

Genomic methods aid study of Seattle 2017-2022 Shigella outbreak

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Shigella colonies on a chromagar plate culture medium are teal, while E. coli colonies are pink. This photograph from the Harborview Medical Center Microbiology Lab in Seattle was taken Jan. 30, 2023. Credit: Jason Matsumoto, Harborview Microbiology Lab

A genomic study of a sustained, multidrug-resistant Shigellosis outbreak

in Seattle enabled scientists to retrace its origin and spread. Additional analysis of the gut pathogen and its transmission patterns helped direct approaches to testing, treatment, and public health responses.

The genomic reconstruction of the 2017-2022 outbreak and a review of the patient care and [public health interventions](#) used are reported Jan 30 in [The Lancet Infectious Diseases](#).

"The aim of the study," the Seattle researchers noted, "was to better understand the community transmission of *Shigella* and spread of antimicrobial resistance in our population, and to treat these multi-drug resistant infections more effectively."

Shigella outbreaks are more frequent in countries without sufficient public health and sanitation resources. But the researchers called *Shigella* an [opportunistic pathogen](#) that can also emerge in regions of high-income countries when conditions allow.

They explained that sustained *Shigella* outbreaks in [urban areas](#) pose a substantial public health challenge for populations trying to cope with harsh living conditions and lack of hygiene facilities.

The lead authors on the paper are Dr. Giannoula S. Tansarli of the Department of Laboratory Medicine and Pathology, and Dr. Dustin R. Long, of the Division of Critical Care Medicine, Department of Anesthesiology, both at the University of Washington School of Medicine.

The senior and corresponding author is Dr. Ferric C. Fang, professor of laboratory medicine and pathology and of microbiology at the UW [medical school](#). He oversees the clinical microbiology lab at Harborview Medical Center and conducts basic science research on how bacteria cause disease. He was assisted by his UW Medicine colleague Dr.

Stephen J. Salipante, a molecular genetics pathologist and an expert on next-generation DNA sequencing technologies.

Shigellosis is caused by *Shigella* bacteria, which can produce inflammation in the lining of the intestine. Its symptoms include fever, stomach cramps and diarrhea, and, in the worse cases, dysentery and dehydration. Some people with Shigellosis become severely ill and require hospitalization. Shigellosis is highly contagious. The transmission of just a few bacteria is sufficient to cause disease.

From 2017 to 2022, all 178 cases of *Shigella* identified by the clinical labs at Harborview Medical Center and UW Medical Center were characterized by species identification, susceptibility testing, and whole genome sequencing. For the study, the researchers retrospectively examined the demographics and the clinical outcomes of the infected patients.

Of the 178 cases, 78, or 45.6%, were in men who have sex with men, and 88, or 51.5% were in persons experiencing homelessness. About half of the *Shigella* isolates were resistant to multiple antibiotics.

The researchers also had data on 143 patients who received antimicrobial therapy. Despite the high presence of drug resistant *Shigella*, nearly 70 percent of patients were found to have received suitable antimicrobial therapy for their *Shigella* infection. The researchers added that rapid diagnostics and culturing of the bacteria for patients seeking care for severe diarrhea, along with assessment of risk factors and detailed local understanding of the populations affected, led to high rates of appropriate treatment. The approach to care improved over time, as clinicians gained more experience with the disease.

The genomic analysis portion of the study revealed sequential outbreaks of several distinct lineages of two species of *Shigella*, *S. flexneri* and *S.*

sonnei. The various at-risk populations were found to carry *Shigella* of different lineages with different drug-resistance traits. This information helped clinicians develop effective treatment guidelines.

How did this *Shigella* outbreak appear in Seattle? The researchers' genomic findings suggest that it came originally from international travelers from areas where *Shigella* was common. It then spread locally and quickly among at-risk groups.

The researchers explained that multi-drug resistant *Shigella* has become a growing global health concern with many outbreaks worldwide. Most of these have affected men who have sex with men. A variety of gut pathogens can be transmitted between men in this way.

However, in the past few years Shigellosis outbreaks also have occurred among people experiencing homelessness in West Coast cities of the United States and Canada.

Whole-genome sequencing enabled the researchers to determine that new *S. sonnei* and *S. flexneri* strains first appeared in Seattle among men who have sex with men. This was quickly followed by transmission within the local population of people experiencing homelessness. This was evidenced by the significant increase in Shigellosis after 2020 in the Seattle-King County area among this population.

The outbreaks were worse in winter, a seasonal characteristic of *Shigella* which might be due to greater overcrowding in shelters and other locations during cold weather. Dr. Fang noted that Shigellosis cases caused by a different *S. sonnei* strain are now being encountered in Seattle this winter.

The Seattle outbreaks followed patterns characteristic of those reported earlier in other countries.

Several public health measures were instituted to limit the spread of *Shigella*. The first was to check for possible sources for contracting *Shigella*. Signs were placed to discourage people from drinking water from decorative fountains in downtown Seattle. Local homeless service providers received prevention resources and guidance. Outreach teams visited encampments and overnight shelters to offer health education and improve the availability of clean water, toilets, handwashing stations, and other sanitation measures.

Many public facilities, such as restrooms, sinks, and drinking fountains, had been closed as part of the COVID-19 pandemic response. Public health officials requested early re-opening of these facilities near encampments and districts where people lived on the streets. They also increased environmental cleaning of alleyways in downtown Seattle that had been used in lieu of restrooms.

The authors noted that the study of the *Shigella* outbreak in Seattle represented the collaborative efforts of local health-care facilities, clinical and academic laboratories, antimicrobial stewardship, infection control, and public health teams.

More information: Giannoula S Tansarli et al, Genomic reconstruction and directed interventions in a multidrug-resistant Shigellosis outbreak in Seattle, WA, USA: a genomic surveillance study, *The Lancet Infectious Diseases* (2023). [DOI: 10.1016/S1473-3099\(22\)00879-9](https://doi.org/10.1016/S1473-3099(22)00879-9)

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