MOLINE NORTH STP
Wastewater Report, September 2023

For updates on your plant in-between these monthly reports, please visit our wastewater dashboard https://iwss.uillinois.edu

LOCATION: MOLINE NORTH STP (Rock Island County)

Catchment Information	
Population Served	25,202
NPDES	IL0029947
zipcode	61265
IL Covid Region	2

SARS-CoV-2 LEVELS IN WASTEWATER

Wastewater is analyzed using digital PCR (dPCR) to determine the concentration of the SARS-CoV-2 virus in a sample. The nucleocapsid protein (N) gene of the virus is targeted in the assay, and results are reported in gene copies per liter of starting wastewater.

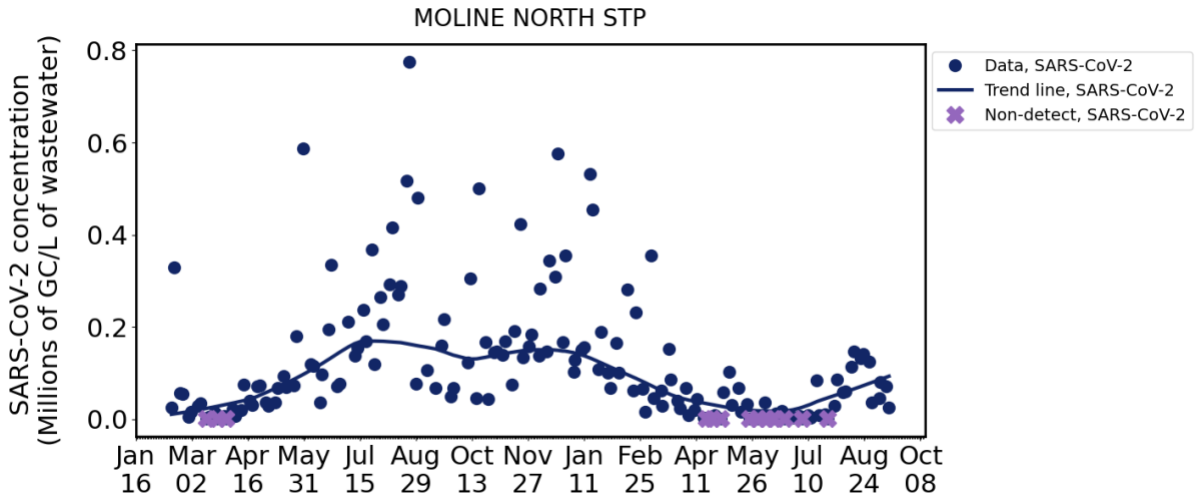

Figure 1. Time series plot of SARS-CoV-2 viral concentrations in millions of gene copies per liter (GC/L) of wastewater.

SARS-CoV-2 SAMPLING RESULTS - LAST 8 SAMPLES

Date	SARS-CoV-2 (GC/L)
2023-09-13	24,825
2023-09-11	70,950
2023-09-06	79,725
2023-09-05	45,450
2023-08-30	36,600

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2023-08-28	124,050
2023-08-23	141,750
2023-08-21	132,300

SARS-CoV-2 LINEAGES IN WASTEWATER

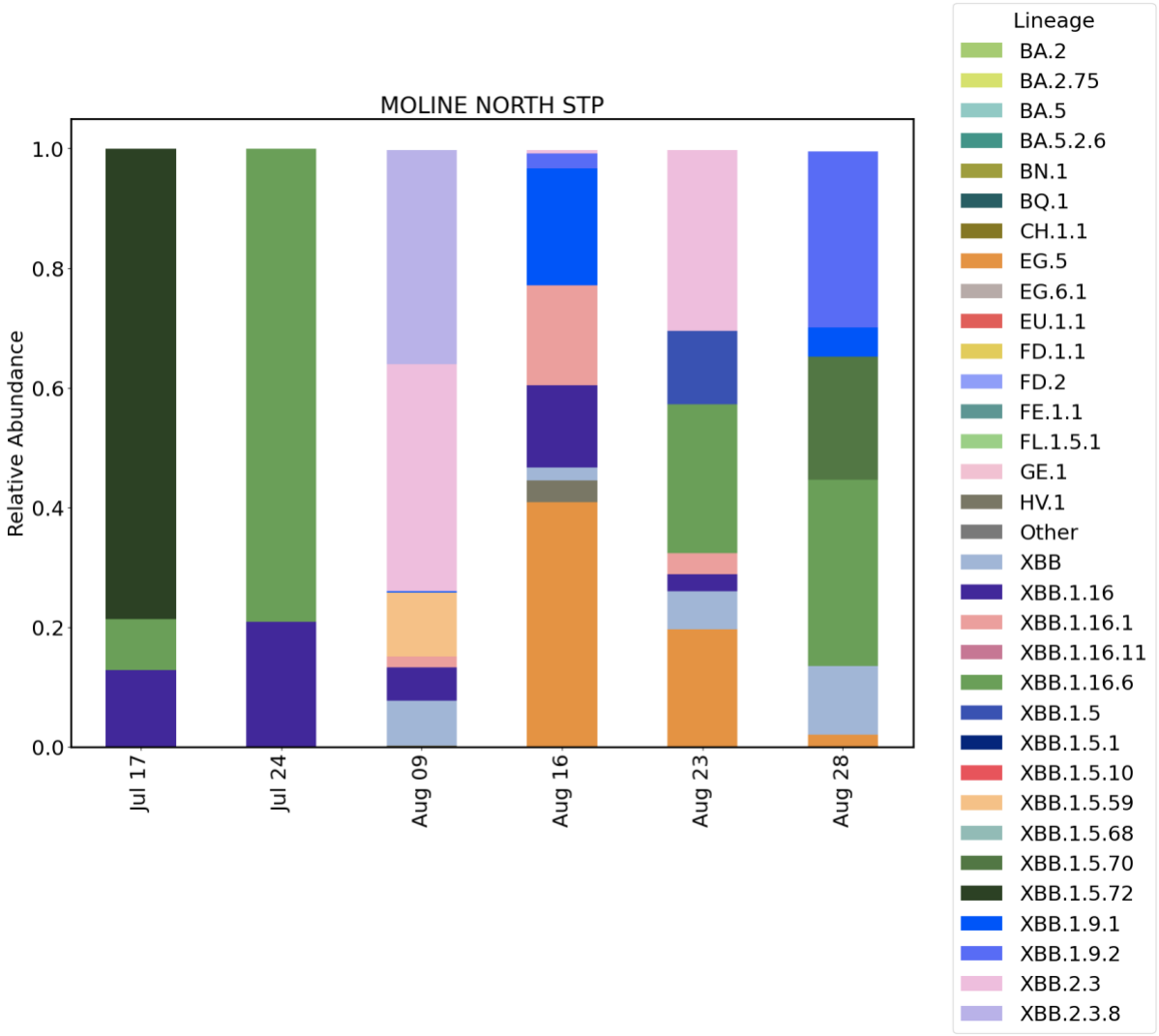

Figure 2. Stacked barplot showing the relative abundances of SARS-CoV-2 lineages in wastewater samples. All lineages in the legend, excluding "Other," are associated with Omicron. The most recently available two months worth of data are shown.

INFLUENZA A/B LEVELS IN WASTEWATER

Wastewater is analyzed using digital PCR (dPCR) to determine the concentration of influenza A and influenza B viruses in a sample. Results are reported in gene copies per liter of starting wastewater.

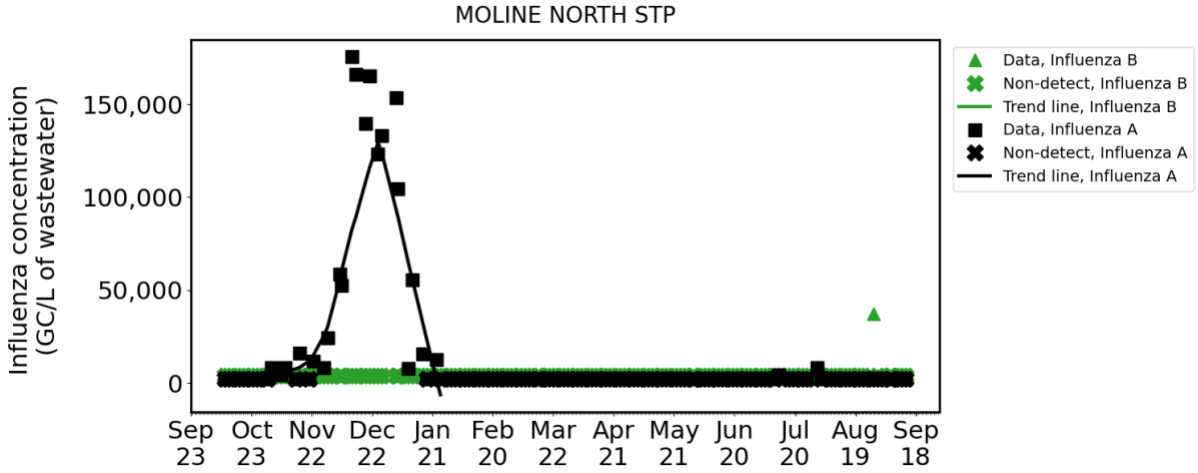

Figure 3. Time series plot of Influenza A/B viral concentrations in gene copies per liter (GC/L) of wastewater.

INFLUENZA A/B SAMPLING RESULTS - LAST 8 SAMPLES

Date	Influenza A (GC/L)	Influenza B (GC/L)
2023-09-13	Non-detect	Non-detect
2023-09-11	Non-detect	Non-detect
2023-09-06	Non-detect	Non-detect
2023-09-05	Non-detect	Non-detect
2023-08-30	Non-detect	Non-detect
2023-08-28	Non-detect	37,200
2023-08-23	Non-detect	Non-detect
2023-08-21	Non-detect	Non-detect

RSV LEVELS IN WASTEWATER

Wastewater is analyzed using digital PCR (dPCR) to determine the concentration of Respiratory Syncytial Virus (RSV) in a sample. Results are reported in gene copies per liter of starting wastewater.

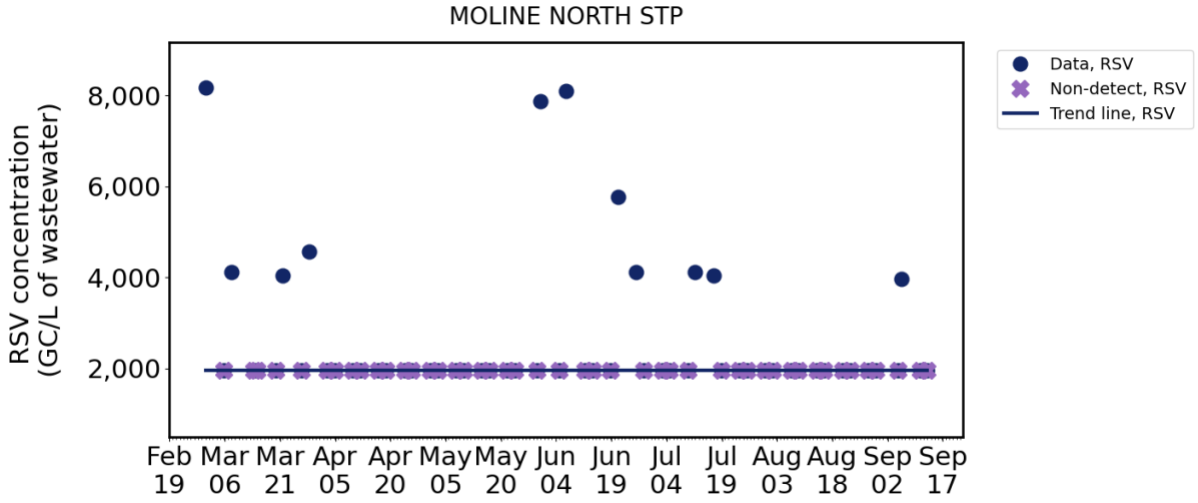

Figure 4. Time series plot of RSV viral concentrations in gene copies per liter (GC/L) of wastewater.

RSV SAMPLING RESULTS - LAST 8 SAMPLES

Date	RSV (GC/L)
2023-09-13	Non-detect
2023-09-11	Non-detect
2023-09-06	3,975
2023-09-05	Non-detect
2023-08-30	Non-detect
2023-08-28	Non-detect
2023-08-23	Non-detect
2023-08-21	Non-detect

Guide to Interpreting Data on SARS-CoV-2, Influenza, & Respiratory Syncytial Virus (RSV) Gene Copies in Wastewater Samples

What do the results mean?

There are several factors to consider when interpreting viral data in wastewater. The rate, magnitude, and duration of shedding may vary from one person to another and from virus to virus, thus how or even whether it is possible to translate viral levels in wastewater into precise community health metrics is an open scientific question. It is only appropriate to monitor and observe the trends of viral gene copies detected in a community over time. The data presented in tables, graphs, and trend assessments show the concentration of RNA copies in the wastewater area from the community where the wastewater was collected. A significant increase in viral gene copies over time is an indicator that cases may be increasing in the community. Wastewater data should not be interpreted in isolation but rather considered alongside other public health metrics.

What does the number that is reported on a sample day mean?

It is a measure of how many gene copies are present in a sample, typically reported as gene copies per liter of wastewater (GC/L). Samples are typically obtained from municipal wastewater treatment plants and reflect inputs of viral material shed by the community served by the treatment plant. This number does not indicate gene copies per person or population.

How are the gene copies measured in the wastewater?

Wastewater samples are first processed to concentrate and isolate genetic material (RNA) that is present in the sample. RNA sequences specific to SARS-CoV-2, influenza A & B, and RSV are then detected and quantified using a molecular biology tool called digital polymerase chain reaction (dPCR). During dPCR, a targeted segment of the RNA is converted to DNA and then amplified (copied many times) so it can be detected by laboratory instruments. Specific methods for sample processing and PCR-based quantification differ among wastewater monitoring projects and analytical laboratories.

What does it mean if a data point for a sample is 0 or a non-detect?

A non-detect means that the amount of SARS-CoV-2, influenza, or RSV RNA in the wastewater sample is below the level that can be reliably detected by the quantification methods used in a given laboratory. A determination of non-detect does not necessarily mean that no viral RNA is present in the sample or in the system – rather that the levels are low enough that they cannot be reliably determined. In some cases, other components of wastewater may interfere with individual measurements, leading to an incorrect non-detection similar to false negatives that can occur from at-home and clinical testing. A non-detect does not necessarily mean that there are no infected individuals within the associated community.

What is the viral gene copy trend line?

The trend line is calculated using Locally Weighted Scatterplot Smoothing (LOWESS), a local regression analysis. It allows us to see the change in trend over time by fitting a curve to the data. This method is useful because it reduces the influence of outliers, and wastewater data can be highly variable. LOWESS is a more complex extension of the moving average.

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Does the number of gene copies in a sample tell us how many people are sick?

There are not presently agreed-upon methods for translating concentration of SARS-CoV-2, influenza, or RSV genetic material in wastewater into a measure of how many people, or even what percentage of a community, have COVID-19, flu, or RSV, respectively. Variability between different wastewater sources, treatment facilities, and communities makes it difficult to translate the SARS-CoV-2, influenza, or RSV concentrations into a measure of how many people are infected in the community. However, an upward or downward trend in viral gene copies per liter of wasterwater generally suggests a similar trend in the number of people infected within a given community.

Can I compare the number of gene copies in a sample from site to site?

Because each community has a different mix of wastewater inputs, different populations, and different wastewater systems, it is not appropriate to compare viral gene copy numbers among communities. Instead, trends in SARS-CoV-2, influenza, or RSV concenentrations from a specific community over time can be used to help understand whether cases or hospitalizations are likely to increase or decrease in the community. Sample collection methods and mechanisms, collection times, and sample variability are other factors that discourage cross-site comparison.

Can I compare the gene copies of different pathogens to one another?

Because each pathogen is distinct, it is not appropriate to compare their viral gene copy numbers, even at the same site. Instead, trends in SARS-CoV-2, influenza, or RSV concentrations (increasing/decreasing) can be used to understand if cases or hospitalizations for each pathogen are likely to increase or decrease in the community.

Guide to Interpreting Data on SARS-CoV-2 Lineages in Wastewater Samples

What are lineages and how are they determined?

Wastewater is sequenced to determine the variants of SARS-CoV-2 virus present in a sample, a proxy for circulating variants in the community. Our sequencing strategy utilizes the entire genome of SARS-CoV-2 to identify mutations that are diagnostic of variants of the virus. Full genome coverage gives us better resolution for distinguishing variants, especially those very similar to each other. Variant names and lineage relationships are determined by the World Health Organization (WHO).

Variant: A genome that contains a particular set of mutations.

Mutation: A change in the genetic information introduced during viral replication.

Lineage: A collection of variants all related to each other based on analysis of the virus genomic sequence.

What is the sequencing plot showing me?

This plot is displaying the relative abundance, or proportion, of lineages found in a wastewater sample collected on a particular date. This plot was generated after comparing sample sequences to a SARS-CoV-2 reference genome and identifying characteristic mutations that are

associated with different variants. We then calculate the percentage of each variant present in the sample. This plot summarize the variant detections; lineages are displayed, as there are often many variants detected that are in the same lineage.

What do the results mean?

The SARS-CoV-2 variants identified in a particular plant's wastewater can provide insight into the variants circulating in the population that the plant serves. This information can be useful, as there tend to be fewer clinical sequences, and those might only reflect a small proportion of the community feeling sick enough to pursue testing. The wastewater samples passively capture the virus shed in wastewater from the community where the wastewater was collected, not just those who are symptomatic. Wastewater data is not interpreted in isolation but rather considered alongside other public health metrics.

Does the number or type of lineages tell us how many people are sick?

We cannot tell how many people are sick from the lineages observed in the wastewater. We can only see relative proportions of the variants that are present in the community served by the wastewater treatment plant. We do pay attention to specific mutations that have been identified as having clinical implications (e.g., for effectiveness of medications or disease severity).

Can I compare the lineages in a sample from site to site?

Yes. We often detect variants in a particular plant first, and then see the relative abundance change over time, with certain lineages becoming more prevalent across the state from plant to plant. We compare these detections to sequence data from across the United States and the world.

Why are the dates of the sequencing data not as current as the gene copies data?

Sequencing results are available about two weeks after sample collection. This is because the quantification of SARS-CoV-2 levels by dPCR happens first, and then genetic material (RNA) is sent for sequencing. Additionally, samples then take multiple days to run on the sequencer and computational processing of sequences takes additional time before results are available.

Why do the lineages in the legend change periodically?

The lineages shown in the sequencing plot of this report are in alignment with the CDC's national genomic surveillance system. As the SARS-CoV-2 virus mutates, new variants emerge. This means there are regularly new variants that contribute to the spread of COVID-19. Some variants will disappear while others will continue to spread and even replace others as the dominant variant. These monthly reports reflect those changes as we continue to monitor for emerging variants of concern.