

Metabolomic analysis of commercial probiotic strains effects (*Bifidobacterium animalis* subsp. *Lactis* and *Lactobacillus plantarum*) on the intestinal metabolism in IBS rat model Nazila. Dardmeh, Masoud. Yavarmanesh, Ali. Moazzami, M. Matin , and Hamid. Noorbakhsh

Introduction

Irritable bowel syndrome (IBS) is the most common gastrointestinal disorder associated with chronic abdominal pain and altered bowel habits. Disrupted gastrointestinal motility, altered gut-brain axis, and other factors linked to the gut microbiome may cause IBS. Recent studies have shown that probiotics effectively alleviate can symptoms of IBS and change metabolomic characteristics. Therefore, a proton nuclear (¹HNMR)-based magnetic resonance metabolomics approach was used to discover



Method

25 female Wistar rats were exposed to repeated Water Avoidance Stress (rWAS), divided into Control, IBS, IBS-P1 (*Bifidobacterium animalis* subsp. *Lactis* BB12), IBS-P2 (*Lactobacillus plantarum* ATCC 14917), and IBS-P1P2 groups (both P1 and P2).

For quantification of metabolites in plasma, a mix containing filtrate (310 μ l), sodium phosphate buffer (150 μ l, 0.4 M, pH 7), D₂O (45 μ l), Millipore water (65 μ l), and TSP-d4 (30 μ l, 5.8 mmol/L United States) was prepared for each sample, and 560 μ L of the final mixture added to a 5-mm NMR tube



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probiotic-derived metabolites in fecal and plasma samples of a rat IBS model.

Preliminary Results

The administration of mixed probiotics significantly reduces CRD pressure threshold values at 60 and 40 mmHg. However, a single probiotic administration is less effective.

OPLS-DA model for plasma metabolites of five groups separated along the first predictive component. 54 plasma metabolites were identified and 15 metabolites were found discriminative.

After intervention in the IBS group received probiotics: Acetoacetate, Myoinositol, Sarcosine, Taurine, and Acetate Arginine, Methionine, Choline, Phenylalanine, Leucine, Valine,

Isoleucine, Threonine, Lactate, and Carnitine

Colorectal distention (CRD)









SCFAs changes in rat feces Acetate, Butyrate, and Propionate



Model parameter were R² Y=0.902, Q² Y=0.583, R² X component 1= 0.173, R² X component 2= 0.883 and cross-validated ANOVA, P=0.05





Conclusion

Our findings demonstrated that probiotic treatment reversed one-carbon metabolism and altered amino acid metabolism in the plasma and fecal samples of the IBS rat model.



