not only an inflammatory factor but also an apolipoprotein that can replace apolipoprotein A1 (apoA1) as the major apolipoprotein of HDL. However, the relationship between genetic polymorphisms of SAA and CAD remains unclear.

Methods 4 Single Nucleotide Polymorphisms (SNPs) (rs12218, rs1059559, rs2229338, and rs2468844) of SAA1 and SAA2 gene were genotyped in 1580 CAD patients and 1914 age- and sex-matched controls by the use of PCR-restriction fragment length polymorphism (PCR-RFLP) analysis.

Results The CC genotype and C allele of rs12218 and the GG genotype and G allele of rs2468844 were more common in the CAD patients than in the control subjects, respectively (all $p < 0.001$). After adjusted for diabetes mellitus, hypertension, smoking, drinking and lipid disorders by use of logistic regression, the SNPs rs12218 (OR=5.906, 95% CI 2.877 to 12.124, $p < 0.001$) and rs2468844 (OR=4.102, 95% CI 2.018 to 8.129, $p < 0.001$) still differed significantly between the CAD patients and control subjects.

Conclusion These data suggest that genetic polymorphisms of SAA1/2 gene significantly increased the risk of CAD in a Chinese Han population.

e0082 MOLECULAR IMAGING OF APELIN ON SURVIVAL AND FUNCTION OF MESENCHYMAL STEM CELLS IN HINDLIMB MICE

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Objective This study was designed to evaluate the contribution of apelin to the therapeutic efficacy of mesenchymal stem cells in hindlimb ischaemia mice.

Methods Mesenchymal stem cells (MSC) expressing firefly luciferase (Fluc) were isolated from β -actin-luc mice and characterised by flow cytometry and bioluminescence imaging (BLI). Male FVB mice underwent femoral artery ligation and received MSC (1×10^6) or MSC with Apelin intra-quadriceps femoris muscle injection. Cell survival was imaged by BLI. Angiogenesis was assessed by immunohistochemistry method. The expressions of AKT and pAKT after cellular therapy were analysed by Western blot.

Results Fluc expression correlated with cell number in all groups. In vivo BLI revealed acute donor cell death of MSC within 2 weeks after transplantation. By contrast, signals of injected cells were still present after 4 weeks in the MSC with apelin group. Immunohistochemistry showed more angiogenesis in the MSC with Apelin group compared to MSC ($p < 0.05$). In vitro apelin treatment of MSC exposed to hypoxia increased cell proliferation. Moreover, considerable increases in phosphorylation of Akt were found in MSC pretreated with apelin.

Conclusions Apelin has beneficial effects on the therapeutic efficacy and survival maintenance of mesenchymal stem cells in hindlimb ischaemia and might constitute an important therapy target in cardiovascular disease.

e0083 MEMBRANE TYPE 1 MATRIX METALLOPROTEINASE ACTIVATION IS ENHANCED BY LOW SHEAR STRESS THROUGH INTEGRIN PATHWAY IN APOE-/- MICE

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Objective Low shear stress and matrix metalloproteinase are involved in atherogenesis and plaque stability. The aim of this study

was to explore the relation and possible mechanism of membrane type-1 matrix metalloproteinase (MT1-MMP) and low shear stress (LSS).

Methods 80 male apoE^{-/-} mice were fed a high-fat diet, and lesions in the left carotid artery were induced by perivascular placement of constrictive collars.

Results Ultrasound-determined shear stress was significantly lower in the left carotid artery than in the right artery (5.61 ± 0.72 vs 9.76 ± 1.48 N/m², $p < 0.01$). Confocal microscopy and dual staining revealed higher MT1-MMP expression in left common carotid artery. Cultured human umbilical vein endothelial cells (HUVECs) exposed to 0.4 N/cm² shear stress (LSS) and 1.2 N/cm² shear stress (PSS). HUVECs subjected to LSS showed a time-dependent increase in MT1-MMP mRNA level. MT1-MMP mRNA level was down-regulated under PSS at 3 and 5 h. MT1-MMP protein showed no change in expression at 1-h LSS, but 3-, 5-, 8- and 16-h treatment produced significantly increased expression and activity. NF- κ B DNA-binding activity was stronger at 30-min and 1-h LSS exposure than with control treatment. Pretreatment with 18 μ M SN50 efficiently inhibited NF- κ B DNA binding activity. In the presence of SN50, MT1-MMP mRNA expression, protein level and activity were significantly attenuated (all $p < 0.01$). MT1-MMP mRNA expression, protein level and activity were inhibited by PD98059 (all $p < 0.01$). To determine the relation between ERK1/2 and NF- κ B with MT1-MMP induced by LSS, HUVECs were incubated with PD98059 for 2 h before LSS. The level of phosphor-IKK α/β was reduced, whereas that of phosphor-IkB α was increased as compared with no PD98059 treatment. As well, NF- κ B DNA-binding activity was decreased. HUVECs were preincubated for 48 h with FAK siRNA and then treated with LSS. The shear stress-induced increase in MT1-MMP mRNA and protein level and activity was significantly inhibited (all $p < 0.01$). As well, LSS-induced ERK1/2 activation was inhibited with 5-min LSS exposure ($p < 0.01$). To examine NF- κ B DNA-binding activity, HUVECs were pretreated for 48 h with FAK siRNA before being exposed to LSS. NF- κ B DNA-binding activity was inhibited with FAK siRNA pretreatment. HUVECs were preincubated for 48 h with integrin β 1 siRNA and then underwent LSS. The shear stress-induced increase in MT1-MMP mRNA expression, protein level and activity was significantly inhibited (all $p < 0.01$). As well, LSS-induced FAK and ERK1/2 activation was inhibited at 5-min exposure ($p < 0.01$). Next, we examined NF- κ B DNA-binding activity with 48-h integrin β 1 siRNA pretreatment before exposure to LSS; NF- κ B DNA binding activity was inhibited by siRNA integrin β 1 pretreatment.

Conclusions MT1-MMP induced by LSS is involved in atherosclerotic plaque, via the integrin β 1-FAK-ERK1/2-NF- κ B pathway.

e0084 IMAGING OF VULNERABLE PLAQUE AND THROMBOSIS WITH MRI IN A RABBIT MODEL

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Objective Our aim is to investigate the feasibility of detecting vulnerable plaque and thrombosis by use of MRI.

Methods 24 male New Zealand White rabbits were divided into two groups: the atherosclerosis group (As group, n=20) and the normal control group (C group, n=4). After induction of atherosclerosis, MRI exams were conducted separately before and after the induction, triggering the plaques' disruption. The rabbits were then massacrred to obtain data of pathology. The animals in the normal control group were fed a standard diet, and we performed MRI exam separately before and after, triggering the plaques' disruption too. After MRI exams, rabbits were massacrred to obtain data of pathology. The in vivo imaging results of MRI were compared with the

histological structure of the specimens, and the concordance of κ was calculated. Furthermore, the effect of plaque's component on the rupture was evaluated with logistic models.

Results 63% (7 of 11) in rabbits in as group had thrombosis after plaques' disruption was triggered. In contrast, vessels in C group were smooth without plaque or thrombus. Sensitivity of MRI for detecting thrombosis' numbers was 71.4%, and specificity was 100%. The correlation of thrombosis' position ($r=0.91$, $p<0.001$) and length ($r=0.88$, $p=0.001$) were detected by MRI and by histopathology were statistically significant. The correlation of area of lipid core ($r=0.9$, $p<0.001$) and area of plaque ($r=0.85$, $p<0.001$) detected by MRI and by histopathology were both statistically significant. The comparison of components with t test showed that thickness of fibrous cap ($p=0.005$), area of lipid core ($p=0.001$) and area of lipid core/area of plaque ($p<0.001$) were significantly different between rupture group and non-rupture group. In addition, for unvaried ordinal regression analysis, the percentage of lipid core area in plaque area was independently associated with the rupture of plaques (OR: 1.277, 95% CI 1.025 to 1.591; $p=0.03$).

Conclusion MRI can be used to detect atherosclerotic thrombosis, and may be become a useful tool to identify vulnerable plaques.

e0085 RELATIONSHIP BETWEEN THE POLYMORPHISM OF APOLOPROTEIN APO B GENE XBAI ECORI AND THE SERUM LIPIDS IN THE LI NATIONALITY OF HAINA

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Objective To study the apolipoprotein (apo) B gene XbaI and EcoRI polymorphism of the Li nationality in Hainan Island and to evaluate their effects on serum apolipoproteins and lipids.

Methods The study was carried out in a natural population of 351 (151 samples from the Li nationality and 200 samples from the Han nationality) individuals aged between 20 and 84 from Li nationality in Hainan area. The XbaI and EcoRI polymorphisms of apolipoprotein (apo) B gene were analysed using PCR and Restriction Fragment Length Polymorphism (RFLP) methods. The levels of serum apoA, apoB, total cholesterol (TC), triglyceride (TG), HDL cholesterol (HDL-C) were also measured, and LDL cholesterol (LDL-C) was calculated.

Results The frequency of the Li nationality's X^+/X^- genotype subgroups was 0.119. The frequency of the Li nationality's X^+ allele was 0.059, which was higher than the Han nationality control group ($p<0.05$). The frequency of the Li nationality's E^-/E^- genotype subgroups was 0.086. The frequency of the Li nationality's E^- allele was 0.043, which was no difference compared to the Han nationality ($p<0.05$). The levels of TC, LDL-C in the Han nationality were higher than those in the Li nationality, but the levels of HDL-C in the Li nationality were higher than those in the Han nationality. There was no difference about the levels of apoB, apoA and TG between the two groups. The levels of LDL-C in the Li nationality's X^+/X^- genotype subgroups were higher than the same group of X^-/X^- genotype subgroups ($p<0.05$), but levels of HDL-C were lower than the X^-/X^- genotype subgroups ($p<0.05$). Also there were no difference in the levels of TG, TC, LDL-C, HDL-C, apoB and apoA in the Li nationality between the E^-/E^- genotype subgroups and the E^+/E^- genotype subgroups ($p<0.05$).

Conclusions The XbaI genotypes and alleles' frequency distribution between Li nationality and Han nationality have significant differences but the EcoRI genotypes and alleles' frequency distribution between Li nationality and Han nationality have no statistical significance ($p>0.05$). Different genotypes of EcoRI and XbaI have different effects on serum apolipoproteins and lipids. The levels of LDL-C of the genotype subgroups which contains X^+ allele was

higher than the genotype subgroups which does not contain the X^+ allele. The X^+ allele can affect lipid levels, but the E^- allele can not affect lipid levels.

e0086 SINOAORTIC DENERVATION DISRUPTED THE CIRCADIAN RHYTHM OF THE OSCILLATION OF MOLECULAR CLOCK AND ACTIVITY OF RAS IN CARDIOVASCULAR

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Objective To observe the profile of blood pressure in sinoaortic denervated (SAD) rats and investigate the expression of clock genes *per2*, *BMAL1*, clock output gene *DBP*, *AT1* and *PCNA* in heart and thoracic aortic of SD and SAD rats, therefore to probe into the influences of the impairment of arterial baroreflex (ABR) on molecular clock and the activity of RAS in peripheral cardiovascular and their interaction.

Methods 72 male Sprague-Dawley rats underwent SAD or sham operation at the age of 12 weeks. 24-h BP and BPV were measured in conscious and unrestrained rats 4 weeks after operation. Rats were housed in a 12 h light/12 h dark cycle (LD12:12) for at least 10 days. Heart and thoracic aorta were taken every 4 h throughout the day to investigate mRNA expression of clock genes (*per2*, *BMAL1*), clock output gene *DBP*, *AT1* receptors and *PCNA* by RT-real time PCR and examine the abundance of *Per2* protein in heart and vessel tissue by Western Blotting respectively.

Results Compared with sham-operated rats, SBPV and DBPV over 24 h of SAD rats were enlarged ($p<0.01$). Clock genes (*Per2* and *BMAL1*), clock output gene *DBP*, *AT1* receptors and *PCNA* oscillated synchronously both in heart and vascular of SAD and sham-operated rats under light-dark cycle. After sinoaortic denervation, the total mRNA abundance of *Per2* decreased significantly both in heart and aorta ($p<0.05$ or $p<0.01$). *BMAL1*, *DBP*, *AT1* and *PCNA* in heart were up-regulated significantly ($p<0.05$ or $p<0.01$), while that of these genes in aortic remained unchanged. More importantly, after operation, the circadian rhythm of mRNA expression of all the above genes both in heart and aortic changed significantly, showing an abnormal expression level of these genes by a rough normal diurnal and nocturnal pattern in heart, or by diurnal oscillation patterns in aorta. Consistent with *Per2* mRNA expression, its protein abundance in heart and aortic decreased simultaneously, and the circadian rhythm was also disturbed. Moreover, all the amplitude of the mentioned genes were significantly weakened or enlarged in SAD rats.

Conclusions The impairment of arterial baroreflex leads to the abnormality in the circadian rhythm of the molecular clocks and the RAS activity was mediated by *AT1* in peripheral cardiovascular. The abnormality of the total RAS activity, circadian rhythm of RAS activity in peripheral tissues, disorders of molecular clock as well as the abnormality of RAS activity may all contribute to the upset of molecular clock in peripheral cardiovascular following sinoaortic denervation. Therefore these abnormalities promote dysfunction of BP regulation and proliferation and remodelling of cardiovascular in SAD rats.

e0087 APPLICATION OF SERUM PROTEIN FINGERPRINT IN DIAGNOSIS OF CORONARY ARTERY DISEASE

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Objective Coronary artery disease (CAD) has emerged as the dominant etiologic factor in patients with heart failure. The