Exploring metabolic signature of protein energy wasting in hemodialysis patients

ABSTRACT

End-stage renal disease patients undergoing maintenance hemodialysis (HD) are vulnerable to the protein energy wasting (PEW) syndrome. Identification and diagnosis of PEW relies on clinical processes of judgment dependent on fulfilling multiple criteria drawn from serum biochemistry, weight status, predictive muscle mass, dietary energy and protein intakes. Therefore, we sought to explore the biomarkers' signature with plasma metabolites of PEW by using 1H-nuclear magnetic resonance for an untargeted metabolomics approach in the HD population, to understand metabolic alteration of PEW. In this case-controlled study, a total of 53 patients undergoing chronic HD were identified having PEW based on established diagnostic criteria and were age- and sex-matched with non-PEW (n = 53) HD patients. Fasting predialysis plasma samples were analyzed. Partial least square discriminant analysis demonstrated a significant separation between groups for specific metabolic pattern alterations. Further quantitative analysis showed that the level of 3-hydroxybutyrate, acetate, arabinose, maltose, ribose, sucrose and tartrate were significantly increased whilst creatinine was significantly decreased (all $p < 0.05$) in PEW subjects. Pathway analysis indicated that PEW-related metabolites reflected perturbations in fatty acid mechanism and induction of glyoxylate and dicarboxylate pathway attributed to gluconeogenesis. These results provide preliminary data in understanding metabolic alteration of PEW and corresponding abnormal metabolites that could potentially serve as biomarkers of PEW.

Keyword: Protein energy wasting; Hemodialysis; Metabolomics; 1H-NMR; Metabolic pathways; Plasma metabolites