

Microbiota and Irritable Bowel Syndrome: A Review

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Abstract

A functional gastro-intestinal condition termed as Irritable Bowel Syndrome (IBS) is referred to as persistent, reoccurring abdominal discomfort and altered bowel routines. The genesis of IBS is multimodulated with no clear explanation for its distinct subtypes. Some of the factors that are commonly engaged comprise sex-related, hereditary, epigenetic, and modifications to how the autoimmune, neurologic, and endocrine supersystems function, as well as management of bile acid generation and brain-gut physiology and permeation. Viral, toxic, dietary and life event-related factors that promote epithelial permeability and elicit mucosal microinflammation, immunological activation and dysbiosis may occur in combination with acquired propensity. Surprisingly, there is substantial evidence that bacterial, viral, and parasite illnesses can cause IBS. In light of some patients' excellent responses to microbiome-related medicines, addressing the microbiota appears to be a potential strategy. However, in many situations, the lack of highly predictive diagnostic biomarkers, as well as the complexity and variability of IBS patients, make care difficult and unsatisfactory, lowering the quality of life of the patient and accelerating the sanitary burden. The current review paper discusses the particular changes and therapies in IBS that target the gut microbiota, such as prebiotics, probiotics, synbiotics and other possible future strategies related to the diagnosis, treatment and prevention of IBS.

Keywords: Dysbiosis, IBS, Microbiota, Probiotic, Prebiotic, Synbiotic

Introduction

IBS: Definition, Morbidity, Prevalence and Manipulation of Microbiome

Globally around 11 per cent of the adult population is affected by Irritable Bowel Syndrome (IBS) and Functional Gastro-Intestinal Disorder (FGID). Till date Rome criteria is used to diagnose IBS, because of the unavailability of sensitive and specific biomarkers (Drossman and Hasler, 2016). IBS is characterized by changes in stool consistency and frequency, abdominal pain and distention, bloating or flatulence. Based on the prevailing bowel patterns, IBS sufferers are divided into four categories: IBS with predominant constipation (IBS-C), IBS with predominant diarrhea (IBS-D), mixed IBS (IBS-M) and unsubtyped IBS.

According to emerging evidence, the causative factors of IBS are antibiotics and infections, bile acids, food, psychological events and sex (Barbara *et al.*, 2016). These factors may cause changes in the epithelial barrier of the gut causing increased permeability of the intestinal membranes, which can cause abnormal sensorimotor and secretory outputs in the gut, due to alterations in the microbiota and activation of neuroendocrine responses

(Enck *et al.*, 2016; Ford *et al.*, 2017). There is a clear association between various gastrointestinal problems (*e.g.*, chronic pain disorders, functional dyspepsia) and psychiatric conditions (*e.g.*, anxiety, depression, fibromyalgia, migraine and pelvic pain) (Doulberis *et al.*, 2017). Though wide range of therapeutic choices are available, the satisfaction resulting from the treatment is low among both the patients and the doctors (Moayyedi *et al.*, 2017). Declining standard of living and rising social, sanitary, and financial costs are the two major effects of linked pathologies and treatment dissatisfaction globally. IBS patients often miss two days of work each month while also being less functional for nine a month (Buono *et al.*, 2017). Furthermore, IBS is associated with higher health-care costs than matched controls without IBS, as well as the financial burden on the migraine and asthma patients (Rahman *et al.*, 2017). The results of various community surveys conducted in India and Bangladesh highlighting the prevalence of IBD, dyspepsia, and overlapping syndromes are shown in Fig 1.

The need of the hour is to achieve an in-depth understanding of pathophysiology of IBS to improve the

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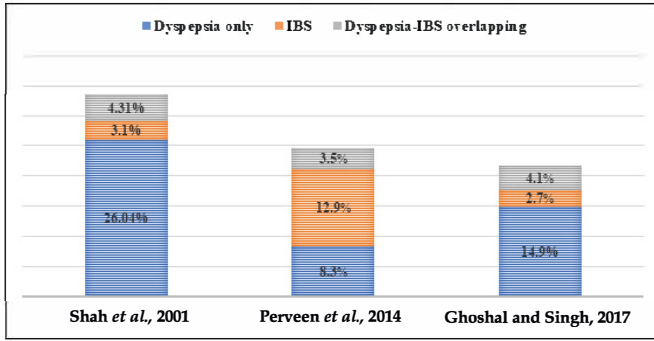


Fig. 1. Prevalence of IBD, Dyspepsia and Overlapping Syndromes

armamentarium and the therapeutic strategies. So, it's worth noting the introduction of novel medications aiming to treat both bowel habits and pain, such as linaclotide and eluxadoline for IBS-C and IBS-D respectively.

The importance of the gut microbiota in creating future treatment options for IBS is becoming clear. The faecal microbiota of IBS patients shows many qualitative and quantitative changes (Dupont, 2014; Distrutti et al., 2016), and there is significant evidence that bacterial, viral and parasite infections emulate the onset of IBS (Klem et al., 2017). Moraes and Quigley (2015) reported that prebiotic/probiotic administration can be an effective strategy in treating IBS, whereas Johnsen et al. (2018) analyzed improvement after fecal transplantation.

The Microbiome in IBS

Dysbiosis as categorized by Levy et al. (2017) is the 'abundance of pathobionts, loss of commensals or diversity', whereas Vangay et al. (2015) classified dysbiosis into four types- 'reductions in energy metabolism capacity, pathogenic populations, essential species and diversification'. Constituents of the intestinal microbiome which can lead to diseases are referred to as Pathobionts (Chow and Mazmanian, 2010). This growing dysbiosis indicates as the indication for IBS

Table 1. IBS and Dysbiosis Percentage

Taxon	Dysbiosis Percentage in IBS	Reference
<i>Lactobacillus</i>	Lower	Labuset al, 2017
<i>Firmicutes/Bacteroides</i>	Lower	Pozueloet al, 2015
<i>Ruminococcaceae</i> or <i>Ruminococcus</i>	Higher	Pozueloet al, 2015
<i>Bifidobacterium</i>	Lower	Parkeset al, 2012
<i>Faecalibacterium</i>	Lower	Carrollet al, 2012
<i>Enterobacteriaceae</i>	Higher	Carrollet al, 2012

(Table 1).

Given the differences in the findings, it is impossible to overlook the significance of microflora in the pathogenesis of IBS. Studies suggests that during the bouts of IBS, there is an increase in the proinflammatory bacterial species including *Enterobacteriaceae*, with decrease in the quantum of *Lactobacillus* and *Bifidobacterium* (Zhuang et al., 2017). A decrease in the percentage of *Lactobacillus* and *Bifidobacterium* was observed in IBS. By interacting with other bacterial species and the host, the genera *Lactobacillus* and *Bifidobacterium* can modify the microbiota and immune system (Parkes et al., 2012).

Several *Lactobacillus* and *Bifidobacterium* species can generate bacteriocins, which are chemicals that have a bactericidal effect *in vitro* against pathogens including *Salmonella* and *Listeria monocytogenes* (Markowiak and Ślizewska, 2017). Additionally, the families of *Lactobacillus* and *Bifidobacterium* may have an influence on the hosts' immune system by interacting with CD209 on dendritic cells to produce an immunomodulatory response (Ruiz et al., 2017). Additionally, IBS patients have decreased amounts of the short chain fatty acid/s generating bacteria like *Bifidobacterium*, *Clostridiales*, *Erysipelotrichaceae* and *Ruminococcaceae* families (Pozuelo et al., 2015).

The link between IBS and methane production is noteworthy, with IBS-D having lower levels and IBS-C having higher levels (Bin Waqar and Rehan, 2019). Only methanogens from the Archaea kingdom synthesize methane by converting hydrogen to methane. The *Methanobacteriales* order is the most prevalent methane generator in the human microbiome. Increased methane production is responsible for slower gastrointestinal transit time and reduction in the anti-inflammatory properties (Suri et al., 2018). The presence of *Methanobacteriales* is connected to the abundance of microbiota within the enterotype of *Clostridiales*, which is related to prolonged evacuation, suggesting that increased methane production in constipated individuals may be attributable to overgrowth of microbes (Tap et al., 2017; Falony et al., 2016; Vandeputte et al., 2016). In fact, the presence of methanogens, exhaled methane, microbial richness and enterotypes richer in *Clostridiales* or *Prevotella* species all correspond with the intensity of IBS symptoms. Despite its great clinical significance, this microbial profile has yet to be explained by genetic variables, dietary variations, or medication use. To understand the pathophysiology of IBS with regards to the role of microbiota, its crucial to

understand the bacterial composition and factors influencing IBS severity. IBS dysbiosis is associated with Psychiatric comorbidity, as IBS-D microbiota transplantation in mice can affect anxiety levels (Socafa *et al.*, 2021). As a result, sex and psychiatric comorbidities could be key factors in explaining the core and particular microbial alterations in IBS.

Treatment of IBS by Intestinal Microbiome Management

While it's unclear whether small intestinal bacterial overgrowth (quantitative) or dysbiosis (qualitative) variations in the intestinal microbiota invoke, or are merely a result of disturbed local gut micro-environmental conditions, in IBS. As a new tool for the management of the affliction, specific interventions to intervene with the gut microbiota are being ascertained. These interventions are based on the following studies.

- Faecal transplantation from IBS patients to mucus rats can transfer several crucial IBS traits, namely systemic bowel intolerance (Crouzet *et al.*, 2013).
- Gastrointestinal infections encourage higher relative risk of getting IBS depending on the molecular mechanisms involved (Klem *et al.*, 2017).
- Some probiotics and prebiotics can help with IBS symptoms (Ford *et al.*, 2014).
- In randomised placebo-controlled trials, dietary treatments that alter the gut microbiota have also been proven to be helpful (Halmos *et al.*, 2014).
- Preliminary findings imply that faecal microbiota transplantation improves symptoms (Tian *et al.*, 2017).

Probiotics, Prebiotics and Synbiotics

Probiotics are live microorganisms that, when taken in appropriate quantities, boost the host's health (FAO/WHO, 2002). Probiotic bacteria should be safe to consume, penetrate the living digestive system in large amounts and give the host possible health benefits. These bacteria can keep the intestinal flora healthy by modifying the environment of the intestine, stimulating the growth of gut microbiota and inhibiting the onset of serious illnesses mediated by microorganisms. *Lactobacillus*, *Bifidobacteria* and the yeast *Saccharomyces boulardii* are among the widely employed probiotic bacteria. Although individual variability exists, there is a mutual synbiotic relationship between the host and the microbiome with human body. The body supports the microbial communities and an appropriate physical

environment, whilst the microbes perform important functions. Hosts' health and advanced diet, immune development, energy metabolism and hosts' defense mechanisms are directly proportional to the composition and functionality of gut microbiota (Thursby and Juge, 2017).

The word prebiotic, which Gibson and Roberfroid first proposed in 1995, is characterized as "non-digestible food component that enhances the overall well-being of the host by significantly fostering the existence and/or functioning of colonic bacteria" (Gibson and Roberfroid, 1995). The commonly adopted definition of prebiotics was established by the International Scientific Organization of Probiotics and Prebiotics (ISAPP) in December 2016. Other compounds than carbohydrates *i.e.*, polyunsaturated fatty acids and polyphenols which can be changed to corresponding conjugated fatty acids, may be included in the group of prebiotics, according to the definition, and they may not work only in the gastrointestinal system (Gibson *et al.*, 2017). Bacterial species that are considered useful to human health and well-being are also used as food by prebiotics. Besides the daily food, the proper selection of the prebiotics can introduce nutraceutical effects, if employed during fermentation. The range of effects influenced by optimized colon actions and metabolism includes increased or improved expression of the short chains of fatty acids, weight of faecal matter, minor lowering of pH of the luminal colon, reduced end-product nitrogen and reactive enzymes, increased binding expression of protein and mineral related active carriers (Ríos-Covián *et al.*, 2016). Many materials and foods are labeled prebiotic on the grounds of fermentability alone (Younis *et al.*, 2015). Multiple whole grains are also called prebiotics since they have various kinds of fibres, some of which are fermentable (Paolella *et al.*, 2014).

Fermentable fibres are important for good health, particularly with respect to other fibres. However, prebiotics are specified additives that are meant to influence individual bacteria, the end results of their fermentation and the host's potential health benefits. Prebiotics as oligosaccharides or more complex saccharides are primarily used selectively by the commensal bacterial species and the organisms that are proven to be beneficial to the host. Before fermentation, prebiotics should be able to withstand the adsorption, absorption and digestion of single resident species of microbiota (Carlson *et al.*, 2018).

However, other complicated saccharides and fibres have

been recently known in addition to most common prebiotics, such as inulin and its derivatives as fructo-oligosaccharides (FOSs) and galacto-oligosaccharides (GOSs). Various type of oligosaccharides are found in natural foods available abundantly in the Indian diets like fruits (watermelon, pomegranate, dates, figs), vegetables (onion, beetroot, green peas, sweet corn, garlic), legumes (chickpea, lentils, red kidney beans, soybeans), cereals (barley, wheat), milk and honey (Longvah *et al.*, 2017).

The most important food prebiotics used in food processing, including infant foods, include fructans and galacto-oligosaccharides (Černáková *et al.*, 2019). These are considered as GRAS (Generally Recognized As Safe) and have been extensively researched for showing health benefits.

Prebiotics may exhibit the following properties:

- Intestinal flora preservation and intestinal transit relaxation (Jandhyala *et al.*, 2015).
- Shift in colonic microflora, leading to regular consistency of stools, avoiding diarrhea and constipation (Gilbert *et al.*, 2018).
- Elimination of excess substances such as glucose and cholesterol, facilitating only the ingestion of essential substances (Carlson *et al.*, 2018).
- Enhancement of *bifidobacteria* development (Cruz *et al.*, 2012).
- Stimulation of the absorption of B vitamins and their development (B1, B2, B3, B6, B9, B12) (Hardman *et al.*, 2016).

The majority of maladies originate in the digestive tract



Fig. 2. Sites harbouring microflora

when the good bacteria find it difficult to control the harmful microorganisms, according to Elie Metchnikoff, widely referred to as the Father of Probiotics. With about 1000 species, 7000 strains, and genes that are nearly 150 times larger than the human genome, the human gut microbiota is a dynamic ecosystem. The microbial ecosystem's interaction with the host symbolises a long evolutionary relationship that is necessary for optimal health throughout life. These microorganisms have an impact on the hosts' metabolism, physiology, and immune system development due to the wide genetic and metabolic variety of the resident microbiota. As a result, the microbiome is now considered a "virtual organ". Every human surface which is exposed to the environment and every body part with an opening to the environment has a microbiome (Munoz-Garach *et al.*, 2016). The Fig. 2 and 3 shows the sites that harbour a normal flora and the distribution of gut microbiota in the human body respectively.

Archae, bacteria, fungus, protozoa and viruses are the range of microbes inhabiting the gastrointestinal tract. The behaviour as well as the makeup of these microbes can have an impact on human health and disease. Probiotics can breach the human gut barrier in an array of ways depending on the region of the intestinal system and the probiotics strains in consideration (Zmora *et al.*, 2018).

Non-specific, species-specific and strain-specific processes also have health consequences that are exerted by probiotics. In terms of non-specific methods, widely used probiotic supplements are divided into species or even genera. These involve inhibiting growth of gastrointestinal pathogenic microorganisms (through

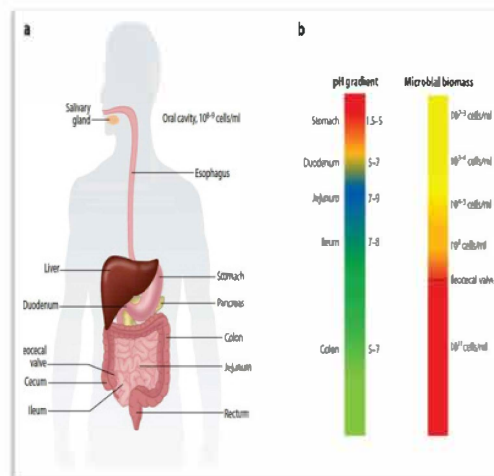


Fig. 3. Distribution of Gut Microbiota

(Source: Munoz-Garach *et al.*, 2016)

promoting invasion resistance, improving intestinal transit, or assisting in the restoration of a disturbed microbiota), generating bioactive metabolites (e.g., short-chain fatty acids) and decreasing colon luminous pH. Vitamin and bile salt synthesis, strengthening of intestinal barrier, activity of enzymes and toxin neutralisation are included in the species-specific mechanisms. The strain specific pathways of cytokine generation, immunomodulation, and influence on the endocrine and neurological systems are unusual and used by just a few strains of a given species. Probiotics can have relatively positive influence on diseases through most of these strategies and on the overall health of the host (Hill *et al.*, 2014).

Because the effects of certain probiotic species and strains may be unique and therapeutic, so the research advice must be species- and strain-specific (Sanders, 2015). Furthermore, combining data from studies of various testiotic types can lead to misleading results on the effectiveness and safety of probiotics.

According to Das *et al.* (2012), probiotics can restore the equilibrium of the intestinal microbiota and confer genetic markers of peripheral or gut microbial disorders functional purposes. The study also led to the conclusion that intestinal luminal conversion by microbial organisms and food is very crucial in establishing the physiology of IBD.

The term "synbiotics" refers to food items or dietary supplements that mix probiotics and prebiotics in a synergistic fashion. Synergistic pro and prebiotic combinations are called synbiotics. The same concept is based on probiotics, prebiotics and synbiotics: the development of foods which multiply "clean" bacteria in the intestine after ingestion. However, it is only valid in case of "mutual synergistic" reinforcement. Synbiotics exhibits its benefits in diarrhoea, IBS, Inflammatory bowel disorder, Ulcerative colitis and Chron's disease (Pandey *et al.*, 2015).

Gibson and Roberfroid in 1995 described synbiotics as "probiotic and prebiotic formulations that support the host by promoting the longevity and implantation of probiotic bacteria additives in the gastric mucosa, triggering the growth and metabolism of one or a few health-promoting bacteria, and hence improve its recipient's health" (Manigandan *et al.*, 2015). Researches are still preliminary on synbiotics to prove their health and overall benefits.

Synbiotics incorporates properties of both probiotics and prebiotics and have been known to address some potential problems in gastrointestinal survival of

probiotics. A good combination of both pro/prebiotic components in one complete product would therefore ensure a higher impact compared with the pro/prebiotic operation alone (Markowiak and Ślizewska, 2017).

Synbiotics along with other natural foods are now considered essential resources to help sustain good health for humans and animals, for disease prevention and/or as alternatives to mitigate disease-related risks. Studies performed on the human gut and animal gut and immunology microbiota relationship have highlighted the role that synbiotics play in mammalian health. Synbiotics affect the microbial ecology of humans and animals' intestines, and play a role in reducing some diseases. These can be the safest and most efficient way to combat colonization issues especially bacterial pathogens and infection with enteric pathogens. Functional prebiotic-like foods or natural antimicrobial supplements as alternatives and bioactive metabolite overexpression in probiotics are essential for improving synbiotic efficacy (Malik *et al.*, 2016).

For human nutrition, following are the popular synbiotic combinations as stated by Markowiak and Ślizewska (2017)

- *Lactobacillus* genus bacteria + inulin.
- *Lactobacillus*, *Streptococcus* and *Bifidobacterium* genus bacteria + fructo-oligosaccharides.
- *Lactobacillus*, *Bifidobacterium*, *Enterococcus* genus bacteria + fructo-oligosaccharides.
- *Lactobacillus* and *Bifidobacterium* genus bacteria with oligofructose.
- *Lactobacillus* and *Bifidobacterium* genus bacteria with inulin

Synbiotics are engineered to have beneficial effects on the host in following ways:

- Boost probiotic survival and implantation in colon.
- Selectively encourage growth or trigger the metabolism of probiotics in the colon.
- Improve the microbial makeup of the GI tract.

Selection of synbiotics depends on certain factors where the selection of pro and prebiotics plays an important role. Proper selection probiotic and prebiotics means these pro and prebiotics should show positive effects on host's health when tried individually and separately. The most appropriate approach appears to be the identification of the characteristics to be exhibited by a prebiotic to get a beneficial impact on the probiotic. Prebiotics must selectively encourage the production of microorganisms with a positive effect on health with

very little (near to absence) stimulation to rest of the microorganisms.

Considering the synergistic effect of synbiotics, Prebiotics are often used as a platform for probiotic strain's growth, intestinal passage along with fermentation. Because of prebiotics usage, probiotic microorganisms gain greater vulnerability to oxygenation, intestinal temperature, pH and other environmental conditions. Such combination shows a synergistic effect which results in the formation of dietary add-ons ensuring an ideal environment for the betterment of the host's health.

Synbiotics acts in two ways:

- By enhanced feasibility of probiotic microorganisms
- By making provision of distinct health effects

The synergistic effect enhances the intestinal metabolic activity, intestinal bio-structure, creation of helpful microbiota and preventing the growth of pathogens inside the gastrointestinal tract. Properties of reducing the levels of metabolites, inhibition of nitrosamines is also observed in synbiotic. It also inhibits carcinogenic stimulants. Their use causes an increase in fatty acids (short-chain), ketones, carbon disulphides and methyl acetates that show a beneficial impact on the health of the host (Markowiak and Ślizewska, 2017).

Microbiome and Gut Dysbiosis

Dysbiosis is described as an "imbalance" due to the growth, loss or changes in the relative amount of microbes in the gut microbial population. Gut microbiomes aid in digestion of food, genotoxic

degradation, and stimulation of adaptive and innate immune responses. These roles have been associated to the occurrence of disease (Messer and Chang, 2018). Cellular sensing and channels are driven by proteins, peptides, and intermediates generated regionally and even at a range which protects the microbiological homeostasis of the host. Ageing, food, disease and stress can all affect the relative quantity and variety of bacterial species in the GI tract and other regions of the body. As demonstrated in Fig. 4, a chronic microbial gut imbalance relates to Inflammatory Bowel Disease (IBD), IBS, obesity, diabetes, cardiovascular, cancer and diseases of central nervous system, in both animal models and human research (Catinean *et al.*, 2018).

Particular bacterial communities, in particular, represent a prospective clinical target for the treatment of infectious and inflammatory conditions. IBS patients, particularly those with persistent *Clostridium difficile*-induced pseudo-membrane colitis, may benefited through IMT (Intestinal Microbiota Transplantation). Dysbiosis of the entire intestinal flora has been attributed to metabolic and inflammatory diseases, with faecal and phage therapy, as well as probiotic and prebiotic regimens, potentially global value in prophylactic and therapeutic implications. (Belizário and Faintuch, 2018).

Dysbiosis with various symptoms was explained by Hedayat *et al.* (2020) as:

- **Local Dysbiosis**, which is characterised by symptoms like bloating, spasms, inflammation with loss of intestinal permeability, mucosal dysplasia, poor nutrition reclamation for buffering

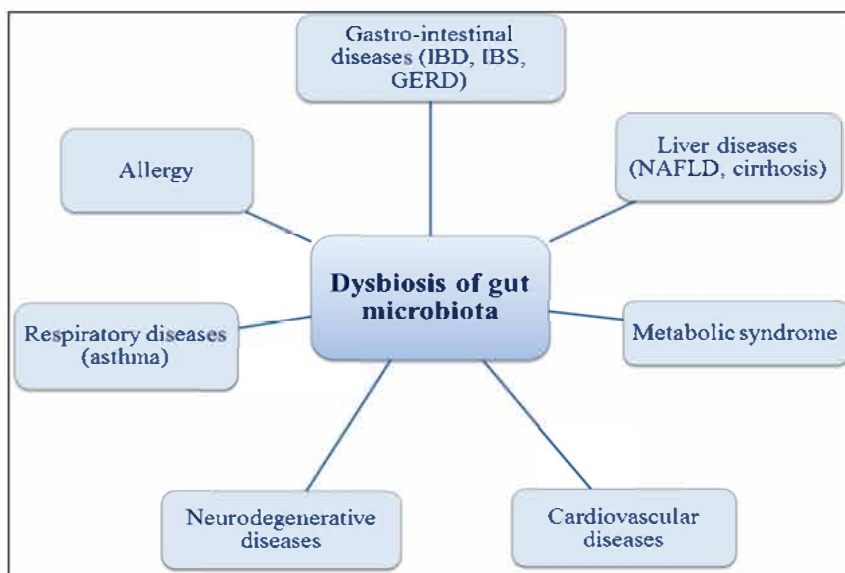


Fig. 4. Gut Microbiota and Associated Health Problems (Source: Catinean et al., 2018)

capacity, and adaptive demands.

- **Regional Dysbiosis**, in which the annexal organs such as the liver, gall bladder and exocrine pancreas are oversolicited and/or congested.
- **Immune Dysbiosis**, which is specific to the development of antigen-antibody complexes in response to partially digested food and its translocated chemical moieties.
- **Systemic Dysbiosis** is the worsening of inflammatory conditions. It shows migraines, arthritis, autoimmune disorders, etc. Changes in the Central Nervous System like brain fog, irritability, changes in mood, fear, anxiety etc. is seen. Endocrine inflammation with modification potential is also altered.

The different types of gut microbiota, as given by Cresci and Izzo (2019), are shown in the Fig.5.

Diet is important in maintaining this complex microbiome since it contains energy-supplying components for the host microbiota. High-fat, high-sugar, and low-fermentable-fiber diets can cause dysbiosis, whereas low-fat, low-sugar, and high-fermentable-fiber diets, specially prebiotic fibre, can optimally promote energy homeostasis, immunological responses, lowering the risk and maintaining general health. Cardenas-Castro *et al.* (2021) studied the *in vitro* gastrointestinal digestion and colonic fermentation of tomato (*Solanum lycopersicum*

L.) and husk tomato (*Physalis ixocarpa* B.). After 48 hours of fermentation, it was discovered that certain phenolic chemicals were liberated and bio transformed by gut bacteria. In both these varieties, the most bioavailable molecule was vanillinic acid, whereas the predominant metabolite was 3-Hydroxyphenylacetic acid. Further research into these chemicals with biological potential is needed.

In individuals with ulcerative colitis, the correlation between the consumption of soy milk and inflammatory markers, gut microbiota and disease severity were studied. The research discovered that soy milk includes a variety of compounds, including phytoestrogens, which may have anti-inflammatory characteristics. It has an impact on the gut flora because to its protein and fibre content. As a result, it can be stated that soy milk shows positive impact on the patients suffering with ulcerative colitis (Sadeghi *et al.*, 2020).

In a mouse diabetes model, Surono *et al.* (2020) explored the impact of functional ingredients in foods on gut microbiota. The research suggests that a 4-week regimen with functional dietary components, specifically starch derived from taro, results in a better gut microbiome in diabetic rats.

In an *in vitro* model, Oleskin and Shenderov (2019) analyzed the effect of probiotics on the growth of *Salmonella enterica*, *Serovar typhimurium* and *Clostridium difficile*. Probiotics suppress pathogens by creating short chain fatty acids such as acetic, propionic, butyric and

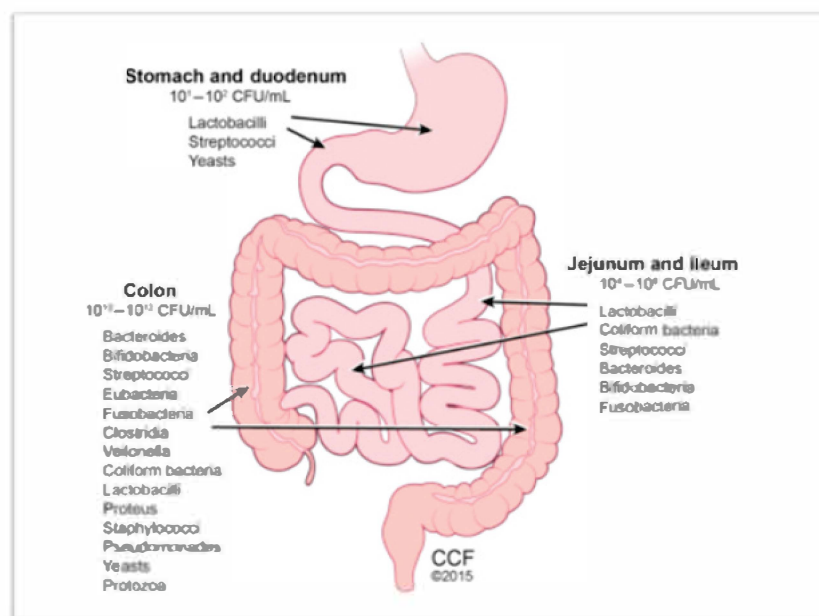


Fig. 5. Types of Gut Microbiota (Source: Cresci and Izzo, 2019)

lactic acids, which also aids in the maintenance of a healthy pH in the intestinal lumen.

Korczak *et al.* (2020) analyzed the effect of oats on gastrointestinal health of animal and human, *in vitro*. The researchers discovered that eating 3 g of glucan per day from oats lowers faecal pH and changes faecal flora. In humans, 40 to 100 g/d of oat bran increased faecal bacterial mass and short-chain fatty acids. The type of oats utilised has an impact on these outcomes.

Dietary changes and probiotic and prebiotic therapy can assist to maintain a healthy microbiota balance in a controlled environment, promoting energy and immunological homeostasis. In a dysbiotic scenario, dietary modifications, probiotic and prebiotic therapy, and, in extreme situations, complete faecal microbiota rebuilding from stool transplantation may contribute in disease response (Tungland, 2018). In the pathogenesis of IBD and IBS, the imbalance in the gut microbiota is considered to play a major role (Carding *et al.*, 2015). Investigation into the efficacy of initiation of treatment against a variety of gastrointestinal and other ailments is progressing.

Waters *et al.* (2015) sought to demonstrate prebiotic, probiotic and synbiotic efficacy in IBS and Chronic Idiopathic Constipation (CIC) and illustrated that prebiotics and probiotics synbiotically prove to be

advantageous for IBS and CIC. The incidence and length of antibiotic-related diarrhoea were also shown to be reduced with the administration of probiotics, in both children and adults (Guo *et al.*, 2019).

Sharma *et al.* (2014) designed a sprouted wheat-based probiotic beverage with a *Lactobacillus acidophilus* NCDC-14 count of $10.43 \log^{10}$ CFU/mL. In cereal-based probiotic fermentations, improved resistance to gastrointestinal conditions as well as a change in gut flora have been documented.

Rose (2014) investigated the effect of whole grains on the microbiota in the gut. The study averred that whole grain oats are unique because it contains certain components, namely sterols, the soluble fiber from β -glucan, ferulic acid, avenacosylates, avenacins, and avenanthramides. These compounds, when metabolized, favorably affect the gut microbiota.

Rathore *et al.* (2012) investigated the effects of probiotics and prebiotics on human health and concluded that probiotics can be used to treat infectious, bacterial or antibiotic-induced diarrhoea, lower serum cholesterol, lower colon cancer risk, improve lactose digestion and alter intestinal microbiota.

The effects of probiotics on gut microbiota were investigated by Das *et al.* (2012) and the results show that probiotics have the potential to reclaim the structure and

Table 2. Class(es) of Probiotics used in Various Diseases/Conditions

S.No.	Reference	Medical Condition	Class(es) of Probiotic
1	Grégoire <i>et al.</i> , 2020	IBD or IBS	LAB and <i>Bifidobacterium bifidum</i> , <i>Saccharomyces boulardii</i> alone, or LAB alone.
2	Kluijfhout <i>et al.</i> , 2020	Gastroenteritis and acute diarrhoea	LAB, <i>Bifidobacterium</i> species, or <i>Saccharomyces boulardii</i>
3	Zommiti <i>et al.</i> , 2020	Intestinal inflammation in Children	LAB
4	Özdemir, 2018	Allergies	LAB
5	Parker <i>et al.</i> , 2018	Antibiotic associated diarrhoea	LAB, or <i>Saccharomyces boulardii</i>
6	Burton <i>et al.</i> , 2017	Lactose Maldigestion	Lactic acid Bacteria (LAB) and <i>Streptococcus salivarius</i> sub sp. <i>Thermophilus</i>

composition of intestinal microbiomes. Furthermore, probiotics were also proved to display positive functions to the phenotypes of intestinal microbes or systemic diseases. The study also stated that diet and bowel luminosity are important for preserving the structure and function of intestine microbial communities *via* intestinal microbes.

A meta-analytical research involving 82 Randomised Controlled Trials (RCT) and more than 10,000 patients studied the ability of probiotic products to avoid antibiotic-related diarrhoea and concluded that probiotic usage did have a positive effect in preventing diarrhoea (Hempel *et al.*, 2012).

Probiotic interventions have been shown to be efficacious as active ingredients in the management of chronic conditions *in vitro* and *in vivo* by Martins *et al.* (2010). Bacterial adhesion to unique intestinal epithelial receptors and subsequent invasion of the host is prevented by *Streptococcus boulardii*, *Streptococcus cerevisiae* and *Streptococcus cerevisiae* BY474 strains that were displayed to captures harmful microorganisms on the cell membrane. Table 2 indicates the circumstances or diseases in which probiotics can be used to prevent and/or cure diseases.

Overall, the outcomes of all of these investigations demonstrate that probiotics are effective therapies for IBS, albeit it is unknown whether specific species and strains are the most helpful. As a result, more research is necessary to confirm the efficacy of probiotics in the treatment of different IBS symptoms.

Emerging Perspectives and Treatment Possibilities in IBS Microbiome Maintenance

Though current understanding of microbiome adjustment is limited at the moment, new options and approaches such as bacterial genetic engineering and tailored microbiota programming, faecal transplantation, bacteriophage therapy, including the use of postbiotics await us in the future.

Conclusion

Dysbiosis appears to play a part in the development of IBS, according to the growing evidence. Probiotics, prebiotics, symbiotics, and dietary manipulation of gut microbiota to treat IBS is becoming more frequent, and while there is currently insufficient evidence about types, formulations, indications, and doses, recent meta-analyses have highlighted positive findings. A number of prospective therapy possibilities, including faecal transplant, are being investigated and evaluated, but more evidence from larger, well-controlled research is

required.

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