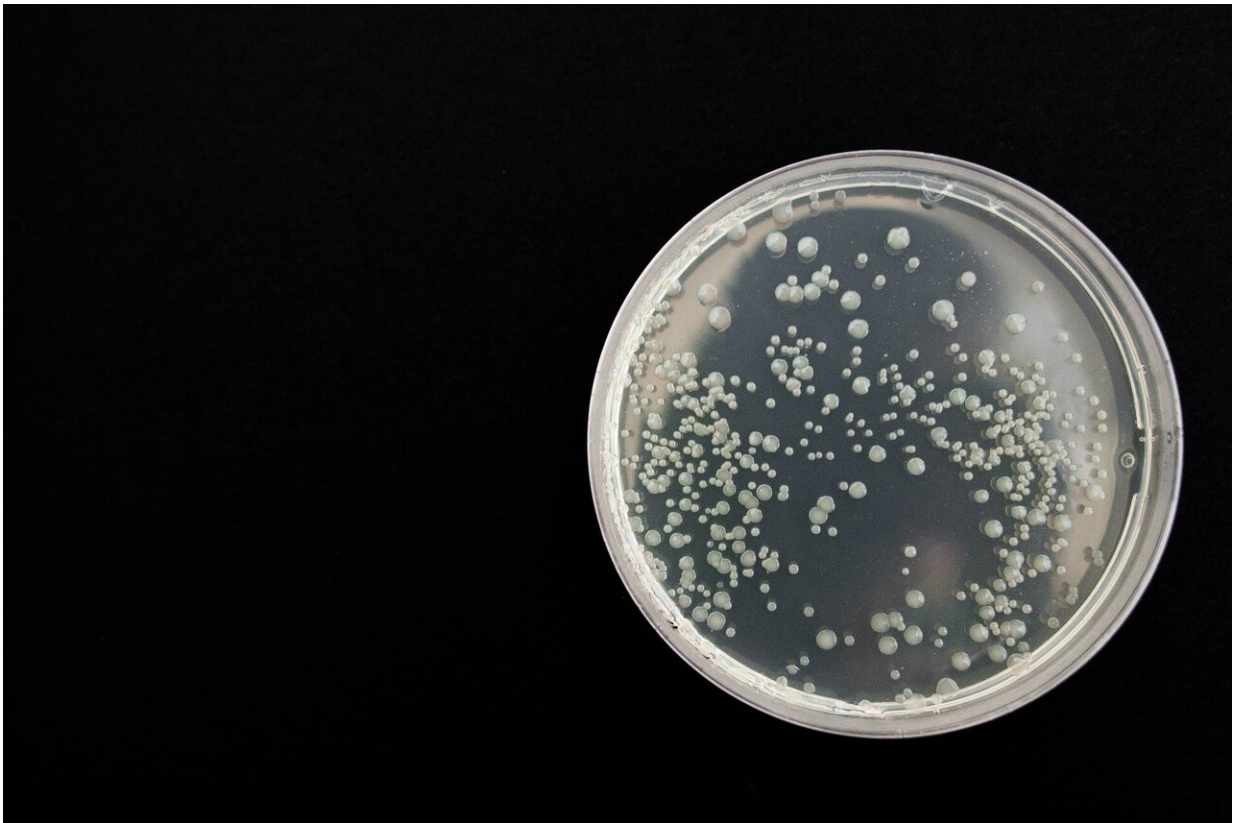


# Drug-resistant hospital bacteria persist even after deep cleaning

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Scientists have used genome sequencing to reveal the extent to which a drug-resistant gastrointestinal bacterium can spread within a hospital, highlighting the challenge hospitals face in controlling infections.

*Enterococcus faecium* is a bacterium commonly found in the gastrointestinal tract, where it usually resides without causing the host problems. However, in immunocompromised patients, it can lead to potentially life-threatening [infection](#).

Over the last three decades, strains have emerged that are resistant to frontline antibiotics including ampicillin and vancomycin, limiting treatment options—and particularly worrying, these strains are often those found in [hospital](#)-acquired *E. faecium* infections.

A team of scientists at the University of Cambridge and the London School of Hygiene and Tropical Medicine has pioneered an approach combining epidemiological and [genomic information](#) to chart the spread of bacteria within healthcare settings. This has helped hospitals identify sources of infection and inform infection control measures.

In a study published today in *Nature Microbiology*, the team has applied this technique to the spread of drug-resistant *E. faecium* in a hospital setting.

Dr. Theodore Gouliouris from the Department of Medicine at the University of Cambridge, and joint first author on the study, said: "We've known for over two decades that patients in hospital can catch and spread drug-resistant *E. faecium*. Preventing its spread requires us to understand where the bacteria lives—its 'reservoirs' - and how it is transmitted.

"Most studies to date have relied on culturing the bacteria from samples. But as we've shown, whole genome sequencing—looking at the DNA of the bacteria—combined with detailed patient and environmental sampling can be a powerful tool to help us chart its spread and inform ways to prevent further outbreaks."

The team followed 149 haematology patients admitted to Addenbrooke's Hospital, Cambridge University Hospitals NHS Foundation Trust, over a six-month period. They took stool samples from the patients and swabs from the hospital environment and cultured them for *E. faecium*.

Genomic analysis of the bacteria was much more effective at identifying hospital-acquired *E. faecium*: out of 101 patients who could be followed up, genomic analysis identified that two thirds of patients acquired *E. faecium*, compared to less than half using culture methods alone.

Just under half (48%) of the swabs taken from the hospital environment were positive for vancomycin-resistant *E. faecium*. This included 36% of medical devices, 76% of non-touch areas such as air vents, 41% of bed spaces and 68% of communal bathrooms tested.

The researchers showed that even deep cleaning could not eradicate the bacteria. The hospital undertook deep cleaning on one ward over a three-day period during the study, when patients were moved elsewhere; however, when the team sampled locations prior to patients returning to the ward, they found that 9% of samples still tested positive for the bacteria. Within three days of patients returning to the ward, around half of the sampled sites tested positive.

Three-quarters (74%) of the patients (111/149) were carriers of the A1 clade—a multi-drug resistant strain of *E. faecium* commonly seen in hospitals that is resistant to the antibiotic ampicillin and which frequently acquires resistance to vancomycin. Of these 111 patients, 67 had strong epidemiological and genomic links with at least one other patient and/or their direct environment.

"The fact that these cases were all linked to another patient or their environment suggests strongly that they had picked up the multi-drug resistant bacteria while in the hospital," said Dr. Francesc Coll from the

London School of Hygiene and Tropical Medicine, joint first author.

Further genomic analysis showed that within this multi-drug resistant strain were several subtypes (defined by how genetically-similar they were). However, it was not uncommon for a patient to be carrying more than one subtype, which—without detailed genomic analysis—could confound attempts to identify the route of transmission of an infection. Notably, despite the circulation of as many as 115 subtypes, 28% of *E. faecium* acquisitions were caused by just two superspreading subtypes. The authors found no evidence of resistance or tolerance to common disinfectants to explain the success of these subtypes.

Six study patients contracted an 'invasive infection', meaning that they had been carrying *E. faecium* asymptotically in their gut, but subsequently developed a symptomatic infection. Comparing the genomes of the infecting and gut strains the authors determined that invasive *E. faecium* infections originated from the [patients'](#) own gut.

"Our study builds on previous observations that drug-resistant strains of *E. faecium* can persist in the hospital environment despite standard cleaning—we were still surprised to find how short-lasting was the effect of deep cleaning," added Dr. Gouliouris.

"We found high levels of hospital-adapted *E. faecium* despite the use of cleaning products and procedures that have proven effective against the bug. It highlights how challenging it can be to tackle outbreaks in hospitals."

Senior author Professor Sharon Peacock from the Department of Medicine at the University of Cambridge added: "The high rates of infection with drug-resistant *E. faecium* in specific vulnerable patient groups and its ability to evade cleaning measures pose an important challenge to infection control. Patient screening, adequate provision of

isolation and ensuite toilet facilities, improved and more frequent cleaning procedures, and stricter health-care worker hygiene practices will all be needed to curtail this global epidemic.

"But this is also a sign of how urgently we need to tackle inappropriate use of antibiotics worldwide, which is widely recognised as posing a catastrophic threat to our health and our ability to control infections."

**More information:** Quantifying acquisition and transmission of *Enterococcus faecium* using genomic surveillance, *Nature Microbiology* (2020). DOI: [10.1038/s41564-020-00806-7](https://doi.org/10.1038/s41564-020-00806-7) , [www.nature.com/articles/s41564-020-00806-7](https://www.nature.com/articles/s41564-020-00806-7)

Provided by University of Cambridge

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