Chicago Department of Public Health
Genomic Sequencing Annual Report 2023

What is genomic sequencing?

The Chicago Department of Public Health (CDPH), in collaboration with the Regional Innovative Public Health Laboratory (RIPHL) at Rush University Medical Center, makes a concerted effort to understand the presence and spread (i.e., prevalence and incidence) of various genetic mutations in bacteria, viruses, and fungi (i.e., target pathogens) of public health interest.

How does CDPH use genomic epidemiology and sequencing data?

Genomic epidemiology makes use of a method called Whole Genome Sequencing (WGS), which looks for specific information within the genetic material of specific pathogens. Public health experts and clinical providers can learn a lot about the current state of diseases in Chicago by understanding which specific types of each disease is circulating—for instance, some are more infectious while others are able to evade a patient's immune system easier. We collect genomic data, summarize it in a variety of ways, and then pass it along to various City officials, Chicago hospitals, and public health providers.

The following sections highlight some of the important genomic sequencing work that was completed in Chicago in 2023, including investigation of SARS-CoV-2, mpox, and *Candida auris*.

How will CDPH sustain and grow the program in 2024?

CDPH will **continue SARS-CoV-2 sequencing** to monitor the variants and their associated mutations of interest circulating in Chicago. We will work to establish automated data exchanges with other public health data sets to enrich analysis and forecasting. Additionally, RIPHL and CDPH will work to **expand advanced molecular detection capacity** to other pathogens of public health importance such as *Legionella* spp. and *Neisseria gonorrhea*. CDPH will also produce educational videos to highlight this work and important public health activity.

SARS-CoV-2

Why did CDPH genetically sequence this virus?

Rapid genetic mutation of SARS-CoV-2, the virus that causes COVID-19, leads to the emergence of different SARS-CoV-2 variants. Hospitals and laboratories across Chicago voluntarily submit SARS-CoV-2 positive clinical specimens for genetic analysis **to understand which variants of SARS-CoV-2 are responsible for clinical illnesses in Chicago**. CDPH and RIPHL study the increase and decrease of these variants because they could be associated with increased transmission or enhanced immune escape. It is important to provide the public and medical community with **advanced warning of potentially more infectious or severe SARS-CoV-2 lineages**.

What did we find?

RIPHL successfully sequenced **nearly 3,000 SARS-CoV-2 specimens during the 2023 calendar year** (> 12,000 since the program began in March 2021). **RIPHL specimens were representative of**

Chicago at-large, with a similar demographic distribution as 2023 Chicago COVID-19 cases (Table 1). XBB, an Omicron sub-lineage that emerged in late 2022 was predominant in 2023 (Figure 1). RIPHL lineage proportions largely follow the CDC COVID-19 tracker for HHS Region 5 and broader US proportions.

How was this information used?

CDPH routinely utilized SARS-CoV-2 genomic reports to understand the landscape of COVID-19 in Chicago. Lineage proportion charts (Figure 1) show which variants are circulating in Chicago and at which proportions. It helps CDPH **identify and understand newly emerged lineages in Chicago** and their potential for increased disease spread.

RIPHL sequences were contributed to national and international public data consortiums including GISAID, and NCBI GenBank. RIPHL SARS-CoV-2 sequences account for 43% of all Chicago-based sequences and 18% of all Illinois-based sequences in GISAID.

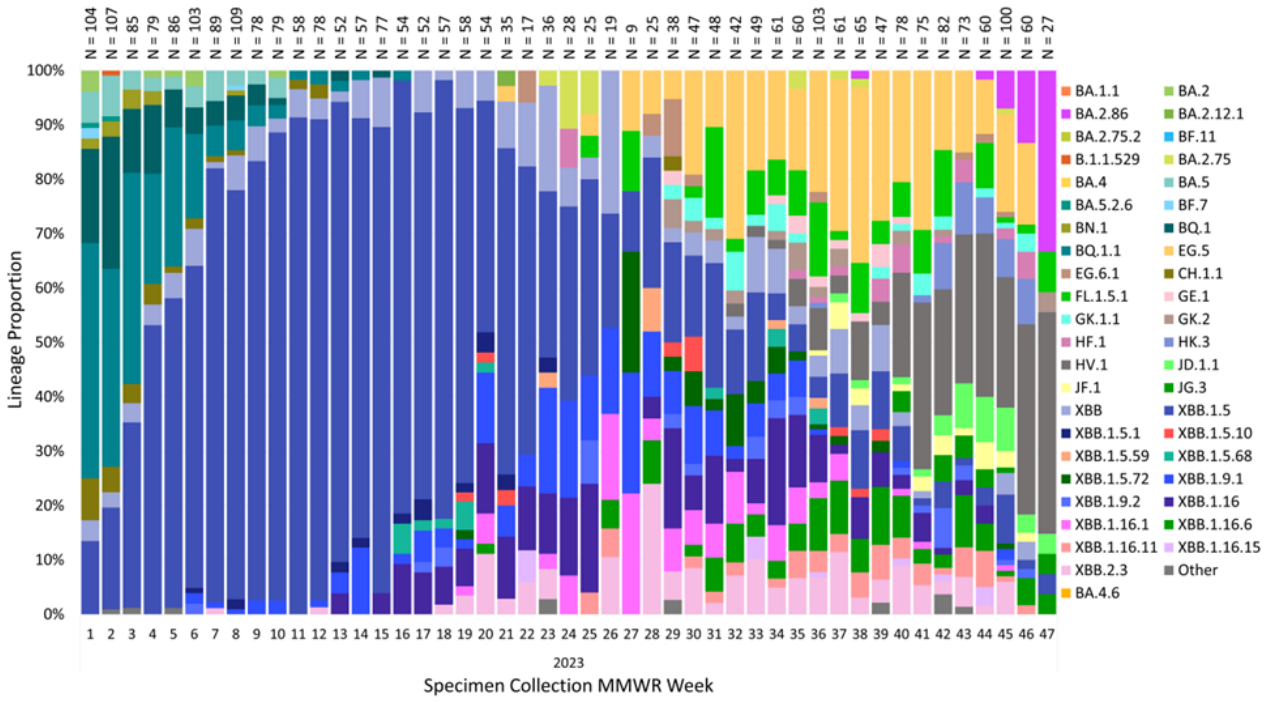
TABLE 1: Demographic distribution of RIPHL-sequenced SARS-CoV-2 specimens and Chicago cases

	RIPHL (N=2058)		Chicago Cases (N=55125)	
	N	%	N	%
Sex				
Female	1243	60%	31929	58%
Male	815	40%	23196	42%
Age				
0-17	551	27%	10724	19%
18-29	311	15%	7797	14%
30-39	255	12%	7988	14%
40-49	221	11%	6605	12%
50-59	199	10%	6909	13%
60-69	210	10%	6620	12%
70-79	177	9%	4904	9%
80+	134	7%	3574	6%
Race/Ethnicity				
Asian Non-Latinx	111	5%	2722	5%
Black Non-Latinx	765	37%	17600	32%
Latinx	601	29%	14333	26%
Other Non-Latinx	163	8%	2554	5%
White Non-Latinx	355	17%	13251	24%
Unknown	63	3%	4665	8%
Region				
Central	94	5%	3031	5%
Far South	177	9%	5935	11%
North	155	8%	11385	21%
Northwest	391	19%	11055	20%
South	354	17%	6025	11%
Southwest	380	18%	8330	15%
West	503	24%	9203	17%
Unknown	4	0.2%	161	0.3%

(note that data only reflects samples collected January 1 through November 8, 2023)

FIGURE 1: SARS-CoV-2 lineage proportions determined from RIPHL clinical samples by MMWR week of specimen collection

Proportion of lineages detected are presented across MMWR weeks (through the most recent data in Week 47, starting 11/19/2023). Date of specimen collection is used to bin results by date. The total number of specimens sequenced per week is noted at the top of each weekly column.



Mpox virus

Why did CDPH genetically sequence this virus?

Mpox caused a global outbreak in 2022 after previously causing only rare human-to-human transmission. While cases in 2023 were much lower than in 2022, the virus is still circulating on-and-off and in limited locations in 2023.

Like all viruses, the mpox virus acquires mutations as it spreads, and when clusters of specimens containing shared mutations are identified, they can be classified into lineages. CDPH began tracking a cluster of mpox illness in the spring and early summer of 2023, a time during which case numbers were very low elsewhere in the country. CDPH sequenced mpox virus samples to determine (i) **the presence of specific mutations which could explain the illness resurgence** and (ii) **possible epidemiologic links based on genomic relatedness** of the virus in patients.

What did we find?

A total of 60 mpox virus specimens (collected between 1/8 and 9/19/2023) were sequenced between 5/24 and 10/4/2023. All but 1 were labeled as lineage B.1.20, a lineage that emerged in late 2022 and became one of the predominant MPXV lineages circulating in 2023 (Figure 2). Analysis

revealed that 57 of 61 (93%) B.1.20 specimens clustered into a single group, **indicating a limited number of introductions to Chicago and close transmission linkages**.

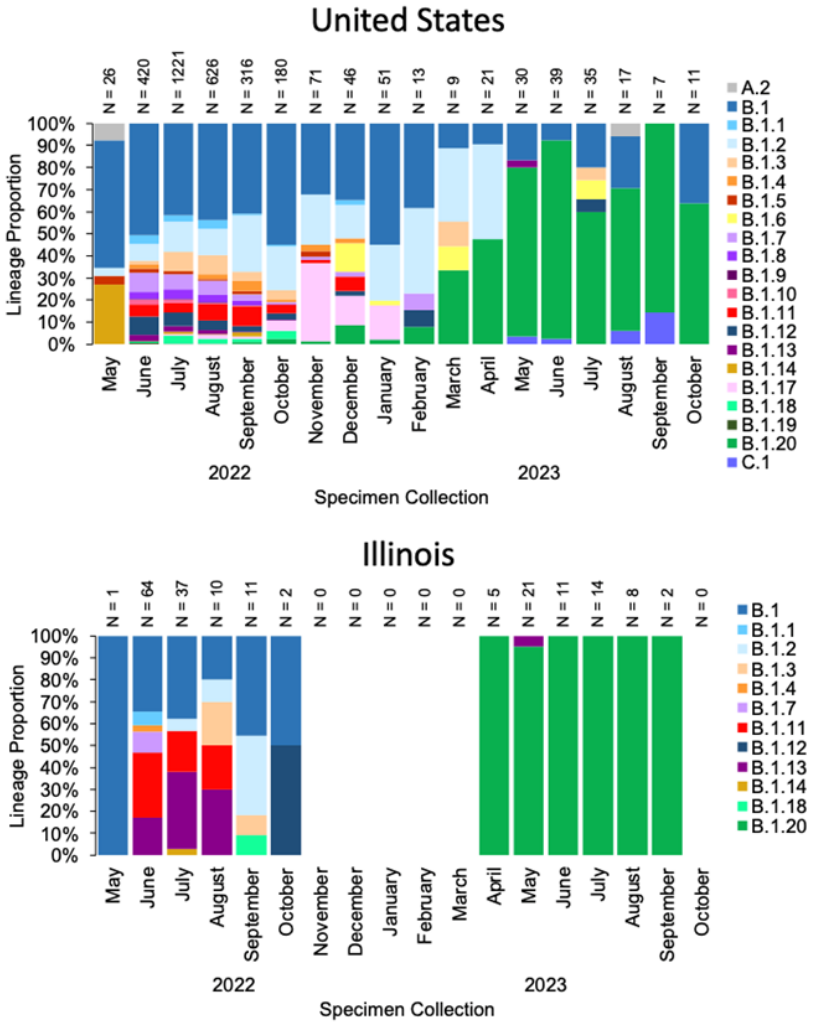
A number of mpox virus lineages from national and international samples in 2023 clustered closely with Chicago sequences suggesting that **this lineage was not limited to Chicago**.

How was this information used?

During the 2023 illness cluster, mpox sequences were analyzed to understand the progression of the epidemic outbreak in the city. **Sequence information helped reveal that infections were not associated with vaccine escape or disease severity** which was encouraging for public health.

Notably, Chicago's mpox sequence data shared to public databases (e.g., GISAID, and NCBI GenBank) contributed to the **designation of a new lineage called B.1.20**.

FIGURE 2: MPXV lineage proportions in the United States (top) and Illinois (bottom) in 2022-2023



The plot displays the proportions of MPXV lineages detected, relative to all specimen collected each month. The total number of specimens sequenced per week is noted at the top of each weekly column.

Candida auris

Why did CDPH genetically sequence this fungus?

Candida auris (*C. auris*) is a fungus that can spread among patients with serious medical conditions in healthcare facilities but does not typically infect healthy individuals. It was first found in the United States in 2013 and Chicago in 2016.

In 2023, CDPH began sequencing Chicago *C. auris* specimens to understand **how it spreads between and within healthcare facilities**, to **identify outbreaks**, and to **monitor resistance to antifungal treatments**.

What did we find?

A total of **350 *C. auris* specimen from the greater Chicagoland were sequenced** during 2023 (collection period 2018-2023). **All sequenced specimens belonged to Clade IV.**

All specimens clustered in a single group, suggesting **that all *C. auris* circulating in Chicago came from a single introduction event around 2016**. We also found that there are some groups of closely related sequences associated with individual facilities, but overall, specimens isolated from different facilities are intermixed. This suggests that *C. auris* is not bounded by the walls of a single healthcare facility. We identified some mutations associated with antifungal resistance; the pace at which these mutations are identified in sequences has increased over time (i.e., we are seeing more antifungal resistance genes as time goes on).

How was this information used?

An investigation of a local outbreak helped **confirm that a healthcare facility's cleaning protocols were sufficient to limit long-term spread of *C. auris* between patients.**

Acknowledgements

The CDPH Lab-based Surveillance program staff for their coordination, analysis and support of the program.

The CDPH Health Care Settings staff for their coordination, analysis, and support of the *Candida auris* sequencing project.

The CDPH Syndemics team for their coordination, analysis and support of the mpox sequencing programs.

The LA County Public Health Lab for their additive mpox virus whole genome sequencing of Chicago mpox specimens.

The laboratory staff at RIPHL and Rush University Medical Center for their laboratory expertise.

Labcorp, IDPH, UChicago Medicine, Rush University Medical Center, UI Health, Asension, Sinai Health System, Advocate Illinois Masonic Medical Center, Lurie Children's Hospital of Chicago, Asension Resurrection, and Northwestern Memorial Hospital, Loyola University for their specimen submission coordination.