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Opinion Article

Microbiome and Gut Dysbiosis in Human Health

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DESCRIPTION

The human gut bacteria is a complicated and constantly changing microbial organism that interacts with the environment as well as other organs such as the brain, heart, liver and immune system. Although these complex multifactorial connections are highly conserved from invertebrates to humans the variety and complexity of human microbiota compositions can result in a setting that is unique to each individual. Nonetheless, commonalities exist between species with a healthy gut microbiome being rich in symbiotic commensal biota and a sick gut microbiome seeing excessive blooms of bacteria. The gut microbiota is thought to be an important part of systemic physiology. Its receptivity to manipulation makes it an important therapeutic target for staying healthy and treating disease. A person's microbiome is a one-of-a-kind collection of bacteria, fungus, viruses and their metabolites, allowing the microbiome to have a highly personalized effect on human health. Moreover it is becoming obvious that an individual's microbiome has an impact that reaches far beyond the gut. The microbiota has local impacts such as modulating intestinal lumen permeability but it can also function as an endocrine system. Historically the state and changes in the gut microbiome have been assessed by culturing faecal sample components and more recently by the use of omics technologies RNA sequencing and DNA sequencing (genomics) (transcriptomics).

The microbiome is described as a "fluid ecosystem of microbes and their theatre of activity, which includes their surroundings and metabolites and is essential to appropriate bodily function." While bacteria populate most human body surfaces such as the skin, nasal passages, oral cavity and urogenital tract the gastrointestinal system is where people interact with germs the most. In fact the colon contains the majority of the human gut microbiome. The microbiome can influence the host's metabolic, immune and even psychiatric disposition through numerous signalling molecules that can result in physiologic and behavioural effects. The gut bacteria, gut-resident lymphocytes and enteric neurons are constantly communicating with other organs.

In each location different bacterial species are tailored to breakdown various nutrients into easily absorbable chemicals. In the colon for example the resident microorganisms specialize in the fermentation of complex carbohydrates which results in the creation of short chain fatty acids. The coexistence of age-related diseases with changes in gut micro biota shows that there is a delicate balance in gut micro biome variety and inhabitant may be advantageous to the host organism. In fact, microbiota can vary from friendly to symbiotic to harmful. From an evolutionary standpoint it makes logical that the bulk of the 'bugs' in the gut are harmless and coexist in the stomach without harming their host. Despite significant advances in micro biome defining a universally 'healthy' microbial signature remains difficult. Because of the richness of the human environment as well as the heterogeneity of study methodologies, analysis and models time demanding and difficult to draw cross-correlation findings across studies. As a result, microbiome investigations frequently produce contradictory or unclear results owing mostly to low reproducibility.

When cross-correlation studies are performed among distinct model systems a larger predictive ability can be expected. By investigating conserved effects across many species in a preclinical setting, the likelihood of clinical failure is expected to be reduced, and it will assist identify what biomarkers. And also the endpoints to test for clinical success. As current emerging approaches for producing more effective targeted therapeutics mature their impact on disease treatment and human health is the rapid growth.

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