Cinnamomi. NXT has been used in the treatment of cardiovascular and cerebrovascular diseases like coronary artery disease in clinic. Due to the complex combination of herbs, the chemical analysis and mechanism are still not clear. In this research, based on UPLC/Q-TOF for ingredients investigation, we used the method of network pharmacology to explore the potential effect of NXT and the evidence of the rationality on herb combinations.

METHODS We used the five principles of drug absorption as a judgment rule to identify the chemical compositions that could be absorbed in blood form the all chemicals of NXT. Moreover, we predicted the main targets and related pathways of absorbable components by PharmMapper, Universal Protein and Molecule Annotation System. Finally, we constructed the networks including multiple components (from different source of herbal medicines) with multiple targets and pathways by Cytoscape.

RESULTS We got 83 chemical compositions from NXT, of which 52 predictions could be absorbed. By analyzing network pharmacological approach, there were 133 targets that could be regulated by these components. In addition, these targets were involved in 85 pathways ($P < 0.01$), including NFAT and Hypertrophy of the heart (Transcription in the broken heart), Nuclear Receptors in Lipid Metabolism and Toxicity, Aspirin Blocks Signaling Pathway Involved in Platelet Activation, VEGF, Hypoxia, and Angiogenesis and Signaling Pathway from G-Protein Families, which were all closely associated with diseases of the cardiovascular and cerebrovascular system.

CONCLUSIONS The 52 main active components of NXT are included amino acids, senkyunolides, flavonoids, and organic acids. NXT plays a dramatic role in the treatment of cardiovascular and cerebrovascular diseases, especially in the pathway NFAT and Hypertrophy of the heart.

GW26-e0097 The relationship of the genetic polymorphism of ApoE and the stability of carotid plaque
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OBJECTIVES The aim of the present study was to investigate the role of genetic polymorphisms of ApoE in carotid artery atherosclerosis and the instability of the plaque.

METHODS 238 subjects were divided into 3 groups: the instable plaque group, stable plaque group and control group according to the result of carotid ultrasound examination. The genotype of ApoE and serum ApoE concentration was measured.

RESULTS • The frequency of $\varepsilon 4$ allele in the CAS subjects was higher than the healthy people. It was higher in instable plaque group than in the stable plaque, and this was statistically significant. • The level of Hs-CRP and MCP-1 in the subjects with $\varepsilon 4$ allele were higher than the subjects without, which indicated that the inflammatory activity in subjects with $\varepsilon 4$ allele was stronger than the subjects without $\varepsilon 4$ allele.

CONCLUSIONS ApoE polymorphism was associated with carotid atherosclerosis and the instability of plaques. Patients with the ApoE4 isoform had a more severe CAS than the subjects without the ApoE4 allele. The genetic polymorphism of ApoE has influenced the atherosclerosis through adjusting the blood-fat or the chronic inflammation status.

GW26-e1073 Cellular repressor of E1A-stimulated gene overexpression in bone mesenchymal stem cells improves the treatment of myocardial infarction in rats
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OBJECTIVES To study the effects of cellular repressor of E1A-stimulated genes (CREG) in bone mesenchymal stem cells (BMSCs) after transplantation into infarcted heart in rats.

METHODS 50ul PBS or 1.5 x 10^6 (Norm) BMSCs, (GFP) BMSCs or (CREG) BMSCs were implanted in myocardial infarction rat models. Cardiac function, fibrosis, apoptosis and angiogenesis were analyzed by echocardiography, masson, western blot and immunofluorescence staining, respectively. ELISA, western blot and matrigel assay were used in vitro to detect vascular endothelial growth factor (VEGF) secretion, signaling molecule expression, and angiogenic tube formation.

RESULTS Compared with group (Norm) BMSCs and group (GFP) BMSCs, prolonged cardiac function (14d LVFV: 51.84±1.14%; LVSF: 42.56±1.22%), decreased fibrosis (14d Fibrotic area: 25.82±1.12%) and apoptosis and increased angiogenesis were found in group (CREG) BMSCs. In vivo and in vitro, VEGF secretion from (CREG)BMSCs was markedly enhanced. In vitro, angiogenic tube formation in (CREG) BMSC supernatants significantly increased. CREG activated hypoxia-inducible factor-1α (HIF-1α), but not HIF-2α. Knockdown of HIF-1α with siRNA decreased VEGF secretion and angiogenic tube formation. Notably, CREG did not influence HIF-1α mRNA synthesis but inhibited the expression of Von Hippel-Lindau (VHL), a key protein that regulates HIF-1α degradation.

CONCLUSIONS Cellular repressor of E1A-stimulated gene overexpression in BMSCs could improve the treatment of myocardial infarction in rats.

GW26-e1424 Study on the regulatory functions and the Mechanism of Protein Kinase C and verapamil to SK2 channels in Human Atrial Fibrillation
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OBJECTIVES Small-conductance Ca²⁺-activated K⁺ (SK) channels are recognized as a new ion channel which associated with atrial fibrillation (AF). This study aims to investigate regulatory functions and the mechanism of protein kinase C (PKC) and verapamil to SK2 in human patients with atrial fibrillation.

METHODS 30 patients undergoing extracorporeal circulation cardiac surgery were divided into 2 groups,18 patients with AF and 15 patients with SR. The regulatory functions of PKC to SK2 channels were detected in isolated human atrial muscle cells with whole-cell patch clamp experiments.

RESULTS The SK2 channel current density at -130mV was (-5.1±0.32) pA/pF in SR group vs.(-1.0±0.73) pA/pF in AF group($P < 0.05$). The ratio of SK2 channel currents in the integrated inward currents was (23.2±2.09)% vs. (12.9±1.81)%($P < 0.05$) in SR group. Verapamil reduced the ratio of SK2 channel currents by PMA in AF group was larger than the SR group. The inhibition ratio of SK2 channel current at -130 mV was (8.59±2.80)% in SR group vs. (20.9±1.70)% in AF group($P < 0.05$). Verapamil reduced the ratio of SK2 channel in the integrated inward currents at -130 mV by (33.5±2.01)% in SR group vs. (20.41±1.34)% in AF group($P < 0.05$). The ratio of SK2 channel currents in the integrated inward currents with verapamil and PMA at -130 mV reduced to (2.18±0.42)% in SR group vs. (4.57±0.45)% in AF group($P < 0.05$).

CONCLUSIONS SK2 channel up-regulated in atrial fibrillation. There is a certain correlation among PKC,verapamil and SK2 channels. We speculate that PKC-related pathway and verapamil-related pathway may regulate the function of SK2 channel.

GW26-e2198 A novel polymorphism of the CYP19 gene is associated with essential hypertension in China
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OBJECTIVES Aromatase which encoded by CYP19 gene is a key enzyme in the conversion of androgen to estrogen and play an important role in the balance of the sex hormone levels. The sex hormone has a causal role in the development of cardiovascular disease. The goal of this study was to investigate the interaction between the SNPs in CYP19 gene and essential hypertension.
METHODS The case-control study including a Han population (410 EH patients and 410 control subjects) and a Uygur population (371 EH patients and 463 control subjects). Individuals was conducted to identify the association of three SNPs in CYP19 with EH by using χ² test or fisher exact test. Differences in lipids and the parameters of echocardiography among individuals with different genotypes were assessed by using one way analysis of variance(ANOVA).

RESULTS For women in Han, the distribution of rs2289105 in CYP19 gene showed a significant difference between EH and controls( P=0.049) and the dominant model (CC vs CT+TT) has a significant lower risk than the homozygous wild-type CC ( P=0.014), the dominant model of rs12050772 (GG vs GT+TT) has a significant lower risk in EH patients ( P=0.021). For men in Uygur, the recessive model of rs4774585 (AA vs AG+GG) has a significant higher risk in EH patients ( P=0.021). ANOVA indicated the left ventricular end-diastolic dimension is significant higher in the homozygous wild-type (GG) group than the other groups ( P=0.015).

CONCLUSIONS The T allele of rs2289105 in CYP19 gene might be a protective genetic marker of EH for women in Han population. The T allele of rs12050772 in Han population and the A allele of rs4774585 in Uygur population could be a protective genetic marker, but further study is needed.

GW26-e2201 Recombinant adeno-associated virus serotype 9 transfection of atherosclerosis mice: determination of the optimal expression time in vivo
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OBJECTIVES To explore the optimal time point of recombinant adeno-associated virus serotype 9-enhanced green fluorescent protein (rAAV9-eGFP) expression in the aorta of atherosclerosis mice.

METHODS Atherosclerosis model was established with high-fat diet and the atherosclerosis model was establisshed with high-fat diet to 30 ApoE-/- mice for 16 weeks. Among them, 25 mice were injected with 5.0×10¹¹ vg (virus genomes) rAAV9-eGFP through the tail vein, while the remaining 5 mice were injected with saline, serving as the control group. The virus-transfected mice were killed at 14, 21, 28, 35 and 60 days after transfection, and aortic tissue was harvested. The expression of enhanced green fluorescent protein was detected with laser scanning confocal microscope. Western blot assays were used to detect the expression of enhanced green fluorescent protein in the aorta. The expression of enhanced green fluorescent protein in vivo was observed and the optimal expression time point was determined.

RESULTS rAAV9-eGFP effectively transfected the aorta of atherosclerosis mice, enhanced green fluorescent protein was expressed in aortic tissue, and the expression intensity increased gradually with the increasing transfection time. The highest expression level was found at 35 days after transfection and then maintained stable at 60 days. There were significant differences at different time points after transfection ( P<0.05).

CONCLUSIONS rAAV9-eGFP can be effectively expressed in the aorta of atherosclerosis ApoE-/- mice and rAAV9-eGFP can be regarded as the optimal vector in the treatment of atherosclerosis.

GW26-e4469 The role of augmented late sodium current in atrial fibrillation
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OBJECTIVES To determine the role of increased late sodium current in atrial fibrillation (AF) by investigating the effect of sea anemone toxin-II (ATX-II) on atrial action potential duration (APD) and effective refractory period (ERP) and the incidence of AF.

METHODS Female New Zealand rabbit hearts were isolated and perfused in Langendorff method. Hearts were paced at right appendage at fixed rate and left atrial and ventricular endo- and epicardial APDs were recorded. Hearts were treated with ATX-II (3 nM) and paced at right atrium in a programmable mode of S1S2 to create AF. Ranolazine and TTX at different concentrations were administered to hearts with AF in order to observe their effectiveness on suppressing AF.

RESULTS When hearts were paced at 350 ms, ATX-II (3-15 nM) significantly prolonged atrial MAPD₉₀ by 46 ± 5 ms (n=6, P <0.001). In the presence of ATX-II (10-15 nM), spontaneous AF were investigated in 64.3% (n=14) of hearts, but TTX (1μM) and ranolazine (10 μM) terminated AF. When hearts were paced at 440 ms, ranolazine alone prolonged atrial and ventricular endo- and epicardial MAPD₉₀ by 17 ± 4 ms, 28 ± 5 ms and 23 ± 6 ms (n=6, P <0.01). However, in the presence of ATX-II (3 nM), ranolazine shortened atrial MAPD₉₀ by 33 ± 4 ms (n=6, P <0.001). ATX-II (1-3 nM) increased AF window, AF burden in concentration dependent manners by 31 ± 11 s and 103 ± 8 ms (n=6, P <0.05), respectively. In the presence of ATX-II (3 nM), ranolazine (3-10 μM) and TTX (0.1-1 μM) significantly reduced AF window and AF burden in concentration dependent manners.

CONCLUSIONS When late sodium current was increased, AF was induced by prolonging atrial MAPD and ERP which was the new mechanism of AF. Both ranolazine and TTX shortened atrial MAPD and exerted the ability of reducing AF window and AF burden and preventing AF.