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Effect of diet on human gut health: A review

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Abstract
Humans have trillions of different bacteria in their guts, including symbiotic species, opportunistic pathogens, and commensal organisms. This microbiota is essential for digestion, aids in the absorption and synthesis of some nutrients, and releases their metabolites. These metabolites may supply a range of growth-promoting and growth-inhibiting substances that may have an indirect or direct impact on human health. A person's daily diet affects the balance of microbial species, especially the majority species that are involved in the fermentation of various substrates. As a result, an unbalanced diet may contribute to the development and spread of human diseases. These include cancer, depression, cancer, inflammatory diseases, and infant health and longevity. The explanation of how nutrition impacts gut health in people will be abridged in this review article.

Keywords: Human gut microbiota, good and bad bacteria, balanced diet, dysbiosis, digestive disorders

Introduction
The human gut microbiome consists of 10^{14} commensal microorganisms that live in and around the human intestinal system. These include bacteria, viruses, fungus, and protozoa (Gill *et al*., 2006) [5]. In this list, bacteria are the group that has been the most thoroughly studied, so they will be the main topic of this review. Gramme positive bacteria make up the majority of the microbiome's major bacterial groupings. gram-negative bacteria and firmicutes *Bacteroidetes* (Flint *et al*., 2007; Walker *et al*., 2011) [4, 19]. Recently, it has been demonstrated that the microbiota may be efficiently separated into various enterotypes, each of which is enriched by distinct bacterial genera and which appears to have a high degree of functional homogeneity (Arumugam *et al*., 2011) [1]. This uniformity persists regardless of the host's age, sex, body mass index, and country of origin.

Microbiome and illness
IBD, inflammatory skin conditions like psoriasis and atopic dermatitis, autoimmune arthritis, type 2 diabetes, obesity, and atherosclerosis have all been linked by studies looking at the makeup and function of the intestinal microbiome in various disease states (Tewari *et al*., 2021) [15]. For instance, IBD patients typically have lesser bacterial diversity, as well as fewer Bacteroides and Firmicutes, all of which may work together to result in lower quantities of butyrate generated from microorganisms. It is believed that butyrate and other SCFAs directly reduce inflammation in the gut (Lucas *et al*., 2017) [11].

In this article, we thoroughly examine the host diet's capacity to influence gut flora in the aim that this information will help us better understand how dietary decisions affect human health through changing the digestive environment.

More than 10 trillion microbial cells make up the human GI tract's various mutualistic microorganisms, which produce a wide range of specialised metabolites, tiny bioactive compounds, and other chemicals that stimulate host metabolic and immunological systems (Tewari, 2019) [16]. As a result, the gut microbiota (GM) is also referred to as a "metabolic organ" having metabolic capability on par with that of the liver (O'Hara and Shanahan, 2006) [12]. The 100 trillion microbes that live on the surface of the human digestive tract are collectively referred to as the gut microbiome. Most of them are commensals, while there are a few potential or opportunistic pathogens. Such modifications result in adjustments to the host's metabolism and immune response systems, which ultimately have an impact on human health. Obesity, type 2 diabetes, and cardiovascular disease are among the numerous medical disorders for which the GMB is known to have a role in the aetiology.

Dietary Changes and the GMB

Within a day, a significant diet shift causes a significant change in the GMB's composition. However, the pattern returns within 48 hours after the new diet is terminated.

Diets high in fat or sugar tend to throw off circadian rhythms. Once more, rapid alterations could occur within 24 hours in response to significant systemic inflammation or stress.

Protein and the GMB

More microbial diversity is linked to higher protein consumption. Consuming light animal and vegetable proteins like those found in whey and beans promotes the growth of commensals like Bifidobacterium (which produces butyrate) and *Lactobacillus*. Additionally, whereas legumes promote the formation of SCFA, whey lowers pathogens like Bacteroides fragilis and Clostridium perfringens. In comparison to strict vegetarians, the GMB is enriched in anerobic bacteria such Bacteroides, Alistipes, Bilophila, and Clostridia but has reduced levels of Bifidobacterium adolescentis after eating large amounts of beef or other animal protein (Lucas *et al*., 2017) [11]. Diets strong in protein and low in carbohydrates have lower levels of Roseburia and Eubacterium rectale. E. rectale levels have been shown to be low in patients with IBD (inflammatory bowel disease). These findings might help to explain why eating more animal protein is associated with a higher risk of IBD. The atherogenic chemical trimethylamine-N-oxide (TMAO), which is connected to a number of bacterial kinds prevalent in meat-eaters at high levels, also raises the risk of CVD (Cho and Caudill, 2017) [3].

Fat and the GMB

Heart-healthy diets contain mono- and polyunsaturated fats but are low in saturated and trans fats, which are often common in Western diets. A higher concentration of anerobes, Bacteroides, Clostridiales, and Enterobacteriales are associated with high dietary fat content; these microorganisms produce more propionate and acetate but less Lactobacillus intestinalis. In rats, the latter has a negative correlation with weight increase. Faecalibacterium prausnitzii is found in greater abundance in foods high in saturated fats. On the other hand, a low-fat diet boosts Bifidobacterium abundance, resulting in lower levels of total cholesterol and fasting glucose. Additionally connected to metabolic inflammation and insulin sensitivity are these alterations brought on by fat (Singh, 2017) [14].

Carbohydrate and the GMB

Under the influence of enzymes, digestible sugars and starches degrade in the small intestine, increasing blood glucose levels and consequently insulin release. Dates, which are high in glucose, fructose, and sucrose, boost *Bifidobacteria* proportions while lowering Bacteroides. Additionally, lactose addition results in a decrease in clostridia and an increase in SCFAs. Diets high in carbohydrates are linked to a rise in the methanogen Methanobrevibacter and the yeast *Candida albicans*. In 85% of patients treated with nystatin, but only in 42% when nystatin was used alone, *Candida* overgrowth was healed by abstaining from dairy, alcohol, cured and fatty meats, simple starches, and sugars (Leeming *et al*., 2019) [10].

Therefore, lactose has positive effects on the GMB. Contrarily, the use of artificial sweeteners is questioned since they more strongly induce intestinal dysbiosis, which leads to glucose intolerance, than do natural sugars like glucose and sucrose. It has been suggested that the FODMAP diet (Fermentable oligosaccharides, disaccharides, monosaccharides, and polyols) can help to improve the GMB and relieve IBS symptoms. The stringent limitations on a variety of plant-based foods make it challenging to maintain over the long run. On the other hand, the specific carbohydrate diet (SCD) has been practised for more than a century (Horn *et al*., 2022) [8].

Foods that contain indigestible carbohydrates include raw oats, whole wheat, soybeans, and galactooligosaccharides (GOS), fructooligosaccharides (FOS), and inulin. These substances are also known as resistant starch and dietary fibre. "Microbiota accessible carbohydrates" (MACs) are provided by these. These are fermented in the colon by gut microorganisms (*LAB* and *Bifidobacterium*), providing the human host with energy and carbon sources, including SCFAs. The fermentation products' higher levels of SCFAs and improved activation of GALT through SCFA receptors and other pathways may have a positive impact on the gut environment. These adjustments are related to immunological and metabolic repair, with decreased inflammatory indicators, increased insulin sensitivity, and normalised post-meal glucose levels. Serum lipids as well as body mass are also decreased (Tomova *et al*., 2019) [17].

Probiotics and the GMB

Probiotics are microbes that are frequently present in fermented foods like yoghurt and cultured milk and can be consumed to enhance gut health and prevent or cure IBD. These microorganisms influence inflammation via influencing the GMB. Notably, they result in decreases in coliforms and total, very low density, and low-density cholesterol, as well as an increase in *Bifidobacteria* and/or *Lactobacilli*. They are related to improved insulin sensitivity at the same time. Such products reduce GI intolerance, and higher serum IgA levels signify a stronger immune response. Additionally, *Bifidobacteria* and *Lactobacilli* are utilised to stop traveler's diarrhoea (Hills *et al*., 2022) [7].

Polyphenols and the GMB

High polyphenol concentrations are found in fruits, tea, cocoa goods, and wine, which may assist to promote beneficial microorganisms. They have anti-inflammatory, anti-cancer, and immunomodulatory properties. Some of these substances are also antibacterial, working to combat the pathogen *Clostridia*, *Salmonella typhimurium*, and *Staphylococcus aureus* (Trinovani *et al*., 2022) [18].

Dietary pattern and the GMB

In general, westernised meals are detrimental to a healthy GMB since they are linked to decreased levels of *Bifidobacterium* and Eubacterium but increased levels of *E. coli* and *Enterobacteriaceae*. Contrarily, plant-based diets, whether vegan or vegetarian, support the growth of the *Bacteroides* and *Bifidobacterium* genus (Heidenreich and Mamic, 2020) [6].

Due to its composition, which is high in whole grains and legumes, nuts, fruits and vegetables, seafood, chicken, olive oil, and wine, and low in red or processed meat, sweets, and dairy products, the Mediterranean diet has a favourable fatty acid profile. Increases in SCFAs are associated with higher concentrations of beneficial LAB, *Bifidobacterium*, Prevotella, and Firmicutes and decreased levels of *Clostridia* (Brostow *et al*., 2021) [2].

GMB and its Physiological aspects

It has been observed that the third pathway through which the entire neuro-endocrine communication affects the role of this gut micro biota. Various neuro-transmitters which are mainly protein in nature and are released from the synaptic cleft can be controlled and altered by bacterial metabolites **(**Qi *et al*., 2021) [13]. Seretonin, dopamine, GABA (gamma amino buteric acid) & nor adrenaline are said to be the key role player regarding gut-brain interactions. In case of various interactions with various immune cells the gut bacteria can be sampled by the protrusions of dendritic cells and can be clearly identified by T lymphocytes and b lymphocytes in terms of increasing immunogenic properties (Kasarello *et al*., 2023) [9]. In a study of Wang *et al*. it has been observed that gut micro-biota may project some positive regulatory effects through which the risk for cardiovascular disease can be prevented (Zhou *et al*., 2023) [21]. During pandemic the respiratory inflammations can be controlled by various probiotics, herbs and fecal micro-biota in a very positive way relieving some clinical symptoms (Wang *et al*., 2023) [20]. The gut micro-biota plays a major role in producing steroidal hormones within woman interacting sexual characteristics. Hence the gut micro biota shows very efficient roles upon the various systems of the body, which are instrumental to the positive as well as negative regulations in response to the specific physiological systems.

Conclusion

A balanced and regular distribution of the various groups of gut bacteria is a result of a nutritious food consumed on a daily basis. Any disruption brought on by an unbalanced diet or food intake may cause the pathogenic groups of the gut microbiome to proliferate and the beneficial groups to decline.

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