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NEWS AND VIEWS

Human Microbiome and Cancer: An Insight

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Recent progress in the field of microbial ecology has led to the discovery of novel microbiota in humans. These organisms perform many biochemical functions for the host and are also associated with disease and disease progression. With the help of high-throughput assays, it is possible to survey the human microbiome, which can help elucidate their functional role in the symbiotic relationship with the host. Cancer, which results in uncontrolled cellular proliferation of the host cells, is a leading cause of death worldwide. Recent studies reveal the role of these microbiota that colonize the gut and associated organs, to be directly involved in cancer progression.

Helicobacter pylori are gram negative, microaerophilic bacteria that colonize the stomach of humans [1]. Experimental analysis has shown the direct involvement of *H. pylori* in gastric adenocarcinoma [2] and gastric Mucosal Associated Lymphoid Tissue (MALT) lymphoma [3]. On the contrary, *H. pylori* have an inverse association in the case of oesophageal adenocarcinoma [4]. *Helicobacter pylori* cause double stranded breaks in the host DNA, which can lead to cancer [5]. Inflammation of the gut also becomes a risk factor for cancer as it disturbs the microbiota and allows new populations to colonize. *E. coli* NC101 is an example of one such strain that colonizes the gut post inflammation and is involved in the causation of colorectal cancer. This strain of *E. coli* secretes colibactin, a toxin that damages cellular DNA, leading to neoplastic growth. When the gene coding for colibactin was removed from the *E. coli* genome, the tumorigenicity was substantially decreased [6].

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Some microorganisms are not directly carcinogenic but play a key role in carcinogenesis. Ethanol, which is not a strong carcinogen, is converted in vitro to acetaldehyde by the action of certain oral microbes, which is a known carcinogen [7]. Interestingly, some gut microbes can also metabolize certain foods of plant origin into biologically active compounds. For example, some gut microbes convert plant lignans into enterolignans, which help to reduce the occurrence of colorectal adenoma [8].

Carcinogenesis is a gradual process and involves alterations in the body at the biochemical, immunological as well at the physiological level(s). The changes that occur in the body can be caused by the microbes or can cause a shift in their population from equilibrium. Therefore, these microbes can also act as potential markers for various cancers. Elevation in the number of three oral bacteria, namely *Capnocytophaga gingivalis*, *Prevotella melaninogenica* and *Streptococcus mitis*, were found to be present in 80 % cases of Oral Squamous Cell Carcinoma (OSCC) and is considered an indicator for the same [9]. The faecal microbe, *Fusobacterium nucleatum*, is an indicator of colorectal carcinoma [10]. Despite all the progress in the field of microbial genomics, we still cannot cultivate all of the human microbiome in an artificial medium. The variation in the microbial constitution is highly individualistic and depends on the physiology, environment etc. Therefore, they cannot be solely considered as an indication of cancer and need to be used along with traditional diagnostic techniques.

As is the case in biology, a system cannot be fully understood until the same experiment can be replicated and similar results produced. Considering the fact that human microbiome has enormous variability, it poses a grave challenge to the scientists. Developing techniques that can overcome this situation is indeed the need of the hour.

Certain microbes residing in the human body are potential indicators but not a complete diagnostic tool in itself. We are still beginning to unravel the mystery of the human microbiome. With gradual advancement in the field of microbial ecology, one will be able to develop novel microbe based diagnostic techniques. This is like a field with no boundaries and the best is still to come.

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