hypertension, with conflicting results. Kazakans of the pasturing area in Xinjiang, China, have higher prevalence of hypertension and mean blood pressure than other populations of Xinjiang. But up to now no study in this population. To investigate the relationship between the G (+252)A polymarphism of ADRB2 gene and essential hypertension in Kazaks of Xinjiang.
Method A total of 276 patients with confirmed hypertensives and 157 healthy control were genotyped for the G (+252)A by PCR restriction fragment length polymorphism (PCR-RFLP) analysis.
Result Compared with control group, there was no significant difference in the distribution of genotypes and allele frequency of G (+252) A polymorphisms in EH group ($p>0.05$). In addition, age, body mass index, systolic blood pressure and diastolic blood pressure had no significant difference in the groups classified according to genotypes ($p>0.05$).
Conclusion G (+252)A polymorphism of β2-AR gene was not related with essential hypertension in Kazaks of XinJiang.

e0163 THE ASSOCIATION OF FURIN GENE CODING POLYMORPHISM WITH ESSENTIAL HYPERTENSION IN KAZAKAN OF XINJIANG

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Introduction The proprotein processing enzyme furin is involved in many blood pressure-regulating factors. In the Golgi, furin appears to activate ENaC. Thus the gene of furin (FUR) may be a candidate gene of hypertension. We investigate the relationship between Furin gene polymorphism and hypertension in Xinjiang Kazakans.
Methods 924 Kazakans was selected randomly from the pasturing area aged in Xinjiang (422 hypertensives, 502 normotensive controls). We sequenced the coding regions of FUR in 94 hypertensive individuals to identify genetic variations of FUR. Genotyping by the TaqMan-PCR method was performed for common SNPs. The possible relationship between the polymorphism and hypertension of Kazakan was analysed.
Results 1. Direct sequencing from 94 hypertension subjects identified 6 SNPs in the Furin gene promoter. 2. The genotypes and allele frequencies of −229C→T, 12690G→C polymorphisms are not significant between these two groups. 3. There was no significance of blood pressure among the three genotypes of −229C→T, 12690G→C polymorphism. In multiple logistic analyses, the genotypes of the −229C>T were excluded as independent variables. None of haplotypes composed of −229C→T and 12690G→C was significantly different in EH and controls.
Conclusion The Furin gene −229C→T, 12690G→C polymorphism might not be associated with essential hypertension in Kazakans.

e0164 DYSREGULATION OF MIR-1 AFTER LEFT VENTRICULAR HYPERTROPHY REVEALS A ROLE OF MIR-1 IN VENTRICULAR ARRHYTHMIA OCCURRED IN THE HYPERTENSIVE HEART

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Clinical studies have shown that the rate of VA in hypertensive patients with LVH was several times higher than the normaltensive ones. Currently the mechanism of VA due to LVH is not yet fully clarified. Growing evidences indicate that microRNAs (miRNAs or miRs) are regulators of gene expression, which are becoming increasingly recognised as important regulators of heart function and diseases. Here we observed that miR-1 was striking because of its more than (2.08±0.21) fold increased in the spontaneously hypertensive rat model (SHRs) with LVH. miR-1 overexpression slowed conduction and depolarised the cytoplasmic membrane by post-transcriptionally repressing Kir2.1 and connexin 43(Cx43), and this likely accounts at least in part for its arrhythmogenic potential. Then we confirmed that in vivo suppression of miR-1 in SHRs could upgrade Cx43 and Kir2.1 protein level. Our data show that miR-1 is a key regulator of cardiac hypertrophy formation and VA due to LVH, suggesting its attractive therapeutic application in ventricular arrhythmia occurred in the hypertensive heart.

e0165 GENETIC VARIATION OF NEDD4L IS ASSOCIATED WITH ESSENTIAL HYPERTENSION IN FEMALE KAZAKH GENERAL POPULATION

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Introduction NEDD4L is a candidate gene for hypertension on both functional and genetic grounds. The study is to investigate the relationships between the variation of NEDD4L and essential hypertension (EH) in Kazakh in China.
Methods We screened the promoter and exons of NEDD4L in 94 Kazakh hypertensive individuals to identify representative variations. Then the representative variations were genotyped in a Kazakh general population, a case-control study was conducted.
Results We did not identify any functional mutations in functional regions of NEDD4L. Three representative variations (296921-296923delTTG, rs2288774, rs2288775) were successfully genotyped in Kazakh population. The distribution of the dominant model (AA vs AG+GG) of rs2288775, the additive model and recessive model (II+ID vs DD) of 296921-296923delTTG differed significantly between case and control in female ($p=0.040$, $p=0.024$ and $p=0.007$ respectively). Logistic regression analysis showed that rs2288775 and 296921-296923delTTG were significantly associated with hypertension (rs2288775: OR=1.479, 95% CI 1.011 to 2.064, $p=0.044$; 296921-296923delTTG: OR=1.908, 95% CI 1.020 to 3.568, $p=0.043$) in female. The frequency of D-C-G haplotype was significantly higher for case than for control in female ($p=0.020$).
Conclusions The genetic variations of NEDD4L may be associated with EH in female Kazakh.

e0166 VARIATION OF ADRB2 IS ASSOCIATED WITH COMMON RISK FACTORS FOR CARDIOVASCULAR

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Introduction Hypertension, overweight/obesity and dyslipidemia are common risk factors for cardiovascular disease. β2-adrenergic receptor (ADRB2) regulates blood pressure, lipid mobilisation, and energy expenditure.
Methods A cross-sectional study was conducted in Kazakh of Xinjiang (169 males, 238 females) aged 30 to 60 years. The widely studied polymorphisms A46G, C79G, C491T and A523C in ADRB2 gene were selected to be genotyped by PCR-RFLP.

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Results 3 polymorphisms (A46G, C79G and A523C) and a mutation (C491T) of ADRB2 were found. Genotype distributions of A523C in control and hypertriglyceridemia, control and hypo-HDL-c individuals were different ($p<0.05$). Logistic regression analysis showed that the OR for hypertension was 2.894 in C523C group against the A523A+A523C group ($p=0.009$); compared the A523A+A523C group, the OR for hypertriglyceridemia in C523C group were 2.666 ($p=0.031$). The frequency of C491T was 1.2% (n=5) and no TT genotype was found. That C491T was found only in hypertensive or dyslipidemia group. All five subjects were diagnosis with hypertension and dyslipidemia. Four out of five individuals with C491T had Hyper-LDL-C. The mean blood pressure and serum LDL-C of the five subjects were much higher than normal value.
Conclusions Variation of ADRB2 may play a causal role in the pathogenesis of the hypertension and dyslipidemia in Xinjiang Kazakans.

e0167 THE RELATIONSHIP STUDY BETWEEN T663A POLYMORPHISM OF αENAC GENE WITH ESSENTIAL HYPERTENSION AND SERUM ELECTROLYTES IN XINJIANG KAZAKHS

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Introduction To study the relationship between the T663A polymorphism in αENaC gene with essential hypertension (EH) and serum electrolytes of Xinjiang Kazakhs.
Methods 516 Xinjiang Kazakhs aged elder than 30 years were recruited in this population based on case-control study from the patural area of Xinjiang, and were divided into hypertensives (EH group) and normotensives (NT group). The gene polymorphism of T663A by PCR-RFLP and the serum electrolytes were examined.
Results The frequencies of AA, AG, GG genotypes were 15.7%, 50.2%, 34.1% and the frequencies of alleles A, G were 40.8%, 59.2%, respectively. The frequencies of AA, AG, GG were 16.3%, 49.1%, 34.6% in EH group and 15.1%, 51.4%, 33.5% in NT group, respectively. The distribution of genotypic and allelic frequencies were not different between EH group and NT group ($p=0.85$; $p=1.0$). No significant difference in levels of blood pressure and K^+, Na^+/K^+ between subjects among genotypes. The T663A polymorphism were excluded as independent variables controlling age and BMI. But the serum Na^+ of the subjects with AA genotype was higher than those subjects with AG and GG genotypes ($p=0.032$).
Conclusions T663A polymorphism might not be associated with EH but the AA genotype of T663A polymorphisms might be associated with the higher level of the serum Na^+ of Xinjiang Kazakhs.

e0168 THE RELATIONSHIP STUDY BETWEEN T3593C POLYMORPHISM OF αENAC GENE WITH ESSENTIAL HYPERTENSION AND SERUM ELECTROLYTES IN XINJIANG KAZAKHS

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Introduction To study the relationship between T3593C polymorphism in the α subunit gene of epithelial sodium channel (ENaC) with essential hypertension (EH) and serum electrolytes of Xinjiang Kazakhs.
Methods More than 500 Xinjiang Kazakhs aged more than 30 years were recruited by cluster sampling from the pasture area of Xinjiang and were divided into hypertensives (EH group) and normotensives (NT group). The genotypes of T3593C were determined by PCR-RFLP method and the serum electrolytes were measured.
Results The frequencies of TT, TC, CC genotypes were 88.39%, 10.63%, 0.98% and the alleles frequencies of T, C were 93.7%, 6.3%, respectively. The distributed genotypic frequencies of TT, TC, CC were 89.33%, 9.88%, 0.79% in EH group and 87.45%, 11.37%, 1.18% in NT group, respectively. The genotypic and allelic frequencies were not different between EH group and NT group ($p=0.78$; $p=0.46$). There was no significant difference in levels of blood pressure and serum electrolytes between subjects with the TT and TC+CC genotypes ($p>0.05$). The T3593C polymorphism were excluded as independent variables which related to the blood pressure and serum electrolytes of subjects controlling FPR age and gender by multiple logistic analysis.
Conclusions The T3593C polymorphism might not be associated with EH and serum electrolytes of Xinjiang Kazakhs.

e0169 IN VITRO EFFECTS OF LOW MOLECULAR WEIGHT HEPARIN ON CLOT RATE

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Objective This study was designed to determine the in vitro effects of different doses and different kinds of Low Molecular Weight Heparin (LMWH) on clot rate (CR), and to determine whether the CR can be used to monitor LMWH.
Methods This study was performed in two phases in vitro. The first, CR was measured with different reagent (glass beads, celite and kaolin) on volunteer (n=20) blood samples spiked with increasing concentrations of LMWH (dalteparin, 0.2–1.8 IU/ml). The second, CR were measured with the same reagent (glass beads) on volunteer (n=20) blood samples spiked with the same concentrations (0.8 IU/ml) of different LMWH (dalteparin, enoxaparin and nadroparin). Regression analysis was performed to establish a regression equation from corresponding anti-Xa LMWH levels.
Results With the increase in doses of dalteparin, CR values were reduced gradually and an exponential relationship was observed between the CR values and dalteparin concentrations ($p<0.01$) for all three reagents. With the same concentrations (0.8 IU/ml) of LMWH, dalteparin showed a more effect on CR (dalteparin 7.4 IU/min vs enoxaparin 8.5 IU/min, nadroparin 8.5 IU/min, $p<0.05$). Compare with the baseline (17.6 IU/min), all three kinds of LMWH induced a significant change in the CR ($p<0.01$).
Conclusions The in vitro studies have shown that, there was an exponential relationship between the CR and dalteparin concentrations for all three reagents. All three kinds of LMWH could significantly reduce the value of CR. CR test may be a suitable method for monitoring the anticoagulant effect of LMWH.

e0170 THE SENSITIVITY OF DIFFERENT REAGENTS FOR LABORATORY MONITORING OF LOW MOLECULAR WEIGHT HEPARIN: AN IN VITRO STUDY

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Objective Because of the lack of Point-of-care testing, the use of low-molecular-weight heparin (LMWH)therapy in some special

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