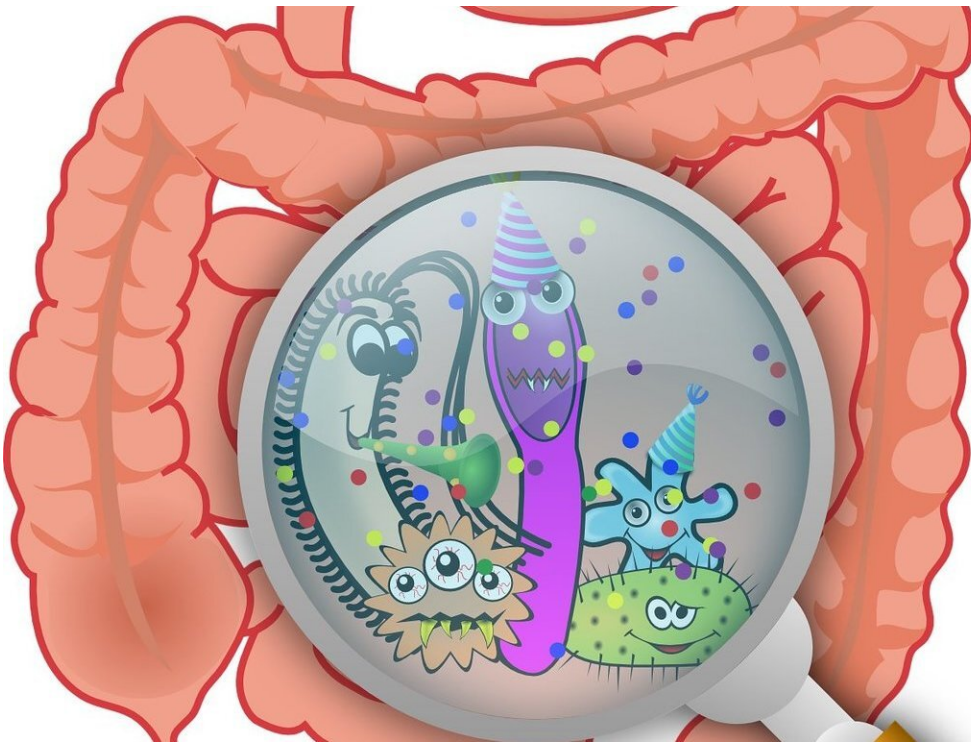


# Unexpected microbiome collapse after admission to intensive care

October 1 2019

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Potentially harmful microbes overwhelm the healthy gut microbiota in intensive care patients, research has found.

Research published in the journal *Microbial Genomics* assessed how the diversity and makeup of the [gut microbiome](#) varied during patients' time

in the intensive care unit (ICU). The gut [microbiome](#) is the complex community of bacteria and other microbes that reside in the gut, and plays an important role in health and wellbeing.

A number of factors are likely to reduce the gut microbial diversity of ICU patients, putting them at greater risk of infection—these include assisted ventilation, enteric feeding and certain medications.

Although the patients tested were admitted to the ICU for a variety of reasons, two-thirds showed a marked reduction in microbial diversity at some stage during their stay. There were 24 patients enrolled in the study, with ages ranging from 25 to 85 years. Reasons for admission varied, and included trauma, heart attack and cancer.

According to Professor Mark Pallen (Quadram Institute, UK), who led the research, a diverse microbiome is important. He said: "The gut microbiome performs many important and diverse roles and many of these roles can be lost if microbial diversity is lost. This is likely to impact on nutrition, gut motility and inflammation in the bowel."

The researchers found that in long-stay ICU patients, the gut microbiome became dominated by bacteria with the potential to become pathogenic: "The gut microbiome is normally home to a very diverse set of microbial species, numbering in the hundreds, with a relatively even spread of abundances. But in ICU patients, a single organism can take over the microbiome so that the vast majority of microbial cells and sequences belong to just one species.

"It was shocking to see how quickly and how often this diverse community can collapse down to stark monolithic domination by a single pathogen among critically ill patients."

The research team used a technique called shotgun metagenomics to

determine which bacteria were present in the gut. This involved extracting and sequencing DNA from faecal samples to determine which microbes were present.

Prof Pallen said, "We saw *Enterococcus faecium* most commonly and this is of concern as this is an important and common pathogen among hospitalised patients. More worrying still, we detected evidence of spread of a single strain between three patients."

*E. faecium* can cause severe infections, particularly at sites where medical devices—such as intravenous cannulas—have been used. If these bacteria get into the bloodstream, they can cause fatal infection. Enterococcal infections are particularly difficult to treat as many species in this group have developed resistance to multiple antibiotics, including the last-resort antibiotic vancomycin.

Domination the gut by a single potential pathogen can put other [hospital patients](#) at risk, according to Pallen. He said, "When a single potentially pathogenic microbe increases substantially in biomass in this particular niche, it is then more likely to spill over into other compartments of the body, for example, the blood or the lungs, where it can cause life-threatening disease. What's more, it is then likely to spread to other patients, facilitating the dissemination of multi-drug resistant pathogens throughout the hospital."

One antibiotic in particular, meropenem, was found to have a [negative impact](#) on healthy gut bacteria in ICU patients. To protect microbial diversity, the researchers suggest that patients could be given medications that absorb or inactivate, such as charcoal, to reduce the impact of antibiotics on the gut microbiome. Another option might be to restore microbial [diversity](#) in ICU patients through faecal microbiota transplants.

**More information:** Anuradha Ravi et al. Loss of microbial diversity and pathogen domination of the gut microbiota in critically ill patients, *Microbial Genomics* (2019). [DOI: 10.1099/mgen.0.000293](https://doi.org/10.1099/mgen.0.000293)

Provided by Microbiology Society

Citation: Unexpected microbiome collapse after admission to intensive care (2019, October 1) retrieved 25 April 2024 from <https://medicalxpress.com/news/2019-10-unexpected-microbiome-collapse-admission-intensive.html>

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