Pathogen Genomics and New Precision Public Health Tools for Infectious Diseases and Outbreak Response

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The findings and conclusions in this presentation are those of the author and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Use of trade names is for identification only and does not imply endorsement by the Centers for Disease Control and Prevention or by the U.S. Department of Health and Human Services.

Seeing Patterns
Solving Puzzles
Targeting Interventions

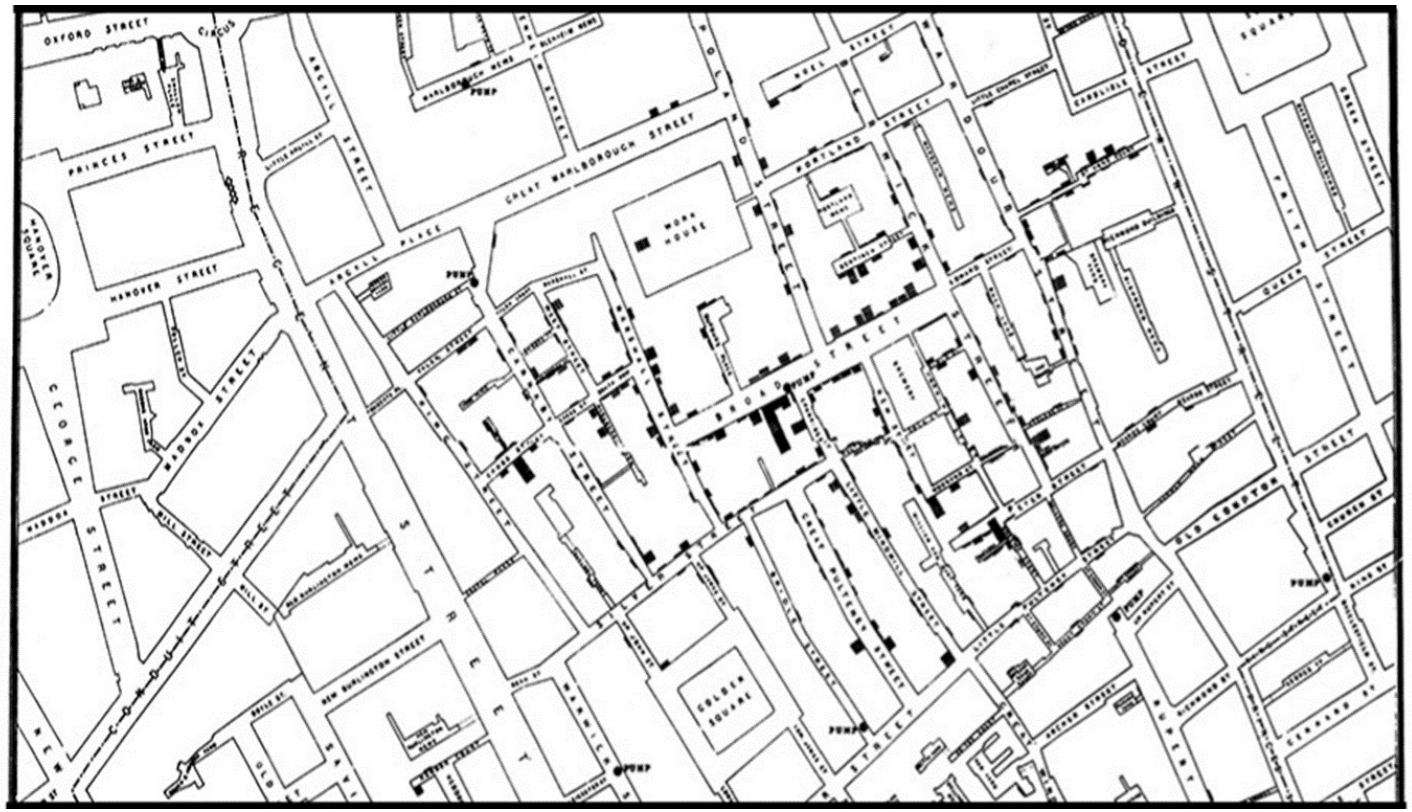
Cholera in London

A dead victim of cholera in Sunderland, 1832, Lithograph with watercolour, IWG (lithographer's monograph). © Wellcome Collection. Attribution 4.0 International (CC BY 4.0)

A COURT FOR KING CHOLERA.

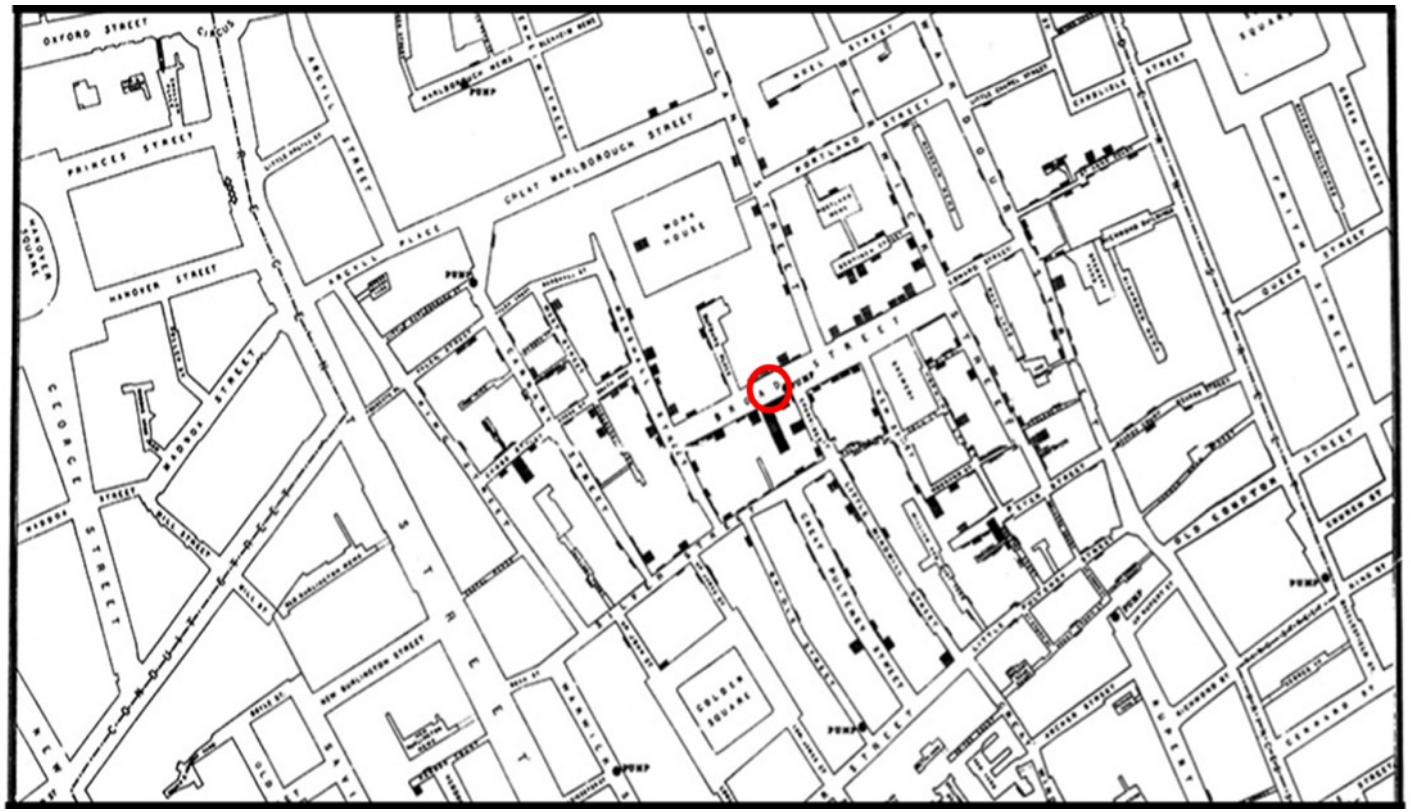
Credit: Punch, or, the London Charivari. © Wellcome Collection. Attribution 4.0 International (CC BY 4.0)

Cholera in London, 1854



commons.wikimedia.org/wiki/File:Snow-cholera-map-1.jpg

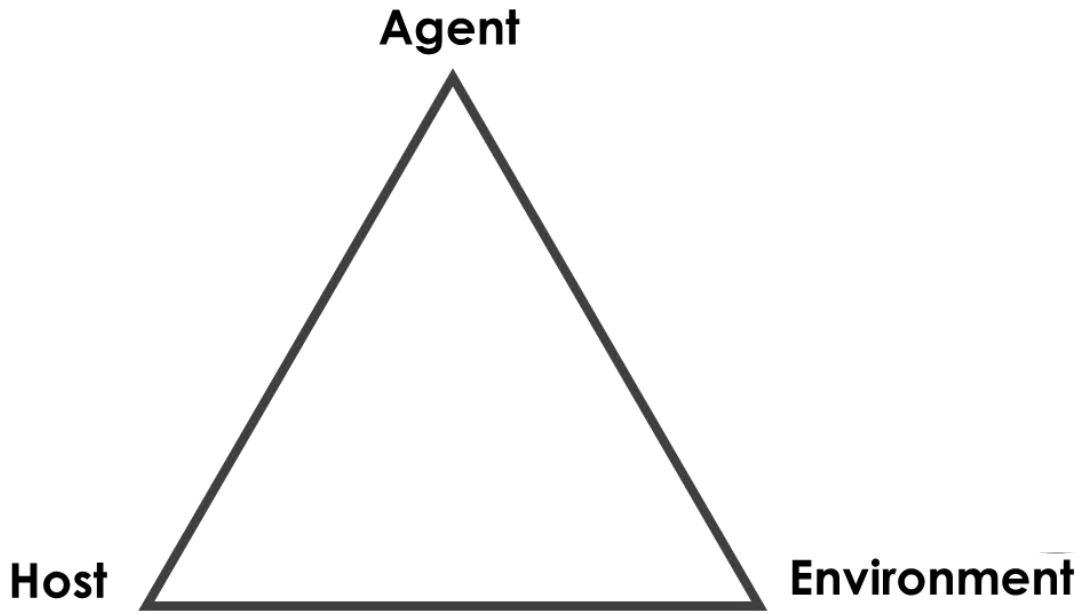
Cholera in London, 1854



commons.wikimedia.org/wiki/File:Snow-cholera-map-1.jpg

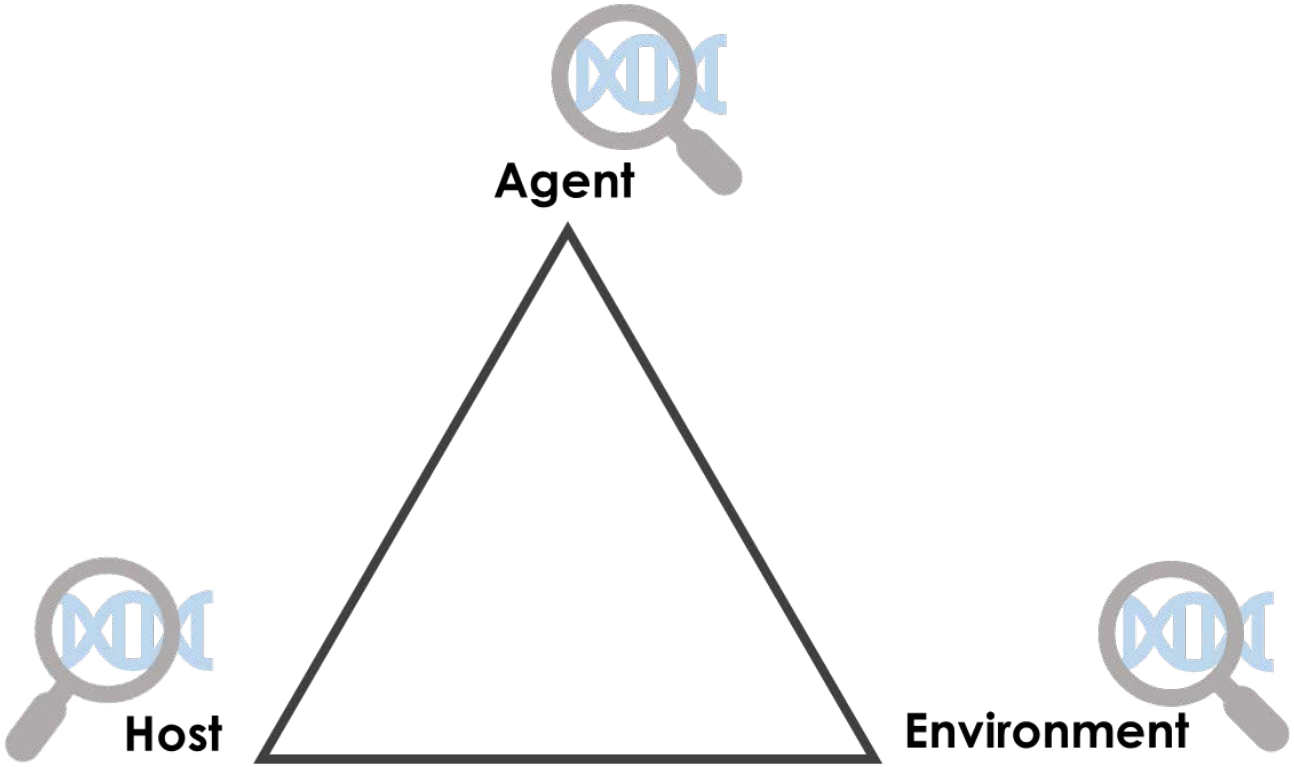
Targeted Intervention

Epidemiologic Triangle of Infectious Disease

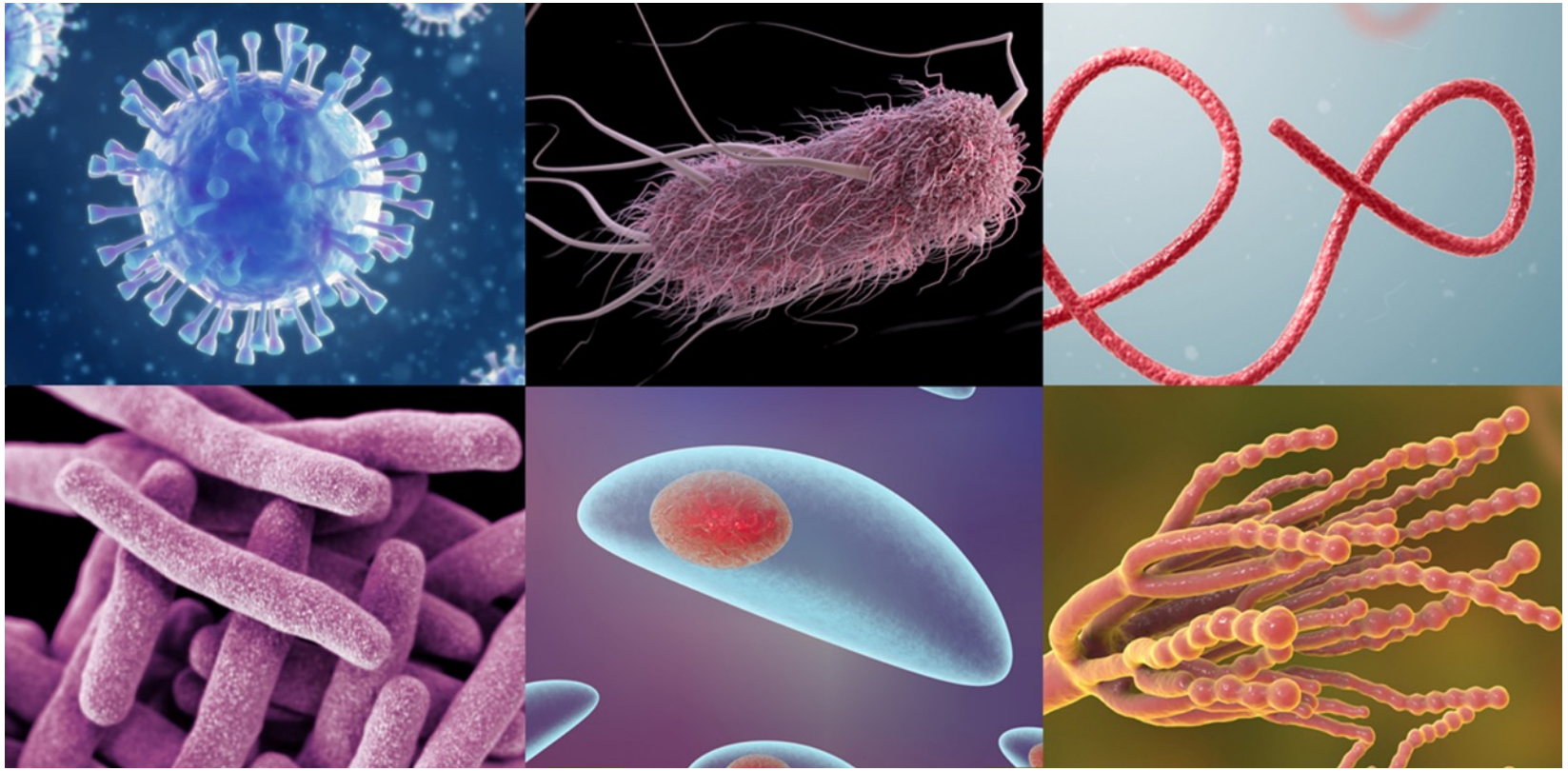


Genomic Epidemiology: Building out the Epidemiologic Triangle

(or…the more we can look at, the better we can see)

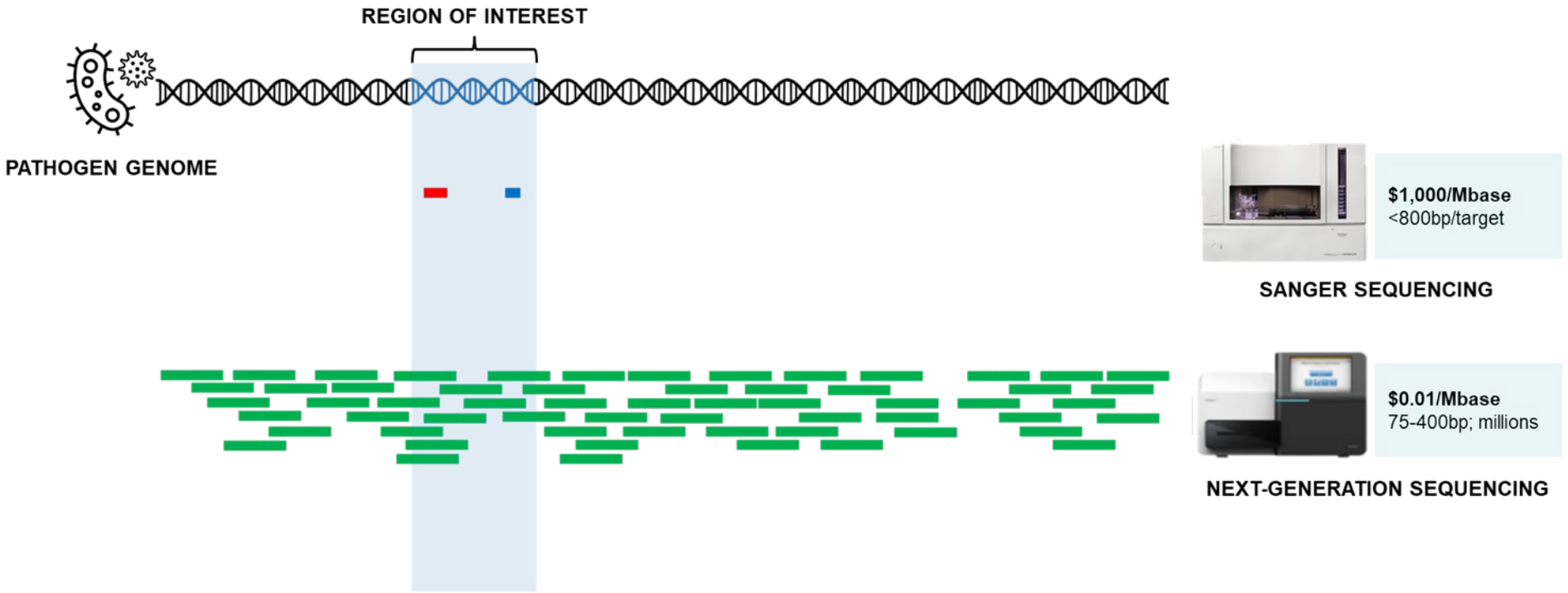


Bringing Focus to Microbial Pathogens



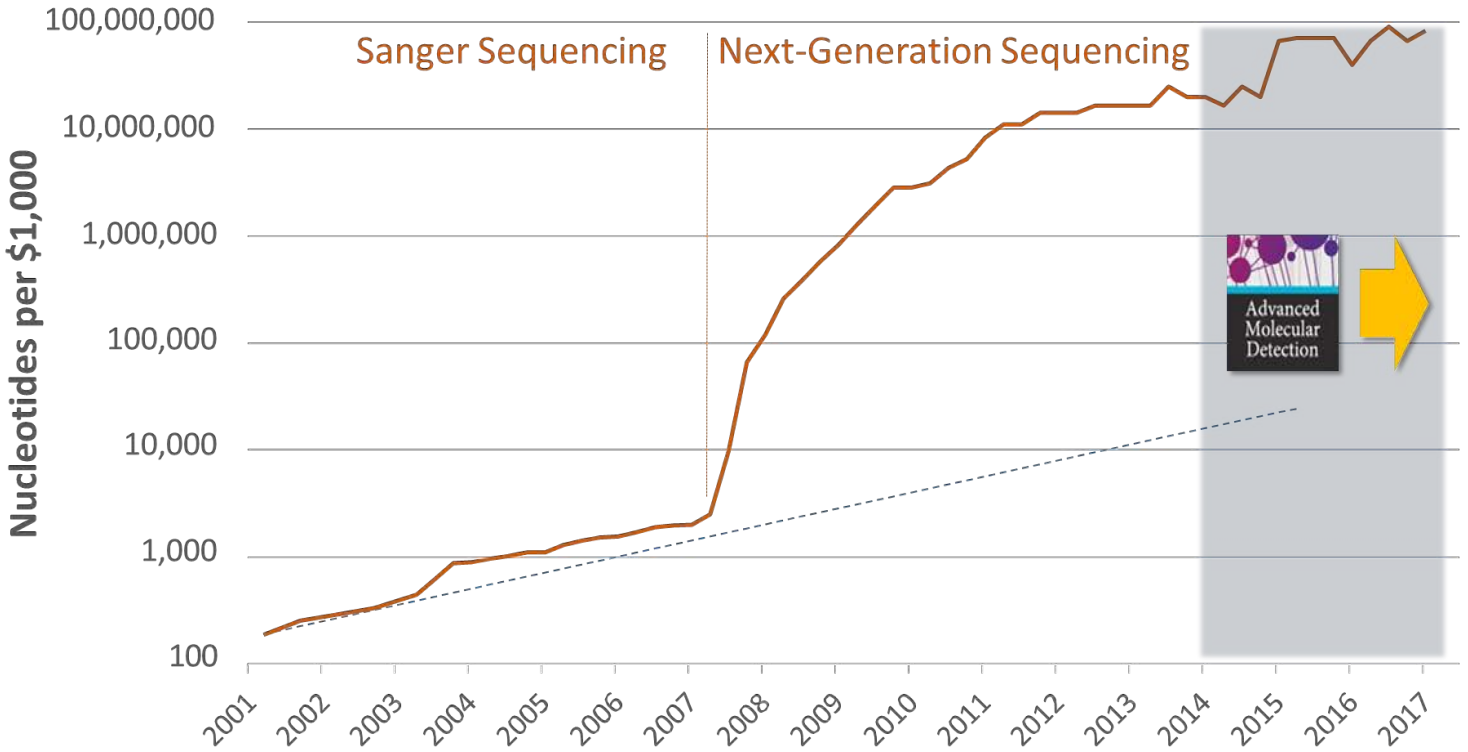
Images: Virus (Getty Images), E. coli (PHIL- CDC), Ebola (Getty Images), Mycobacterium tuberculosis (PHIL - CDC), Toxoplasma gondii (Getty), Fungi Penicillium (Getty)

Sequencing in Public Health



bp = base pair

The Deep Impact of Next Generation Sequencing



Adapted from NHGRI (https://www.genome.gov/sequencingcosts

Next Generation Sequencing Technologies

Short Read ("2nd Generation")

Illumina
MiSeq

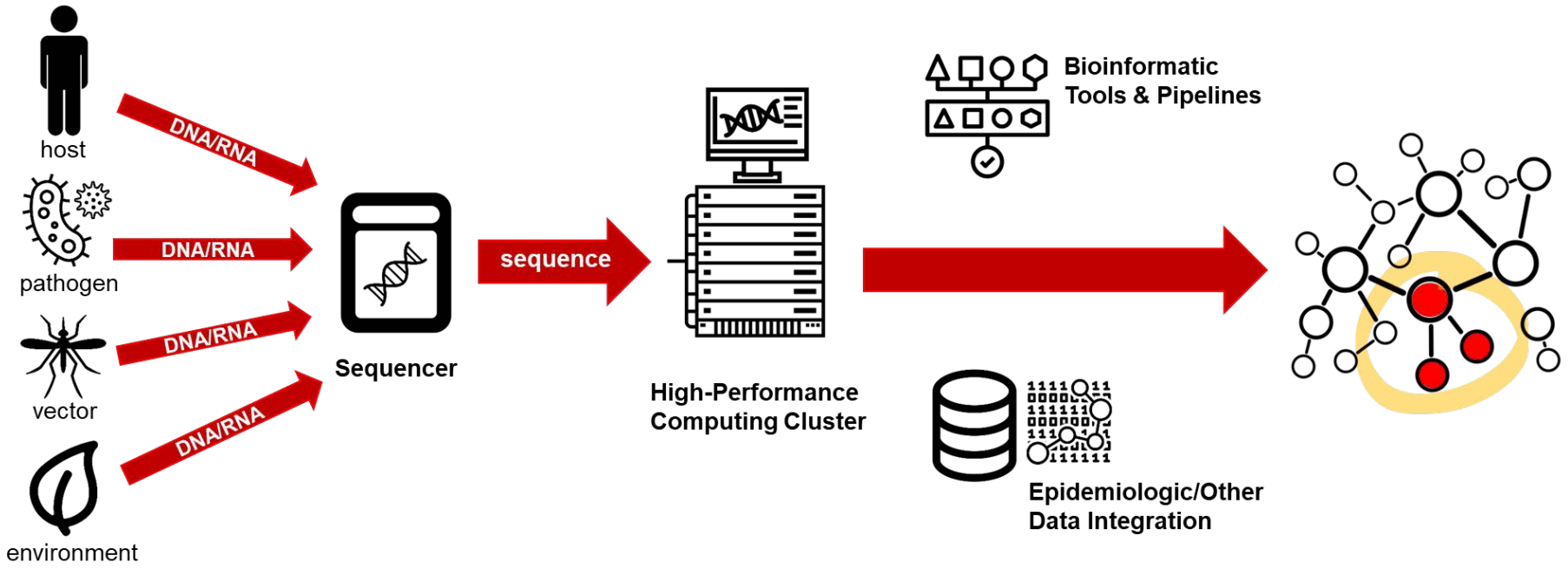
ThermoFisher
("IonTorrent")
Ion S5

Single Molecule, Long-Read
("3rd Generation")

PacBio
Sequel

Oxford Nanopore
MinION

How is NGS Used in Public Health?

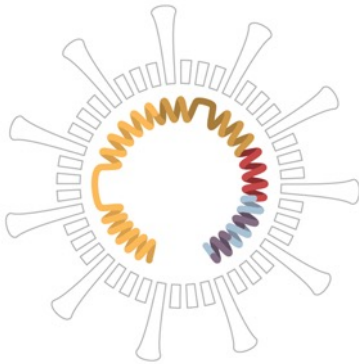


Armstrong G, et al. (2019)NEJM 381(26): 2569-2580.

Some Definitions

- **Strain**: a subdivision of a species
- **Phenotype**: an observable set of characteristics of an organism
- **Genotype**: the genetic makeup of an organism
- **Genome:** the entire set of genetic material of an organism
- **Genomics**: the study of genomes
- **Metagenomics**: the study of the ensemble of genomes from a mixture of organisms

Utility of Sequencing

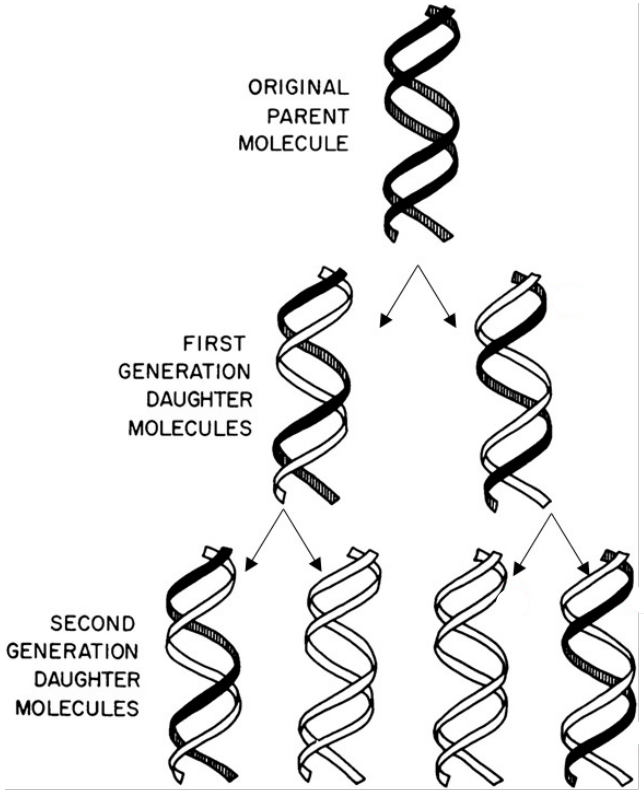


- Identification: a genomic "fingerprint"
- Comparison: of "fingerprints" to each other
  - ***Link*** pathogens with similar sequence
  - ***Sort*** pathogens into subgroups for epidemiologic analysis
- Function: biologically meaningful code that can be used to infer characteristics of an organism
- Universality: same methods for all microbial pathogens

Identification
(Genetic Information is Structured)

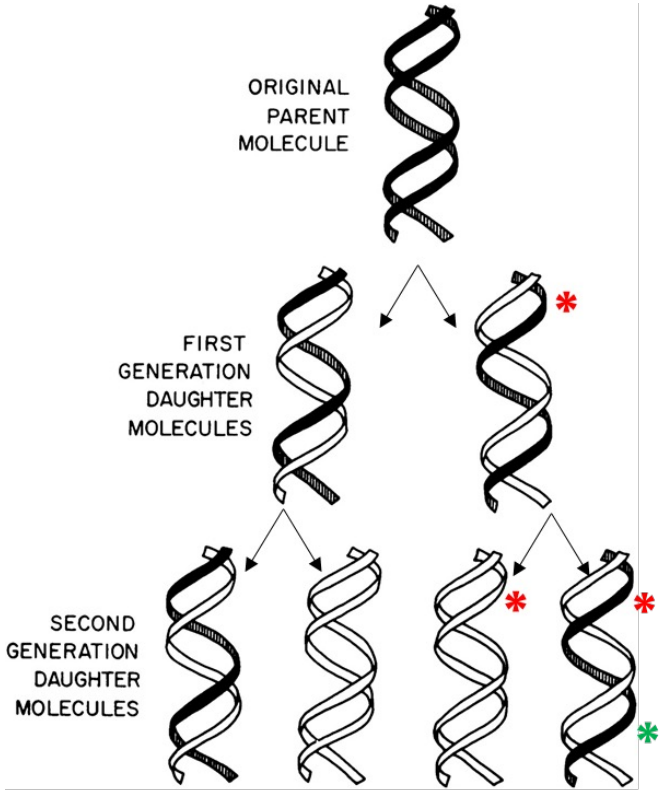
More Data ~ Higher Resolution

Linking and Sorting (Genetic Information is Propagated)



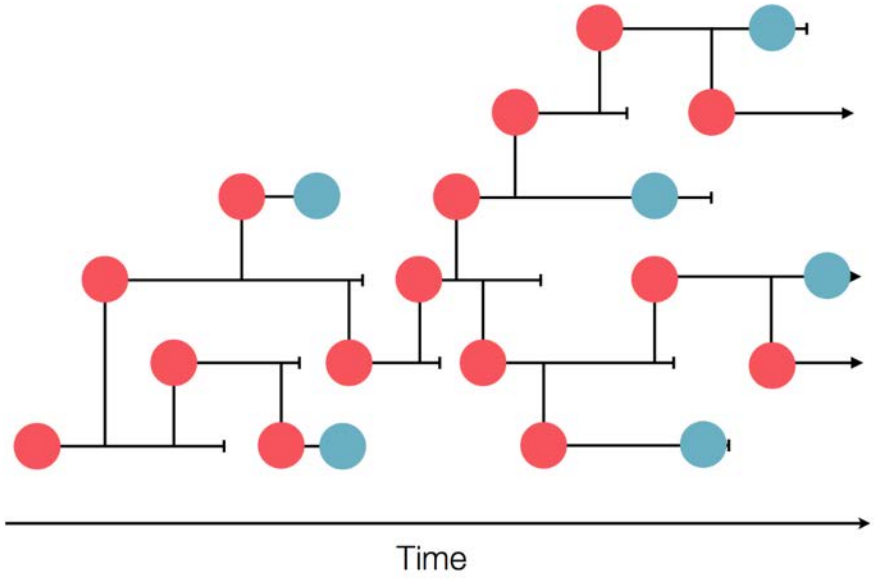
Adapted from M Meselson and FW Stahl (1958) PNAS 44(7).

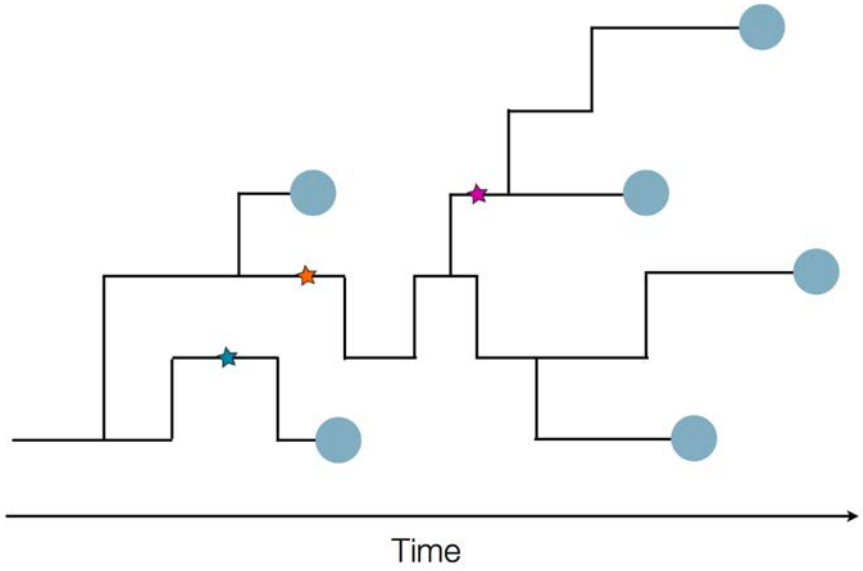
Genomes are imperfectly Copied as Microbes Replicate and Spread



Inferring Relationships

Pathogens mutate as they spread, providing a “fingerprint” that can be used to infer ancestral relationships among sampled individuals.





Images from Trevor Bedford Group: https://docs.nextstrain.org

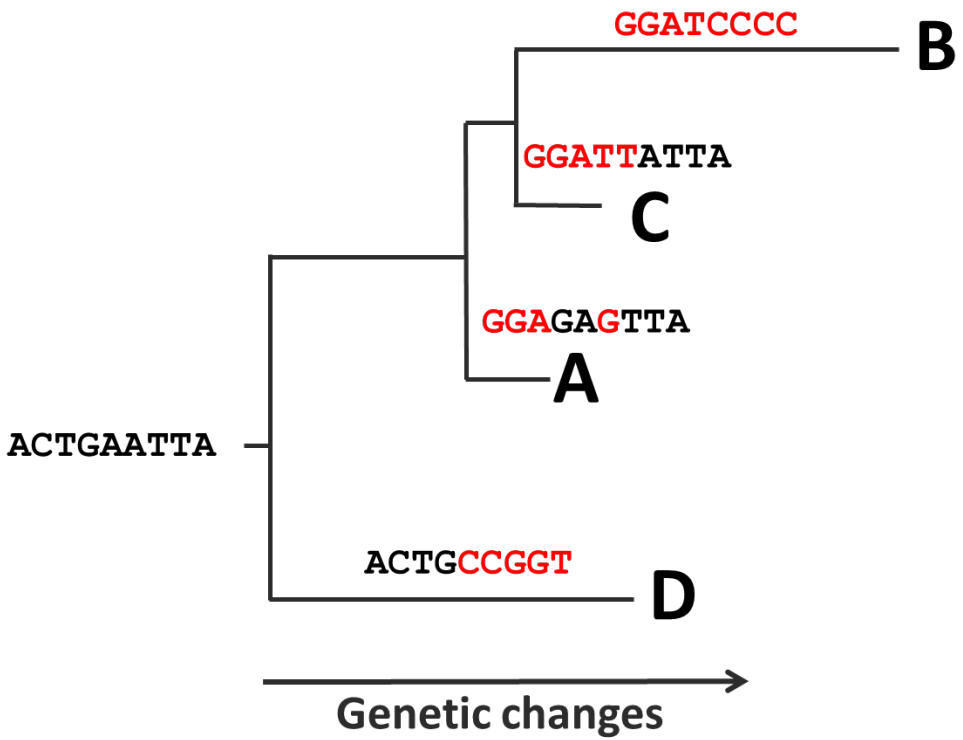
Sequences are Related Evolutionarily

Isolate	Fingerprint
Ancestor	**ACTGAATTA**
A	**GGAGAGTTA**
B	**GGATCCCCC**
C	**GGATTATTA**
D	**ACTGCCGGT**

www.cdc.gov/amd/training/covid-19-gen-epi-toolkit.html

Relationships are Shown by Phylogenetic Trees

Isolate	Fingerprint
Ancestor	ACTGAATTA
A	GGAGAGTTA
B	GGATCCCCC
C	GGATTATTA
D	ACTGCCGGT



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Phylogenetic Trees Reveal Groupings

Isolate	Fingerprint
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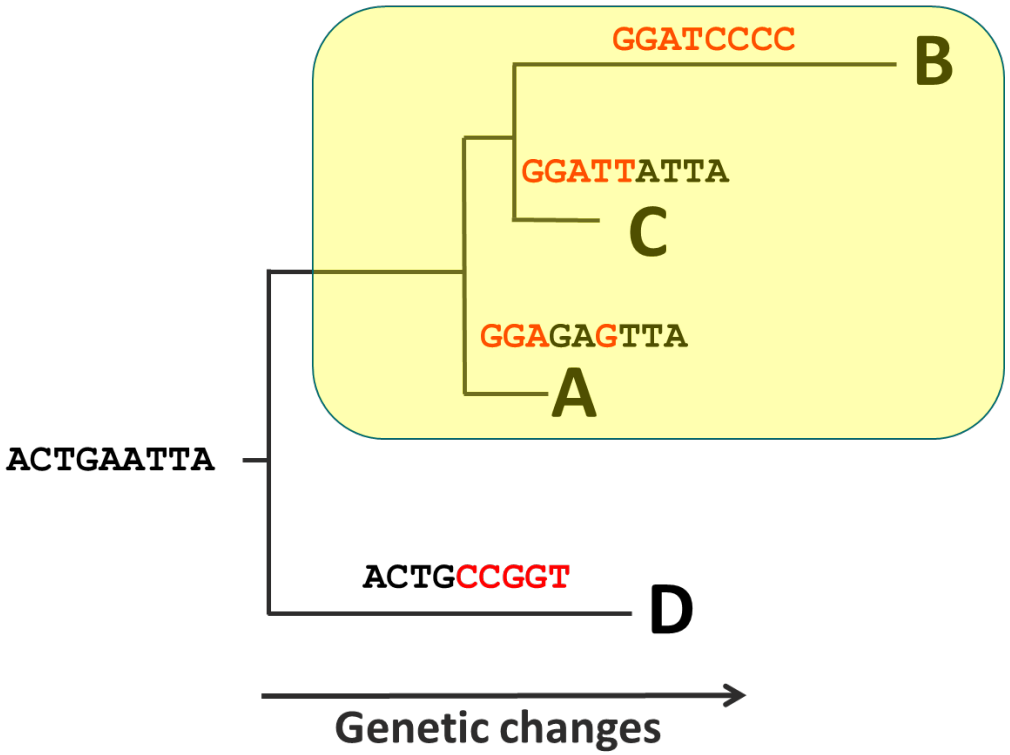
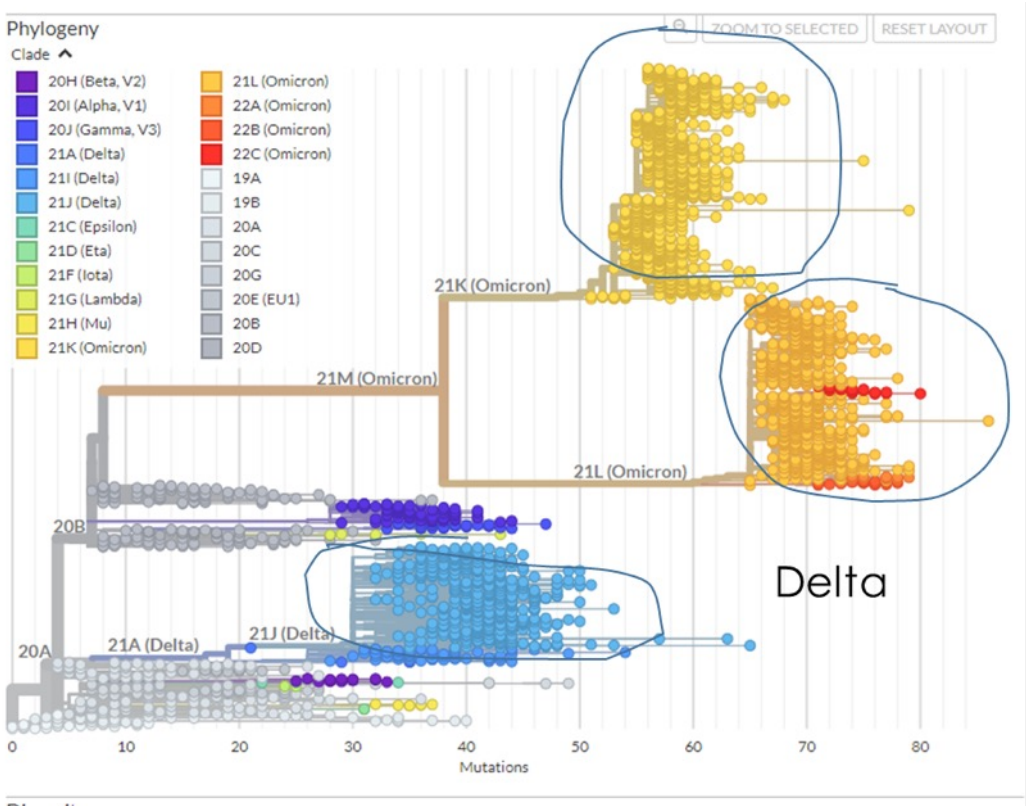


www.cdc.gov/amd/training/covid-19-gen-epi-toolkit.html

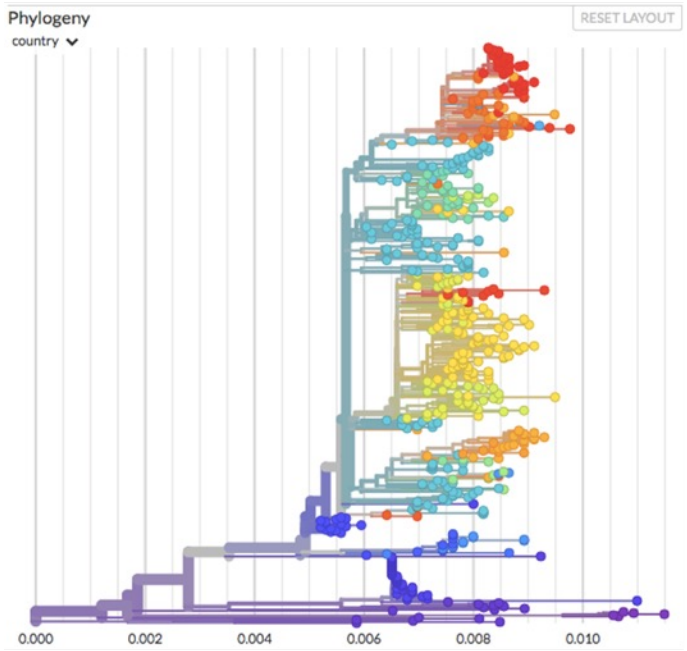
Sorting and Categorizing



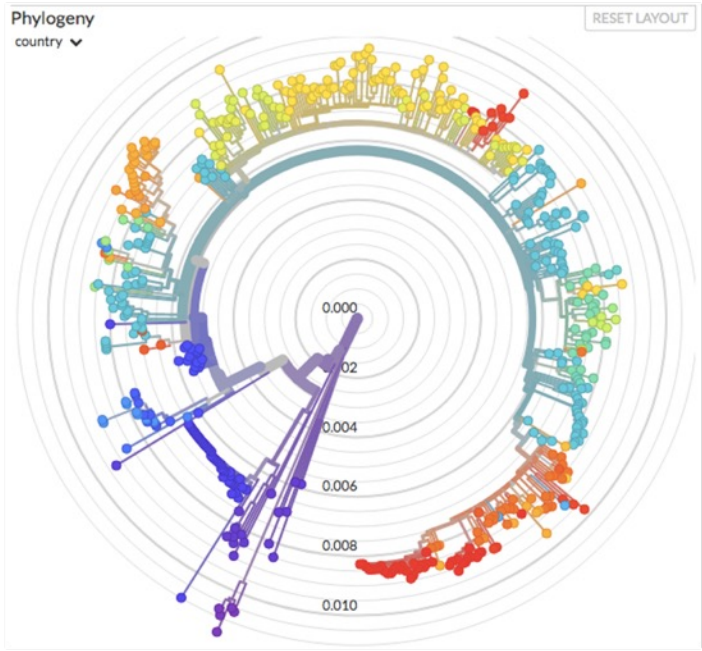
Omicron

Source: nextstrain.org

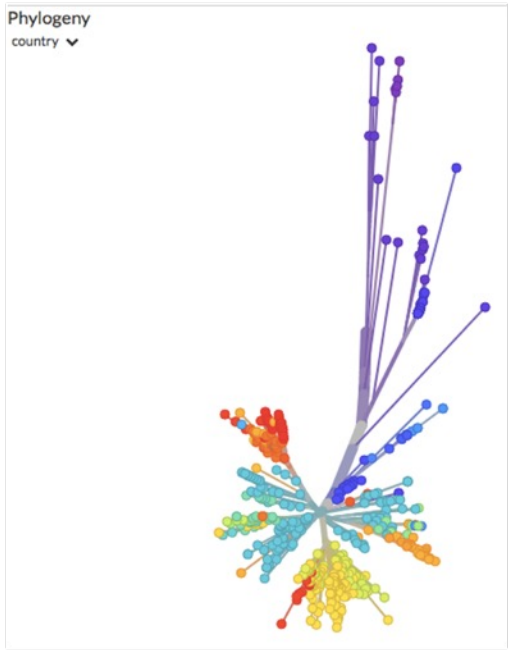
Same Tree, Different Representations



Rectangular Rooted trees
(when outgroup is known)



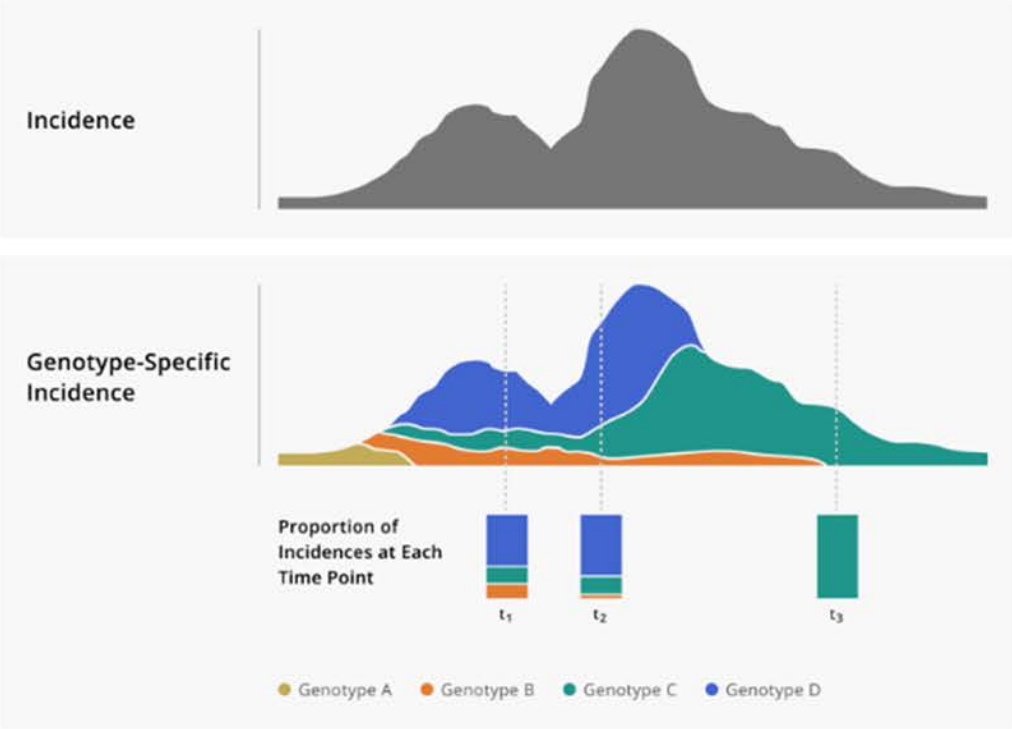
Radial Rooted trees
(when outgroup is known)

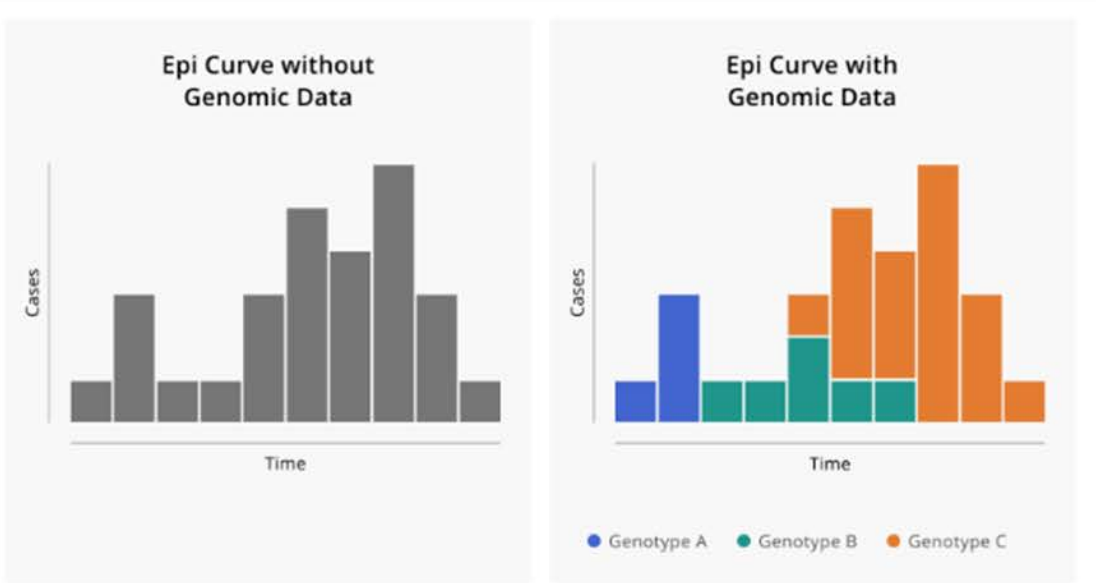


Unrooted tree
(direction of evolution unknown)

Adapted from Nathan Grubaugh Source: nextstrain.org

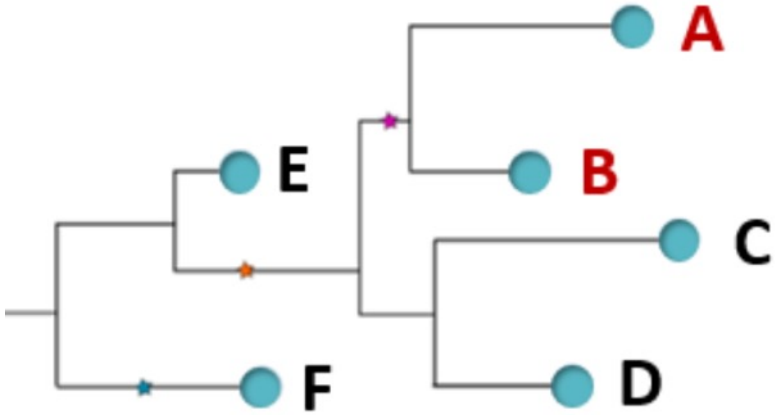
Increased Granularity

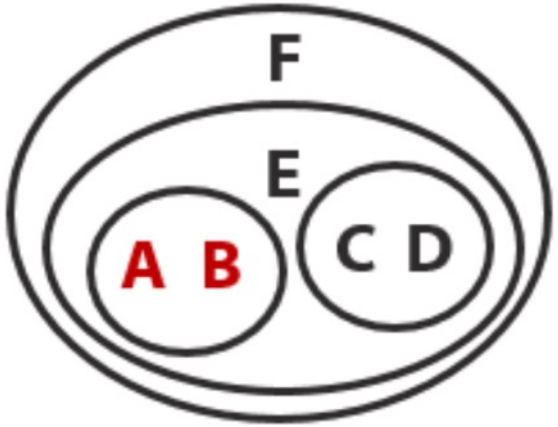




https://alliblk.github.io/genepi-book

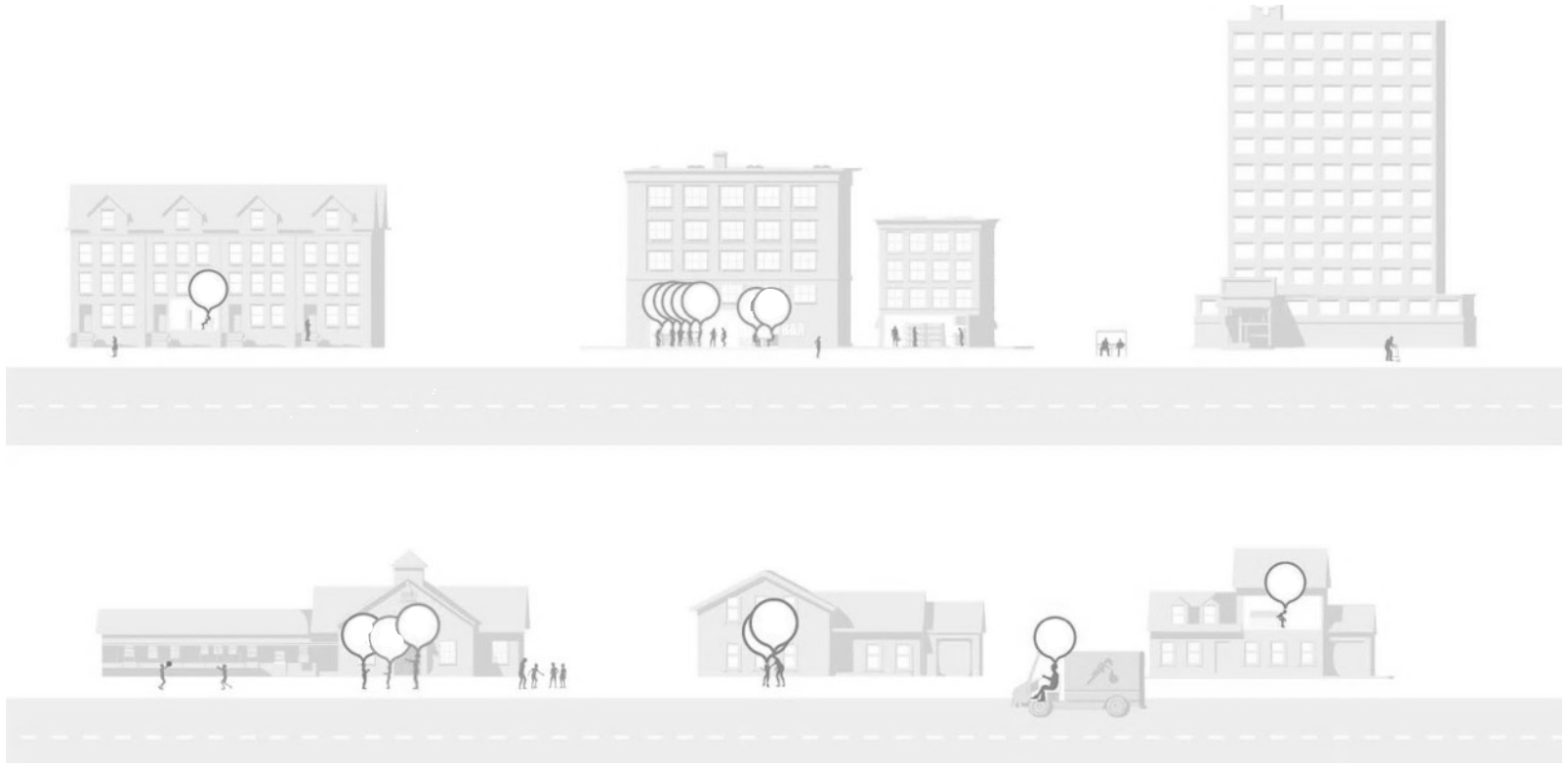
Strains that are Phylogenetically Closer are More Likely to Share an Epidemiological Link





Images from Trevor Bedford Group: https://docs.nextstrain.org

Linking: Host-only View



Adapted from The Washington Post article: https://www.washingtonpost.com/graphics/2020/health/coronavirus-genetic-code/

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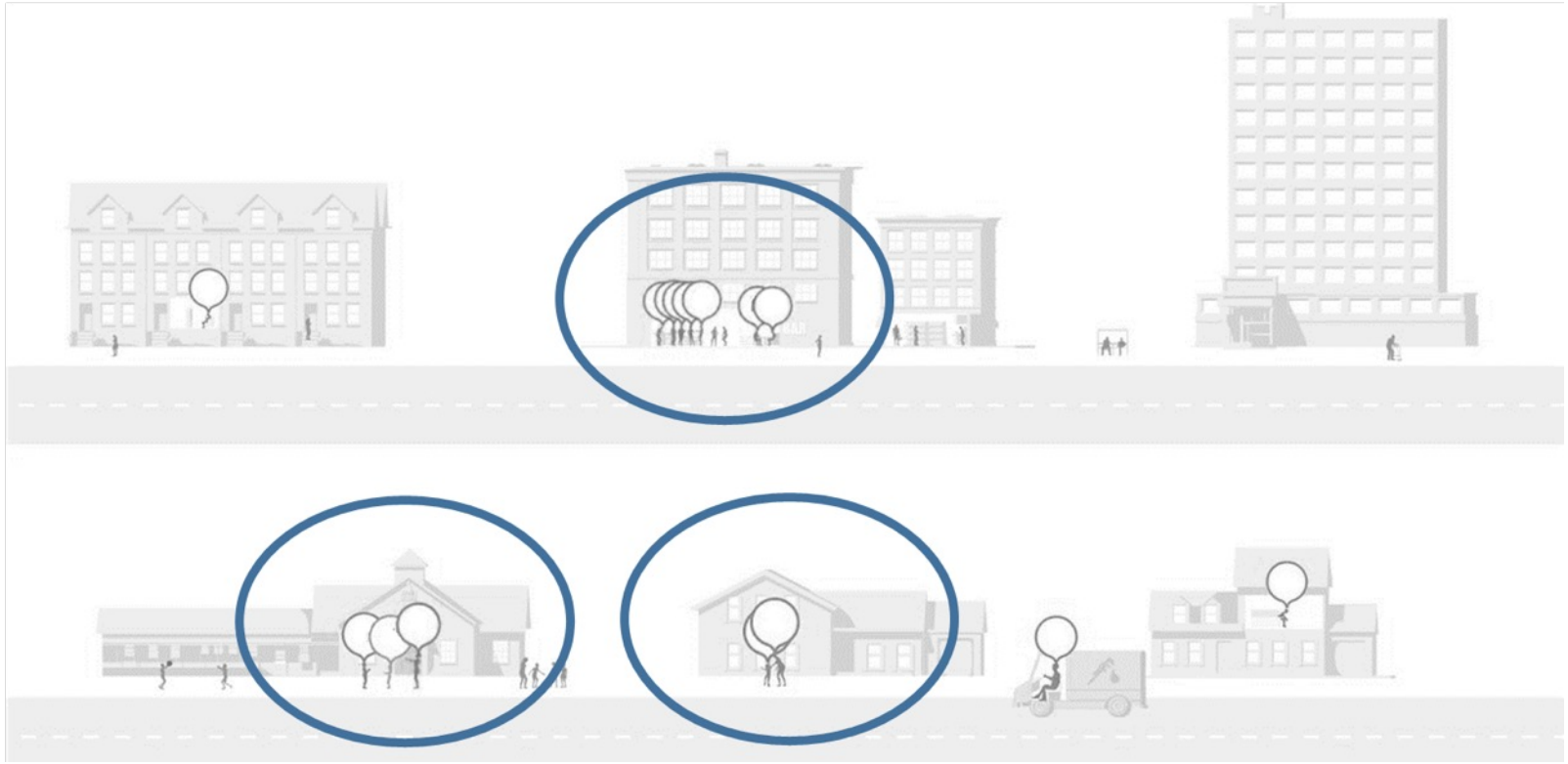

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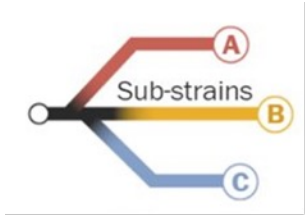
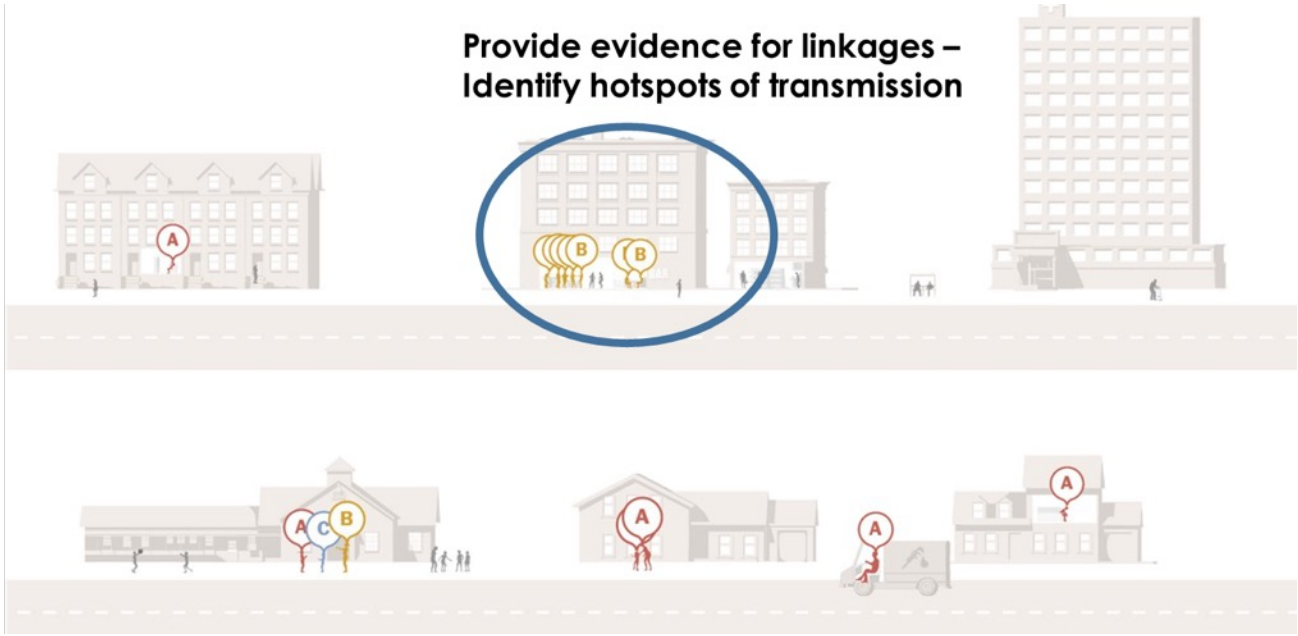
Linking: Host + Pathogen View





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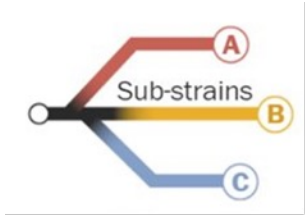
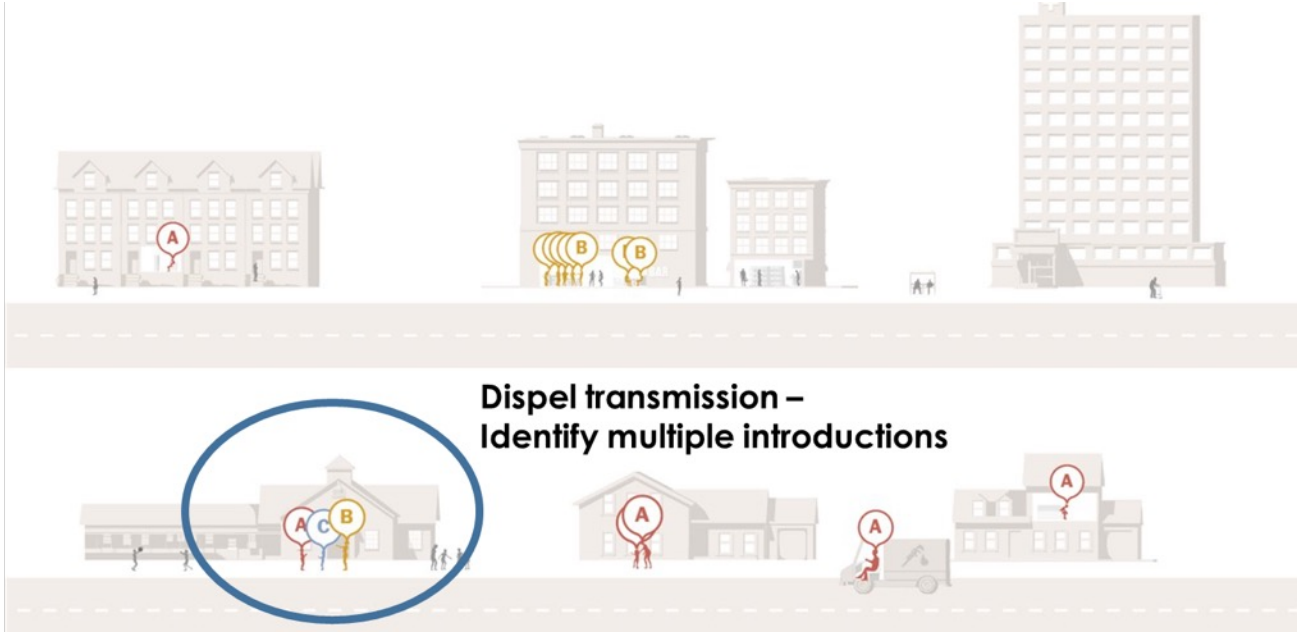
Linking: Host + Pathogen View





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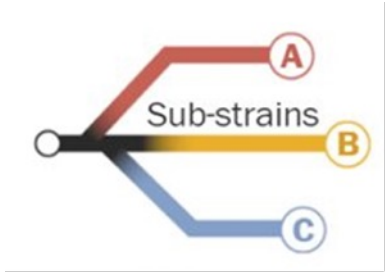
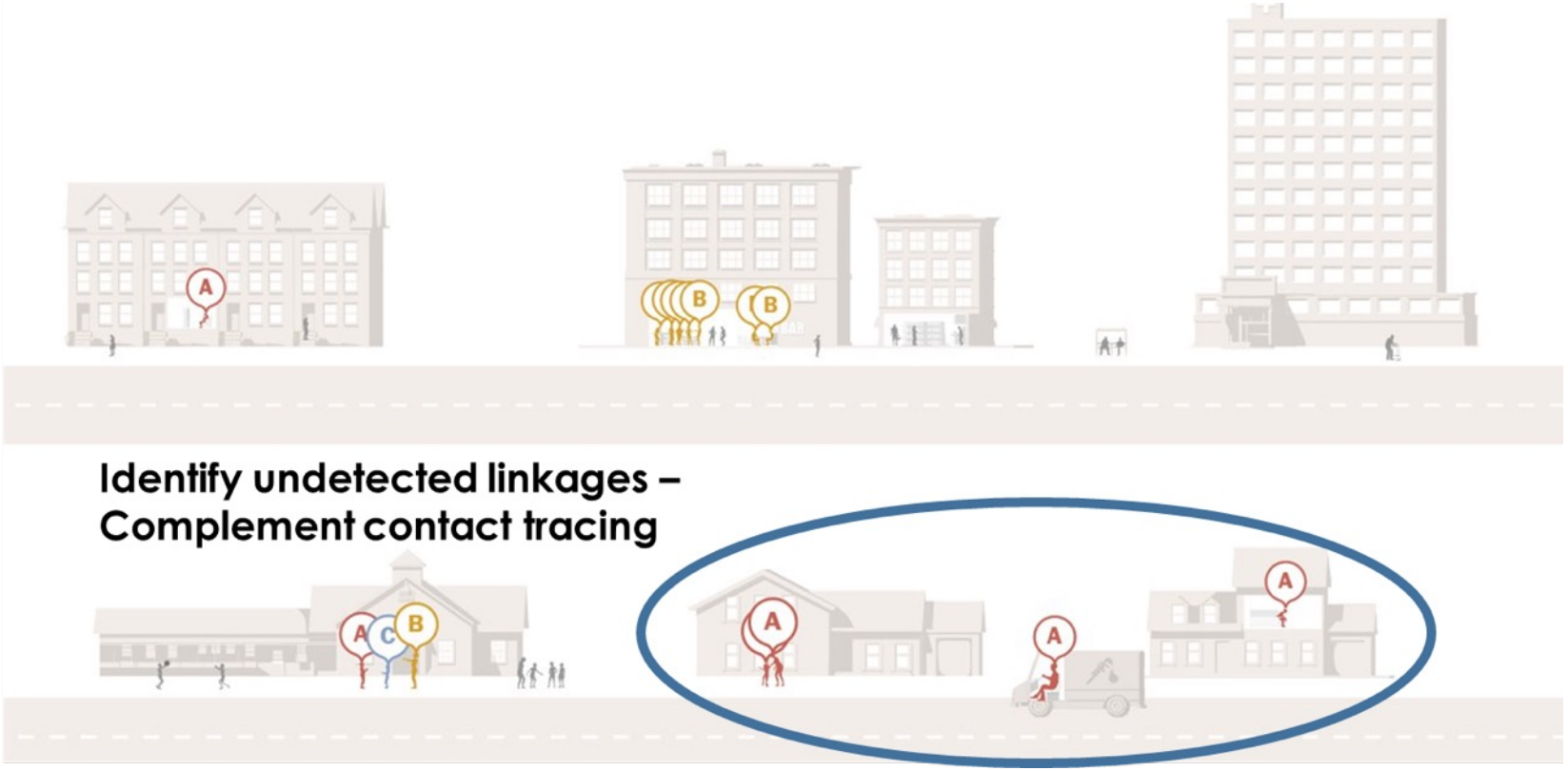
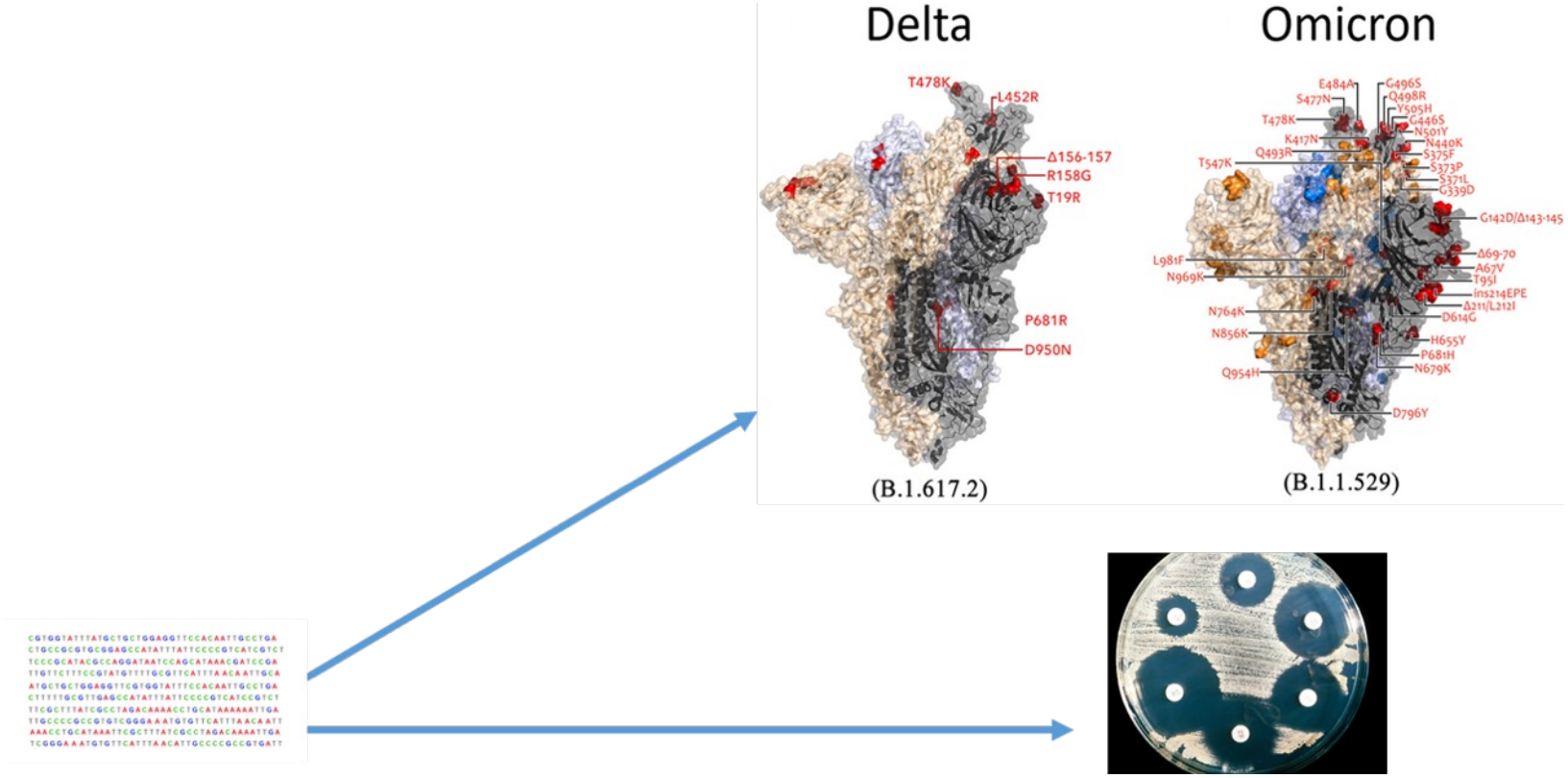
Linking: Host + Pathogen View





Decoding
(Genetic Information is a Biological Code)

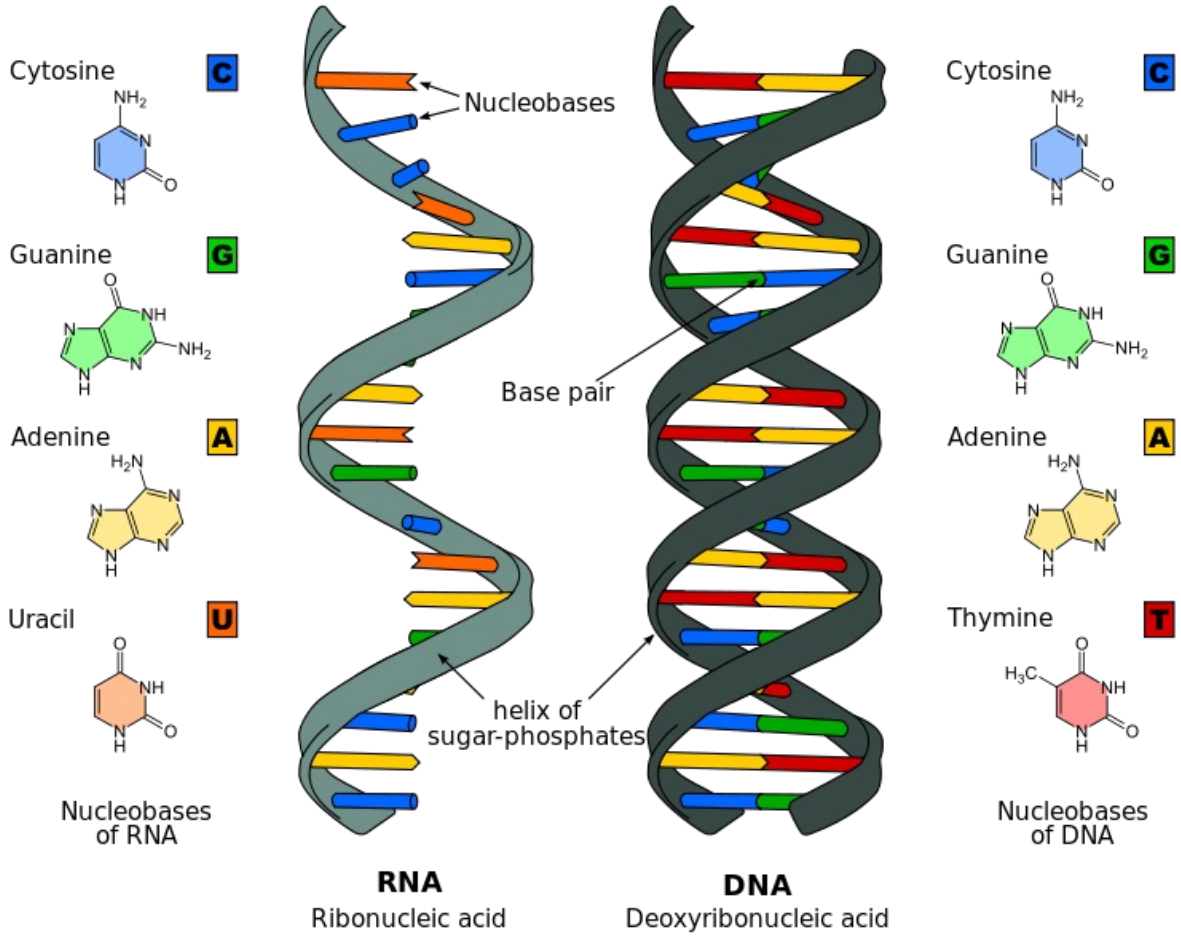


Kumar S, et al. (2021) J Med Virol, doi: 10.1002:mv.27526

Phenotypes Inferred from Genotype

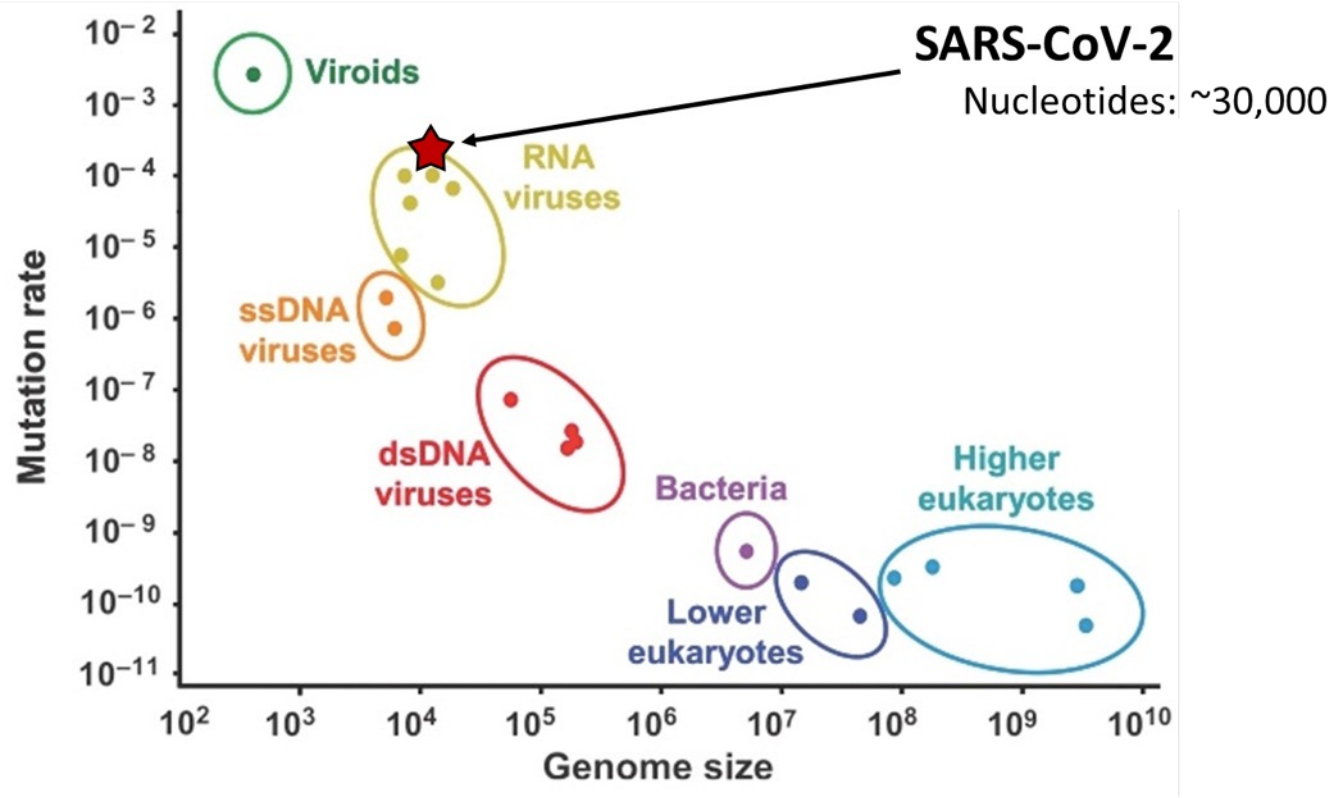
- Bacteria
  - Antibiotic resistance (many examples)
  - Serotype, serogroup (e.g., pneumococcus, meningococcus, *E. coli, Salmonella)*
  - Virulence factors (e.g., STEC)
- Viruses
  - Serotype, antigen type (e.g., influenza, enteroviruses)
  - Antiviral resistance (e.g., oseltamivir resistance in influenza, HIV resistance)
- Eukaryotic pathogens
  - Species (blood pathogens)
  - Resistance (malaria)

Universality: Nucleotides are the Building Blocks of Genomes



"Chemical structures of nucleases" by Roland1952 licensed under CC by 3.0

Variations in Genome Size

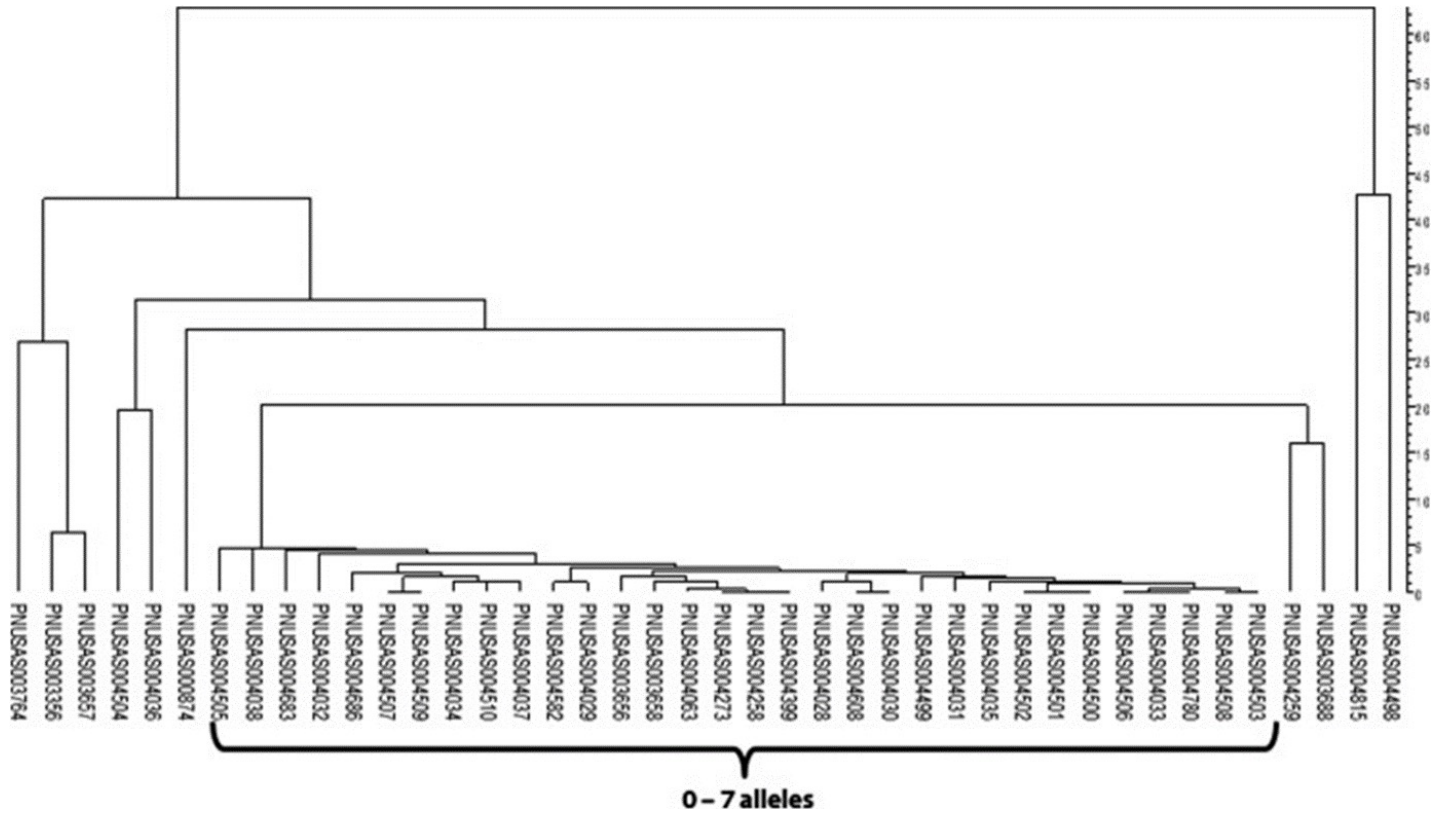


Analyzing Different Types of Data Together

- Pathogen genetic relatedness

- Source type (human, food, animal, environment, etc.)
- Time
- Place
- Social Contact
- Clinical Features
- Many more possibilities…

Closely Related Isolates



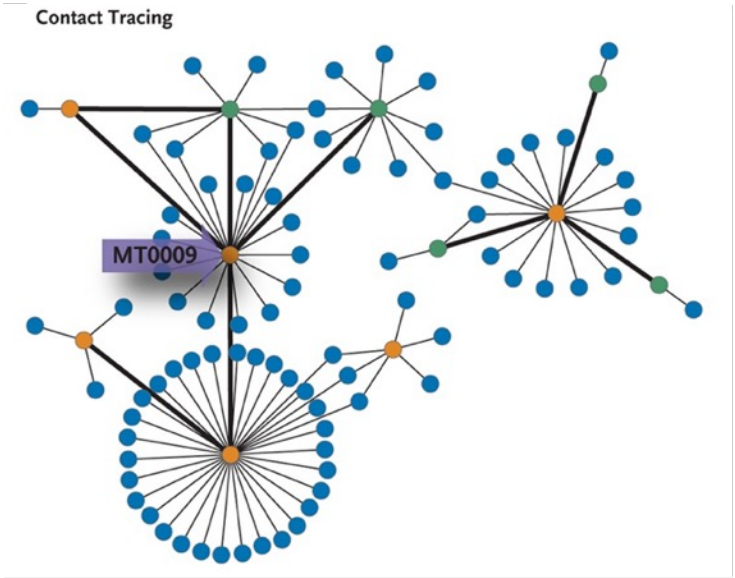
Brown E , et al. (2019) 16 (7)441-450.

Genomic Data + Source Type

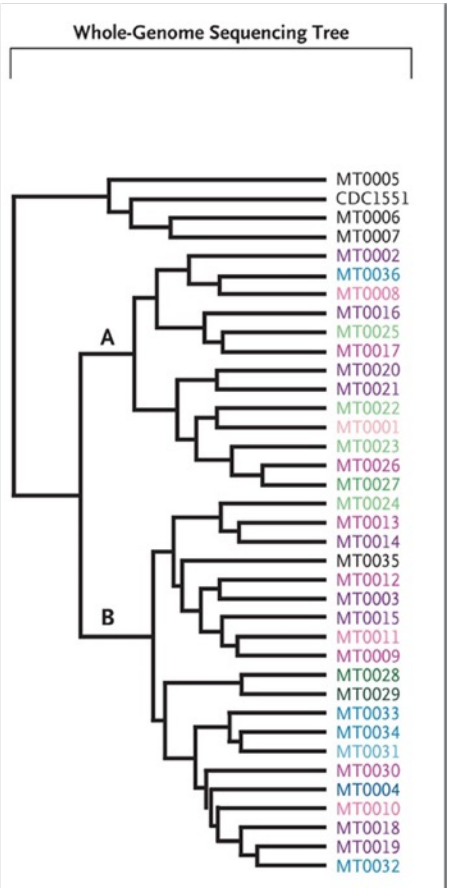
Stevens EL, et al. (2022) J Food Prot. 1; 85(5).

Multiple Streams of Information

Host



Pathogen



Adapted from Gardy JL, et al. (2011) NEJM 364(8):730-9.

Key Question

Where is transmission occurring?

SARS-CoV-2: Where is Transmission Occurring?

- Outbreaks in multiple congregate settings in Minnesota March-June, 2020
- Long-term care facilities, meat-packing plant
- Hypothesis 1
  - Transmission among cases is primarily occurring in the congregate setting
  - Expected sequencing result: SARS-CoV-2 genomes from most cases in the congregate setting are *closely related, supporting a single introduction*

- Hypothesis 2
  - Cases are exposed to SARS-CoV-2 in the community, outside the congregate setting
  - Expected sequencing result: SARS-CoV-2 genomes from most cases in the congregate setting are *distantly related, supporting multiple introductions*

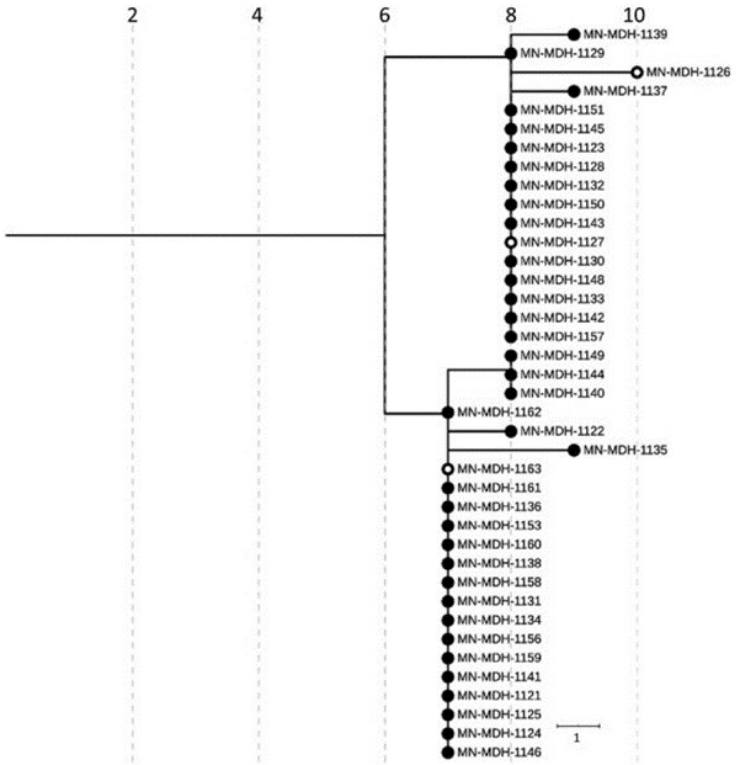
- Implications: focus of prevention efforts

www.cdc.gov/amd/training/covid-19-gen-epi-toolkit.html

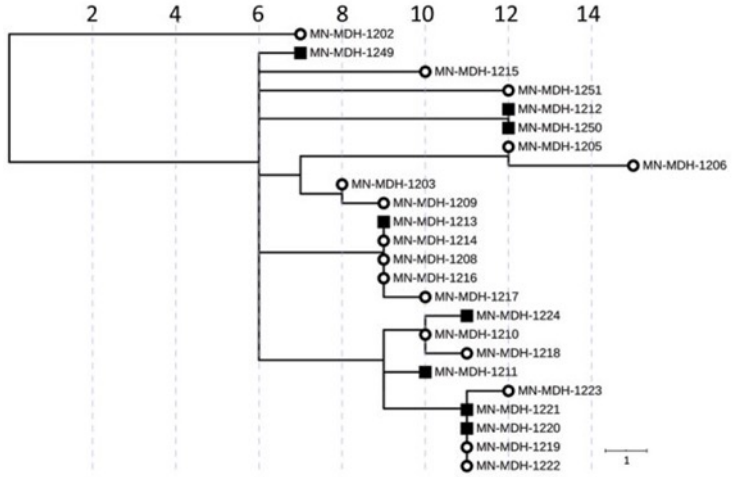
Adapted from The Washington Post article: https://www.washingtonpost.com/graphics/2020/health/coronavirus-genetic-code/

Different Patterns in Different Facility Types

Long-term Care Facility



Meat-packing Plant



Lehnertz NB, et al. (2021) Emerg Infect Dis. 27(8):2052-2063.

Different Patterns in Different Facility Types

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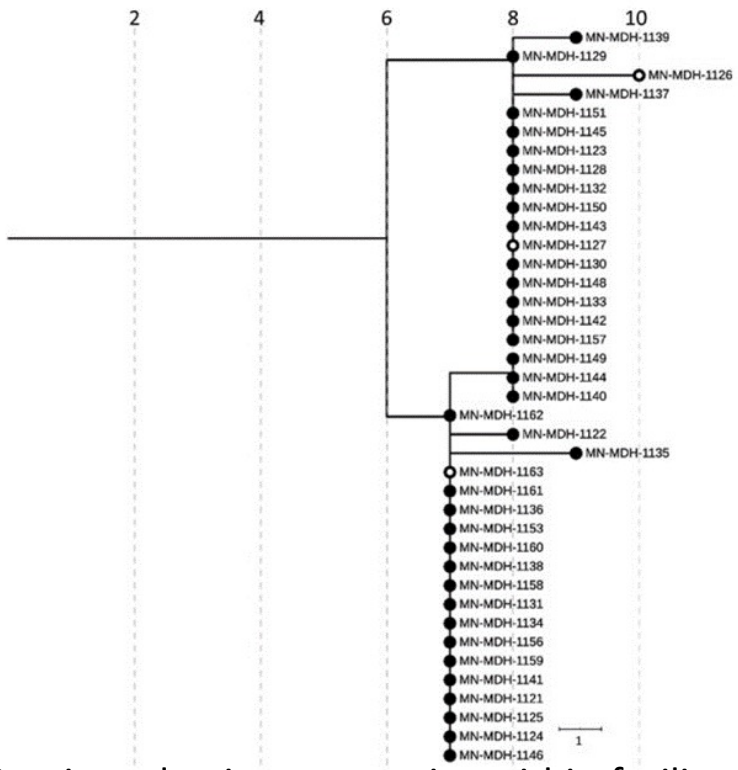

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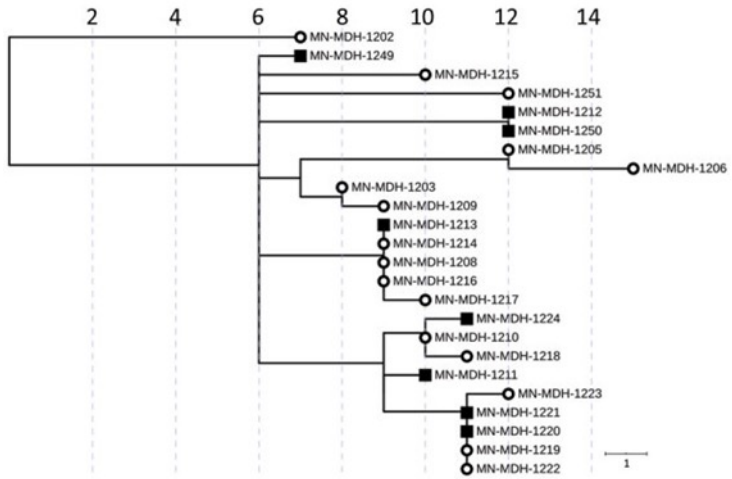
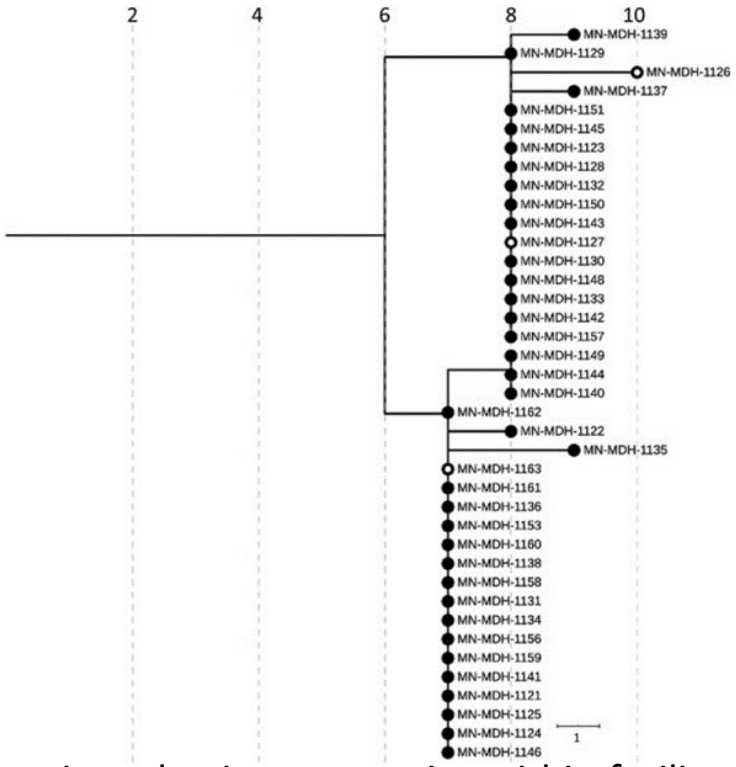


- Few introductions, extensive within-facility transmission
- Prevention target: Infection-control practices

Lehnertz NB, et al. (2021) Emerg Infect Dis. 27(8):2052-2063.

Different Patterns in Different Facility Types

Long-term Care Facility



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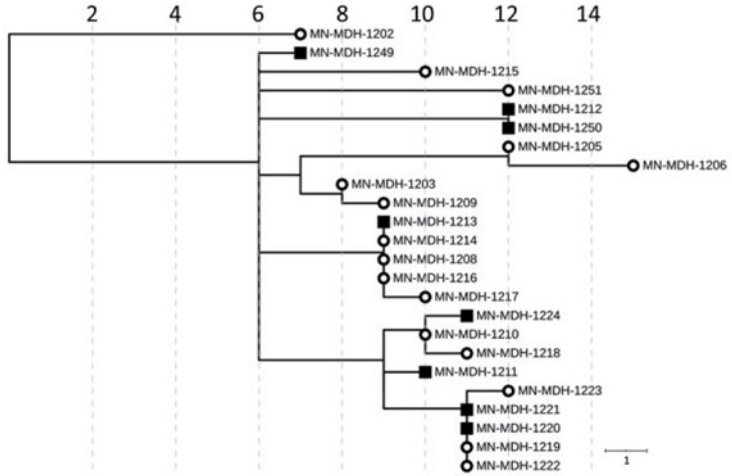
Meat-packing Plant



- Multiple introductions, limited within-facility transmission
- Prevention target: community transmission

Lehnertz NB, et al. (2021) Emerg Infect Dis. 27(8):2052-2063.

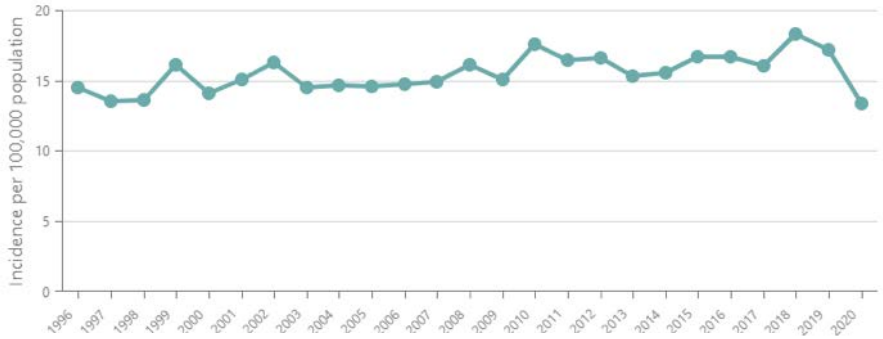
Foodborne Illnesses

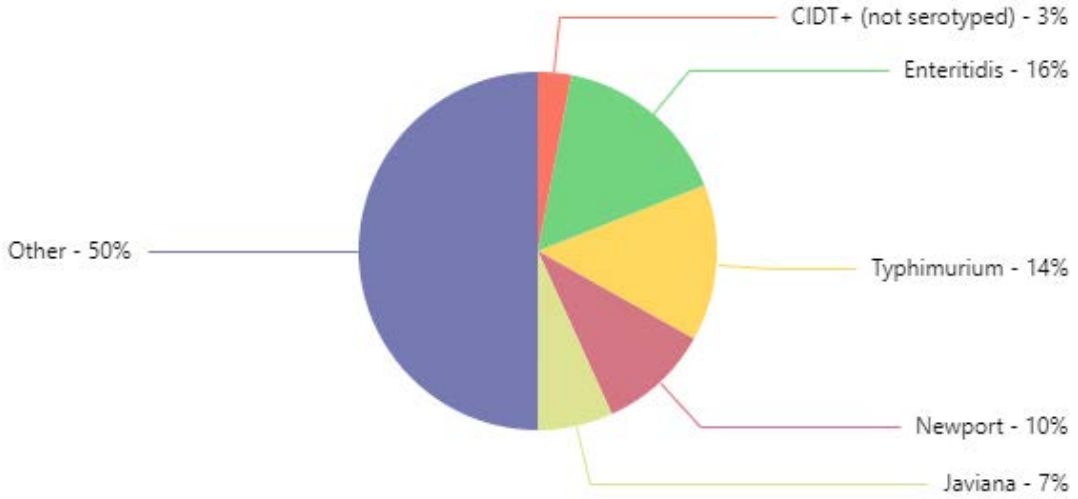
CDC estimates that each year 48 million people get sick from a foodborne illness, 128,000 are hospitalized, and 3,000 die.

https://www.cdc.gov/foodsafety/foodborne-germs.html

Foodborne Illness

Salmonella Infections by Year; 1996-2022





PulseNet surveillance

PFGE WGS

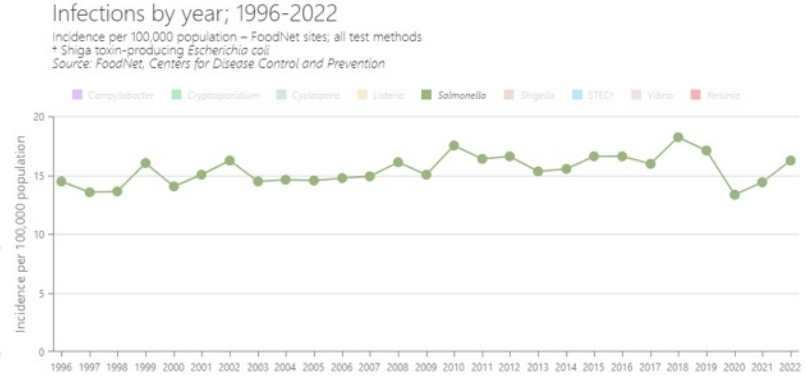
Pulsed-Field Gel Electrophoresis || Whole Genome Sequencing

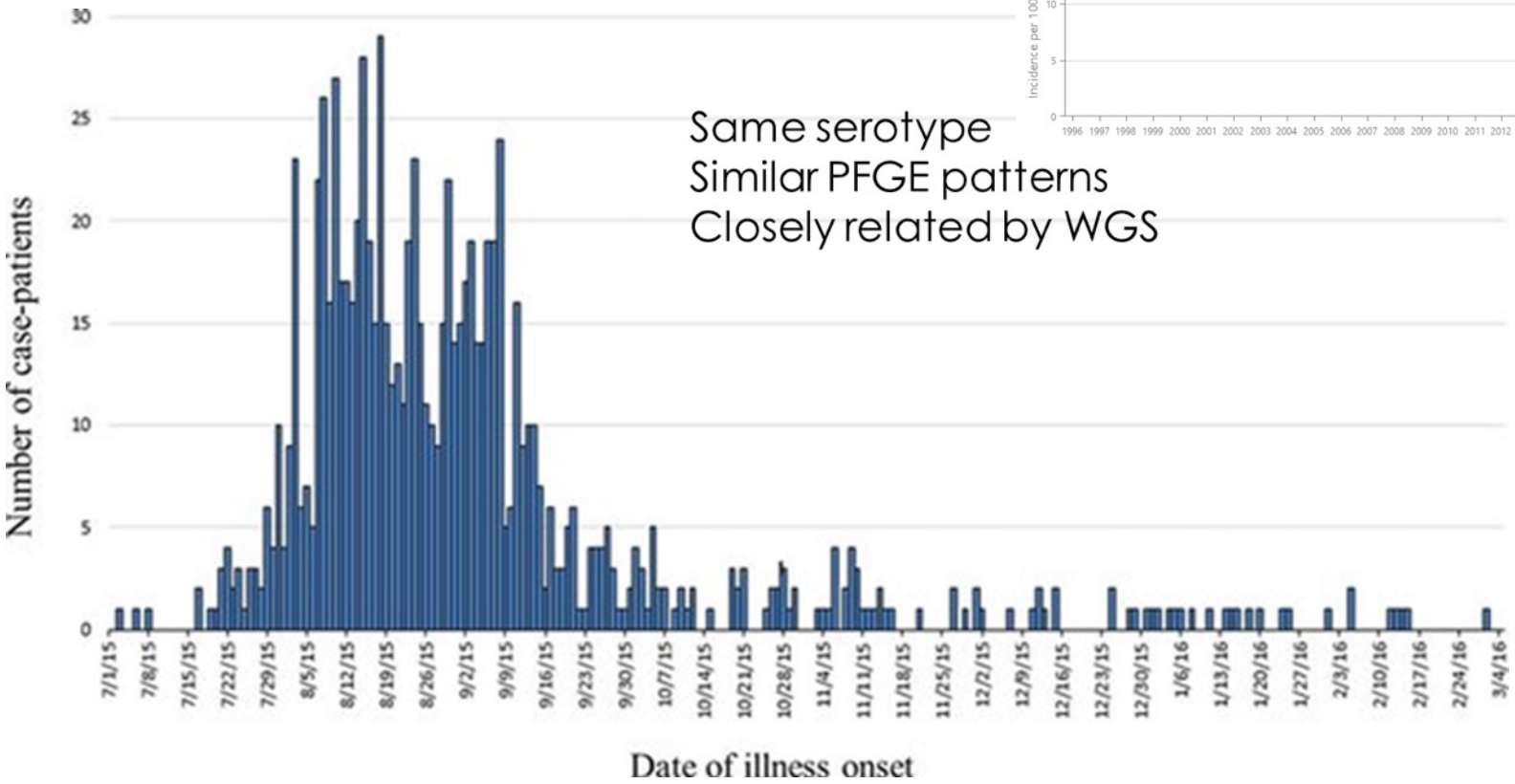
Adapted from https://www.cdc.gov/foodnet/index.html

Key Question

Is there an outbreak?

An Outbreak: *Salmonella* Poona (Genomic Data + Time)

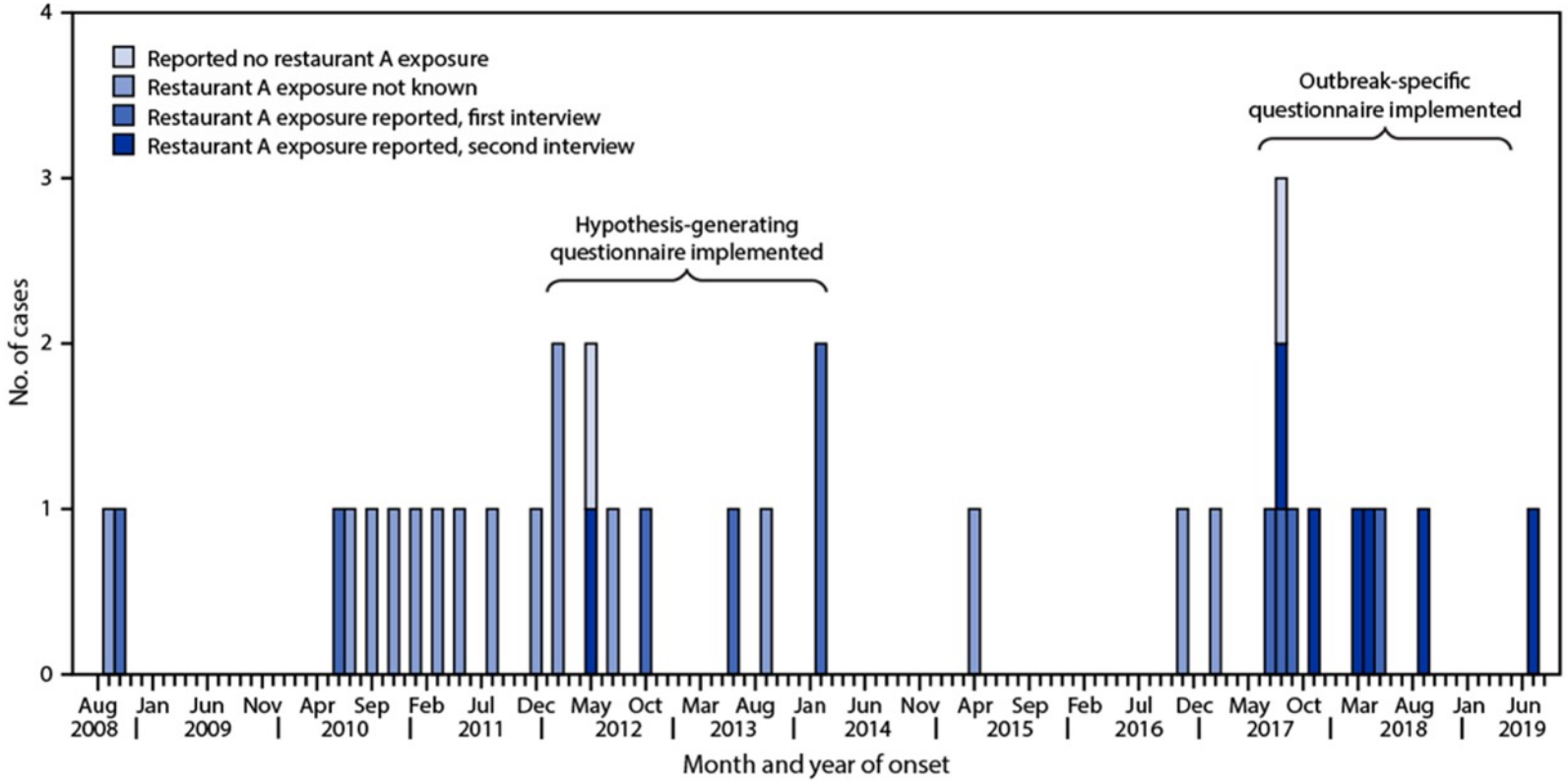




Same serotype
Similar PFGE patterns
Closely related by WGS

Laughlin M, et al. (2019) Epidemiology and Infection. 147, e270, 1-6.

Also an Outbreak: *Salmonella* Mbandaka (Genomic Data+ Time)



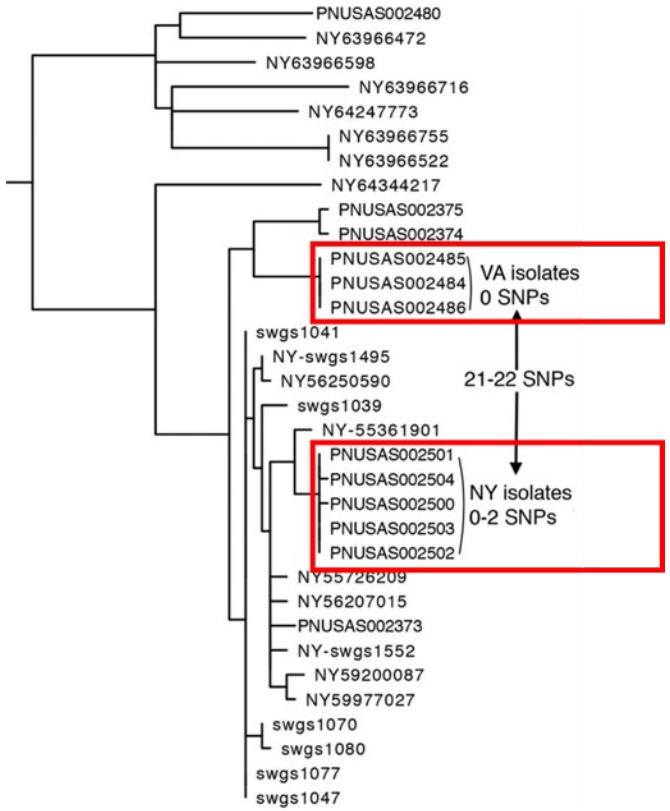
Nettleton WD, et al. (2021) MMWR 70(33): 1109-1113.

One Outbreak or Two?

Concurrent *Salmonella* Enteritidis outbreaks
at correctional facilities in Virginia and New York

Two Separate Outbreaks

Concurrent *Salmonella* Enteritidis outbreaks
at correctional facilities in Virginia and New York

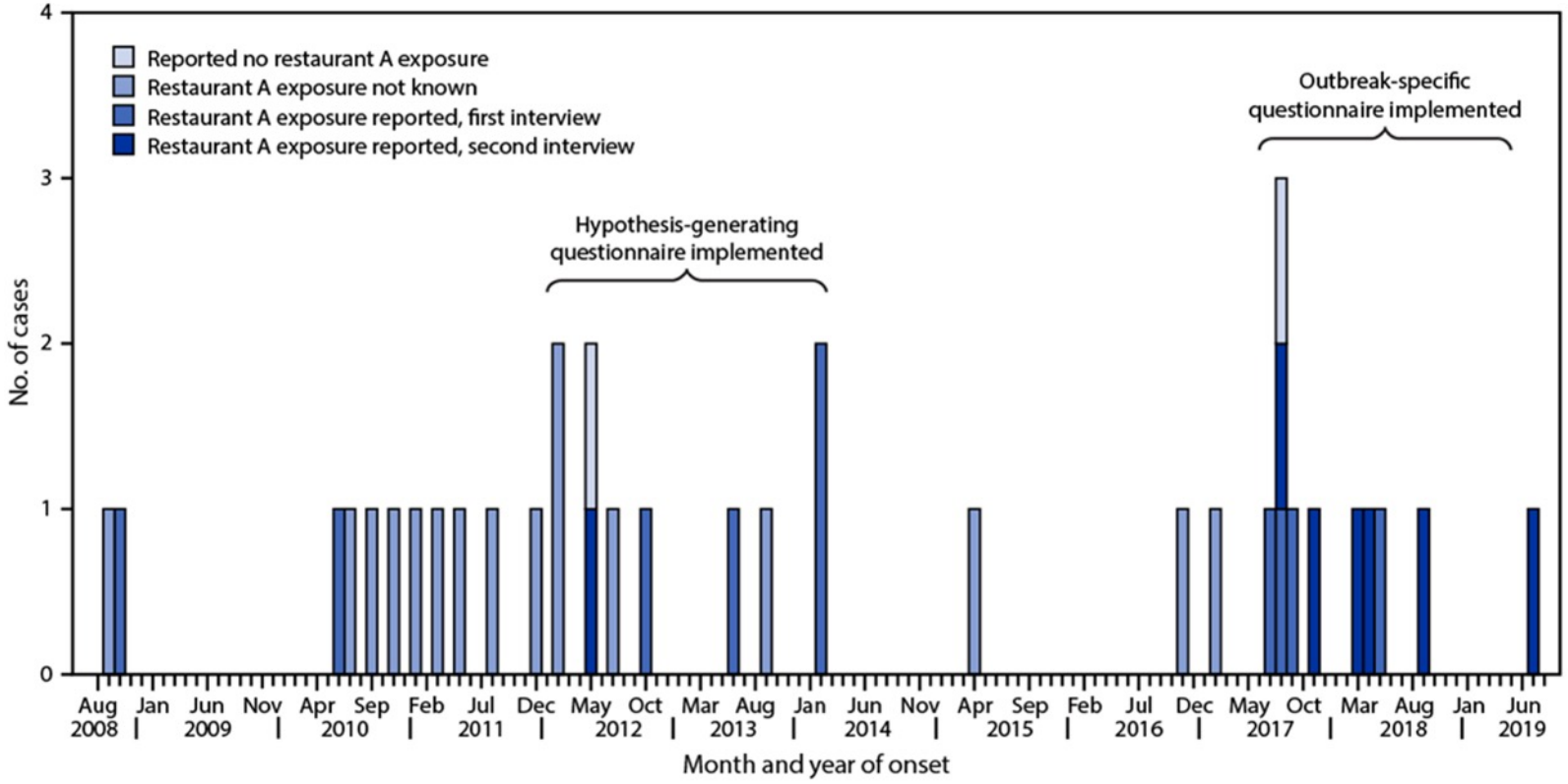


Kubota KA, et al. (2019) Public Health Rep; Nov/Dec 2019; 134(2_supple):22S-28S.

Key Question

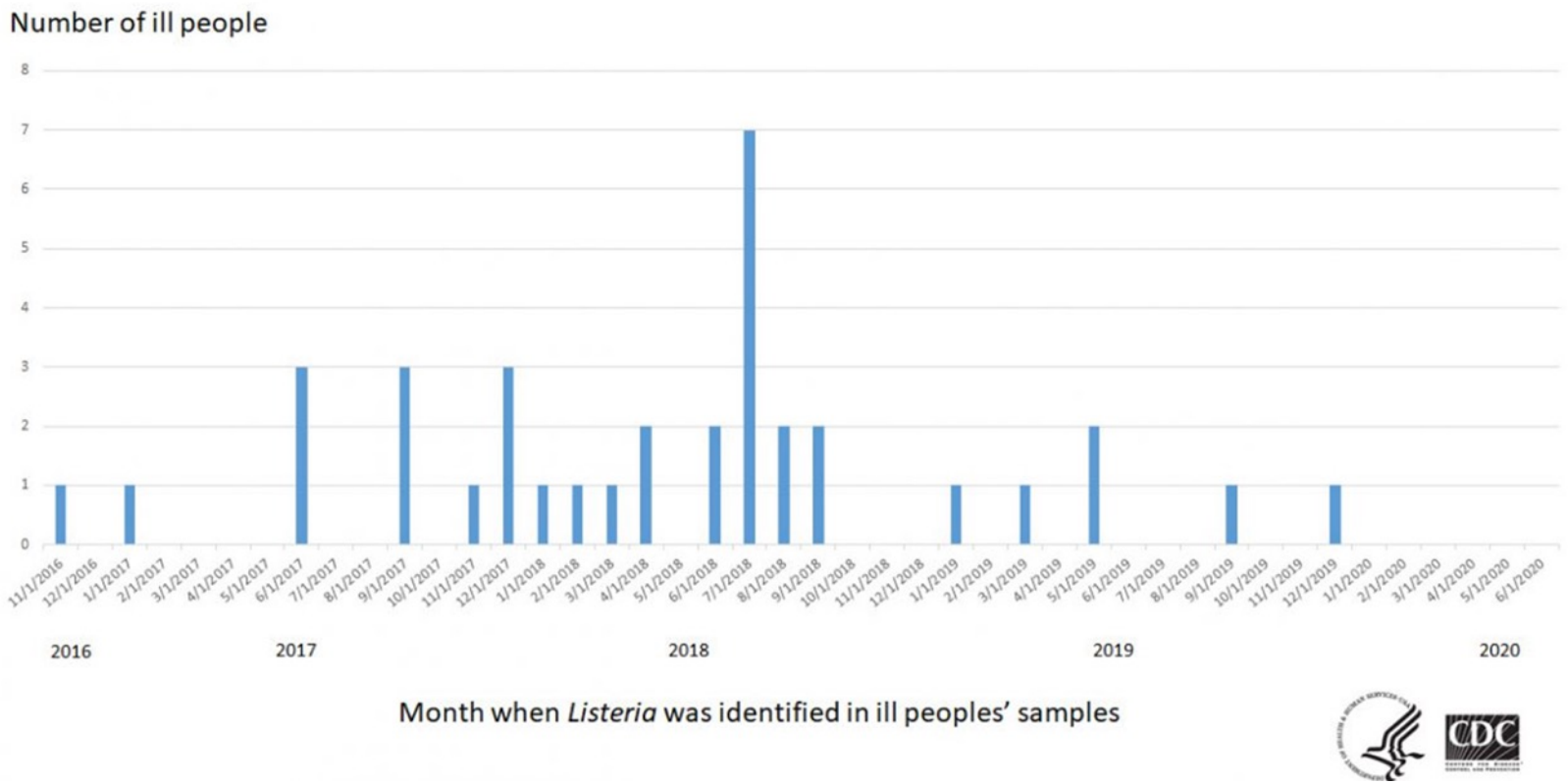
What is the source of infection?

Also an Outbreak: *Salmonella* Mbandaka (Genomic Data+ Time)



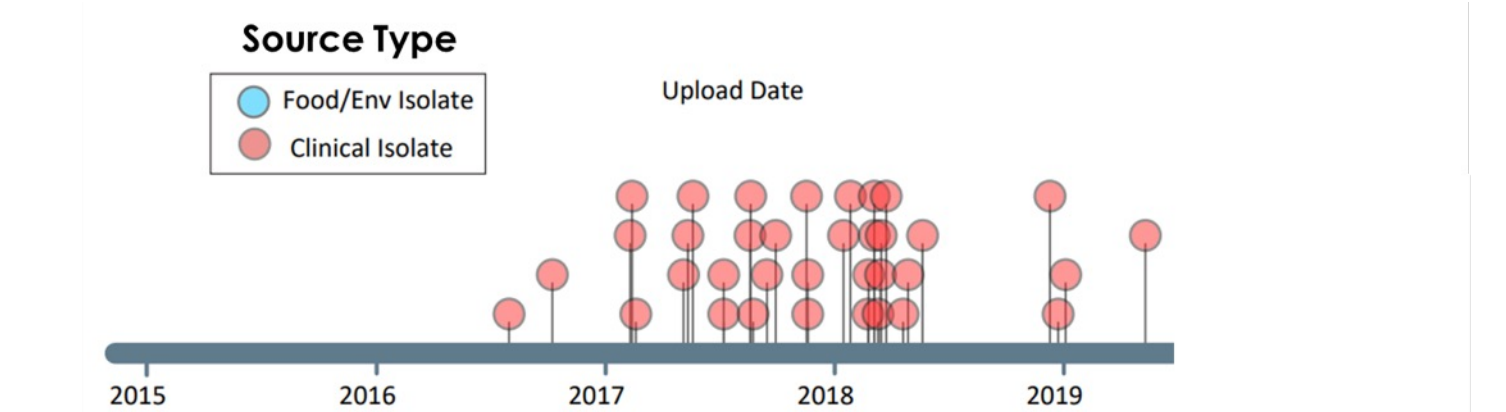
Nettleton WD, et al. (2021) MMWR 70(33): 1109-1113.

Solving a *Listeria* Outbreak with Global Data



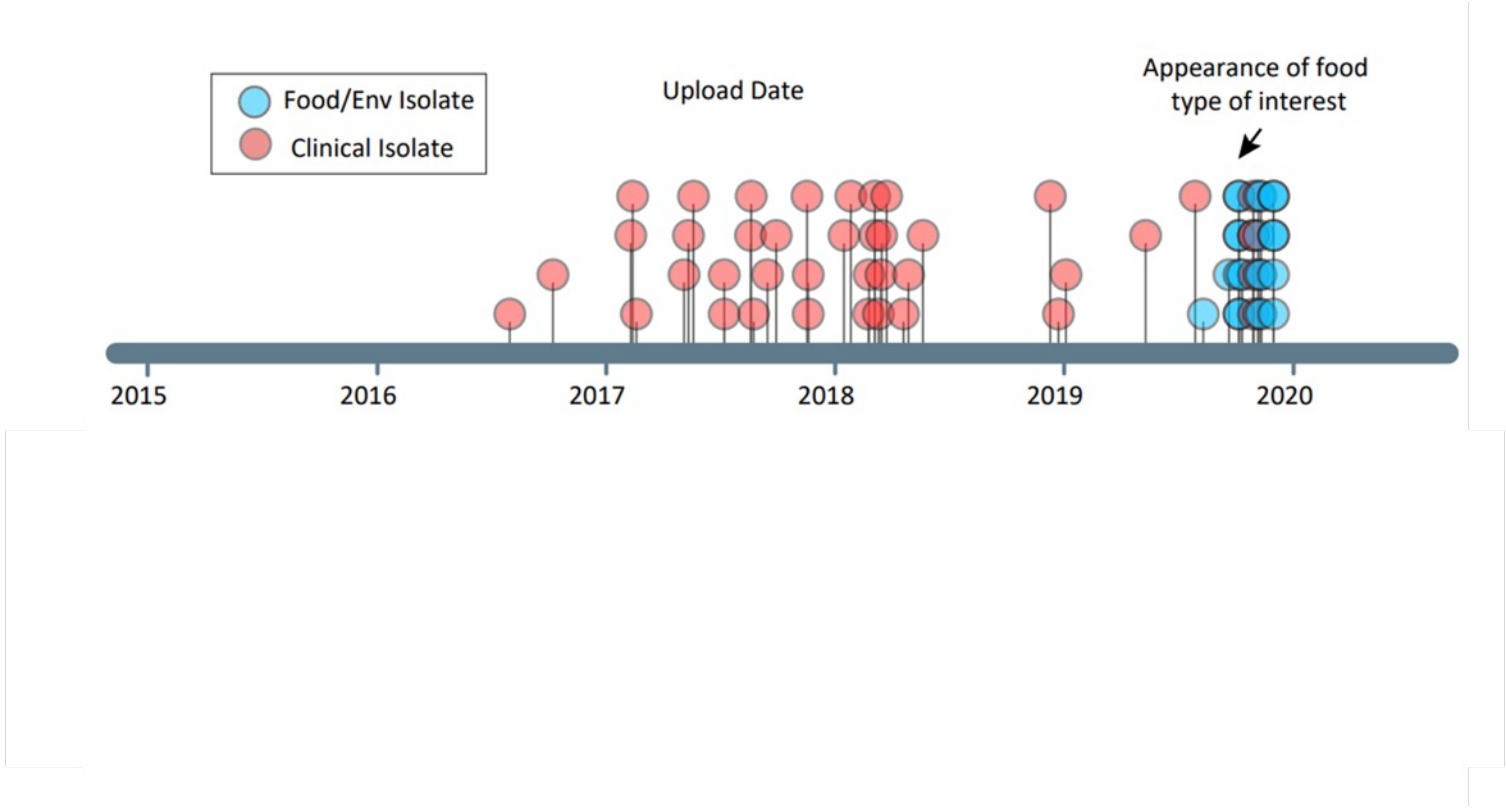
Source: https://www.cdc.gov/listeria/outbreaks/enoki-mushrooms-03-20/epi.html

Genomic Database: Source Type + Place



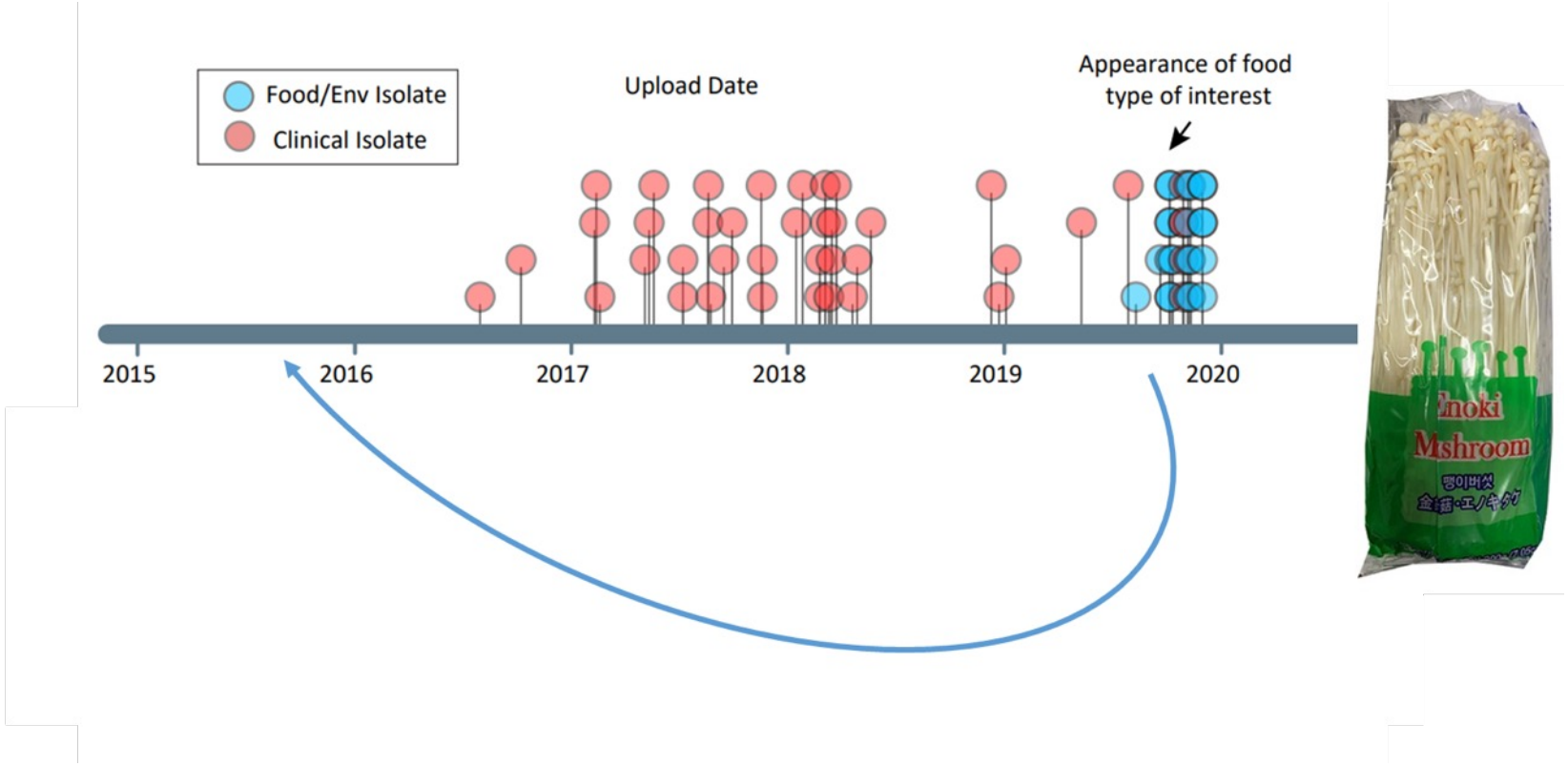
Adapted from Pettengill JB, et al. (2020) *The Lancet Microbe*; 1(6):E233-E234.

Genomic Database: Source Type + Place



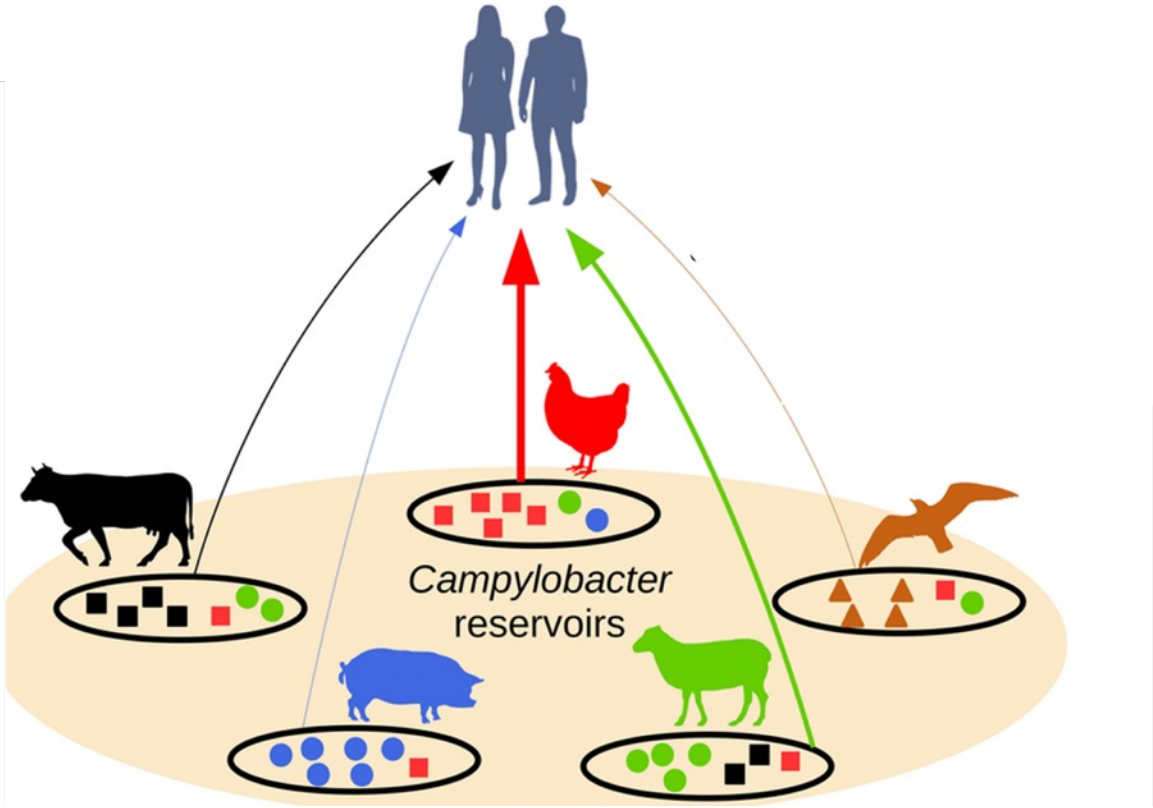
Adapted from Pettengill JB, et al. (2020) *The Lancet Microbe*; 1(6):E233-E234.

Genomic Database: Source Type + Place



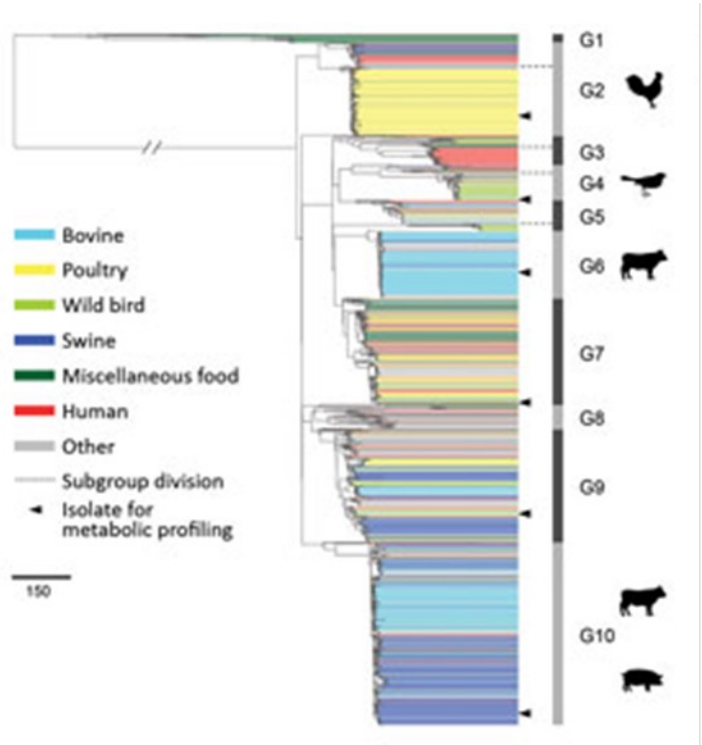
Adapted from: Pettengill JB, et al. (2020) *The Lancet Microbe*; 1(6):E233-E234.
Photo from: https://www.fda.gov/food/outbreaks-foodborne-illness/outbreak-investigation-listeria-monocytogenes-enoki-mushrooms-march-2020

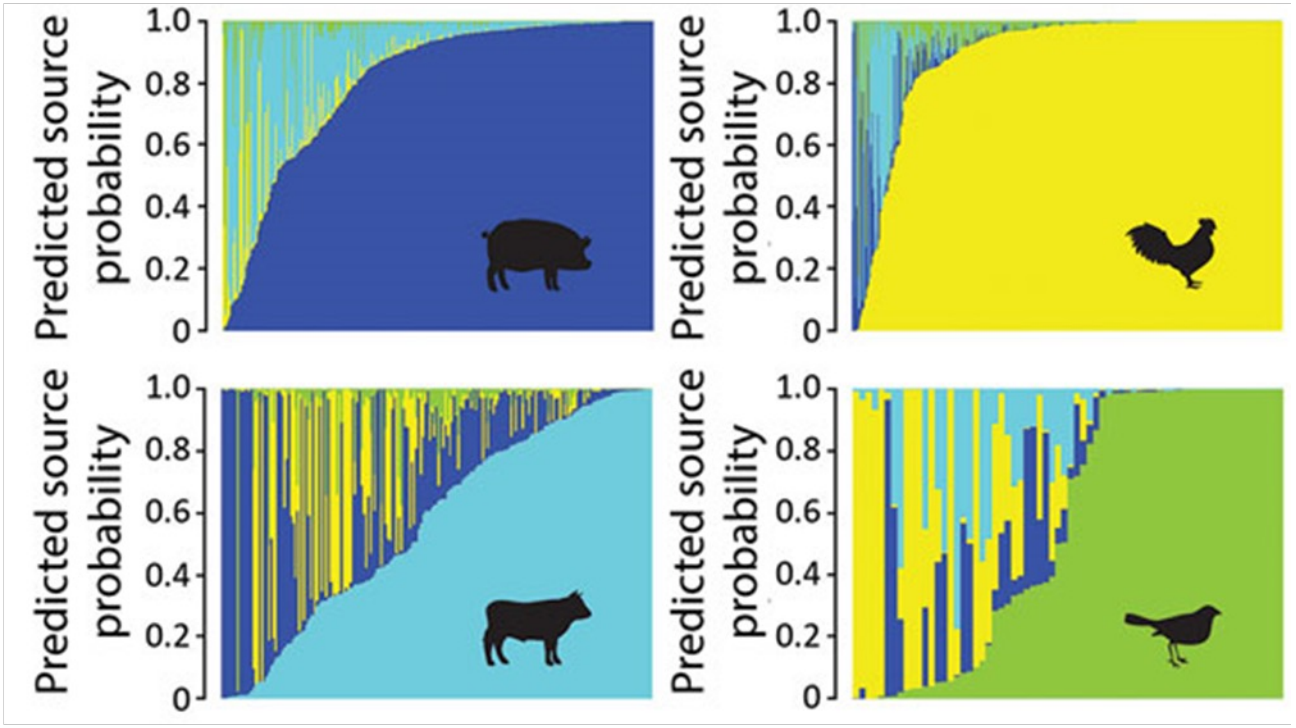
Pathogen Genomics of Source for Source Attribution and Prediction



Adapted from Perez-Reche FJ, et al. (2020) 10: 12124.

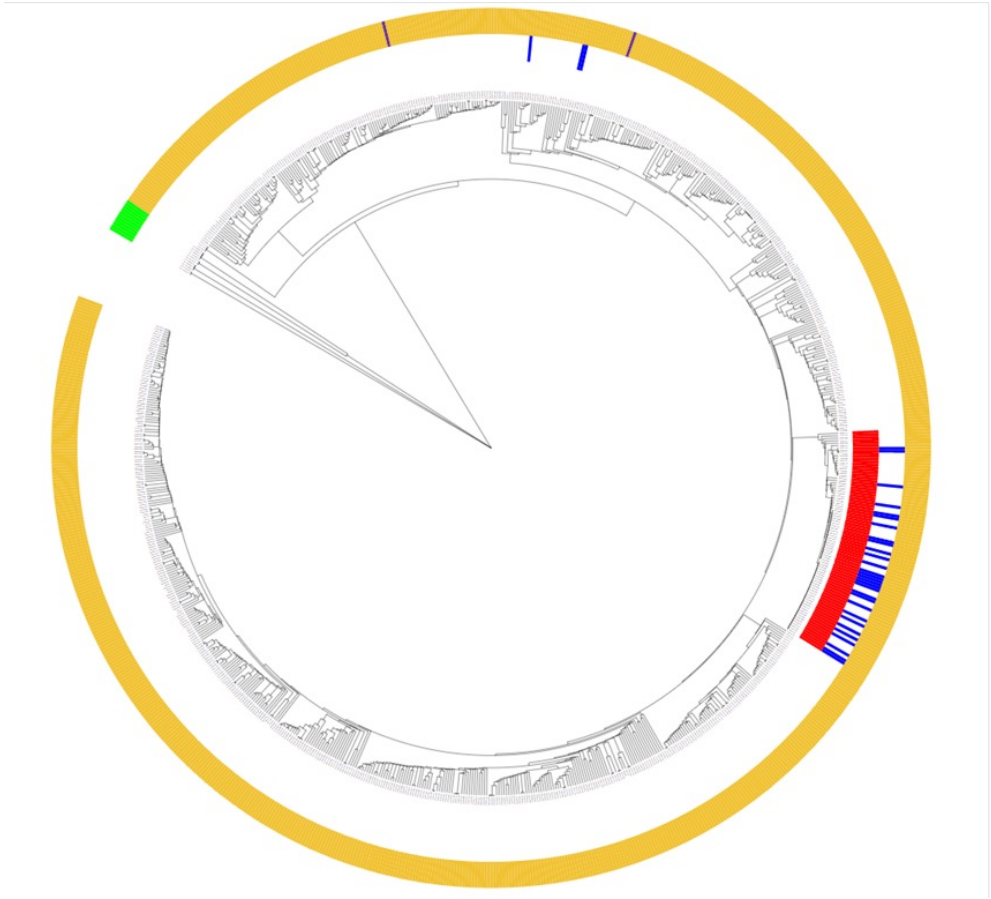
Pathogen Genomics + Source Type: *Salmonella* Source Attribution

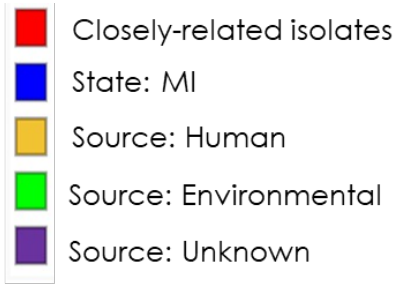




Adapted from Zhang S, et al. (2019) Emerging Infectious Diseases, 25(1).

Ongoing Monitoring





Salmonella Newport (Genomic Data + Place)

Courtesy of Molly Leeper, PulseNet

The Problem

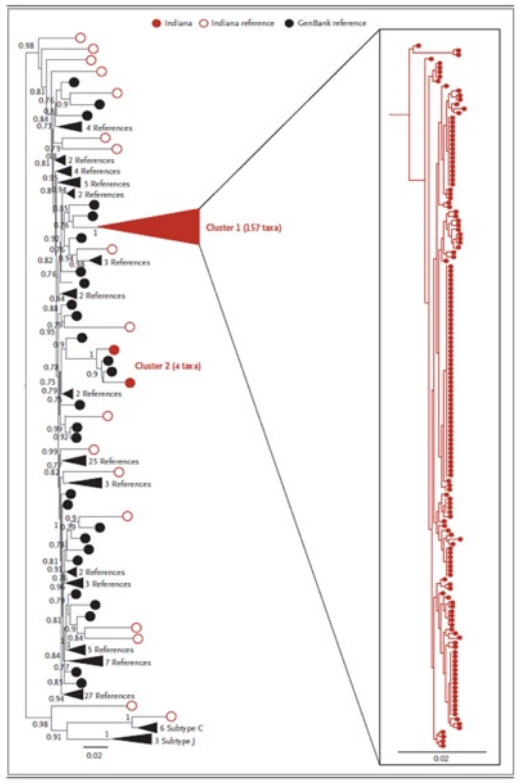
January, 2015: 11 new diagnoses of human immunodeficiency virus (HIV) infection reported in a small community in Indiana

Key Questions

Are the cases part of a transmission chain?

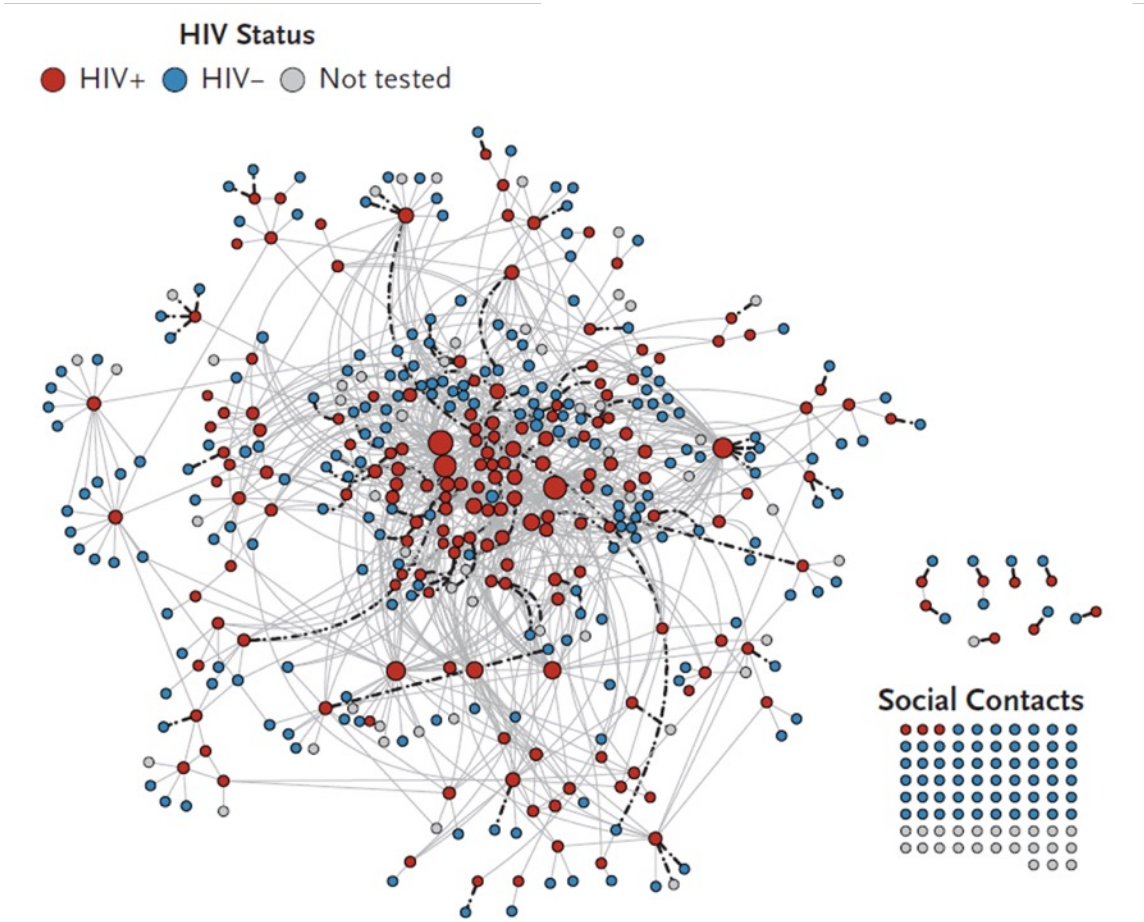
How is transmission occurring?

Highly Related Sequences



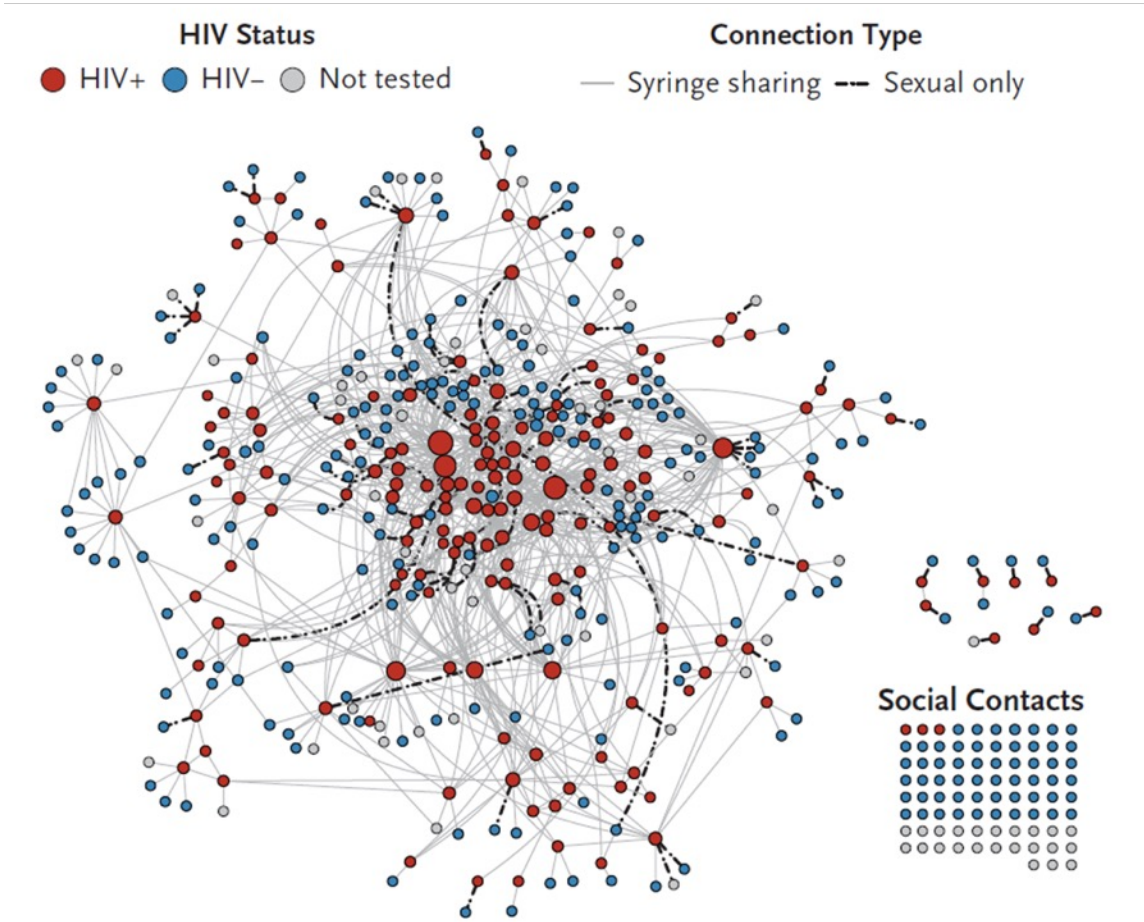
Adapted from Peters P, et al. (2016) NEJM. 375(3): 229-39.

Social Network



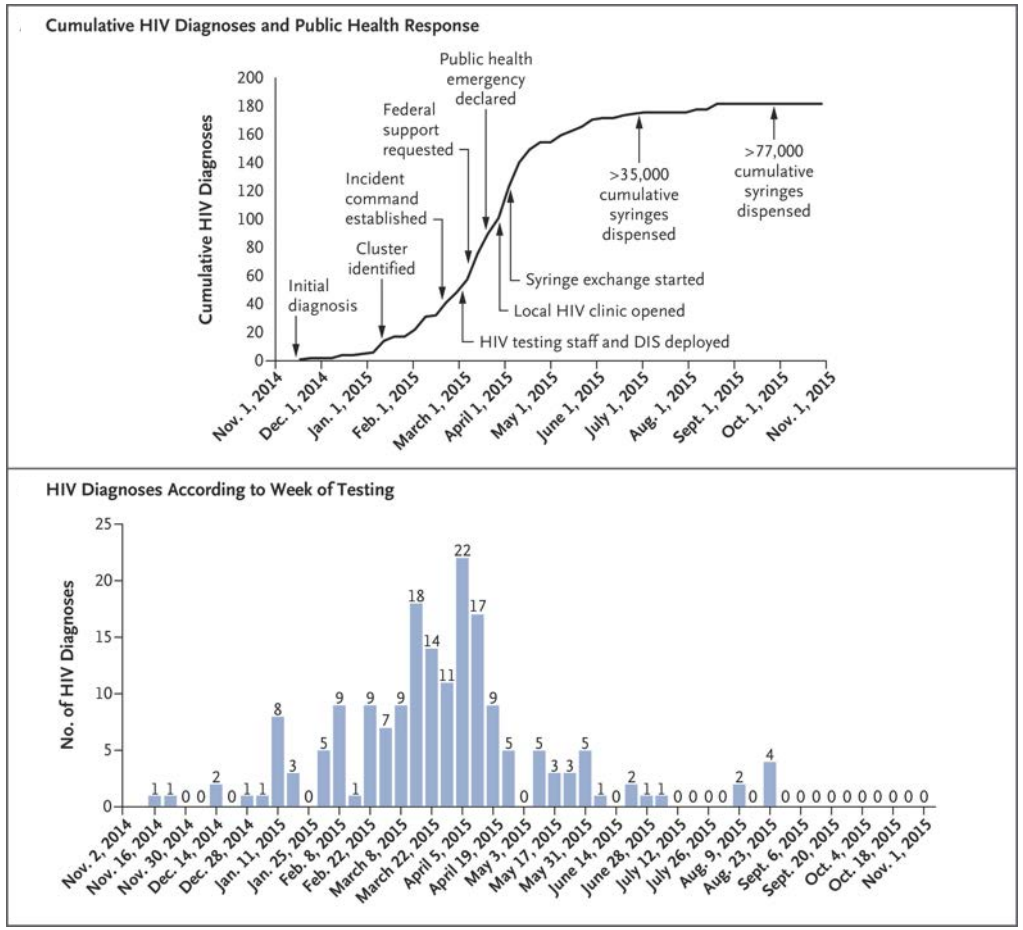
Adapted from Peters P, et al. (2016) NEJM. 375(3): 229-39.

Social Network + Connection Type



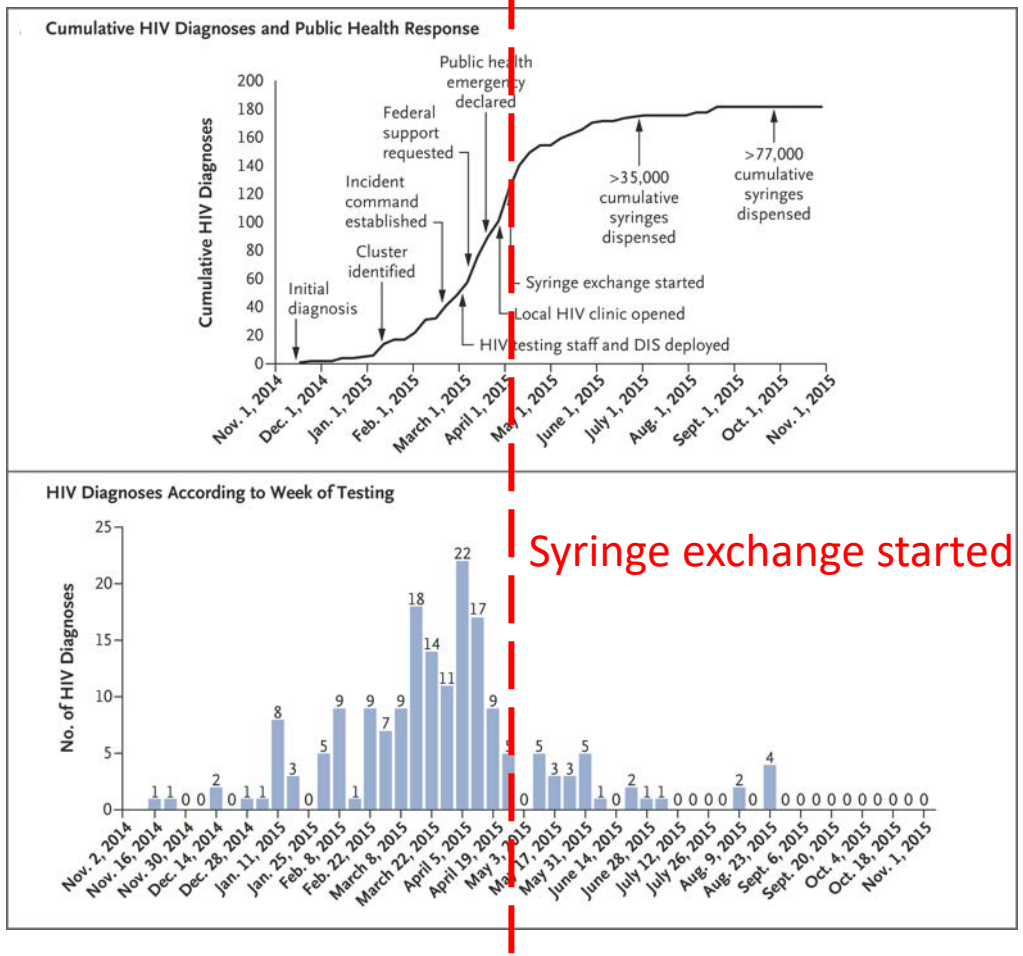
Adapted from Peters P, et al. (2016) NEJM. 375(3): 229-39.

Targeting Prevention to Mode of Transmission



Adapted from Peters P, et al. (2016) NEJM. 375(3): 229-39.

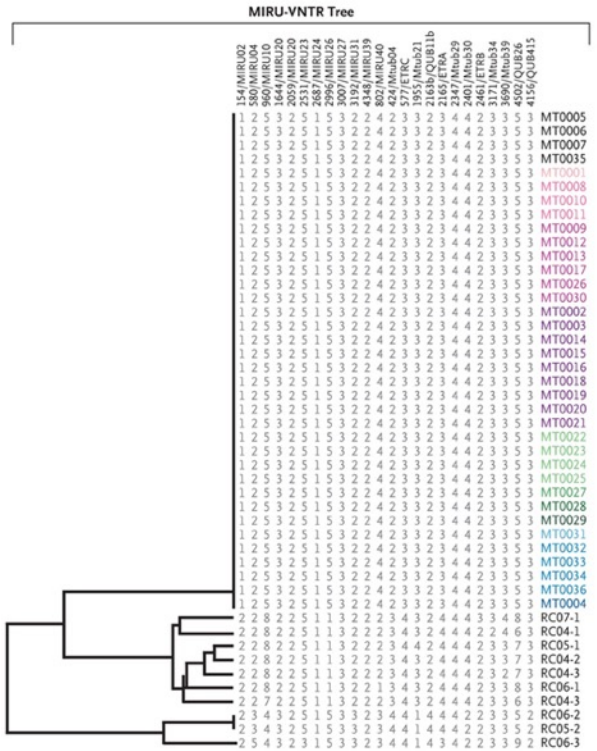
Targeting Prevention to Mode of Transmission



Adapted from Peters P, et al. (2016) NEJM. 375(3): 229-39.

Defining the Problem: A Tuberculosis Outbreak?

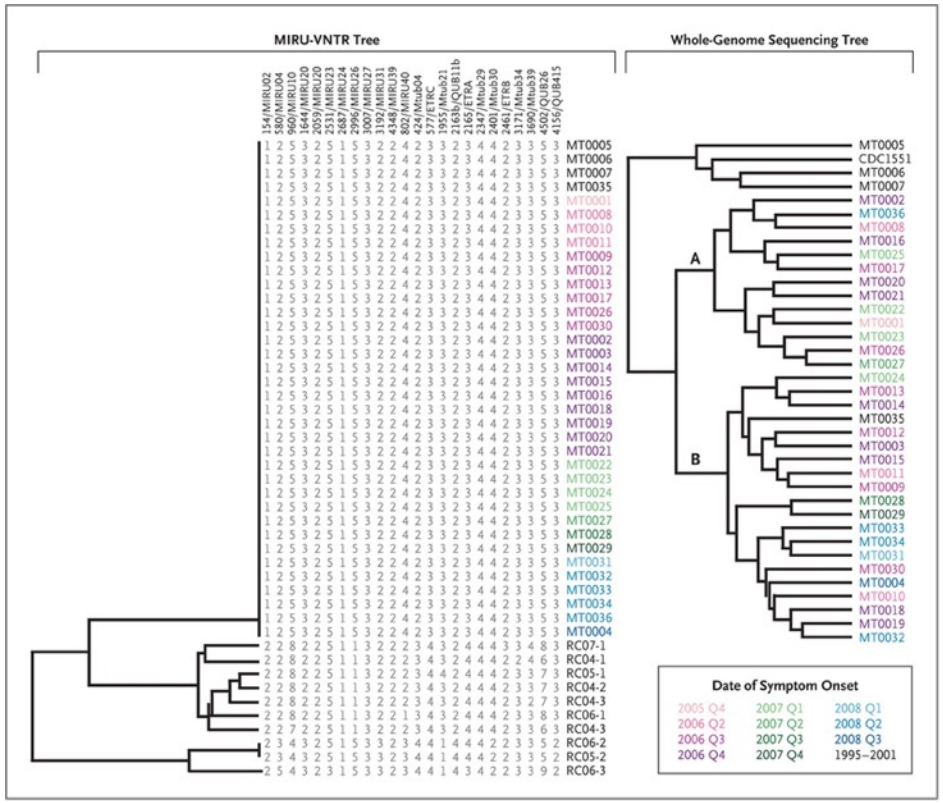
41 cases of tuberculosis over 3 years



Adapted from: Gardy JL, et al. (2011) NEJM 364(8):730-9.

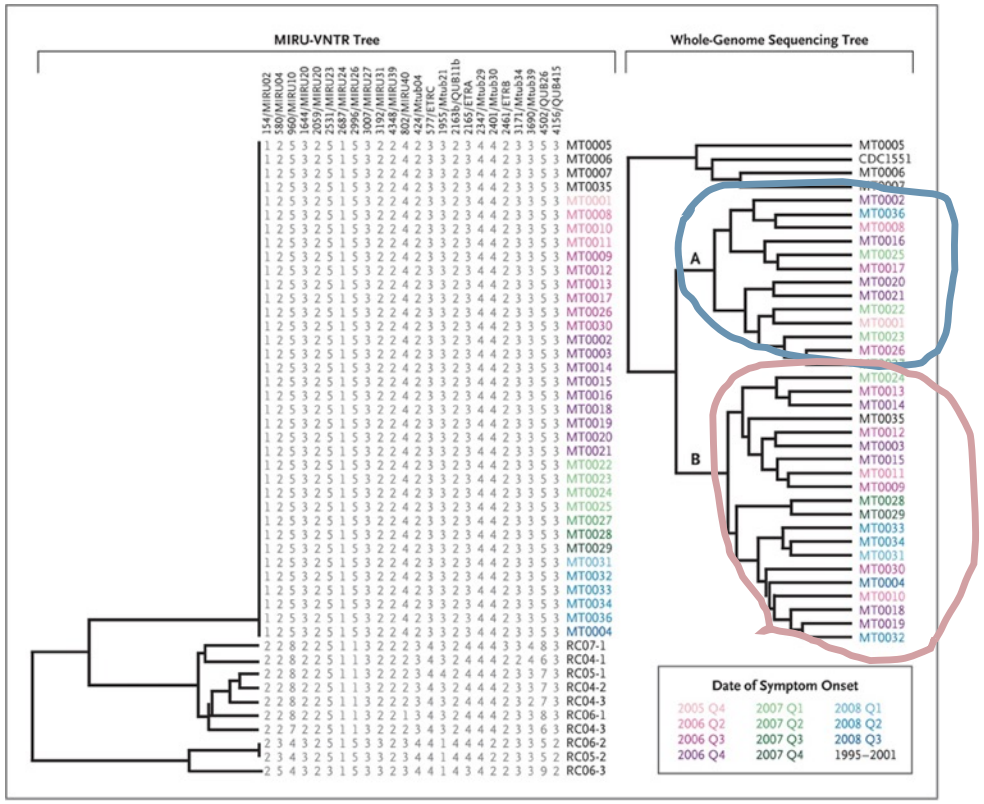
More Data ~ Higher Resolution

A Higher Resolution View



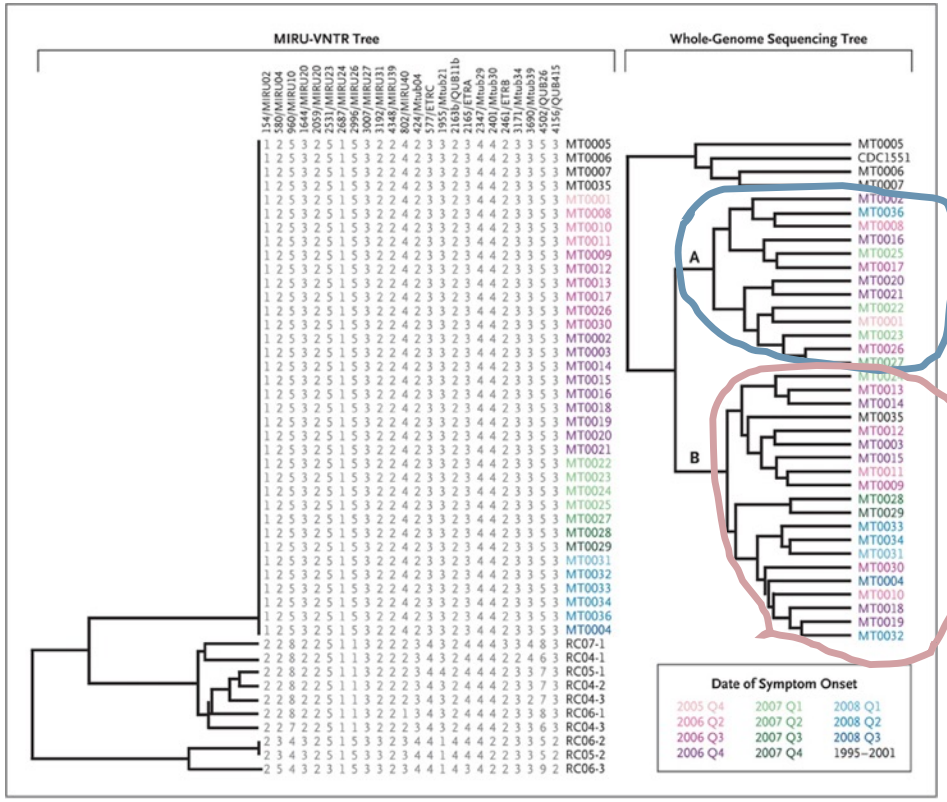
Adapted from: Gardy JL, et al. (2011) N Engl J Med 364(8):730-9.

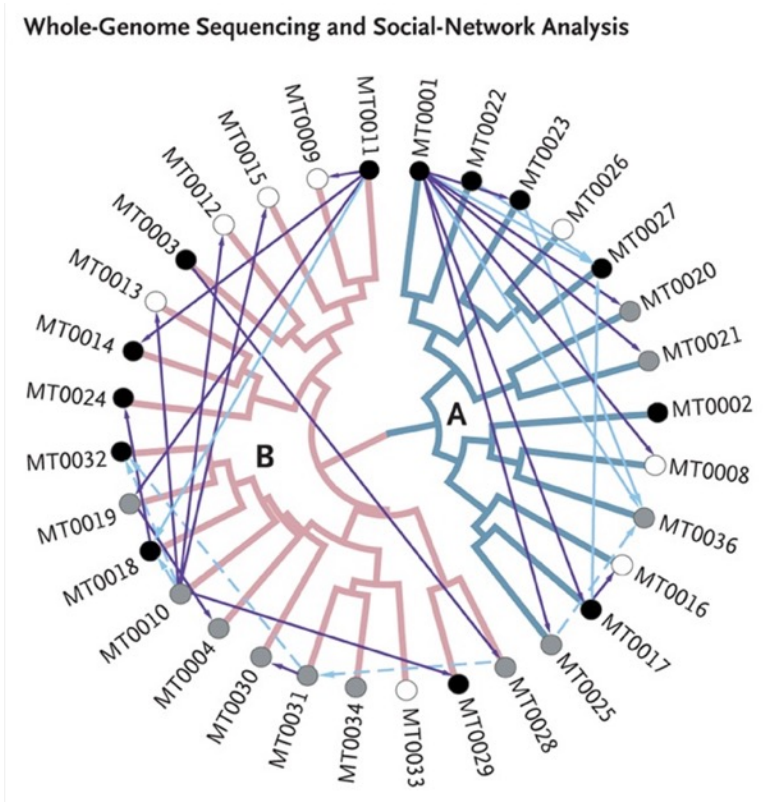
A Higher Resolution View: Two Outbreaks



Adapted from: Gardy JL, et al. (2011) N Engl J Med 364(8):730-9.

Two Outbreaks, Two Networks





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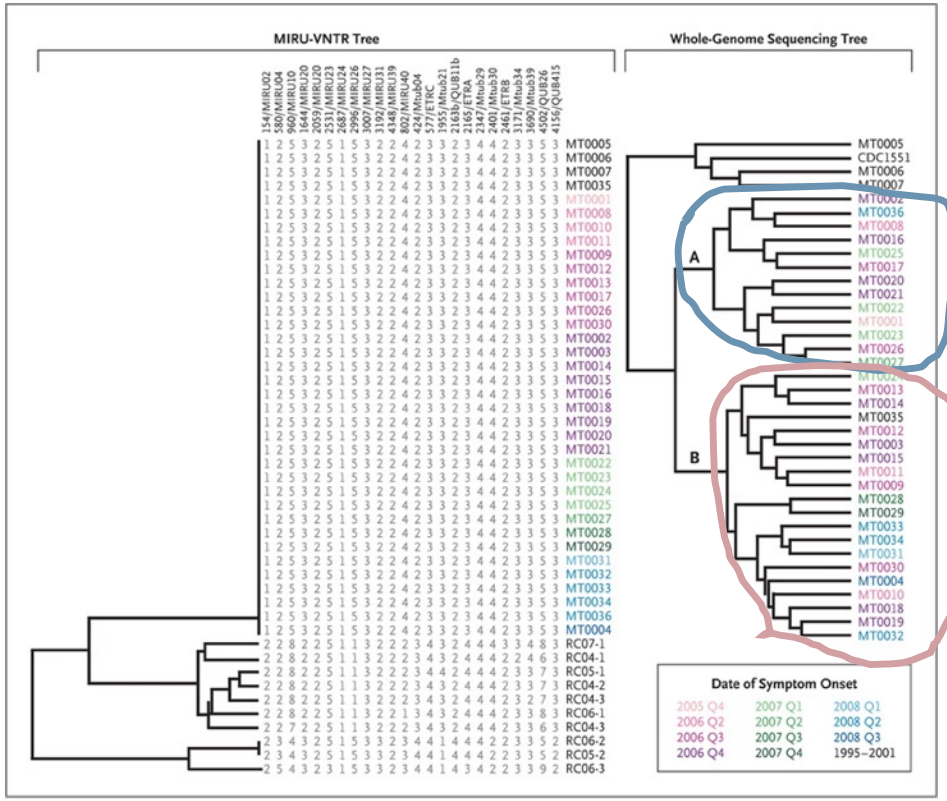
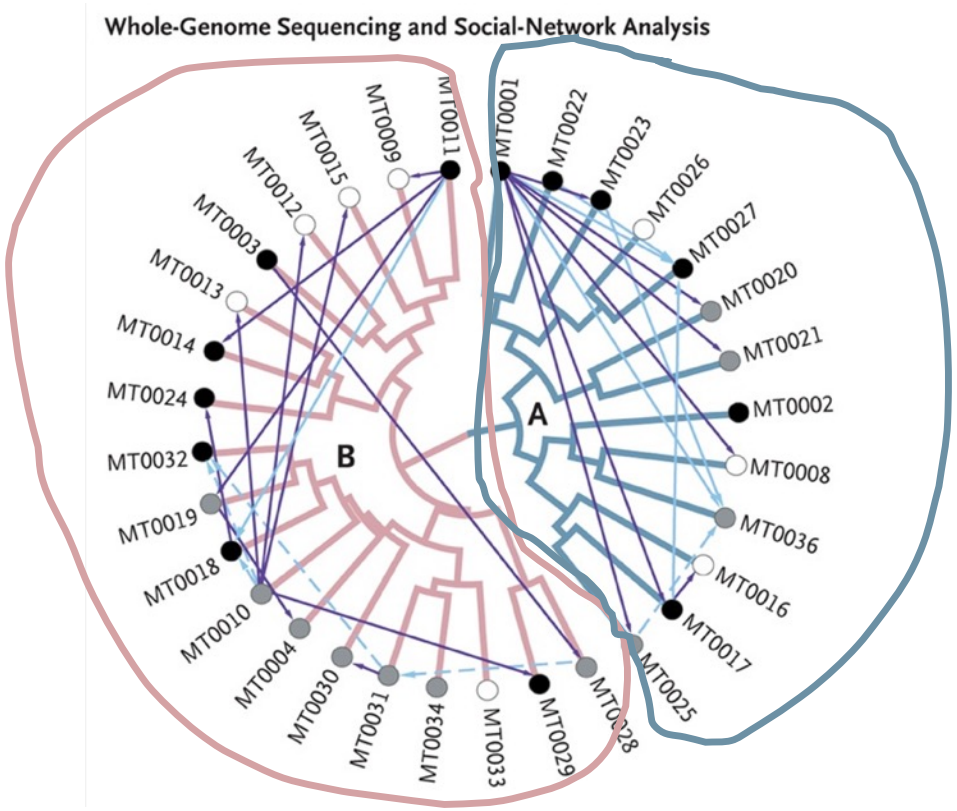
Two Outbreaks, Two Networks





Adapted from: Gardy JL, et al. (2011) N Engl J Med 364(8):730-9.

An Unusual Infection

March 2021, Kansas:

A 53 year old woman with multiple medical conditions including chronic lung disease developed shortness of breath, cough, malaise and weakness.

The patient was hospitalized, treated with broad spectrum antibiotics but developed encephalopathy, hypotension, and respiratory distress.

The patient was transferred to the ICU but despite aggressive treatment died on day 9 of hospitalization.

Blood cultures grew *Burkholderia pseudomallei*.

Adapted from: Gee JE, et al. N Engl J Med 2022;386:861-868.

Burkholderia pseudomallei

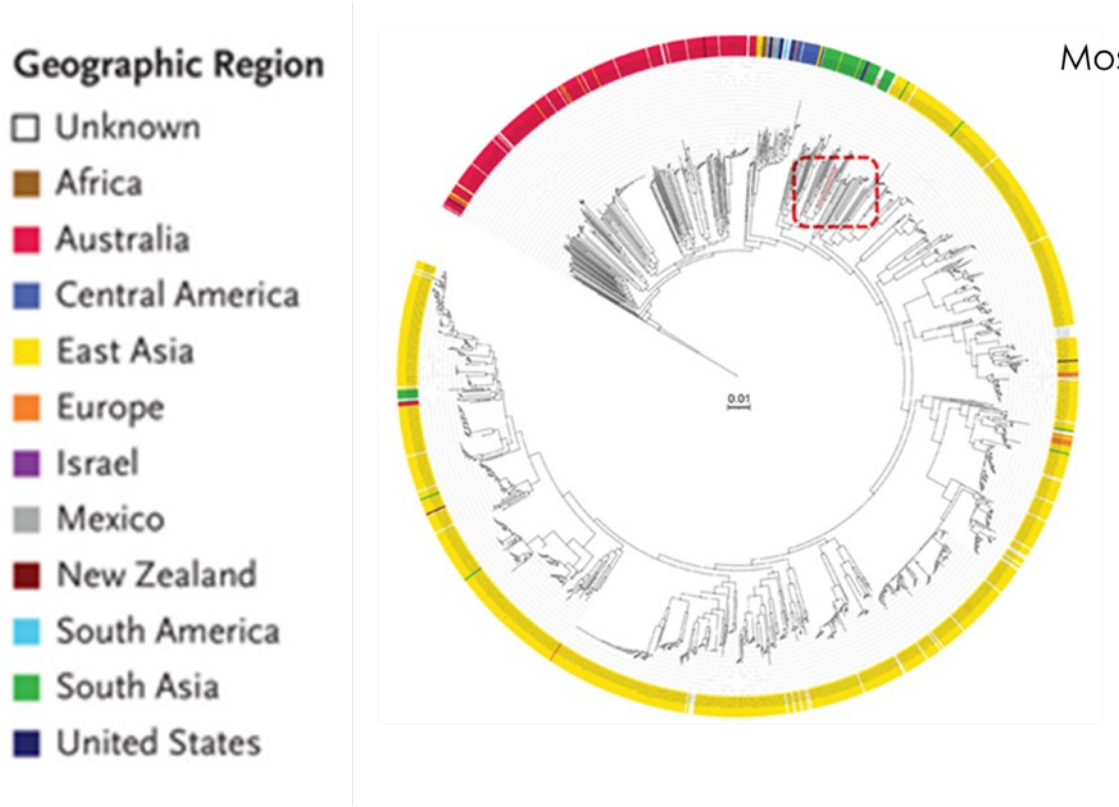
- Cause of melioidosis (fatality rate 10-50%)
- Found in contaminated soil and water
- Infection through inhalation, ingestion, skin contact
- Can infect any organ of the body
- Disease predominately in tropical climates, especially in Southeast Asia and northern Australia
- Most cases in the U.S. linked to recent travel to endemic areas

https://www.cdc.gov/melioidosis/index.html

An Unexpected History

Adapted from Gee JE, et al. N Engl J Med 2022;386:861-868.

A Bacterial Strain Similar to Strains Found in South Asia



Most similar to strains from South Asia

Adapted from Gee JE, et al. N Engl J Med 2022;386:861-868.

Another Report

Adapted from Gee JE, et al. N Engl J Med 2022;386:861-868.

Another Report

Adapted from Gee JE, et al. N Engl J Med 2022;386:861-868.

Key Question

Are these cases related?

Whole Genome Sequencing Results

- Genomic sequences nearly identical → common source
- Strain had BimBm gene variant associated with neurological involvement in mouse model

Key Question

What is the source of infection?

Multistate Investigation of Non-travel Associated *Burkholderia pseudomallei* Infections (Melioidosis) in Three Patients: Kansas, Texas, and Minnesota—2021

Print

Distributed via the CDC Health Alert Network
June 30, 2021, 2:30 PM ET
CDCHAN-00444

Sample Testing

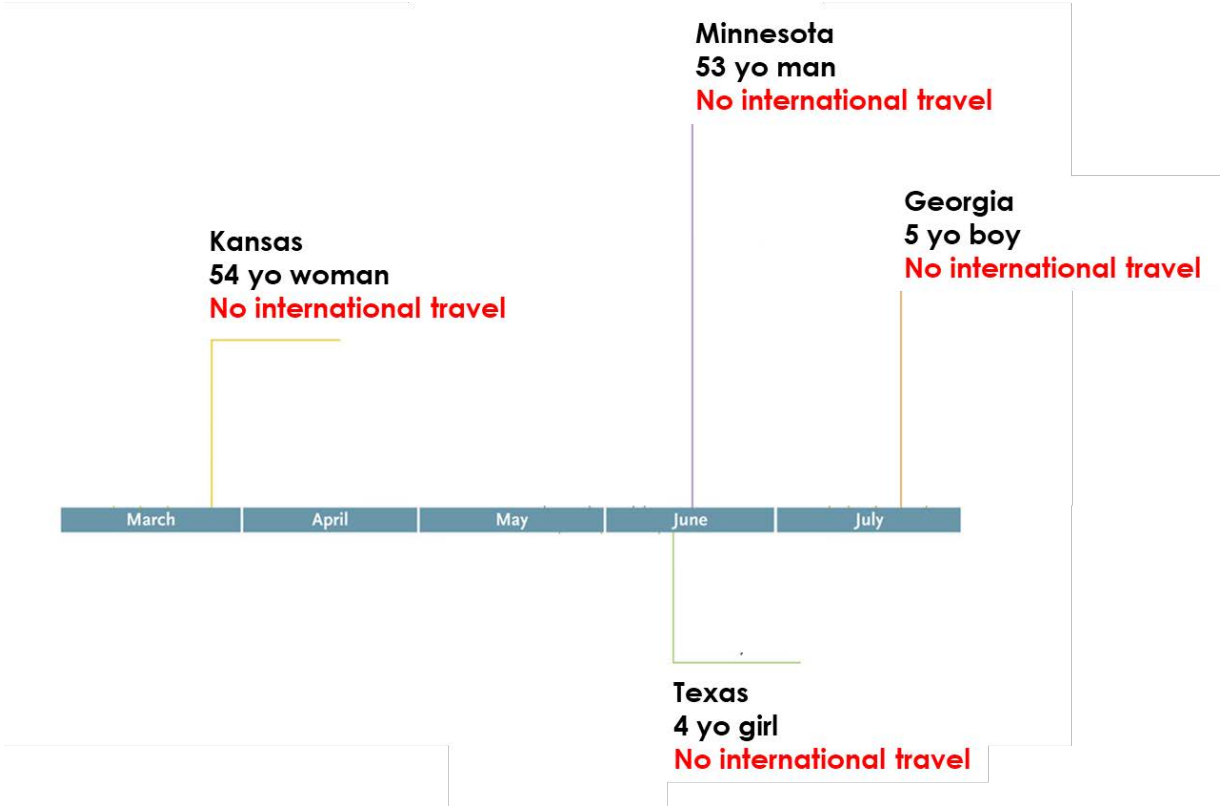
- >100 samples from products, soil, water in and around patient homes
- No samples positive for *Burkholderia pseudomallei*

New Case Identified: Multistate Investigation of Non-travel Associated *Burkholderia pseudomallei* Infections (Melioidosis) in Four Patients: Georgia, Kansas, Minnesota, and Texas—2021

Print

Distributed via the CDC Health Alert Network
August 9, 2021, 11:40 AM ET
CDCHAN-00448

Another Report



Adapted from Gee JE, et al. N Engl J Med 2022;386:861-868.

Source Implicated in Fatal Case in Georgia: Multistate Outbreak of Non-travel Associated *Burkholderia pseudomallei* Infections (Melioidosis) in Four Patients: Georgia, Kansas, Minnesota, and Texas–2021

Print

HAN HEALTH ALERT NETWORK

This is an official CDC HEALTH UPDATE

Distributed via the CDC Health Alert Network
October 22, 2021, 6:15 PM ET
CDCHAN-00455

Source Implicated in Fatal Case in Georgia: Multistate Outbreak of Non-travel Associated *Burkholderia pseudomallei* Infections (Melioidosis) in Four Patients: Georgia, Kansas, Minnesota, and Texas–2021

Print

HAN HEALTH ALERT NETWORK

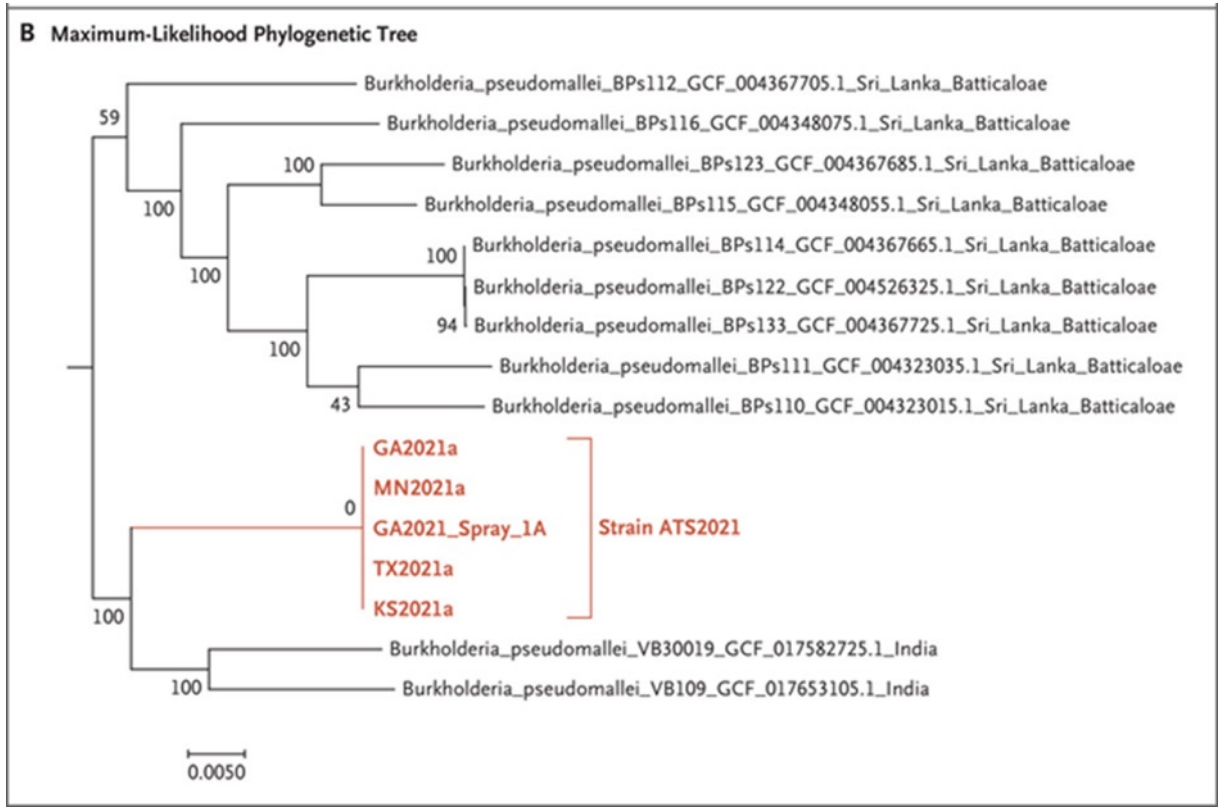
This is an official CDC HEALTH UPDATE

Distributed via the CDC Health Alert Network
October 22, 2021, 6:15 PM ET
CDCHAN-00455

"Testing…has identified the bacterial DNA of *Burkholderia pseudomallei* in an aromatherapy room spray."

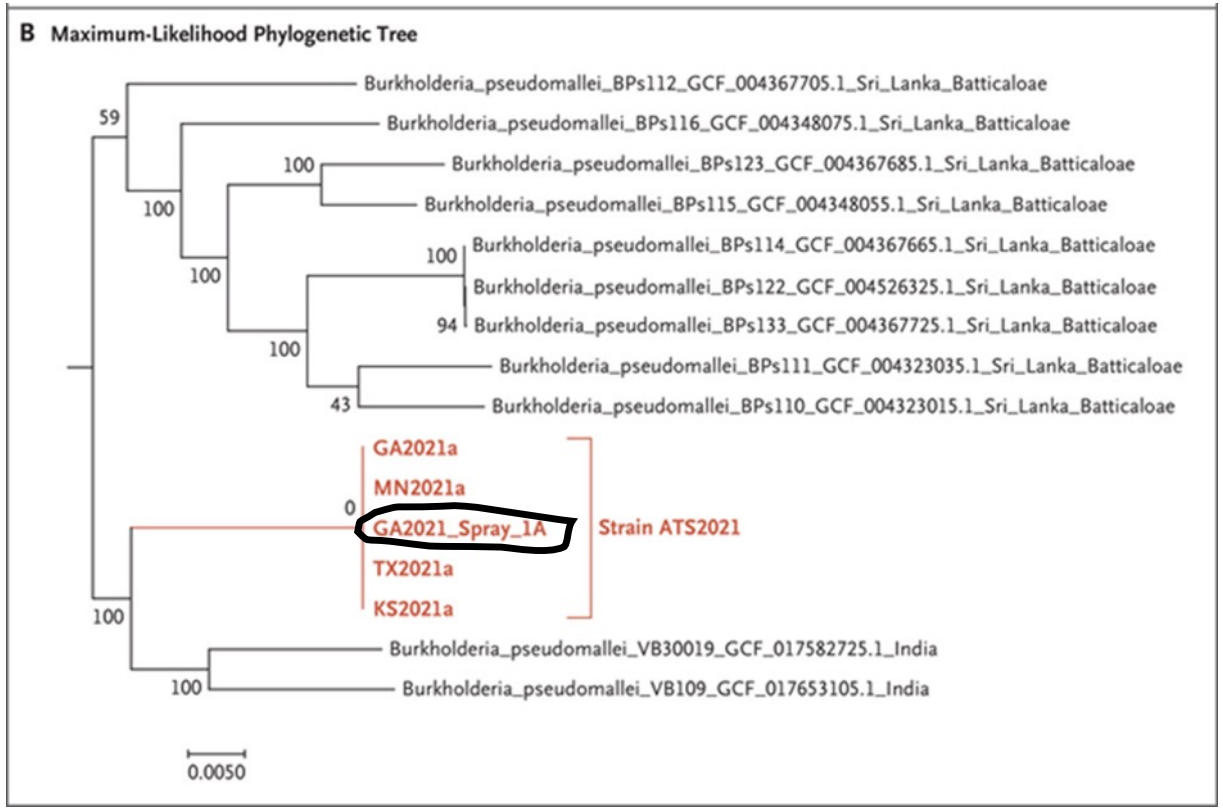
"Whole genome sequencing results from the positive sample are pending."

Identical Sequences: Product and Clinical Samples



Adapted from Gee JE, et al. N Engl J Med 2022;386:861-868.

Nearly Identical Sequences: Product and Clinical Samples



Adapted from Gee JE, et al. N Engl J Med 2022;386:861-868.

Source Identified and Case Definition Established: Multistate Investigation of Non-travel Associated *Burkholderia pseudomallei* Infections (Melioidosis) in Four Patients: Georgia, Kansas, Minnesota, and Texas – 2021

Print

"Whole genome sequencing…confirmed that the strain of *Burkholderia pseudomallei* in bottles of aromatherapy room spray matches the bacterial strain that sickened all four patients."

HAN
HEALTH ALERT NETWORK

NVH
This is an official CDC HEALTH UPDATE

Connecting the Dots

- Strain from Georgia patient matched strain in bottle of aromatherapy spray
- All strains from patients in four states matched each other
- All patients had exposure to the same aromatherapy product
- Same strain found in unopened bottle of spray in a store in another state
- Strain was similar to strains from South Asia
- Aromatherapy spray imported from India

"…the proverbial needle in a haystack."

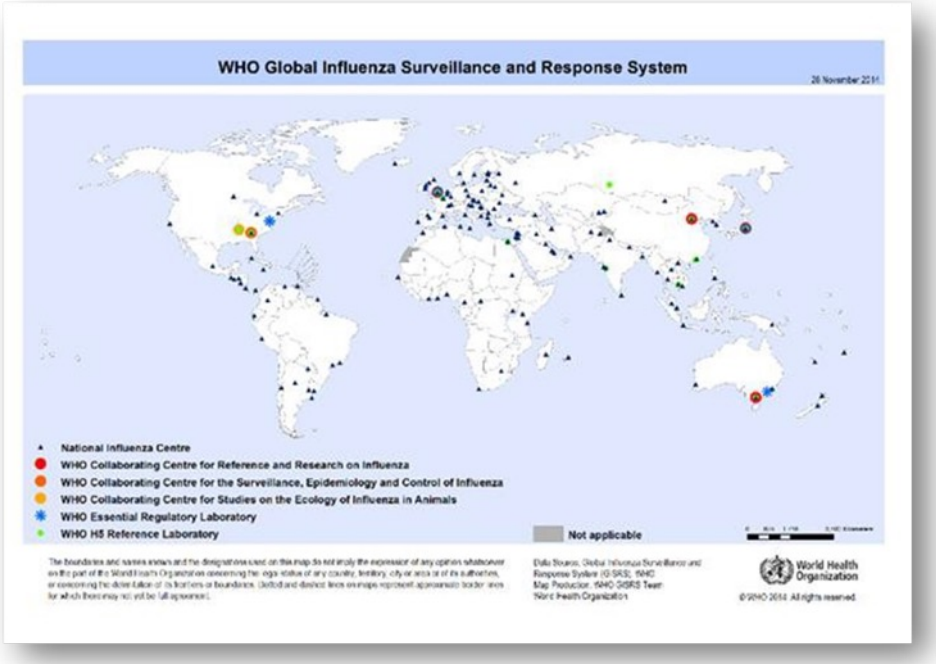
https://www.cdc.gov/media/releases/2021/p1026-melioidosis-outbreak.html

Targeted Intervention

Recall of 3,900 bottles of aromatherapy spray

Impact of Next Generation Sequencing on Influenza Vaccine Strain Selection

- CDC is an important contributor to influenza surveillance and prevention
  - Serves as US National Influenza Center and WHO Collaborating Center for Surveillance, Epidemiology and Control of Influenza
  - Analyses 8,000 – 12,000 influenza samples/year in support of surveillance and selection of vaccine strains
    - Vaccine is produced in a "just in time" fashion
    - 150 Million vaccine doses/year in the US
- Evolution of influenza is very rapid
  - Critical to find variants quickly
  - Antigenic drift
  - Reassortment
- AMD improves characterization
  - High throughput NGS sequencing for influenza surveillance
  - Antigenic inference



On the Front Lines: Transforming Influenza Surveillance

In the Field

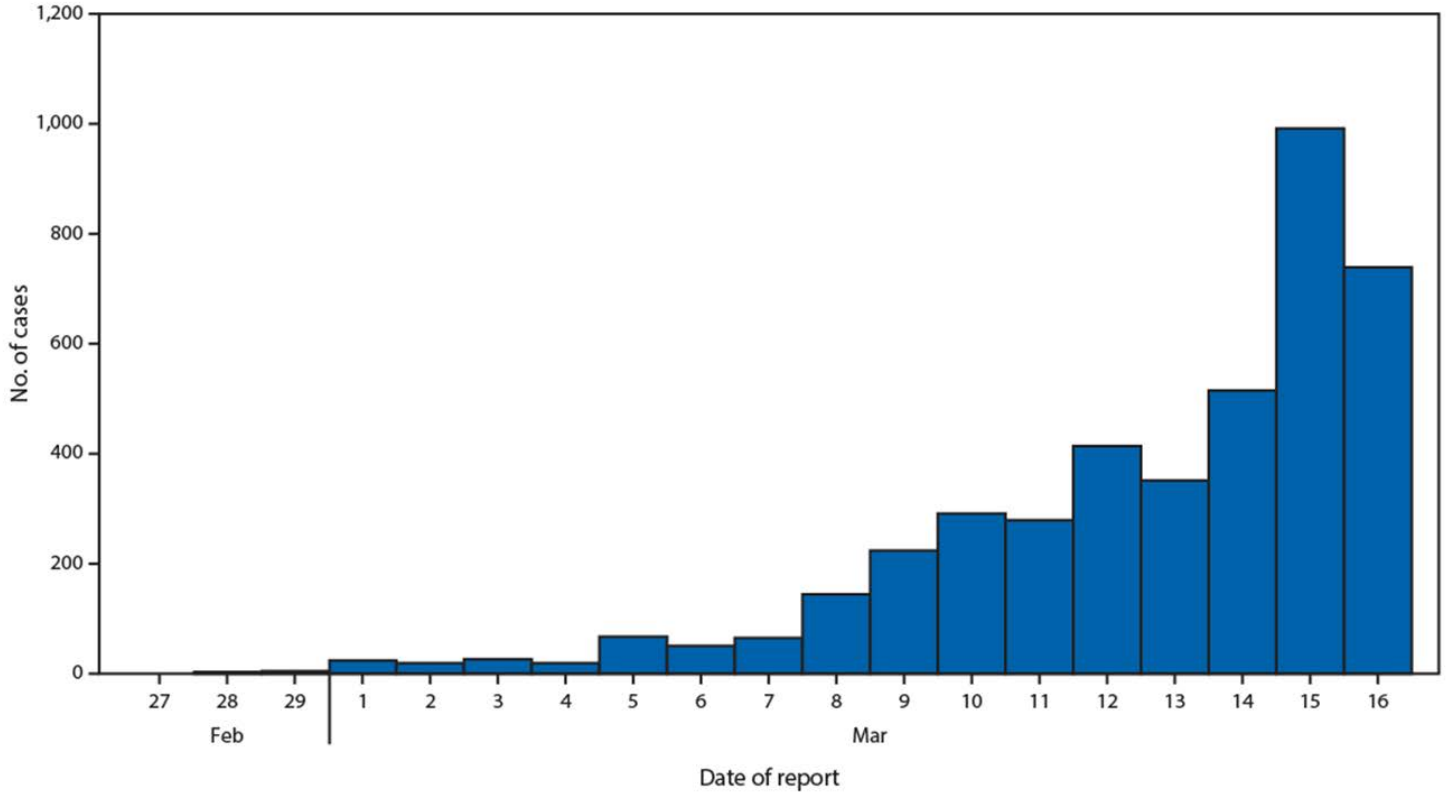
COVID-19

Late December, 2019 – reports of patients with pneumonia of unknown cause

January 10, 2020 – novel coronavirus identified by sequencing

Host View: Counting

Number of new COVID-19 cases reported daily — United States, February 12–March 16, 2020



Adapted from: MMWR (2020) 69:343-346.

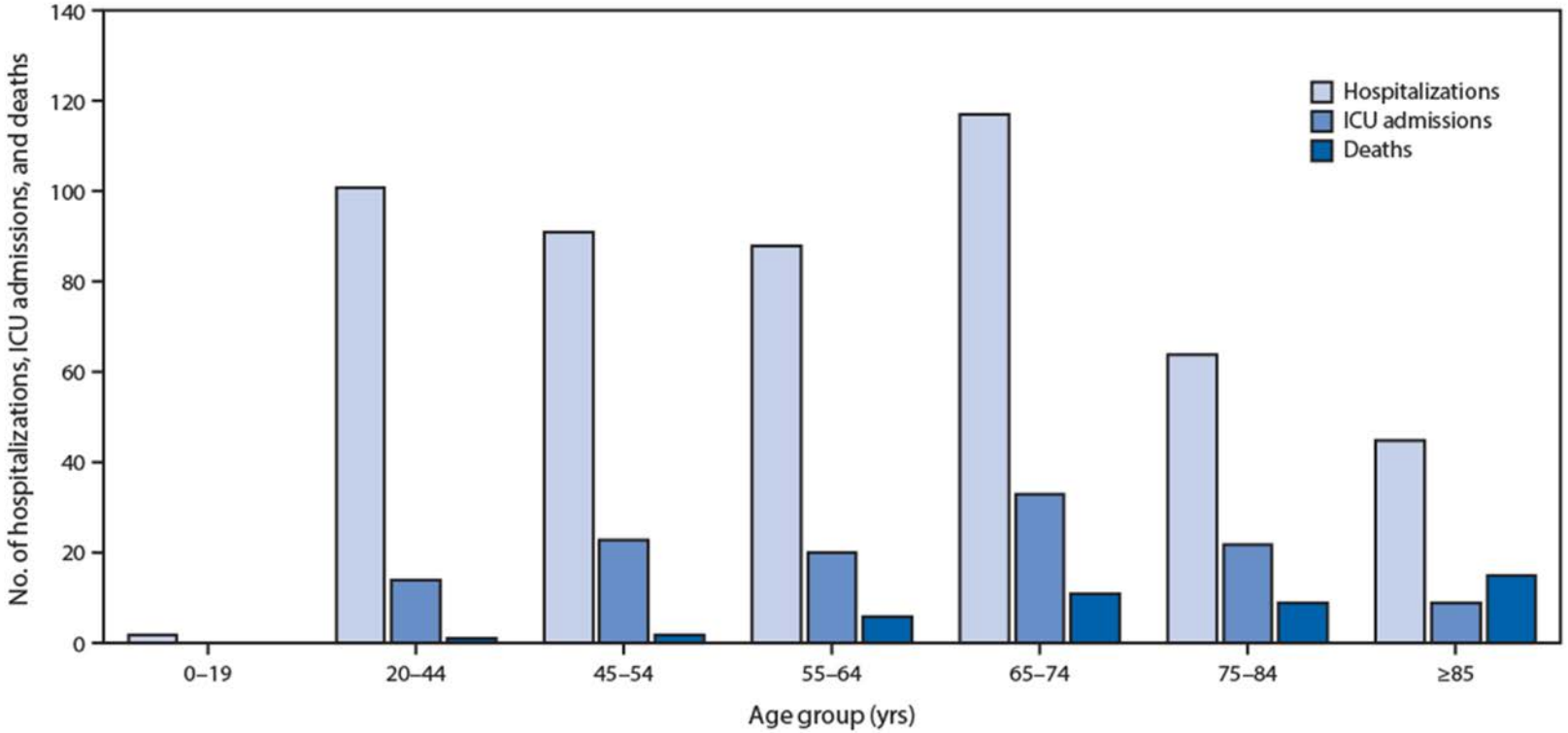
COVID-19: A New Infectious Disease

Host

- Who is affected?
- What are the characteristics of disease?
- What are risk factors for severe disease?

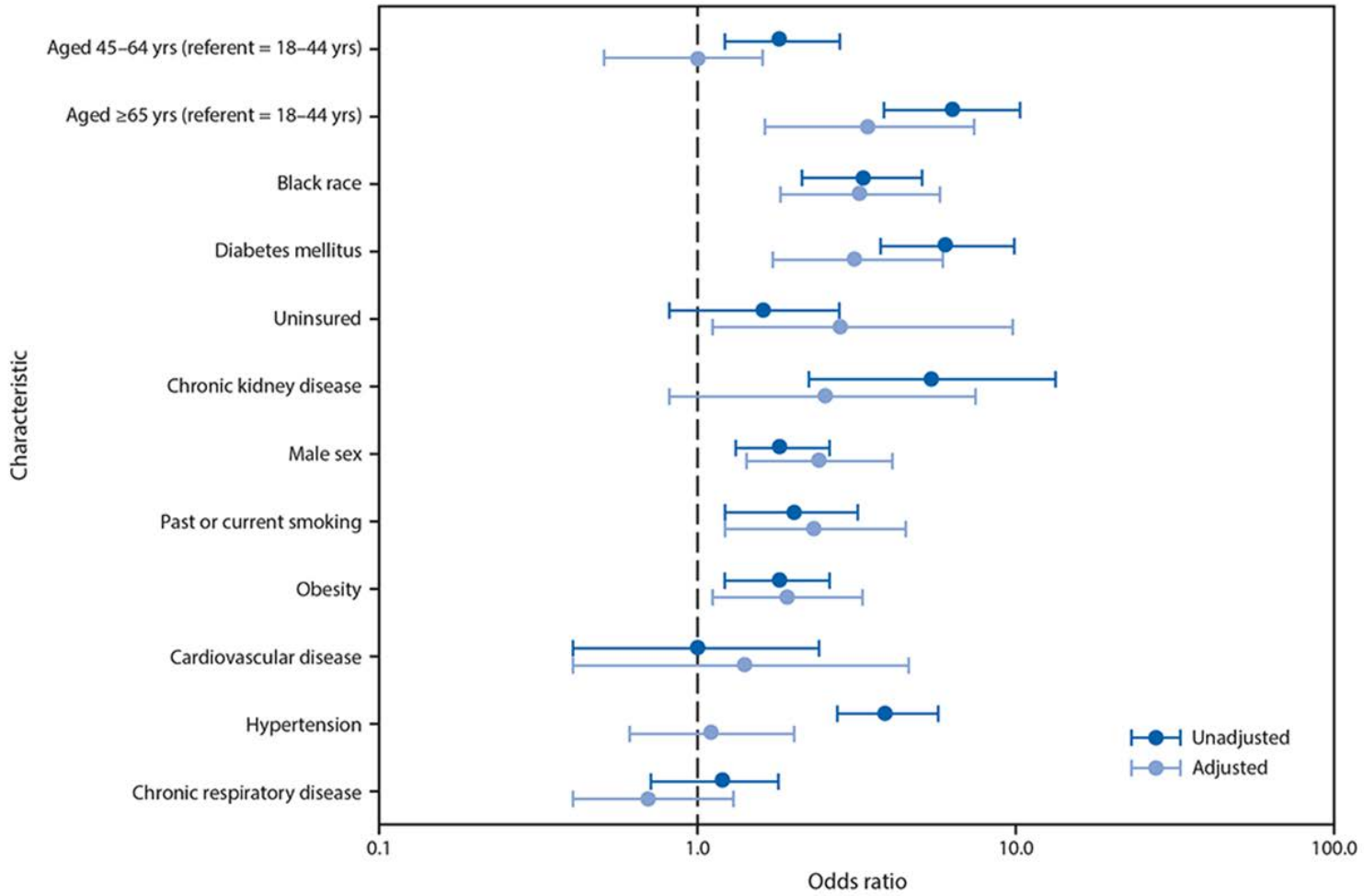
COVID-19 Host View: Sorting

COVID-19 hospitalizations, intensive care unit admissions, and deaths, by age group — United States, February 12– March 16, 2020



Images from Trevor Bedford Group: https://docs.nextstrain.org

Host View: Risk Factors for Severe Disease



Jackson BR, et al. (2021) Clin Infect Dis. 73(11) :e4141-e4151.

COVID-19: A New Infectious Disease

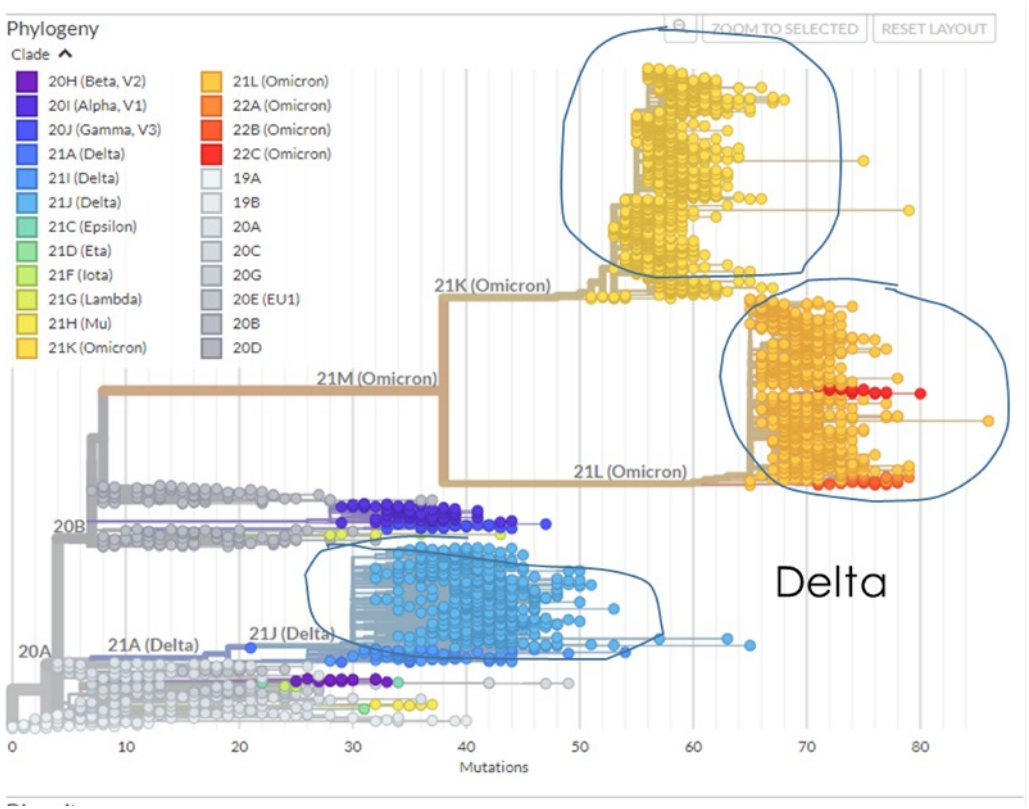
Host

- Who is affected
- What are the characteristics of disease?
- What are risk factors for severe disease?

Pathogen

- Where is transmission happening?
- How is the virus changing?
- What features of the virus affect severity of disease?
- Do changes in the virus impact vaccine efficacy? Treatment response? Severity of disease? Transmissibility?

Identifying Variants



Omicron

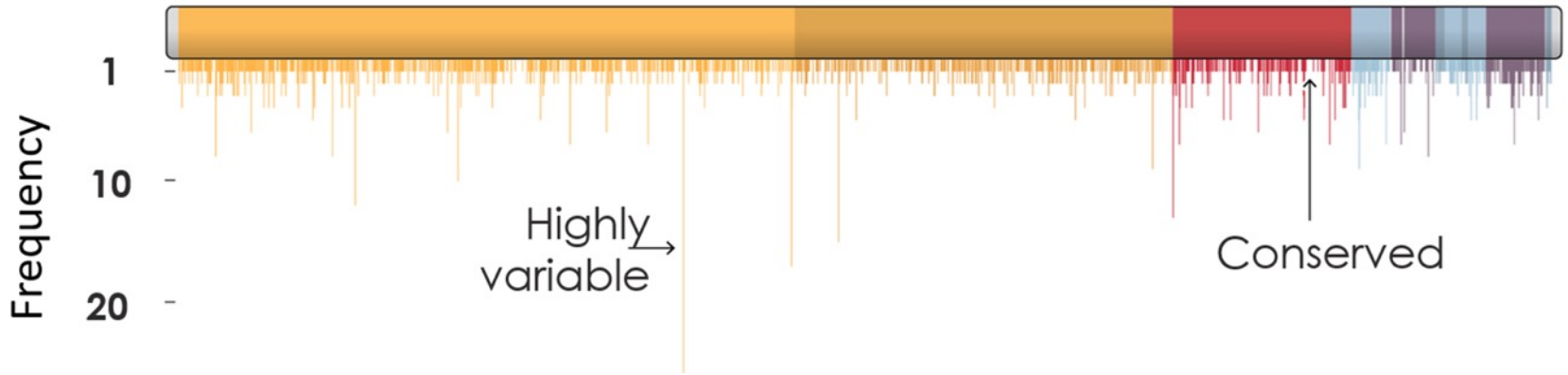
Source: nextstrain.org

SARS-CoV-2

SNP = Single Nucleotide Polymorphism

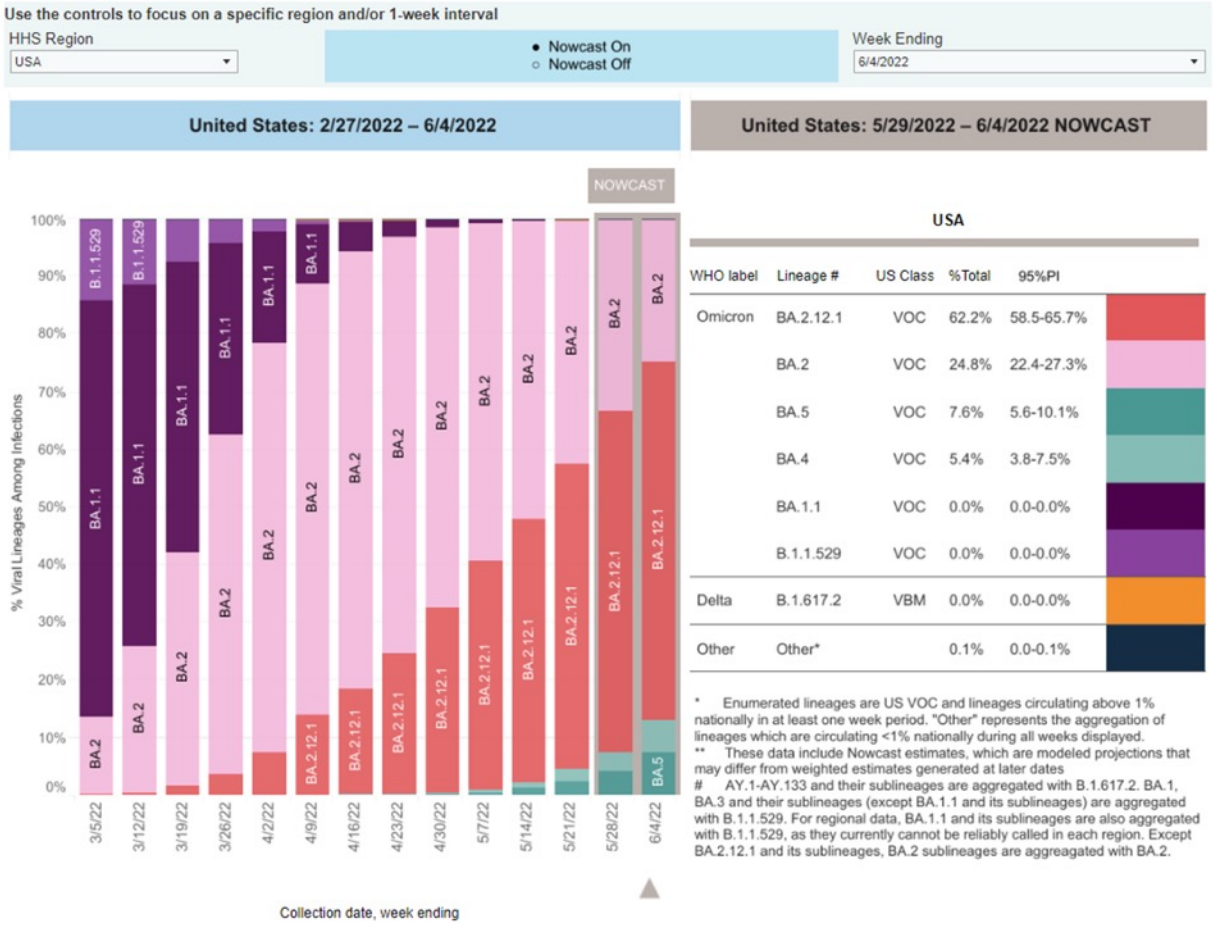
- ATGTT**C**CTC sequence
- ATGTT**G**CTC reference

SNPs occur across the genome with varied frequency:



Genome image adapted from The New York Times www.nytimes.com/interactive/2020/04/30/science/coronavirus-mutations.html

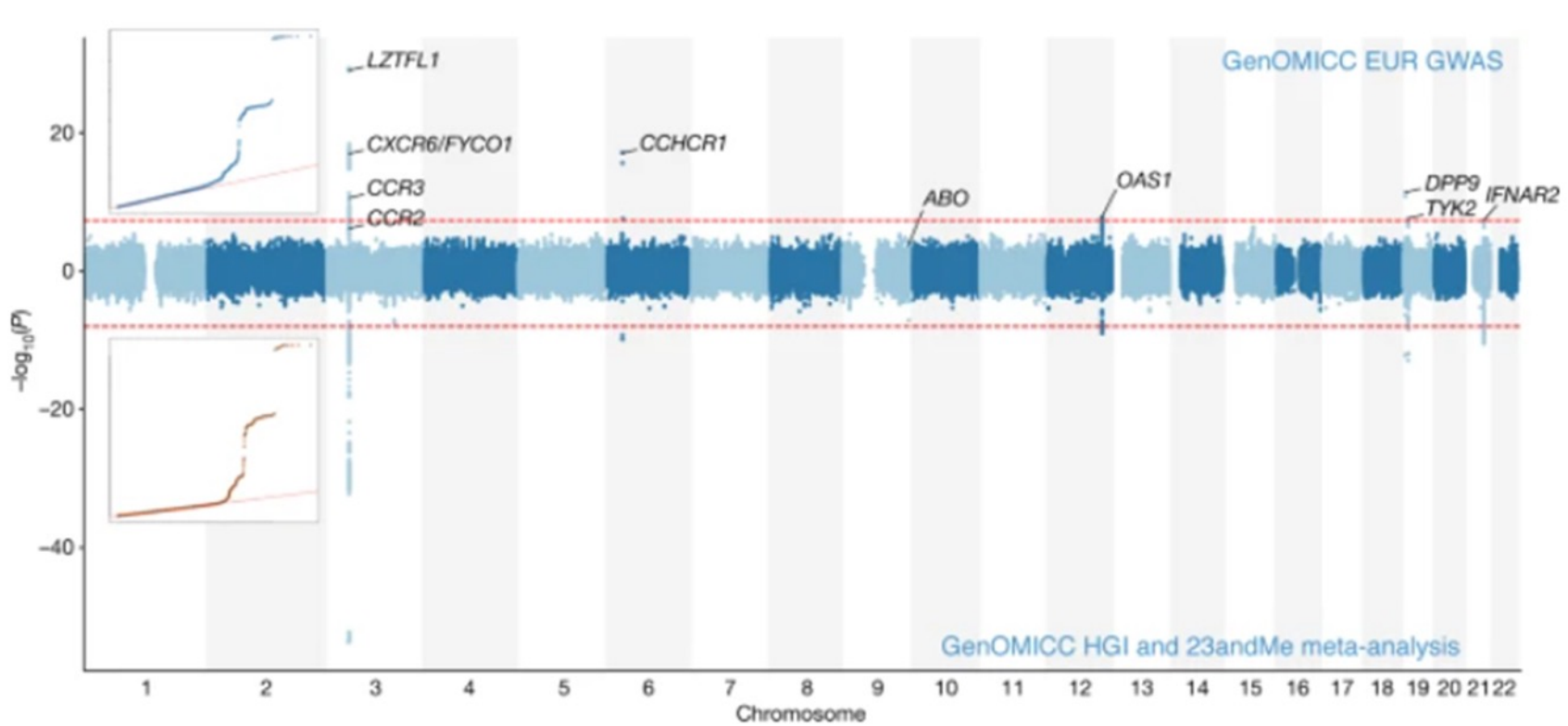
SARS-CoV-2 Variant Surveillance



https://covid.cdc.gov/covid-data-tracker/#variant-proportions

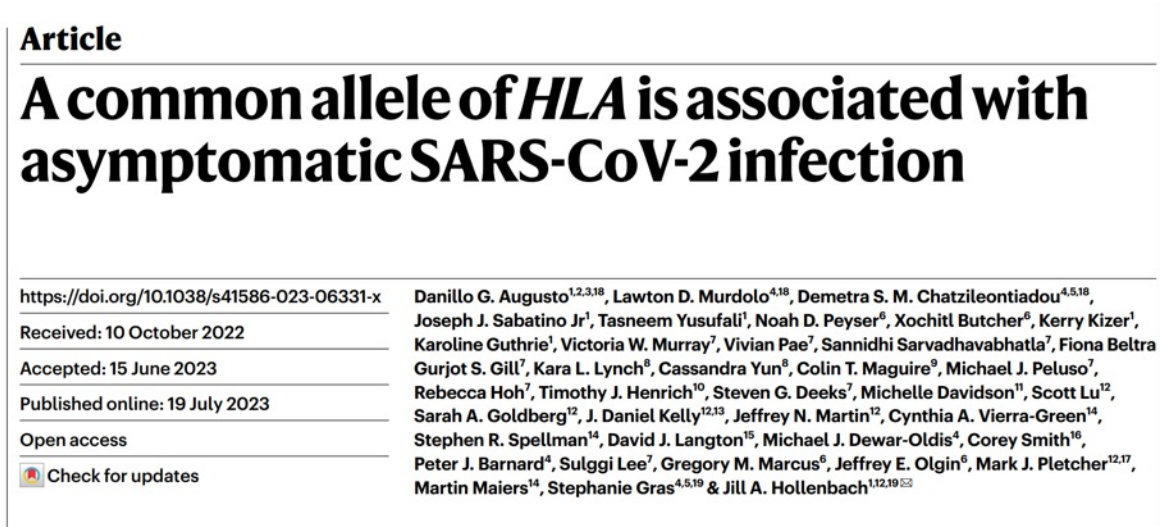
COVID-19 Clinical Spectrum of Disease

COVID-19 Critical Illness – Human Genetics



Pairo-Castineira E, et al. (2021) Nature 591, 92-98.

Host Factors Associated with Severity of Disease



Article

A common allele of *HLA* is associated with asymptomatic SARS-CoV-2 infection

https://doi.org/10.1038/s41586-023-06331-x

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Open access

Check for updates

Danillo G. Augusto[1,2,3,18], Lawton D. Murdolo[4,18], Demetra S. M. Chatzileontiadou[4,5,18], Joseph J. Sabatino Jr[1], Tasneem Yusufali[1], Noah D. Peyser[6], Xochitl Butcher[6], Kerry Kizer[1], Karoline Guthrie[1], Victoria W. Murray[7], Vivian Pae[7], Sannidhi Sarvadhavabhatla[7], Fiona Beltra Gurjot S. Gill[7], Kara L. Lynch[8], Cassandra Yun[8], Colin T. Maguire[9], Michael J. Peluso[7], Rebecca Hoh[7], Timothy J. Henrich[10], Steven G. Deeks[7], Michelle Davidson[11], Scott Lu[12], Sarah A. Goldberg[12], J. Daniel Kelly[12,13], Jeffrey N. Martin[12], Cynthia A. Vierra-Green[14], Stephen R. Spellman[14], David J. Langton[15], Michael J. Dewar-Oldis[4], Corey Smith[16], Peter J. Barnard[4], Sulggi Lee[7], Gregory M. Marcus[6], Jeffrey E. Olgin[6], Mark J. Pletcher[12,17], Martin Maiers[14], Stephanie Gras[4,5,19] & Jill A. Hollenbach[1,12,19] ✉

Augusto DG, et al. (2023) Nature Aug; 620(7972):128-136.

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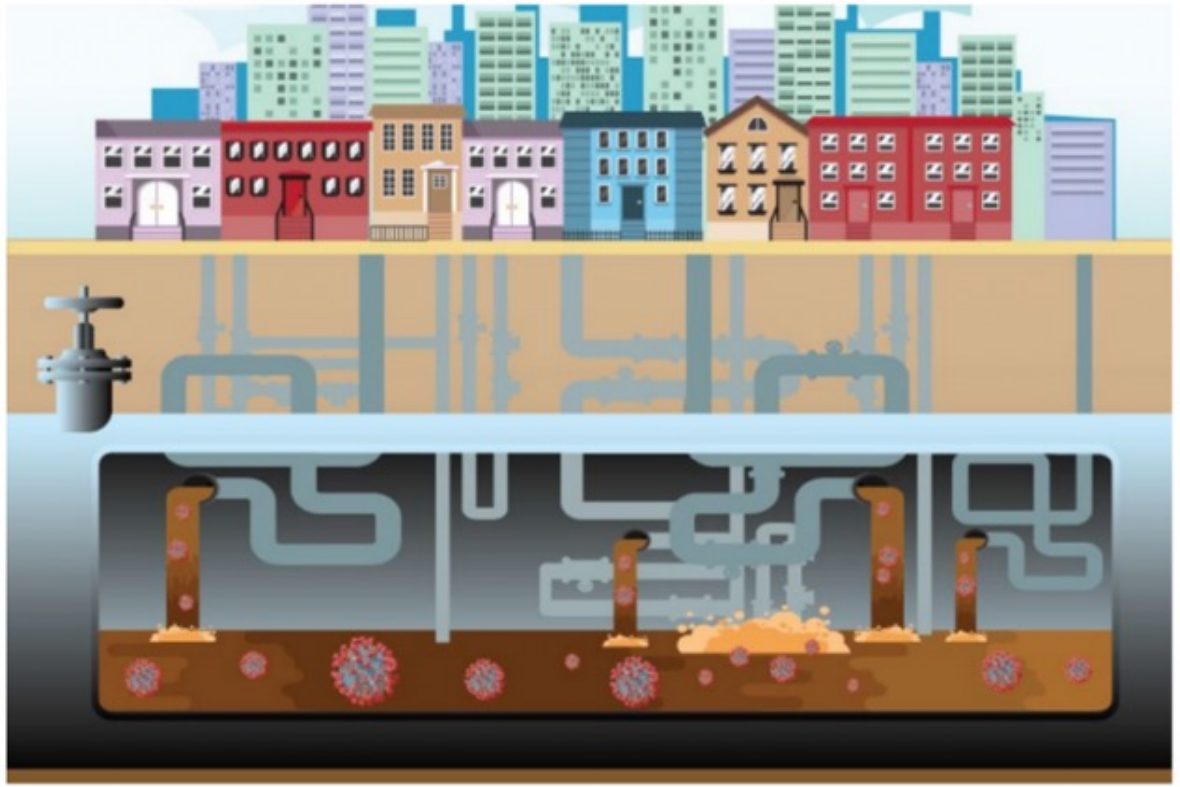
Advanced Molecular Detection (AMD)

CDC > Advanced Molecular Detection (AMD) > What's New > 2022

- Advanced Molecular Detection (AMD)
- Who We Are +
- What We Do +
- What's New –

Wastewater Surveillance: A New Frontier for Public Health



https://www.cdc.gov/amd/whats-new/wastewater-surveillance.html

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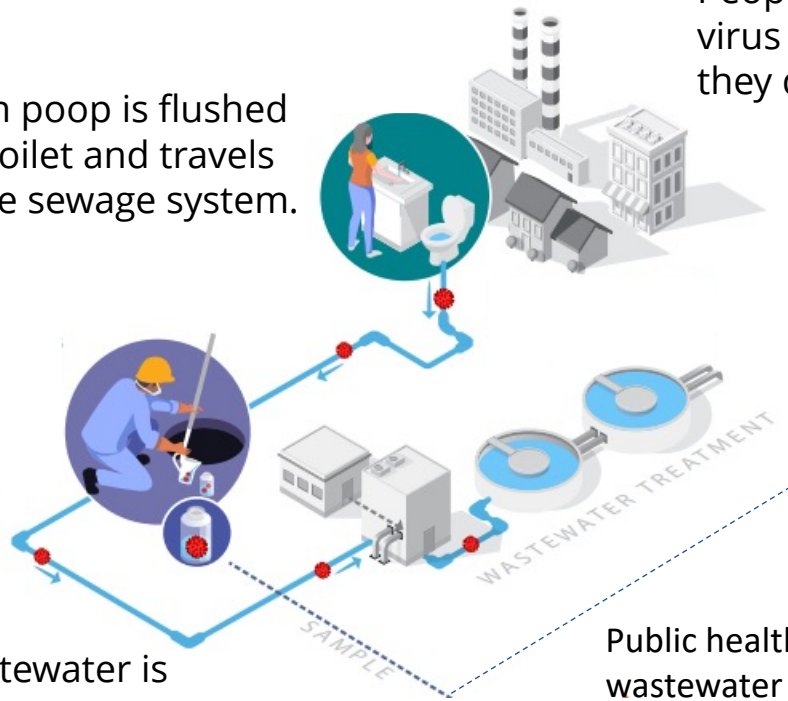
Wastewater Surveillance

People with COVID-19 can shed the virus in their feces (poop), even if they don't have symptoms.

The virus in poop is flushed down the toilet and travels through the sewage system.



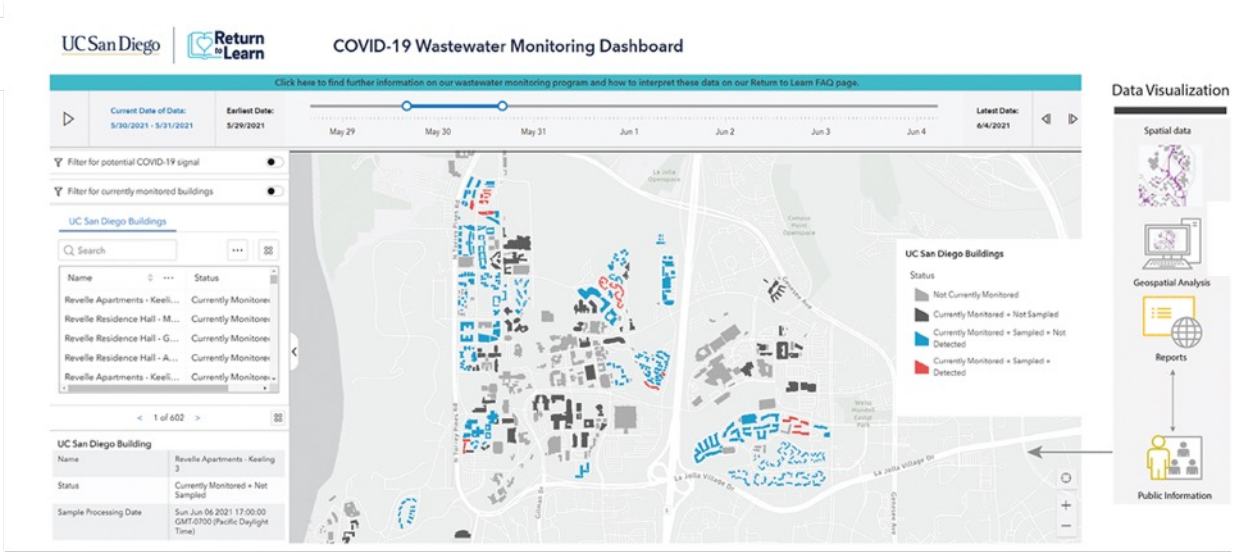
Laboratories test for the virus and measure virus levels in the wastewater.

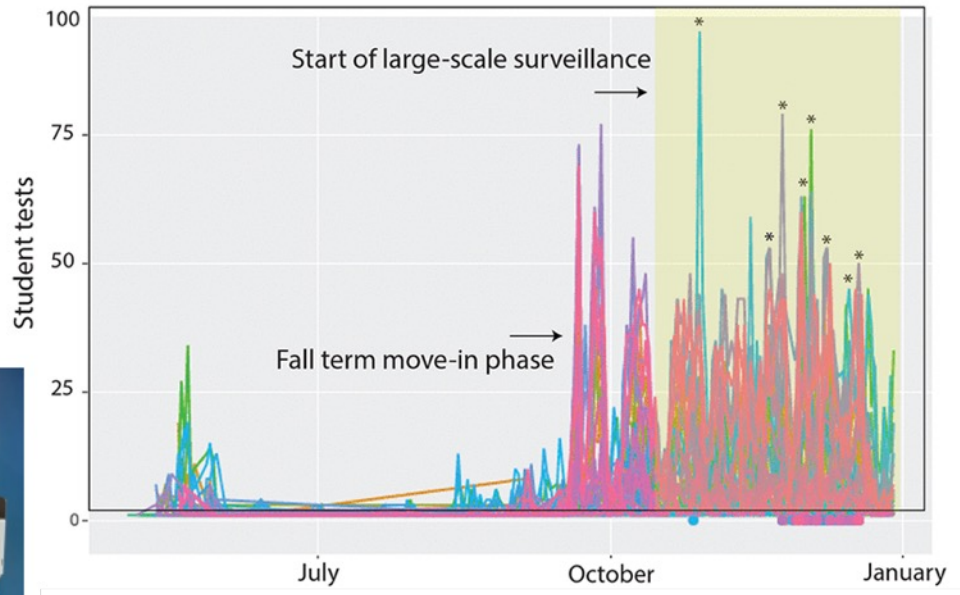
Before wastewater is treated, wastewater technicians take samples to get information about the virus.

Public health officials use wastewater data to better understand COVID-19 trends in communities and make decisions, such as where to have mobile testing and vaccination sites.

Adapted from www.cdc.gov/nwss

Wastewater Surveillance to Public Health Action





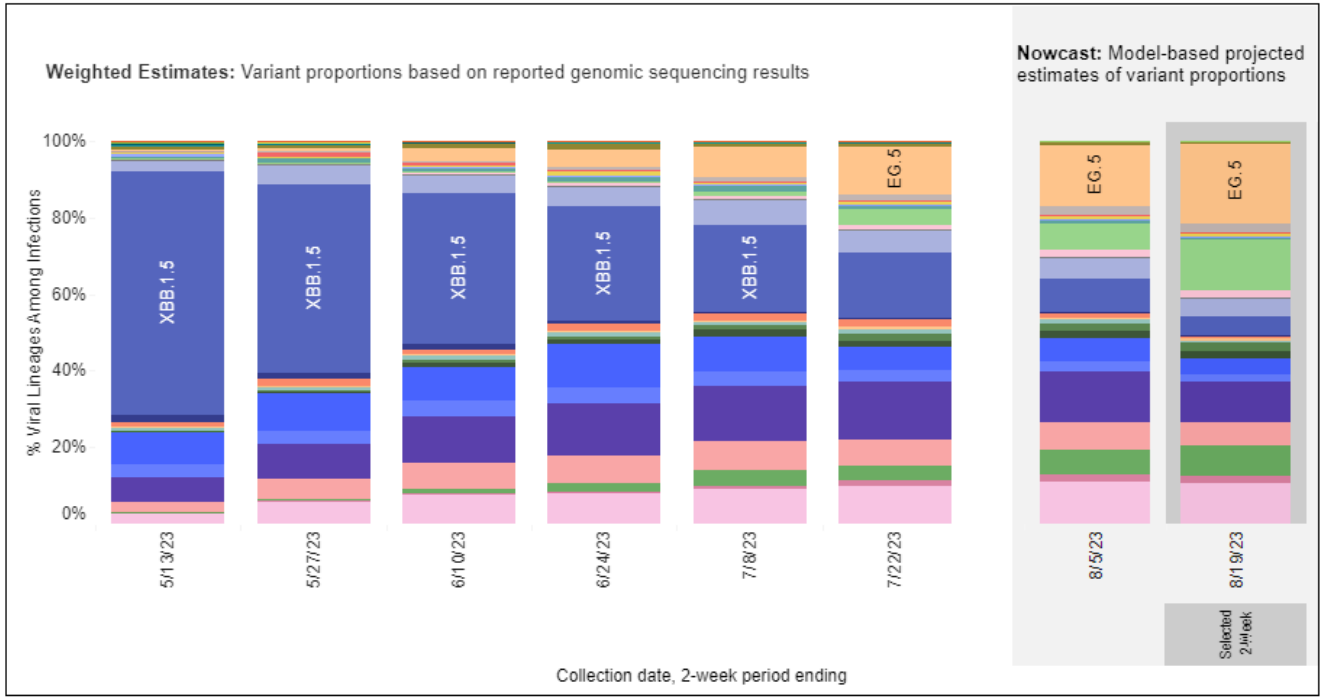
Adapted from Karthikeyan, et al. (2021mSystems; 6(4):e0079321.

Photo: https://www.reuters.com/business/healthcare-pharmaceuticals/uc-san-diego-offers-students-covid-test-kits-by-vending-machine-2021-01-06/ machine | Reuters

SARS-CoV-2 Variant Tracking by Wastewater Monitoring

Weighted and Nowcast Estimates in United States for 2-Week Periods in 4/30/2023 – 8/19/2023

Hover over (or tap in mobile) any lineage of interest to see the amount of uncertainty in that lineage's estimate.



Nowcast Estimates in United States for 8/6/2023 – 8/19/2023

USA

WHO label	Lineage #	US Class	%Total	95%PI
Omicron	EG.5		20.6%	17.8-23.8%
	FL.1.5.1		13.3%	9.4-18.4%
	XBB.1.16		10.7%	9.2-12.4%
	XBB.2.3		10.6%	8.6-13.0%
	XBB.1.16.6		8.0%	6.4-10.1%
	XBB.1.16.1		5.9%	5.1-6.9%
	XBB		5.1%	4.0-6.4%
	XBB.1.5		4.7%	4.0-5.6%
	XBB.1.9.1		4.1%	3.5-4.8%
	XBB.1.5.70		2.4%	1.7-3.4%
	EG.6.1		2.3%	1.6-3.3%
	XBB.1.16.11		1.9%	1.1-3.4%
	XBB.1.5.72		1.9%	1.5-2.4%
	XBB.1.9.2		1.8%	1.4-2.3%
	GE.1		1.8%	1.1-2.7%
	XBB.1.5.10		1.0%	0.7-1.4%
	FE.1.1		0.9%	0.5-1.5%
	FD.1.1		0.8%	0.5-1.4%
	CH.1.1		0.8%	0.5-1.2%
	XBB.1.5.68		0.6%	0.4-1.0%
	XBB.1.5.59		0.4%	0.3-0.8%
	EU.1.1		0.2%	0.1-0.3%
	XBB.1.5.1		0.1%	0.1-0.1%
	BA.2.12.1		0.0%	0.0-0.2%
	BA.2		0.0%	0.0-0.0%
	FD.2		0.0%	0.0-0.0%
	BA.5		0.0%	0.0-0.0%
	BQ.1		0.0%	0.0-0.0%
	BQ.1.1		0.0%	0.0-0.0%
Other	Other*		0.1%	0.0-0.1%

* Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one 2-week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all 2-week periods displayed.

BA.1, BA.3 and their sublineages (except BA.1.1 and its sublineages) are aggregated with B.1.1.529. Except BA.2.12.1, BA.2.75, XBB and their sublineages, BA.2 sublineages are aggregated with BA.2. Except BA.2.75.2, CH.1.1 and BN.1, BA.2.75 sublineages are aggregated with BA.2.75. Except BA.4.6, sublineages of BA.4 an aggregated to BA.4. Except BF.7, BF.11, BA.5.2.6, BQ.1 and BQ.1.1, sublineages of BA.5 are aggregated to BA.5. Except the lineages shown and their sublineages, sublineages of XBB are aggregated to XBB. Except XBB.1.5.1,XBB.1.5.10,FD.2,EU.1.1,XBB.1.5.68 and XBB.1.5.70 sublineages of XBB.1.5 are aggregated to XBB.1.5 Except FL.1.5.1, sublineages of XBB.1.9.1 are aggregated to XBB.1.9.1. Except XBB.1.16.1,XBB.1.16.11 sublineages of XBB.1.16 are aggregated to XBB.1.16. Except FE.1.1, sublineages of XBB.1.18.1 are aggregated to XBB. For all the other lineages listed, their sublineages are aggregated to the listed parental lineages respectively Previously, FL.1.5.1, GE.1, EG.6.1, FD.1.1, was aggregated to XBB.1.9.1, XBB.2.3.10, XBB.1.9.2, and XBB.1.5.15 respectively. Lineages BA.2.75.2, XBB, XBB.1.5 , XBB.1.5.1, XBB.1.5.10, FD.2, XBB.1.9.1, XBB.1.9.2, XBB.1.16, XBB.1.16.1, XBB.2.3, BN.1, BA.4.6, BF.7, BF.11, BA.5.2.6 ,BQ.1.1, EU.1.1, XBB.1.5.68, FE.1.1, EG.6 XBB.1.5.72 , FL.1.5.1, GE.1, EG.6.1,XBB.1.16.11, FD.1.1 and XBB.1.5.70 contain the spike substitution R346T.

https://covid.cdc.gov/covid-data-tracker/#variant-summary

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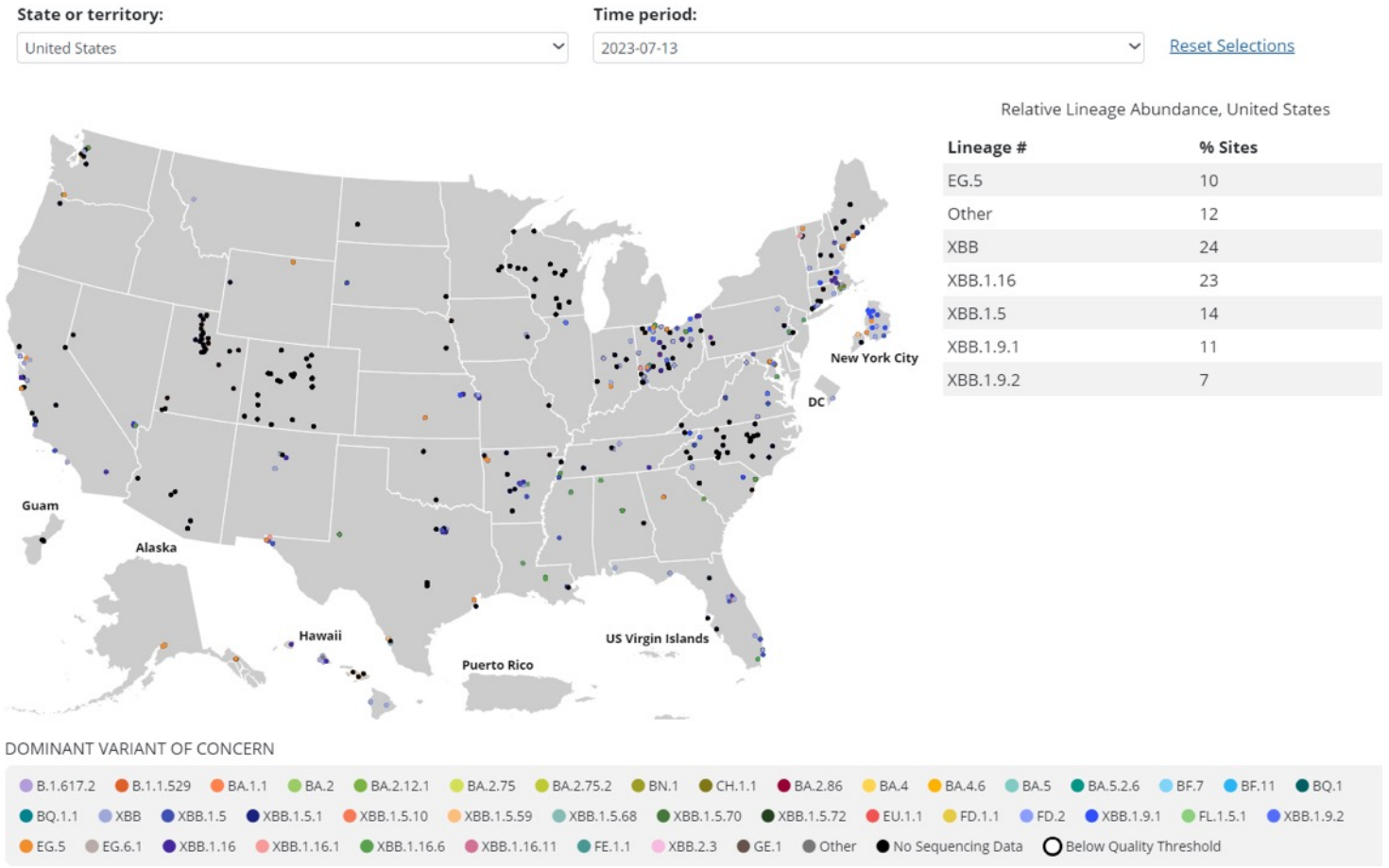
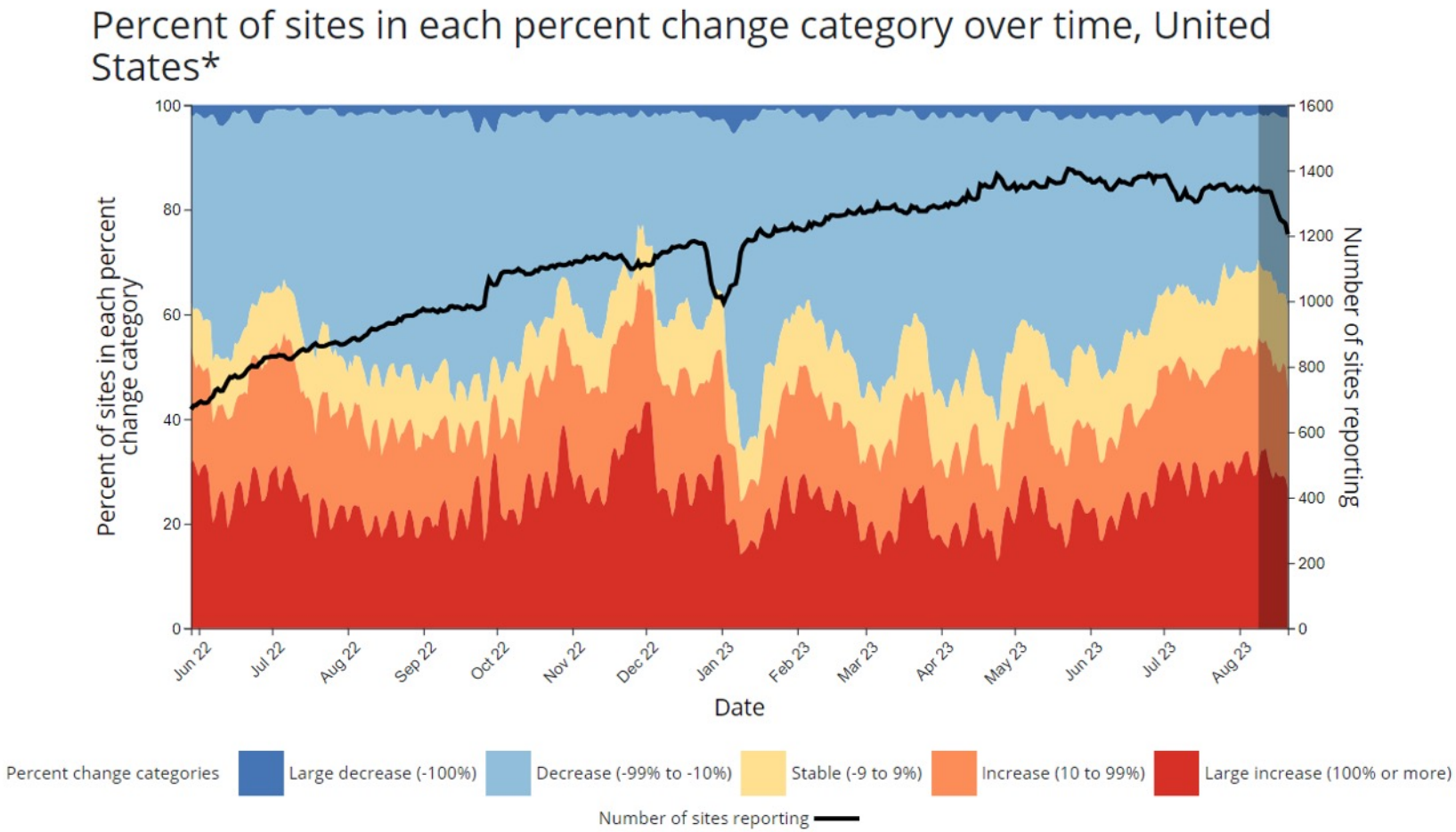
National Wastewater Surveillance System



https://covid.cdc.gov/covid-data-tracker/#wastewater-surveillance

Wastewater Metric Chart: SARS-CoV-2



https://covid.cdc.gov/covid-data-tracker/#wastewater-surveillance

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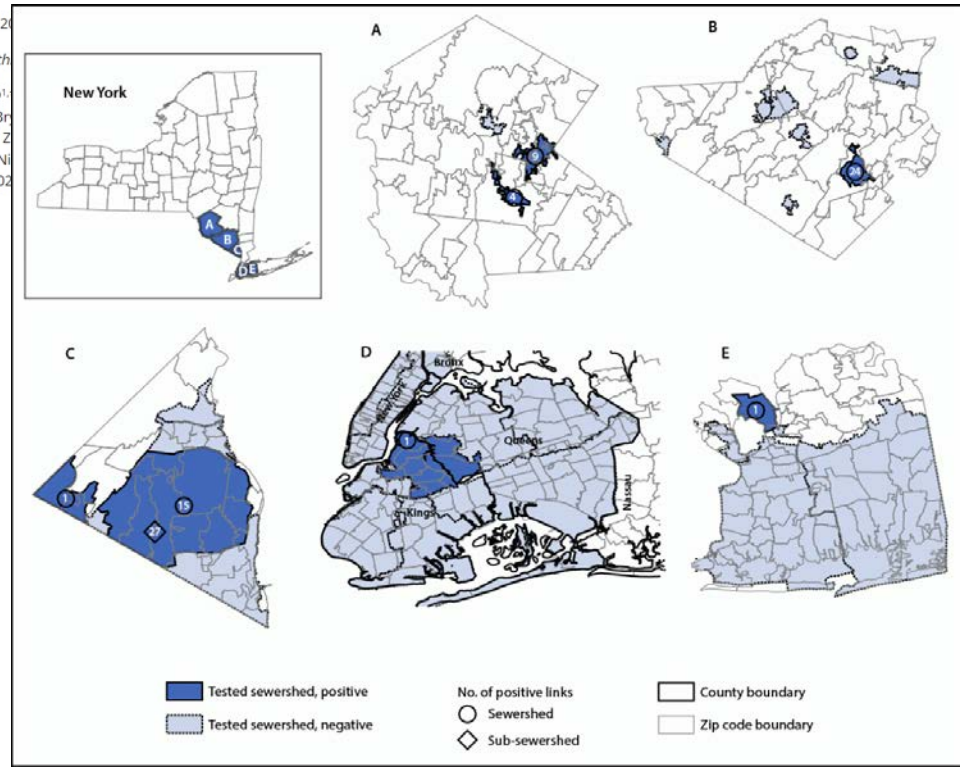
Morbidity and Mortality Weekly Report (*MMWR*)

Wastewater Testing and Detection of Poliovirus Type 2 Genetically Linked to Virus Isolated from a Paralytic Polio Case — New York, March 9–October 11, 2022

Weekly / November 4, 2

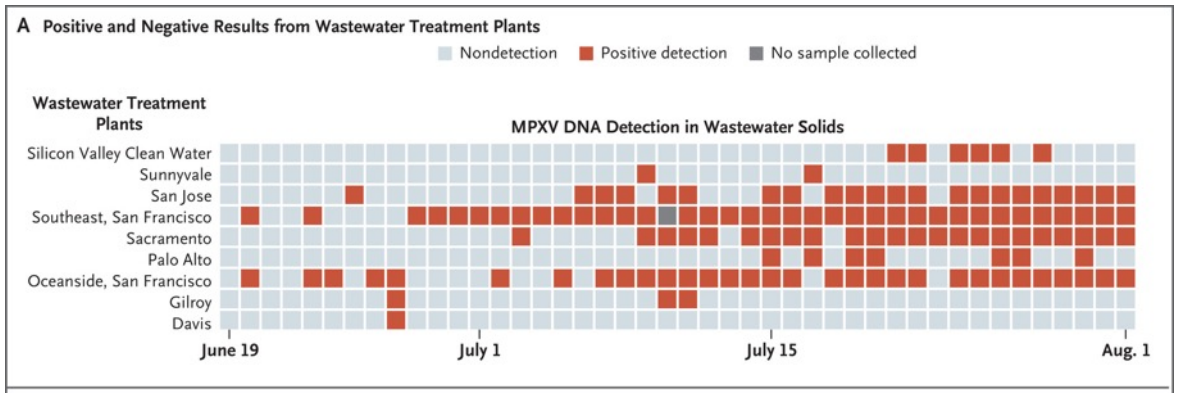
On October 28, 2022, th

A. Blythe Ryerson, PhD[1]; Emily Lutterloh, MD[2]; Br Gelman, DPM[8]; Jane R. Z Adriana Lopez, MHS[1]; Ni Rosenberg, PhD[2,11,*]; 202



The NEW ENGLAND JOURNAL of MEDICINE

Use of Wastewater for Mpox Outbreak Surveillance in California



Ryerson AB, et al. (2022) MMWR ;71:1418–1424.
Wolfe MK, et al. (2023) NEJM 388(6): 570-572.

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CDC > Advanced Molecular Detection (AMD) > What's New > 2022

Advanced Molecular Detection (AMD)

- Who We Are +
- What We Do +
- What's New –

CDC launches Traveler-based SARS-CoV-2 Genomic Surveillance Program

Print

Early warning detection system for new SARS-CoV-2 variants active at four US International airports

PARTICIPATING AIRPORTS

Seattle (SEA)	New York City (JFK)
San Francisco (SFO)	Newark (EWR)
Los Angeles (LAX)	Washington D.C./Dulles (IAD)

https://wwwnc.cdc.gov/travel/page/travel-genomic-surveillance#impact
https://www.cdc.gov/amd/whats-new/airport-genomic-surveillance.html

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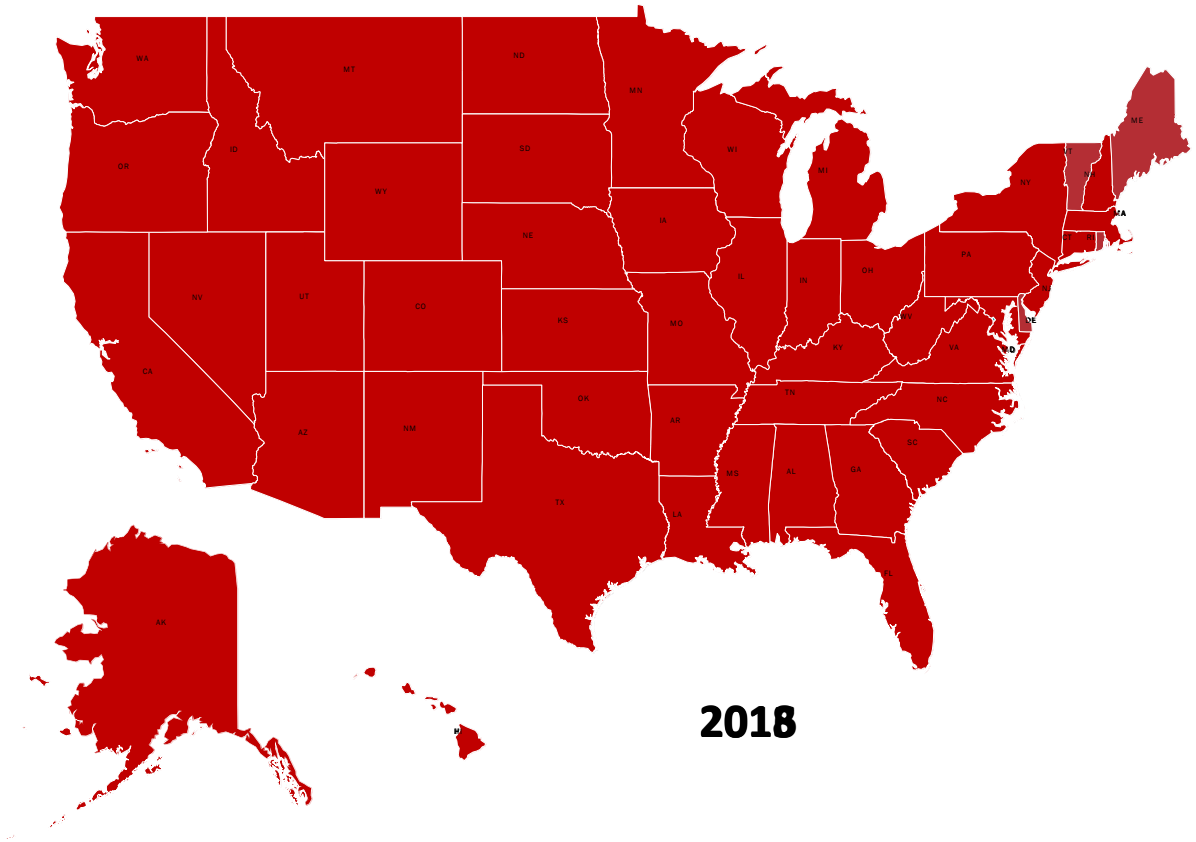
NGS Capacity in the States (2013-2018)



- Growing list of applications
  - **PulseNet**
  - **Healthcare-associated infections**
  - Bacterial meningitis
  - Cryptococcus
  - Cyclospora
  - **Viral hepatitis**
  - Gonococcus
  - Influenza
  - **Legionella**
  - Malaria
  - Streptococcus
  - Tickborne diseases
  - **Tuberculosis**
  - …

AMD Workforce Development

APHL FELLOWSHIP PROGRAMS

APHL-CDC Infectious Disease Bioinformatics Fellowship

I am a Public Health Bioinformatician

Bioinformatics is revolutionizing the way the world tracks and detects infectious diseases. In public health, the use of Next Generation Sequencing (NGS) technology has reshaped outbreak investigations and pathogen surveillance. Bioinformaticians are crucial for this transition to the use of NGS in public health. They develop pipelines and help interpret the data, identifying and characterizing pathogens; playing a vital role in the public health engine that keeps us all healthy.

The US Centers for Disease Control and Prevention (CDC)'s Advanced Molecular Detection initiative is spearheading use of NGS technology in public health laboratories. The Association of Public Health Laboratories (APHL) and CDC Office of Advanced Molecular Detection (OAMD) are offering exciting fellowship opportunities for graduates of bioinformatics and related programs to apply their skillset and become part of the public health engine.

Opening in Fall 2022

"The work is both satisfying and gratifying. I'm getting to use my knowledge and my position to make an impactful and meaningful difference in people's lives by preventing illness and fighting the spread of disease through modern surveillance and computational techniques.

— Logan Fink, 2018 Fellow
Colorado Department of Public Health and Environment

Learn more about this and other APHL-CDC Fellowship Programs:
www.aphl.org/fellowships

Follow Us! #APHLFellows

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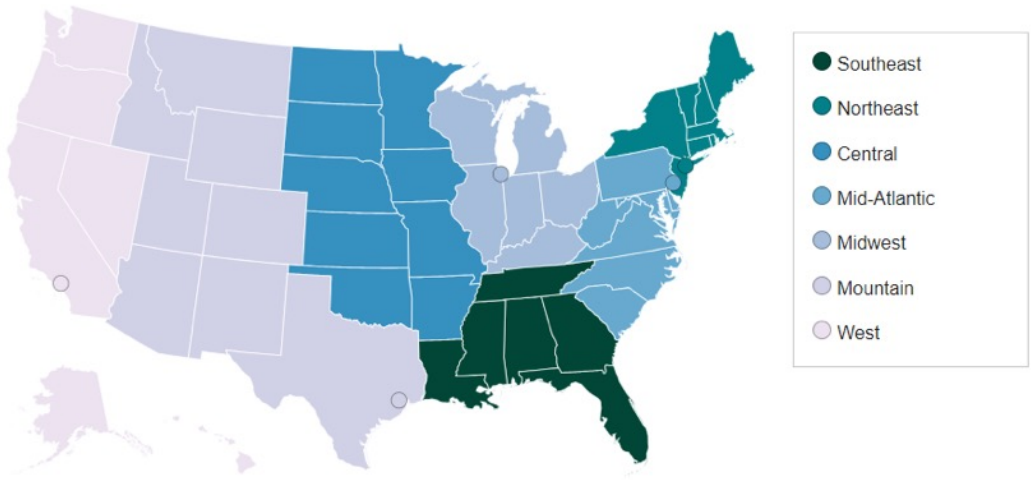
Workforce Development



Download Data (CSV)

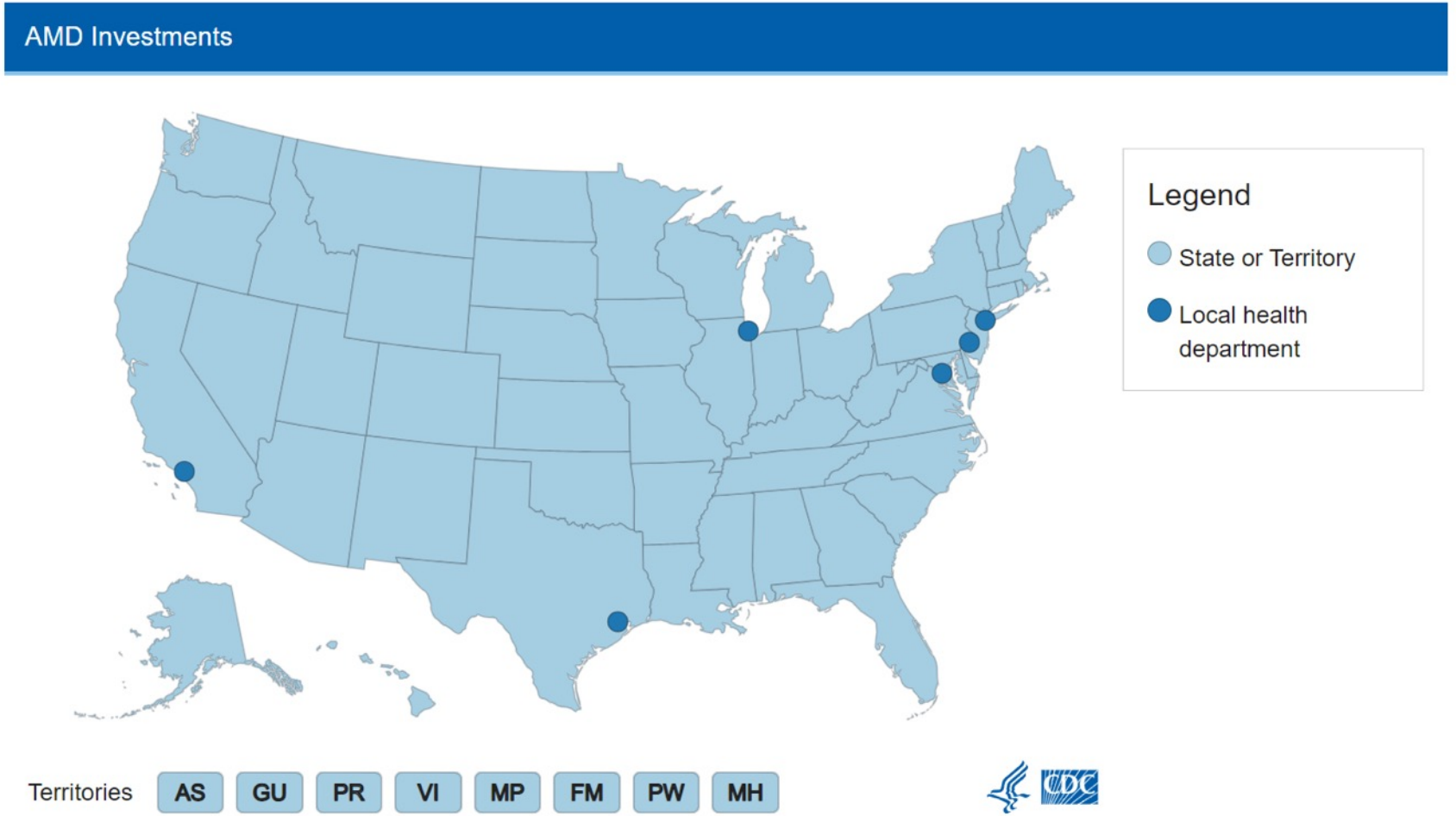
Data Table +

AMD Regional Workforce Development Training Leads provide support to labs within the region and across regions on cross-cutting AMD training to help staff develop the critical skills necessary to extract, analyze, and interpret sequencing data. Regional training may incorporate local or regional resources or collaboration with academic institutions.

AMD Regional Bioinformatics Support Leads act as regional consultants. Often referred to as Bioinformatics Regional Resource, or BRRs, they provide support to labs within the region and across regions to help develop national bioinformatics. The state public health lab serving as the BRR may also be the AMD Training Lead for the region. In addition to assisting with training, BRRs assist state and local staff with data analysis. They also consult with local or state IT departments, CDC, and other partners on how to implement or expand the use of AMD technologies.

https://www.cdc.gov/amd/investments/index.html

AMD Investments: 64 Jurisdictions



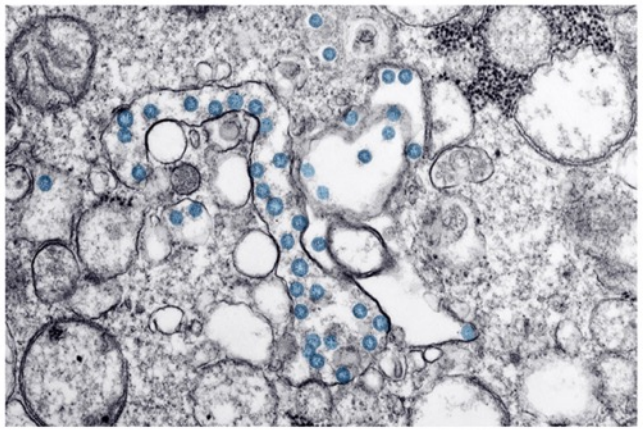
https://www.cdc.gov/amd/investments/index.html

The New York Times

The Coronavirus Outbreak › | LIVE Latest Updates | Maps and Tracker | Living at Home | Newsletter

Labs Across U.S. Join Federal Initiative to Study Coronavirus Genome

The project, announced by the C.D.C., will help trace patterns of transmission, investigate outbreaks and map how the virus is evolving, which can affect a cure.



Virus particles, marked in blue, that were taken from an early Covid-19 patient in the U.S. C.D.C./E.P.A., via Shutterstock

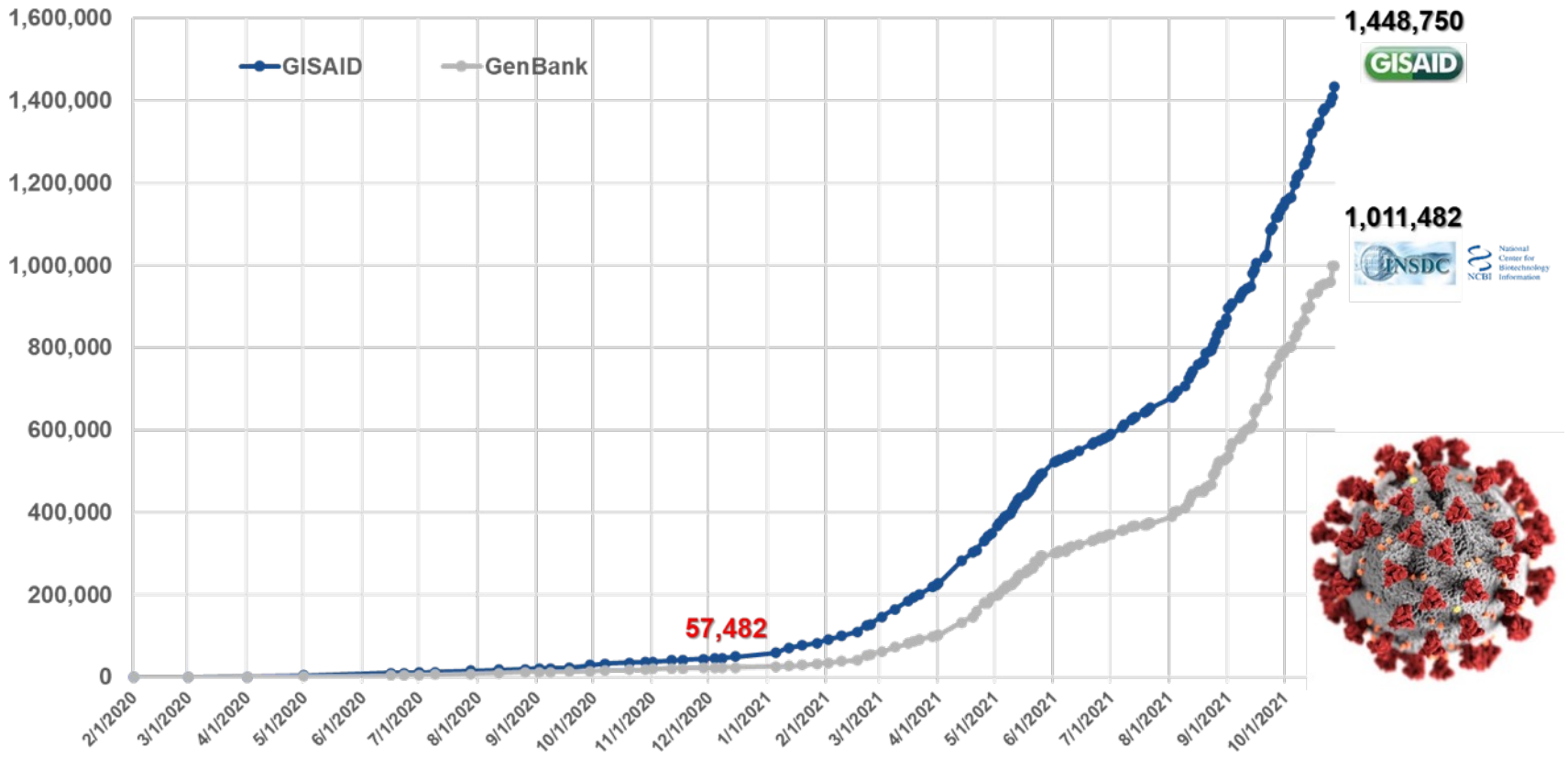
By Sheri Fink

Published April 30, 2020 Updated May 6, 2020

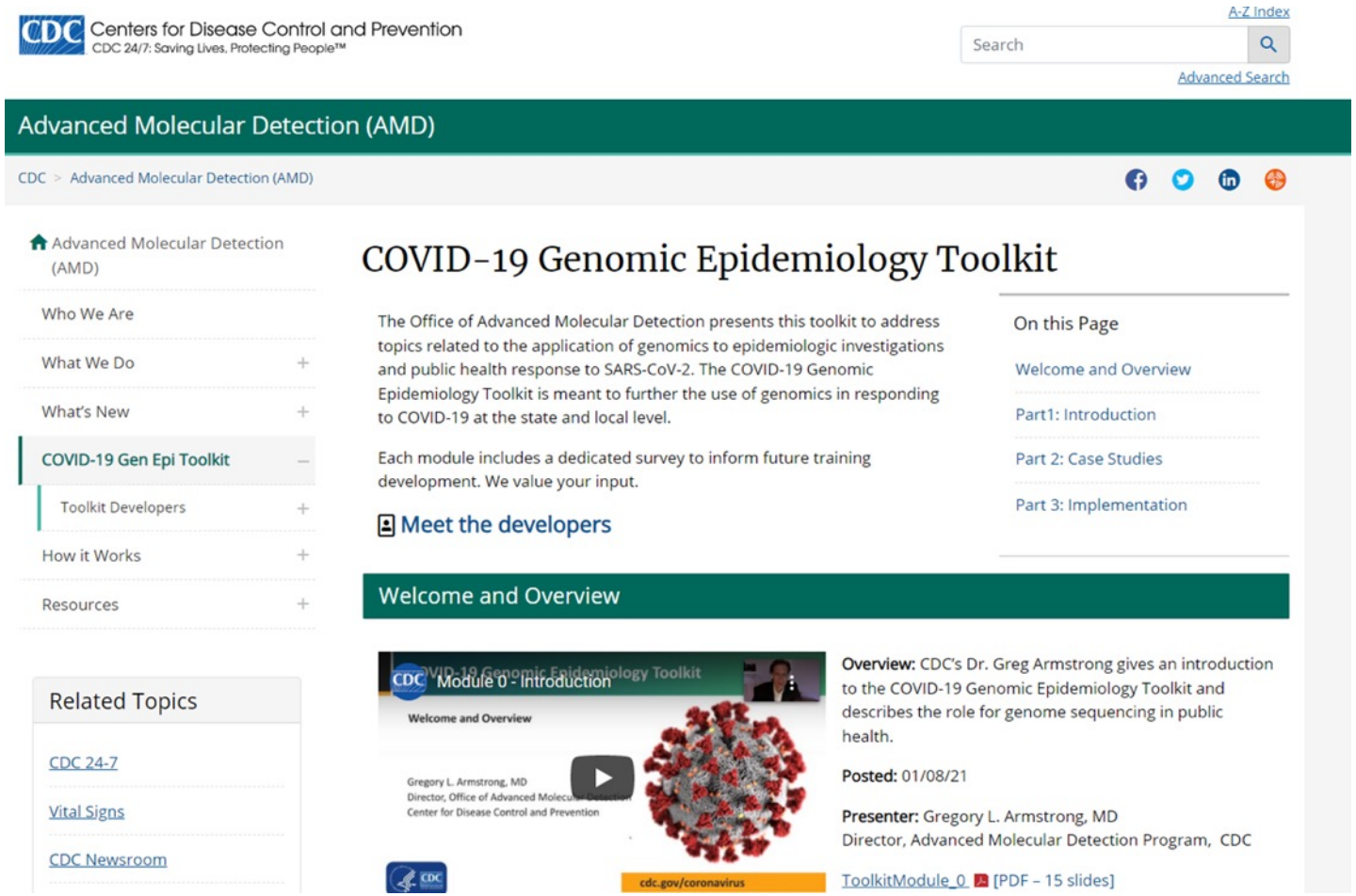
The Centers for Disease Control and Prevention on Thursday announced a national initiative to speed research into how the coronavirus was spreading around the country, bringing together at least 75 public health, academic and commercial institutions studying its genome.

https://www.nytimes.com/2020/04/30/science/coronavirus-genetic-sequencing.html

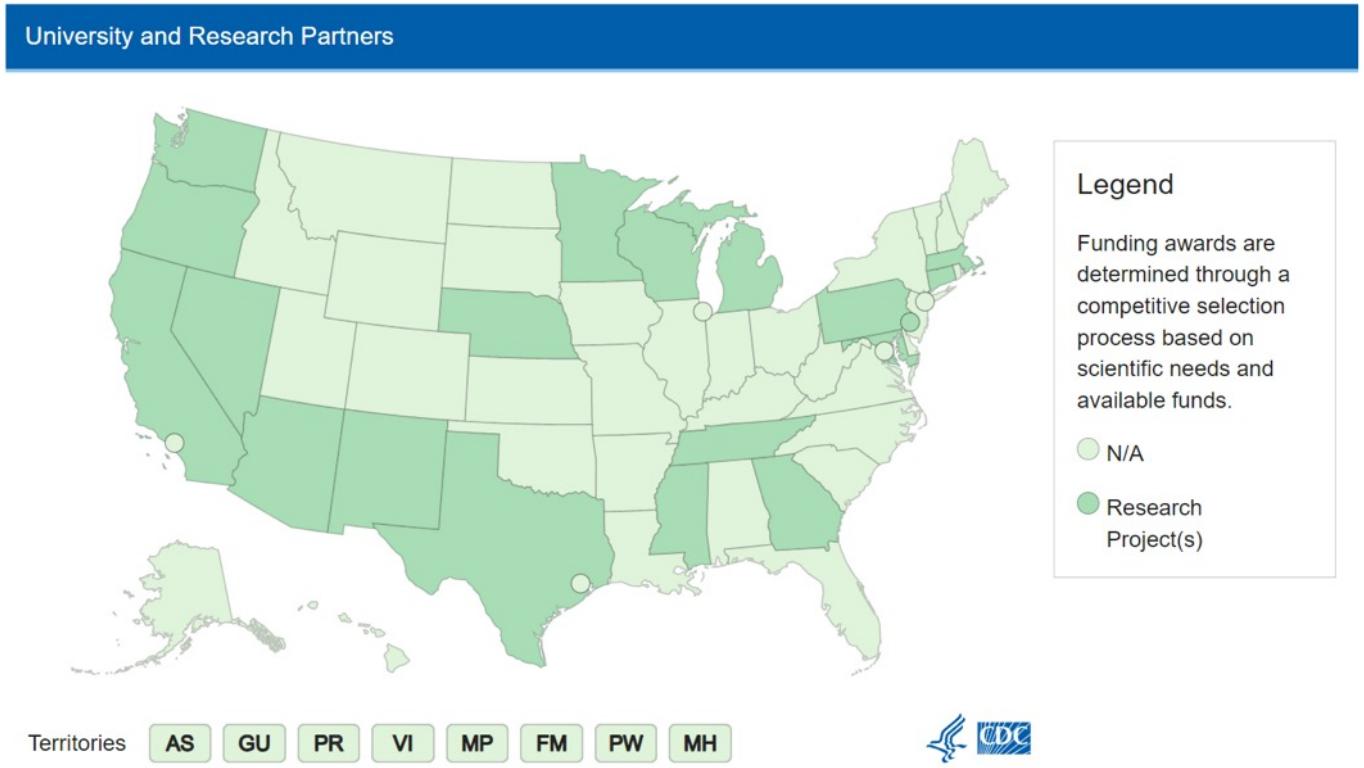
Public SARS-CoV-2 Sequence Data from US Laboratories



COVID-19 Genomic Epidemiology Toolkit



Innovation: Broad Agency Announcement Awards



39 Research Awards to Date

Bioinformatic analysis tools

Patterns of SARS-CoV-2 spread

Host markers associated with COVID-19 severity

Multi-modal data integration and analysis

Transmissibility of SARS-CoV-2 variants

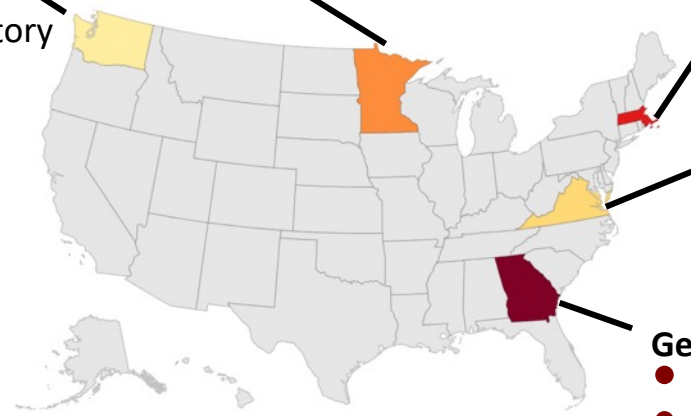
https://www.cdc.gov/amd/investments/index.html

Pathogen Genomics Centers of Excellence Network

Minnesota Department of Health
- University of Minnesota
- Mayo Clinic
- University of Pennsylvania College of Veterinary Medicine

Massachusetts Department of Health
- Broad Institute of MIT and Harvard
- Boston University
- Mass General Brigham hospital network
- Yale University
- Fathom Information Design
- Theiagen Genomics
- Harvard Medical School

Washington State Department of Health
- University of Washington
- Fred Hutchinson Cancer Center
- Washington Animal Disease Diagnostic Laboratory
- Public Health – Seattle & King County



Virginia Division of Consolidated Laboratory Services
- Virginia Department of Health
- Virginia Commonwealth University
- University of Virginia

Georgia Department of Public Health
- University of Georgia
- Georgia Tech Research Institute
- Emory University
- Augusta University
- Georgia State University
- University of Texas Health Science Center at Houston

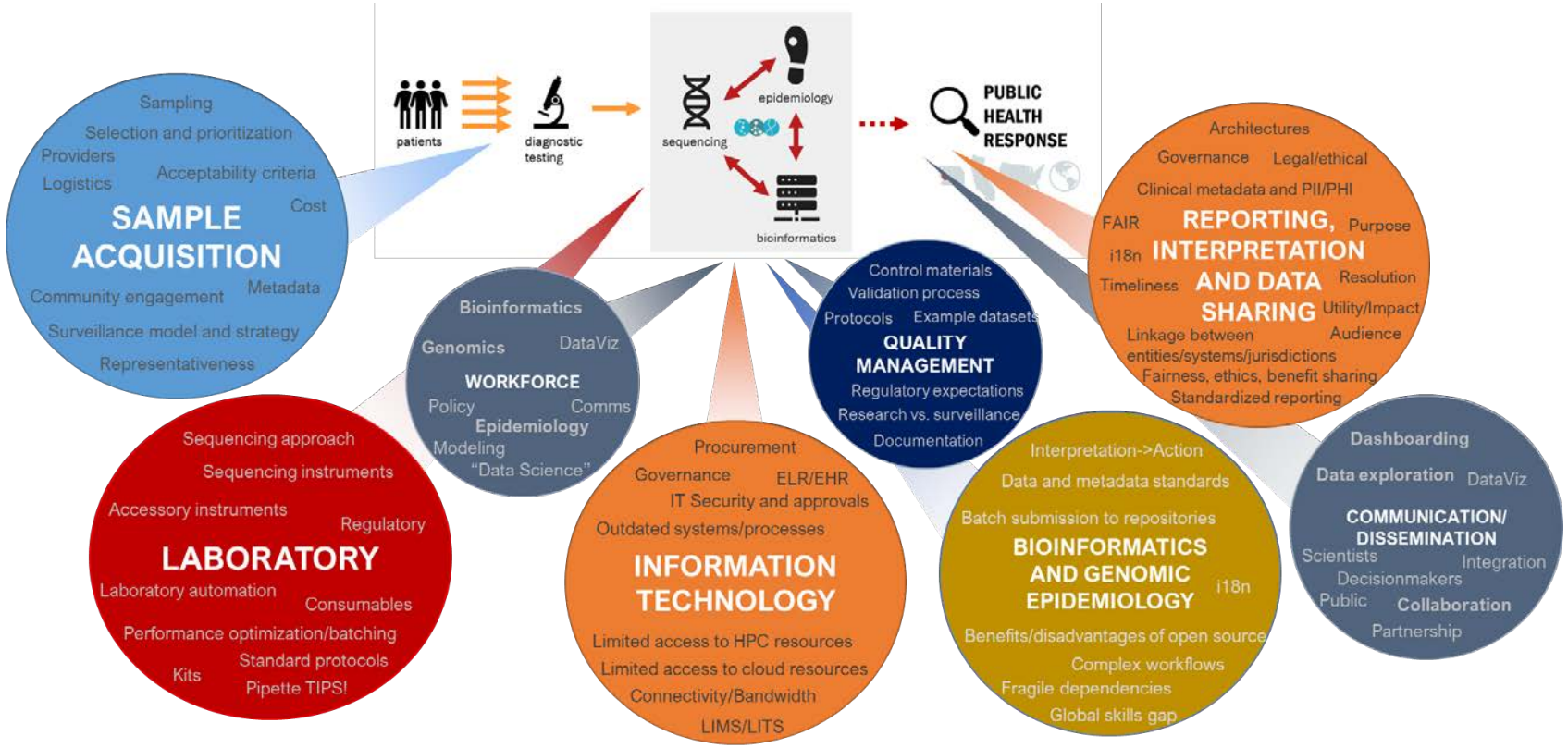
Pathogen Genomics Centers of Excellence

Innovation

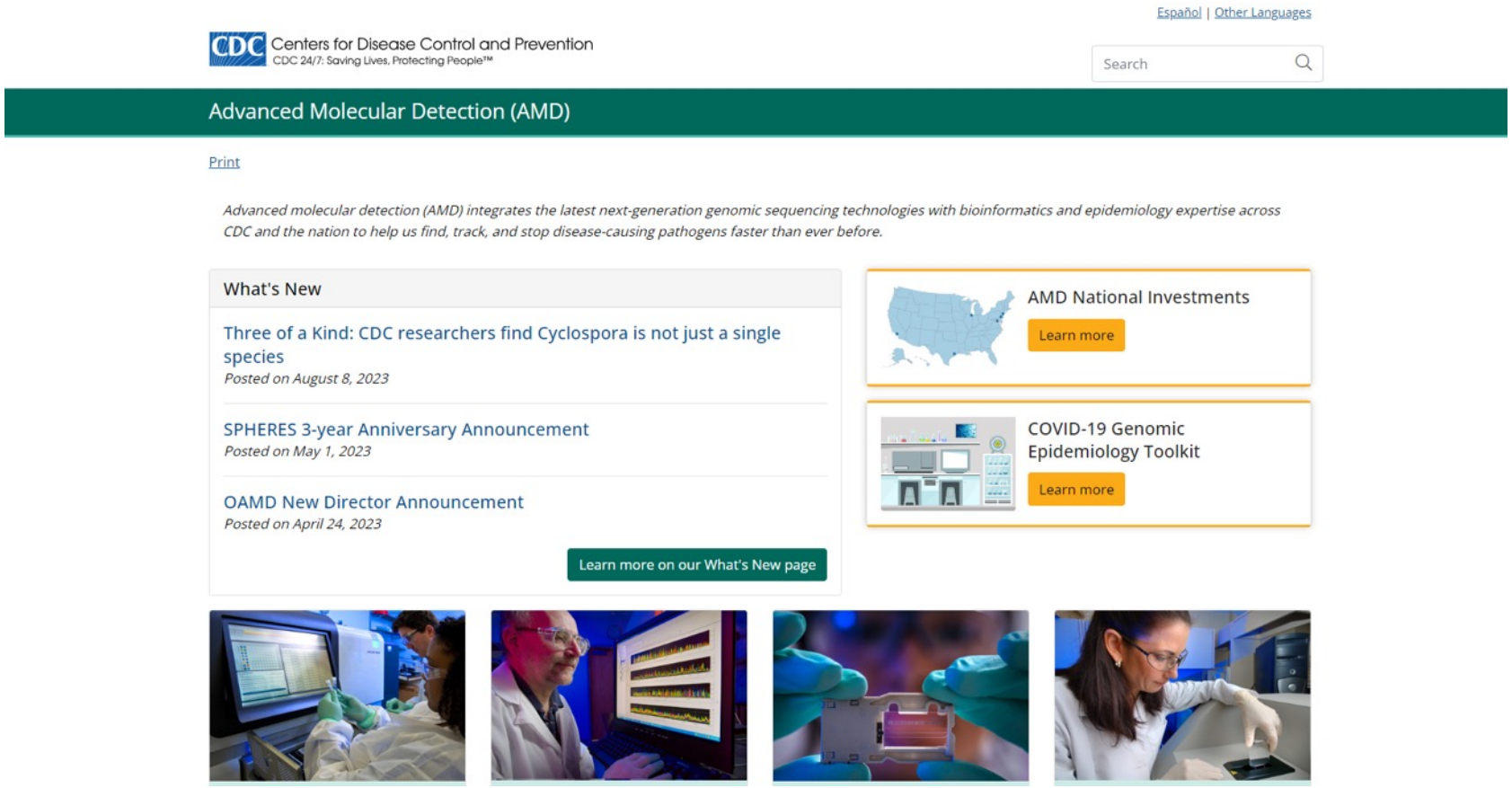
Education

Response

Challenges and Opportunities nd



Resources



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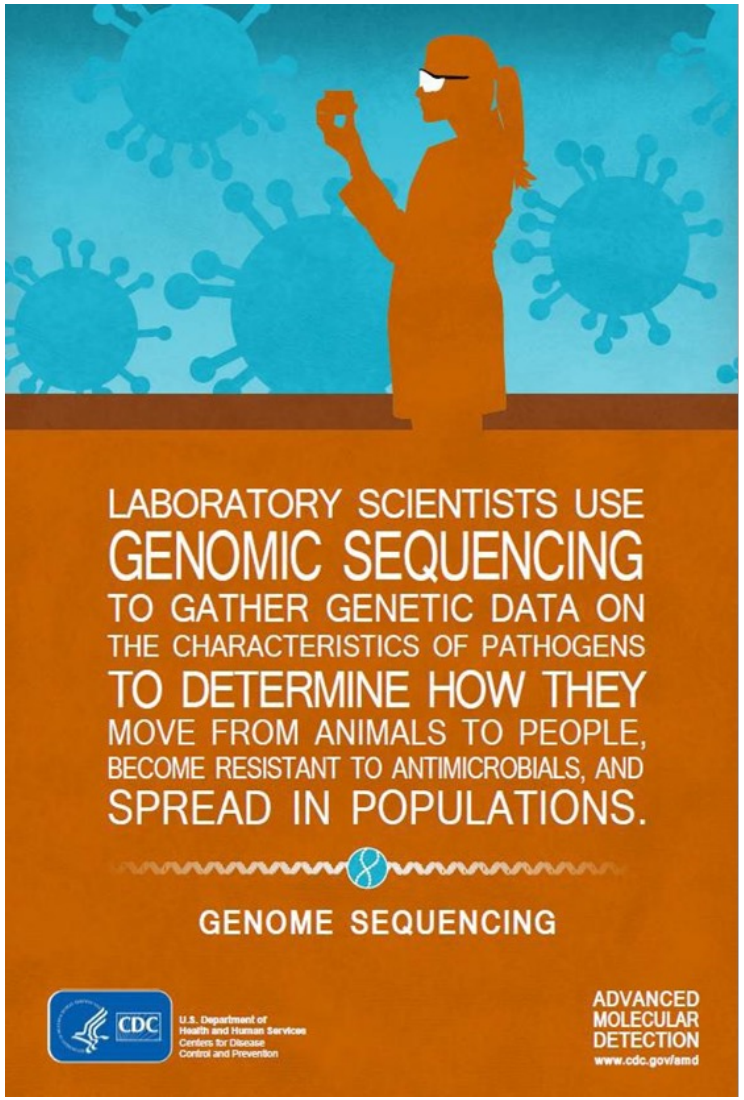

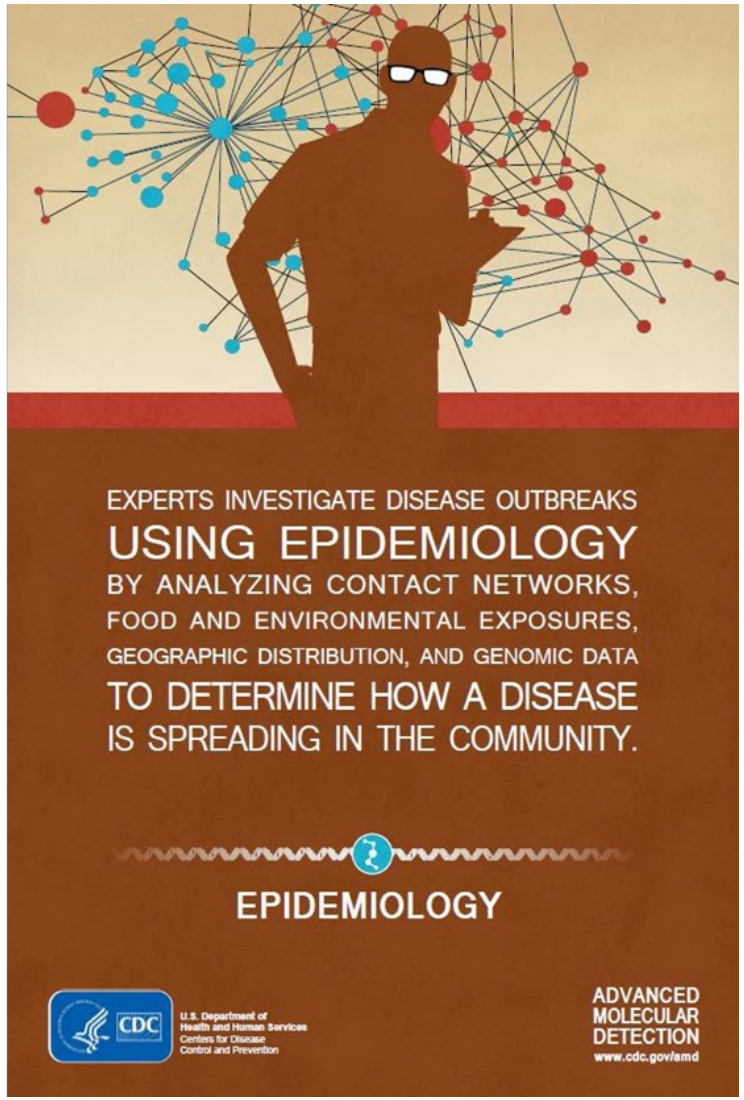

Thank you. http://www.cdc.gov/amd