70 kDa protein 1, heat shock protein beta-1 and heat shock protein beta-7 were up-regulated, while 3 proteins as heat shock protein HSP 90-beta, peroxiredoxin-5 and stress-70 protein were down-regulated in LAA of AF patients. Those proteins may exert a protective effect against AF-induced cardiac myocytes damage. Western blotting has further validated the content of desmplakin, cytochrome c oxidase subunit 5B and heat shock protein-1 in the LAA between AF and SR patients with mitral valve disease. Also, the reliability of the iTRAQ proteomic studies was validated.

**Conclusions:** In summary, those up-regulated cardiac cytoprotection-related proteins suggested that there is an adaptive response in the LAA tissues to atrial stress and cardiac myocytes damage induced by AF. While, the down-regulated proteins may demonstrated that the adaptive ability was started to impaired during the permanent atrial fibrillation. The adaptive response of the cardiac cytoprotection-related proteins may be involved in the matrix of AF.

**GW25-e3536**
Short-term High-dose Rosuvastins Reduces Levels of Adhesion Molecules in Patients with Acute Coronary Syndrome undergoing Percutaneous Coronary Intervention
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**Objectives:** This study sought to the expression profile long noncoding RNAs (lncRNAs) in oxidized low-density lipoprotein (ox-LDL) treated human umbilical vein endothelial cells (HUVECs) compared to normal HUVECs through microarray analysis.

**Methods:** The global lncRNAs and miRNAs expression profiles in ox-LDL treated HUVECs compared with normal HUVECs were analysed through the Arraystar Human lncRNA Array v2.0. Four upregulated lncRNAs (ENST0000043178, AK094119, ENST00000447336, chr8:4977604-49797329+2+) were validated by quantitative real-time transcriptase polymerase chain reaction (qRT-PCR). GO analysis and pathway analysis were performed in the standard enrichment computation method.

**Results:** Approximately 141 lncRNAs and 113 miRNAs were identified to be different expression. The cut-off change ≥2.0, P-value cut-off is 0.05. ox-LDL treated HUVECs compared with normal HUVECs. Four upregulated lncRNAs were validated by qRT-PCR. GO analysis showed that the highest enriched GOs targeted by up-regulated transcripts were biological regulation (ontology: biological process) and that the highest enriched GOs targeted by the down-regulated transcripts were cellular metabolic process (ontology: biological process). Pathway analysis indicated that 4 pathways corresponded to up-regulated transcripts and those 22 pathways corresponded to down-regulated transcripts (P-value cut-off is 0.05).

**Conclusions:** Our data reveal that clusters of lncRNAs are aberrantly expressed in ox-LDL treated HUVECs compared with normal HUVECs, which indicate that lncRNAs differentially expressed in endothelial cells may play a partial or key role in endothelial dysfunction and damage. This study may provide novel insights into the mechanism and potential targets for the future treatment of atherosclerosis.

**GW25-e4278**
Hesperetin blocks the proliferation of pulmonary artery smooth muscle cells induced by platelet-derived growth factor-BB
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**Objectives:** The proliferation of pulmonary artery smooth muscle cells (PASMCs) contribute to the development of pulmonary vascular remodeling which will ultimately lead to pulmonary hypertension. In this study, we investigated the effect and molecular mechanisms of hesperetin on the platelet-derived growth factor (PDGF)-BB-induced proliferation of primary cultured rat PASMCs.

**Methods:** PASMCs were incubated with different concentrations of hesperetin (12.5μmol/L, 25μmol/L, 50μmol/L, 100μmol/L) in the presence of PDGF-BB (20 ng/ml) or not. Cell proliferation was determined by CCK-8 assay.

**Results:** The toxicity of hesperetin on PASMCs was determined by the trypan blue exclusion test. Cell cycle progression was determined using a Cell cycle and Apoptosis Analysis Kit. The mRNA expression of cyclin D1, cyclin E, CDK2, CDK4 and p27 were measured. Further studies showed that hesperetin inhibits the cell cycle associated with the inhibition of the mRNA expression of cyclin D1, cyclin E, CDK2, and CDK4, as well as an increase of the mRNA expression of p27 in PDGF-BB-stimulated PASMCs. Further studies showed that the beneficial effect of hesperetin on blocking the proliferation of PASMCs is related to suppression of the P38 and AKT/GSK3β signaling pathway, but has little effect on the ERK1/2 and JNK signaling pathways.

**Conclusions:** These results demonstrate that hesperetin suppresses PDGF-BB-induced PASMC proliferation through the P38 and AKT/GSK3β signaling pathway and suggests that it may be a feasible therapy for pulmonary vascular remodeling diseases.

**GW25-e4349**
Effects of OX40-OX40 ligand interaction on the levels of ROS and Cyclin A1 in C57BL/6J mice atherosclerosis
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