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Commentary

Systemic Inflammations Produced by Gut Microbiota

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DESCRIPTION

Chronic inflammation-related disorders have a strong correlation with gut microbial dysbiosis. Prebiotics and probiotics, which are typically recommended, and are not significantly, improved the overall condition of these disorders. Therefore, there is an immediate requirement for the development of new prebiotics and probiotics which target particular disorders. In this, providing a succinct overview of current knowledge of the normal gut microbiota, microbiome, and their functions in maintaining gut integrity and mucosal immunity.

As a result of microbial dysbiosis, chronic intestinal inflammation develops, resulting in leaky gut syndrome and systemic chronic inflammation in the host. Many diseases, including obesity, type 2 diabetes mellitus, liver inflammations, decreased lung function immunity, Colorectal Cancer (CRC), obesity-induced Chronic Kidney Disease (CKD), and some brain/neuro problems, were subsequently carried. The method for appropriate prebiotic, probiotic and derived postbiotics implantation for the treatment of disorders is provided. Although the efficacy of these drugs is promising, more study is needed before any recommendations can be made for the majority of clinical circumstances.

Billions of living bacteria are present on the luminal surface of the intestines; their total number can exceed 1014 in the colon, which is between 1 and 100 times more cells than an adult produces. From a lower density at around 102/ml in the stomach to about 1011/ml in the colon, these bacteria form a population density gradient. There are currently 52 identified bacterial phyla identified, with approximately five to seven phyla known to live in the mammalian gastrointestinal tracts, according to the results of targeted 16S rRNA gene sequencing. Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria, four of these major phyla, dominate the remaining and constitute up to 97% among all bacteria. A complete and balanced bacterial ecosystem forms due to optimal interactions among the different bacterial phyla. Using the shotgun sequencing approach in combination to focused 16S rRNA gene sequencing provides more accurate result. The gut microbiota's whole DNA has been sequenced. The Open Reading Frames (ORFs) or genes are then annotated, and their functions are predicted using bioinformatics tools like Gene Ontology (GO) or the Kyoto Encyclopedia of Genes and Genomes (KEGG). These may connect the DNA sequences of these bacteria to putative biological metabolic pathways and functions. Results acquired from the shotgun sequencing approach (the metagenomics approach) are referred to as "Microbiome" in contrast to the term "Microbiota," which are essentially phylogenetically evaluated by targeted 16S rRNA gene (mainly V3-V4 domain) sequencing. The total number of genes in the microbiota, estimated by metagenomics analysis to be around 3.3 million, and is higher than the 25,000 genes in humans. Therefore, compared to transmissions from the microbiota, those acquired from the microbiome provide significantly more information. Along with the gut microbiome, fungi and viruses also colonise the gastrointestinal tracts to produce the gut mycobiome and the gut virome, respectively. Microbiota colonise the intestines from conception and begin to stabilise during the first years of a person's life. Microbiota exhibit greater complexity and diversity in healthy individuals. In contrast, as people age increases, the diversity of the microbiota decreases, the most significant environmental factors affecting the composition of the microbiota are nutrition, delivery method, drug use (including antibiotic use), and ageing.

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