

Common bacteria on verge of becoming antibiotic-resistant superbugs

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Bacteria that cause many hospital-associated infections are ready to quickly share genes that allow them to resist powerful antibiotics. The illustration, based on electron micrographs and created by the Centers for Disease Control and Prevention, shows one of these antibiotic-resistant bacteria. Credit: CDC/James Archer

Antibiotic resistance is poised to spread globally among bacteria frequently implicated in respiratory and urinary infections in hospital settings, according to new research at Washington University School of Medicine in St. Louis.

The study shows that two genes that confer resistance against a particularly strong class of antibiotics can be shared easily among a family of [bacteria](#) responsible for a significant portion of hospital-associated infections.

Drug-resistant germs in the same family of bacteria recently infected several patients at two Los Angeles hospitals. The infections have been linked to medical scopes believed to have been contaminated with bacteria that can resist carbapenems, potent antibiotics that are supposed to be used only in gravely ill patients or those infected by [resistant bacteria](#).

"Carbapenems are one of our last resorts for treating bacterial infections, what we use when nothing else works," said senior author Gautam Dantas, PhD, associate professor of pathology and immunology. "Given what we know now, I don't think it's overstating the case to say that for certain types of infections, we may be looking at the start of the post-antibiotic era, a time when most of the antibiotics we rely on to treat bacterial infections are no longer effective."

Dantas and other experts recommend strictly limiting the usage of carbapenems to cases in which no other treatments can help.

The study, conducted by researchers at Washington University, Barnes-Jewish Hospital and the National University of Sciences and Technology in Pakistan, is available online in Emerging Infectious Diseases.

The researchers studied a family of bacteria called Enterobacteriaceae,

which includes *E. coli*, *Klebsiella pneumoniae* and *Enterobacter*. Some strains of these bacteria do not cause illness and can help keep the body healthy. But in people with [weakened immune systems](#), infections with carbapenem-resistant versions of these bacteria can be deadly.

The Centers for Disease Control and Prevention named carbapenem-resistant Enterobacteriaceae as one of the three most urgent threats among emerging forms of antibiotic-resistant disease. Studies have shown the fatality rate for these infections is above 50 percent in patients with weakened immune systems.

Two genes are primarily responsible for carbapenem-resistant versions of these disease-causing bacteria. One gene, KPC, was detected in New York in 2001 and quickly spread around most of the world, with the exception of India, Pakistan and other South Asian countries. This gene was present in the bacteria that recently contaminated medical equipment in a Los Angeles hospital where two patients died.

A second carbapenem resistance gene, NDM-1, was identified in 2006 in New Delhi, India. It was soon detected throughout South Asia, and most patients infected by bacteria with NDM-1 have had an epidemiological link to South Asian countries.

Dantas and his collaborators were curious about why the two resistance genes seemed to be geographically exclusive. For the study, they compared the genomes of carbapenem-resistant bacteria isolated in the United States with those of carbapenem-resistant bacteria isolated in Pakistan.

Based on the apparent geographic exclusivity of the two resistance genes, the scientists expected to find that bacteria from the two regions were genetically different. Such differences could explain why the two resistance genes weren't intermingling. But the researchers' results

showed otherwise. The bacteria's high genetic similarity suggests that the [antibiotic resistance](#) genes could be shared easily between bacteria from the two geographic regions.

The researchers also sequenced a special portion of bacterial genetic material called plasmids. Most of a bacteria's DNA is found in its chromosome, but bacteria also have many extra, smaller and circular bits of DNA known as plasmids that easily can pass from one bacterial strain to another. A plasmid is like a bacterial gene delivery truck; it is the primary way antibiotic [resistance genes](#) spread between bacteria.

The researchers identified a few key instances in which the plasmids carrying NDM-1 or KPC were nearly identical, meaning they easily could facilitate the spread of antibiotic resistance between disease-causing bacteria found in the United States and South Asia. Recent evidence suggests that this intermingling already may be happening in parts of China.

"Our findings also suggest it's going to get easier for strains of these bacteria that are not yet resistant to pick up a gene that lets them survive carbapenem treatment," Dantas said. "Typically, that's not going to be a problem for most of us, but as drug-resistant forms of Enterobacteriaceae become more widespread, the odds will increase that we'll pass one of these superbugs on to a friend with a weakened immune system who can really be hurt by them."

More information: Pesesky MW, Hussain T, Wallace M, Wang B, Andleeb S, Burnham C-AD, Dantas G. KPC and NDM-1 are harbored by related Enterobacteriaceae strains and plasmid backbones form distinct geographies. *Emerging Infectious Diseases*, June 2015; dx.doi.org/10.3201/eid2106.141504

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