GW23-e2238

DETECTION AND ANALYSIS ON PLASMA METABOLITES DISORDER IN CORONARY HEART DISEASE (UNSTABLE ANGINA PECTORIS) PATIENTS BASED ON NMR METABOLOMICS

doi:10.1136/heartjnl-2012-302920af.8

Qi Shi, Huihui Zhao, Jianxin Chen, Wei Wang, Wei Wang. *Beijing University of Chinese Medicine*

Objectives To discuss the characteristics of plasma metabolites in coronary heart disease (unstable angina pectoris, UAP) patients, and explore the composition and concentration changes of the plasma metabolites. Explain the metabolic rules in vivo, pathogenesis and biological essence of UAP patients in the disease state.

Methods 45 cases of UAP in-patients, aged from 45 to 75, diagnosed and confirmed by coronary angiography, were selected.15 cases of healthy people were selected as the control group. Varian UnityInova 600 M superconducting Fourier (nuclear magnetic resonance, NMR) spectrometer was applied to detect the plasma metabolites. Collect the data with the methods of CPMG and LED. Free induction decay signal was transferred into one dimensional NMR

Results 39 endogenous metabolites had been detected. The micro molecule substances were aerf-glucose, β-glucose, β-hydroxy isobutyric acid, β-hydroxybutyric acid, phenylalanine, alanine, acetone, choline, methionine, dimethylamine, glycine, glutamate methylamine, glutamine, creatine, creatinine, inositol, methylamine, lysine, leucine, tyrosine, hippuric acid, ornithine, taurine, praline, carnitine, lactic acid, tryptophan, threonine, aspartic acid, valine, isoleucine, acetyl glutamic acid, histidine, N acetyl glycoprotein. The macro molecule substances were unsaturated fatty acids, lipid compound, lipid, LDL/VLDL and HDL.

OPLS/O2PLS-DA integral matrix figures results showed: distribution region of UAP patients and healthy people could be

completely separated along the t (1) axis direction. The fitting degree of the modes was well, and there were no special nodes, cross or overlapping nodes.

44 identifiable variables were selected with the VIP value higher than one. These variables have lager contributions to the classification because the locations were far from the origin in the corresponding load and S figures. T test was applied to these variables, and compared with the healthy people, 37 identifiable variables had significant differences. Finally, we obtained 25 characteristic metabolites related to the UAP patients after the integration of the 37 variables. Among these 25 metabolites, β-hydroxy isobutyric acid of the UAP patients was down-regulated while the other 24 were up-regulated compared with the control group.

Cluster analysis results show that the UAP group could be distinguished with the control group base on the 25 characteristic metabolites.

Conclusions Application of metabonomics method can successfully discriminate plasma constituents of UAP patients from healthy people, and find the different metabolites preliminarily. Further studies showed pathogenesis of the UAP may involve the metabolic processes of amino acids, glucose, lipids, energy, coagulation, renal function impairment and