Role of Microbiome on Human Health

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Abstract:

The human body is called as "super organism" that is made up of extensive number of commensal microbes, including bacteria, fungi and viruses, there are 10 times more microbial cells exist in a human body than its own body cells.[1] Collectively it is termed as human microbiome. The indigenous microbial community is also called as microbiota. The major presence of them colonizes the gastrointestinal tract (GIT). A Metagenomic analysis of the human microbiome has revealed that the human stomach has 3.3 million distinct genes- 150 times more genes that human genome. [2] Furthermore, the research of bacterial diversity revealed that approximately 1000 different species of bacteria reside in human stomachs, with the bulk of them falling into the Bacteroides and Pharmaceutics categories.[2] The microbiome plays a crucial role in growth and development of the immune system, central nervous system and the GIT system and is also responsible for essential metabolic pathways.[3] Our daily lifestyle like diet, drug uses antibiotic or non-antibiotic and other environmental factors like air, water, soil etc. can affect the composition of the gut microbiota. There are both beneficial and harmful microbiotas present in the guts of a human body. The researchers highlighted that manipulation of gut microbiota can be employed to prevent obesity, inflammatory bowel disease and colorectal cancer. Furthermore, when frequency of abundance at phylotype level is ignored, most individuals have a core microbiota of 50–100 bacterial species, and most human guts studied to date have a core microbiome harbouring over 6000 functional gene groups. [1] The recent study of on gut microbiota is how to use/ manipulate them to cure/regulate diseases. The researchers now focus on sequencing of the next generation (NGS). It is a novel technique for variant/mutation identification and sequencing of DNA and RNA. In a short amount of time, NGS can sequence tens of thousands of genes or the entire genome. [4]

Keywords:

Human microbiome; Microbiota; Metagenomic; Microbiome dysbiosis; Next-generation sequencing

Introduction:

Based on the genetic potential that the local microbial community carries, humans can think of as "super organism". The microbial population which is named as microbiota develops simultaneously along with human growth. [5] In reaction to shifting environmental conditions, the composition, and gene expression change. The huge and most varieties of microbes are found in the gastrointestinal tract or the GI tract. [6]

There are approximately 1000 microbial species living in our guts. The microbiome in human body is either directly or indirectly involves in lots of diseases, the microbiome most commonly causes the inflammatory and autoimmune diseases. Gut microbiota directly affect the metabolic pathways, they perform microbe metabolite host interaction. The interaction is commonly observed between intracellular symbiotic bacteria at the scale of individual epithelial host cells. This kind of interaction produces specialized metabolites from the host-microbe interface. The sudden change or imbalance in bacterial composition can causes certain changes in bacterial activity, which farther affects the other system of a human body. *Lactobacillus, Streptococcus, Staphylococcus* these types of bacteria mainly effect on the stomach, Duodenum, Jejunum and ileum. *Bifidobacteria* is mostly found in colon. [7] The imbalance of these can cause lots of dysfunction of a human body. As example:

Heart-gut axis: thrombotic episodes, atherosclerosis, and cardiovascular disorders. [8] There is more effect done by gut microbiome that is helpful for a human body, as example:

Digesting breast milk: gut microbiome starts to affect a host body the moment they are born. There are some bacteria called Bifidobacteria first start to grow inside foetus' intestine then digest the carbohydrates in breast milk that are very crucial for growth.

Digesting fibre: human digestive system cannot digest fibre. The bacteria inside the human body produce short chain fatty acid, which helps to digest the fibre. It is a very useful substance for intestinal well-being. Fibre helps lower the risk of cancer, diabetes, heart disease, and weight gain.

The gut microbiota aids in immune system regulation by controlling the work of the immune system.

Helping control brain health: according to the modern research, gut microbiome may also affect the CNS or the central nervous system. [3]

Most of the microbes of gut microbiome are beneficial to human health, but having unhealthy microbes can lead to lots of diseases. Recent studies shows that gut microbiota can effect on weight. A sudden

imbalance in microbiome is called the dysbiosis. Recent study shows that dysbiosis can causes to weight gain.

As per it is there are both symbiotic and pathogenic microorganism present in a human body. The researchers are now focusing on a new technology called next generation sequencing. With this process scientists can manipulate thousands of genes or the whole genome in a short period of time. Interestingly in this process, it targets a particular amplicon sequence of the 16S ribosomal RNA gene (16S-seq), a marker gene specific to bacteria. This method helps to identify and classify bacterial species present in a sample. It enables Metagenomic studies, where the entire genetic material of a microbial community is sequenced. This method not only identifies bacteria but also other microorganism, their functional genes, and potential interactions with the microbiota. So in near future NGS technologies will provide powerful tools for characterizing and understanding the complexities of the human microbiota. [9]

Role of Microbiome in Human Health and Disease:

The trillions of bacteria which make up the microbiome (including bacteria, viruses, and fungi) living on and inside the host body. [10] Recent research suggests that the microbiome plays a crucial role in human health, with disruptions to its composition and function linked to diseases such as inflammatory bowel disease (IBD), obesity, and cancer. In this article, we will explore the mechanisms by which the gut microbiome contributes to immune function and nutrient metabolism, as well as the potential for new treatments based on emerging research. [10]

The gut microbiome is the largest and most diverse among all the microbiome present inside the human body. It is composed of trillions of microorganisms, including over 1000 different bacterial species. These bacteria play a significant role in digestion and metabolism, as they help break down complex carbohydrates and produce important vitamins and nutrients. The microbiota residing in the gut also has a key role in modulating the immune system, which provides protection against harmful pathogens. Changes in the gut microbiome can lead to alterations in immune function, contributing to the development of inflammatory disorders, such as IBD, and other diseases.

Dysbiosis, or the disruption of healthy gut flora, has been linked to several diseases. Inflammatory bowel disease is one such condition where the gut microbiome has

been shown to play a critical role. Studies have also associated dysbiosis with other conditions, including allergies, autoimmune disorders, diabetes, obesity, and even some cancers. In obesity, for example, certain bacterial strains like Formicates have been found to be more abundant in the gut microbiome, contributing to inflammation, insulin resistance, and the deposition of fat in adipose tissues. While research in this area is still on-going, the microbiome's impact on human health has significant implications for disease management and prevention.

Host-Pathogen Microbiome:

The gastrointestinal, respiratory, and urogenital tract mucosal linings establish a barrier against pathogens, commensals, chemicals, medicines, and poisons by their on-going interaction with the external environment. These surfaces have intricate architectures that allow for tissue-specific functions. These architectures are made up of several cell types arranged into three-dimensional (3-D) patterns. Infections can arise because of the biological, chemical, and biomechanical properties that characterize the micro environmental niches along these surfaces. [11] In order to choose where and when to activate particular virulence programs during different infection stages, pathogens have evolved to detect specific host structures, polarity, and changes in local environmental signals (pH, temperature, oxygen levels, nutrients, hormones, physical forces, etc.). [9] A major obstacle in tissue engineering for infectious illness studies is accurately modelling host-pathogen interactions in the laboratory requires recreating the spatiotemporal properties of dynamic 3-D microenvironments as they occur in vivo. [11]

In vitro investigations of infectious diseases have traditionally focused on the interaction between a single bacterium and a single host cell type, which is frequently cultured as flat 2-D monolayers.[12] composition and localization, oxygen levels, transport processes, and biomechanical forces (e.g., fluid shear, stretch, compression). [12] Technological developments in bioinformatics and Next Generation Sequencing (NGS) have transformed host-pathogen system research. Now that the genomes of model and non-model animals have been sequenced, scientists may learn more about how specific genes behave in different scenarios and how host-pathogen interactions affect molecular settings like global gene expression. [14] A plethora of web-based software applications and open-source R packages have been created to

assist researchers in comprehending the host-pathogen microbiome. Quality control, taxonomic categorization, diversity metrics, annotation, functional analysis, sequence classification, metabolic pathway reconstruction, and statistical analysis are among the activities that these tools allow researchers to do. [13]

Host-pathogen interactions play a significant role in human biology, resembling a conflict between two adversarial systems. Pathogens, functioning as invaders, can exploit host cells for their advantage and evolve rapidly, sometimes outpacing the human immune response, as seen in HIV infection. This interplay between hosts and pathogens leads to phenotypic changes and is considered a primary driver for phenomena like speciation and the evolution of sex. Despite the importance of these interactions, many aspects remain poorly understood, particularly at the molecular level. There is a critical need for further research into the molecular dynamics governing host-pathogen interactions and the regulatory mechanisms underlying phenotypic alterations in the host. [14]

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The Potential of Microbiota Manipulation in the Future for Disease Treatment:

In microbiome research, manipulating the microbiota is a rapidly growing tool as therapeutic. [12] By manipulating the gut microbiota, many diseases can be cured. An imbalance in microbiome, which is called as dysbiosis, is the cause of many dysfunctions and diseases. A recent study says that by manipulating the gut microbiota, the reversing of dysbiosis can be possible. Some of the tactics being studied or used at the moment include the use of targeted antibiotics to eliminate specific microbiota, probiotics and

prebiotics to promote the growth of good bacteria, and fecal microbiota transplantation to restore bacterial populations. [10] A better knowledge of the host-microbiome interactions influencing disease will be possible thanks to these investigations. Now on, scientists are mainly focusing on a new technique, Next Generation Sequencing. NGC have significantly advanced the understanding of the human microbiota. In this process, first the sample is collected from different sites including skin, mouth, gut, urogenital tract etc. Then the genetic material of the microorganism is extracted from the collected samples. [14] This can involve isolation of DNA for bacterial and archaeal communities or RNA for studying gene expression of microbiota. Then comes the most interesting part, the technique specifically targets the 16S ribosomal RNA. This gene presents in all bacteria and contains variable regions that allow for the identification of different bacterial species. 16s rRNA sequencing provides information on taxonomic composition. Beyond taxonomic profiling, NGS enables the study of functional aspects of the microbiota; functional Metagenomic involves sequencing the Metagenome to identify genes related to specific functions such as metabolism, virulence and antibiotic resistance. Through the understanding of the individual variation in the microbiota through NGS have implications for personalized medicine, which allows for the development of targeted interventions, such as probiotics or prebiotics. NGS produced massive datasets, and tools for bioinformatics are necessary for handling and interpreting the data. Data analysis involves tasks such as taxonomic classification. These advances contribute to the understanding of health and disease and open a new avenue for developing microbiota based interventions for personalized medicine.[15]

Conclusion:

Comprehensive studies on the community structure of individual gut microbiota have been carried out with the rapid development of DNA sequencing techniques. However, because there is currently no in vitro culture system for uncultivable gut bacteria to study their physiological functions and fermentation characteristics in large colons, few studies have been able to correlate the microbiota community structure with host phenotype. A typical three-stage continuous culture system was established to simulate the nutritional and environmental conditions of the human gut (Macfarlane and Macfarlane, 2007) [16] based on data obtained from two human victims of sudden death, of which there was apH increase along the longitudinal axis of

the colon and a distally decreased production of short chain fatty acids (Macfarlane et al., 1992). [16]

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