MICROBIOTA

Manipulating the microbiota could affect colorectal cancer development

"The gut microbiome is linked to various physiological functions associated with colon cancer," explain Patrick Schloss, Grace Chen and Joseph Zackular, authors of a recent study published in *mBio*. "We wanted to determine whether changes in the gut microbiome are actively driving tumorigenesis or just a collateral effect of this process," they add.

To answer this question, the researchers used a mouse model of inflammation-associated colorectal cancer. Next-generation sequencing of the 16S rRNA gene was used to show how changes in the gut microbial community were associated with the development of tumours. Tumour-bearing mice had enrichment of Bacteroides, Odoribacter and Akkermansia genera and decreases of Prevotellaceae and Porphyromonadaceae family members when compared with healthy mice.

Germ-free mice were then colonized with microbiota from either healthy or tumour-bearing mice. An increased

number and size of tumours developed in mice that received microbiota from tumour-bearing mice. "Finally, we used a broad-spectrum antibiotic cocktail to alter the microbiome of conventional mice, and these mice developed few, if any, tumours," describe Schloss, Chen and Zackular.

These findings indicate that a causal link exists between dysbiosis of the gut microbiota and colon tumorigenesis. Therefore, the researchers conclude that manipulating the microbiota composition is a potential strategy to prevent colorectal cancer development.

Zackular *et al.* are now investigating therapies—including diet, probiotics and prebiotics—that would modulate the gut microbiota to prevent or limit colorectal cancer progression.

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Original article Zackular, J. P. et al. The gut microbiome modulates colon tumorigenesis. *mBio* 4, e00692–13