

Perspective A SCITECHNOL JOURNAL

## Assessing the Impact of Gut Microbiota on Gastrointestinal **Cancer Progression**

## Yang Mien\*

Department of Pathology, Huazhong University of Science and Technology, Wuhan,

\*Corresponding Author: Yang Mien, Department of Pathology, Huazhong University of Science and Technology, Wuhan, China; E-mail: yang\_mien@hust22.cn Received date: 21 July, 2024, Manuscript No. JCEOG-24-148878;

Editor assigned date: 23 July, 2024, PreQC No. JCEOG-24-148878 (PQ);

Reviewed date: 06 August, 2024, QC No. JCEOG-24-148878;

Revised date: 13 August, 2024, Manuscript No. JCEOG-24-148878 (R); Published date: 20 August, 2024, DOI: 10.4172/2324-9110.1000422

## **Description**

Gastrointestinal (GI) cancers, which include cancers of the stomach, liver, pancreas, colon and rectum are among the most common and lethal forms of cancer worldwide. The development of GI cancers is influenced by several factors, including genetic predisposition, environmental exposures and lifestyle choices such as diet and smoking. In recent years, studies have increasingly recognized the significant role that gut microbiota, the vast community of microorganisms living in the human digestive tract plays in the initiation and progression of GI cancers. Trillions of microbes reside in the human gut, including bacteria, fungi, viruses and archaea collectively known as the gut microbiota. These microorganisms are involved in critical functions such as digestion, metabolism and immune regulation.

The gut microbiota maintains a symbiotic relationship with its host, helping to protect the intestinal lining, produce essential nutrients and modulate inflammatory responses. However, disruptions in the balance of the gut microbiota known as dysbiosis can lead to adverse health outcomes, including increased susceptibility to gastrointestinal cancers. Several mechanisms have been proposed through which gut microbiota influences cancer development. One of the most wellestablished links is through chronic inflammation. Certain bacterial species can induce inflammatory responses in the gut, which over time may damage the epithelial lining of the GI tract. This chronic inflammation develops a favorable environment for mutations, DNA damage and uncontrolled cell growth all of which are precursors to cancer.

Inflammatory Bowel Diseases (IBD) such as Crohn's disease and ulcerative colitis are known risk factors for colorectal cancer. Patients with IBD exhibit significant alterations in their gut microbiota, with an over-representation of pro-inflammatory bacteria such as Escherichia coli and Enterococcus faecalis and a reduction in beneficial species like Bacteroides and Lactobacillus. The pro-inflammatory bacteria produce substances like Reactive Oxygen Species (ROS) and Reactive Nitrogen Species (RNS) that cause DNA damage in the epithelial cells, promoting the formation of cancerous lesions. Some bacteria in the gut microbiota produce metabolites that can directly promote cancer. For instance, certain species of Fusobacterium which are frequently found in patients with colorectal cancer, produce virulence factors that promote cancer cell growth.

Additionally, gut bacteria can convert dietary components into harmful substances. For example, Bacteroides fragilis produces enterotoxins that activate inflammatory pathways and have been implicated in colon cancer development. Moreover, some bacterial species convert bile acids into secondary bile acids, which have been associated with an increased risk of colorectal cancer due to their toxic effects on the intestinal epithelium. Some microorganisms have the ability to directly influence the host's DNA integrity through the production of genotoxins. For example, Escherichia coli strains that carry the Polyketide Synthetase (PKS) island produce colibactin, genotoxin that induces double-stranded breaks in DNA. This leads to genetic mutations that can accelerate cancer progression, particularly in the colon and rectum.

Colorectal Cancer (CRC) is one of the most studied cancers in relation to gut microbiota. Several studies have demonstrated that patients with colorectal cancer have distinct microbial profiles compared to healthy individuals. Notably, there is a higher abundance of pathogenic bacteria like Fusobacterium nucleatum and Parvimonas micra in the tumor tissues of CRC patients. These bacteria are believed to promote cancer progression by modulating immune responses, promoting tumor cell adhesion and activating oncogenic pathways. Fusobacterium nucleatum, for instance has been shown to promote tumorigenesis by interacting with epithelial cells through specific virulence factors and recruiting immune cells that develop a pro-tumor inflammatory environment. Conversely, beneficial bacteria such as Faecalibacterium prausnitzii, which are known for their antiinflammatory properties, are often depleted in CRC patients, further contributing to a pro-carcinogenic state.

The gut microbiota is also implicated in the development of gastric cancer, particularly through its interactions with Helicobacter pylori, a bacterium known to cause gastric ulcers and cancer. H. pylori induces chronic inflammation in the stomach lining, which over time leads to the development of gastric lesions and cancer. Recent studies suggest that the broader gastric microbiome, beyond H. pylori may also play a role in gastric carcinogenesis. Imbalances in the gastric microbiota can disrupt mucosal integrity and enhance the inflammatory response further increasing cancer risk.

The role of gut microbiota in gastrointestinal cancer progression, modulating the microbiome provides a potential for cancer prevention and treatment. Probiotics, which are live beneficial bacteria and prebiotics, which are substances that promote the growth of beneficial bacteria, have shown potential in restoring healthy gut microbiota and reducing cancer risk. In animal models, probiotic supplementation has been found to reduce the incidence of colorectal tumors by enhancing immune responses and reducing inflammation. Clinical trials are currently exploring the use of probiotics and prebiotics as adjunct therapies for GI cancers.

## Conclusion

The gut microbiota plays a significant role in the progression of gastrointestinal cancers through mechanisms such as chronic inflammation, the production of carcinogenic metabolites and direct DNA damage. Understanding the complex interactions between the microbiome and the host provides new opportunities for cancer



Citation:

prevention and treatment. By restoring a healthy balance of gut microorganisms through probiotics, Fecal Microbiota Transplantation (FMT) and other microbiome-modulating therapies, it may be possible

to reduce cancer risk and improve treatment outcomes. As studies in this field continues to advance, the gut microbiota may become a key target in the fight against gastrointestinal cancer.

Volume 13 • Issue 2 • 1000422 • Page 2 of 2 •