International Scholars Journals

Advanced Journal of Microbiology Research ISSN 2736-1756 Vol.16 (4), pp.001, December, 2022.
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Perspective

Infectious symbiotic microbes and diseases

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Received: 25-Nov-2022, Manuscript No. AJMR-22-81756; Editor assigned: 28-Nov-2022, PreQC No. AJMR-22-81756 (PQ); Reviewed: 12-Dec-2022, QC No. AJMR-22-81756; Revised: 19-Dec-2022, Manuscript No. AJMR-22-81756 (R); Published: 26-Dec-2022

DESCRIPTION

Since the late nineteenth century, the germ theory of disease has dominated almost all facets of clinical microbiology and established the groundwork for a new branch of medicine called infectious diseases. Numerous illnesses have been shown to have a microbiological aetiology and are categorised as infectious diseases under the direction of the one pathogen-one disease paradigm. The paradigm also offers fundamental guidelines for research and development of specialised diagnosis using pathogen isolation and identification, specialised antibiotic treatment, and efficient vaccination prevention. One of public health's major contributions to the significant decline in infant and child mortality and the twenty-first century increase in life expectancy was the establishment of the notion of infectious diseases.

But until the last decade, when technological advancements in high throughput sequencing and bioinformatics made it possible to examine the entire microbial community in the human body, the restriction to one pathogen in one disease sharply narrowed our vision by choosing and focusing on single colonies and ignoring the vast majority. Commensal bacteria have developed a symbiotic relationship with human hosts over millions of years of mutual hosting, serving critical roles in immune system development, digestion of food substances beyond our capacity, and the prevention of harmful bacterial invasion. If these functions are essential to humans, then a disruption in the bacterial population should have an impact on a person's susceptibility to various diseases.

The association of bacterial microbiota with cancers of the colon, pancreas, mouth, and possibly the oesophagus as well as the landmark discovery that *Helicobacter pylori* induces peptic ulcer and is strongly associated with cancer of the stomach have recently brought the human microbiome to the forefront of cancer research. Three reviews in this issue compile the most recent developments in cancer cause in relation to the human microbiome. Animal models of colitis-associated colorectal cancer have provided important insight into the need to study both the host genetics and the microbes in this disease. These models show that while inflammation caused by the knockout of immune-related genes or the presence of bacteria and bacterial metabolites is necessary, neither factor alone is sufficient to promote tumorigenesis.

Recent research on microbiome change in HIV infection is covered under the section on the role of microbiome in microbial and inflammatory illnesses. Studies of the microbiome in HIV infection frequently focus on determining whether the microbiome plays supporting roles in the development and progression of the disease given that HIV is the known cause of AIDS. According to several recent studies, changes in the microbiome after HIV infection may stimulate the immune system, which speeds up viral replication and causes CD4+ T-cell depletion, shortening the time it takes to progress to the AIDS stage.

Few exogenous variables are known to alter the human microbiome, except than food and antibiotics. Two reviews in this issue look at clinical practises that influence the gut microbiome. PPIs, which are frequently prescribed to treat gastro *Helicobacter gastritislux* disease and *Helicobacter gastritis*, may affect the gastrointestinal microbiome by reducing gastric acid secretion, causing hyperparathyroidism and hypergastrinemia, interfering with nutrient absorption, and inhibiting bacterial proton pumps. PPIs promote gastric dysbiosis, result in small intestinal bacterial overgrowth, and raise the risk of *Clostridium difficile* infection, according to studies. However, they also deplete esophageal gram-negative bacteria and aid in the removal of the *H. pylori* infection.

High-throughput, low-cost sequencing technologies could replace established techniques used in clinical microbiology laboratories to detect and identify single pathogens, such as colony picking, selective media, and specific PCR. These techniques allow for the detection of specific pathogens for the diagnosis of infectious diseases as well as the profiling of the entire microbial population for microbiome diseases or micro ecological diseases.

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