American Journal of Biology and Natural Sciences
https://biojournals.us/index.php/AJBNS
**ISSN: 2997-7185**

# Microbial Communities and their Role in Digestion within the Human Gastrointestinal Tract

**Zeina Thamer Hussein**
Samarra University  Department of Pathological analysis Pathological Analysis
zeinathamer372@gmail.com

**Sharoq Edan Najem**
Samarra University, College of Applied Sciences, Department of Pathological Analysis

**Zahraa Hussein Jawad**
University of Kufa College of Science Department of Pathological Analysis

**Elaf Jamal Fadil**
AL-Huda University College Department of Medical Laboratory Techniques
elafjalani@gmail.com

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**Received:** 2024, 15, Jan
**Accepted:** 2025, 21, Feb
**Published:** 2025, 24, mar

**Annotation:** The human gastrointestinal (GI) tract hosts a complex microbial community essential for digestion, metabolism, and immune regulation. Despite extensive knowledge of microbial diversity, a key gap remains in understanding how microbial community dynamics and interactions contribute to digestion under varying physiological and dietary conditions. This study reviews the structure, composition, and function of gut microbiota, emphasizing their roles in carbohydrate fermentation, protein metabolism, and nutrient cycling. Using 16S rRNA gene sequencing and metagenomic analyses, recent findings reveal that microbial composition shifts rapidly in response to diet, antibiotics, and host factors, influencing health outcomes. Results highlight the dominance of Firmicutes and Bacteroidetes in digestion and their metabolic flexibility in adapting to environmental changes. These insights underscore the importance of preserving microbial balance for digestive health and suggest potential interventions through diet and microbiome-targeted therapies.

**Keywords:** gut microbiota, gastrointestinal tract, digestion, microbial diversity, Firmicutes, 16S rRNA, human health.

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## 1. Introduction

The diverse microbial community that inhabits the human gut has an extensive metabolic repertoire that complements the activity of mammalian enzymes and includes functions essential for host digestion [1]. The collective genomes of the gut microorganisms (microbiome) provide metabolic capabilities that extend beyond the human host, making the gut microbiota a key factor in shaping the biochemical profile of the diet and its impact on host health and disease. Within the human gut, there exists a mass of microorganisms so large that they outnumber the host's cells. Most of this microbial diversity is contained within the colon, the site of the largest collection of bacteria in the human body, working symbiotically with the host to digest otherwise indigestible polysaccharides. Due to the complexity of the tasks carried out by these microorganisms, the gut microbiota is not confined to simply one species, but is spread amongst several different phyla with 90% belonging to just two: Firmicutes and Bacteroidetes. To fully understand digestion within the human gastrointestinal tract, the different microbial communities involved must be examined, as well as the metabolites produced through the fermentation process carried out by these microorganisms. All the microorganisms living in the human body collectively form a "metaorganism," with the gut microbiome capable of greatly influencing the host's metabolism. The host's internal environment changes throughout the length of the gut, and different microorganisms have adapted to live in these varied conditions. The initial part of the small intestine is inhabited by aerophilic microorganisms, such as Streptococcus, Lactobacillus, and Veilonella, which are all normally derived from the host during birth. These form the dominating microflora within the gut of infants until feeding allows other microorganisms to become established in the colon. [2][3][4]

## 2. Anatomy of the Human Gastrointestinal Tract

The gastrointestinal tract (GIT) is a long, muscular tube that functions as the food processor for the human body. The GIT consists of the mouth, esophagus, stomach, small intestine (SI), large intestine (LI), rectum, and anus. The intestine is essentially segmented into the: duodenum, jejunum, and ileum in the SI and the cecum, colon, and rectum in the LI, which is further divided into the ascending colon, transverse colon, descending colon, and sigmoid colon. The mucosa is highly folded into finger-like villi within the SI. In contrast, the colon is relatively smooth with no villi on the mucosa.

The mucosa overlay is a layer composed of simple columnar epithelium with crypts and villi. Paneth cells, Goblet cells, enterocytes and enteroendocrine cells line the crypts and villi. The layer beneath the mucosa is characterized by a dense aggregation of lymphoid tissues known as Peyer's patches. The SI is distinguished by its abounding nutrient availability, influencing a complex microbial flora to colonize its mucosa. Approximately 10^14 microbial cells are reported to inhabit the colon, with the large majority of the organisms being strict anaerobes. Many mutualistic relationships with the host exist, including digestion of food, production of nutrients, and prevention of the entrance of pathogenic organisms. Despite these advantages, the continued shedding of bacteria and susceptibility of bacterial attachment and invasion by various pathogens foster a high turnover of bacterial groups. The bacterial group responsible for adhesion and invasion of pathogenic organisms are referred to as the Bridgehead bacterial groups, with increased fitness to grow on mucus and survive exposure to acid, although it is unknown if the Bridgehead organisms are a physiological group of organisms, or simply a coincidental group commonly observed within the gut. [5][6][7]

## 3. Microbial Diversity in the Gastrointestinal Tract

The human gastrointestinal (GI) tract is a complex ecosystem of intense interactions among bacteria, viruses, archaea, fungi, and host gastrointestinal cells. These interactions are known to affect the physiology of the host cells and play important roles in health and the development of systemic human diseases. Despite the importance of such interactions, little is known about the nature, extent, and importance of these interactions in higher organisms, particularly in the natural environment of a complex GI tract. The human GI tract is a natural habitat for a wide diversity of microorganisms. In the large intestine, there are on average, 100 thousand microbes per gram of colonic content, comprising between 500 and 1000 species [8]. The bacterial density increases from the stomach to the colon reflecting the microbial activity in the particular environment. It is known that a close interaction among the active organisms and gut epithelial cells plays important roles in human health. The community of microbes present on the mucosal surface is different than the one present in gut contents, indicating that the mucus layer and enterocyte surfaces harbor a distinct set of organisms.

The upper GI tract is considered, in general, a sterile environment because of the impact of gastric acid during food ingestion. However, the mucosal layer of the small intestine has been recently shown to contain a small yet active and complex community of bacteria. These results indicate the bacteria are in close interaction with the gut epithelium in the upper part of the small intestine, and in many cases are proposed to help protect the host against pathogens. The human microbiota was traditionally studied by taking samples from feces and isolating and culturing microbes. However, a vast majority of microorganisms in the GI tract cannot be cultivated. Recent reports have shown that microbes from the human GI tract are not always easy to cultivate. Additionally, different bacterial species may require different growth conditions to cultivate. Thus, cultivation-dependent techniques alone may be insufficient to correctly identify species. DNA-based techniques permit the identification of a wide range of bacteria, independently of their ability to grow under artificial conditions. By employing direct sequencing of 16S rRNA gene amplicons, up to 80% of the bacteria in a sample can be identified. This technique has been used to study natural microbial communities such as soil, water, and encrusting communities. [9][10][11]

## 4. Functions of Microbial Communities in Digestion

The human gut is home to an astonishingly large number of approximately 10^14 bacterial cells, which comprise a vast and diverse array of bacterial species and individual members. One of the major roles that the gut microbiota plays is the fermentation of dietary carbohydrates, particularly those that cannot be digested by human enzymes. The various by-products that arise from carbohydrate fermentation are of crucial importance for maintaining the health of the colonic environment and the overall well-being of the mammalian host. For numerous bacterial species thriving in this rich ecosystem, proteins serve as a significantly richer energy source and carbon source than carbohydrates. As a response to the limitation of carbohydrate availability, gut bacteria have developed mechanisms to degrade host-secreted mucus glycoproteins for their nutritional needs. Recent data suggests that the dynamics of the human gut cannot simply be characterized as a chaotic environment where bacteria merely compete against one another for the limited resources available. Instead, it represents a highly organized and structured ecosystem, characterized by a complex network of interactions amongst the host, the gut microbiota, and the various colonic food sources present. To support health, it becomes essential to cycle nutrients effectively between luminal spaces and mucus-adherent microenvironments found within the colon. This nutrient cycling is essential and plays a significant role in determining the composition, variety, and overall function of the gut microbiota, which in turn is crucial for maintaining the health of the mammalian host. Specifically, the bacteria- and peptide-rich biofilm layer that forms in the gut is digested by a community dominated primarily by Firmicutes, which includes notable species such as Akkermansia muciniphila, as well as members of the Betaproteobacteria group. This intricate balance and interaction among the microbiota not only support digestion but also contribute to broader aspects of health and disease prevention in the host. [12][13]

## 5. Factors Influencing Microbial Composition and Activity

1. Diet The most obvious factor that influences microbial composition and activity in the colon is the diet. Temporary alterations, or changes in the long term diet, markedly affect the microbiota in a very short time-scale. Although the overall structure of the microbial communities is influenced, it is the metabolic capacity of the microbiota that shows the most marked changes. This is caused by the provision of novel substrates and the disappearance or reduction in availability of other substrates. 2. Host lifestyle and physiology Additional factors that disturb the microbiota include interruptions to its habitual activity/development. This can be seen with the use of antibiotics or acute infection, both of which reduce overall diversity and evenness in the microbiota. Similarly, faecal frequency is also well known to affect the composition of the microbial population. A healthy microbiota of aged individuals has characteristic differences to that of youth so host physiology also plays a role. 3. Other factors Numerous other factors have also been postulated to affect the microbial composition of the colon. Historical factors include birth delivery mode, antibiotic exposure, and compound exposures that would permanently affect physiological development after birth. Lack of exposure to pathogens can prevent immunological development in childhood. Epidemiological studies have linked obesity with low-grade inflammatory responses, and in turn this could affect the microbiota. Exosomes secreted by various cells have been shown to interact with and carry bacteria, changing their distribution and ability to interact with cells. Additionally, altered electrolyte concentration has been shown to affect efficacy of excreted antibiotics, leading to nM concentrations effecting toxin production and host microbiota interactions. [14][15][16]

## 6. Conclusion

Slow and gradual digestion as promoted by nature is the healthiest method for digesting food. When a meal is eaten in 10 minutes, it is considered fast food that does not allow for sufficient chewing and therefore results in inefficient digestion. When a meal is taken in 30 to 40 minutes, though it is not rapid, the large food particles can ferment or putrefy because of the body’s temperature, humidity, and digestion enzymes.

The gastrointestinal (GI) tract may exist from the mouth to the anus, but in reality, the GI tract is similar to a large tube 8 meters in length. This tube is where the human body absorbs and digests food, and it is filled with bacteria, most of which exist in the large intestine. To industrialism and urbanization, people shy away from natural and fresh foods, and frequently eat processed, high-calorie and high-fat easily prepared foods. This unbalanced and harmful diet deprives the body of a diverse intestine-friendly bacteria community. Due to these eating behaviors, the majority of the GI tract length is used only for the transference and digestion of food. Because of this, U-Tube surgery has become popular, as it reduces the stomach volume from 1000 milliliters (mL) to 100 mL, allowing it to hold only one-tenth of its original food amount.

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