

ISSN: 2644-2981 Global Journal of Nutrition & Food Science

ris Publishers

# **Short Communication**

Copyright © All rights are reserved by Tulika Mishra

# **Impact of Diet on Gut Microbiome**

## Tulika Mishra\*

Pathological Processes & Therapeutics, American University School of Medicine, Oranjestad, Aruba

**\*Corresponding author:** Tulika Mishra, Pathological Processes & Therapeutics, American University School of Medicine, Oranjestad, Aruba.

Received Date: May 15, 2023 Published Date: May 26, 2023

#### Abstract

In recent years there has been a growing interest in the field of gut microbiota and its relationship with food. It is now well known that gut microbiota is related to many diseases. Healthy gut microbiota is related to the diet that we consume. The human gut commensal mainly consists of anaerobes that belong to Bacteroidetes or Firmicutes. These commensals convert dietary fibers into Short-chain fatty acids which are further required in many metabolic processes. Production of vitamins, Short-chain fatty acids, etc depends upon the substrate that has been provided to the gut microbiota, and that substrate is the diet. Consumption of protein, fat diet, digestible and nondigestible carbohydrates, Fruits, seeds, vegetables, Probiotics, and Prebiotics have their own impact on gut microbiota. Therefore, the aim of this review is to discuss the impact of various dietary molecules on the gut microbiota.

Keywords: Gut Microbiome; Dietary components; Short-chain fatty acids; Bifidobacterium; Lactobacilli

Abbreviations: gastrointestinal (GI), short-chain fatty acids (SCFAs)

## Introduction

Our relationship with commensal microorganisms is intimate. Since the time of birth, commensal enters the germ-free system of a neonate and proliferates dramatically in a favorable manner. The gastrointestinal (GI) tract alone harbors 10 times more bacterial cells than eukaryotic cells in the entire human body [1]. These microbial species help in regulating various biological processes including stimulation of the immune system, neurological health benefits from the gut-brain axis, and aid in the uptake of nutrients from food in the large intestine [2]. It is very well documented that Food is a major source of energy that promotes growth and development, it even affects gut microbiota. The dietary changes may significantly change the gut microbial population [3]. These commensals are present throughout the gastrointestinal tract, although their density and species vary according to the anatomical site and other factors. As the pH of the stomach is low, so the density of commensals is also low. Contrary to this, the intestine is the most favorable anatomical site for these commensals. The human gut microbiota mainly consists of anaerobes.

The human gut microbiota is mainly populated with bacteria that belong to Bacteroidetes (Bacteroides or Prevotella species) or Firmicutes (mostly Clostridium and Lactobacillus species) that are gram-positive, in addition to this 1% comprise of Fungi and Archaea [4].

The mutual relationship between the gut microbiota and host is beneficial for both. The microbiota is backed by the food that humans eat while the microbiota helps in digestion, establishing the immune system, endocrine system, and mental health. Disturbance in microbiota balance can result in many metabolic and brain-related diseases. Most of the microorganisms are found to be present in the colon where they metabolize the food that we eat into vitamins, essential amino acids, and other products such as butyrate, propionate, and acetate [5,6]. The maintenance of gut microbiota is very much dependent upon dietary habits. Although, other factors also play a role, but major role is played by dietary habits. The studies showed differences in gut microbiota between people and across geographies and lifestyles [7,8].

#### **Effect on Metabolism**

The gut microorganism metabolizes the food provided by the host into vitamins, molecules required for other processes, antimicrobial substance, etc. the dietary fibers and mucin are converted into short-chain fatty acids (SCFAs) which mainly includes acetate, propionate, and butyrate. Short-chain fatty acids (SCFA) are mainly found in the cecum and proximal colon. Butyrate is commonly produced by Coprococcus comes, Coprococcus eutactus, Eubacterium rectale, Eubacterium hallii, Faecalibacterium prausnitzii, and is used by the colonic epithelial cell as a source of energy and is also utilized for the differentiation of T regulatory cells. Acetate is commonly produced by most enteric bacteria, e.g., Akkermansia mucinophila, Bacteroides spp., Bifidobacterium spp., Prevotella spp., Ruminococcus spp Clostridium spp., Streptococcus spp and is utilized to improve Epithelial integrity. Propionate is commonly produced by Bacteroides spp., Phascolarctobacterium succinatutens, Dialister spp., Veillonella spp., Salmonella spp., Roseburia inulinivorans, Ruminococcus obeum. Propionate, and butyrate indirectly affect the peripheral organs by stimulating hormones and the nervous system. In addition to this SCFA stimulates water and sodium absorption, decreases colonic pH, stops high-fat diet-induced obesity, reduces circulating cholesterol, and restrains the growth of pathogens [9].

Production of vitamins, SCFA, etc depends upon the substrate that has been provided to the gut microbiota, and that substrate is the diet. Even the presence of different types of microorganisms in the gut is also diet driven [10].

## Food Components & Gut Microbiota

Consumption of protein has been reported to increase gut commensal Bifidobacterium and Lactobacillus and decrease pathogenic Bacteroides fragilis and Clostridium perfringens. Plantbased proteins have also been found to increase intestinal SCFA levels whereas animal protein enhances Bacteroides and reduces fecal SCFA. Many of the important species like Bifidobacterium spp., Lactobacillus spp. etc. are associated with increased production of SCFA which are considered anti-inflammatory and play an important role in the mucosal barrier. Consumption of red meat increases the risk of cardiovascular disease as it increases the level of trimethylamine-N-oxide which is a proatherogenic compound [6].

The fat diet also influences the gut microbiota, it is believed that high-fat diets and saturated fatty acid diets should be avoided instead intake of monounsaturated and polyunsaturated is found to be helpful to regulate gut microbiota and inflammation [11].

The microbiome of the gut is also influenced by the presence of Digestible (Sugars, starch) and nondigestible carbohydrates (fibers) in the diet. It has been proved that Sugars increase the relative abundance of Bifidobacteria and reduce the number of Bacteroides and Clostridium species. The addition of non-digestible carbohydrates as in whole grain and wheat bran prompts a boost in gut Bifidobacteria and Lactobacilli. The addition of Prebiotics in the diet also encourages shifts in immune markers, resulting in reductions in the pro-inflammatory cytokine IL-6 [6].

Fruits, seeds, vegetables, tea coca products, and wine are rich in polyphenols. The addition of polyphenols in the diet in the form of fruits, vegetables, etc. increases Bifidobacterium and Lactobacillus and reduces the numbers of Clostridium perfringens and Clostridium histolyticum. Fruit polyphenols are found to be active against enteropathogens Staphylococcus aureus and Salmonella typhimurium. Even different types of diets also affects the gut microbiome. Studies have shown that consumption of Western diet (high in animal protein and fat, low in fiber) reduces the beneficial Bifidobacterium spp. and Eubacterium spp. Gluten free diet increases Enterobacteriaceae and Clostridiaceae spp. and reduces beneficial Bifidobacterium, Lactobacillus, Ruminococcus bromii [7].

Prebiotics are another substance that enhances the gut microbiota. These substances can be obtained from various sources, including soybeans, raw oats, and honey. The most popular prebiotics are plant oligosaccharides. Nondigestible carbohydrates, including polysaccharides (resistant starch, pectin, and dextrin) and oligosaccharides, such as fructooligosaccharides, galactooligosaccharide, mannan oligosaccharides, raffinose oligosaccharides, arabinoxylan oligosaccharides, lactulose, and inulin, possess prebiotic properties [12]. Prebiotics are fermented by gut microbiome and produce short-chain fatty acids. These short-chain fatty acids improve intestinal membrane integrity and absorption of minerals, lowering both glycemic levels and body weight, improving immunity, and modulation of metabolic, cardiovascular, and inflammatory biomarkers. The intake of prebiotics favors the growth of beneficial bacteria, such as Lactobacillus and Bifidobacterium, which are responsible for the inhibition of the proliferation of harmful bacteria [13].

Probiotics are another highly beneficial substance for the gut microbiome. These are live microorganisms that can be taken by consuming a large range of fermented products. Most common fermented products include yogurt, kefir, sauerkraut, tempeh, and kimchi. The most common probiotics bacteria include Lactobacillus, Lactococcus, Leuconostoc, Pediococcus, Propionibacterium, Bifidobacterium, Bacillus, some Streptococcus, Enterococcus, Escherichia coli) and yeast (Saccharomyces) genera. As most of the probiotics do not colonize the gut, therefore for better results their continuous consumption is encouraged [13].

Unevenness in the gut microbiota can influence the health of the individual. It is very well-documented that dysbiosis is associated with many diseases including obesity, type 2 diabetes, asthma, allergies, and inflammatory bowel disease. A balanced diet is very important for healthy gut microbiota.

#### Acknowledgments

None.

# **Conflict of Interest**

No conflict of interest.

### References

- 1. Hooper L, Gordon J (2001) Commensal host-bacterial relationships in the gut. Science 292: 1115-1118.
- Naliyadhara N, Kumar A, Gangwar SK, Devanarayanan TN, Hegde M, et al. (2023) Interplay of dietary antioxidants and gut microbiome in human health: What has been learnt thus far? J Functional Foods 100: 105365.
- Rothschild D, Weissbrod O, Barkan E, Kurilshikov A, Korem T, et al. (2018) Environment dominates over host genetics in shaping human gut microbiota. Nature 555(7625): 210–215.
- Consortium THGP (2012) Structure, function and diversity of the healthy human microbiome. Nature 486(7402): 207-214.
- 5. Simpson HL, Campbell BJ (2015) Review article: dietary fiber-microbiota interactions. Aliment Pharmacol Ther 42(2): 158-179.
- Singh RK, Chang HW, Yan D, Lee KM, Ucmak D, et al. (2017) Influence of diet on the gut microbiome and implications for human health. J Transl Med 15(1): 73.
- Graf D, Cagno R, Fak F, Flint HJ, Nyman M, et al. (2015) Contribution of diet to the composition of the human gut microbiota. Microb Ecol Health Dis 26: 26164.

- Yatsunenko T, Rey FE, Manary MJ, Trehan I, Dominguez-Bello, et al. (2012) Human gut microbiome viewed across age and geography. Nature 486: 222-227.
- Daliri EBM, Wei S, Oh DH, Lee BH (2017) The human microbiome and metabolomics: Current concepts and applications. Crit Rev Food Sci Nutr 57(16): 3565-3576.
- 10. Flint HJ, Duncan SH, Louis P (2017) The impact of nutrition on intestinal bacterial communities. Curr Opin Microbiol 38: 59-65.
- 11. Cândido FG, Valente FX, Grześkowiak LM, Moreira APB, Rocha DMUP, et al. (2018) Impact of dietary fat on gut microbiota and low-grade systemic inflammation: mechanisms and clinical implications on obesity. Int J Food Sci Nutr 69(2): 125-143.
- Farias DP, Araújo FF, Neri-Numa IA, Pastore GM (2019) Prebiotics: Trends in food, health and technological applications. Trends Food Sci. Technol. 93:23–35.
- Oniszczuk A, Oniszczuk, T, Gancarz M, Szymańska J (2021) Role of Gut Microbiota, Probiotics and Prebiotics in the cardiovascular diseases. Molecules 26(4): 1172.