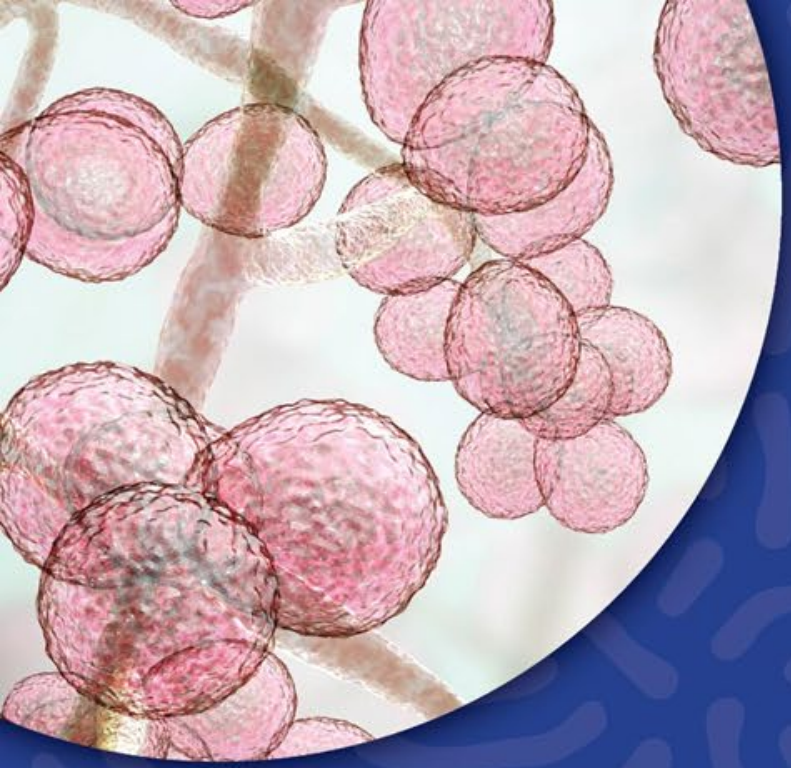

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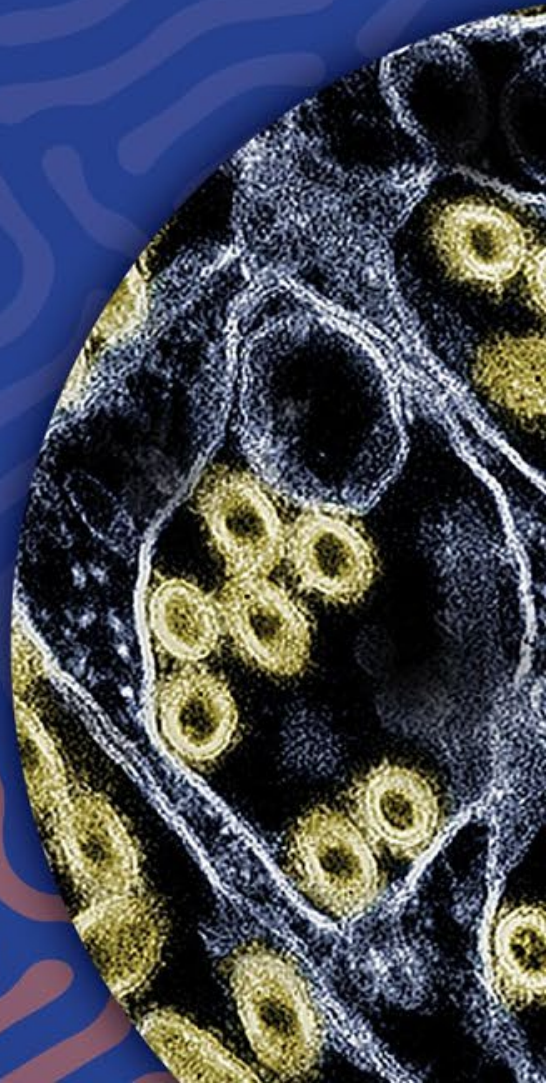

The State of the Science: Wastewater Surveillance

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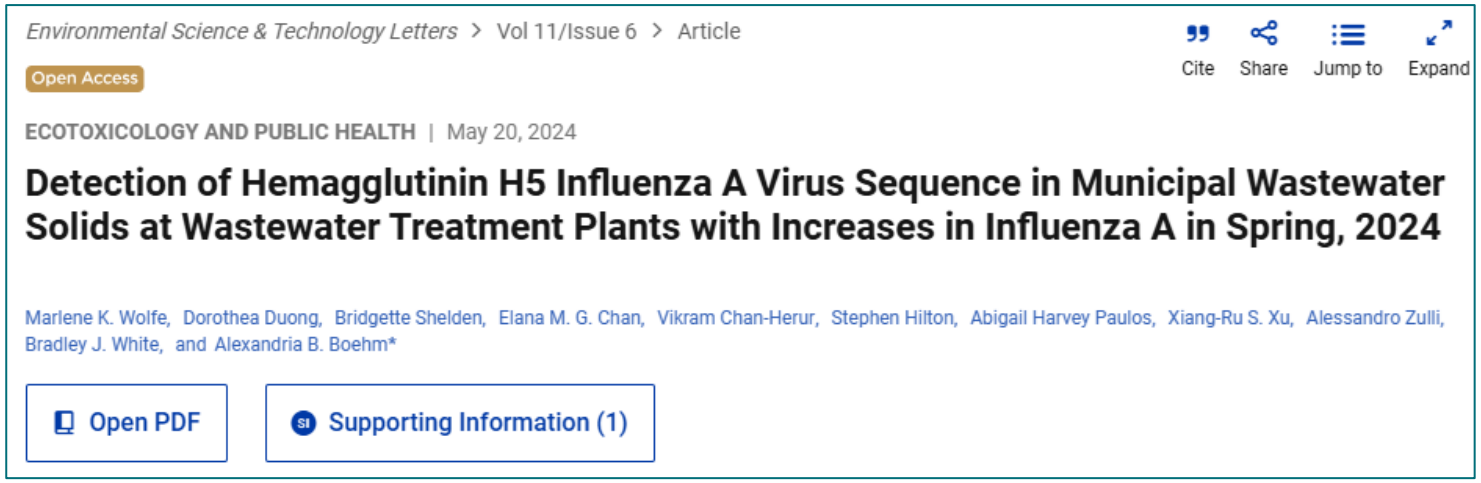
Shannon Matzinger, PhD
Genomic Surveillance Program Manager
Colorado Department of Public Health and Environment

H5N1 in Wastewater



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ECOTOXICOLOGY AND PUBLIC HEALTH | May 20, 2024

Detection of Hemagglutinin H5 Influenza A Virus Sequence in Municipal Wastewater Solids at Wastewater Treatment Plants with Increases in Influenza A in Spring, 2024

Marlene K. Wolfe, Dorothea Duong, Bridgette Shelden, Elana M. G. Chan, Vikram Chan-Herur, Stephen Hilton, Abigail Harvey Paulos, Xiang-Ru S. Xu, Alessandro Zulli, Bradley J. White, and Alexandria B. Boehm*

Open PDF Supporting Information (1)

Morbidity and Mortality Weekly Report

Avian Influenza A(H5) Subtype in Wastewater — Oregon, September 15, 2021–July 11, 2024

Rebecca Falender, DVM[1]; Tyler S. Radniecki, PhD[1]; Christine Kelly, PhD[1]; Paul Cieslak, MD[2]; David Mickle[1]; Harrison Hall[3]; Ryan Scholz, DVM[3]; Melissa Sutton, MD[2]

H5N1 in Wastewater

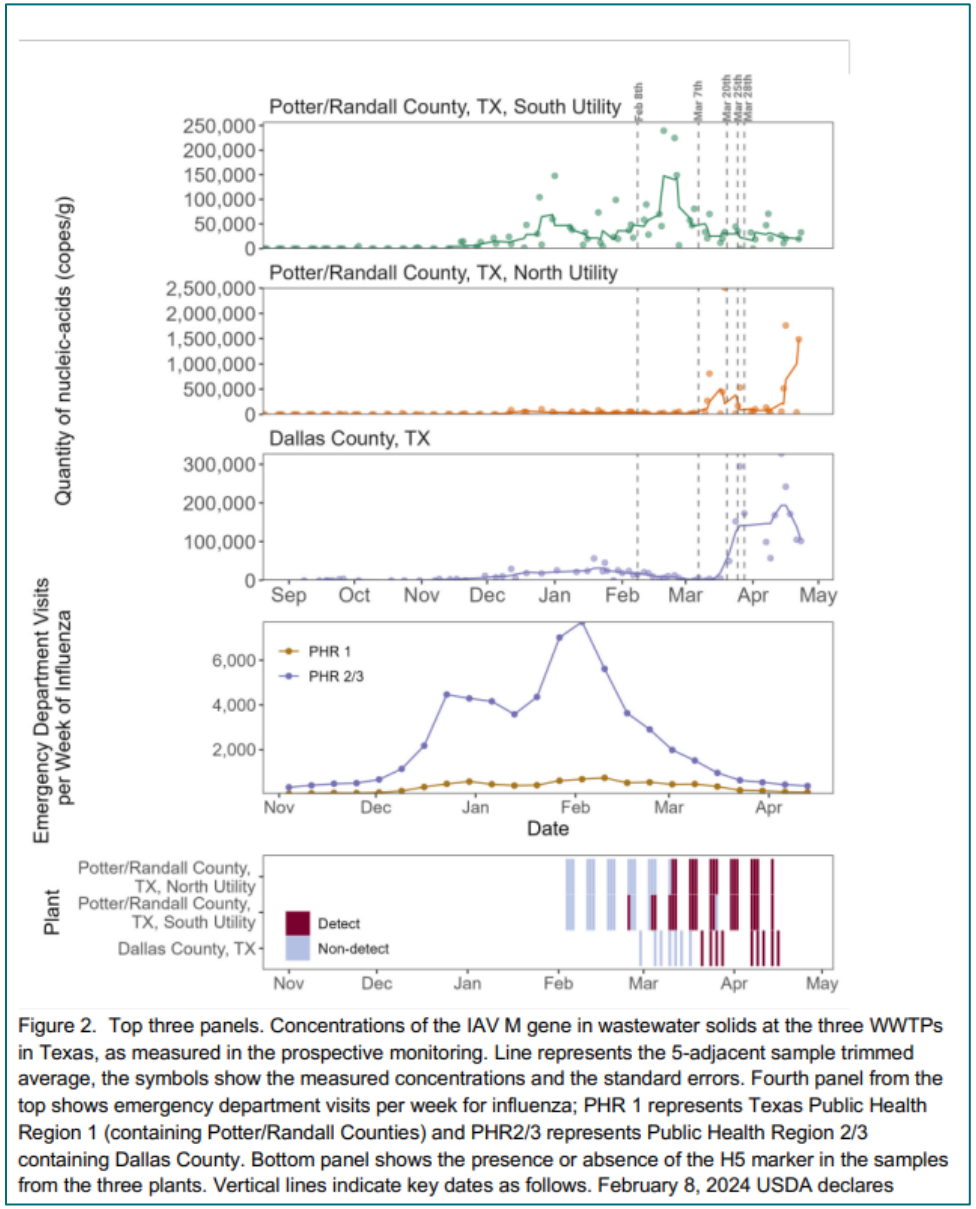
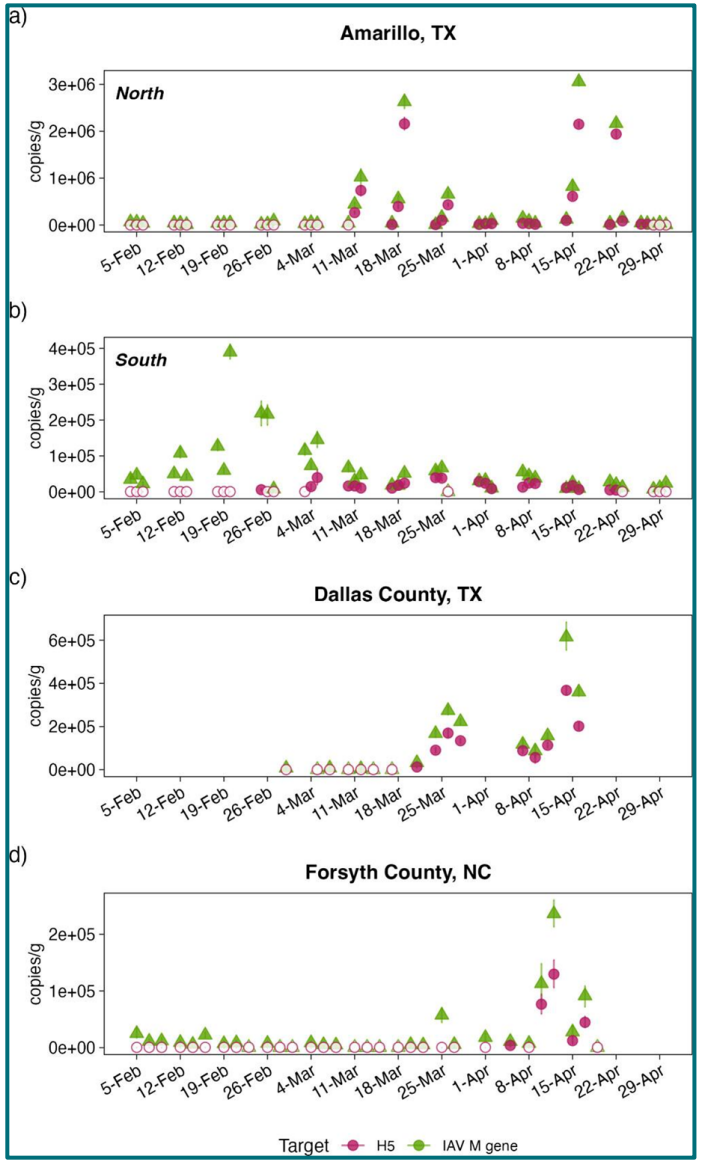


Figure 2. Top three panels. Concentrations of the IAV M gene in wastewater solids at the three WWTPs in Texas, as measured in the prospective monitoring. Line represents the 5-adjacent sample trimmed average, the symbols show the measured concentrations and the standard errors. Fourth panel from the top shows emergency department visits per week for influenza; PHR 1 represents Texas Public Health Region 1 (containing Potter/Randall Counties) and PHR2/3 represents Public Health Region 2/3 containing Dallas County. Bottom panel shows the presence or absence of the H5 marker in the samples from the three plants. Vertical lines indicate key dates as follows. February 8, 2024 USDA declares



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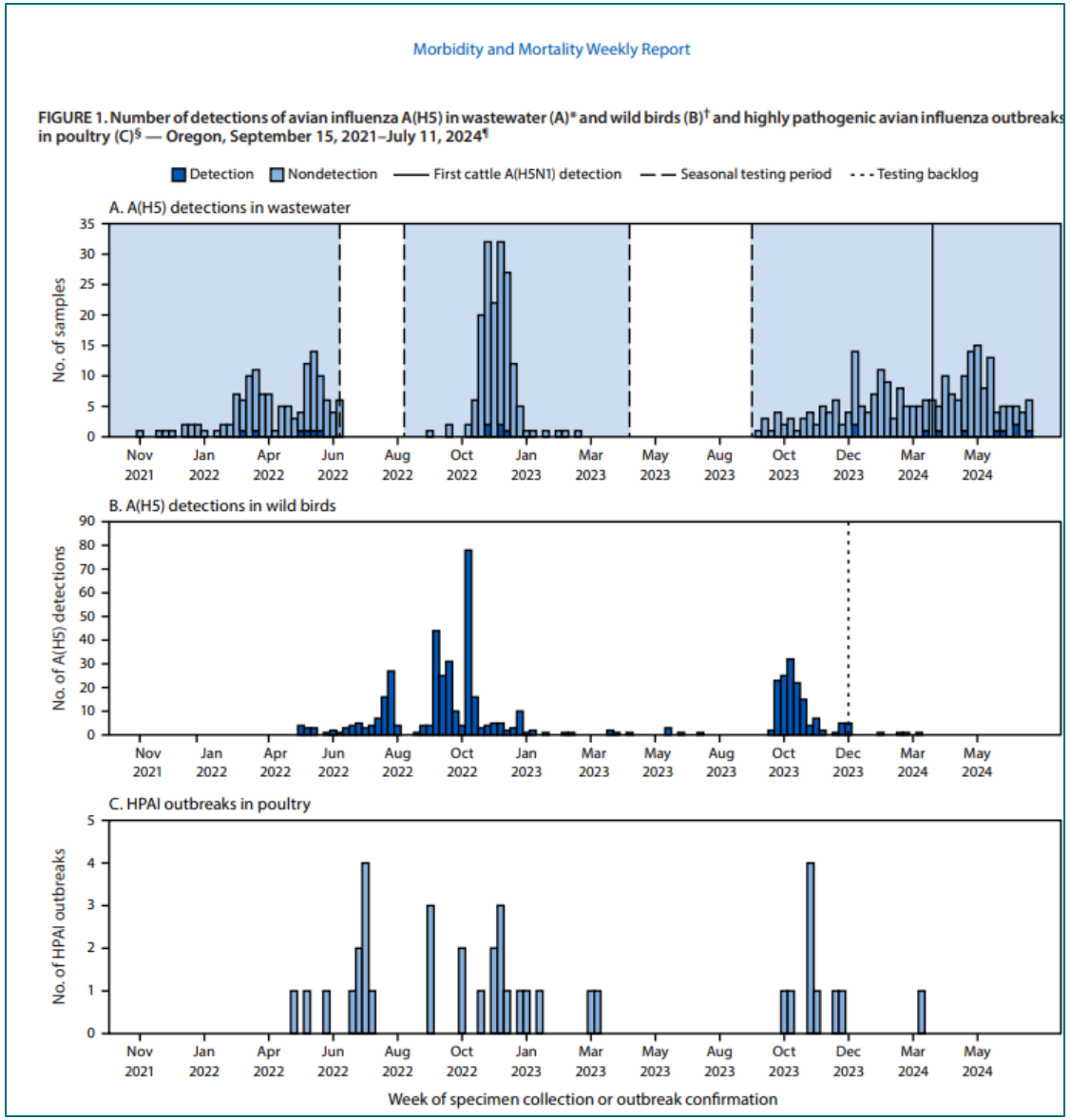
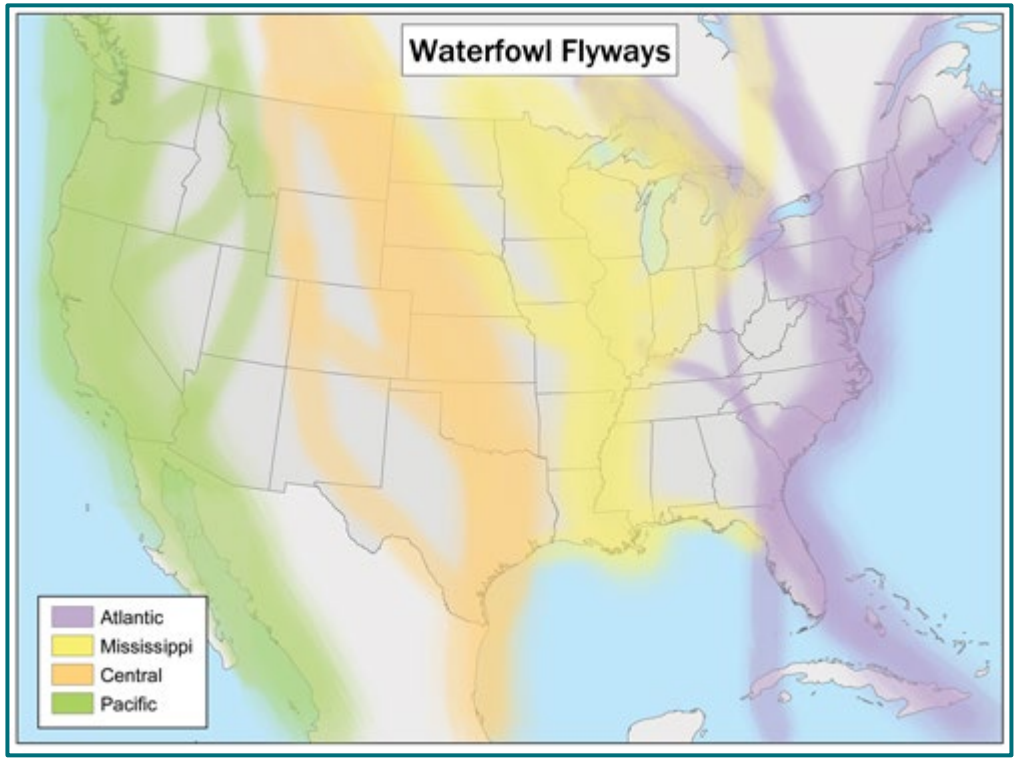
H5N1 in Wastewater





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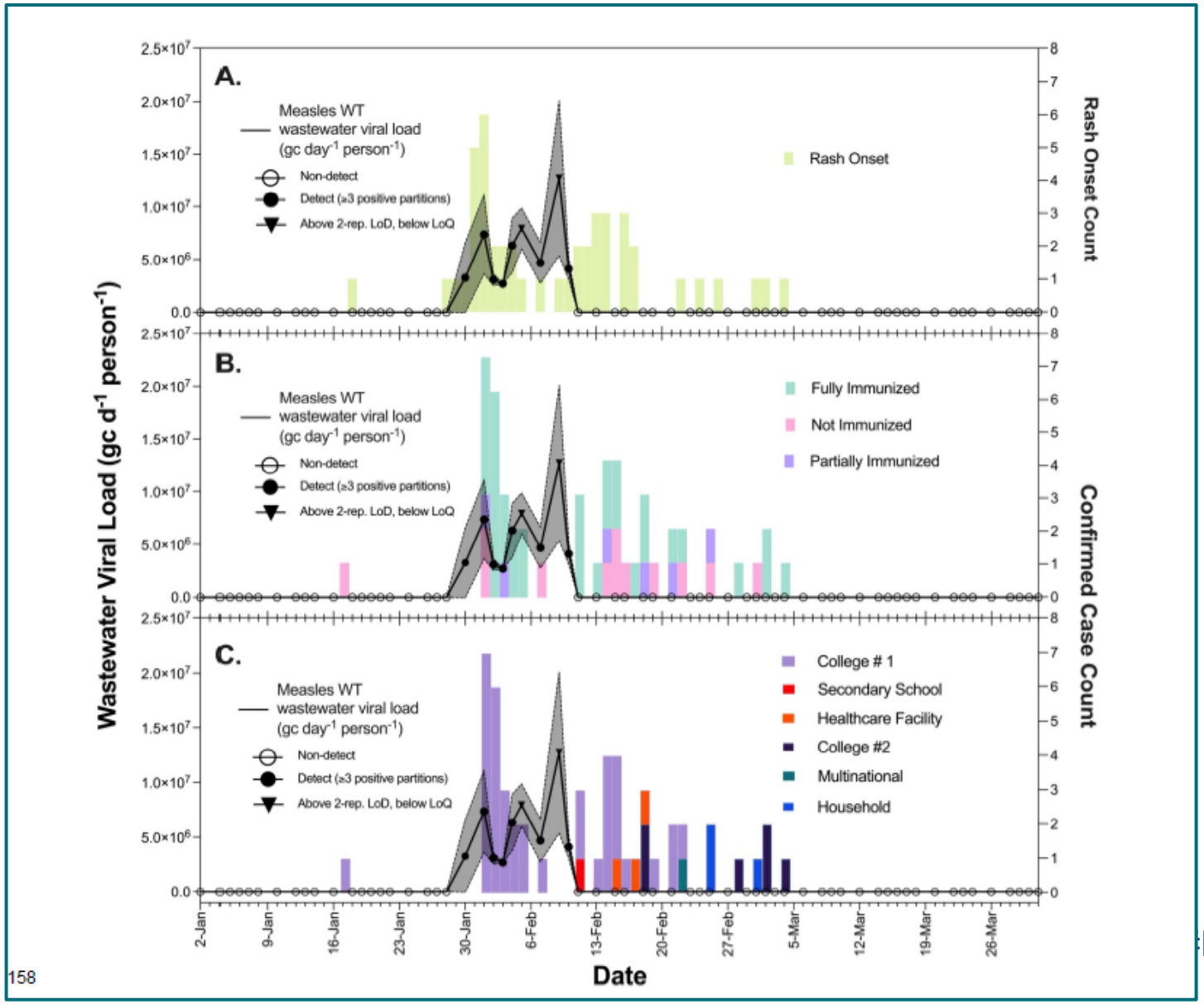
Measles in Wastewater

Retrospective Wastewater Based Tracking of Measles Outbreak in Canton of Vaud, Switzerland: January – March 2024

Charles Gan, Melissa Pitton, Jolinda de Korne-Elenbaas, Ludovico Cobuccio, Alessandro Cassini, Christoph Ort, Timothy R. Julian

doi: https://doi.org/10.1101/2025.03.11.25322836

Measles in Wastewater



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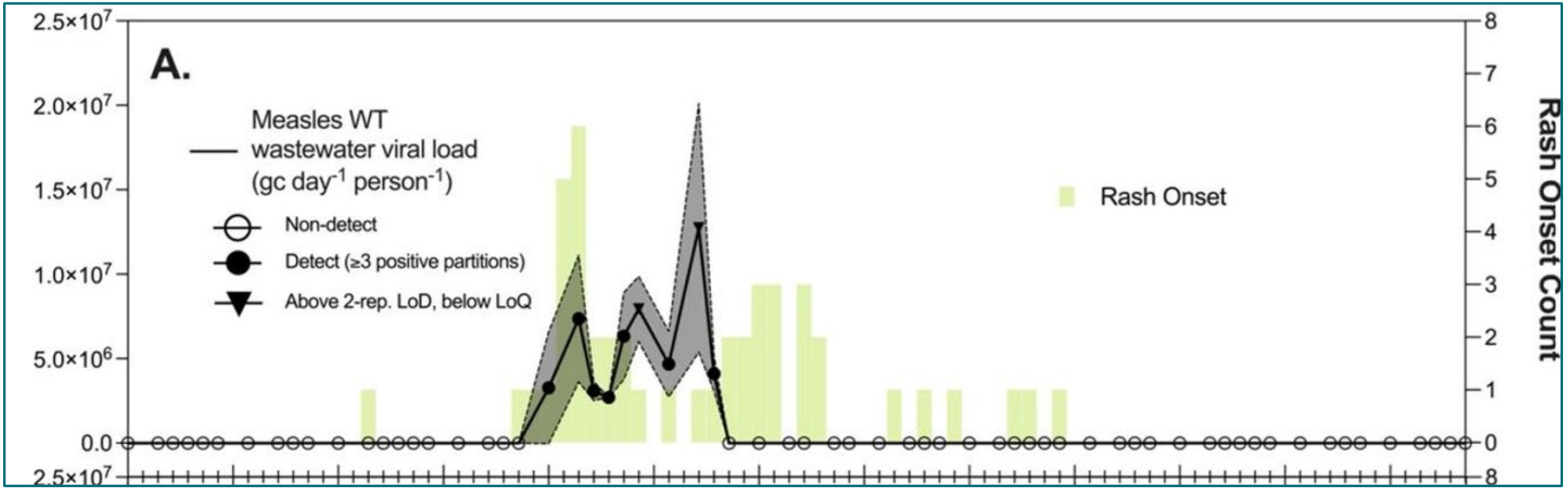
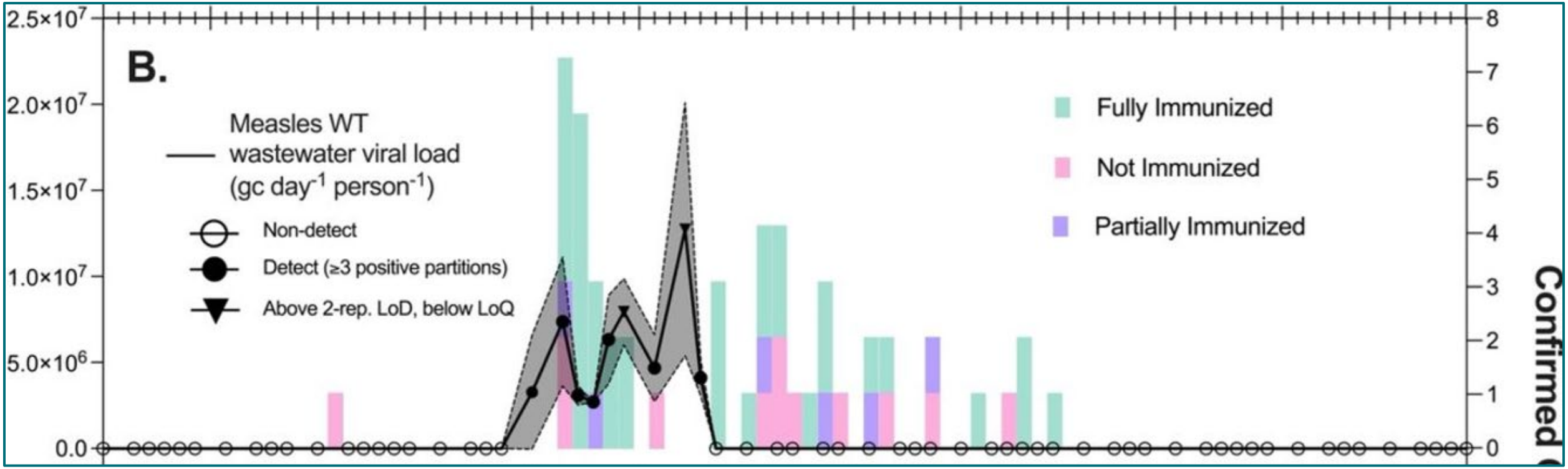
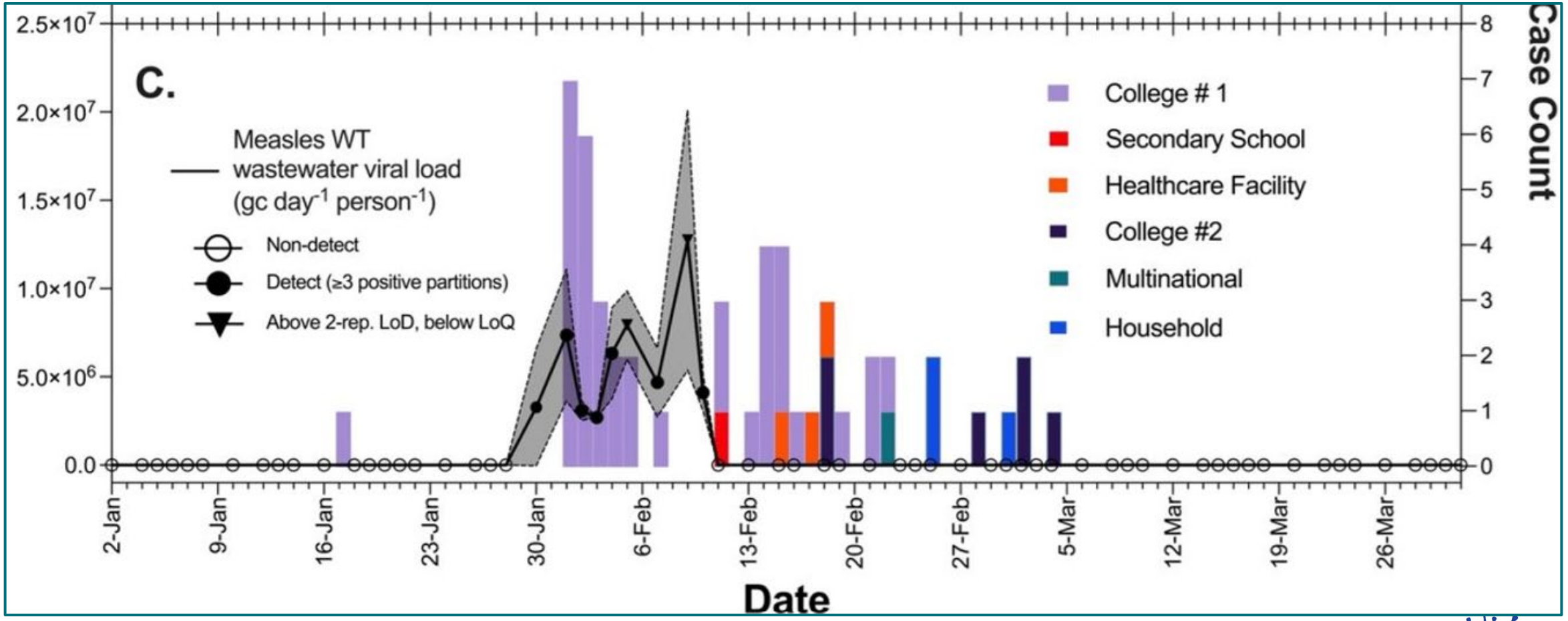
Measles in Wastewater



Measles in Wastewater



Measles in Wastewater



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Sequencing Approaches

AMERICAN SOCIETY FOR MICROBIOLOGY | mBio

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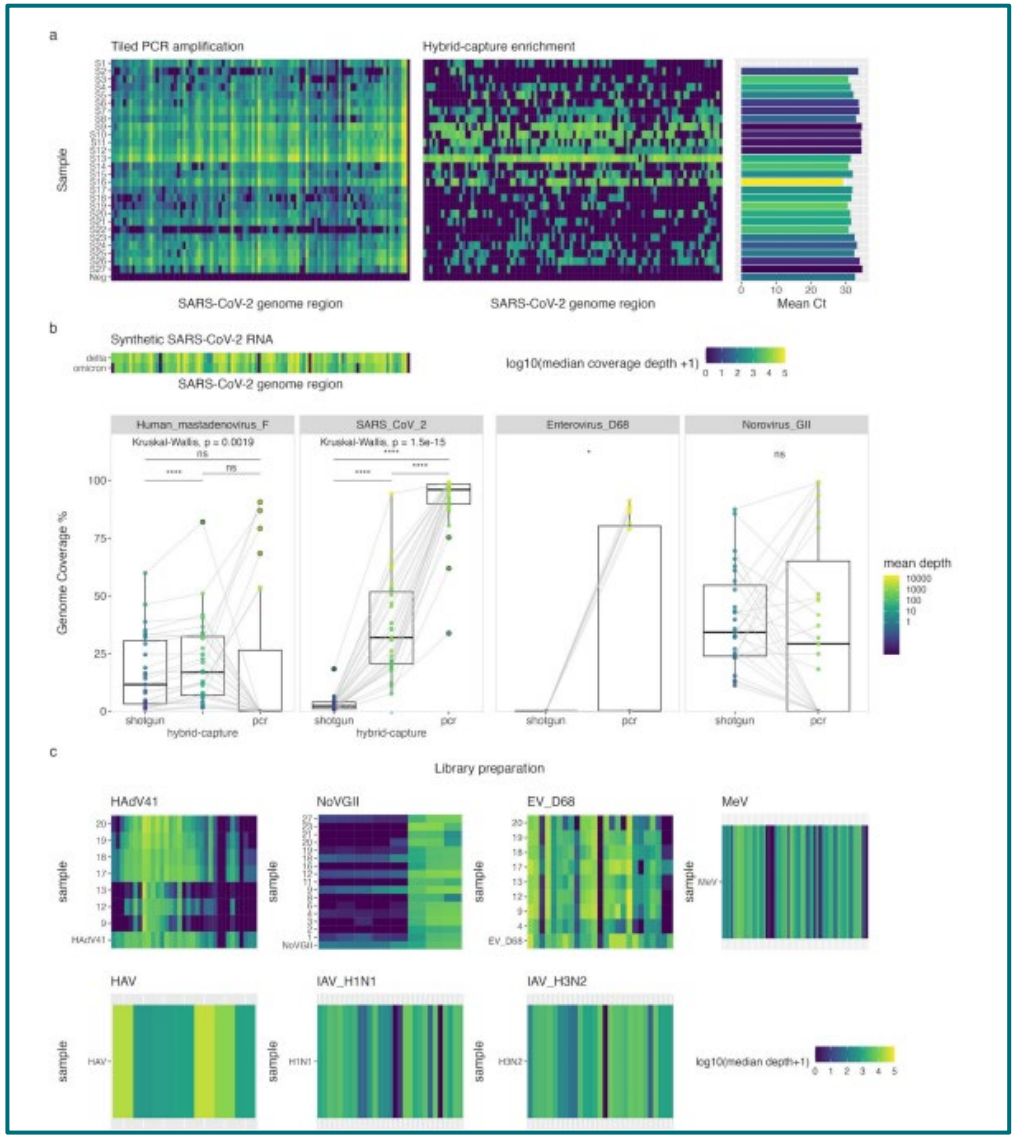
| Environmental Microbiology | Research Article

Comparison of metagenomic and targeted methods for sequencing human pathogenic viruses from wastewater

Harry T. Child,[1] George Airey,[2] Daniel M. Maloney,[3] Abby Parker,[4] Jonathan Wild,[4] Suzie McGinley,[4] Nicholas Evens,[5] Jonathan Porter,[5] Kate Templeton,[4] Steve Paterson,[2] Ronny van Aerle,[6,7] Matthew J. Wade,[7] Aaron R. Jeffries,[1] Irene Bassano[8]

Sequencing Approaches



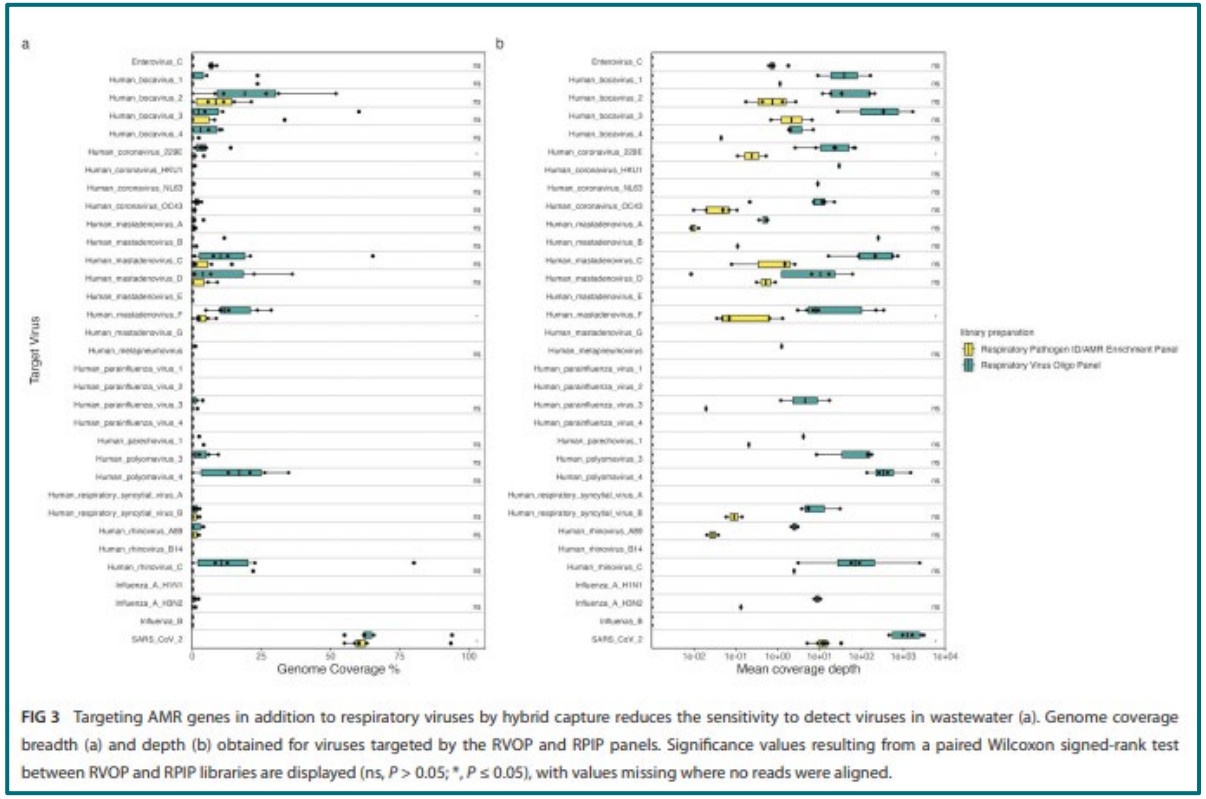


FIG 3 Targeting AMR genes in addition to respiratory viruses by hybrid capture reduces the sensitivity to detect viruses in wastewater (a). Genome coverage breadth (a) and depth (b) obtained for viruses targeted by the RVOP and RPIP panels. Significance values resulting from a paired Wilcoxon signed-rank test between RVOP and RPIP libraries are displayed (ns, $P > 0.05$; *, $P \leq 0.05$), with values missing where no reads were aligned.

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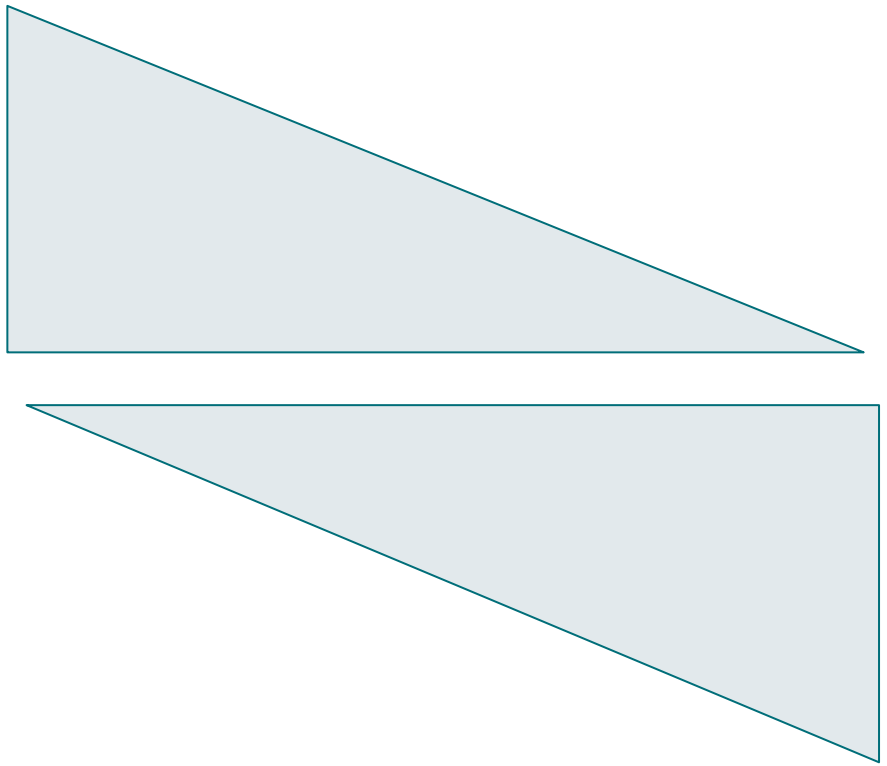
Sequencing Approaches

AGNOSTIC

HYBRID CAPTURE

TARGETED

SEQUENCE ALL THE THINGS



SEQUENCE ALL THE VERSIONS

Takeaways

- Wastewater can provide non-invasive community level insight and strengthen clinical and syndromic data
- The use will be pathogen dependant necessitating longitudinal studies to compare with other datastreams
- Wastewater can add value especially in areas of low clinical surveillance or pathogens with low clinical surveillance already established.
- Prioritize ways to make this system more sustainable in combination with clinical data

Thank You!

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email: shannon.matzinger@state.co.us