Public health response to COVID-19 epidemics using real-time genomic epidemiology and science communication

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COVID-19 timeline

The arrival of an invisible enemy

- 1st COVID-19 patient hospitalized in Wuhan
- Genome sequence of SARS-CoV-2
- 1st travel associated case identified in U.S.
- Travel restricted from Iran to U.S.
- 1st reported case in Connecticut
- 1st reported case outside of China (Thailand)
- Travel restricted from China to U.S.
- 1st "community acquired" case identified in U.S.
- Travel restricted from Europe to U.S.

Credit: Joseph Fauver
Early response to COVID-19

Joining efforts to respond to the first wave of cases in Connecticut

Before the first COVID-19 cases in Connecticut (on March 6th), Yale launched its SARS-CoV-2 surveillance initiatives

Multidisciplinary consortium of Yale laboratories: IMPACT

Yale SARS-CoV-2 Surveillance Initiatives

**YSFPH**
Albert Ko
Nathan Grubaugh
Anne Wyllie
Arnau Cassanovas
Many others...

**YSM**
Akiko Iwasaki
Craig Wilen
Maria Tokuyama
Alice Lu-Culligan
Many others...

**YNHH**
Charles Dela Cruz
Shelli Farhadian
Melissa Campbell
Alison Nelscon
Many others...

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Our contribution

- Genomics
- Phylogenetics
- Science Communication

Public health response to COVID-19 epidemics using real-time genomic epidemiology and science communication
Genomics
Sample processing and testing

Supporting our local hospital (YNHH) during a public health crisis

Sample Collection

RNA Extraction & Testing

MinION Sequencing

Tiled Amplicon Generation

Sample Collection

RNA Extraction & Testing

MinION Sequencing

Tiled Amplicon Generation

Isabel Ott  Chaney Kalinich  Mary Petrone  Chantal Vogels  Anne Wyllie  Nathan Grubaugh
Comparing primer-probe sets

 mContext

Except for one primer-probe set (RdRp-SARSr, Charité), all the others have shown comparable sensitivities.

Primer–probe sets used in the US (CDC N1 and N2) are consistent/sensitive enough to prevent false negatives.
Fast sequencing of positive samples

Getting an in-depth understanding about SARS-CoV-2 lineages

Day 1: we generated 9 genomes (>90% coverage at >20X depth) within 24 hours of receiving the RNA samples.

Sample Collection

MinION Sequencing

Tiled Amplicon Generation

RNA Extraction & Testing
Phylogenetics
Revealing the origins of the first lineages circulating in Connecticut

Coast-to-coast viral spread around early March 2020

Rapid phylogenetic analysis of 9 viral genomes using a Nextstrain pipeline revealed early patterns of viral spread

First introductions of SARS-CoV-2 in Connecticut likely came from the West Coast (WA) and from Europe (EU)

Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States

Emma Hodcroft
Estimating the risk of viral introductions

The impact of domestic or international flights at spreading the coronavirus

We selected 5 **domestic** and 5 **international** locations representing travel origins with the highest numbers of COVID-19 cases.

When travel ban from Europe was enacted, **domestic air travel** posed higher risk of viral spread in the U.S.

The **high COVID-19 prevalence** and the large **passenger volumes** within the US favored local viral spread.

From 9 to 241 genomes, week after week

More routes of viral spread were revealed

April 3rd, n=18
April 7th, n=13
April 14th, n=30
April 22nd, n=15
April 29th, n=16

May 5th, n=19
May 27th, n=05
June 9th, n=37
June 17th, n=38
June 24th, n=41
From 9 to 241 genomes, week after week

Importations from New York seeded most outbreaks in CT from mid-March
Science Communication
COVIDTracker

An online platform for sharing results, data, and protocols

We created an easy to maintain, online platform: covidtrackerCT.com

Weekly reports about the spread of COVID-19 in Connecticut

Open Science: sharing protocols, data and analysis pipelines

Accessible, jargon-free language to communicate our findings to the general audience and policymakers

We're using a variety of tools, including viral sequencing, case surveillance, test development, and wastewater surveillance, in order to learn more about how SARS-CoV-2 is spreading in Connecticut.

Chaney Kalinich

Cole Jensen

Peter Neugebauer

covidtrackerCT.com

Yale SARS-CoV-2 Surveillance Initiatives

Public health response to COVID-19 epidemics using real-time genomic epidemiology and science communication
Communicating science in real time

COVIDTracker: an online platform for sharing data, protocols and results

Informative articles

Weekly reports

Protocols

covidtrackerCT.com
Our approach

Samples, data analysis and communication

PLOS BIOLOGY

Real-time public health communication of local SARS-CoV-2 genomic epidemiology


Published: August 21, 2020 | https://doi.org/10.1371/journal.pbio.3000869
Concluding remarks

Our research shows that...

- **Collaborations** involving universities, hospitals and public health departments were **essential** to properly **respond to the epidemic** in Connecticut.

- **Quick access** and **processing** of COVID-19 samples by an **interdisciplinary team** were crucial to generate genomic data and make them available **in real time**.

- Accurate results obtained via **fast phylogenetic tools** (e.g. nextstrain) can provide **actionable** information about viral spread, even when genomic data is limited.

- **Clear and accessible** scientific content coming from researchers to the general public plays an **important role at fighting misinformation**.
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