

Study describes new strategies for investigating microbial outbreaks

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Credit: University of Texas at San Antonio

In a new study published in *Frontiers in Microbiology*, Mark Eppinger, assistant professor in the Department of Biology at The University of Texas at San Antonio (UTSA) describes innovative strategies to track disease-causing pathogens like *E. coli*. Eppinger hopes his research will aid in halting and preventing large-scale outbreaks.

"When there's an outbreak of human pathogenic *E. coli*, a timely response is very important," he said. "Usually, at first no information is

available about where the disease originated."

Eppinger, a member of the UTSA South Texas Center for Emerging Infectious Diseases, calls the method he developed at UTSA a form of whole genome sequence typing of outbreak strains. According to the researcher, each outbreak features unique characteristics. The outbreak strains have subtle traits that make them distinguishable from other strains, which makes it possible for Eppinger to compare and contrast them to other [outbreaks](#).

He likens the investigation to looking at a parking lot full of the same blue car. They all look very similar, but Eppinger is looking for the tiniest differences such as a dent, a scratch or a broken tail light.

"No detail is too small," he said. "We can use these differences to trace the outbreak back to its contaminated source by looking to see if these traits existed in other reported outbreaks of the same pathogen."

Finding similarities between outbreaks allows for the pathogen to be traced back to a certain country or region, or even to a singular location. The more quickly investigators can find the source of an outbreak, the faster they can contain the outbreak.

Eppinger's strategies can also aid in identifying how lethal the pathogen can be. In his study, he focused on outbreaks of *E. coli*, which has recently affected restaurants like Chipotle and companies like Totino's, which sells frozen pizza products.

"Some outbreaks can be more severe than others," he said. "As a result of the 2006 outbreak, which spread through spinach, nearly half the people effected were hospitalized and a large portion had permanent kidney damage."

By studying strains from different past *E. coli* outbreaks with his techniques, Eppinger is able to measure the amount of toxin produced in each strain, which is a direct mediator of disease and shows how severe the resulting illness could be.

"In terms of outbreak investigation, you can ask a person where they've eaten, where they work and if they've traveled recently," Eppinger said. "If we get an outbreak strain, we can map it directly to other outbreak strains and pinpoint the origin. The answer is there in these tiny details."

More information: Brigida Rusconi et al, Whole Genome Sequencing for Genomics-Guided Investigations of Escherichia coli O157:H7 Outbreaks, *Frontiers in Microbiology* (2016). [DOI: 10.3389/fmicb.2016.00985](https://doi.org/10.3389/fmicb.2016.00985)

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