GW26-e1471
Effect of homocysteine on the cultured rat vascular smooth muscle cell phenotype transformation
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OBJECTIVES To verify whether homocysteine (Hcy) could induce the dedifferentiation of vascular smooth muscle cells (VSMCs).
METHODS The primary culture and identification of rat VSMCs was conducted, using VSMCs in passage-4 for the following experiments. The VSMCs were divided into 4 groups: control group, Hcy (100 umol/L) modulation group, Hcy (500 umol/L) modulation group, Hcy (1000 umol/L) modulation group. MTT were used to investigate the proliferation of VSMCs. Transwell chambers and wound healing were employed to test the migratory ability of VSMCs. ICC were used to detect the VSMCs’ morphology structure. Western blotting used to investigate the expressions of SM-actin, SM-MHC, Calponin, OPN in VSMCs of every group.
RESULTS Compared with control group, the proliferation and migration ability of VSMCs were significantly increased in the Hcy modulation group, P<0.01. The expression of SM-actin had no significant difference between each group. The expression of SM-MCH and Calponin increased and OPN decreased in the Hcy group compared with control group, P<0.01. This effect of Hcy were positively correlated with its concentrations.
CONCLUSIONS Hcy could induce the dedifferentiation of VSMCs, this maybe the mechanism by which Hcy increased the proliferation and migration ability of VSMCs.

GW26-e2181
Association of LPA genetic polymorphisms with coronary artery disease in the Xinjiang Han and Uygur population of China
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OBJECTIVES Lipoprotein (a) (Lp(a)) is well known as an independent risk factor for coronary artery disease (CAD) and primarily determined by variation in the LPA gene coding for the apolipoprotein (a) moiety of lipoprotein (a). Our study was purposed to evaluate the association between the human LPA gene polymorphisms and CAD in Xinjiang Han and Uygur population of China.
METHODS 831 Han people (392 CAD patients and 439 control subjects) and 828 Uygur people (312 CAD patients and 317 control subjects) were selected for the present case-control study. Both patients and participants were genotyped for the same three single nucleotide polymorphisms (SNPs) (rs1801693, rs6913877 and rs9363559) of LPA gene by a Real-time PCR instrument.
RESULTS The rs1801693, rs6913877, and rs9363559 polymorphisms were found to be associated with CAD in Han population. For male, the distribution of SNPs (rs1801693) in genotypes, alleles and the recessive model (CC vs CT+TT) showed a significant difference (all P<0.05), the significant difference in the recessive models (CC vs CT+TT) was retained after adjustment for covariates just for the male (OR:0.552, 95% confidence interval [CI]:0.351-0.886, P<0.01). For total, the distribution of SNP2 (rs6923877) in genotypes and the dominant model (GG vs AG +AA) showed a significant difference (both P<0.05), the significant difference in the dominant models (GG vs AG +AA) was retained after adjustment for covariates (OR:1.473, 95% confidence interval [CI]:1.002-2.152, P=0.049). For female, the distribution of SNP3 (rs9364559) in the alleles, the dominant model (AA vs AG +GG) and retained after adjustment for covariates also showed the significant difference(for the alleles: P=0.021,for the dominant model: P=0.045, adjustment for covariates: OR:0.576, 95% confidence interval [CI]:0.350-0.898, P=0.016).
CONCLUSIONS Polymorphisms rs1801693, rs6923877 and rs9364559 of LPA gene are associated with CAD in Han population of China.

GW26-e2197
Ethnic disparities in recommended anthropometric cut-off values to identify the clustering of cardiovascular risk factors effectively in ostensibly healthy Chinese population in Xinjiang
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OBJECTIVES To investigate validity of widely recommended anthropometric cut-off points in screening for the clustering of cardiovascular risk factors in Chinese population of different ethnic.
METHODS 13090 participants (Uygur, Han and Kazakh, respectively) without hospital admission for cardiovascular disease were selected from the Cardiovascular Risk Survey (CRS). Sensitivity, specificity of body mass index (BMI;<30), waist circumference (WC;<88 cm ),waist-hip ratio (WHR;<0.85), and waist-height ratio (WHRH;<0.50) cut-off points for the clustering of cardiovascular risk factors (dyslipidemias, hypertension and hyperglycemia) were calculated for each ethnic. Cut-off points yielding high sensitivity together with modest specificity were considered valid.
RESULTS The sensitivity of WC ≥88 cm for one or more risk factors was 57% in Han participants, and 81%, 83% in Uygur and Kazakh participants. The specificity of WC ≥88 cm for one or more risk factors was 72%, 53% and 49% at the three ethnic (Han, Uygur and Kazakh, p<0.05). WC ≥88 cm yielded ≥80% sensitivity for two or more risk factors across all ethnic. For WHR, specificity decreased in Uygur and Kazakh participants compared with Han participants (p<0.0001), being 33% and 35%. BMI, WHR and WHRH cut-off points were not better than WC.
CONCLUSIONS Validity of recommended anthropometric cut-off points in screening asymptomatic population varies with ethnic. In Han population, WC ≥88 cm yielded high sensitivity and modest specificity for two or two more risk factors, however, sensitivity for one or more risk factor was less than optimal. Our results support ethnic-specific screening cut-off points for Chinese population.

GW26-e2203
Haplotype-Based Case-Control Study of the Human CYP4F2 Gene and Essential Hypertension in the Chinese Han population
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OBJECTIVES CYP4F2 is responsible for metabolizing arachidonic acid to 20-hydroxyeicosatetraenoic acid (20-HETE), which plays a crucial part in the regulation of blood pressure in humans. The aim of the present study was to assess the association between the human CYP4F2 gene polymorphism and essential hypertension (EH) in the western Chinese Han population.
METHODS Four CYP4F2 SNPs were genotyped (rs1558193, rs3093166, rs3093194, rs2108622) by the TaqMan® SNP Genotyping Assay in Real-Time PCR system. We examined the association between the four SNPs and EH using a haplotype-based case-control study that involved 405 EH patients and 396 control subjects.
RESULTS For men, the distribution of SNP1 (rs1558193) alleles and the dominant model (CC vs CT+TT)showed a significant difference between EH and control participants (for allele: P=0.029; for dominant model: P=0.009). The significant difference in dominant model was retained after adjustment for covariates (OR:1.505, P<0.05). The significant difference in dominant model was retained after adjustment for covariates (OR:1.505, P<0.03). For men, the frequency of the C-A-G-T haplotype was significantly higher for EH patients than for control subjects (P=0.039).
CONCLUSIONS The CC genotype of rs1558193 in CYP4F2 gene and the C-A-G-T haplotype could be a risk genetic marker of EH in the male Chinese Han population.

GW26-e2336
Association between the NFKB1-94ATTG ins/del polymorphism (rs28362491) and coronary artery disease: A meta-analysis
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OBJECTIVES It has been reported that single nucleotide polymorphisms (SNPs) rs28362491 in NFKB1-94ATTG ins/del might be associated with the susceptibility to coronary artery disease (CAD). Owing to mixed and inconclusive results, we conducted a meta-analysis to systematically summarize and clarify the association between the SNPs and CAD risk.