



Children with Hirschsprung disease exhibited alterations in host–microbial co-metabolism after pull-through operation

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Abstract

Purpose This study aims to compare the fecal metabolome in post pull-through HD with and without HAEC patients and healthy young children using nuclear magnetic resonance (NMR) spectroscopy.

Methods Fresh fecal samples were collected from children under 5 years of age in both post-pull-through HD patients and healthy Thai children. A total of 20 fecal samples were then analyzed using NMR spectroscopy.

Results Thirty-four metabolites identified among HD and healthy children younger than 5 years were compared. HD samples demonstrated a significant decrease in acetoin, phenylacetylglutamine, and *N*-acetylornithine (corrected *p* value = 0.01, 0.04, and 0.004, respectively). Succinate and xylose significantly decreased in HD with HAEC group compared to HD without HAEC group (corrected *p* value = 0.04 and 0.02, respectively). Moreover, glutamine and glutamate metabolism, and alanine, aspartate, and glutamate metabolism were the significant pathways involved, with pathway impact 0.42 and 0.50, respectively (corrected *p* value = 0.02 and 0.04, respectively).

Conclusion Differences in class, quantity, and metabolism of protein and other metabolites in young children with HD after pull-through operation were identified. Most of the associated metabolic pathways were correlated with the amino acids metabolism, which is required to maintain intestinal integrity and function.

Keywords Hirschsprung disease · Hirschsprung-associated enterocolitis · Metabolome · Nuclear magnetic resonance spectroscopy

Introduction

Metabolomics is the latest branch of “-omics” science or systems biology suite, referring to the study of the chemical products or metabolites produced by cells and organisms, such as amino acids, carbohydrates, fatty acids, and other products of cellular metabolic functions. The definition of

metabolomics is “an analytical description of complex biological samples and aims to characterize and quantify all the small molecules in such a sample” [1]. In our body, the gut is one of the organs where most substances are produced. Hosts and their gut microbes coproduce many small molecules during the metabolism of food and xenobiotics. Most of them play important roles in the communication between host cells and host’s microbes, known as host and microbial co-metabolism and signaling [2]. Some of the main metabolites that regulate host–microbiota interactions include short chain fatty acids (SCFAs), bile acids, choline, phenol, polyamines, lipids, etc. The levels and relative ratios of metabolites reflect metabolic functions, and abnormal values often indicate disease including infectious diseases, metabolic disorders, inflammatory bowel diseases, and cardiovascular diseases [3–8].

The analytical techniques for metabolomics are constantly being developed and any biological samples can be examined, for example, urine, blood, serum, feces, tissues,

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