

Microbiologists discover how gut bacterial resources are hijacked to promote intestinal illnesses

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Dr. Vanessa Sperandio of the UT Southwestern Medical Center. Credit: UT Southwestern

UT Southwestern Medical Center microbiologists have identified key bacteria in the gut whose resources are hijacked to spread harmful foodborne *E. coli* infections and other intestinal illnesses.

Though many *E. coli* bacteria are harmless and critical to gut health, some *E. coli* species are harmful and can be spread through contaminated

food and water, causing diarrhea and other intestinal illnesses. Among them is enterohemorrhagic *E. coli* or EHEC, one of the most common foodborne pathogens linked with outbreaks featured in the news, including the multistate outbreaks tied to raw sprouts and ground beef in 2014.

The UT Southwestern team discovered that EHEC uses a common gut bacterium called *Bacteroides thetaiotaomicron* to worsen EHEC infection. *B. thetaiotaomicron* is a predominant species in the gut's microbiota, which consists of tens of trillions of microorganisms used to digest food, produce vitamins, and provide a barrier against harmful microorganisms.

"EHEC has learned to how to steal scarce resources that are made by other species in the microbiota for its own survival in the gut," said lead author Dr. Meredith Curtis, Postdoctoral Researcher at UT Southwestern.

The research team found that *B. thetaiotaomicron* causes changes in the environment that promote EHEC infection, in part by enhancing EHEC colonization, according to the paper, appearing in the journal *Cell Host Microbe*.

"We usually think of our microbiota as a resistance barrier for pathogen colonization, but some crafty pathogens have learned how to capitalize on this role," said Dr. Vanessa Sperandio, Professor of Microbiology and Biochemistry at UT Southwestern and senior author.

EHEC senses changes in sugar concentrations brought about by *B. thetaiotaomicron* and uses this information to turn on virulence genes that help the infection colonize the gut, thwart recognition and killing by the host immune system, and obtain enough nutrients to survive. The group observed a similar pattern when mice were infected with their

equivalent of EHEC, the gut bacterium *Citrobacter rodentium*. Mice whose [gut](#) microbiota consisted solely of *B. thetaiotaomicron* were more susceptible to infection than those that had no [gut microbiota](#). Once again, the research group saw that *B. thetaiotaomicron* caused changes in the environment that promoted *C. rodentium* infection.

"This study opens up the door to understand how different microbiota composition among hosts may impact the course and outcome of an infection," said Dr. Sperandio, whose lab studies how bacteria recognize the host and how this recognition might be exploited to interfere with bacterial infections. "We are testing the idea that differential gastrointestinal microbiota compositions play an important role in determining why, in an EHEC outbreak, some people only have mild diarrhea, others have bloody diarrhea and some progress to hemolytic uremic syndrome, even though all are infected with the same strain of the pathogen."

Provided by UT Southwestern Medical Center

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