O-008 - TARGETED METABOLOMICS ANALYSIS FOR PROPIONATE METABOLISM DISORDERS

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BACKGROUND: Disorders of propionyl-CoA metabolism result mostly from a defect in propionyl-CoA carboxylase or methylmalonyl-CoA mutase in propionic acidemia (PA) or methylmalonic aciduria (MMA) respectively. These disorders are the most frequent forms of branched-chain organic acidurias. Global metabolomic profiling offers novel opportunities for the study of these diseases. ***OBJECTIVE:*** this study aims to evaluate the targeted metabolomics profiles of patients with disorders of propionate metabolism. ***METHODS:*** We analyzed 98 dry blood samples for 9 PA and 20 AMM patients using targeted metabolomics approach. Data were processed using multivariate analysis with the MetaboAnalyst 4.0 software. ***RESULTS:*** Hierarchical clustering analysis (HCA) clearly distinguished between the metabolomic profile of AMM and PA patients. The first tree principal components account the 61.3% of variance explained, Orthogonal partial least squares-discriminant analysis (orthoPLS-DA) classification modeling analysis have satisfactory results (Q2: 0.675 R2Y: 0.803). Our metabolomics studies revealed alterations of specific metabolites and glycine was the main important metabolite responsible of the differentiation with a VIP value of 1.7 in almost all principal components, and has a 6.13 fold change rate. C3/C2, the classical biomarker used in newborn screening was higher in AP patients with a fold change rate of 0.5. ***CONCLUSIONS:*** Besides classical biomarkers of propionate metabolic defects, metabolomics analysis could discover others that could facilitate differential diagnosis and might be important for a better understanding of pathogenesis, treatment optimization and clinical follow-up.