Medical Xpress

What's in your gut? Certain bacteria may influence susceptibility to infection

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The specific composition of bacterial species in a person's gut may protect against or increase susceptibility to *Campylobacter*, the most common cause of human bacterial intestinal inflammation, according research published this week in *mBio®*, the online open-access journal of the American Society for Microbiology. The study also found that *Campylobacter* infection can yield lasting changes to one's gut bacteria composition.

"It has been known for a long time that the microbiota, or microorganisms in the gut, can protect a person from colonization by organisms that cause intestinal tract disease. However, very little is known about how human gut microbiota influences susceptibility to these organisms, and to *Campylobacter* in particular," said senior study author Hilpi Rautelin, MD, PhD, professor of clinical bacteriology at Uppsala University and Uppsala University Hospital in Sweden. "We wanted to see if the composition of the human gut microbiota plays a role in susceptibility to *Campylobacter* infection."

Rautelin and colleagues followed 24 workers at three poultry slaughterhouses in Sweden. In 2010, they collected fecal samples from the workers once a month from June to September, during the summer peak of *Campylobacter*-positive chicken flocks, and again the following February. Fecal samples were cultured for *Campylobacter* and analyzed by sequencing for all bacteria. While all participants tested negative for *Campylobacter* at the beginning of the study, seven participants became culture positive for the organism during the study. Only one of the

Campylobacter-positive participants experienced symptoms of illness.

Those who became *Campylobacter*-positive had a significantly higher abundance of *Bacteroides* and *Escherichia* organisms than those who remained culture negative, suggesting that these bacterial species likely play an important role in colonization resistance. This group also had a significantly higher abundance of *Phascolarctobacterium* and *Streptococcus* species than those in the *Campylobacter*-negative group, which had an overrepresentation of Clostridiales, unclassified Lachnospiraceae, and *Anaerovorax* species.

"Elevated proportions of *Bacteroides* and *Escherichia* species in the gut microbiota may predispose humans to *Campylobacter* infection," Rautelin said. "These particular species have been shown to have an important role for susceptibility to gut pathogens and *Campylobacter* in particular in some mouse model studies."

Following the individuals' fecal microbiota compositions over time, the researchers observed that the *Campylobacter*-negative individuals had small differences but those who tested positive for *Campylobacter* showed significant changes by the February sample. Researchers do not yet know the implications of these changes, Rautelin said.

Whether microbiota composition alone or together with an individual's immune status also plays a significant role in the eradication of *Campylobacter* from the intestines remains to be studied, she said.

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