METABOLITE PROFILING OF PREITONEAL DILAYSIS EFFLUENT BETWEEN LOW AND HIGH-AVERAGE TRANSPORT PATIENT- A PILOT STUDY

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OBJECTIVES

It is known that outcome of peritoneal dialysis patient is associated with the capacity of solutes and water clearance. However the high molecular weight solutes in peritoneal dialysis effluent (PDF) and their clinical consequences have not been well studied. This study aims to explore the endogenous metabolite remove by peritoneal dialysis, especially under different characteristics of peritoneal membrane transport.

METHODS

A cross-sectional study collected PDF from no-diabetic continuous ambulatory peritoneal dialysis (CAPD) patients underwent fast peritoneal equilibration test (PET) in a single centre from March 2012 to November 2012. Among patients with characteristic of high-average transport (HA) and low-average transport (LA), paired cases were selected, based on the gender, age, PD Kt/V, residual renal function (RRF) and duration of treatment. Ultra-performance liquid chromatography (UPLC) coupled with Q-TOF mass spectrometry were performed to investigated the metabolic profile in the PDF sample. After raw data acquisition and transformation by Agilent Masshunter Qualitative Analysis software, paired t-test and fold change analysis were conducted to screen the feature difference. The different metabolites were defined by Agilent Mass Profiler Pro software finally.

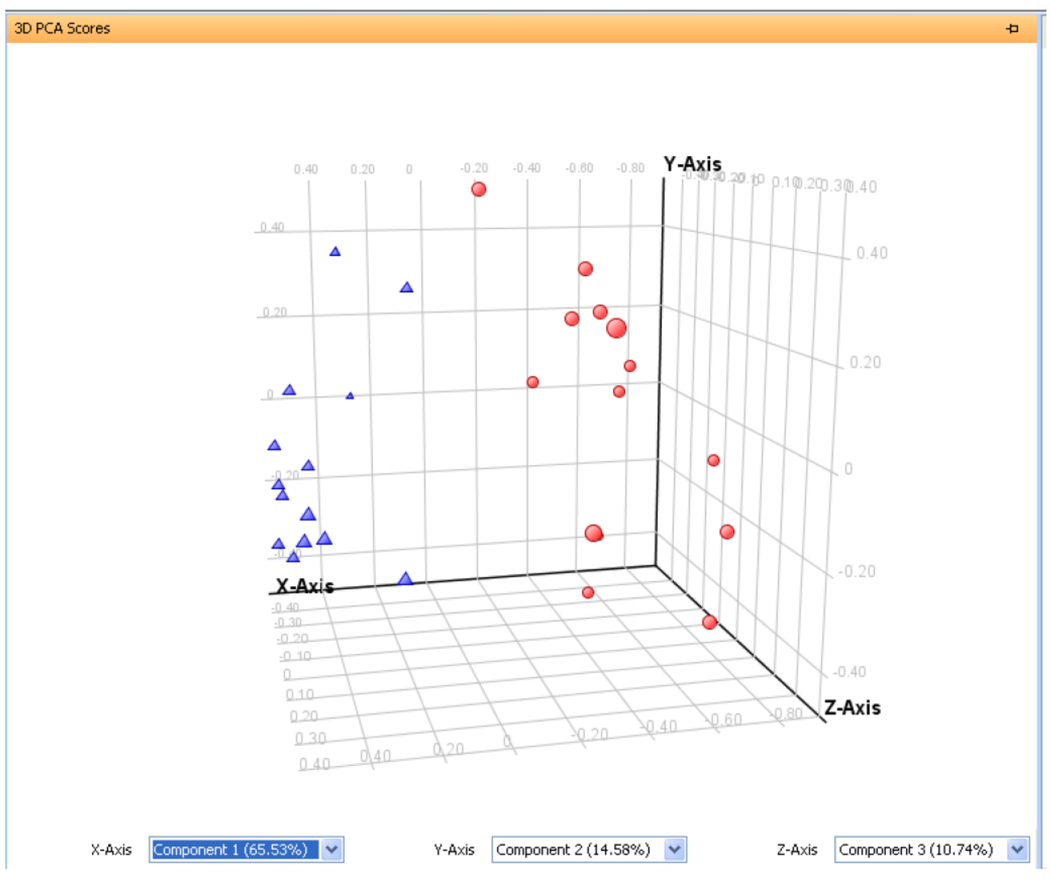
RESULTS

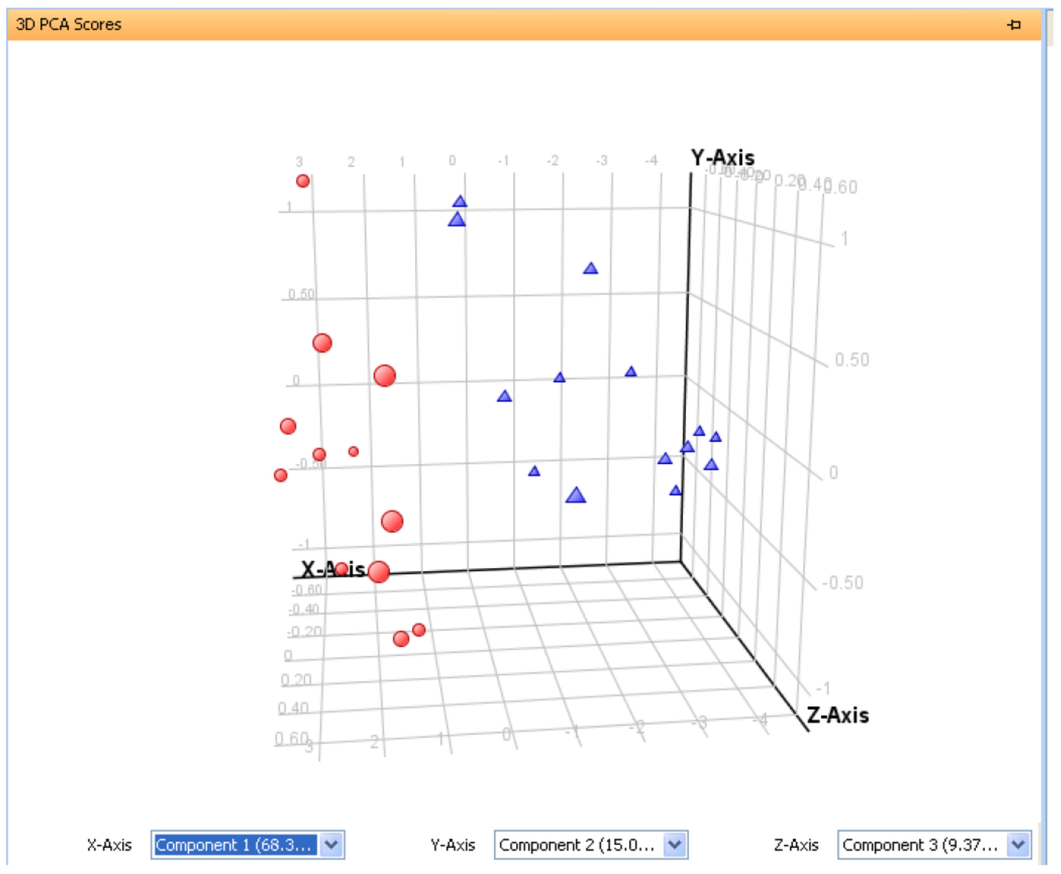
Twenty paired PDF samples from cases (female/male, 8/12; age, 58.4±16.3 years; dialysis duration, 14.3±5.6 months) with feature of HA and LA were defined. The metabolomics analysis indicated that distribution of 14 metabolites from 6 metabolic pathway (energy metabolism, lipid metabolism, carbohydrate metabolism, tricarboxylic acid cycle and amino acids metabolism) between HA and LA group had significant difference ($p<0.05$).

Tab.1 Different Metabolites and involved pathway between HA and LA group

No.	Identification	mass	Formula	Corrected p-value	Related Pathway
1	(Phenylalanine)	165.1691	$C_9H_{11}NO_2$	0.047	amino acids metabolism
2	(Histidine)	155.0695	$C_6H_9N_3O_2$	0.040	amino acids metabolism
3	(Pyruvic acid)	88.0160	$C_3H_4O_3$	0.026	amino acids metabolism
4	(isoleucine)	131.0950	C6H13NO2	0.047	amino acids metabolism
5	(glutaminate)	145.0618	C5H9N2O3	0.043	amino acids metabolism
6	(Tryptophan)	204.2252	$C_{11}H_{12}N_2O_2$ (L-)	0.001	amino acids metabolism
7	(Glycine)	75.0320	$C_2H_5NO_2$	0.047	amino acids metabolism
8	(α-oxoglutarate)	146.0215	$C_5H_6O_5$	0.026	tricarboxylic acid cycle
9	(Taurine)	125.0146	$C_2H_7NO_3S$	0.017	amino acids metabolism
10	(3-hydroxybutyric acid)	104.0470	$C_4H_8O_3$	0.043	lipid metabolism
11	(citrate)	192.0270	$C_6H_8O_7$	0.017	tricarboxylic acid cycle
12	(glucose)	180.1559	$C_6H_{12}O_6$	0.009	carbohydrate metabolism
13	(Acetoacetate)	101.0244	$C_4H_5O_3$	0.015	energy metabolism
14	(phosphorylcholine)	219.0427	$C_5H_{14}ClNO_4P$	0.019	lipid metabolism

Fig.1 3D PCA plots with the scores of principal components between HAblue(HA) and red(LA)





CONCLUSIONS

Current metabonomics results provided new insight into the effect of solutes remove by peritoneal dialysis in clinical outcome.