

Scientists discover uncommon superbug strain in greater Houston area

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Houston Methodist Research Institute scientists used genome sequencing to discover that an otherwise rare strain of a superbug was found in more than one-third of the Houston patients studied. This strain is resistant to many commonly used antibiotics.

"Finding the otherwise uncommon strain in our city was a very surprising discovery," said James M. Musser, M.D., Ph.D., senior author and chair of the Department of Pathology and Genomic Medicine at the Houston Methodist Research Institute and Houston Methodist Hospital. "Because *Klebsiella pneumoniae* is a common and important cause of human infections, we urgently need to identify potential vaccine targets or other new treatments, and develop new and rapid diagnostic techniques."

In the largest published study to date on the bacterial pathogen *Klebsiella pneumoniae*, researchers sequenced the genome of more than 1,700 strains causing infections in patients over a four-year period. The study appears in the May 16 issue of *mBio*, an online journal published by the American Society for Microbiology.

Musser said the reason why this particular strain is prevalent in the Houston area is a mystery, but is a focus of intensive ongoing research. *K. pneumoniae* is one of the most common causes of infections in hospitalized patients in the United States.

The team's discovery documents the occurrence of an especially strong group of antibiotic-resistant bacteria in a city of approximately six million people. Musser said *K. pneumoniae* is a challenging pathogen because it causes serious infections, especially in hospitalized patients. *K. pneumoniae* typically doesn't cause disease when it lives inside human intestines. However, when it moves into other parts of the body, the bacteria can cause a range of illnesses, including pneumonia; bloodstream, wound or [surgical site infections](#); meningitis; and [urinary tract infections](#).

Musser's team collaborated with scientists at the Argonne National Laboratory and University of Chicago to sequence and analyze the genomes of 1,777 *K. pneumoniae* strains causing infections between September 2011 and May 2015 in patients in the Houston Methodist system.

Unexpectedly, the otherwise uncommon clone type 307 was the most abundant strain of *K. pneumoniae* circulating. This organism also has been periodically identified in parts of Europe, Africa, Asia and South America. However, until now, clone type 307 has not been documented to be an abundant cause of infections in one city.

"Incorporating sophisticated and novel computational and molecular strategies allowed us to rapidly identify the drug-resistant strains," said S. Wesley Long, M.D., Ph.D., first author and associate director of the Clinical Microbiology Laboratory at Houston Methodist Hospital. "The faster we can successfully identify which antibiotics this strain is sensitive to, the faster a treating physician can target the appropriate therapy to these ill patients. Our discoveries also give us the tools to begin to understand how the germ is spreading throughout the Houston area."

Earlier this year, *K. pneumoniae* made national and international

headlines when the Centers for Disease Control documented the first case of an elderly Nevada woman who died from a rare form of this superbug after she failed to respond to all 26 antibiotics used in the United States.

"Fortunately, the strain 307 identified in our study remains susceptible to certain antibiotics that can be used to successfully treat infected patients," said Long.

More information: S. Long, R. Olsen, T. Eagar, S. Beres, P. Zhao, J. Davis, T. Brettin, F. Xia, J. Musser. *mBio*, (Online May 16, 2017). [DOI: 10.1128/mBio.00489-17](https://doi.org/10.1128/mBio.00489-17)

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