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Gut Microbiota and Its Influence on Developing Irritable Bowel Syndrome: A Review

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ABSTRACT

Introduction: Irritable Bowel Syndrome (IBS) has a global prevalence of 11%, and it is amongst the most frequent gastrointestinal diseases. It is characterised by an impaired bowel function displaying symptoms such as changed stool habits accompanied by abdominal pain and discomfort. A major risk factor attributed to IBS is a dysbiotic gut that leads to inflammation and abnormal intestinal immune activity. Diet is known to alter gut microbiota. Therefore, a diet rich in Fermentable Oligosaccharides, Disaccharides, Monosaccharides and Polyols (FODMAP) is considered to be a risk factor since it causes visceral hypersensitivity, impaired gut motility and dysbiosis, promoting faster fermentation by gut microbiota and causing gas.

Aim: This review highlights the association of gut microbiota with IBS and an increase in studies of genome sequencing that help in the early identification of chronic disease development.

Materials and Methods: We searched PubMed, Medline, and Google Scholar for articles published in English between 2000 and December 2021 using the keywords "gut microbiota," "microbiota," "pathogenesis," "inflammatory bowel diseases," and "irritable bowel syndrome". An average of 200 research publications was examined; those that did not include gut-related variables or the risk of acquiring noncommunicable diseases were excluded.

Results: Studies have shown that patients suffering from IBS have a distinct gut microbiota, and certain bacteria are linked to the intestinal symptoms. There is a reduced microbial diversity in IBS patients. There was an abundance of *Firmicutes* and a decreased number of *Bacteroidetes*. There is a direct relationship between IBS and the number of harmful bacteria like *E. coli, Clostridium* and *Ruminococcus*. Faecal bacterium *prausnitzii* was lower in IBS patients, making it a "good gut signature". Contrary to popular belief, *Lactobacillus* and *Bifidobacterium*, which are used as probiotics, were increased in patients with IBS.

Conclusion: Gut microbiota is now being studied immensely and is regarded as the "second brain". Recent microbiome gene sequencing has displayed a great number of links between gut microbiota composition and the development of gastrointestinal disorders such as IBS.

Keywords: Bowel function, Global prevalence, Gut dysbiosis, Gut-related variables

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