Testimony before the Committee on Environmental Protection (jointly with the Subcommittee on COVID Recovery and Resiliency) meeting on Friday, March 11, 2022.

Dear Chair Gennaro and Committee members,

I am John Dennehy, a Professor of Biology at Queens College and The Graduate Center of The City University of New York. I operate a virology laboratory at Queens College that is working with the NYC Department of Environmental Protection and the Department of Health and Mental Hygeine to monitor SARS-CoV-2 in NYC wastewater.

Since SARS-CoV-2 is shed in feces, SARS-CoV-2 genetic material can be extracted from community wastewater and assayed to provide estimates of SARS-CoV-2 community prevalence. This approach is especially powerful since it randomly samples all community members and can detect viruses shed by individuals not seeking medical attention, such as asymptomatic individuals or those who choose to test at home. Additionally, SARS-CoV-2 genetic material isolated from wastewater can be sequenced using high-throughput sequencing technologies to identify currently circulating variants. Given the continuing evolution of SARS-CoV-2 and the appearance of variants of concern such as Omicron, sequencing efforts documenting not only current dominant variants, but also minority variants circulating at low levels in sewersheds, are imperative. The fact that Omicron's origin and early spread was not observed strongly motivates efforts to detect and monitor novel variants.

My laboratory has been monitoring circulating SARS-CoV-2 variants in all 14 NYC sewersheds since January 2021. Variant frequencies in these sewersheds closely tracked variant frequencies estimated from clinical sampling in the same areas. However, in some sewersheds, we noted the presence of cryptic SARS-CoV-2 variants not observed in clinical samples from anywhere in the world[1,2]. Concerningly, these variants show considerable overlap with the Omicron variant of concern, suggesting convergent evolution due to similar selective pressures. We have not been able to identify the sources of these variants, but we speculate that they have arisen from either long-term infections of immunocompromised patients or from an animal reservoir. Given that both the Alpha and Omicron variants of concern are hypothesised to have arisen during long-term infections, it is crucial to identify the sources of these cryptic SARS-CoV-2 variants to prevent the emergence of new variants of concern.

Thank you for the opportunity to comment today. I am available to answer any questions.

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[1] Smyth DS, Trujillo M, Gregory DA, Cheung K, Gao A, Graham M, Guan Y, Hoxie I, Kannoly S, Kubota N, Lyddon TD, Markman M, Rushford C, San K, Sompanya G, Spagnolo F, Suarez R, Daniels M, Johnson MC & Dennehy JJ. 2022. Tracking cryptic SARS-CoV-2 lineages detected in NYC wastewater. *Nature Communications*: 13, 635. https://doi.org/10.1038/s41467-022-28246-3.

[2] In New York City Sewage, a Mysterious Coronavirus Signal, Emily Anthes, *New York Times*, 2022/02/03.