

Team helps track down deadly bloodstream infection

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The Translational Genomics Research Institute (TGen), working with international investigators, have discovered the source of a potential deadly blood infection in more than 50 South American cancer patients.

Using advanced genomic sequencing, TGen was able to track a potentially deadly and therapy-resistant fungus, *Sarocladium kiliense*, to a tainted anti-nausea medication given to dozens of [cancer patients](#) in Chile and Colombia, according to a report in *Emerging Infectious Diseases*, published by the U.S. Centers for Disease Control and Prevention.

"Contamination of medical products, particularly with environmental fungi, poses growing concern and a [public health threat](#), especially in vulnerable populations such as cancer patients," said Dr. David Engelthaler, Director of Programs and Operations for TGen's Pathogen Genomics Division in Flagstaff, Ariz.

"Increased vigilance and the use of advanced technologies are needed to rapidly identify the likely sources of infection to efficiently guide epidemiologic investigations and initiate appropriate control measures," said Dr. Engelthaler, Arizona's former State Epidemiologist.

This bloodstream-infection outbreak, from June 2013-January 2014, included a cluster of cases at eight hospitals in Santiago, the capital of Chile. All of the patients received the same four intravenous medications. But only one—ondansetron, an anti-nausea

medication—was given exclusively to cancer patients.

All of the patients infected with *S. kiliense* received ondansetron from the same source, a pharmaceutical company in Columbia. Two of three lots of unopened ondansetron, tested by the Chilean Ministry of Health, yielded vials contaminated with *S. kiliense*, forcing a recall of all ondansetron in Chile made by the Colombian manufacturer.

Subsequently, Colombian officials discovered 14 other cases in which patients, given ondansetron from the same Colombian pharmaceutical firm, were infected with *S. kiliense*. The source of the contamination was identified only as "pharmaceutical company A" in the CDC report.

Read the full CDC report here:

<http://wwwnc.cdc.gov/eid/article/22/3/pdfs/15-1193.pdf>

S. kiliense has been implicated previously in healthcare-related infections, but the lack of available typing methods has precluded the ability to substantiate sources.

"The use of whole-genome sequence typing (WGST) to investigate fungal outbreaks has become integral to epidemiologic investigations," Dr. Engelthaler said. "Our WGST analysis demonstrated that the patient isolates from Chile and Colombia were nearly genetically indistinguishable from those recovered from the unopened medication vials, indicating the likely presence of a single-source infection."

Provided by The Translational Genomics Research Institute

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