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Decreased Diversity of the Bacteria Microbiome in the Gut is Associated With Risk of Colorectal Cancer

Decreased diversity in the microbial community found in the human gut is associated with colorectal cancer, according to a new study published December 6 in the *Journal of the National Cancer Institute*.

Previous studies suggest a role for the gut microbiota in colorectal cancer (CRC), but comprehensive epidemiological studies comparing samples from case and control subjects that also consider potential confounders and adjust for multiple comparisons inherently involved in microbiome analysis have not been reported.

Jiyoung Ahn, Ph.D., from Department of Population Health at New York University School of Medicine in New York, NY, and colleagues compared samples and data from participants enrolled in a case-control study. DNA was extracted from fecal samples from 47 case subjects and 94 sex- and body mass index-matched control subjects and was sequenced to determine the gut microbial community structure of case vs control subjects. Odds ratios to determine the relationship between gut microbiota of case subjects vs control subjects were calculated using logistic regression analysis after adjusting for age, sex, BMI, race, smoking, and sequencing batch. They found decreased bacterial diversity in the gut was associated with CRC risk.

The authors highlight several trends in abundance of some key bacteria in the fecal samples they analyzed from case and control subjects that contribute to the decreased diversity associated with CRC risk which they report. Case subjects showed decreased levels of Clostridia, which include some bacterial family members that ferment dietary fiber, to butyrate, which is a major colonic metabolite that may inhibit inflammation and carcinogenesis in the colon. Also of note, increased levels of *Fusobacterium* and *Porphyromonas*, bacteria related to inflammation in in the mouth and gastrointestinal track was observed for case vs control subjects.

The authors write, "Because of the potentially modifiable nature of the gut bacteria, our findings may have implications for CRC prevention."

In an accompanying editorial, Volker Mai, Ph.D., M.P.H., and J. Glenn Morris, Jr., M.D., M.P.H., T.M. from the University of Florida at Gainesville FL, say the findings by Ahn et al. are exciting. However, they also write, "CRC occurrence is known to be influenced by host genetics, as well as factors such as obesity, nutrition and exercise; given that these factors also influence microbiota, separation of cause and effect among all of these factors may become quite difficult." Mai and Morris conclude that prospective cohort studies are therefore warranted.

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