Interaction between diet composition and gut microbiota and its impact on gastrointestinal tract health

Muhammad Shahid Riaz Rajoka a, Junling Shi a,∗, Hafiza Mahreen Mehwish b, Jing Zhu a, Qi Li a, Dongyan Shao a, Qingsheng Huang a, Hui Yang a

a Key Laboratory for Space Bioscience and Space Biotechnology, School of Life Sciences, Northwestern Polytechnical University, Xi’an 710072, Shaanxi, People’s Republic of China
b Department of Biotechnology, University of Agriculture, Faisalabad, Pakistan
Received 15 May 2017; received in revised form 20 July 2017; accepted 26 July 2017
Available online 8 August 2017

Abstract
A substantial amount of emerging research is indicating that the gut microbiota has a significant impact on human health. Alterations of gut microbiota have clear consequences on intestinal homeostasis, physiology, gut microbiome, immune system and host metabolic pathways. Diet composition plays an important role in the control of gut microbial populations and, thus, in the prevention, management and treatment of certain diseases such as cancer, diabetes. A comprehensive analysis of previously reported results revealed that the gut microbiota can be modulated by diet and the composition of gut microbiota can be influenced by various diet components. The symbiotic relationship between different gut microbial communities regulates the immune system and, therefore, any dysbiosis can dysregulate the immune system. Further research is needed to fully understand the mechanisms involved in the interactions between diet composition, gut microbiota and associated diseases.

© 2017 Beijing Academy of Food Sciences. Production and hosting by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Keywords: Gut microbiota; Dysbiosis; Probiotics; Human health

1. Introduction
Over the past decades, the interaction between nutrition and the gut microbiota and its impact on human health has gathered increasing interest. Initial studies were primarily focused on the classification of microbial species forming the gut microbiota and the relationship of gut microbiota composition with the host health status [1]. Recent studies started to investigate the interaction between food and gut microbiota relative to the health of the host [2]. Current exciting research is beginning to unravel how the composition of food modulates the gut microbiota [3].

It has been found that the human-associated microbial communities are crucial for proper development of human and various hypotheses have been proposed to understand such relationship. One hypothesis is that the microbial communities of the mother affect fetal development and, consequently, the health of the offspring [4]. As a result, therapeutic interventions and diagnostic measurements which target the microbiota of the mother could prevent a negative impact on offspring health and premature birth [5]. Another assumption is that, after birth, the changing pattern of microbial populations relative to human development can be used to determine the importance of the microbiota in the development of individuals with healthy growth phenotypes. Therefore, it could be deduced that deviations from normal microbial communities lead to abnormal development such as precocious maturation or immaturity [6].

The human body hosts at least 10^{14} microorganism and harbors more microbes than body cells [3,7]. All human-associated microbes are collectively known as microbiota and the microbiota encoding genes form the microbiome [6,8]. It is estimated
that the human gastrointestinal tract has 10 million genes which are associated with different microbial species and all genes have some beneficial impact on the health of the host, with possible effects on the homeostasis of the immune system, conversion of food into useful nutrients and protection against pathogenic microorganisms invading. However, due to the differences of diets, the microbiota differs widely from individual to individual and each person carries hundreds of microbial species that remain unchanged throughout adulthood [9–11].

The gut microbiota consists of bacteria, archaea, fungi, protozoa and viruses [12]. The microbial communities interact with each other and with their host, causing influence on the physiology and health of the host. The human gut microbiota is composed of both anaerobic and aerobic microbial communities [13]. Most gut microorganisms are strictly anaerobic bacteria and difficult to be cultured in vitro. At present, it is estimated that less than 30% of the gut microbial populations have been successfully cultured. However, this does not imply that all other bacterial species are unculturable, but rather that the optimal growth conditions for these microbes have not yet been discovered [14]. The development of high-throughput sequencing techniques has revolutionized the research process on currently uncultured microbes providing an insight into their mechanisms [15]. The dominant bacterial species in the human gastrointestinal tract are divided into three phyla: the phylum Bacteroidetes (e.g. Porphyromonas, Prevotella etc.), the phylum Firmicutes (e.g. Ruminococcus, Clostridium, Eubacteria etc.) and the phylum Actinobacteria (Bifidobacterium). Other bacteria such as Lactobacilli, Streptococci and Escherichia coli (E.coli) are found in small numbers. Based on the evidence from genomic technologies, the Bacteroidetes and Firmicutes phyla were found to be the dominant bacterial populations in the gastrointestinal (GI) tract (Fig. 1) [16,17].

The GI tract is currently reported to be sterile during gestation and become colonized after birth. Colonization of bacteria in the GI tract depends upon various factors such as type of childbirth and method of postnatal feeding [18]. The gut microbial population is transferred from mother to child and its composition is affected by various genetic factors [19,20]. The microbiota populations are also affected by diet and can be involved in the development of various diseases such as cancer, metabolic diseases and obesity. High-carbohydrate diets favor the Prevotella genus, whereas high-fat and high-protein diets promote the development of Bacteroidetes and Firmicutes species [21–23].

A disturbance in the interaction between nutrition, metabolism and microbiome may constitute an important factor in the deregulation of normal host homeostasis. Such disturbances in the structure and function of microbiota have been found to be related to the development of various diseases. It is, therefore, necessary to clearly define the range and composition of a normal, healthy microbiota. MetaHit and the Human Microbiome Project are conducting an in-depth analysis of the human-associated microbial communities and their function in maintaining the host homeostasis using various techniques [24–28].

After analyzing the currently available data, this review gives a comprehensive summary on the reports to illustrate how the interaction between microbiota and food affects human physiology and, thus, generate useful information for the prevention of multiple diseases.

2. Impact of diet on GIT microbiota

Protein, fat and carbohydrates are the most comment and major components in diets of human. The type and amount of protein, fat and carbohydrates present in the diet have been widely found to influence the composition of the gut microbiota in the host. This effect is related to the metabolites of the components present in diets. Short chain fatty acids, acetate and butyrate are reported as the end products of microbial-mediated degradation of protein and carbohydrates in the GIT tract (GIT). Short chain fatty acids produced by GIT microbiota are the most extensively studied metabolites of diets and have been found to have a physiological effect on the health of the host [29].

Degradation of the protein in diets normally happens at the distal end of the colon, where the conditions are suitable for the secretion of proteolytic bacteria. The normal end products of protein degradation are amino acids, ammonia, amines and short chain fatty acids. High concentrations of ammonia have been found to be related to the development of malignant growths [30–33]. Gathered results showed that the rats feeding on diets consisting of protein isolated from whey cheese or containing cysteine or threonine resulted in a significant increase in bifidobacteria or lactobacilli counts in their feces [34–36]. Also of note, the protein isolated from whey cheese could alter the microbiota composition in a dose-dependent manner. Furthermore, it was observed that the mice that were fed high fat diets along with the whey-isolated protein tended to have an increase in Lactobacillaceae counts and a decrease in Clostridiaceae counts compared with the mice fed on a normal diet [37].

Dietary fiber is an important food component derived from plants. However, fiber concentration is lower in processed foods than in raw vegetables. Dietary fibers pass from the small intestine to the colon where they are partially metabolized by bacterial species and the remaining fibers are then excreted through feces. Some polysaccharides such as insulin, starch and oligosaccharides are the typical examples of dietary fibers which can be degraded by bacteria. However, certain fibers, such as cellulose, cannot be completely degraded by bacteria when passing through the colon [38]. In the GI tract, some carbohydrates, such as starch and non-starch polysaccharides, cannot be directly metabolized by the host. These complex carbohydrates normally act as an important energy resource for microbial growth and can be degraded by proteolytic enzymes into short chain fatty acids and various gases. These carbohydrates are also referred to as prebiotics that are defined as the non-digestible component of food that benefits the host by stimulating the growth of the microbiota. Prebiotics are very important to induce changes in the composition of the gut microbial populations and confer multiple benefits to the host health. Prebiotics such as insulin, fructooligosaccharides and oligosaccharides act as important stimulants which promote the growth of bifidobacteria and lactobacilli [39–41]. Recent studies indicate that the consumption of prebiotics can modu-
late the gut microbial population and improve the hosts health [42].

It has been widely reported that the consumption of modern western diets containing less fiber and vegetables tended to result in the loss of some important microbial species in the western (urban) communities compared to rural communities. As previously mentioned, diets have a strong impact on the microbial diversity of individuals from different populations. For instance, when comparing an individual whose diet is high in fat and low in fiber with an individual on the opposite diet (e.g. high fiber and low fat), the latter tends to have a smaller amount of pathogenic bacteria and a large amount of beneficial microbes, such as *Prevotella* and *Xylanibacter* [43–45]. The balance of GIT microbial composition can be achieved as a result of symbiosis which regulates the immune system and protects the host from various diseases (Fig. 2).

The Mediterranean diet, which is based on a balanced intake of fruits, grains, monounsaturated fat, vegetables and polysaturated fats, is considered the standard for a healthy life style. It has been found that such diets have anti-inflammatory capabilities and can be used to reduce inflammation in diseases. Individuals fed on the Mediterranean diet have lower numbers of *Bacillaceae*, *Proteobacteria* and *acute phase C-reactive proteins*, but higher *Clostridium* and *Bacteroidetes* populations [46,47]. Vegetarian diets are also recognized as healthy and beneficial diets because they can protect the host from various chronic, metabolic and inflammatory disorders. Recent investigations showed that vegetarian diets could increase the number of *Faecalibacterium prausnitzii*, *Clostridium clostridioforme* and *Bacteroides Prevotella*, but decrease the ratio of *Clostridium cluster XIVa* species [48–50].

Small amounts of dietary fat can be digested and absorbed but some fat components cannot be metabolized and pass to the colon where they affect the microbial composition and are then excreted in feces. Consequently, the consumption of high-fat foods tends to induce substantial changes in the composition of GI tract microbiota [51,52]. Mice fed on high-fat diets have different microbiota composition from those that have been fed control or balanced diets [53]. High fat content and increased calorie consumption have the capability to induce changes in the microbial composition of the GI tract [54,55]. Table 1 highlights the impact of various dietary components on host microbiota and health status.

It has been also found that the children feeding on vegetarian diets rich in plant-based polysaccharides, fibers and starches had a significant increase in the number of *Firmicutes*, *Xylanibacter*, *Bacteroidetes* and *Prevotella* compared with those consuming a carbohydrate rich European diet. Therefore, it was suggested that children should be provided with a plant-based polysaccharide rich diet which confers protection against inflammatory disease [44].

Currently, it is clear that the composition of the microbiota differs among individuals living in different geographic regions and also depends on the long-term diet pattern. However, further investigation is required to identify the effects of long term and short term dietary patterns on the microbiota composition.

### 3. Impact of GIT microbiota on various diseases

The GIT microbiota has recently become a major subject of clinical research. Various studies have described the role of microbiota in ameliorating liver disease, irritable bowel syndrome, chronic inflammation, constipation, food allergies and cancers [43,60–64]. The gut microbiota interacts with the lymphoid tissue and epithelium, and, thus, plays an important role in the regulation and development of the host defense system [65,66]. The gut microbiota is involved in the regulation of antimicrobial peptides, mucin gene expression and paracellular permeability of the paneth cells of the small intestine. Moreover, a healthy microbiota is necessary for the maturation of the B cells and T cells, and the maintenance of proper immunoglobulin levels in the serum [67–69]. Recent studies showed that several diseases might be associated with the change in composition and metabolic activities of gut microbiota [70–72]. Changes in the composition and function of GI tract microbiota have also been linked to aging, obesity, neurodevelopmental disorders, cirrhosis, cardiovascular diseases and cancer [73–83].

#### 3.1. GIT microbiota and cancer prevention

The intestinal microbiota has been increasingly recognized to be involved in the pathogenesis of diseases, even some kind of...
Balance of GIT microbial composition could be achieved through symbiosis which regulates the immune system and protects the host from various diseases. Symbiosis could occur through the consumption of balanced diets. Dysbiosis, which could be caused by an imbalanced diet, dysregulates the immune system of the host which then becomes susceptible to inflammation and diseases.

Table 1
Influence of dietary components on host health and GIT microbiota.

<table>
<thead>
<tr>
<th>Dietary component</th>
<th>Influence on microbiota</th>
<th>Influence on host health</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Less vegetable, fish and fruits</td>
<td>Reduced microbiome [50]</td>
<td>Enhance of inflammation, triglyceride level, lipoproteins cholesterol Not fully understood</td>
<td>[50]</td>
</tr>
<tr>
<td>Shift from vegetarian to animal centered diets</td>
<td>Enhances Enhanced Bacteroides and reduces reduced Prevotella counts [56]</td>
<td>Not fully understood</td>
<td>[56]</td>
</tr>
<tr>
<td>Low carbohydrate intake</td>
<td>Decreases Decreased Eubacterium rectale, Bifidobacterium and Roseburia species [52]</td>
<td>Not fully understood</td>
<td>[52]</td>
</tr>
<tr>
<td>High protein diet</td>
<td>Causes a rRiched Bacteroides associated enterotype, and decreases decreased Firmicutes [22,56]</td>
<td>Decrease in weight</td>
<td>[22,56]</td>
</tr>
<tr>
<td>Reduced food intake</td>
<td>Decreases Decreased overall microbial diversity [53]</td>
<td>Overall poor and declining health</td>
<td>[53]</td>
</tr>
<tr>
<td>Western diet</td>
<td>Reduces Reduced Bacteroidetes and increases increased Firmicutes [57–59]</td>
<td>Inducing obesity</td>
<td>[57–59]</td>
</tr>
<tr>
<td>Plant-based, polysaccharide rich diet</td>
<td>Reduces Reduced Firmicutes and increases increased Bacteroidetes [59]</td>
<td>Increasing gut transit time</td>
<td>[59]</td>
</tr>
</tbody>
</table>
population tends to decrease [58]. However, a decrease in Bac-
teroidetes and an increase in the Firmicutes population, with normal levels of Firmicutes has recently been reported [74]. These microbial communities have a higher capacity to harvest food energy and produce low levels of inflammation. The decrease in microbiota composition in obese individuals is thought to be related to the reduction in insulin sensitivity and the stimulation of inflammation [23,74]. Research based on animal models found that host genetics and some environmental factors alter the microbiota composition and induce obesity [57,94]. The increase in harvesting food energy in the obese individuals is due to the hydrogen transfer between the microbiota phyla, since there is a consequent increase in hydrogen-using and hydrogen-producing microbes in those individuals [95]. The low level of chronic inflammation is found to be a major factor which causes obesity and enhances the level of macrophages, T cells, tumor necrosis factor, interleukin and mast cells [96].

In obese mice, Bifidobacterium species increase significantly and, thus, modulate the inflammation by producing glucagon peptide-2 and reducing lipopolysaccharide translocation [97]. The first finding demonstrating the role of microbiota in stimulating obesity came from a study that used germ free mice and showed the resistance to diets. Here, induced obesity depended on the macronutrient composition of the diets and improved the fat storage on microbiota colonization from the conventional donor [98–100].

Overall, the results of these studies indicate a link between dysbiosis and obesity, and suggest that the microbiota can enhance the host fat storage. However, the mechanisms responsible for the induction of obesity are very complex and still not completely understood.

### 3.3 GIT microbiota and type 2 diabetes

Type 2 diabetes alters the composition of gut microbiota and microbiota function such as the secondary metabolite bile acids and butyrate products. These functions are crucial for insulin sensitivity. The status of gut microbiota can be used to successfully distinguish between type 2 diabetes patients and healthy individuals in Chinese and European populations. Type 2 diabetes was linked to higher amounts of Lactobacilli and lower amounts of Roseburia when comparing the two populations [77,78,101–103]. However, the current understanding of the effect of GIT microbiota on type 2 diabetes is very limited. Further research is necessary to elucidate the interaction between the microbiota and the metabolism of the host, as well as to determine its impact on type 2 diabetes.

### 3.4 GIT microbiota and cardiovascular diseases

Cardiovascular diseases are the leading cause of death worldwide. The first indication of a link between GIT microbiota and cardiovascular diseases came from studies concerned with impaired dental health, cardiovascular diseases, infectious agents and atherosclerosis. Recent studies showed that certain bacterial strains used for the prevention of cardiovascular diseases exhibited antimicrobial activities [104–106]. Bacterial DNA identified from atherosclerotic plaques demonstrated the
Table 2
Effect of lactic acid bacteria on gastrointestinal cancer cells.

<table>
<thead>
<tr>
<th>LAB</th>
<th>Cell lines</th>
<th>Results</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Pediococcus pentosaceus</em> GS4</td>
<td>HCT-116</td>
<td>Induction of apoptosis, proliferation inhibition and downregulation of NF-kB and p-Akt</td>
<td>[90]</td>
</tr>
<tr>
<td><em>Kluyveromyces marxianus</em> YAS</td>
<td>Caco-2 and HT-29</td>
<td>Inhibition of cell proliferation, induction of apoptosis and upregulation of apoptosis-related genes</td>
<td>[91]</td>
</tr>
<tr>
<td><em>Lactobacillus brevis</em> SBL8803</td>
<td>SW-620, Caco-2 and HT-29</td>
<td>Reduction of cell viability</td>
<td>[87]</td>
</tr>
<tr>
<td><em>Lactobacillus plantarum</em> A7</td>
<td>Caco-2 and HT-29</td>
<td>Inhibition of cell proliferation</td>
<td>[84]</td>
</tr>
<tr>
<td><em>Lactobacillus acidophilus</em></td>
<td>Caco-2</td>
<td>Inhibition of cell proliferation, reduction of migration and invasion ability</td>
<td>[88]</td>
</tr>
<tr>
<td><em>Lactobacillus casei</em> NCIMB 701359</td>
<td>Caco-2 and SW-480</td>
<td>Induction of apoptosis, inhibition of proliferation</td>
<td>[57]</td>
</tr>
<tr>
<td><em>Lactobacillus pentosus</em> B281, <em>Lactobacillus plantarum</em> B282</td>
<td>Caco-2 and HT-29</td>
<td>Inhibition of cell proliferation</td>
<td>[81]</td>
</tr>
<tr>
<td><em>Lactobacillus rhamnosus</em>, <em>Lactobacillus crispatus</em></td>
<td>HT-29</td>
<td>Inhibition of cell proliferation</td>
<td>[82]</td>
</tr>
<tr>
<td><em>Lactobacillus paracasei</em> subp. paracasei X12</td>
<td>HT-29</td>
<td>Arrest cell cycle through the regulation of mechanistic target of rapamycin (mTOR) signaling pathway</td>
<td>[89]</td>
</tr>
<tr>
<td><em>Lactobacillus casei</em> ATCC 393</td>
<td>HT-29 and CT-26</td>
<td>Inhibition of cell proliferation</td>
<td>[84]</td>
</tr>
<tr>
<td><em>Lactobacillus reuteri</em></td>
<td>Caco-2</td>
<td>Caused significant cytotoxicity in treatment of up to 72h</td>
<td>[57,89]</td>
</tr>
<tr>
<td><em>Lactobacillus fermentum</em></td>
<td>Caco-2 and SW-480</td>
<td>Inhibition of cell proliferation</td>
<td>[84]</td>
</tr>
</tbody>
</table>

presence of a microbial load in the plaques which was, therefore, associated with influencing the development of cardiovascular diseases [107,108]. However, Metagenomic analysis of the fecal microbiome of healthy individuals and atherosclerosis patients showed a decrease in beta-carotene production gene (anti-inflammatory) and an increase in the peptidoglycan synthesis gene (proinflammatory) in the afflicted population [109].

3.5. GIT microbiota and parkinson’s disease

Parkinson’s disease is the most common neurodegenerative disease, affecting 1%–2% of the population over the age of 65 years. In recent decades, it was discovered that changes in neurodegenerative disorders occur through bidirectional communication in the gut-brain axis [110–112]. The gut-brain axis, or interaction, is developed during stress responses and it is believed that neuronal degeneration in conjunction with cognition and gastrointestinal disorders occur together. Hence, the neuro-hormonal factors and the gut microbiota influence the gut and brain function. It has been accepted that the gut microbiota influences the function of the central nervous system by establishing the pathway known as microbiota-gut-brain axis [113]. Dysfunctions in the microbiota-gut-brain axis result in the development of Parkinson’s disease as evidenced by various disease symptoms [114,115]. Pain is experienced by approximately 45%–85% of Parkinson’s disease patients. However, it has been noted that changes in the microbiota are associated with different types of pain such as migraines, autoimmune related pain, inflammatory pain and visceral pain in patients with rheumatoid arthritis [116–118]. The communication pathways are very complex involving neurochemical signaling molecules which are used to facilitate this communication process. The gut microbiota stimulates the production of short-chain fatty acids and certain neurotransmitters. These factors contribute to the development of Parkinson’s disease and the associated pains [119,120]. Therefore the microbiota has the potential to modulate the pain in Parkinson’s disease patients.

4. Conclusions

Over the past decades, researchers have established a link between the alteration of gut microbial composition and various diseases. Diet affects the host health status by modulating the composition of the gut microbiota. It has been found that normal gut microbiota affects the development of the immune system, nutrient absorption, tissue generation, morphogenesis, and bone homeostasis metabolism. In this paper, we summarized the recent developments concerning the relationship between diseases and the gut microbiota. The modulation of the gut microbiota is a hot topic of interest and may benefit the health of the host (Fig. 3). However, there is still a substantial gap in our understanding of how diet modulates the microbiota and how microbiota modulates the immunity of the host. New tools and new approaches are needed for further investigations, as the modulation of the GIT microbiota represents a promising new method for the prevention, management and treatment of various diseases.

Disclosure statement

The authors declare that there are no conflicts of interest.
Acknowledgements

This study was supported by the National Key Technology R&D Program (grant number 2015BAD16B02) and the National Natural Science Foundation of China (NSFC) (grant number 31201408 and 31471718).

References


