Development of a rapid, uniform, state-wide surveillance program for COVID variants in New York State wastewater

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Results

Chemistry on Absolute quantification was performed with the Qiagen Digital PCR system for compared to other methods (ARTIC/Illumina, ClearLabs Dx, and AmpliSeq/QIAcuity) with results available within 25 hours of initiation of testing.

A sampling network of more than 200 sewer sheds was established in NYS during 2021-23 for the detection of SARS-CoV-2 in wastewater (see Figure 1).

The NYS sequencing consortium, established in 2021 for SARS-CoV-2 sequencing of positive clinical samples, was expanded for sequencing of positive wastewater samples in 2022. Comparison of the sequencing data across the five consortium sites was tested with a proficiency testing panel and demonstrated a high consistency in the detection and percentage composition of lineages detected (Figure 2).

After the initiation of SARS-CoV-2 sequencing from wastewater across the state, data processing and visualizations demonstrated the interesting variation in lineage distribution across the counties, regions and state over time (figures 3, 4 and 5) and the ability to visualize individual lineages by county and sewer shed source (figure 6).

A network was established for the rapid monitoring of SARS-CoV-2 lineages in NYS wastewater.

A proficiency testing panel clearly demonstrated a high degree of consistency in the detection and percentage lineage composition from the five participating sequencing laboratories.

Conclusions

Methods

- To assure rapid, sensitive, and uniform results in this new WW program across the state, Thermofisher GeneXus instruments were installed at all five sites.
- Data from previous testing demonstrated greater sequence depth and coverage from samples at lower viral loads, with AmpliSeq chemistry on GeneXus compared to other methods (ARTIC/Illumina, ClearLabs Dx, and AmpliSeq/QIAcuity) with results available within 25 hours of initiation of testing.
- An evaluation panel comprising 16 samples was prepared at the Wadsworth Center and distributed to the five sites, containing total nucleic acid from multiple SARS-CoV-2 isolates, representing multiple circulating variants.
- Each sample contained varying percentages (from 5-75%) of up to six different lineages.
- Purity of the isolates was verified by Whole Genome Sequencing (WGS) on GeneXus followed by Freyja analysis
- Absolute quantification was performed with the Qiaagen QiaCayct Digital PCR system for each isolate and by real-time RT-PCR using the New York State SARS-CoV-2 assay.
- Sequencing data from the laboratories was uploaded to a centralized cloud and assessed for performance and consistency.
- Participating sequencing laboratories started receiving SARS-CoV-2 positive wastewater nucleic acid extracts from throughout the state in November, from four contracted detection laboratories.
- Sequencing data was uploaded to a Google Cloud account at Syracuse University, where analysis included deconvolution with Freyja and other software to determine composite lineages. Sequence data flow is shown in Figure 1.

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