

Overview of the Ohio Wastewater Monitoring Network

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Ohio Wastewater Monitoring Network (OWMN)

Goal

Sepa

- Monitor trend of SARS-CoV-2 RNA at specific locations (vs compare sites)
- Serve as early indicator of COVID-19 community spread
- Prioritize resources

Statewide network

- Started July 2020
- leveraged expertise and resources
 - Ohio Universities
 - US EPA-ORD

• 67 locations twice a week

- Sequencing to screen for possible presence of SARS-CoV-2 variants
 - Variants of Concern (VOC)
 - Variants of Interest (VOI)





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Athens WTP Eastern Regional WRF

https://coronavirus.ohio.gov/wps/portal/gov/covid-19/dashboards/otherresources/wastewater

Public Health Application

- To serve as an early warning of infection in communities and an understanding of case trends
- The focus is on <u>trends or significant changes</u> in the number of viral gene copies detected.
- Currently action is taken when at least 3 samples show a sustained increase of at least 10-fold (1 log)
- State actions when increases are observed:
 - Notify the local health district and utility

Sepa

- Provide information on how to interpret the data and link to message toolkit
- Notify the state pandemic testing team for linkages to establish pop-up testing sites
- Provide case data by sewershed to local health district (this extraction to be provided soon)
- Participation in the CDC National Wastewater Surveillance System
- Toolkit link: <u>https://coronavirus.ohio.gov/wps/portal/gov/covid-19/healthcare-providers-and-local-health-districts/for-local-health-districts-and-governments</u>

Accomplishments

- Built statewide network that represents wastewater flow from nearly 5 million residents
- Almost I year of weekly data collected

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- All data is publicly available on the Ohio coronavirus dashboard and is updated daily
- Provided nearly 500 warnings to local health communities
- Expanded to include genomic sequencing of wastewater to pair with clinical data and inform public health decisions

Lab Method Logistics

• Twice weekly samples

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- Report data within 2 days of sample receipt
- No prescribed method; labs decide
- Supply chain shortages
- Low target concentration
- Sample hold time: 4°C 72 hours
- No sample pasteurization



Quality Assurance/Quality Control

• Matrix Spike to assess method recovery efficiency

- Coronavirus recommended: human (OC43), murine (MHV), bovine (BCoV)
- Inhibition control to monitor for PCR amplification inhibition
- RT-qPCR standards/RT-ddPCR positive control
- Human fraction measurements
 - crAssphage

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- Pepper mild mottle virus
- Monthly Interlaboratory Method Validation
 - Pick a site with sufficient concentration of SARS-CoV-2
 - Each lab gets 0.5 L
 - Each lab processes and analyzes sample
 - Report data to Project Coordinator





OH Network Lab Methods

LAB	LOD (copies/L)	Processing Method	Nucleic Acid Extraction	Quantitative Analysis Method	RT-PCR Standard Curve/ Control	Inhibition Control	Matrix Spike	Fecal Indicator
А	850	Centrifugation, filtration	Qiagen RNeasy PowerWater Kit	RT-qPCR	DNA plasmid	Dilution	MHV	crAssphage
В	135	Centrifugation, filtration	Qiagen Allprep DNA/RNA Kit	RT-qPCR	DNA plasmid	Dilution	BCoV	crAssphage
С	133	Tween, solids removal hollow fiber ultrafiltration (InnovaPrep)	Qiagen PowerMicrobiome Kit	RT-ddPCR	DNA plasmid	Luciferase Control RNA	OC43	crAssphage
D	7,440	Filtration	Trizol, garnet bead beating, alcohol precipitation	RT-qPCR	DNA plasmid	Luciferase Control RNA	BCoV	PMMoV
E	500	Centrifugation, filtration	Trizol and RNA purification kit	RT-qPCR	Synthetic RNA	Luciferase Control RNA	BCoV	crAssphage
F	3,000	Promega, add protease, supernatant through GFA/silica column	Promega Wastewater Large Volume TNA Capture Kit	RT-qPCR	DNA plasmid	Promega probe	OC43	PMMoV
G	231	Centrifugation, filtration	Qiagen RNeasy PowerWater Kit/Trizol-chloroform	RT-ddPCR	SARS-CoV-2 genomic RNA	Luciferase Control RNA	OC43	crAssphage
н	891	Acidification, Filtration, extract filter	Qiagen Allprep PowerViral DNA/RNA Kit	RT-qPCR	Synthetic RNA	Mouse lung RNA	OC43	PMMoV



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LAB	LOD (copies/L)	Processing Method	Nucleic Acid Extraction	Quantitative Analysis Method	RT-PCR Standard Curve/ Control	Inhibition Control	Matrix Spike	Fecal Indicator
А	850							
В	135		:					
С	133	1				1 1		
D	7,440					I I		
E	500	5	8	2	3	4	3	2
F	3,000	t :						
G	231					1 1		
н	891	r Numbe	r of different proce	dures emp	oyed at the vari	ous processin	g/analysis	steps

Validation Results (April 2021)



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N2 RNA concentrations from 8 labs span >2 orders of magnitude



RNA sequences with deletions of nucleotides that result in absence of spike aa 69-70 increases over time RNA sequences with nucleotides that change spike aa 501 increases over time

Genome/Genetic Sequencing

Pooled sample

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- Cannot assemble a genome
- Focus on mutations that cause amino acid substitutions, signatures of VOC/VOI

Genome/Genetic Sequencing

- 3 labs, different methods
- Tiled amplicon approach
- Short read seq via Illumina
- Short term spike amino acid changes for CDC's VOC/VOI
- Report (for each site)
 - Read depth
 - Number of alternative alleles



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OH Network Insights

- How do current practices (eg. methods, protocols, technologies, best practices, etc.) successfully contribute toward comparable, high quality data/results/decisions?
 - Using a consistent method, trends of SARS-CoV-2 RNA in a sewershed can be evaluated
 - Implementation of Quality Control parameters allow for confidence in lab measurements
 - Frequent communication/regular meetings facilitate interlab discussion and troubleshooting
- How do current practices compromise efficiency and reduce confidence in data/results/decisions?
 - Too many labs/methods result in measurement variation
 - Varied experience leads to measurement variation
 - Supply shortages lead to method changes
- What is needed to increase comparability and confidence in data and results?
 - Standardized methods/procedures
 - Standardized quality control samples/reagents
 - Statistical models to quantify uncertainty
- What types of standards could potentially help to fill these needs?
 - Matrix Spike
 - Extraction controls
 - RT-qPCR standards
 - RT-ddPCR controls
 - Inhibition controls
 - Sequencing controls

*⇒***EPA**

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