

Researchers use gut bacteria composition to genetically classify colorectal tumors

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Ran Blekhman, Ph.D., from the University of Minnesota. Credit: Dr. Blekhman

By analyzing the types of gut bacteria present around colorectal tumors, researchers have found a way to predict key genetic mutations in the tumors themselves, a method that could eventually inform the

development of colorectal cancer diagnostics and therapeutics. Their findings were presented at the American Society of Human Genetics (ASHG) 2015 Annual Meeting in Baltimore.

Led by Ran Blekhman, PhD, Assistant Professor of Genetics, Cell Biology, and Development at the University of Minnesota and senior author on the study, the researchers examined the genetic differences between colorectal [tumor](#) cells and healthy colon cells from 44 adults with [colorectal cancer](#). They looked for correlations between specific mutations in the tumor cells and the composition of the tumor microbiome - the types of bacteria present in the tumor's immediate environment and their relative abundance - and found relationships between the two.

"Ours was the first study to analyze both of these factors together," said Michael B. Burns, PhD, a postdoctoral researcher in Dr. Blekhman's laboratory. "Previous studies have found associations between certain mutations and colorectal [cancer](#), and between certain microbiome characteristics and cancer, but had not integrated the two," he explained.

The researchers found that in general, the more [cancer-associated mutations](#) a person's tumor cells had, the more varied his or her tumor microbiome was. In fact, specific mutations in tumor cells were associated with the presence of specific types of bacteria in the microbiome. Together with Dan Knights, PhD, Assistant Professor of Computer Science and Biotechnology at the University of Minnesota, Dr. Blekhman and colleagues developed a method to predict the types of mutations present in a tumor based on its microbiome. On average, the method correctly predicted about half of the most common mutations found in the tumor.

"We found that it could be possible to genetically classify the colorectal tumor a person has without having to do a biopsy and dissect it," Dr.

Blekhman said. "This could eventually provide a non-invasive and inexpensive approach to inform diagnosis and treatment."

In the longer term, he added, this research could also inform the development of new treatments for colorectal cancer. "By studying interactions between tumors and the bacteria in their microbiomes, we would better understand the bacteria's role in causing tumors to form and grow - if they even have such a role - and eventually, we may be able to treat cancer by changing aspects of its microbiome," Dr. Blekhman said.

The researchers caution that their current findings show only a correlation between microbiome composition and mutations in colorectal tumors. As yet, there is no evidence that bacterial changes cause colorectal cancer, but Dr. Blekhman and colleagues plan to study this question experimentally. They also plan to evaluate whether colorectal tumor microbiome composition can be assayed from stool samples, and if this data can also be used to predict the type of [mutations](#) present in the [tumor cells](#).

Provided by American Society of Human Genetics

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