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New Research on Respiratory Diseases and Gut Microbiota

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Abstract

A wide variety of microorganisms, including bacteria, fungi, and viruses, colonise the skin, intestines, respiratory and urogenital tracts, as well as other human body surfaces. The gut is the most heavily and densely colonised organ. The microbiome is essential for the growth of the immune system and tissue homeostasis. Dysbiosis of the gut microbiota influences lung health and respiratory conditions by affecting not just the immune responses of the GI tract but also the immunity of distal organs like the lung. We present a review of recent research on the associations and underlying mechanisms of the relationship between the gut microbiota and common respiratory illnesses like asthma, chronic obstructive pulmonary disease (COPD), cystic fibrosis (CF), lung cancer, and respiratory infections, as well as the development of probiotics as a therapeutic intervention for these illnesses.

Unknown is how the gut microbiota affects or contributes to autoimmune diseases' systemic immunity. Aryl hydrocarbon receptor, a ligand-activated transcription factor, shapes the immune system and affects host metabolism, making it a master modulator of host-microbiota interactions. Manipulation of the gut microbiota is a potential clinical therapy for autoimmune diseases. Additionally, therapeutic optimization while minimising potential side effects is crucial in these conditions. For the purpose of identifying potential future effective therapeutics based on the gut microbiota for preventing autoimmune diseases, we present studies relating gut microbiota dysbiosis to autoimmune pathways implicated in disease development.

Keywords: Gut microbiota; Central nervous system; prebiotics; probiotics; Intestine; Gut barrier; Gut mucosa.

Introduction

The gut microbiota, a varied microbial community that resides in the digestive tract, is a complicated ecosystem. In recent years, the gut microbiota has transformed into a kind of endocrine organ, secreting various substances that maintain homeostasis and control how the human body works. The gut microbiota ecology is mostly made up of Firmicutes and Bacteroides. Increasing evidence points to a connection between aberrant gut microbiota composition and a number of diseases, such as metabolic disorders and inflammatory bowel disease (IBD) [1]. Eating prebiotics (such as inulin-type fructans and certain polyphenols) dramatically increases the presence of A. muciniphila and improves metabolic disorders. A. muciniphila is more prevalent when consuming a high-fat, high-sucrose diet, according to prior mouse research. The host's diet is hypothesised to affect the composition of the gut microbiota and metabolites derived from the microbiota, resulting in interactions between the host and its microbiome [2]. A growing amount of research has focused on the host's metabolism of microbe-produced metabolites such short-chain fatty acids (SCFAs), amino acids, and their derivatives. The consequences of the interconnections between nutrition, microbiota, and host emphasise the therapeutic potential for illness prevention and treatment. Identify imidazole propionate as a metabolite produced by bacteria that derives from histidine and is more prevalent in type 2 diabetes sufferers. In this overview, we'll discuss the microbial origins of a few key metabolites produced by diets as well as their astounding effects on host physiology [3].

Up until the middle of the 20th century, infectious diseases were the main global health concern, but today, cardiovascular and metabolic disorders are the main causes of morbidity and mortality worldwide. Though bacteria were once thought to pose a risk to health, it is now well known that under normal circumstances, a pool of microbes exists in some body compartments, such as the gut, that is primarily composed of non-pathogenic microorganisms ("nice guys") that are crucial in preventing the progression of a number of chronic diseases. In addition, recent studies have linked illnesses linked to dysbiosis of the gut microbiota to elevated oxidative stress. According to recent studies, the beneficial bacteria in the gut microbiota may encourage physiological cross-talk with other systems, including the brain, cardiovascular organs, and tissues related to metabolism, helping to prevent and treat the progression of hypertension and the metabolic syndrome. According to other research, disturbance of the gut microbiota (caused and promoted by sedentary lifestyles and urban diets) may enhance the bioavailability of reactive oxygen species (ROS) and oxidative stress [4].

Modern research on the effects of probiotic kefir on the prevention and management of gut dysbiosis in cardio metabolic illnesses is included in the review. The authors discuss the benefits of this kind of nutraceutical on heart failure patients' autonomic control of cardiovascular function. They also offer new details and information about the molecular mechanisms via which kefir lessens oxidative stress in these circumstances. In order to keep readers informed about the mechanisms underlying probiotic treatment of chronic diseases, the paper contains five schematic diagrams [5].

As a result, the three terms-gut microbiota, food, and chronic diseases-used in the title of this special issue, which looked so unrelated until the last century, now have a bigger significance in the current century. To learn more about the interactions, whether they are influenced by food and the microbiota or by medical procedures,

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additional in-depth research is required. The term "gut microbiota" refers to trillions of commensal bacteria that are present in the intestine in a specific proportion and whose balance can be easily thrown off by dietary choices, way of life, and environment. The microbial community is needed in the committed stage through which food would be transformed into tiny molecules and metabolites, regulating both directly and indirectly host metabolism, gut barrier integrity, inflammatory status, and intestinal shape [6].

A large body of research has shown the relationship between intestinal microbiota and diseases, such as colorectal cancer, brain ischemia-reperfusion injury, liver fibrosis, and cardiovascular diseases, since Hippocrates stated that "all diseases originate in the gut" centuries ago. About 50% of the dry weight of adult faeces and between 0.2 and 2.0 kg of the weight of an adult are accounted for by the gut bacteria. The microbiome, which vastly outnumbers the human genome, is described as the large genome of microbial genes and their functions. Although the gut community's traits may be passed down the generations, environmental factors can also change the community's makeup. In contrast, gut dysbiosis contributes to conditions such as atherosclerosis, hypertension, heart failure, arrhythmia, cardiac tumours, and others. Appropriate gut microbiota structure and metabolite functions are crucial for maintaining homeostasis. However, the mechanisms underlying it are complex and remain unknown [7].

Materials and Methods

A simulated in vitro digestion-fermentation procedure, intended to resemble natural digestion in the human oral, gastric, and intestinal chambers, was applied to the standardised polyphenol combination. Before and after the digestion-fermentation process, the antioxidant profile of propolis was assessed. The impact of propolis extract on the gut microbiota was examined using next-generation sequencing (NGS) of the 16 S rRNA amplicon. Through the use of chromatography and UV detection, the profile of the short-chain fatty acids (SCFA) produced by the microbiota was also examined [8]. From February 5 through March 17, 2020, in Hong Kong, we conducted shotgun met genomic sequencing analysis on faecal samples from 15 individuals who had the coronavirus disease 2019 (COVID-19). From the beginning of hospitalisation until discharge, faeces were sampled two or three times per week. The severity of the illness was determined by whether there was radiographic evidence of pneumonia or not; it might be mild, moderate, severe, or critical (respiratory failure requiring mechanical ventilation, shock, or organ failure requiring intensive care). We compared the microbiome data from 15 healthy people and 6 subjects with community-acquired pneumonia (controls). We examined the gut microbiome patterns in relation to illness severity and variations in SARS-CoV-2 faecal shedding [9].

All of the host's mucosal surfaces are covered by the ommensal microbiota, which is made up of numerous bacteria, although the majority of them live in the gastrointestinal tract, which is the focus of this article. Amazingly, just 10 trillion of the 100 trillion cells that make up the human body are human, whereas 90 trillion are bacteria. Our met genome, sometimes known as our second genome, is made up of the genes from various bacteria. It should therefore come as no surprise that this diverse collection of gene products contributes significantly to physiological homeostasis [10].

The interaction between the gut microbiota and its host is crucial for the development of the immune system, as well as for the metabolism of drugs, the synthesis of vitamins, and the prevention of harmful bacteria adhering. The maturation of the immune system throughout the neonatal period is one of the microbiota's most significant functions. The development of a diversified diet and microbiota and the first emergence of adaptive immunity in humans are related, which shows that intestinal mucosal immunity has evolved to tolerate a variety of microorganisms and dietary antigens [11].

Discussion

The physiology, diet, and immunity of human hosts depend on the gut microbiota. Actually, the relatively steady intestinal flora helps maintain gut internal homeostasis. The aetiology of diabetes, obesity, hyperlipidaemia, cardiovascular disease, colon cancer, IBD, IBS, and other intestinal disorders has been related to intestinal flora dysregulation in a growing body of studies. Numerous investigations compared the microbial number and composition of IBD patients or experimental models to that of healthy controls [12]. IBD patients, especially those with UC and Crohn's disease (CD), have 25% less faecal microbial genes than healthy people, and their microbial compositions are very different. Despite the fact that both CD and UC are IBD, UC has a different mucosal microbiota than CD. For instance, CD has both a rise in the faecal bacterium prausnitzii and a decrease in the variety of flora, whereas UC does not. Additionally, there were notable differences in the mucosa-associated intestinal flora of ulcerated regions and those without ulcerations in UC, particularly in the lactobacilli and the Clostridium leptum subgroup, both of which have been related with the disease. Although the composition of the commensal intestinal microbiota in humans and mice differs, gut inflammatory diseases share a similar loss of intestinal microbial diversity, which affects the abundance and composition of the flora [13].

Conclusions

A rising body of research suggests that the gut microbiota and host immunology, as well as the stomach and lung, interact significantly and intricately. Asthma, COPD, CF, lung cancer, and respiratory infections are examples of prevalent respiratory conditions that are hypothesised to have a connection to the aetiology or advancement of gut microbial symbiosis. It is still early to understand the mechanism involving the gut-lung axis, thus more research is required. Our knowledge of the function of gut microbiota in the lung and the development of efficient and cutting-edge therapeutic approaches for respiratory diseases depend on future research into gut microbiota modification and enhancement, as well as the balance of gut and lung immunity via diet, probiotics, and FMT [14].

Studies on both humans and animals have provided evidence that the role of the gut microbiota and its metabolites in CVDs is well understood. Verification of the makeup of the gut flora and in-depth mechanistic investigation are now possible thanks to high-throughput technologies. However, because the connections between gut microbiota and disease development are so intricate, they also involve metabolic balance, immunological modulation, the inflammatory response, gut barrier integrity, etc. Additional research into the underlying systems is required, with the potential for application to clinical treatment [15].

Conflicts of Interest

None

Acknowledgments

None

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