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A Brief Review on Human Gut Microbiota

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Abstract

The gut microbiota, a diverse and dynamic collection of microorganisms found in the human gastrointestinal (GI) tract, has a significant impact on the host during homeostasis and illness. The formation of the human gut microbiota during infancy is influenced by a variety of variables. One of the primary factors affecting the gut microbiota over the course of a lifetime is thought to be diet. In keeping immunological and metabolic balance and warding off infections, intestinal bacteria are essential. Numerous inflammatory illnesses and infections have been linked to altered gut bacterial makeup, or dysbiosis. Understanding inter-individual variability, the variety of bacterial populations in and around the GI tract, functional redundancy, and the necessity of separating cause from effect in dysbiosis-related situations are all necessary for properly interpreting these results. The evolution and makeup of the human GI microbiota, as well as its effects on gut integrity and host health, are summarised in this review, which highlights the need for mechanistic investigations that concentrate on host-microbe interactions.

Keywords: Gastrointestinal tract; Gut microbiota; Symbiosis

Introduction

One of the greatest interfaces (250-400 m2) between the host, external variables, and internal antigens in the human body is the gastrointestinal (GI) tract. Around 60 tons of food and many environmental microbes from the environment travel through the human GI tract in a lifetime, posing a serious danger to gut integrity [1]. The phrase "gut microbiota" refers to the assortment of bacteria, archaea, and eukarya that colonise the GI tract and has co-evolved with the host over thousands of years to develop a complicated and beneficial connection [2,3]. According to estimates, there are more than 1014 microorganisms living in the GI tract, which contains around 10 times as many bacterial cells as human cells and more than 100 times as much genetic material (microbiome) as the human genome [4]. The ratio of bacterial to human cells, according to a newly updated estimate, is really closer to 1:1 [5]. The host and the microorganisms living inside it are sometimes referred to as a "superorganism" because of the enormous number of bacterial cells in the body [6]. Through a variety of physiological processes include enhancing gut integrity or reshaping the intestinal epithelium [7], obtaining energy [8], defending against pathogens [9], and controlling host immunity [10], the microbiota provides the host with a number of advantages. The changed microbial composition known as dysbiosis, however, has the potential to disrupt these systems. A role for the microbiota in many intestinal and extra-intestinal disorders has slowly emerged as more advanced technologies to profile and characterise complex ecosystems are developed [11,12]. The growth and makeup of the human GI microbiota, as well as its effects on gut integrity and host health, are discussed in this overview. Prior to around 10 years ago, labor-intensive culture-based techniques were the primary source of knowledge regarding the adult human gut microbiota [13]. Due to the development of culture-independent technologies like high-throughput and affordable sequencing techniques, our capacity to study the breadth of the gut microbiota has recently considerably increased. Since the bacterial 16S ribosomal RNA (rRNA) gene is present in all bacteria and archaea and contains nine highly variable sections (V1-V9) that make it easy to identify across species, targeting this gene is a common strategy [14,15]. Earlier methods emphasised sequencing the 16S rRNA gene in its entirety. The significant bias and insensitivity of culturing methods were emphasised in an early investigation utilising this method since 76% of the rRNA sequences recovered from an adult male faecal sample belonged to unknown and uncharacterized species [16]. The goal of 16S rRNA sequencing has recently switched to more thoroughly analysing small sub regions of the gene. However, using shorter read lengths can result in mistakes. Due to their increased resolution and sensitivity, whole-genome shotgun metagenomics may offer more accurate estimates of microbiota composition and diversity. The Human Microbiome Project and MetaHit data combined have given researchers the most complete picture of the microbial diversity associated with humans to date [17,18]. Data from these investigations was compiled to identify 2172 human-isolated species, which were divided into 12 distinct phyla, with 93.5% of these species belonging to the Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes. The only known member of the Verrucomicrobia phylum, an intestine species called Akkermansia muciniphila, was isolated from one of the 12 recognised phyla, making up three of them. 386 of the known species in humans are strictly anaerobic, hence they often inhabit mucosal areas like the GI tract and oral cavity.

Dr. Tim Spector presented his recent and earlier study on twins in the UK during the 23rd International Symposium on Glycoconjugates. The results are excellent and are assisting in understanding how much the genotype accounts for specific traits or illnesses. In Taiwan, myopia is one such instance. As he said, the rate of myopia in children is substantially greater than anticipated, even though the environmental component only accounts for 10% of variability and the hereditary component accounts for the majority of it. In this instance, the phenotype is being forced by the environment. Along with these intriguing findings, he also revealed his current research focus, which is the examination of the gut flora as part of the British Gut project. Both this one and the American Gut project can provide insight into the current significance of gut bacteria for biomedicine. Although

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many of these situations are still in the early stages of experimentation, the scientific community's interest is expanding and the process of consolidating it is progressing steadily.

We must not lose sight of the fact that medications taken orally are immediately absorbed through the gastrointestinal tract, and any possible impact on the human gut microbiota should be carefully considered, since some components may change the population and produce dysbiosis. This is significant since research has demonstrated that the human gut microbiota plays a critical role in immune function and overall health. In addition, it may be used as a biomarker for either the oral bacterial population or the gut microbiota. Understanding how the microbiota functions is important for the development of new drugs because it will help us determine whether our treatments are having an impact on the balance of the microflora and because we might be able to use probiotics or antimicrobials to control the numbers and proportions of bacteria in the population. In this way, new medicine formulations may contain these added ingredients to boost the proportion of some groups or control others.

The transplantation of microbiota from healthy donors is a novel therapeutic procedure that is presently only performed in patients with Clostridium difficile infections who do not respond to conventional antibiotic therapies. These recent advancements as an alternative therapy are exciting, but they run the risk of becoming a harmful procedure if not carried out by a licenced expert (and this sector is extremely new) especially given the recent DIY faecal microbiota transplantation trend. Failure to assess the microbiota for appropriateness in terms of safety with regard to pathological agents may result in the spread of new illnesses. Therefore, it is crucial to identify the basic bacterial population of a healthy person. This collection can aid in the earlier improvement of a patient's condition, speed up their recovery following antibiotic therapy, or, in the event of a viral illness, assist in lowering the viral load [19]. It has been mentioned that the taxonomic makeup of the microbiota varies significantly across people and is influenced by factors including dietary habits, place of residence, age, and even circadian rhythms. The formation of a core collection of bacteria in healthy persons can be facilitated if we consider the transcriptomics profile of that bacterial population because the species makeup is so variable. We may strive for a core set of transcripts in this metabiome, even if the species mix may not be entirely homogenous. Since the transcriptome has been shown to be more conserved amongst bacteria, it stands to reason that various bacterial species will react similarly to a certain class of biotic or abiotic stimuli. For instance, the more conserved genes involved in bacterial glycolytic metabolism, which are found in many species, would be expressed when this pathway was required [20,21]. Reducing to the ludicrous, when people are overheated, they perspire to release heat, regardless of their race, nation, religion, or geographic location. Something comparable can be presented on a molecular level. Furthermore, characterising this group of bacteria in the healthy may benefit greatly from the metabolomic component. Since all of these methods and technologies are fundamentally complimentary, there is a lot of room for innovation.

Discussion

Recent articles have linked viral infections to the microbiome, and curiously, the microbiome of the host itself has been shown to influence host immunity. Apart from any potential medicinal ramifications, the basic science topic of characterising the microbiome of people who have viral infections is intriguing in and of itself. It has been proposed that the microbiota may indirectly influence viral infections brought on by the HBV (Hepatitis B virus) through the immune system. Additionally, recent studies in mice have shown that the gut microbiota plays a significant role in the clearance of the virus by promoting adult liver immunity.

Conclusion

It is essential to characterise the human gut microbiota, and several initiatives have been created in this manner. Knowing the components of a healthy microbiota and the consequences that dysbiosis may have is crucial for the development of new medications since some of them may have adverse effects on the immune system indirectly through the bacterial population. It may also be useful for creating more effective medications, such specific kinds of antibiotics to eradicate particular species or probiotics to spread the most practical varieties. Future ideas and discoveries are expected to come from this area of study.

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Conflict of Interest

Author declares no conflict of interest.

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