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Bacterial Biomarkers in the gut of Inflammatory Bowel Disease by Metagenomic analysis- Review article

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ABSTRACT :

Microbiota within the intestines and the host interact with each other and there by affect the host's health status, which in turn affects the structure of gut microbiota. With advances in metagenomics, metabolomics and bioinformatics, as well as traditional culturing, the causality and association between gut microbiota of the Crohn's disease, ulcerative colitis of gut have been well studied. Our aim was to systematically review the literature on the Inflammatory Bowel Disease (IBD) gut microbiome and its usefulness to provide microbiome-based biomarkers. A review of the online bibliographic database PubMed was carried out. The IBD intestinal microbiome was often characterized by decreased species richness and diversity, as well as decreased temporal stability, whereas alterations in the gut microbiome appeared to play a critical role in determining the start of IBD. Several studies have found that various microbial taxa, such as bacteria, fungi, viruses, and archaea, are enriched or reduced in IBD. The decrease in helpful bacteria and the increase in harmful bacteria are the two key traits in this sense. There were also significant differences between remission and relapse IBD status. Changes in the composition and abundance of the gut microbial community have proven to be useful as diagnostic indicators. The gut microbiota is important in IBD. A deeper understanding of the human gut microbiota could lead to novel targets for illness diagnosis, prognosis, treatment, and possibly cure.

Keywords: Gut microbiota, inflammatory bowel disease, Crohn's disease, ulcerative colitis, biomarkers.

INTRODUCTION:

The gastrointestinal system is the human body's most densely inhabited microbial environment. Despite its well-established host-beneficial roles, intestinal microbiota has been implicated with a number of pathological disorders, including Crohn's disease (CD) and ulcerative colitis (UC). While some of these microbes are important immune system regulators, others can infect the human body and cause diseases such as IBD, diabetes, obesity, cancer, autoimmune, and neurological disorders. Deciphering the function and makeup of our gut microbiome, the collective genomes of the microbial population that lives in the human gut, is critical in this regard (1).

The global frequency of IBD has been steadily increasing, primarily in tandem with industrialization, with corresponding increases in health-care expenses. (2). Although the aetiology and pathogenesis of IBD are not fully understood, genetic polymorphisms suggest that unique immune responses to unbalanced gut microbiota play a major role in disease pathogenesis. (3,4).

GWAS have identified over 160 single nucleotide polymorphisms (SNPs) related with IBD, many of which are involved in pathways that alter the host response to microbial stimuli. The NOD2 gene, the first to be linked to IBD susceptibility, recognises components of the bacterial cell membrane (5,6).

The diversity of the faecal microbiome is lower in IBD patients compared to healthy controls (HC).The large alterations in the variety of gut microbiota in the condition of new-onset CD (before to therapy) are strongly connected to disease status(7-9).

The incidence and prevalence of inflammatory bowel diseases (IBD), such as Crohn's disease (CD) and ulcerative colitis (UC), have increased globally during the last 50 years (10). Particularly in typically low-incidence locations like Asia, South America, and southern and eastern Europe(11). Furthermore, IBD is one of the major risk factors for the development of colorectal cancer (CRC)(12), which is a major source of morbidity and mortality worldwide (13).Furthermore, populations in developed nations have seen an increase in the incidence of Clostridium difficile infections (CDI) over the previous 15 years (14). The recent advancement of high throughput sequencing technologies, such as Roche 454, Ion Torrent, and Illumina, allows for profiling of the bacterial population harboured by the intestinal tract, i.e. gut microbiota, and characterization of changes in this microbiota, sometimes referred to as gut dysbiosis, which is associated with the majority of major intestinal diseases (15).

We did a review to gather all known evidence on the relationship between the gut microbiome and IBD. Our goal was to describe the links between IBD and dysbiosis, as well as the potential clinical translation of microbiome-based biomarkers.

MATERIALS AND METHODS:

Search Strategy

An electronic search was undertaken utilizing the MEDLINE database via PubMed Up to August 2020 to identify published literature on the gut microbiome and IBD. Furthermore, the reference lists of the included research were reviewed in order to uncover additional relevant studies.

Eligibility Criteria:

The inclusion criteria were intestinal microbiome studies comparing IBD patients with controls; performed on fecal, intestinal lavage or intestinal tissue samples; focused on human adults; written in English.

Studies were excluded if they were abstracts from conference proceedings, letters to the editor, reviews, or if they only included one patient. These conditions included IBD and other conditions such as irritable bowel syndrome, Clostridium difficile infection, and primary sclerosing cholangitis

RESULTS:

The notion of a healthy microbiome is complicated by the significant variances discovered between the microbiomes of apparently healthy persons, according to articles that were found and examined in the PUBMED database. The microbiome is distinct among healthy individuals around the world. Despite this variance, healthy individuals have a broad and diversified microbial gut population that coexists in a state of relative equilibrium. A microbial species imbalance known as dysbiosis is frequently linked to inflammatory activity and a dysfunctional gut barrier. The major changes identified in IBD patients' guts are described in the sections that follow.

The articles reviewed here show that, despite the trillions of resident microorganisms found in the gastrointestinal system, which include bacteria, archaea, fungus, and viruses, most current research on the microbiome is mostly focused on bacteria.

Biologic dysbiosis

It has often been demonstrated that IBD is accompanied with an unbalanced bacterial composition and a disease-dependent reduction of biodiversity. The abundance of beneficial microorganisms such as *Clostridium* groups IV and XIVa, *Bacteroides, Suterella, Roseburia, Bifidobacterium* species and *Faecalibacterium prausnitzii* is reduced, whereas some pathogens such as *Proteobacteria* members (including invasive and adherent *Escherichia coli*), *Veillonellaceae, Pasteurellaceae, Fusobacterium* species, and *Ruminococcus gnavus* are increased [4]. The majority of studies have shown that the microbial community is less diversified and commensal bacteria are decreased in IBD patients [16, 17, 18, 19, 20, 21, 22, 23].

Escherichia coli, Salmonella, Yersinia, Desulfovibrio, Helicobacter, and *Vibrio* are only a few of the many genera in the phylum *Proteobacteria* that have been linked to an increase in IBD patients [24,25,26,27,28].

There is more evidence that the *Firmicutes* phylum's anti-inflammatory commensal bacterium *F. prausnitzii* is usually decreased in CD than in UC, where it is occasionally raised and in other occasions decreased [29, 30, 31, 32]. Additionally, it has repeatedly been observed that individuals with IBD have a specific decrease in *Roseburia* species [24,33,34, 26, 35]. The mucin degrader *R. gnavus*, which belongs to the same phylum, is frequently increased in IBD

patients' guts, which may reduce the stability of the barrier and exacerbate inflammation [24, 36, 37, 26, 38, 39, 40].

CONCLUSION:

The decrease in healthy bacteria and the rise in pathogens are the key characteristics of IBD gut dysbiosis. Persuasive studies have assessed the value of the gut microbiome as a tool for targeting non-invasive indicators for IBD. A reliable biomarker may support early IBD diagnosis, IBD categorization, and illness outcome prediction. In general, the discovery of microbiome-based biomarkers would be advantageous for IBD clinical management since they would offer less invasive diagnostic tools, permit individualised treatments, and lessen the financial burden of IBD on the healthcare system. These microbiome data collectively represent a priceless data source that can be continuously mined to uncover associations between the microbiome and IBD for a deeper pathophysiological understanding that may promote the development of clinical strategies, including disease prevention, treatment, stratification, and assessment of high-risk population.

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