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Human Metagenomes' hidden association with chronic diseases (overview)

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The prevalence of numerous irrelevant chronic diseases has risen dramatically in recent decades. Long-term antibiotic use for chronic disease is on the rise, just till today, nothing is clear about the importance of the resistance and its link to host microbiomes.

The immune system is made up of a complicated but well-organized network of cell types that constantly monitor and maintain their surroundings. The microbial flora is shaped by the immune system's cells and their surrounding environment's regulated homeostatic interaction.

The properties of the identifying antibodies have been the focus of chronic diseases research, such as chronic prostatitis or autoimmune disease. However, as our understanding of the genes linked to disease states grows, we realize that humans must be seen as superorganisms in which a slew of bacterial genomes – the metagenome – coexist with our own. According to the National Institutes of Health, 90 percent of the cells in Homo sapiens are microbial, not human. Some of these bacteria produce compounds that disrupt the expression of genes linked to chronic illness.

Moreover, During the initial years of life, complex connections between the microbiome and the immune system appear to be crucial to later life health outcomes, but they have not been studied at the community level.

On the other hand, in follow up previous studies, some researchers theorize that the loss of specific bacterial species from our ancestral microbiota, has changed the setting in which immunological and metabolic development occurs in early life, leading to an increase in disease. This worrying trend shows that we need to emphasize our efforts on understanding and reverse the underlying causes that are causing our microbiota to vanish or change.

Recent Publications

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