ACTA SCIENTIFIC MICROBIOLOGY (ISSN: 2581-3226)

Volume 3 Issue 1 January 2020

Socio Scientific Article

Human Microbiome- The Microbial Derived Intelligence in Our Body

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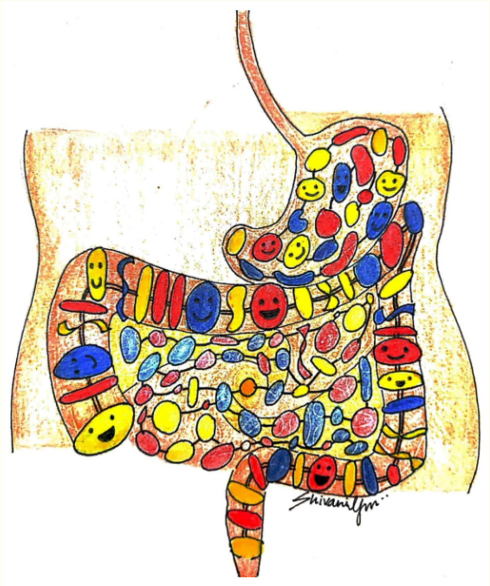
Received: November 18, 2019; **Published:** December 04, 2019

DOI: 10.31080/ASMI.2020.03.0449

Abstract

Human Gut Microbiome (HGM), or gastrointestinal (GI) microbiota, includes a varied group of microorganisms that live in the digestive tract of humans. HGM consists of the largest number of bacteria and the greatest number of species compared to other areas of the body. The microbial constitution of the gut microbiota varies across the digestive tract. Evolving research on the human microbiome and its role in human wellness and disease are currently in the limelight, by virtue of which, researchers of diverse clinical specialty areas are attempting to fit this potential into existing disease models. Tremendous data has demonstrated a strong association of the gut microbiome with host metabolism, immune and neuroendocrine homeostasis, and the possible dysregulation or alteration of the gut microbiome.

Keywords: Human Microbiome; Microorganisms



Figure

Human microbiome

Humans have been living with tiny living partners, since ages. These micro-sized partners (1-10 micrometer) consist of a variety of microorganisms such as bacteria, fungi, yeasts, and viruses. These microbes are present on the and inside the human body. These microbes together are referred to as ‘Human microbiome’ of an individual. The microbial makeup for a given site in the body varies from person to person, not only in type but also in numbers. Bacteria of the same species found throughout a particular organ of multiple subtypes, preferring to inhabit distinctly specific locations in the organ. Therefore, such microbial makeup of a person is like a signature of that individual. Evaluation of the ‘microbiome’ of a person involves both classical microbiological identification methods and several high-end molecular biology techniques.

'Microbiome research' is the study that emphasizes community-level analysis of data derived from genome-enabled technologies. The type and the number of microbial fauna depend upon secretions from our skin or other body parts and nutrient spectrum con-

Citation: Girish B Mahajan and Dipali Rahul Phatak. “Human Microbiome- The Microbial Derived Intelligence in Our Body". *Acta Scientific Microbiology* 3.1 (2020): 30-32.

tent. Resident micro-flora consists of organisms which are regularly present in a specific area and when disturbed it re-establishes itself, for example, *Escherichia coli* in the intestine. Their growth in a given area depends upon physiological factors such as temperature, moisture, and availability of certain nutrients and inhibitory substances. The skin is the human body's largest organ, colonized by a diverse milieu of microorganisms (almost 1000 genera), most of which are harmless or even beneficial to their host. Now you can imagine this huge number of microbes is like an important organ of our body. The community of these microbes plays an important role in our physical, social and mental health, though the ways scientists aren't yet clear about. Scientists have explored significant roles of the Human microbiome in varied aspects of human life. Let us understand some of these to realize how microbes are like another 'brain' working in a different way to control human activities.

Human Gut Microbiome-what is it exactly and how is it studied?

Human Gut Microbiome (HGM), or gastrointestinal (GI) microbiota, includes a varied group of microorganisms that live in the digestive tract of humans. HGM consists of the largest number of bacteria and the greatest number of species compared to other areas of the body. The microbial constitution of the gut microbiota varies across the digestive tract. Overall the number of microorganisms (with 300 to 1000 different species) inhabiting the GI tract has been estimated to exceed 10^{14}, which is ~10 times more than the number of human cells and over 100 times more than the human genome. The microbiota offers many benefits to the host by regulating, an array of physiological functions such as strengthening gut integrity or shaping the intestinal epithelium, harvesting energy, protecting against pathogens and regulating host immunity.

A simple way to study gut microbiome is using samples from gut material and gut inner surface for cultivation, purification, and characterization of microbes. For this, a diverse range of nutrient, selective and differential media are used. Axenic microbes obtained in this way are identified by a polyphasic approach. Additionally, there are genetic ways and tools to identify other uncultivable microbes in our gut. All these studies, through various iterations provide an insight into the role of this microbiome in different aspects of our health.

Human gut microbiome and cancer

We are aware that certain chemicals and other substances have the capacity to induce cancer in humans. For example, tobacco consumption in any form has been linked with respiratory or mouth cancer. It will be surprising to note that, similar to chemicals, the presence of certain microbes in the gut enhances the occurrence of gut cancers and some other gut microbiome sets may reduce the risk of such cancer. It's also shown that gut microbiota plays an important role in the development of liver carcinoma. Stool samples of patients with colorectal cancer have higher proportions of microbes called *Escherichia* and *Fusobacterium* than healthy controls. A bacterium, *Helicobacter pylori* indirectly promotes carcinogenesis by changing the composition of gastric microbiota. The direct influence of *H. pylori* on carcinogenesis is exerted mainly through two toxic substances released by it: VacA and CagA. Cancer growth may also be supported by a pro-inflammatory environment created by gut microbiota. Other mechanisms of induction of cancer by microbes involve interactions between host factors (fat-rich diet, obesity, etc.), stress due to lack of oxygen, genotoxicity, antigen-presenting white blood cells, etc. Scientific facts suggest that change in microbiota in the gut may reduce the risk of such cancers. An accurate study of the relationship between gut microbiota and gastrointestinal cancers needs to be explored further. Such studies will substantially impact routine clinical practice and patient care.

Microbiome and obesity

Obesity, defined as excess adipose (fatty) tissue, is a disease; the incidence of which is increasing alarmingly in both industrialized and developing countries. According to the World Health Organization (WHO), more than 1.9 billion adults are overweight and over 0.6 billion are obese, worldwide. Obesity predisposes the person to a number of diseases, including diabetes, heart diseases, and several cancers. The essential basis of obesity is an energy imbalance between calories consumed and expended.

One of the modes by which the gut microbiota may impact our metabolism is the production of short-chain fatty acids (SCFAs), principally acetate, propionate, and butyrate from dietary polysaccharides otherwise inaccessible to humans. Humans get approximately 10% of their daily energy supply from these SCFAs produced by gut bacteria, and it has been observed that SCFA profiles are altered in obese individuals. Besides caloric intake, these SCFAs also act as signalling molecules and may control satiety, making them an essential factor of the microbiota–host cross-communication in the context of obesity. One well-established example in animals is wherein; obese mice display an increased proportion of a group of bacteria called Firmicutes and a lower proportion of Bacteroidetes in their microbiota compared with wild-type counterparts. These results imply that bacterial species within the human gut microbiota may be effective in preventing obesity development. It also raises the curiosity of whether gut microbiota transplant (Fecal microbiota transplant) in humans and dietary interventions targeting the gut microbiota could be a new therapeutic strategy for obese patients.

Microbiome and autism

Autistic people are prone to repetitive behaviour and may sometimes face difficulties in communicating their thoughts. Scientists do not know exactly what causes autism spectrum disorder (ASD), but they believe that both genetic and environmental factors play a role. Recently in a study, featured in the prestigious scientific journals titled "Cell', researchers from the California Institute of Technology (Caltech) in Pasadena identified differences in the microbiomes of people with and without ASD. Though several such studies have been reported, researchers are still unable to resolve whether observed microbiome changes are a consequence of having ASD or if they contribute to the symptoms in a different way.

In another study, the Caltech team reported that children with autism received a new type of therapy called microbiota transfer therapy. The results showed a 45% improvement in measurements of language, social interaction, and behaviour. Such studies have created huge expectations towards remedial ways for ASD.

Microbiome and diabetes

A healthy microbiome is characterized by bacterial diversity and richness. Gut microbiota mostly comprise of Firmicutes (64%), Bacteroidetes (23%), Proteobacteria (8%), and Actinobacteria (3%). Lack of bacterial diversity and overgrowth of bacteria results in dysbiosis, an imbalance in the gut's microbial composition. Alteration in the proportion of bacteria is thought to result in metabolic diseases. The microbiome of patients with type-2 Diabetes Mellitus (T2DM) is characterized by reduced levels of Firmicutes and Clostridia and an increased ratio of Bacteroidetes:-Firmicutes (this ratio correlates with plasma glucose concentration).

Perspectives and future direction

Evolving research on the human microbiome and its role in human wellness and disease are currently in the limelight, by virtue of which, researchers of diverse clinical specialty areas are attempting to fit this potential into existing disease models. Tremendous data has demonstrated a strong association of the gut microbiome with host metabolism, immune and neuroendocrine homeostasis, and the possible dysregulation or alteration of the gut microbiome. The field of Human Microbiome research is still relatively new but fast-growing, showing several promising studies on the modulatory role of the human microbiome in human wellness and disease. Future applications of microbiome-based disease diagnosis, prognosis monitoring, prophylaxis and treatments that exhibit great potential in revolutionizing the current measures in disease management and treatment are definitely worth looking forward. We envisage specific probiotics will soon over-rule the existing drugs for several metabolic disorders.

Acknowledgment

The authors are very thankful to their respective affiliation institutes for encouraging publishing of such awareness articles for wide readers of the journal. Authors of the article hereby gratefully acknowledge the Editor and senior management of the monthly periodical titled 'Abhineet' published by 'Asha Foundation (https://indiaasha.org/)' for approving the copyrights for the publication of the article, which was published in 'Abhineet' in the joint issue of September-2019. The authors are also thankful to Shivani G. Mahajan for drawing, painting and providing the apt and creative painting for this article.

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