(The lesion severity of any coronary artery which was over 50% are diagnosed coronary heart disease), a non-CHD group (n=38), single vessel disease group (n=31), multiple vessel disease group (n=86).

We analysed the association between plasma TMAO, Choline, Betaine, Carnitine, Buytrobetaine and the severity or extent of coronary artery stenosis. TMAO, choline, betaine, carnitine and buytrobetaine were given the correlation analysis and the gensini scores analysis. We still use the binary classification of stepwise logistic regression analysis methods to analyze Vascular risk factors for coronary heart disease (CHD).

RESULTS The differences of TMAO between a normal group, mild stenosis group, moderate stenosis group and severe stenosis group were statistically significant (P<0.05).Each two groups were compared, the level of TMAO in moderate stenosis group and severe stenosis group are higher than normal group and mild stenosis group [2.77 (1.49,9.74) vs 8.37(5.4,16.61), 2.77(1.49,9.74) vs 8.36 (4.85,16.78), 4.66(3.1,6.25) vs 8.37(5.4,16.61), 4.66(3.1,6.25) vs 8.36 (4.85,16.78), P<0.0083]. The differences of TMAO between a non-CHD group, single disease group, multiple vessel disease group were statistically significant (P<0.05); Each two groups were compared, the level of TMAO in single vessel disease group and multiple vessel disease group are higher than a non-CHD group [4.37(2.34,6.85) vs 8.37(5.04,25.38), 4.37(2.34,6.85) vs 8.36(4.89,13.88), P<0.016]. There was no significant difference between Choline, Betaine, Carnitine, Buytrobetaine and the severity or extent of coronary artery stenosis.

Spearman correlation analysis showed that the TMAO was significantly positively correlated with Gensini cores (r=0.244, P=0.002). Choline, Betaine, Carnitine and Buytrobetaine are uncorrelated with Gensini cores.

We put the cardiovascular risk factors for binary logistic regression analysis, The severity of coronary artery lesions of patients positively correlated to the level of TMAO(OR 1.221,95%CI 1.078-1.382,P<0.05),diabetes(OR 2.856,95%CI 1.04-7.846,P<0.05) and negatively correlated to the level of APO-A1(OR 0.061,95%CI 0.008-0.49,P<0.05).

CONCLUSIONS Our findings show that the TMAO level is associated with the severity or extent of coronary artery stenosis assessed by coronary angiography,suggesting that plasma TMAO level may reflect plaque progression.

TMAO is the independent risk factors for coronary artery atherosclerosis disease,there is significant correlation between different levels of TMAO and coronary atherosclerosis disease.

GW28-e0971

Serum fibroblast growth factor 21 and new-onset metabolic syndrome

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OBJECTIVES Fibroblast growth factor 21 (FGF21) is a crucial metabolic regulator with multiple favorable effects on glucose homeostasis and lipid metabolism. Since serum FGF21 level has been implicated as a potential marker for the early identification of metabolic syndrome (MetS), we investigated the association between serum FGF21 level and the development of MetS in a population-based prospective study.

METHODS We conducted a prospective study of 221 randomly sampled adults without MetS from a general population-based cohort study who were examined from 2005-2008 (baseline) and also from 2008-2011 (follow-up). Baseline serum FGF21 levels were analyzed using enzyme-linked immunosorbent assay.

RESULTS During the average 2.8-year follow-up period, 82 participants (36.6%) developed new-onset MetS. Serum FGF21 levels were significantly higher in patients with new-onset MetS compared to those without MetS (209.56 ± 226.80 vs. 110.09 ± 81.10, $p<0.001$). Multivariate adjusted models showed the odds for MetS development were more likely in patients with serum FGF21 levels in the highest quartile compared to those in the lowest quartile (3.84, 95% confidence interval: 1.59-9.28).

CONCLUSIONS Serum FGF21 level was an independent predictor for new-onset MetS in a population-based prospective study.

DIABETES

GW28-e0919

Associations between aldehyde dehydrogenase 2 (ALDH2) rs671 genetic polymorphisms, lifestyles and diabetes risk in Chinese Han people

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OBJECTIVES Diabetes is a multiple factor disease which was influenced by gene, environment, and lifestyle. Several studies confirmed that the aldehyde dehydrogenase 2 (ALDH2) rs671 polymorphism is associated with diabetes. However, the evidence remains inconclusive. Whether lifestyle affects the development of diabetes in different genotype groups have not been clarified, either. We sought to identify associations between ALDH2 rs671 polymorphism, lifestyles, and diabetes in Chinese Han people.

METHODS The subjects were adult Chinese Han people who received heath examination in the period from December 2015 to December 2016. Detection of the ALDH2 r671 polymorphism was determined by polymerase chain reaction. Lifestyle data were collected using self-administered questionnaires. Basic characteristics and fasting venous blood sample were collected at baseline.

RESULTS 3519 subjects were eligible for participation. The frequencies of the ALDH2 rs671 genotype were 67.1% (GG), 30.2%(GL), 2.7%(LL), respectively. ALDH2 rs671 polymorphism was significantly associated with diabetic risk (GG vs. GL+LL: OR=1.33, 95% CI=1.07-1.66, P=0.01). In different groups, the association between lifestyle and diabetic risk were also significant difference. In the homozygous group, smoking and drinking were significantly increased the risk of diabetes rather than in heterozygous group(smoking: OR=1.53, 95% CI:1.31-1.79, P<0.001; drinking: OR=1.62, 95% CI:1.33-1.99, P<0.001). Pickled foods intake was significantly increased the risk of diabetes in homozygous group (OR=1.71, 95% CI: 1.15-2.54,P=0.008). Fried foods intake was significantly decreased the risk of diabetes in heterozygous group(OR=0.45, 95% CI: 0.28-0.70,P=0.001).

CONCLUSIONS Our study suggested that ALDH2 rs671 polymorphism might be able to be used as a predictor for the risk of diabetes in Chinese Han people. Smoking, drinking and pickled foods intake were risk factors for diabetes in the homozygous group, while fried food intake is a protective factor in heterozygous group.

GW28-e1087

Heart failure in diabetic patients: features of clinical hemodynamic parameters

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OBJECTIVES To analysis of clinical and hemodynamic parameters in cohort of patients with T2DM and chronic heart failure (CHF).

METHODS Included 134 patients with CHF of both sexes hospitalized in the cardiology department of Moscow region. All patients were divided into two group: group I (patients with CHF and T2DM, n = 66, 61.8 ± 7.2 years, 28 men, 38 women), and group II (patients with CHF without diabetes, n = 68; 62.3 ± 7.7 years, 33 men, 35 women). The following were performed: assessment of the symptoms of the disease using the Clinical State Assessment Scale (SHOCS); ECG at rest in 12 standard leads; Transthoracic echocardiography; Laboratory blood tests; X-ray of the chest; Test with a 6-minute walk.

RESULTS Patients with CHF and T2DM had a relatively high functional class of HF, a severity of symptoms (according to SHOCS 13.7 ± 2.2 points against 11.1 ± 2.2 points, p <0.05), as well as more pronounced morphofunctional changes: a significant decrease in LVEF by 5.5%, as well as an increase in the time of delay in the blood flow of early diastolic filling, accompanied by a decrease in the E/A ratio. The revealed features of the clinical course were accompanied by impaired biochemical indices. The study of the anamnesis of patients with CHF and diabetes in this cohort allowed to reveal insufficient control (less than 80%) of glycemia among patients with diabetes and