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Short Communication

Stability Disruptions in Inflammtory Bowel Disease (IBD)

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DESCRIPTION

The microbiota "organ" is the gastrointestinal tract's major bioreactor, populated by 1014 bacteria and identified by microbiome that indicates 100 times of the human genome, a complex interaction and a positive interaction occurs under this physiological conditions. Inflammatory Bowel Disease (IBD) is characterised by a disruption of this homeostasis. Whether an altered microbiome promotes to IBD is still unknown. It is hypothesized that a complicated interaction between genetic predisposition, the immune system, and environmental variables is the pathophysiology of Inflammatory Bowel Disease (IBD). Metagenomic study on the human microbiome has recently produced significant information that is helpful to assemble IBD. IBD-related therapeutic possibilities using bacteria, host-microbe interactions, and the composition of the intestinal microbiota. Moreover, an interpretation on the potential role of bacteriophages in the development and treatment of IBD is provided [1,2].

The multifactorial pathophysiology of Inflammatory Bowel Diseases (IBD), which affects millions of individuals worldwide and is influenced by a number of components. A significant characteristic of IBD is an imbalanced gut microbiota. The therapeutic potential of bacteria and potential bacteriophage roles in IBD includes the composition of the gut microbiota, interactions between microbes and their hosts, IBD pathogenesis, development, and prognosis depend on the microbiome. Chronic inflammatory conditions of the gastrointestinal tract with a complex pathogenesis brought upon with multiple genetic, immunological, and environmental variables and are described as Inflammatory Bowel Disease (IBD) [3,4].

IBD refers to Crohn's disease (CD) and Ulcerative Colitis (UC), two gastrointestinal disorders with clinical, pathological, and epidemiological characteristics. Their frequent phases of disease symptoms, which are characterized by diarrhoea, weight loss, stomach discomfort, and rectal bleeding. According to growth projections, there are presently 2 million people living with IBD in Europe and more than 1 million persons in the United States. The number of bacteria in a healthy adult bowel is 1014, which is 10 times more than there are human cells. More than 100 bacterial species are characterized by 200 bacterial strains that constitute the gut microbiome. Metagenomics developments have demonstrated the complexity of this system. Three phyla, Firmicutes, Bacteroidetes, and Proteobacteria, account for more than 90% of these bacterial species. It is believed that the interaction between the Gastro-Intestinal (GI) tract and its microbiome, which is dynamic and beneficial to both individuals, is a key factor in determining both health and disease. The intestinal immune system offers defence to prevent an excessive amount of intraluminal germs from entering the bloodstream. In order to survive with microbes and their byproducts, probiotics activate homeostatic mechanisms based on molecular reactions mediated by epithelial cells, macrophages, dendritic cells, T and B-lymphocytes [5].

The gut provides the microbiota with a nutrient-rich environment, and the microbiota in turn offers a wide range of metabolic functions, such as the digestion and absorption of non-digestible substrates, a barrier effect against pathogenic microorganisms, and modulation of immune responses. The chronic inflammation present in IBD and other chronic inflammatory illnesses may result from a certain level of disruption of this symbiosis. Colorectal cancer is more likely to occur in IBD patients, and the risk increases with the severity and duration of colitis and the level of inflammation. The major sources to the pathogenesis of CAC (Colitis-Associated Cancer) are the intestinal microbiota, oxidative stress, and the mucosal inflammatory reaction [6,7].

CONCLUSION

The gut microbiota influences IBD-related bacterial therapeutic potential as well as potential bacteriophage functions. CAC is more likely to occur in IBD patients, and the risk increases with the severity and duration of the colitis. The gut microbiota contains a wide variety of bacterial species, some of which are protective and some of which promote the development of CAC. By regulating the intestinal flora, probiotics may reduce the pro-inflammatory effect. Several bacterial species are present in the natural microbiota, which contribute to the development of CAC. Probiotic bacteria are associated with the preventive role; they also regulate the gut flora, which has the potential to reduce the pro-inflammatory response and the risk of developing and progressing colitis.

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