

Diversity in Microbial Communities and their Metabolism Related to Human Health

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Abstract

Human gut microbiome contains a range of 1000 different microbial species with defined functions, which have coevolved with human beings over thousands of years. In recent years, the gut microbiota has become the interest of extensive research. Gut microbiota is an essential organ of the human body. In our food, these microorganisms contribute from flavoring products to the synthesis of vitamins and antioxidants essential to living beings. The gut microbiota has been linked with the development of a number of chronic gastrointestinal and systemic diseases, such as irritable bowel syndrome (IBS), inflammatory bowel diseases (IBD), and metabolic diseases like obesity, diabetes, fatty liver disease. Here, we review some significant recent studies that have discussed the understanding of microbial diversity of human gut and the impacts on human health and diseases.

Keywords: Gut Microbiota; Microbial Community; Gut Microbiome; Isoflavones; Gut Dysbiosis; Microbial Metabolism

Abbreviations

IBS: Irritable Bowel Syndrome; IBD: Inflammatory Bowel Disease; GI: Gastrointestinal

Introduction

The communities of microorganism, which exist in nature, live in various complex forms of life on the Earth and play an important role in human health. These communities contain a wide range of species and in the community each of them may play a different role. The activity of these microbial communities exhibit an universal implications for habitability and biosphere of Earth and complexity of them has made hard to understand their response to any change in their environment. In nature, microbes generally do not exist in isolation. The concurrence of mixed microbial communities are affluent with opportunities for interaction. They account for one third of all planetary biomass and play a critical role in global ecosystem and sustaining human life. Despite the importance of these microbes and the habitats affected by them, scientists are still struggling to identify them and understand how these organisms are connected by the metabolic activity to form cooperative communities; mainly, how these microbes together to acquire nutrients and energy from the environment [1,2]. Understanding and identifying the core microbiome of any given environment is of crucial importance for predicting and assessing the environmental change both locally and globally [3]. The human microbiota is formed by trillions of commensal microbes, which is a colonization of different bacteria, archaea, fungi and some viruses in healthy human body. There are several supporting evidences that these microbes have co-evolved with their human hosts and play an important role in maintaining their health [4]. There is a remarkable diversity in abundance of microbes living on and within the healthy human body is illuminated by recent studies. With the help of high

throughput sequencing technologies and some nongenomic techniques, the role of the gut microbiota in human health and disease has become clearer [4]. The purpose of this review is to briefly discuss the microbial diversity of the human gut and the impacts of it on human health and diseases.

Microbial diversity in gut microbiome

In human intestinal tract, it is estimated that approximately 1000 different bacterial species coexist with more than 3 million genes, it is approximately 150 times more than human genes. In total, gut microbiota can weigh up to 2 kg. The majority of these microorganisms in gut have beneficial effects but some of them are often considered as pathogens in opportunistic situations [5]. The healthy human gut microbiota is mainly dominated by *Bacteroidetes*, *Firmicutes*, *Actinobacteria* and *Proteobacteria* with minor contributors, including *Fusobacteria* and *Verrucomicrobia*. Among them *Bacteroidetes* and *Firmicutes* are generally the most abundant of the gut microbiome [6]. The bacteria from gut microbiota mostly belongs to the genera *Bacteroides*, *Bifidobacterium*, *Clostridium*, *Eubacterium*, *Ruminococcus*, *Peptococcus* and *Peptostreptococcus*. Some other genera such as *Lactobacillus*, *Escherichia*, *Faecalibacterium* and *Roseburia* are present in lesser number. Among all bacteria in the gut *Bacteroides* spp. alone constitute approximately 30% [7-9]. Enriched intake of diet from animal sources favors *Bacteroides* spp. and plant-based diet favors *Prevotella* spp. The ratio of *Prevotella* spp. to *Bacteroides* spp. is used as an useful index for clinical diagnosis of some diseases [10]. Lactic acid bacteria, chiefly *Lactobacillus* spp. and *Bifidobacterium* spp., and Butyrate-producing bacteria, *Butyricoccus* spp., *Roseburia* spp., including some *Clostridium* groups, are believed to have beneficial effects in the host as anti-inflammatory and anti-tumorigenic [11-13]. Dysbiosis caused by a variety of conditions can increase the risk of disease when the delicate balance in host and microbiota are directly or indirectly perturbed.

Role of gut microbial metabolism in human health

Gut microbiota is an essential organ of the human body. The development of gut microbiota depends on the interaction of genetic factors, diet and disease, contact with the environment, which makes a unique microbiota in each individual [14]. The gut microbes provide a wide variety of important functions in our body. They play an important role in digestion of complex lipids and polysaccharides, synthesizing nutritional factors and some vitamins, development of systemic and intestinal immune system and help in the protection by secretion of anti-microbial products against some pathogenic bacteria. Some very essential products of microbiota are vitamins such as folic acid, riboflavin, conjugated linoleic acids, and secondary bile acids [4]. It is known that microbes intensely populate the most part of the gastrointestinal tract. Due to the presence of hydrochloric acid, the stomach and the small intestine have fewer microorganisms [14]. The large intestine has highest concentration of microorganisms, mainly *Lactobacillus* spp., *Escherichia coli*, *Klebsiella* spp. and *Proteus* spp. that help in the degradation of food [15,16]. Gut microbes are also helpful in maintenance of gut integrity by epithelium renewal and also important for detoxification of the deleterious xenobiotics. These functions are vital and important, because ablation of gut microbiota with broad spectrum antibiotics can lead significant consequences, such as inappropriate development of the gut immune system and the development of antibiotic-associated *Clostridium difficile* colitis [17,18].

Gut microbes have major contribution in host fermentation, reduction of sulfate and nitrate, esterification, and hydrolysis of glycosides from plant foods, and other endogenous compounds which are excreted in bile and end up in the large intestine [19]. According to some studies, soy protein has potential effects on hot flushes and bone loss in perimenopausal women because the two major soy isoflavones, genistein and daidzein, have weak estrogenic properties. Isoflavones, are metabolized by gut microbes as many other flavonoides. Daidzein is metabolized by formation of equol, an active isoflavone, only in about 30 to 50 percent of individuals depending on the population and depending on gut microbial composition [20,21]. Plant lignins are present in fruits, grains, nuts and in some other foods, which are metabolized to produce enterodiol and enterolactone by microbes of gut microbiota. Enterodiol and enterolactone are considered to be protective in breast cancer. It is shown in some studies that the formation of enterodiol and enterolactone are highly variable among individuals due to difference in their gut microbiota [22]. Some cruciferous vegetables such as broccoli, cauliflower, cabbage and their vegetable relatives are reported as cancer-preventing vegetables. They lower risks of various cancers like breast, lung, prostate, colorectal and pancreatic cancers. Gut microbes extract chemopreventive isothiocyanate from cruciferous vegetables [23].

Gut microbiota and disease

Any kind of alteration in composition and functional potential of our gut microbiota can be linked with number of diseases. Gut dysbiosis can disturb intestinal homeostasis, cause metabolic abnormalities, and activate immune or inflammatory responses [24]. Any change in gut microbial community is believed to be major contributory factor for immune related, infectious, cancerous, and metabolic disorders, including irritable bowel syndrome (IBS) and inflammatory bowel diseases (IBD) such as Ulcerative Colitis and Crohn's Disease; systemic diseases such as type 2 diabetes and obesity; neonatal necrotizing enterocolitis, gastrointestinal cancers mainly colorectal cancer, and infectious diseases [4,24]. According to some recent studies, fatty liver disease can be associated with altered metabolites which are either produced or influenced by gut microbes. Gut microbiota plays an important role in regulating bile acid and choline levels that are supposed to be associated with fatty liver disease [25]. There are evidences that gut microbes extending beyond the intestine and affecting systemic processes, for e.g. metabolism and organ functions of brain and liver, cardiovascular system, and others. Several metabolomics studies have identified number of compounds in blood those are specifically derived and dependent on the presence of gut microbes [26].

Conclusions

The microbial community of our gut evolves with us and plays an important role in human health and diseases. We know that the gut microbiota influences host metabolism, physiology of the body and immune system development while any alternation of the microbial community can result in chronic gastrointestinal (GI) disease. Understanding the part of microbial populations can help in the development of appropriate therapeutic approaches. And manipulation of the gut microbiota is considered as a potential therapeutic option to treat some chronic gastrointestinal (GI) diseases. The concept of altering gut community by microbial intervention, such as fecal microbiota transplantation in case of antibiotic-associated *Clostridium difficile* colitis; is currently a topic which is receiving considerable interest.

The revolution in molecular technologies is providing the tools necessary to study the gut microbiota, which will help to elucidate the relationships between the gut microbes and intestinal pathologies more accurately. Targeting the specific components of the gut microbiota will potentially allow the removal of the harmful microbes and enrich with the beneficial microbiome that contribute to our health.

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Conflict of Interests

All the authors declare that there are no conflicts of interest related to this review article.

Informed Consent

Consent was obtained from all individual participants included in the presentation of review article.

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