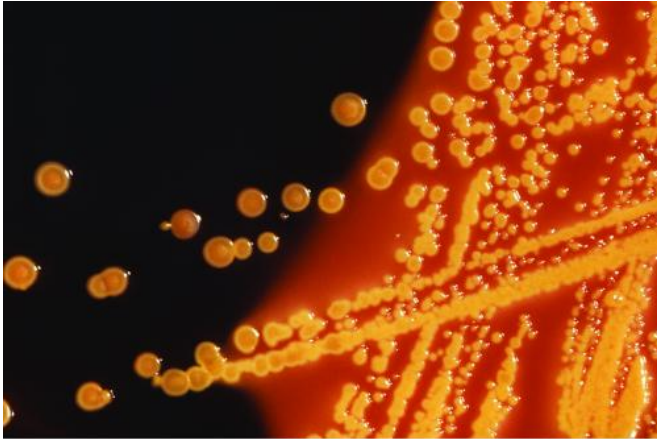


Epidemic of *Escherichia coli* infections traced to one strain of bacteria

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Colonies of *Escherichia coli* bacteria growing in a laboratory culture are shown. Credit: Centers for Disease Control and Prevention

In the past decade, a single strain of *Escherichia coli*, or *E. coli*, has become the main cause of bacterial infections in women and the elderly by invading the bladder and kidneys, according to a study published today in the American Society for Microbiology's open access journal *mBio*.

Besides becoming more resistant to antibiotics, the strain H30-Rx gained an unprecedented ability to spread from the urinary tract to the blood, leading to the most lethal form of bacterial infections—sepsis— and posing a looming threat to the more than 10 million Americans who annually suffer from [urinary tract infections](#) (UTIs).

This new study could help trace the evolutionary history of this superbug and possibly lead to the development of a vaccine, according to Lance B. Price, Ph.D., the study's lead author. Price is professor of environmental and occupational health at the George Washington University School of Public Health and Health Services (SPHHS), and is an associate professor in the Pathogen

Genomics Division of the Translational Genomics Research Institute (TGen).

Previous research suggested that the ST131 group of *E. coli* – a family of many genetically related strains of bacteria—had independently gained resistance to antibiotics through separate genetic events. The ST131 group had been identified as a major source of superbugs—microbes resistant to multiple antibiotics—among UTI bacteria. If true, the existence of many different resilient strains would prove a formidable threat with multiple ways of evading the immune system and medical treatment, according to the new study.

Using advanced genomic techniques, Price and collaborators—James R. Johnson of the Veterans Affairs Medical Center and the University of Minnesota, and Evgeni V. Sokurenko of the University of Washington School of Medicine—discovered that the ST131 strains represented genetic clones abruptly evolved from a single strain of *E. coli*.

By gaining mutations in two genes, a strain called H30 gave rise more than a decade ago to the H30-R clone, which became fully resistant to the then-wonder-drug known as Cipro. Soon after, a new clone evolved from H30-R called H30-Rx, which is resistant to several extended-spectrum antibiotics, such as third-generation cephalosporins.

Using whole-genome sequencing—spelling out, in order, each molecule of DNA—researchers analyzed the genomes of *E. coli* samples from patients and animals in five countries over 44 years, 1967-2011. They created a family tree tracing how the superbug clones emerged as the result of discrete genetic events.

"Astoundingly, we found that all of the resistance could be traced back to a single ancestor," Price said. "Our research shows this superbug then took

off, and now causes lots of drug-resistant infections."

H30-Rx, appears to be much more adept than other *E. coli* at ascending from the bladder to the kidneys and then into the bloodstream, where it can be lethal, and the study suggests that H30-Rx may be responsible for 1.5 million UTIs and tens of thousands of deaths annually in the United States.

This study shows that, by focusing on H30-Rx, researchers might find a vaccine that could prevent many infections. Vaccines for highly resistant strains of superbugs could protect people from ever getting sick in the first place, Price said.

"This strain of *E. coli* spreads from person to person and seems to be particularly virulent," Johnson said. "This study might help us develop better tools to identify, stop or prevent its spread by finding better ways to block the transmission of the [superbug](#), or by finding a diagnostic test that would help doctors identify such an infection early on—before it might have the chance to turn lethal."

Sokurenko added, "We now know that we are dealing with a single enemy, and that by focusing on this strain we can have a substantial impact on this worldwide epidemic."

The study, The epidemic of ESBL-producing *Escherichia coli* ST131 is driven by a single highly pathogenic subclone, H30-Rx, appears today in the peer-reviewed online-only scientific magazine *mBio* – the flagship journal of the American Society for Microbiology and the American Academy of Microbiology.

Provided by George Washington University

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