SF-RAD:

Correlative analysis of wastewater trends with clinical cases and hospitalizations through five dominant variant waves of COVID-19

> Funded by NIH RADx-rad Grant 1U01DA053941-01

- Data standardization and informatics infrastructure
- Aims 2. Wastewater characterization
 - 3. Integration with human health surveillance







Helena

Policy

Chris

PIs: Helena Solo-Gabriele, Stephan Schürer, Chris Mason, Professor, UMiami hmsolo@miami.edu

Stephan

SARS-CoV-2

Wastewater-Based Surveillance

Ø RADx[™] Radical





Human Surveillance

Student Campus Residents, UMiami Gables/Marine (Sep. 2020)

Fall'20/Spring'21

- Students tested weekly (nasal swab, qPCR) Supplemented by breath test
- COVID results and total tests by building/dorm room Summer/Fall'21
- Unvaccinated students tested weekly
- All students tested when wastewater exceeds

University Hospital, UMiami Medical (Sep. 2020)

- Treat known COVID patients
- Electronic medical records pulled regularly

Miami-Dade County Residents, FDOH WWTP (Jan. 2021)

- Positives by zip code
- Number of tests by zip code
- Augment with Biobot wastewater data (Apr. 2020)

Pilot, Miami-Dade County Public Schools, MDCPS (Jan. 2022)

- In collaboration with RADx-UP project (Gwynn, PI)
- 9 Schools (4 Elementary, 2 Middle, 3 High Schools)

Sample Collection Plans



Undergraduate Campus



Undergraduate Campus



Undergraduate Campus



Hospitalizations



—Hospitalizations

-O-WASD SARS-CoV-2

Detection and anticipation of SARS-CoV-2 Variants of Concern (VOCs) in wastewater with amplicon NGS



ARCTIC amplicon preparation and Illumina NovaSeq6000 NGS

Hospital Wastewater



C. auris (gc/L)



Additional Targets RADXSM Radical UNIVERSITY A CATALYZER Weill Cornell VALANIE Weill Cornell Yale SPHASE

Table 1: Included on the Viral Surveillance Panel.1

	Adenovirus	R Hepatitis B virus	Parechovirus	Dengue virus 1	Lujo hemorrphagic fever virus	Sapovirus	
-	Aichivirus	R Hepatitis C virus	Parvovirus		SARS 00V		
	Astrovirus	R Hepatitis E virus	Poliovirus	Dengue virus z	Macnupo virus	SARS-COV	Canalaa auris
		R Human		Dengue virus 3	Marburg virus	R SARS-COV-2	
	Chapare virus	Immunodeficiency Virus 1	Polyomavirus	Dengue virus 4	MERS-CoV	Tick-borne encephalitis virus	
R 	Chikungunya virus	Human Immunodeficiency Virus 2	Respiratory syncytian virus	Eastern equine encephalitis virus	Metapneumovirus	Torque Teno virus	-
	Coronavirus-229E	Influenza A virus	Rhinovirus	Ebola virus	Monkeypox virus	Variola virus	-
	Coronavirus-HKU1	Influenza B virus	Rift Valley fever virus	Enterovirus	Nipah virus	R Venezuelan equine encephalitis virus	
	Coronavirus-OC43	Japanese encephalitis virus	Rotavirus	Guanarito virus	Norovirus	R West Nile virus	
	Coronavirus-NL63	Junin virus	Rubella virus	Hantavirus	Omsk hemorrhagic fever virus	Western equine encephalitis virus	
	Coxsackievirus	Kyasanur Forest disease virus	Sabia virus	Hendra	Oncolvtic human		_
	Crimean-congo	n-congo rhagic Lassa fever virus rus	Salivirus	henipavirus	papillomavirus	🕅 Yellow fever virus	
	haemorrhagic fever virus			Hepatitis A virus	Parainfluenza virus	<u>R</u> Zika virus	-

Discovery, geography, and phylogeny of noroviruses, aichiviruses, and myriad bacteria



Anti-microbial resistance (AMR) genes are significantly higher in hospital sewage



Acknowledgments Questions (hmsolo@miami.edu)

