



Wastewater Analysis Offers a New Way to Monitor HIV in Communities

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Human immunodeficiency virus 1 (HIV-1) detection in wastewater offers a novel approach to monitor the virus in communities. Baylor College of Medicine researchers and colleagues at collaborating institutions report in [Nature Communications](#) that their method, called hybrid-capture genetic sequencing, allows them to analyze viral genomes in detail and specifically identify viral signals coming from community wastewater. Analysis of sites with available clinical data showed that wastewater HIV signals strongly coincided with the number of people known to be living with HIV in that community, providing evidence that wastewater HIV signals can track HIV burden.

“HIV-1 is a retrovirus that has infected 90 million people and caused more than 40 million deaths,” said co-corresponding author [Dr. Thomas Giordano](#), section chief of infectious diseases and professor of medicine at Baylor. “Despite advances in diagnostics, preventive measures and treatment, HIV-1 continues to spread – there were 1.3 million new diagnoses globally in 2023. Controlling HIV is challenging because it is difficult to identify people who are undiagnosed or not receiving consistent care; these groups account for 80% of new transmissions.”

Current HIV surveillance methods rely heavily on clinical diagnoses and viral load reporting, which depends on individuals accessing care. As a result, people who do not seek or delay seeking medical attention remain largely invisible to public health systems.

“There is an urgent need for a complementary surveillance strategy capable of detecting undiagnosed or untreated infections,” said co-corresponding author [Dr. Anthony Maresso](#) professor of molecular virology and microbiology at Baylor. “In the current study, we show that wastewater analysis may offer the possibility of finding geographic locations with untreated HIV. This would help identify communities where resources for HIV prevention and treatment need to be present or increased.”

Wastewater analysis was first developed at Baylor for poliovirus surveillance in the mid-20th century. During the COVID-19 pandemic, Baylor and collaborators pioneered the use of wastewater surveillance to track SARS-CoV-2 virus at the population and community levels,

successfully mirroring case rates, predicting hospitalizations and enabling early detection of new viral variants.

Since May 2022, the Texas Wastewater and Environmental Biomonitoring ([TexWEB](#)) group has implemented weekly-to-monthly viral sequencing of wastewater across major Texas cities. This program has now detected more than 400 human and animal viruses in wastewater, enabled monitoring and early detection of viral outbreaks including, avian influenza virus, mpox and measles, and generated a sequencing-based tracking dashboard for public health reporting.

“In the current study, we used this approach to analyze wastewater collected from 40 sites across 15 cities in Texas from mid-2022 through the end of 2024. Instead of using tests that look only for short specific genetic sequences of HIV, we used an advanced sequencing approach that allowed us to detect HIV genetic material and examine which sections of the HIV genome were present,” said first author [Dr. Justin Clark](#) assistant professor of molecular virology and microbiology at Baylor.

Across more than 2,000 wastewater samples, HIV genetic material was detected repeatedly, though at low levels, showing that HIV can indeed be found in wastewater in a consistent and measurable way. “It’s important to remark that it’s highly unlikely that HIV signals in wastewater represent infectious virus,” Giordano said. “Decontamination protocols in labs and wastewater facilities break down any virus that end up in wastewater.”

Unexpected results

“When we looked closely at some of the HIV signals, we detected, the sequences appeared to come from non-circulating lab strains rather than virus circulating in the community, which suggested contamination,” Clark said. “But the interesting thing is that we do not work with HIV in our lab. That meant that any ‘contamination’ had to have happened before we received the wastewater samples.”

The team then looked at where these sequences were coming from and found them concentrated near medical and research centers.

“We saw this as a clue,” Clark said. “Certain HIV sequences belonging to HIV variants that circulated in the 1980s have been developed into research tools called lentiviral vectors. These are not live virus but sections of its genetic material that are used in many types of research. Our detailed analysis of wastewater HIV sequences suggests that lentiviral contamination from research activity was confounding the data. To filter out this confounding factor, we developed an approach that classifies HIV sequences as circulating (community-derived) or non-circulating (vector-derived.) Earlier research had not looked for or filtered out these other signals.”

Once the researchers eliminated the confounding factor, they uncovered a significant association between HIV signals in wastewater and diagnosed HIV in communities.

“Our study also addresses the need to maintain site anonymity, which is important for HIV

surveillance given ongoing stigma and criminalization,” Giordano said. “We have another component of this study – reaching out to focus groups, communities, individuals and advocates to make sure we take into consideration people’s points of view.”

“This study establishes a foundation for sequencing-based HIV wastewater surveillance and highlights lentiviral vector contamination as an overlooked confounding factor that must be addressed in future monitoring efforts for HIV-1 and other disease-causing microbes with synthetic counterparts,” Maresso said.

The following authors also contributed to this work: Dylan Chirman, Harihara Prakash, Austen Terwilliger, Matt Ross, Mike Tisza, Sara J. Javornik Cregeen, Jason T. Kimata and Faith E. Fletcher, all at Baylor College of Medicine. Marlene McNeese and Loren Hopkins are at Houston Health Department. Jennifer Deegan, Catherine L. Troisi, Eric Boerwinkle, Kristina Mena and Fuqing Wu are affiliated with the University of Texas Health Science Center at Houston, and Marc Johnson and Devon Gregory are with the University of Missouri School of Medicine.

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