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**Effects of a high-fat diet on intestinal microbiota and gastrointestinal diseases**

Yang XJ *et al.*Effects ofhigh-fat diet

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**Abstract**

Along with the rapid development of society, lifestyles and diets have gradually changed. Because of overwhelming material abundance, high-fat, high-sugar, and high-protein diets are common. Numerous studies have determined that diet and its impact on gut microbiota are closely related to obesity and metabolic diseases. Different dietary components affect gut microbiota, thus impacting gastrointestinal disease occurrence and development. A large number of related studies are progressing rapidly. Gut microbiota may be an important intermediate link, causing gastrointestinal diseases under the influence of changes in diet and genetic predisposition. To promote healthy gut microbiota and to prevent and cure gastrointestinal diseases, diets should be improved and supplemented with probiotics.

**Key words:** Intestinal microbiota; Gastrointestinal diseases; High-fat diet

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**Core tip:** Along with the rapid development of society, lifestyles and diets have gradually changed. Because of overwhelming material abundance, high-fat, high-sugar, and high-protein diets are common. Numerous studies have determined that diet and its impact on gut microbiota are closely related to obesity and metabolic diseases. Different dietary components affect gut microbiota, thus impacting gastrointestinal disease occurrence and development. A large number of related studies are progressing rapidly. In this review, we summarize the relationship between a high-fat diet, gut microbiota, and gastrointestinal diseases.

Yang XJ, Zhang M. Effects of a high-fat diet on intestinal microbiota and gastrointestinal diseases. *World J Gastroenterol* 2016; In press**INTRODUCTION**

Along with the rapid development of society, lifestyles and diets have gradually changed. Because of overwhelming material abundance, high-fat, high-sugar, and high-protein diets are common. Numerous studies have determined that diet and its impact on gut microbiota are closely related to obesity and metabolic diseases[1]. Different dietary components affect gut microbiota, thus impacting gastrointestinal disease occurrence and development. A large number of related studies are progressing rapidly. In this review, we summarize the relationship between a high-fat diet, gut microbiota, and gastrointestinal diseases.

**BASIC COMPOSITION OF INTESTINAL MICROBIOTA**

The intestinal tract is the primary site of bacterial colonization in the human body. These complex and diverse bacteria form the gut flora. There are more than 1000 bacterial species in the human gut, and this number can reach as high as 1 × 108 species. The intestinal flora is primarily composed of anaerobes, facultative anaerobes, and [aerobe](http://fanyi.baidu.com/#auto/auto/aerobe)s. Anaerobes comprise more than 99% of gut microbes.The intestinal flora of the human body primarily includes Firmicutes, Bacteroidetes, Actinomycetes, Proteobacteria, Verrucomicrobia, and Archaebacteria. More than 90% are Firmicutes or Bacteroidetes. The Firmicutes, Bacteroidetes, Proteobacteria, and Actinomycetes comprise 64%, 23%, 8%, and 3% of the gut microbiota, respectively[2]. The intestinal flora of the human body is established in infancy and gradually stabilizes with age. By approximately 2 years of age, it is similar to the adult intestinal flora[3]. The intestinal flora composition differs by age group. The proportion of Firmicutes and Bacteroidetes in infants, adults, and the elderly is 0.4, 0.9, and 0.6, respectively[4].

**EFFECT OF A HIGH-FAT DIET ON INTESTINAL MICROBIOTA**

Diet is an important factor determining intestinal flora composition. It plays a critical role in the colonization, maturation, and stability of the intestinal flora. Both animal and human experiments have demonstrated that dietary changes can rapidly affect intestinal flora structure. Within 4 days of eating a specific dietary component, the human intestinal flora composition will change significantly[1,5].

Animal experiments have indicated that dietary structure affects intestinal flora. The proportion of Bacteroidetes decreased, and the proportion of Firmicutes increased, which increased the proportion of Mollicutes, in the intestinal tracts of mice fed a high-fat and high-sugar diet compared with mice fed a low-fat and high-sugar diet[6]. Intestinal flora diversity is reduced in mice fed a high-fat and high-sugar diet. However, control diet consumption gradually reversed these changes. Furthermore, one study investigated varying proportions of dietary fatty acids in mice for 8 weeks. A diet high in saturated fatty acids led to an increased proportion of intestinal Firmicutes and decreased intestinal flora diversity[7]. This study suggests that dietary fats and saturated fatty acid intake may affect intestinal flora composition. One study found that converting a low-sugar, low-fat diet to a high-sugar, high-fat diet caused a rapid decline in the number of Bacteroidetes in the intestines[8]. Another study also suggested that the number of *Bacillus bifidus* was reduced in mice fed a high-fat diet[9]. Animal studies have demonstrated a significant reduction in the number of lactic acid bacteria, *Bacillus bifidus*, and *Enterococcus*, in the intestinal tract of the group fed a high-fat diet. Furthermore, the phylum Bacteroidetes displayed a decreasing trend, while the *Bacillus fusiformis* displayed an increasing trend[10-11].

Human experiments have also demonstrated that dietary composition affects intestinal flora. Compared with Italian children, who consume a large amount of plant protein, fat, sugar, and starch, the proportion of Bacteroidetes in the intestinal flora of African children was high, while the proportion of Firmicutes was low[12] (Table 1).

**RELATIONSHIP BETWEEN INTESTINAL MICROBIOTA AND GASTROINTESTINAL DISEASES**

The composition and proportion of gut microbiota are closely related to human health. Upsetting the gut microbiota equilibrium can cause enteric dysbacteriosis and a variety of gastrointestinal and systemic diseases[13].

***Intestinal microbiota and inflammatory bowel disease***

Inflammatory bowel disease (IBD) comprises a group of inflammatory conditions of the colon and small intestine, including Crohn’s disease (CD) and ulcerative colitis (UC), the cause and pathogeny of which are not completely understood. Gut microbiota are closely related to IBD occurrence and development. Although the specific bacteria involved in IBD have not been identified, the gut microbiota in patients with IBD differ from those of healthy individuals. One study[14] determined that the total number of mucosa-associated bacteria in the IBD group was higher than that in the control group. In the CD group, *Streptococcus* was dominant in the inflammatory mucosal region, while in the UC group, lactic acid *Bacillus* was dominant. Studies have demonstrated that the number of *Faecalibacterium prausnitzii* decreased in patients with CD[15]. Their secretory products have immune regulatory activity *in vitro*[16]. IBD pathogenesis includes intestinal flora imbalance, increased pathogenic bacteria, toxin damage to the intestinal epithelium, immune function abnormalities, and immune tolerance imbalance. Intestinal bacteria can induce epithelial endoplasmic reticulum stress, leading to intestinal mucosal barrier damage and increased intestinal permeability. Probiotic supplements in patients with IBD can effectively alleviate symptoms and delay disease progress[17-18].

***Intestinal microbiota and irritable bowel syndrome***

Irritable bowel syndrome (IBS), affecting approximately 5%–25% of the population, comprises a group of symptoms, including abdominal pain and changes in bowel movement patterns, without any evidence of underlying damage. The mechanisms of IBS are unclear. One study found that 3–36% of intestinal infections can cause persistent symptoms of IBS, which suggests that gut microbiota play an important role in IBS onset[19]. Intestinal flora may affect gastrointestinal motility, visceral sensitivity, the inflammatory response, and the brain-gut axis, which lead to IBS. A number of studies have confirmed that the intestinal flora of patients with IBS differs from that of healthy individuals[20-21]. At present, however, intestinal flora composition results in patients with IBS have been inconsistent, and some have been contradictory. These inconsistencies may be owing to differences in specimen collection, molecular detection methods, or definitions of IBS[22]. The majority of studies have found that the Bacteroidetes are reduced, while the Firmicutes are increased in the intestinal flora of patients with IBS. However, it is not yet determined whether the changes in intestinal flora directly cause or are secondary to IBS. In the future, treatment of the intestinal flora imbalance may become an option for patients with IBS[23].

***Intestinal microbiota and tumors***

Colorectal cancer is a common gastrointestinal tumor, the incidence and mortality rates of which are increasing each year. Most colorectal cancers are due to old age, lifestyle factors, and underlying genetic disorders. Additionally, changes in the gut microbiota are closely related to colorectal cancer occurrence and development[24]. Many studies have detected imbalances in the gut microbiota of patients with colorectal cancer, while those of healthy individuals are in equilibrium. Furthermore, some reports have suggested that changes in the gut microbiota can cause cancer directly. However, it is unclear which species of bacteria play a primary role in causing cancer[25-27]. There are two theories regarding the pathogenesis of colorectal cancer associated with intestinal flora. First, some intestinal bacteria may either directly or indirectly affect intestinal epithelial cells, causing genetic mutations. These bacteria are defined as “Alpha-bugs”[28]. Their direct effects include secreting toxic proteins, and the indirect effects include changes in intestinal flora that are more likely to cause mucosal immune responses and changes in colonic epithelial cells.When gene mutations accumulate, it can lead to colorectal cancer. The second theory is named the “driver-passenger”model[29]. Following colorectal cancer incidence, primary pathogens (defined as “drivers”) are [replace](http://fanyi.baidu.com/#auto/auto/replace)d by opportunistic pathogens (defined as “passengers”), which are more viable in the intestinal tumor microenvironment. Possible mechanisms of intestinal flora-induced colon cancer are summarized as follows: (1) the carcinogen precursor is absorbed by the stomach and then secreted into the intestinal cavity by the liver, and the active ingredient is released by intestinal flora activity; (2) the carcinogen precursor in food is released by intestinal flora activity; and (3) metabolites produced by intestinal flora induce carcinogenic effects. Many studies have explored the role of probiotics in colon cancer prevention[30]; however, there is not yet a consensus.

***Intestinal microbiota and liver disease***

The intestinal blood flows through the portal vein system to return to the liver. The liver affects intestinal function by secreting bile into the enterohepatic circulation. The physiological link between the two organ systems is called the “intestine-liver axis”. Studies have indicated that changes in intestinal flora play an important role in liver disease incidence and progression[31]. Intestinal probiotics can improve liver disease and are now widely used in its clinical treatment[32]. Nonalcoholic fatty liver disease (NFALD) is one of the most rapidly growing chronic liver diseases. A number of studies have indicated that intestinal flora play an important role in NFALD development[33]. Bacterial overgrowth and intestinal permeability are the primary mechanisms underlying endotoxemia and inflammatory reaction-initiated liver disease. One study confirmed the relationship between intestinal bacterial overgrowth and NFALD[34]. In another study, the relationship between intestinal permeability and NFALD was demonstrated in animal experiments[35]. Alcoholic fatty liver was also associated with gut-derived [endotoxemia](http://fanyi.baidu.com/#auto/auto/endotoxemia). Specifically, ethanol intake in the intestinal tract may cause intestinal mucosal injury and intestinal flora disorder, resulting in increased endotoxin-induced intestinal epithelial permeability, bacterial translocation, and [endotoxemia](http://fanyi.baidu.com/#auto/auto/endotoxemia)[36]. The intestinal flora in patients with liver cirrhosis is dramatically disordered. One study demonstrated a significant decrease in *Bacillus bifidus* and lactic acid *Bacillus* in the intestinal tract of patients with liver cirrhosis, suggesting the possibility of intestinal bacterial translocation and increased infection[37]. The occurrence of primary hepatocellular carcinoma is also associated with intestinal flora imbalance[38].

**CONCLUSION**

In summary, gut microbiota may be an important intermediate link, causing gastrointestinal diseases under the influence of changes in diet and genetic predisposition. A diet that is high in fat especially high in saturated and trans fat is closely related to obesity, metabolic syndrome and gastrointestinal diseases; in substitution, polyunsaturated fats such as omega-3, omega-6 and omega-9 in right proportion are suggested. To promote healthy gut microbiota and to prevent and cure gastrointestinal diseases, diets should be improved with low-fat, low-sugar, high fruits and vegetable intake and complex fibres, and supplemented with probiotics or increase fermented dairy products consumption such as yogurt and buttermilk. It is essential for patients with GI diseases to not only change their dietary composition, but also establish a healthy eating habit and pattern to promote healthy microbiota as well as to alleviate diseases-associated syndromes. Maintenance of normal gut microbiota may be potentially key means of preventing GI diseases in the future.

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Grade E (Poor): 0

**Table1 Effect of a high-fat diet on intestinal microbiota**

|  |  |  |  |
| --- | --- | --- | --- |
| **Diet** | **Intestinal flora** | **Animal experiments** | **Human experiments** |
| **High**-fat diet | Bacteroidetes  Firmicutes | decreased  increased | decreased  increased |
| **Low**-fat diet | Bacteroidetes  Firmicutes | increased  decreased | increased  decreased |