balance of microorganisms in the gastrointestinal tract, allowing a potentially harmful bacterium known as vancomycin-resistant *Enterococcus* (VRE) to take over as much as 99 percent of the population of intestinal microbes.

VRE, which is highly resistant to most antibiotics, is a common cause of infection in hospitalized patients, particularly in patients receiving treatment for cancer. After it reaches a high density in the intestine, VRE can cross the intestinal lining and invade the bloodstream. Before this study, it was known that VRE could colonize in the gastrointestinal tract, but it was not known that it could become such an overwhelming part of the bacterial flora.

“Clinicians prescribe antibiotics to treat particular infections, but they sometimes forget that these drugs also kill many normal bacteria that inhabit our mouths, stomachs, small intestines, and colons,” explains Eric G. Pamer, Chief of Memorial Sloan Kettering’s Infectious Diseases Service and senior author of the paper, published in the *Journal of Clinical Investigation*. [PubMed Abstract] “We think our study is a first step toward identifying the breadth of the impact of antibiotic treatment.”

Carles Ubeda, a research colleague working with Dr. Pamer, collaborated with the Center’s Genomics Core Laboratory and Computational Biology Center to use high-throughput, multiparallel DNA-sequencing methods — which allow analysis of many samples at one time — to study the balance of micro-organisms in the intestines of mice during treatment with several common antibiotics. They found that the frequency of harmful bacteria, including VRE, remained increased even weeks after treatment ended.

“The ultimate goal is to identify members of the normal intestinal flora that provide resistance to common pathogens causing infections in hospitalized patients,” Dr. Pamer adds. “This may enable us to develop effective probiotic agents [supplements that contain beneficial bacteria] that could be used to enhance resistance to harmful pathogens.”

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