

Characterization of the Intestinal Microbiota: A Signature in Fecal Samples from Patients with Irritable Bowel Syndrome

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Abstract : Irritable bowel syndrome (IBS) is a common bowel disorder which is usually diagnosed through the abdominal pain, fecal irregularities and bloating. Alteration in the intestinal microbial composition is implicating to inflammatory and functional bowel disorders which is recently also noted as an IBS feature. Owing to the potential importance of microbiota implication in both efficiencies of the treatment and prevention of the diseases, we examined the association between the intestinal microbiota and different bowel patterns in a cohort of subjects with IBS and healthy controls. Fresh fecal samples were collected from a total of 50 subjects, 30 of whom met the Rome IV criteria for IBS and 20 Healthy control. Total DNA was extracted and library preparation was conducted following the standard protocol for small whole genome sequencing. The pooled libraries sequenced on an Illumina Nextseq platform with a 2×150 paired-end read length and obtained sequences were analyzed using several bioinformatics programs. The majority of sequences obtained in the current study assigned to bacteria. However, our finding highlighted the significant microbial taxa variation among the studied groups. The result, therefore, suggests a significant association of the microbiota with symptoms and bowel characteristics in patients with IBS. These alterations in fecal microbiota could be exploited as a biomarker for IBS or its subtypes and suggest the modification of the microbiota might be integrated into prevention and treatment strategies for IBS.

Keywords : irritable bowel syndrome, intestinal microbiota, small whole genome sequencing, fecal samples, Illumina

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