

New colon cancer culprit found in gut microbiome

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Changes in the gut bacteria of colon cancer patients indicate that some virulent bacteria could be linked to the progression of the disease, according to research published in the open access journal *Genome Medicine*. The findings could eventually be used to identify a virulence signature in these cancers and help doctors predict how bacterial changes in patients' guts could affect their prognosis.

The human [gut microbiome](#), the collection of microorganisms, their genomes and habitat that contributes to maintaining a healthy intestine, is thought to play an active role in colon cancer progression. Previous studies have shown that changes in the bacterial community occur in the gut microbiome of colon cancer patients, with tumors harboring increased bacterial diversity and an abundance of pathogenic [bacteria](#) compared to surrounding healthy tissue.

Although researchers have uncovered a variety of potentially pathogenic bacteria associated with colon cancer, little work has been done to determine if there is a single signature that might unify their findings.

Lead author Michael Burns from The University of Minnesota, USA, said: "It was surprising that the results were so clear. We were able to clearly identify the presence of two virulent strains of bacteria, including the discovery of a new potential culprit, *Providencia*."

"This has obvious implications for colon [cancer patients](#) and by analyzing the similarities among these pathogens, we have uncovered a single signature of colon cancer when analyzing the gut microbiome that might help researchers identify these cancers in the future."

This was the first study to focus on the pathogenic potential of the bacterial genes present in the colon cancer 'tumor microenvironment', the environment

of surrounding blood vessels, immune cells and other cells. The genes of the gut microbiomes were predicted in 44 primary tumor and 44 patient-matched normal colon tissues to analyze the general microbial function.

The team in Ran Blekhman's lab noted changes in the abundances of helpful, harmless, and [pathogenic bacteria](#), including *Fusobacterium* and *Providencia*. *Fusobacterium* has previously been implicated as a cancer-causing group of bacteria, but this is the first time that *Providencia* has been linked to colon cancer.

Analyzing the major changes that take place in the gut microbiome could help researchers categorize the role particular bacteria play and identify the key players.

Additionally, by showing that the microbial genes predicted to be present in colon cancer tissue are enriched for virulence functions, clinicians could use this signature to uncover what bacterial changes in the gut mean for a patient's health.

At this stage, the research cannot determine a definite causal link between *Providencia* species and colon cancer. While the study's methods are robust for analyzing human [gut](#) samples, more research will be needed to assess the interactions between [gut bacteria](#) and the progression and development of [colon cancer](#).

More information: Virulence Genes are a Signature of the Microbiome in the Colorectal Tumor Microenvironment, Michael B Burns, Joshua Lynch, Timothy K Starr, Dan Knights and Ran Blekhman, *Genome Medicine* 2015. [DOI: 10.1186/s13073-015-0177-8](https://doi.org/10.1186/s13073-015-0177-8)

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