significance for the prevention and treatment of cardiovascular and cerebrovascular disease. Inwardly rectifying subfamily J, member5 (KCNJ5) gene has become an important candidate gene in PA research. Meanwhile, the KCNJ5 gene expression have been implicated in the development of obesity and appears to be a key feature of metabolic syndrome (MetS).However, the relationship between the genetic variation of KCNJ5 gene and lipid metabolism is complex and still remains poorly understood. Aim of our study was to assess whether KCNJ5 gene polymorphisms are associated with dyslipidemia among patients with PA.

METHODS Patients hospitalized at the Center for Hypertension of the People's Hospital of Xinjiang Uygur Autonomous Region were selected from January2010 to December 2011. A total of 494 subjects who diagnosed with primary aldosteronism were recruited base on a history and laboratory tests. 338of whom (68.4%) were diagnosed with dyslipidemia, and 156 individuals were confirmed without dyslipidemia (31.6%).The polymorphisms of rs2604204, rs3740835, rs4937391, rs6590357, rs11221497, rs138295501 among the patients with primary aldosteronism (PA) were genotyped by Taqman polymerase chain reaction (PCR), Blood samples were collected from all subjects and genotyping was performed on DNA extracted from blood cells. Lipid levels were measured by conventional methods and were analyzed.

RESULTS When all dyslipidemia cases were compared against non-dyslipidemia controls, we found that the rs3740835 variant was associated with dyslipidemia in the PA population (P=0.023). Also, the frequencies of AA haplotype of rs3740835 significantly increase prevalence of dyslipidemia compared with (AC+CC) genotype.

CONCLUSIONS Our study demonstrates the polymorphisms of rs3740835 of KCNJ5 gene may play a role in the development of lipid metabolism abnormality in patients with PA.

GW26-e0113

Interactions of several single nucleotide polymorphisms and alcohol consumption on blood pressure levels

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OBJECTIVES Hypertension is a complex trait that is considered to result from an interaction between an individual's genetic background and various environmental factors. Both single nucleotide polymorphisms (SNPs) and alcohol consumption modulate blood pressure levels, but the interactions of SNPs and alcohol consumption on blood pressure levels are limited. This study aimed to detect the interactions of ten SNPs and alcohol consumption on blood pressure levels in the Bai Ku Yao population, an isolated and conservative subgroup of the Yao minority in China.

METHODS A total of 1224 unrelated participants of Bai Ku Yao were recruited by a stratified randomized sampling. There were 616 non-drinkers (male/female, 414/202) and 608 drinkers (414/196). Two groups were matched for age, sex, and area of residence. Information on demographic characteristics, socioeconomic status, lifestyle factors, personal and family history of disease, medical and medication history, and physical activity was obtained with standardized questionnaires. Genotyping of the ATP-binding cassette transporter A1 rs2066715, acyl-CoA:cholesterol acyltransferase-1 rs1044925, low-density lipoprotein receptor rs5925, hepatic lipase gene rs2070895, endothelial lipase gene rs2000813, methylenetetrahydrofolate reductase rs1801133, the E3 ubiquitin ligase myosin regulatory light chain-interacting protein rs3757354, proprotein convertase subtilisin-like kexin type 9 rs505151, peroxisome proliferator-activated receptor delta rs2016520, and Scavenger receptor class B type 1 rs5888 was performed by polymerse chain reaction and restriction fragment length polymorphism combined with gel electrophoresis, and then confirmed by direct sequencing. The association of genotypes and blood pressure levels was tested by analysis of covariance, and the interactions of the SNPs and alcohol consumption on blood pressure levels were detected by using a factorial regression analysis after controlling for potential confounders. A P value of $\leq$ 0.005 was considered statistically significant after Bonferroni correction.

RESULTS The genotypic frequencies of rs5925, rs2070895, rs1801133 and rs3757354 were significantly different between nondrinkers and drinkers. The levels of systolic (rs2066715 and rs2070895), diastolic (rs2070895) and pulse pressure (rs2066715, rs1044925 and rs1801133) in nondrinkers, and systolic (rs1044925 and rs5888), diastolic (rs1044925 and rs2000813) and pulse pressure (rs505151 and rs5888) in drinkers were different among the genotypes (P < 0.005-0.001). The interactions of genotypes and alcohol consumption on systolic (rs2066715, rs1044925, rs5925, rs2070895, rs1801133, rs3757354, rs2016520, and rs5888), diastolic (rs2066715, rs1044925, rs5925, rs2000813, rs3757354 and rs2016520) and pulse pressure (rs1044925, rs2070895, rs1801133, rs3757354 and rs505151) were observed (P < 0.005-0.001).

CONCLUSIONS The differences in blood pressure levels between the nondrinkers and drinkers might be partially result from the different interactions of these SNPs and alcohol consumption. The observed associations and interactions between these SNPs and blood pressure variation in this isolated ethnic subgroup may also be the major characteristics of this condition in the other ethnic groups, especially in the Chinese minorities.

GW26-e1253

Apelin and APLN single nucleotide polymorphisms and combined hypertension and central retinal artery stenosis in a Chinese population

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OBJECTIVES Apelin activity plays a role in regulating blood pressure. This study explored the relationship between single nucleotide polymorphisms (SNPs) in the Apelin gene (APLN) with hypertension and hypertension with central retinal artery equivalent (CRAE) stenosis in a coastal Chinese population.

METHODS All subjects answered an epidemiological survey for demographic and disease characteristics. Apelin levels were determined and three APLN SNPs, rs56204867, rs3115757, and rs3761581, were evaluated. CRAE was measured using fundus photography.

RESULTS Apelin levels were significantly lower in subjects with hypertension and hypertension with CRAE stenosis (0.23 $\pm$ 0.10 ng/ml and 0.21 $\pm$ 0.08 ng/ml, respectively) compared with control subjects (0.25 $\pm$ 0.11 ng/ml; P< 0.001). Linear regression analysis showed hypertension and hypertension with CRAE stenosis was associated with age, being male, systolic blood pressure, abnormal blood lipids, and Apelin levels. Genetic analysis indicated that in both males and females SNP rs3761581 was associated with hypertension and that more males carrying rs56204867 and rs3761581 T-A haplotype had hypertension (61.88%) and hypertension with CRAE stenosis (56.82%) than control males (39.33%).

CONCLUSIONS In this Chinese population, Apelin and APLN SNP rs3761581 was associated with combined hypertension with CRAE, indicating that the expression of APLN gene products may be involved in vascular injury.

GW26-e1527

Value of neutrophils count in predicting surgery related acute kidney injury in CKD with hypertensive patients: a cohort study

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OBJECTIVES As a component of routine blood cell, the presences of neutrophils (polymorph nuclear leukocyte, PMN) have been proved to a predictor of morbidity and mortality in several clinical settings. However, it is not known whether episodes of acute kidney disease (AKI) associate with a higher neutrophils in vulnerable groups, such as CKD with hypertensive patients. To address this gap in knowledge, this study investigates whether surgery related AKI in CKD patients is associated with neutrophils.

METHODS The counts of neutrophils were measured in 998 patients admitted to the third Xiangya Hospital from October 2008 through February 2013. We divided patients into quintiles according to the counts of WBC or subtypes.

RESULTS We divided patients into quintiles according to the counts of WBC or subtypes. After adjustment for multiple covariates, the 4th quintiles of neutrophil counts had greater ORs for AKI (2.44, 95%CI 1.37-4.33) compared with the 1st quintile. Incident of AKI increased 1.30 fold for every $3*10^9$/L increase in the admission neutrophil counts.

CONCLUSIONS The count of neutrophils, as an easy and quick measurable index, is an independent predictor of AKI in CKD with hypertensive patients.