

Opinion Article

Human microbiome and its impact on health

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DESCRIPTION

Microbes that are both beneficial and potentially dangerous make up the microbiome. The majority are symbiotic (meaning they benefit both the human body and the microbiota) while a tiny number are harmful (promoting disease). Pathogenic and symbiotic bacteria coexist peacefully in a healthy body.

The microbiome is a collection of microorganisms (fungi, bacteria, and viruses) that live in a certain environment. Microorganisms that dwell in or on a specific region of the body, such as the skin or the gastrointestinal system, are commonly referred to as bacteria. These microbes are dynamic and alter in response to a variety of events in the environment, including exercise, nutrition, medicine, and other exposures.

The gut microbiome is made up of the genomes of bacteria, archaea, viruses, and fungi that live in the digestive tract. The amount of information available about the bacteria that live in our guts is rapidly increasing. Until recently, human population heterogeneity was attributable to different gene allelic forms. There are billions of bacteria in the human intestine, with a genome larger than all of the human cells in the body. In the gut, bacteria are distributed spatially, with the colon harbouring the greatest diversity and number of germs. Because of its proximity to the environment, the colon contains more aerobes than the small intestine. It has been challenging to culture commensals because of their anaerobic nature, particularly in the upper gut. Advances in omics-based techniques have contributed to a better knowledge of the gut ecology and the many factors that influence its microbial makeup. This technique has paved the way for a slew of new studies on the role of gut microbiota in immune system homeostasis, which has ramifications for health and illness. The National Institutes of Health's (NIH) human microbiome research, which began and detected bacteria on numerous surfaces of the human body. Firmicutes, bacteroidetes, proteobacteria, and actinobacteria

are the most common phyla in humans, with firmicutes and bacteroidetes dominating the intestine. The colonisation of the gut occurs at birth and is impacted by vaginal or C-section delivery. During maturation, however, the microbiota changes as a result of exposure to diverse environmental variables. Each individual's microbiota is unique, much like their genetic imprint, yet roughly one-third of the species are shared by most individuals. Intestinal microbiota is influenced by a variety of factors, including cleanliness, food, geographic location, and host genotype. In addition, research in people and animals have revealed that sex hormones and age play a role in shaping the microbial composition of the intestine. Humans and commensals have coevolved and have a symbiotic relationship. Microbes in the intestine outcompete pathogens and maintain epithelial integrity, which may be a crucial element in preventing inflammation. Diverse microbial populations are important for sustaining the gut ecology and for extracting energy from food and creating micronutrients. In exchange, the microorganisms get food and a good habitat to flourish in.

The microbiome is anticipated to play a role in bladder cancer development and treatment at various stages. Because of the difficulty of directly infusing strains into the bladder, the potential to impact the bladder microenvironment through the use of probiotics has been limited until recently.

Pathogens, carcinogens, and other poisons are all attacked by bacteria, and bacteria are the first line of defence. Because they can metabolise chemotherapeutic medicines and affect how the host responds, pharmaceutical and other firms are likely to invest heavily in research in this field. The fast increasing ability to determine and manipulate the microbiome of the urinary system has considerable appeal as medicine progresses toward more personalised methods. The extent to which this has an impact on bladder and other urinary malignancies remain to be established, but significant discoveries are expected in this field over the next ten years.

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