

Monitoring SARS-CoV-2 using wastewater-based epidemiology

October 22 2021



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Alternative viral detection methods have been critical in the fight against COVID-19, helping to reduce the burden on our healthcare system. In a new study published in *Applied and Environmental Microbiology*,

University of California, Irvine researchers demonstrate the efficiency of wastewater-based epidemiology (WBE) to monitor the presence and genetic diversity of SARS-CoV-2 among other viruses in Southern California.

COVID-19 mitigation strategies require accurate and affordable detection methods to help minimize the spread of SARS-CoV-2. Clinical-based detection methods remain the gold standard; however, WBE, which represents the collective waste of the human population in a given locale, can detect viral pathogens and potentially serve as an early warning detection system during a viral outbreak. Therefore, a better understanding of the ability of WBE to precisely detect and track viral pathogens could provide insights into the system's ability to serve as a valuable tool in the fight against infectious diseases like COVID-19.

Working with researchers at the Southern California Coastal Water Research Project, the UCI team monitored wastewater representing 16 million people in Southern California between August 2020 and January 2021.

"When the pandemic hit, and we heard about wastewater monitoring efforts, we immediately thought of the wastewater collection in our lab that we were using to hunt for phages—viruses that infect bacteria and could be used as alternatives to antibiotics," said Katrine Whiteson, Ph.D., associate professor of molecular biology & biochemistry and co-corresponding author. "I am proud of the team of students mobilized by Jason Rothman in our lab to process and concentrate the wastewater to search for viruses."

In order to assay RNA viruses in several Southern California sewersheds, a research team led by Whiteson and Rothman, Ph.D., a Hewitt Foundation Postdoctoral Fellow, collected and analyzed 94 wastewater influent samples across seven treatment plants over five months. The

wastewater samples were subjected to metatranscriptomic sequencing and droplet digital PCR to characterize RNA viromes and SARS-CoV-2 viral load.

The researchers found that the viral load of specific waste treatment plants correlated with the weekly average of reported COVID-19 cases in that county. Because the team gathered samples longitudinally, they confirmed that the relative abundance of SARS-CoV-2 increased throughout the study in specific plants. Additionally, the researchers optimized their purification technique and detected SARS-CoV-2 single nucleotide variants in certain samples.

"Our study shows the usefulness of wastewater-based epidemiology and its importance in helping monitor COVID-19 across Southern California," said Rothman, the study's first author and co-corresponding author.

During the study, the team determined that the wastewater samples were rich in viral diversity, with most viruses being plant-infecting. Other human viruses of interest remained prevalent throughout the pandemic, including norovirus. The diversity and composition were dependent on the location of the waste treatment plant, which was also the case for human pathogenic viruses like SARS-CoV-2. The team suggests that future studies continue to refine their sample preparation methods and more comprehensive monitoring to help determine how pathogenic viruses change over time.

"Our team was able to use cutting edge sequencing approaches to monitor not just the presence but also the diversity of [wastewater](#) representing 16 million people in Southern California," said Whiteson.

More information: Jason A. Rothman et al, RNA viromics of Southern California wastewater and detection of SARS-CoV-2 single

nucleotide variants., *Applied and Environmental Microbiology* (2021).
[DOI: 10.1128/AEM.01448-21](https://doi.org/10.1128/AEM.01448-21)

Provided by University of California, Irvine

Citation: Monitoring SARS-CoV-2 using wastewater-based epidemiology (2021, October 22)
retrieved 27 June 2024 from <https://medicalxpress.com/news/2021-10-sars-cov-wastewater-based-epidemiology.html>

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