论著

基于磁共振的新疆汉族不同性别健康人群血清和尿液代谢组学差异分析

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摘要： 目的:寻找新疆汉族不同性别人群体液差异性代谢成分。方法:对92例不同性别汉族健康人血清和尿液样本进行研究。血清和尿液样本采用磁共振方法进行测试, 并采用正交偏最小二乘判别分析(OPLS-DA)法进行模式识别分析, 最后以R^2X, R^2Y, Q^2等参数评价和分析结果。结果:男性血清极低密度脂蛋白、低密度脂蛋白、不饱和脂类、肌酸酐和丙酮等代谢物含量比女性高, 而女性血清中柠檬酸、胆碱、葡萄糖及多种氨基酸(包括异亮氨酸、亮氨酸、缬氨酸、丙氨酸、瓜氨酸、赖氨酸、蛋氨酸、谷氨酸、苯丙氨酸、苏氨酸、酪氨酸、1-甲基组氨酸、甘氨酸等)含量高于男性;男性尿液中甲酸、丙二酸、牛磺酸、肌酸酐等代谢物含量比女性高, 而女性尿液中马尿酸、γ-氨基丁酸、琥珀酸盐、柠檬酸和谷氨酸等代谢物含量高于男性。血清分析的模型参数为R^2X=0.64, R^2Y=0.70, Q^2=0.67, 尿液分析的模型参数为R^2X=0.17, R^2Y= 0.70, Q^2=0.44。结论:新疆健康人群血液和尿液中包含了多种与性别有关的代谢成分, 这种差异性代谢产物的发现在临床代谢组学研究中具有积极的意义。

关键词： 代谢组学　健康人群　代谢差异

Gender related metabonomic analysis of serum and urine samples from Xinjiang healthy Han subjects with magnetic resonance

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Abstract: Objective: To investigate gender variability in the metabolic serum and urinary profile of healthy Han population in Xinjiang.
Methods: Serum and urinary samples from 92 healthy Han people in Xinjiang were tested by magnetic resonance based metabonomics and pattern recognition analysis performed with orthogonal partial least-squares discriminant analysis (OPLS-DA). The quality of the model was described by parameter R^2X, R^2Y, and Q^2.
Results: The serum in males had higher levels of very low density lipoprotein, low density lipoprotein, unsaturated lipids, creatinine and acetone than in females, whereas females had higher levels of citrate, choline, glucose and amino acids (including isoleucine, leucine, valine, alanine, citrulline, lysine, methionine, glutamate, phenylalanine, threonine, tyrosine, 1-methyl histidine and glycine) than in males. The urine of males had higher levels of formate, malonic acid, taurine, creatinine than that of females, while females had higher levels of hippurate, γ-aminobutyric acid, succinate, citrate and glutamate than males. The model parameters of serum were R^2X=0.64, R^2Y=0.70, and Q^2=0.67, and those of urine were R^2X=0.17, R^2Y=0.70, and Q^2=0.44.
Conclusion: The blood and urine from Han population in Xinjiang contain a variety of gender related metabolites, which plays an important role in the research of clinical metabonomics.

Keywords: metabonomics　healthy population　metabolic difference

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