

## REVIEW ARTICLE

# Gut Microbiota as the Key to Mental and Physical Health

Paulina Emanowicz, Paulina Średnicka, Michał Wójcicki, Agnieszka Zapaśnik

Prof. Waclaw Dąbrowski Institute  
of Agricultural and Food Biotechnology,  
State Research Institute,  
Department of Microbiology  
36 Rakowiecka St.,  
02-532 Warsaw, Poland

**Correspondence**

[paulina.emanowicz@ibprs.pl](mailto:paulina.emanowicz@ibprs.pl)

Prof. Waclaw Dąbrowski Institute  
of Agricultural and Food Biotechnology,  
State Research Institute,  
Department of Microbiology  
36 Rakowiecka St.,  
02-532 Warsaw, Poland

**Abstract**

The gut microbiota plays a crucial role in maintaining optimal physical and mental health by regulating essential metabolic processes, enhancing immunity, and preserving the integrity of the intestinal barrier. A balanced diet rich in plant-based ingredients positively influences the gut microbiome, reducing the risk of various diseases. Dysbiosis of the gut microbiota, induced by factors such as a low-fiber diet or stress, may lead to increased intestinal permeability, predisposing individuals to diseases, particularly inflammatory bowel diseases. Research on the gut-brain axis also underscores the significant impact of gut microbiota on emotional aspects. A comprehensive understanding of the relationship between diet, gut microbiota, and the nervous system is essential for the development of effective therapeutic and preventive strategies in the realm of both physical and mental health.

**KEYWORDS**

gut microbiota, dysbiosis of gut microbiota, gut-brain ax

**Introduction**

The human gastrointestinal tract is home to over 100 trillion microorganisms with a unique gut microbiota profile. According to recent research, the contents of the colon weigh approximately 200-250g, of which about 100g are bacteria representing the gut microbiome [Daniel, 2020]. The gut microbiota is a crucial participant in nutrient metabolism, influencing the growth and regulation of the immune system, removing pathogens, maintaining intestinal barrier integrity, and ensuring homeostasis [Liang et al., 2023]. Additionally, it plays a significant role in regulating the epithelial barrier and shaping the interaction of microbial communities with its functions.

Maintaining proper gut microbiota through a balanced diet, probiotics, and prebiotics can promote overall health and prevent the development of various diseases. In this context, proper nutrition, particularly the high consumption of fruits and vegetables, has the potential to reduce the risk of many diseases. Studies indicate that a diet rich in these components can not only support gut microbiota balance but also promote health through a balanced influence on oxidative reactions. As a result, approaching diet as a means to support gut microbiota health becomes not only a step towards maintaining general health but also an effective preventive strategy against various health problems [Liang et al., 2023].

Current research confirms that there is biological communication between our brain, gastrointestinal tract, and gut microbiota. Contrary to appearances, gut microorganisms play a crucial role in influencing emotional aspects by generating and regulating signals transmitted from the gut to the brain. These signals have the ability to amplify and, in some cases, prolong emotional states [Camara-Lemarrroy et al., 2018].

Various factors such as disease states, unhealthy dietary habits, epithelial damage, mucus layer disorders, and gut microbiota dysbiosis can negatively impact gut permeability. Consequently, this may lead to the occurrence of leaky gut syndrome, which is a significant factor in the etiology of inflammatory conditions both within the digestive system and beyond [Lopetuso et al., 2015].

**Impact of Diet on Maintaining Intestinal Barrier Integrity**

Fruits, vegetables, and other plant-based foods contain phytochemicals, including compounds such as polyphenols, flavonoids like anthocyanins (ACN), and carotenoids. Phytochemicals can reduce gut permeability and improve its function by reducing pro-inflammatory cytokines. For instance, polyphenols can modulate the gut microbiota by promoting the presence of bacteria such as *Akkermansia muciniphila* (family *Verrucomicrobia*) and *Fae-*

*calibacterium prausnitzii* (family *Ruminococcaceae*), which are extremely important for gut health [Kumar Singh et al., 2019; Liang et al., 2023].

Dietary fiber also significantly impacts the gut microbial ecosystem. Gut bacteria can transform it to produce short-chain fatty acid (SCFAs) derivatives like acetate, butyrate, and propionate. SCFA production in the gut lumen plays a crucial role in maintaining gut homeostasis, particularly in processes such as water and salt absorption in the colon. SCFAs are an important energy source for colonocytes that form the colon epithelium, with butyrate especially supporting their growth, and preventing mucosal atrophy. Thus, they play an essential role in maintaining the integrity of the intestinal epithelial barrier, a key defensive mechanism of the body.

Studies by Peng et al. [2009] confirm the critical role of butyrate and acetate in maintaining the integrity of the intestinal epithelial barrier. This mechanism includes increasing the expression of tight junction proteins such as claudin-1 and initiating the redistribution of zonulin-1 and claudin-1. It is noteworthy that not all bacteria in the microbiota can produce butyrate, with the primary producers being bacteria such as *Faecalibacterium prausnitzii* [Benus et al., 2010; Korsten et al., 2023].

However, some environmental factors can impair gut barrier function and contribute to the secretion of pro-inflammatory cytokines. For instance, a Western diet low in fiber and high in simple sugars, particularly fructose, increases gut permeability by reducing the expression of tight junction proteins. Impaired gut barrier function is associated with the induction of inflammatory states, which consequently leads to intestinal and systemic diseases [Odenwald, Turner 2017].

Scientific research indicates that in inflammatory conditions of the colon, such as Crohn's disease, there is a noticeable increase in oxidation, which is associated with a reduction in thiols acting as antioxidants, leading to a decrease in anaerobic bacteria, which predominate in normal gut microbiota [Aw, 2003]. This disease is characterized by thiol depletion and oxidative stress, which leads to changes in the microbiota and a reduction in the number of *F. prausnitzii*, which maintains the intestinal epithelial barrier. This confirms that consuming dairy products, fruits, and fiber, which are primary sources of flavins and thiols, promotes "gut health" and enables their utilization by anaerobic bacteria in niches where oxygen gradients exist, such as the intestinal mucosa [Khan et al., 2013].

### Dysbiosis

Many aspects of a modern lifestyle directly impact the gut microbiological profile; these include medications, a diet high in refined carbohydrates, diseases, hospitalization, surgeries, smoking, alcohol abuse, processed foods low in fermentable fiber, and chronic stress. All these factors can disrupt microbiota function and cause tight junction breakdown in the intestinal barrier. This change leads to dysbiosis, a loss of balance in the population and function of microorganisms, and increased intestinal permeability [Camara-Lemarroy et al., 2018; Liang et al., 2023].

Gut microbiome dysbiosis leads to an increased influx of macromolecules through the intestinal barrier, such as lipopolysac-

charides (LPS), resulting in local intestinal inflammation and low-grade systemic inflammation [Huang et al., 2018; Korsten et al., 2023]. The link between dysbiosis and inflammation can be identified by any pathological increase in bacterial numbers resulting from changes in intestinal permeability [Caparrós et al., 2021].

There is growing evidence that the reach of gut microorganisms extends beyond the intestines and affects systemic processes. They are involved in maintaining metabolic processes and organ functions such as the brain (gut-brain axis), cardiovascular system (gut-heart axis), and liver (gut-liver axis), among others [Liang et al., 2023].

### Inflammatory Bowel Disease

Inflammatory Bowel Disease (IBD) is a chronic gastrointestinal disorder. IBD includes Crohn's Disease (CD) and Ulcerative Colitis (UC). It is noteworthy that the gut microbiota of patients with active CD is less stable compared to patients with inactive CD or healthy individuals without IBD [Sepelri et al., 2007]. The long-term effects of gut microbiota disruption, along with an increased abundance of pathogens in the intestines, can significantly impact intestinal permeability even during periods of disease stabilization without inflammation [Vivinus-Nébot et al., 2014]. The development of CD has been shown to be associated with increased intestinal permeability. This confirms that altered intestinal barrier function contributes to pathogenesis, and any abnormalities can serve as a biomarker for the risk of developing CD [Turpin et al., 2020].

Individuals suffering from IBD typically exhibit differences not only in the composition but also in the diversity of microbial populations compared to healthy individuals (see Table 1). Patients with IBD show reduced microbiome diversity. IBD microbiota is characterized by an increased number of bacteria from the *Proteobacteria phylum*, such as the *Enterobacteriaceae* family, and certain representatives of the *Bacteroidetes phylum* [Liang et al., 2023; Santana et al., 2022]. In IBD patients, a particularly noticeable decrease in the relative abundance of the *Firmicutes phylum* is observed, including the highly metabolically active commensal bacterium *Faecalibacterium prausnitzii* and *Akkermansia muciniphila* from the *Verrucomicrobia family* [Miquel et al., 2013; Caparrós et al., 2021; Kowalska-Duplaga et al., 2019].

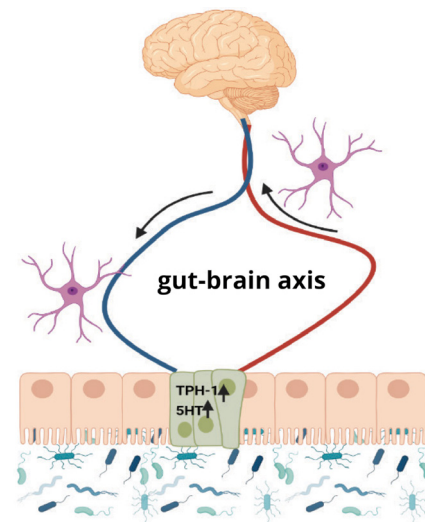
Additionally, it has been shown that in CD patients, there is a significant increase in the bacteria *Ruminococcus gnavus* and *Fusobacterium nucleatum* from the *Ruminococcaceae* and *Fusobacteriaceae* families respectively compared to the control group [Gevers et al., 2014; Clooney et al., 2021]. Conversely, the presence of *Ruminococcus albus* and *Eubacterium rectale* from the *Ruminococcaceae* and *Lachnospiraceae* families decreases in CD. Bacteria from the genera *Eubacterium* and *Roseburia* are among the most significant in classifying CD compared to the control group [Mukherjee et al., 2020].

### Gut-Brain Axis

The gut-brain axis enables bidirectional communication between the central nervous system and the enteric nervous system, connecting emotional and cognitive areas of the brain with gut functions. In recent years, there has been significant advancement in understanding the concept of the gut-brain connection [Irum et al., 2023]. The main goal of exploration in this field is to identify

**Table 1.** Changes in the composition of gut microbiota in patients with IBD

Microbiome Component	Presence in IBD	Mechanisms of Action	Bibliography
<b>Family Ruminococcaceae</b>			
<i>Faecalibacterium prausnitzii</i>	-	A commensal bacterium that is metabolically active and participates in butyrate production. Butyrate plays a crucial role in gut physiology, offering benefits such as protection against pathogen invasion, modulation of the immune system, and supporting anti-inflammatory activity	[Caparrós i in. 2021, Jacobs i in. 2016, Kowalska-Duplaga i in. 2019, Miquel i in. 2013]
<i>Ruminococcus albus</i>	-	Participates in the metabolism of short-chain fatty acids (SCFAs) and plays a protective and anti-inflammatory role.	[Clooney i in. 2021]
<b>Family Lachnospiraceae</b>			
<i>Eubacterium rectale</i>	-	Involved in the production of short-chain fatty acids (SCFAs), primarily butyrate. Plays a crucial role in modulating inflammation and maintaining the integrity of the intestinal barrier.	[Jacobs i in. 2016, Clooney i in. 2021]
<b>Family Verrucomicrobiaceae</b>			
<i>Akkermansia muciniphila</i>	-	A commensal bacterium that is metabolically active and involved in the production of SCFAs. It plays a crucial role in protecting against pathogen invasion, modulating the immune system, and supporting anti-inflammatory activity	[Lo Presti i in. 2019, Zhang i in. 2021]
<b>Family Bacteroidaceae</b>			
<i>Bacteroides</i>	+	Involved in mucin metabolism, playing a role in the degradation of the protective mucus layer	[Lo Presti i in. 2019, Zhang i in. 2021]
<b>Family Enterobacteriaceae</b>			
<i>Escherichia Coli</i>	+	Associated with the epithelium, it can infect and damage single layers of intestinal epithelial cells and synthesize α-hemolysin	[Gevers i in. 2014, Price i in. 2019]
<b>Family Fusobacteriaceae</b>			
<i>Fusobacterium nucleatum</i>	+	Involved in pro-inflammatory reactions	[Vich Vila i in. 2018, Mottaweia i in. 2016]



**Figure 1.** Interactions between the brain-gut-microbiota axis and serotonin signaling. Enterochromaffin cells (highlighted in green) dominate in the production of over 90% of serotonin (5-HT) in the body. The synthesis of 5-HT in these cells is regulated by, among others, SCFAs, which increase their stimulating effect on ECC along with increased availability of tryptophan (TPH-1) in the diet.

novel therapeutic strategies and preventive measures for mental disorders by gaining an in-depth understanding of the relationship between the gut and the brain and the role of gut microbiota in shaping mental illnesses and their therapeutic consequences. Progress has been noted in treating depression and anxiety, stemming from research on the positive impact of gut microbiota on behavior and brain function.

The most commonly used pharmacotherapeutic substances in treating mental disorders are selective serotonin reuptake inhibitors (SSRIs) such as Prozac, Paxil, and Celexa. These drugs work by increasing the availability of serotonin by inhibiting its reuptake in neuronal synapses. It is worth noting that serotonin is synthesized and stored in enterochromaffin cells within the gut. These serotonin-carrying cells are susceptible to the influence of diet, chemicals released by specific species of gut microorganisms, and neurological signals transmitted by the brain. The com-

plex interaction between diet, gut microbiota, and the nervous system plays a crucial role in modulating serotonin activity and can affect the regulation of our emotional state (Figure 1) [Emeran, 2018].

Clinical practice has shown that oral therapy with the bacterium *Lactobacillus rhamnosus* JB-1 is effective in treating anxiety and depressive behaviors [McVey Neufeld et al., 2019].

Studies comparing the gut microbiota of individuals with untreated depression, individuals with bipolar disorder, and healthy control individuals have been conducted. It was observed that the gut microbiota of patients with untreated depression differed from that of the control group of the same age, gender, and body mass index. Patients with untreated depression had more bacteria from the family *Enterobacteriaceae* and the genus *Alistipes*, and fewer from the genera *Faecalibacterium*, *Coprococcus*, and

*Dialister* [Zheng et al., 2020]. Additionally, some studies have shown that gut microbiota dysbiosis may play a causal role in developing depressive behaviors through pathways mediated by host metabolism.

In individuals with bipolar disorder, similar to cases of patients with depression, reduced abundance of bacteria such as *Faecalibacterium*, as well as the families *Ruminococcaceae* and *Lachnospiraceae*, and bacteria of the genera *Akkermansia* and *Sutterella*, was found. These observations suggest a connection between the composition of gut microorganisms and the symptoms and severity of the disease reported by patients [Evans et al., 2017; Painold et al., 2019].

### Conclusions

Microorganisms present in the gut play a crucial role in maintaining gut health, and their dysbiosis is associated with various diseases. Diet significantly influences the composition of gut microbiota, which in turn affects the body's homeostasis. Plant-based components, such as polyphenols and fiber, positively impact gut microbiota, improve the integrity of the intestinal barrier, and regulate oxidative reactions. Gut microbiota dysbiosis, resulting from factors such as a low-fiber diet or stress, can lead to increased intestinal permeability and inflammation. Inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are closely correlated with gut microbiota dysbiosis, manifesting as reduced bacterial diversity. The intensively studied gut-brain axis highlights the significant role of gut microorganisms in regulating emotional aspects through communication between the brain, gastrointestinal tract, and gut microbiota.

The impact of diet on gut microbiota is crucial for both mental and physical health. The complex interactions between diet, gut microbiota, and the nervous system are essential for maintaining body homeostasis, representing a critical area of research for developing therapeutic and preventive strategies for various diseases.

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