THE IMPACT OF GUT MICROBIOTA ON GASTROINTESTINAL HEALTH: A REVIEW

Abstract

The gut microbiota, a dynamic and diverse population of microorganisms found in the human gastrointestinal system, has a major influence on the host during both homeostatic and disease states. One of the key determinants of how the gut microbiota changes throughout a person's lifetime is nutrition. A viable approach for managing digestive health may be based on the gut microbiome. As a person ages and is exposed to different environments, the composition of microbes changes accordingly. Eubiosis and dysbiosis are as crucial concepts for understanding their function in health and disease. The current knowledge about the human gastrointestinal microbiota and its impact on gut health, the role of diet on gut microbiota, and the role of microbiota epigenetics are vast.

Keywords: Gut microbiota, gastrointestinal tract, gastrointestinal health, eubiosis, dysbiosis

Authors

Priyaalini G
Assistant Professor
Department of Food Science and Nutrition
Dr. N.G.P. Arts and Science College of Arts and Science
Coimbatore, Tamil Nadu, India.

Rakeshwari M
Assistant Professor
Department of Food Science and Nutrition
Dr. N.G.P. Arts and Science College of Arts and Science
Coimbatore, Tamil Nadu, India.

I. INTRODUCTION

One of the strongest interfaces between the host, environmental factors, and antigens in the human is the gastrointestinal system (250–400 m2). Significant harm to intestinal health is posed by about 60 tons of food that travel through the human gastrointestinal tract in an average lifespan, combined with a diverse range of environmental bacteria (Bengmark, 1998). The term "gut microbiota" refers to a variety of microorganisms (bacterial species, archaea, and eukaryotic organisms) that inhabit the gastrointestinal tract and have co-existed with the host over a long time to create a unique and beneficial relationship (Neish, 2019).

Recent developments in genome sequencing methods and bioinformatics have made it feasible to extensively understand these bacteria, their function, and also how they interact among themselves and their hosts in both health and diseases. The healthy gut microbiota performs specific roles in the host's nutrient metabolism, the metabolism of xenobiotics and drugs, and the preservation of the structural integrity of the gastrointestinal tract mucosal barrier, immune regulation, and defense against pathogenic organisms (Jandhyala et al. 2015).

The normal human gut microbiota is influenced by many factors. They are a method of delivery (vaginal or cesarean), the diet during infancy (breast milk or formula feeds), food consumption throughout the life stage (vegetarian or nonvegetarian sources), and the use of antibiotics or antibiotic-like compounds that are obtained from the environment or the gut commensal community. This review highlights our current knowledge of human gut microbiota and its effects on gut integrity, gastrointestinal health, and disease.

II. DEVELOPMENT OF THE GUT MICROBIOTA FROM BIRTH TO THE ADULT STAGE

Labor and delivery provide the very first significant exposure to a sophisticated microbiota and also serve as the primary pathway for intergenerational microbiota transmission in humans. When the chorioamniotic membrane ruptures, the baby is exposed to various microbial populations from the mother's vagina and perineum. The chance of being infected by opportunistic microbiomes increases with prolonged labor (Bahn et al. 1998). After birth maternal milk called colostrum a single superfood with a complex biological composition, has a nutritive, immunological, hormonal, and prebiotic effect on the neonate, which encourages the development of the intestinal microbiota (Pacheco et al. 2015).

Bacteria can colonize on an epithelial mucosal layer, digested food particles, or survive freely in suspension in the liquid phase in the large intestinal tract and bowel. After exclusive breastfeeding has ended, the baby's gastrointestinal system gets matured enough to handle dietary particles reaching the post-absorptive site and bringing in new substrates. During this point, dentition starts. The microbial complexity of the gut progressively develops until the age of three years as a result of these solids change in the hindgut, promoting bacterial communities with essential metabolic activities. A complex diet's enhanced chemical diversity as well as the host's gut and immunological maturation may be responsible for the growth of gut microbial diversity (Yatsunenko et al. 2012).

The method of birth, diet, genetics, state of health, gestational age, and other factors can all have an impact on how the gut microbiota develops.

III. DISTRIBUTION OF GUT MICROBIOTA

The distribution and makeup of the gut microbiota differ along the length of the gastrointestinal tract, and also within the lumen, mucus layer, and epithelium (Shin et al. 2019).

IV. ROLES OF THE GUT MICROBIOTA

The gut microbiota carries out a broad range of different tasks, including assisting with food digestion, producing vital vitamins, synthesizing metabolites, preventing the colonization of pathogenic bacteria, regulating the gut immune system, metabolizing drugs, detoxifying the body, and preserving the physiological homeostasis of the gastrointestinal tract (Eisenstein, 2020). Therefore, it is essential for preserving human health to practice eubiosis or maintain a healthy proportion of helpful bacteria.

V. FACTORS AFFECTING VARIATIONS IN HUMAN GUT MICROBIOTA

The microbial composition and abundance may be influenced by some intrinsic variables, including mucus, pH, and intestinal permeability. Additionally, other extrinsic factors including antibiotics (Maier et al. 2018), analgesics (Wang et al. 2022), psychotherapies (Pu et al. 2022), and nutritional components (Haikonen et al. 2022) have an equally significant role. The gut microbiota demonstrates persistence, resilience, and symbiotic interactions with the host when things are going well.

A person's healthy gut microbiota is shaped by several factors and changes continuously throughout their lifetime. It is now clear that the delivery method significantly affects the baseline microbial profile. Lactobacillus and Prevotella genera are the best examples of bacteria from the mother's vagina that initially colonize the intestines of vaginally born infants (Gaskins, 1999). Contrarily, in cesarean delivery, the infant's intestine is primarily colonized by the skin flora of the mother, as evidenced by Streptococcus, Corynebacterium, and Propionibacterium dominance (Dominguez-Bello et al. 2010).

Breast milk or formula feeds after primary inoculation has a substantial impact on the microbiota's initial development, but dietary practices, lifestyle decisions, life events, and environmental factors, such as antibiotic use, have a longer-term impact (Sekirov et al. 2010). Infants that consume formula have gut niches dominated by anaerobic Streptococci such as Enterococcus, Enterobacteria, Bacteroides, Clostridia, and others, while infants who breastfeed have gut niches dominated by Bifidobacterium and Lactobacillus. These bacteria are capable of digesting the indigestible glycan known as human milk oligosaccharides (HMO), which is present in breast milk. The gut-associated lymphoid tissue (GALT), which plays a role in developing innate immunity during development, is said to be maintained by pre-term microbiota. Children may develop diseases as a result of abnormal gut microbiota colonization (Sherman et al. 2015).

Even as adults, diet remains the primary factor in determining composition, diversity, and richness. A gut microbiome with greater diversity and richness is typically associated

with diets high in fruits, vegetables, and fiber. It has been demonstrated by numerous studies that the gut microbiome exhibits significant seasonal and geographic variations. Nevertheless, these variations also had different dietary habits as contributing factors. The majority of studies on antibiotics have focused on their bactericidal and bacteriostatic effects on pathogens, but in recent years, there have been many investigations into how antibiotics affect the ecology of the gut's bacterial population more broadly.

A large amount of research has demonstrated that the use of antibiotics has numerous short- and long-term consequences on the ecology of the normal gut microbiota. It has been established that multi-drug resistant bacterial genes existed thousands of years before antibiotics were developed, highlighting the effects of contact with environmental small compounds with growth-inhibitory qualities (Dethlefsen et al. 2007).

VI. GASTROINTESTINAL DISORDERS

It is well known that each person's microbiome, which is the entirety of the genomic information contained inside the microbiota, is unique who appear to be in good health and undergoes changes due to factors such as aging, nutrition, and lifestyle (Shanahan et al. 2021).

A change in the ratio of beneficial to pathogenic microbes, a shift in the distribution of colonic bacteria, and a significant increase in the proportion of bacteria in the small intestine can all be signs of dysbiosis, a microbial imbalance in the gut (Ghoshal and Srivastava, 2014). GI disorders including colon cancer, celiac disease, inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS) might arise as a result of alterations in the gut microbiota.

VII. ROLE OF DIET ON GASTROINTESTINAL MICROBIOTA

Dietary habits can considerably affect the composition and functionality of our gut microbiota since different microorganisms require various settings to grow and survive. High fiber intake and switching Saturated Fatty Acids (SFAs) for Poly Unsaturated Fatty Acids (PUFAs) both are protective factors (Soliman, 2019; Micha and Mozaffarian, 2010).

The findings of the Kaczmarek et al. (2017) study show that the human gut microbiota's composition and function alter as the day progresses, which may be related to the human body's circadian rhythm, the microbial community itself, or dietary habits. The timing of meals and the length of overnight fasts were behavioral factors that also predicted bacterial abundance.

Food additive compounds used in the food preparation, the method of heat processing used to prepare the meal (roasting, steaming, and frying), the duration and intensity (uncooked, moderately cooked, and well-cooked), and several other elements like dietary patterns all have an impact on how food affects gut flora (Yu et al. 2021).

VIII. ROLE OF MICROBIOTA EPIGENETICS

The gut microbiota ferments the food consumed by the host to create metabolites. Metabolites produced by the microbiota act as a substrate, control its actions of the epigenetic modifying enzymes, affect the expression of the host genes, and trigger immunological inflammation in intestinal epithelial cells (IECs), all of which contribute to the development of several metabolic abnormalities (Woo and Alenghat, 2022). Probiotics, prebiotics, dietary supplements, histone deacetylase (HDAC) inhibitors, fecal bacteria transplantation (FMT), as well as other epigenetic medications, are now being developed rapidly (Li et al. 2022).

IX. CONCLUSION

More learning about the microbial pathogenesis of gut microbial alterations and the host's interactions with those microbes gives a better outcome to treat and control gastrointestinal tract dysmotility and associated metabolic manifestations. The revelatory findings on how gut microbiota changes and their impact on human health and disease, the statement of Hippocratic "all disease begins in the gut" is gradually gaining acceptance among microbiologists, gastroenterologists, endocrinologists, and epidemiologists. Generally, the first-line treatment is based on the type and stage of disease; these include diet, prebiotics, or probiotics and antimicrobials which are primarily aimed at changing the composition of the host microbiota. There aren't many studies that are conclusive about the adaptability of diet to keep a healthy microbiome because of the diversity of human nutrition and the significant influence that societal and cultural variables have on it. It is necessary to conduct more studies on the link between diet and gut flora.

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