Wastewater Based Epidemiology for Tracking the Prevalence of COVID-19 in Communities

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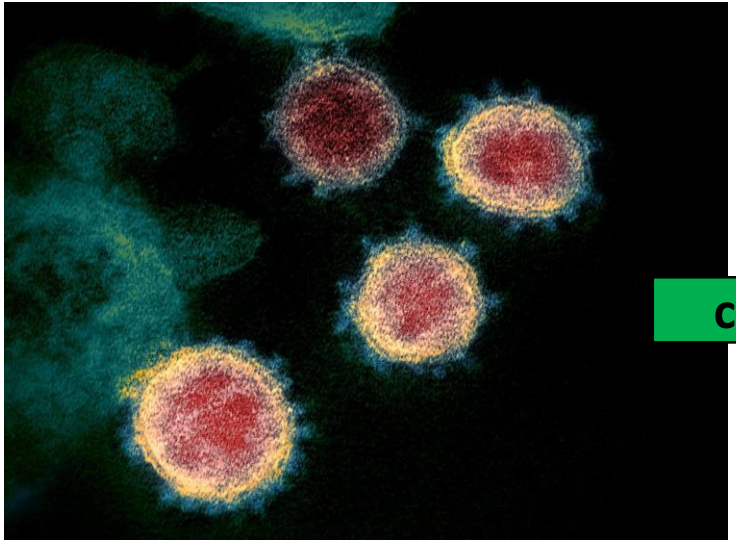
Acknowledgements

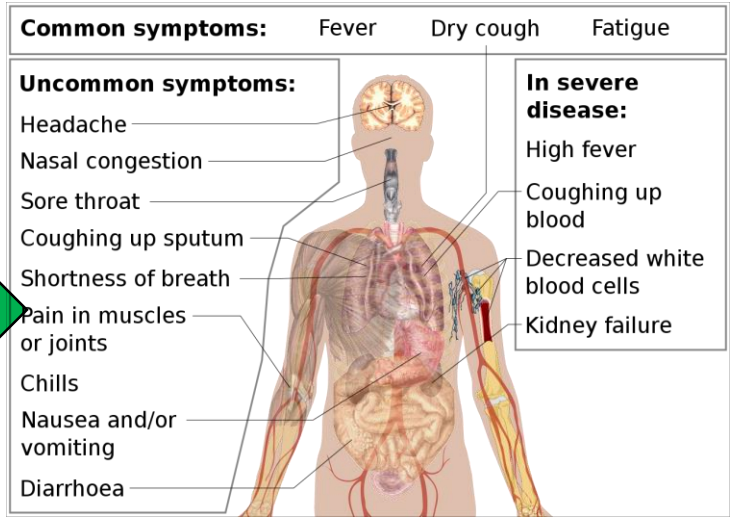
Agenda – Utility Perspective

- Background
- Poop never lies!
- Current WBE studies on COVID-19
- How to determine prevalence in community
- Outbreak prevention
- Ongoing research
- Communications

Background



causes



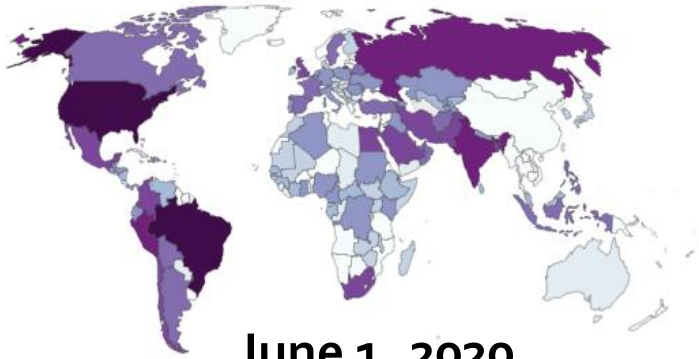
SARS-CoV-2 virus

COVID-19 disease

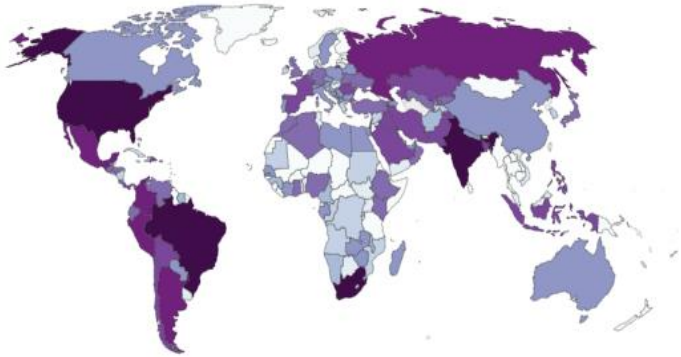
Progress of Current Pandemic

Feb 1, 2020

April 1, 2020



June 1, 2020

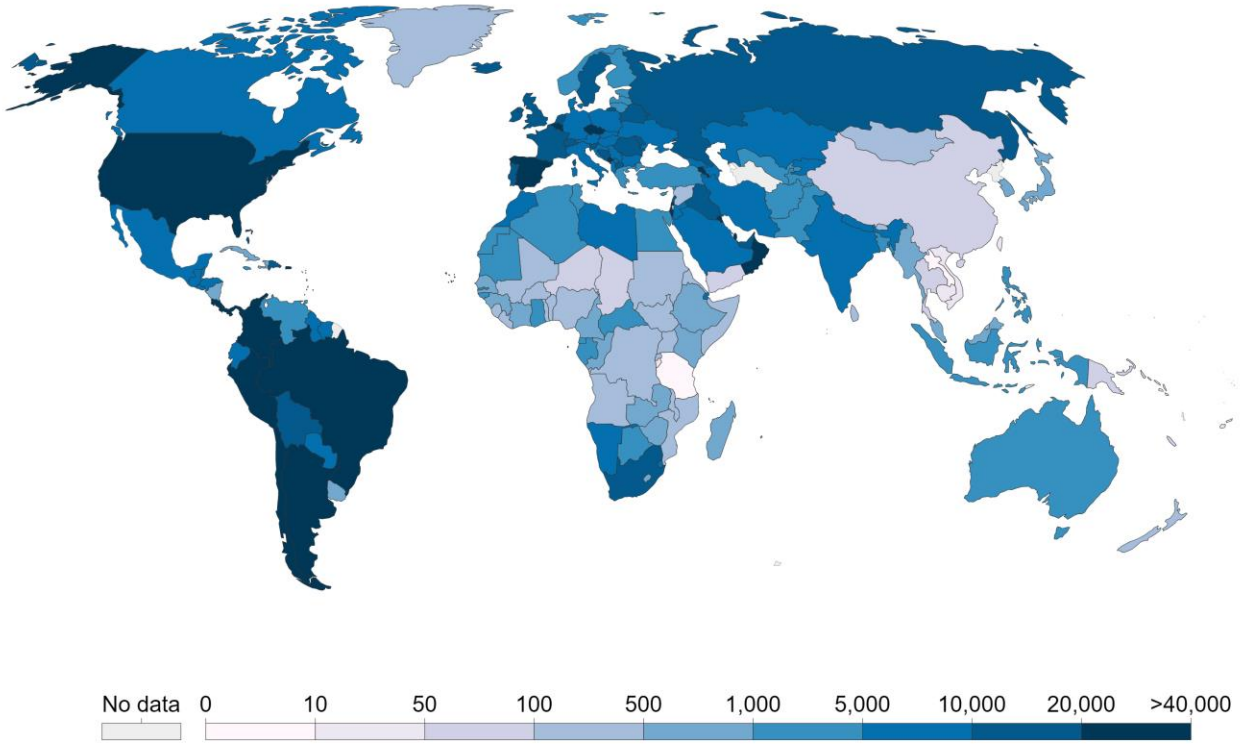


August 1, 2020

Cumulative confirmed COVID-19 cases per million people, Oct 28, 2020

The number of confirmed cases is lower than the number of actual cases; the main reason for that is limited testing.

Our World in Data



Source: European CDC – Situation Update Worldwide – Last updated 28 October, 11:35 (London time)

CC BY

Summary: The countries with the most cumulative COVID-19 cases:

- U.S.A.
- India
- Brazil

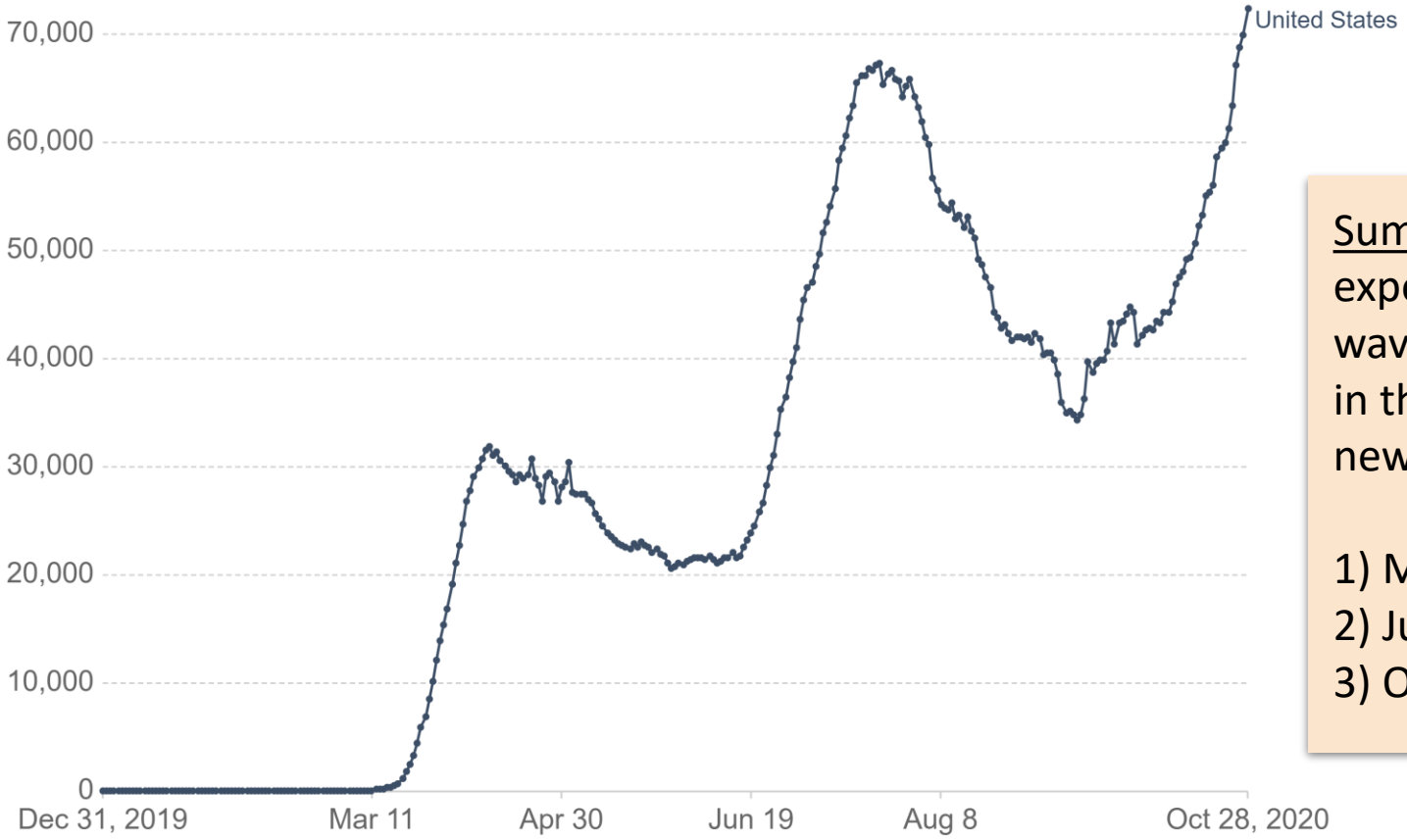
Summary: Taking population into account (cases per capita), the worst-hit regions so far are the U.S., South America, and Europe.

Graphic and data obtained from https://ourworldindata.org/coronavirus

Daily new confirmed COVID-19 cases

Shown is the rolling 7-day average. The number of confirmed cases is lower than the number of actual cases; the main reason for that is limited testing.

Our World in Data

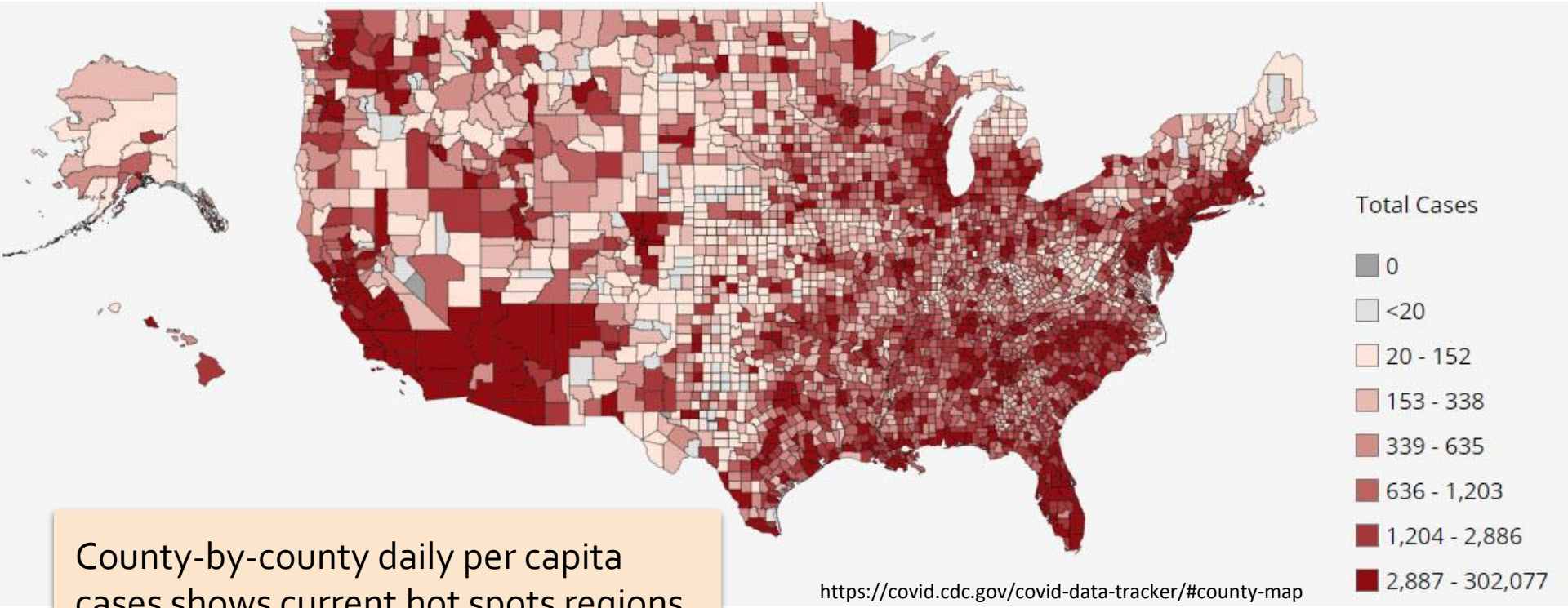


Source: European CDC – Situation Update Worldwide – Last updated 28 October, 11:35 (London time)

https://ourworldindata.org/covid-cases

<u>Summary</u>: The U.S. experienced three waves of rapid increase in the number of daily new cases.

1) March - April
2) June – July
3) October – current



https://covid.cdc.gov/covid-data-tracker/#county-map

County-by-county daily per capita cases shows current hot spots regions in the USA:

- East
- South
- Southwest

Updated: Oct. 28

Limitations with Clinical Data

- Limited test availability
- Test effectiveness (false negative & false positive)
- Asymptomatic carriers
- Infected / symptomatic people not getting tested
- Unreported cases
- Lag in reporting cases
- Reoccurrence of infection / disease
- Increased testing

How can we measure prevalence of SARS-CoV-2 infection in a community without relying solely on testing data?

POOP NEVER LIES!

China CDC Weekly

Notes from the Field

Isolation of 2019-nCoV from a Stool Specimen of a Laboratory-Confirmed Case of the Coronavirus Disease 2019 (COVID-19)

Yong Zhang[1,&]; Cao Chen[1,&]; Shuangli Zhu[1]; Chang Shu[2]; Dongyan Wang[1]; Jingdong Song[1]; Yang Song[1]; Wei Zhen[1]; Zijian Feng[3]; Guizhen Wu[1]; Jun Xu[2,#]; Wenbo Xu[1,#]

nature

https://doi.org/10.1038/s41586-020-2196-x

Accelerated Article Preview

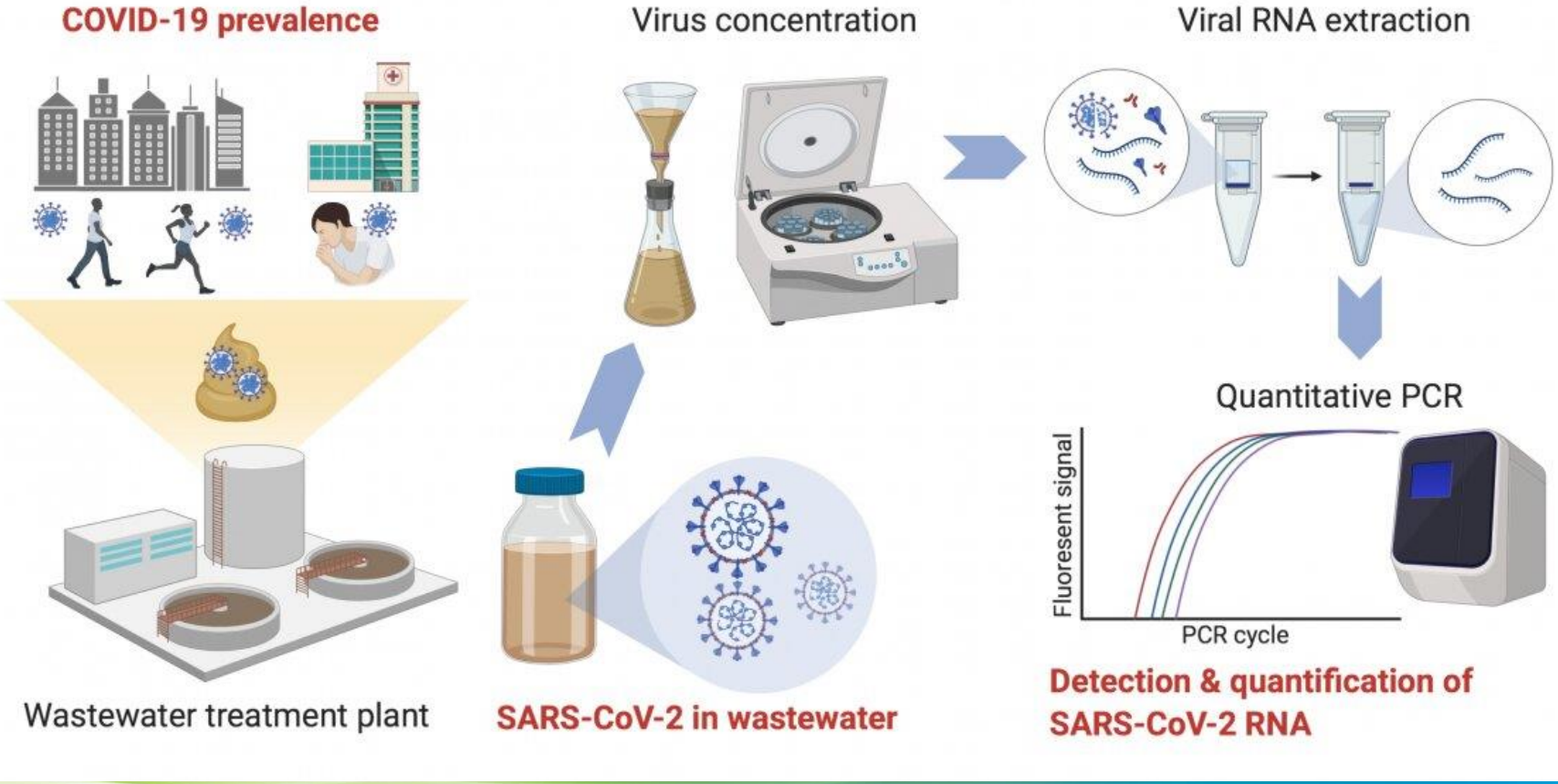
Virological assessment of hospitalized patients with COVID-2019

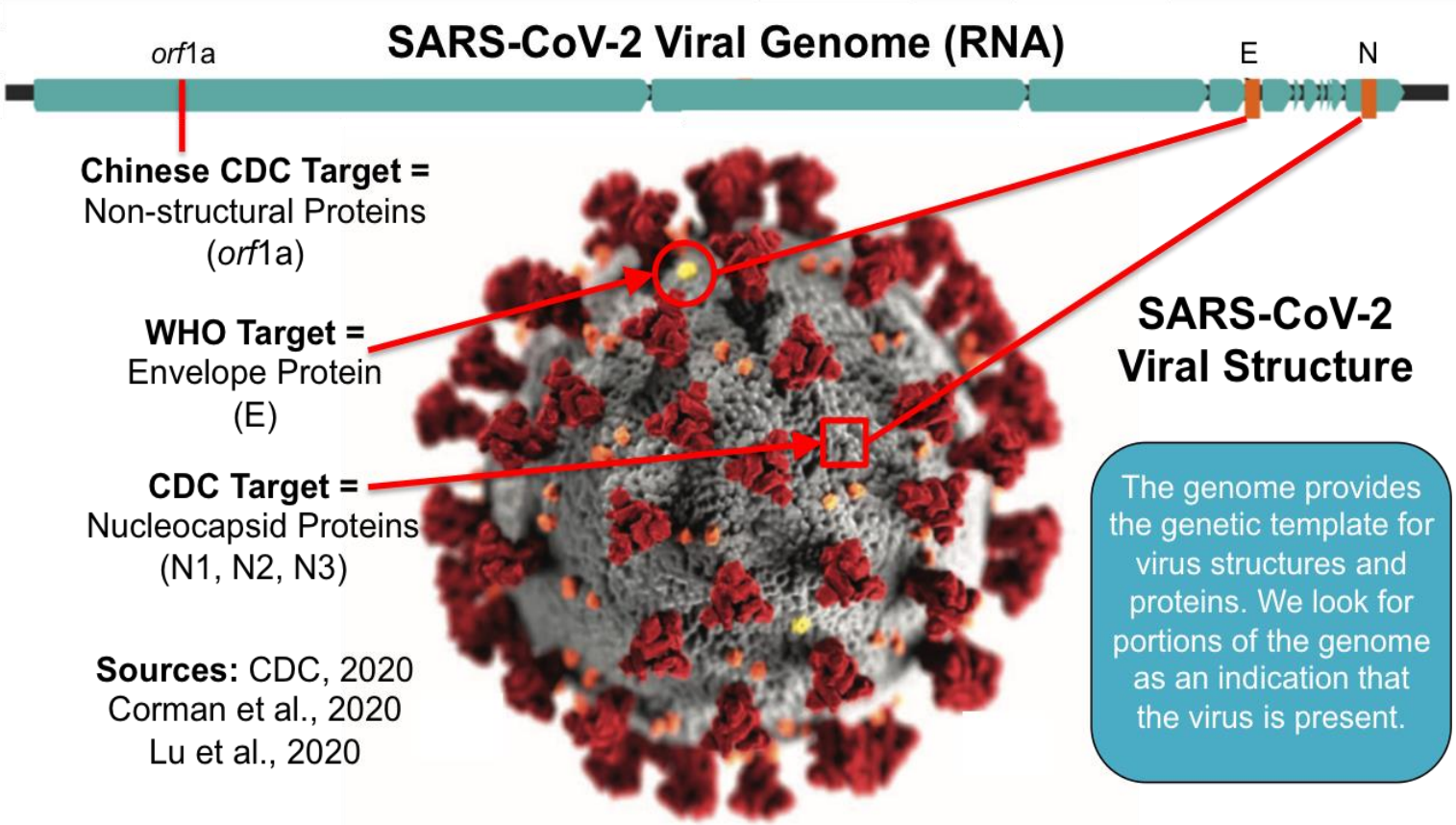
Received: 1 March 2020

Accepted: 24 March 2020

Accelerated Article Preview
Published online 1 April 2020

Roman Wölfel, Victor M. Corman, Wolfgang Guggemos, Michael Seilmaier, Sabine Zange, Marcel A. Müller, Daniela Niemeyer, Terry C. Jones, Patrick Vollmar, Camilla Rothe, Michael Hoelscher, Tobias Bleicker, Sebastian Brünink, Julia Schneider, Rosina Ehmann, Katrin Zwirglmaier, Christian Drosten & Clemens Wendtner


COVID-19 prevalence
Virus concentration
Viral RNA extraction
Quantitative PCR
Fluoresent signal
PCR cycle
Wastewater treatment plant
SARS-CoV-2 in wastewater
Detection & quantification of SARS-CoV-2 RNA



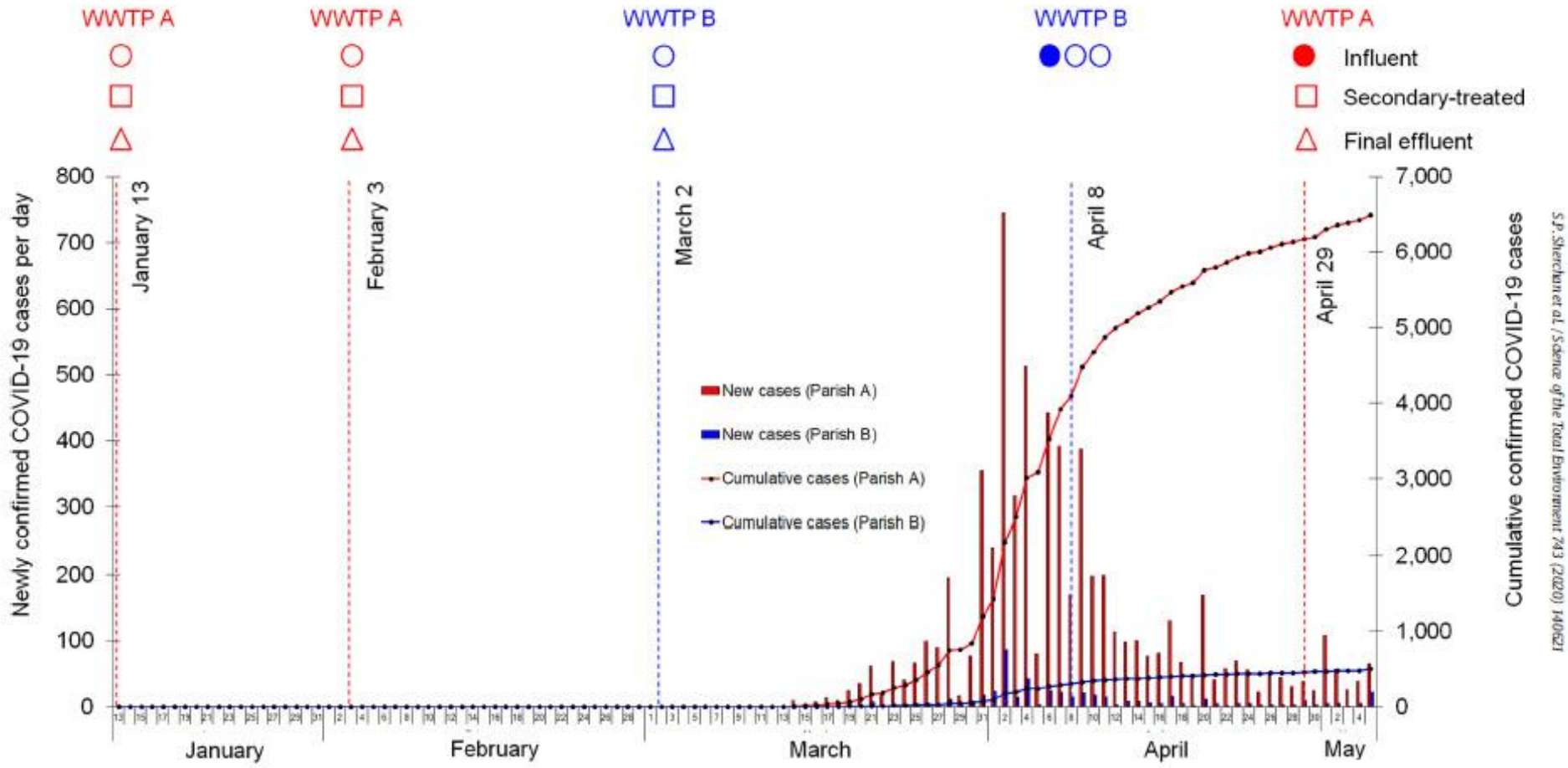
Reference: Dan Garrity, Southern Nevada Water Authority

Wastewater Surveillance

- Potential early warning tool
  - Can identify change in community infection rate before clinical testing
- Pooled testing approach
  - Captures symptomatic *and* asymptomatic infections
- Can help determine actual conditions
  - May overcome clinical testing artifacts (ie., test lags)

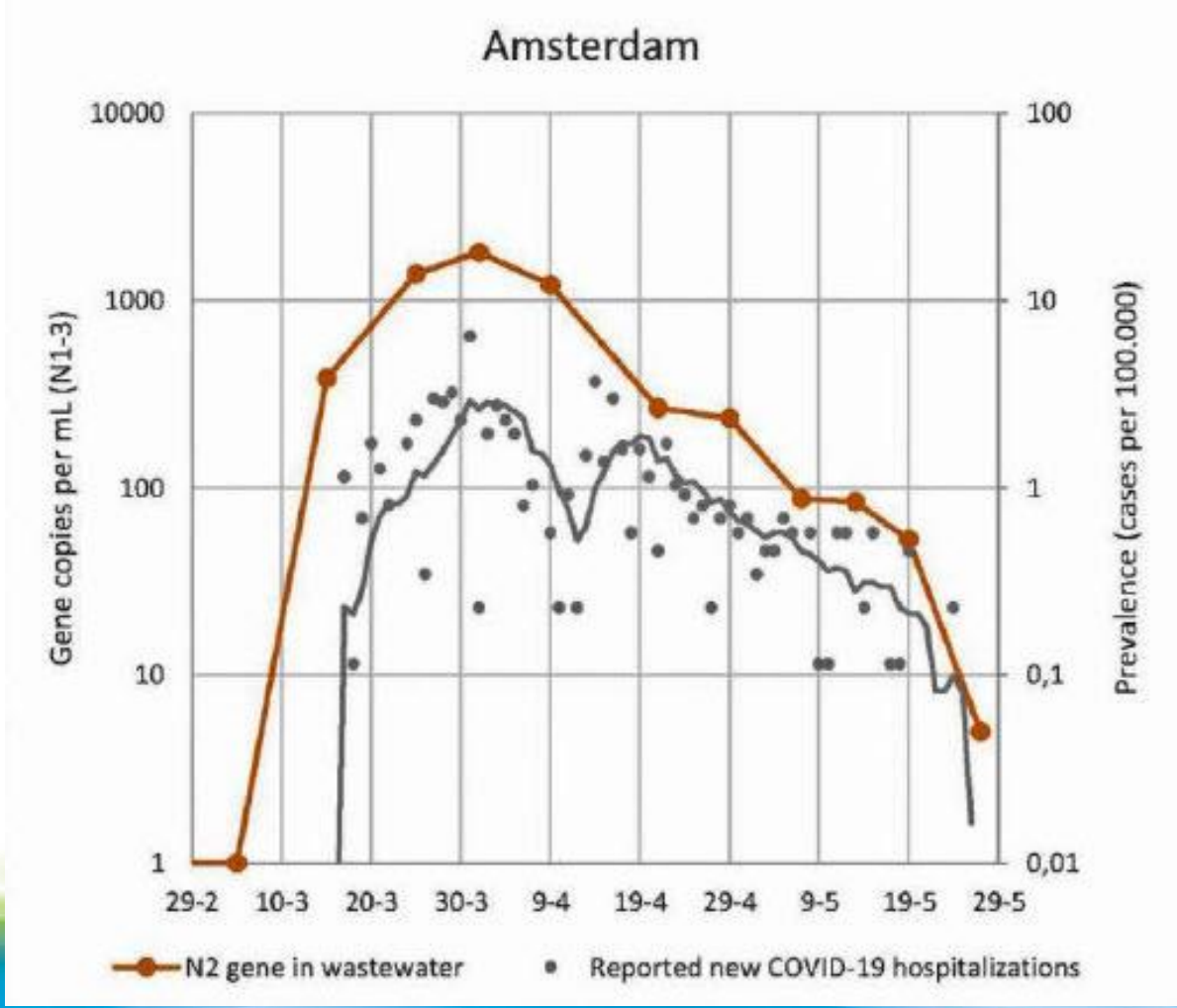
Reference: Dan Garrity, Southern Nevada Water Authority

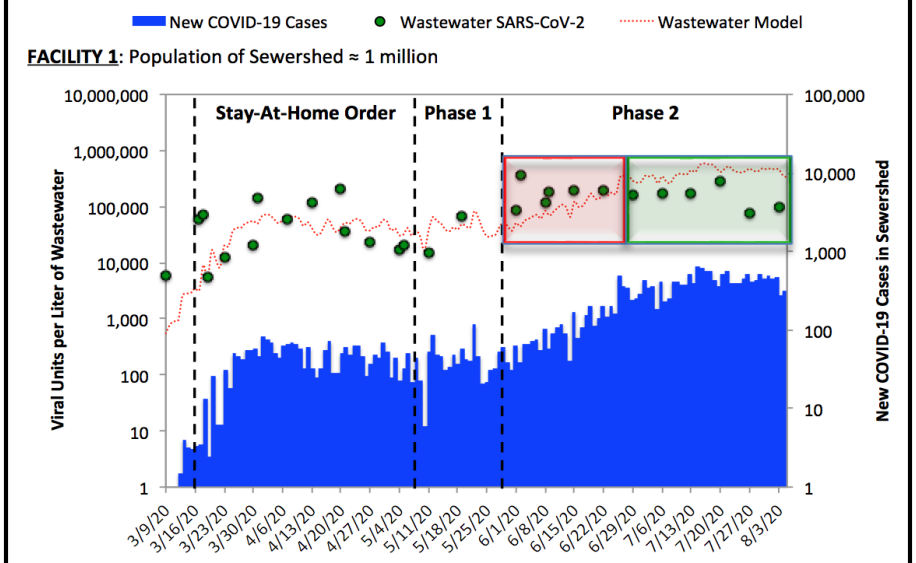
Current WBE Studies

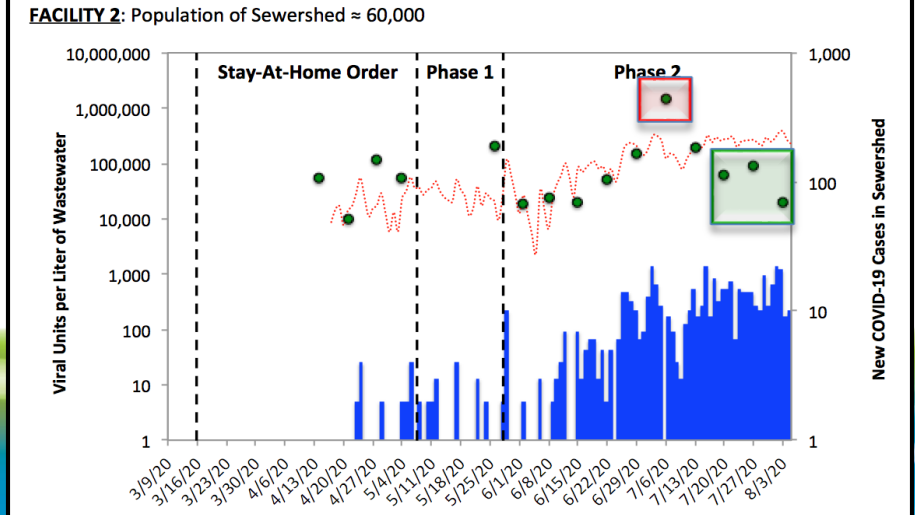


S.P. Sherchan et al. / Science of the Total Environment 743 (2020) 140621

Fig. 1. SARS-CoV-2 RNA detection in wastewater and confirmed COVID-19 cases in southern Louisiana, USA. Circles, squares, and triangles represent sample types, i.e., influent, secondary-treated, and final effluent, respectively. Red and blue symbols represent samples collected from WWTPs A and B, respectively. Closed and open symbols denote positive and negative SARS-CoV-2 RNA detections, respectively. Bars and line plots denote new and cumulative COVID-19 cases, respectively, in parishes A (red) and B (blue) where respective WWTPs (A and B) are located. Epidemiological data on confirmed COVID-19 cases in each parish in the State of Louisiana were retrieved from the USA facts (https://usafacts.org/visualizations/coronavirus-covid-19-spread-map/). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)


Amsterdam
10000
1000
100
10
1
Gene copies per mL (N1-3)
100
10
1
0,1
0,01
Prevalence (cases per 100.000)
29-2
10-3
20-3
30-3
9-4
19-4
29-4
9-5
19-5
29-5
N2 gene in wastewater
Reported new COVID-19 hospitalizations



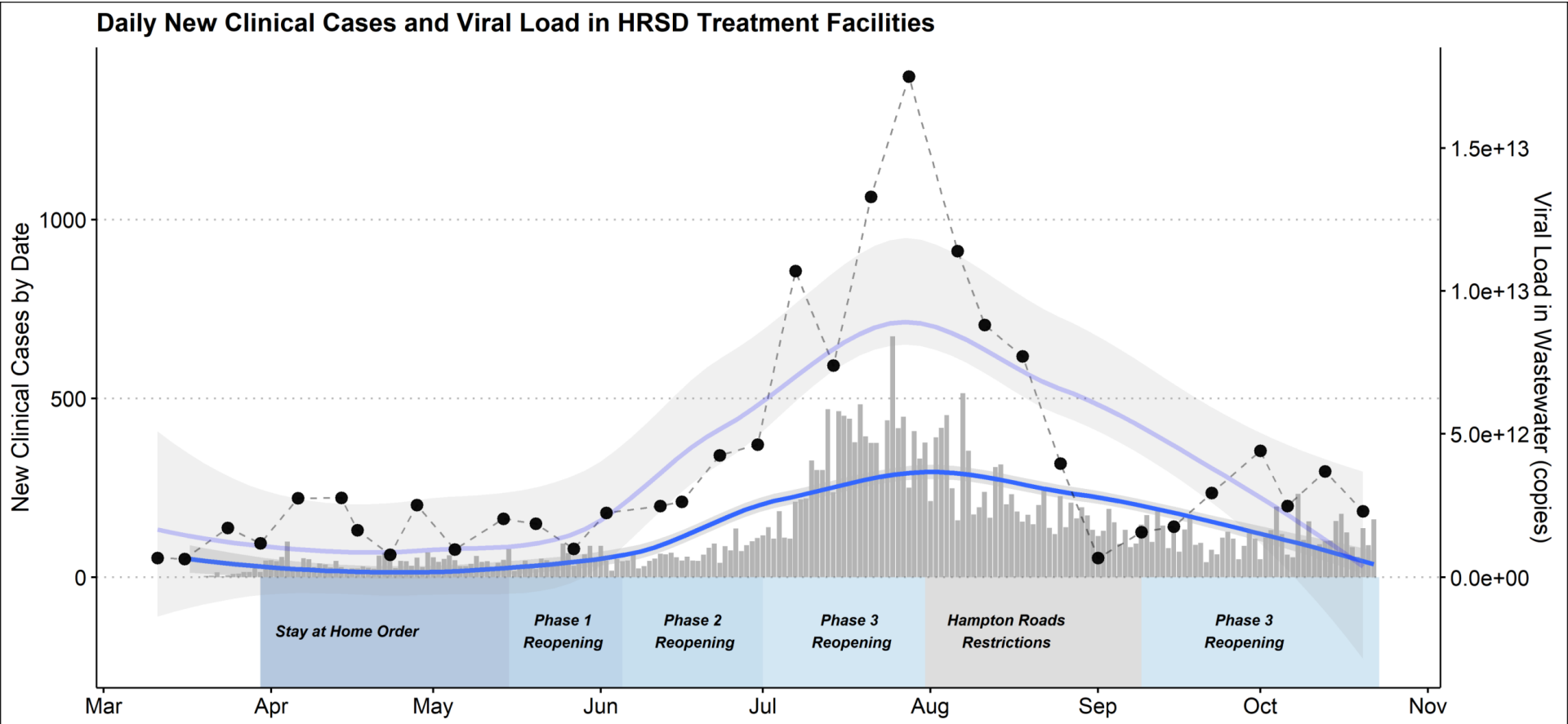


SNWA

- Genetic 'fingerprint' in wastewater appeared to be correlated with new daily cases
- Wastewater surveillance confirms that infections in Southern Nevada increased in June/July (not just more testing) but decreased in July/August
- Clinical testing did not accurately characterize actual conditions in the community at all times, possibly due to test lags

Reference: Dan Garrity, Southern Nevada Water Authority

Hampton Roads, VA



Reference: Raul Gonzalez, Hamptons Road Sanitation District

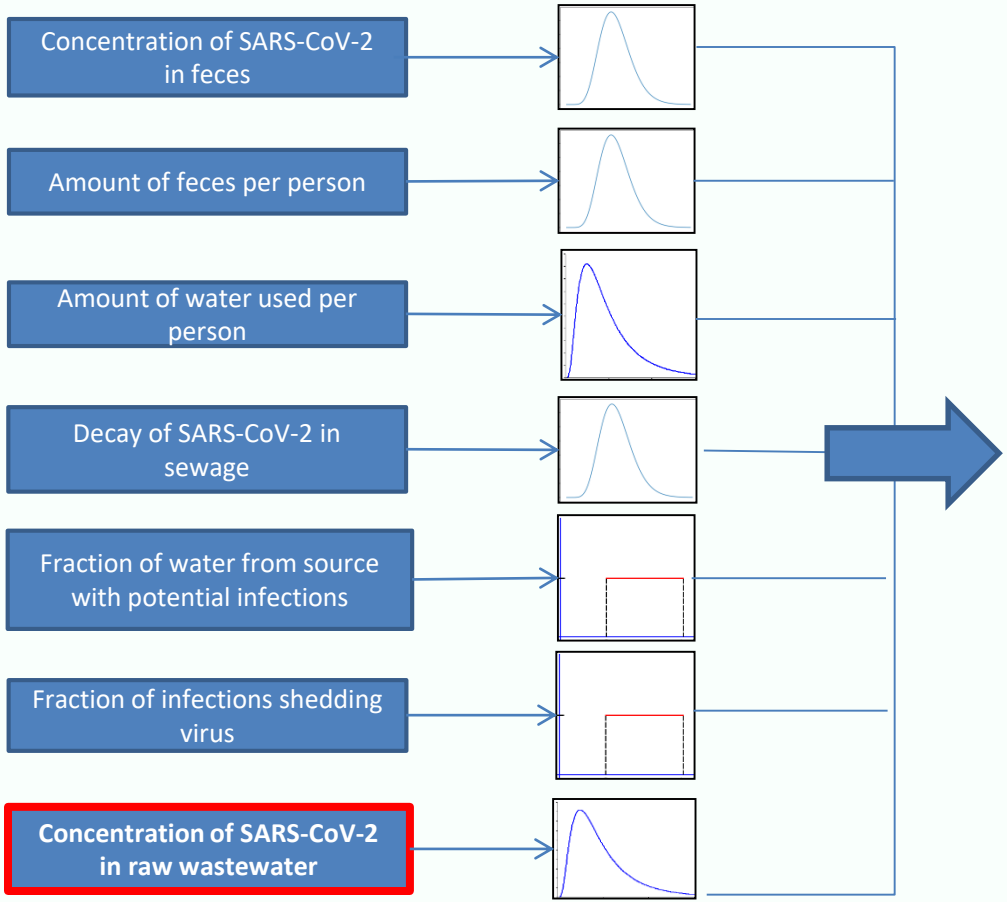
*Trend lines created using lowess smoothing function

How to determine the prevalence of SARS-CoV-2 infection in a community from PCR data?

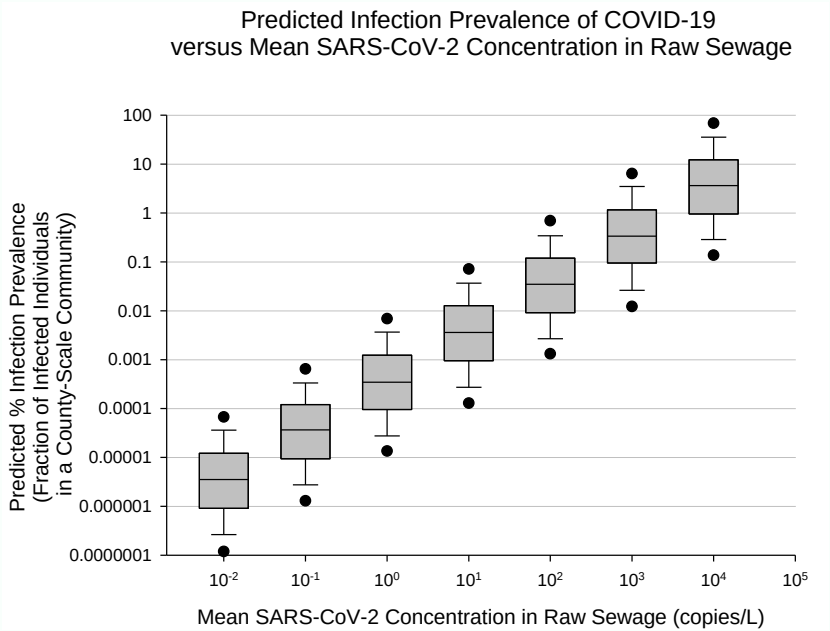
$$\text{Infections (persons)} = \frac{\text{Concentration (gene copies/L)} \times \text{Wastewater Flow Rate (L/day)}}{\text{Feces Production Rate (grams/person-day)} \times \text{Fecal Shedding Rate (gene copies/gram)}}$$

Shedding rate is still under investigation

CDC Sewage Model Framework | Monte Carlo Simulation

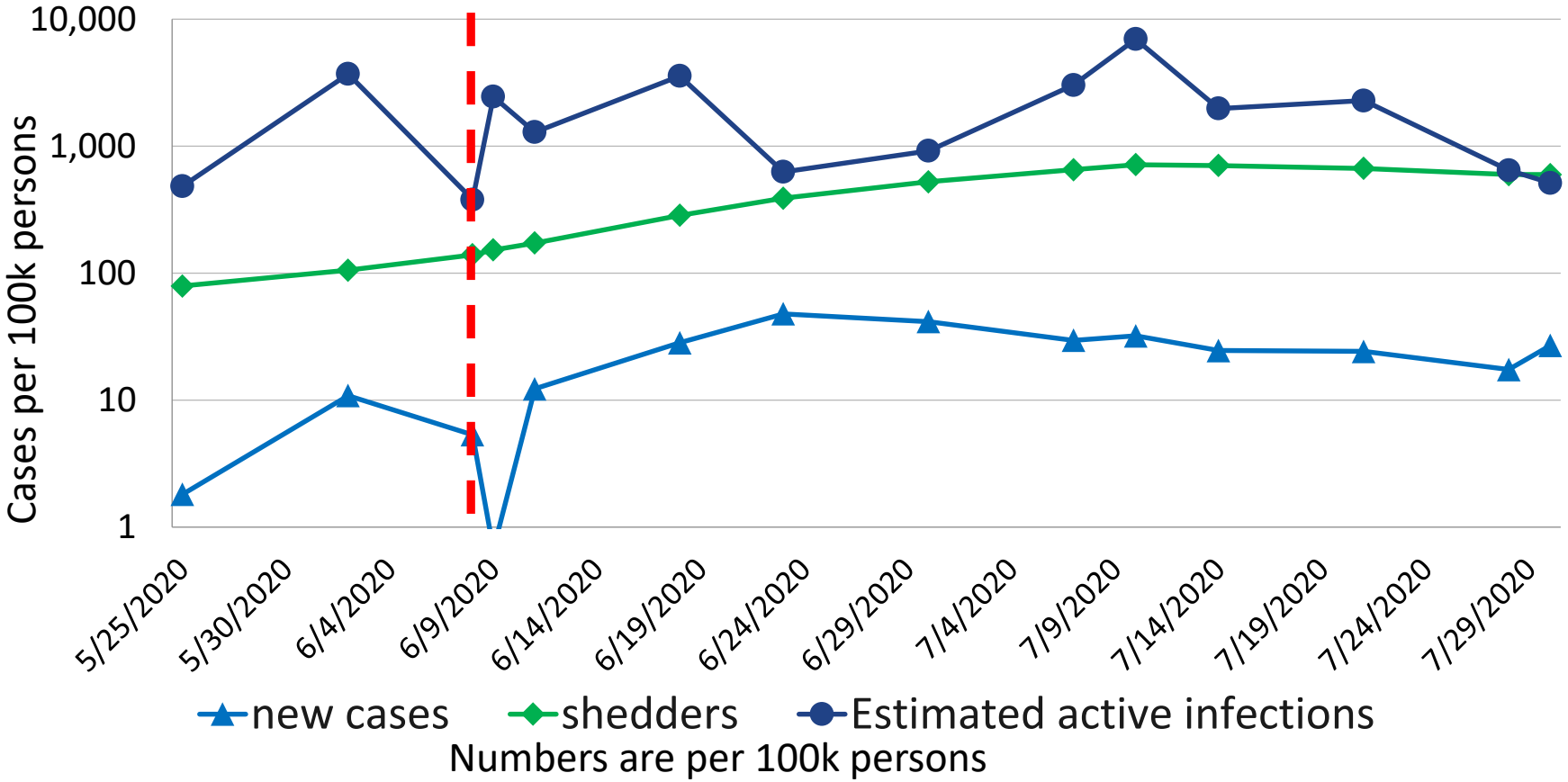


Daily Prevalence of infections in community



Reference: Amy Kirby and Mia Mattioli, CDC

Pima County, AZ



Assumptions & Limitations

- Shedding rate is unknown
  - Variable by person?
  - Severity of illness?
  - Duration? Decrease over time?
- Homogeneity in wastewater sample
  - Weather
  - Dilution
  - Decay
  - Processing
- Variability in sample processing
  - Concentration efficiency
  - Detection variability
- Reported infections = true numbers
  - Ignore limitations of testing
  - Asymptomatic captured in water but not reported
- Population
  - What about commuters/visitors?

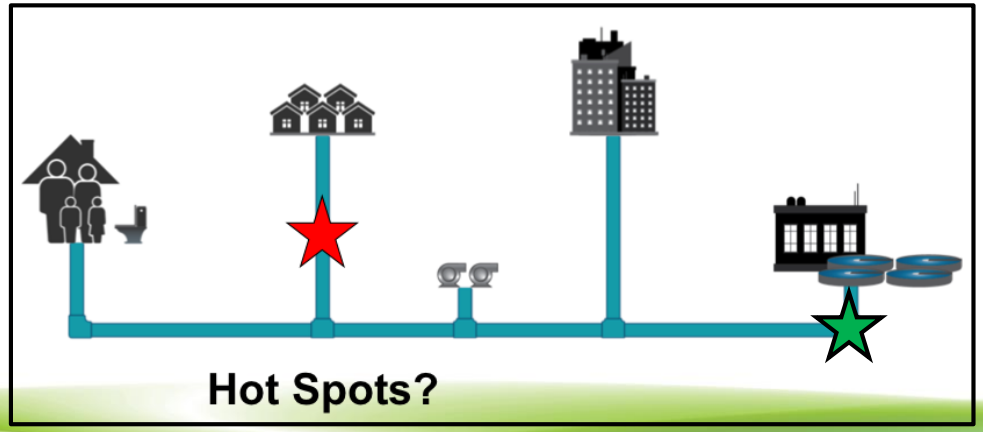
Outbreak Prevention

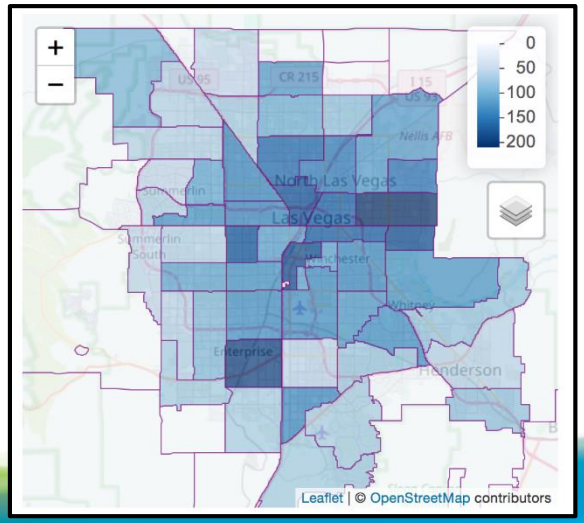
- 16 dorms/buildings
- Sampling manhole specific to individual buildings
- Closed/Control System
- Positive detection 2 days after classes began
- Swab/Antibody testing confirmed 2 infected persons
- Infected persons removed; concentration returned to negative
- Defined community: asymptomatic vs symptomatic is known

Ongoing Research

Localized Surveillance

- Identify 'hot spots' for prioritized sampling
- Characterize community healthy by geographic location





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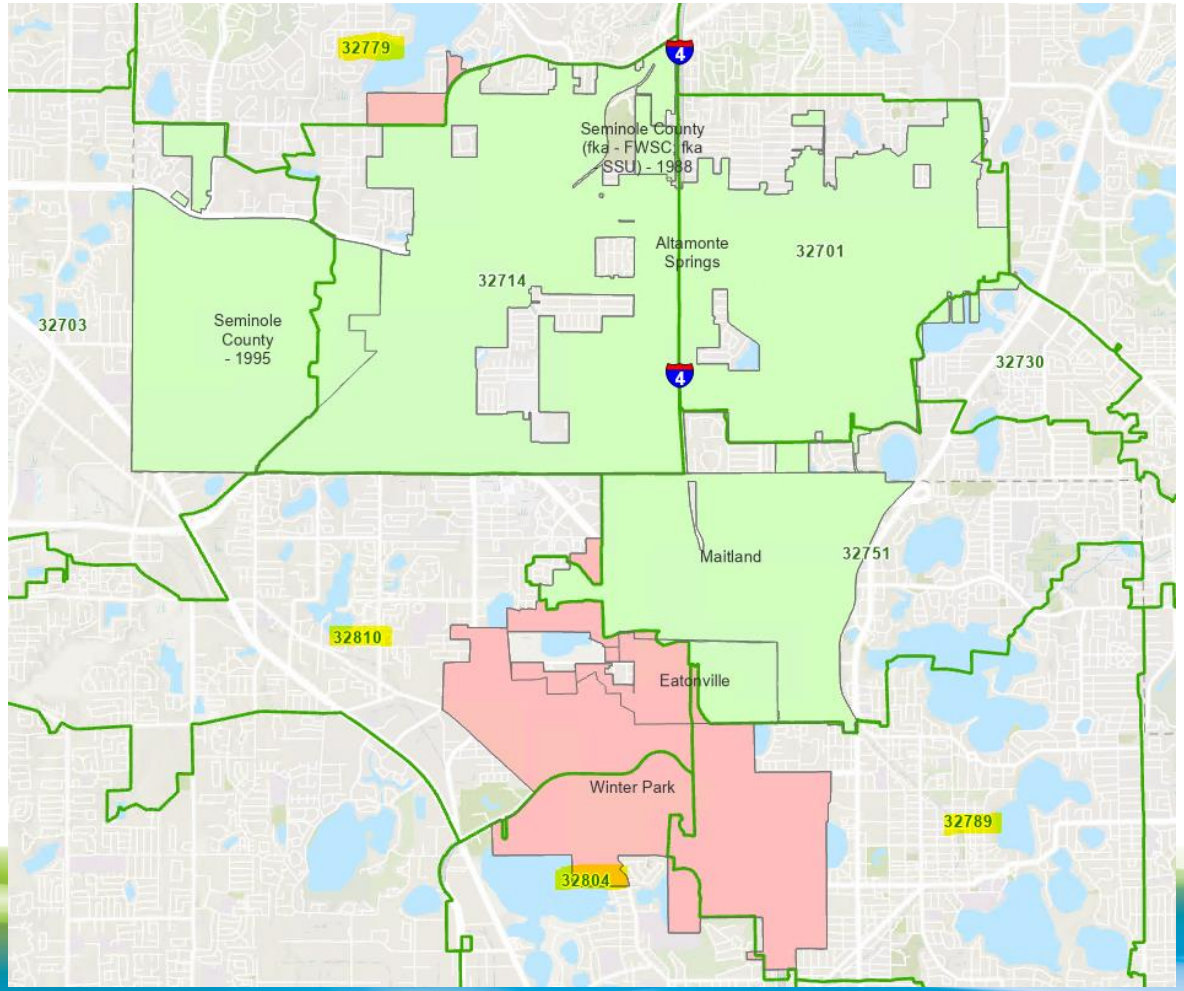

County boundaries and testing data does not overlap with wastewater service area.

Working with local health officials to get testing data per zip code.

Zip code clinical data is prorated and compared with service area wastewater results.

Potential Targets: long-term care facilites, schools, airports, theme parks, etc.

Communication

Communication is key!

- Estimates are not exact!
  - Shedding rate is still under investigation
- Models are meant to be used in *tandem* with other data to influence public health intervention
- No standard method for processing samples
- Variability across samples
- Correlation between model estimates and actual infections is still being determined

Questions?

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