membrane potential, citrate synthase activity and mtDNA copy number (P<0.05). Furthermore, HG cells showed decreased SIRT1 expression and PGC-1α acetylation. Additionally, mRNA and protein expression of PGC-1α downstream genes (NRF-1, NRF-2, ERR-α and TFAM) were reduced in HG group. Resveratrol reversed these changes in HG group, but this effect was diminished in HG+ sh-SIRT1 group.
Conclusions: Resveratrol protects against cardiac apoptosis and improves cardiac function in diabetic mice through enhancing mitochondrial biogenesis and function. SIRT1 plays an important role in the resveratrol beneficial effects against diabetic cardiomyopathy.

GW25-e4357

Ghrelin receptor deficiency aggravates instability of atherosclerotic plaque and vascular inflammation in low-density lipoprotein receptor-null mice

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Objectives: Ghrelin has been found to be associated with anti-inflammation, inhibition of atherosclerotic plaque formation and plaque stability in cardiovascular system. We investigated whether ghrelin affected the atherosclerotic plaque and immune inflammation of atherosclerosis.
Methods: We crossed ghrelin receptor knock out mice (GHSR-/-) into a low-density lipoprotein receptor-null (LDLR-/-) mouse line. In this model, atherosclerotic lesions were promoted by feeding a high-fat, high-cholesterol Western-type diet for 18 weeks, following a standard protocol. Serum lipid levels, atherosclerotic plaque on aortic arches, and the expression of ICAM-1 and VCAM-1, T cell, macrophage and smooth muscle cell of atherosclerotic plaque were observed.
Results: Though the serum lipid levels and atherosclerotic plaque area on aortic arches were not significantly different between in GHSR+/+/LDLR-/- mice and GHSR -/-LDLR-/- mice, the protein expression of ICAM-1 and VCAM-1 in atherosclerosis plaque were increased in GHSR -/-LDLR-/- mice than that in GHSR+/+/LDLR-/- mice. T cell and macrophage were more, while the smooth muscle cells of atherosclerosis plaque were less in GHSR -/-LDLR-/- mice than that in GHSR+/+/LDLR-/- mice.
Conclusions: In conclusion, ghrelin receptor deficiency aggravates instability of atherosclerotic plaque and vascular inflammation but not atherosclerotic plaque area, which will provide novel avenues for the treatment of atherosclerosis patients.

GW25-e4400

Study on the relationship between the serum level of GDF15a and infarction area for rats with myocardial infarction

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Objectives: Through detecting the serum level of growth differentiation factor 15a (GDF 15a) of the rats with different myocardial infarction area, to explore the relationship between the serum level of GDF15a and myocardial infarction area and the prediction effect of GDF15a on myocardial infarction area.
Methods: 1. Experimental animals: 30 healthy Wistar rats, male, weighing 200～300 g, are selected. Rats are randomly divided into high ligation group, low ligation group and sham operation group with 10 rats in each group. 2. Myocardial infarction model set up: Rats are injected with 10% chloral hydrate and fixed on the operation board, assisted respiration with endotracheal intubation, connected to electrocardiograph (ECG) and monitored. In high ligation group, the coronary arteries of rats are ligated about 3mm from the aortic root which is between the left atrial and pulmonary arterial cone. In low ligation group, the coronary arteries are ligated about 2 mm from the tip of left atrial appendage. Method used in sham operation group is similar to low ligation group but without coronary artery ligation. Penicillin is applied in order to prevent postoperative infection. 3. Rats serum GDFl5a detection: 2ml blood sample is taken from the abdominal aorta of each rat in 24h after operation, GDFl5a is then detected using ELISA method. 4. Infarction area computation: Each rat is sacrificed after blood sampling, heart is harvested, the left ventricular long axis transverse segment which is below the left coronary artery ligation point is collected and sectioned, the thickness of the slices is 4μm. The slices are then HE stained and used to do heart-pathological monitoring and compute infarction area. Infarction area (%)= [(The endocardial length of the left ventricular infarct / Total endocardial circumference) /2 + (The epicardial length of the left ventricular infarct / Total epicardial circumference) /2] ×100%. Calculation is implemented by the professional image analysis software IPP 6.0. 5. Statistical method: Measurement results are showed in the manner of average±standard deviation (SD), ANOVA and t test are applied to calculate statistical significance, all analysis are done using statistical software SPSS 17.0.
Results: Three rats in high ligation group are dead in 24h after operation compared to one rat in low ligation group. Result 1: Serum GDFL5a detection results for each group: the contents of GDFL5a are respectively 1190.2±61.4ng/L in high ligation group, 931.6±93.0ng/L in low ligation group and 637.2±61.2ng/L in sham operation group. ANOVA result for the average comparison of three groups is F=117.8 with P<0.001, which shows that this result has statistical meaning and the content of GDFl5a in high ligation group is significantly higher than the ones in low ligation group and sham operation group. Result 2: Computation of infarction area between three groups: The infarction areas are respectively 57.7±4.0 in high ligation group, 38.6±4.6 in low ligation group and 0 in sham operation group. T-test is applied to compare the areas between high ligation group and low ligation group, t=8.7 with P<0.001, which shows that this result also has statistical meaning and infarction area in high ligation group is significantly larger than the one in low ligation group.
Conclusions: The serum level of GDFl5a rises for the rats with cardiac obstruction, its level rises with an increasing infarction area, this phenomenon shows that the serum level of the GDFl5a has certain prediction effect on the infarction area.

GW25-e4408

Magnolol administration in prehypertension postpones the development of hypertension and the underlying mechanisms

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Objectives: Patients with prehypertension are more likely to progress to manifest hypertension than those with optimal or normal blood pressure. However, the mechanisms underlying the development from prehypertension to hypertension still remain largely elusive and the drugs for antihypertensive treatment in prehypertension are absent. Here we determined the effects of magnolol (MAG) on blood pressure and aortic vasodilatation to insulin, and investigated the underlying mechanisms.
Methods: Four-week-old male spontaneous hypertensive rats (SHR) and age-matched normotensive Wistar-Kyoto (WKY) control rats weretreated with vehicle (distilled water) or MAG (100 mg/kg/day, o.g., once daily) for 3 weeks. Additionally, human umbilical vein endothelial cells (HUVECs) were exposed to glucose (25 mmol/L) and saturated FFA palmitate (16:0; 500 μmol/L) (HG/HF) for 18 hours and treated with MAG (10μmol/L) for 48 hours.
Results: MAG significantly decreased blood pressure in seven-week-old SHR (SBP: 131±6 vs. 160±11 mmHg in vehicle-treated SHR, DBP: 106±5 vs. 127±8 mmHg, n=8, P<0.01), improved insulin-induced aorta vasodilation (relaxation: 57.4%±2.4% vs. 42.2%±5.3%, n=6, P<0.01), restored Akt and eNOS phosphorylations stimulated by insulin, and increased PPARγ and decreased TRB3 expressions (n=5-6, P<0.05). Furthermore, in cultured HUVECs, MAG incubation increased PPARγ, decreased TRB3 expressions, and restored insulin-induced phosphorylated Akt and eNOS levels and NO production (P<0.05), which was blocked by both PPARγ antagonist and siRNA targeting PPARγ (P<0.05).
Conclusions: Treatment of young SHRs with MAG beginning at the prehypertensive stage decreases blood pressure via improving vascular insulin resistance, which is at least partly attributable to upregulated PPARγ, downregulated TRB3 and consequently increased Akt and eNOS activations in blood vessels. These results indicate that MAG may be used as an antihypertensive drug early administrated at the prehypertensive stage.

GW25-e4516

Genotype-phenotype analysis on a large cohort of Chinese LQTS patients

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Objectives: Long QT syndrome (LQTS) is an inherited cardiac disorder characterized by syncope or even sudden death. Although a variety of clinical index could point to a diagnosis of LQTS, gene-screening remains to be the golden standard for LQTS diagnosis. In addition, while 15 genes have been identified as LQTS causing genes, 90% of the mutationslie mainly in KCNQ1, KCNH2, SCN5A– the causing genes of LQT1-3. So, in the present study, we aim to evaluate the diagnostic value of the clinical data by analyzing the genetically diagnosed LQTS patients. Besides, we also investigated the mutation spectrum and gene distribution of Chinese LQTS patients.
Methods: 214 LQTS patients, selected from the Chinese Channelopathy Registry Study, were enrolled into this study. Patients were evaluatedbased on QTcandclinical manifestations. Individuals were clinically diagnosed as LQTS if presenting a prolonged QT interval (QTc≥450ms for male; QTc≥470ms for female) and/or documented TdP (Torsade de Pointes), ventricular fibrillation as well as cardiac arrest.

Mutational screening of KCNQ1, KCNH2, SCN5A genes was performed by PCR and direct DNA sequence analysis. LQTS phenotype were evaluated for all putative LQTS patients.
Results: For the total cohort of the LQTS patients, 173 patients were genotype-positive for LQTS, while 41 negative. We compared the phenotypes between the two groups. Statistical results indicate that differences of average QTc, Schwartz score,-percentages of patients with syncope, and Schwartz score>4 between the two groups are significant (P<0.05), while those of age of first syncope, gender (female vs. male), percentages of patients with QTc>480ms and TdP not (P>0.05).

Overall, 173 of 214 (81%) LQTS patients were found to harbor at least one putative LQTS-causing mutation. Among them, 99 mutations were identified: 42 were in KCNQ1, 54 in KCNH2, 3 in SCN5A. In this set of mutations, 42 were novel, including 15 in KCNQ1, 27 in KCNH2, and none in SCN5A. To be specific, most of mutations (71 of 99, 72%) were missense, while frame-shift mutations, splice sites, nonsense and inframe deletions account for 15% (15/99), 5% (5/99), 5% (5/99), 2% (2/99), respectively.Most frameshift mutations (11 of 15, 73%) were found in KCNH2 (representing 20% of all KCNH2mutations), while 80% (4/5) of the splice mutations were identified