

SARS-CoV-2 variants in Chicago (April 2021)

Background

Like all viruses, SARS-CoV-2 – the virus that causes COVID-19 – constantly changes through genetic mutation. These genetic mutations can lead to the emergence of new SARS-CoV-2 variants. Though the emergence of these new variants is expected, some variants are concerning to public health authorities because they might be able to spread more easily from person-to-person, cause more severe disease, or reduce the effectiveness of currently available COVID-19 vaccines.

CDC classifies the most concerning variants as “variants of concern” (VOCs) or “variants of high consequence”. [As of April 2021, CDC has classified five VOCs and no variants of high consequence.](#)

Variant	First detected	Reasons for concern
B.1.1.7	United Kingdom	Spreads more easily from person-to-person, likely causes more severe illness.
P.1	Japan/Brazil	Likely moderately reduces the effectiveness of some COVID-19 vaccines and monoclonal antibody treatments.
B.1.351	South Africa	Spreads more easily from person-to-person, likely moderately reduces the effectiveness of some COVID-19 vaccines and monoclonal antibody treatments.
B.1.427	US (California)	Spreads more easily from person-to-person, likely moderately reduces the effectiveness of some COVID-19 vaccines and significantly reduces the effectiveness of some monoclonal antibody treatments.
B.1.429		

Identifying SARS-CoV-2 variants in Chicago

Testing for variants is not like diagnostic testing to detect SARS-CoV-2 infection. Variants are identified through specialized laboratory analysis called genomic sequencing, which can only be done in certain advanced laboratories, can only be performed on a small subset of positive specimens that meet specific technical criteria, and takes some time (usually weeks) for results to be returned. A small but increasing proportion of all confirmed cases are now being sequenced.

CDPH is involved in surveillance for variants in Chicago in several ways:

- CDPH collaborates with the Illinois Department of Public Health (IDPH) to perform genomic sequencing on specimens from some Chicago residents,
- CDPH submits specimens, through the IDPH laboratory, to the [CDC’s National SARS-CoV-2 Strain Surveillance System](#),
- CDPH has partnered with Rush University Medical Center to establish and operate the Regional Innovative Public Health Laboratory (RIPHL), which is beginning to collect a small number of specimens each week from Chicago hospitals for routine genomic sequencing,
- CDPH is in contact with other laboratories performing genomic sequencing on specimens from Chicago residents, to conduct investigations and report data for surveillance purposes.

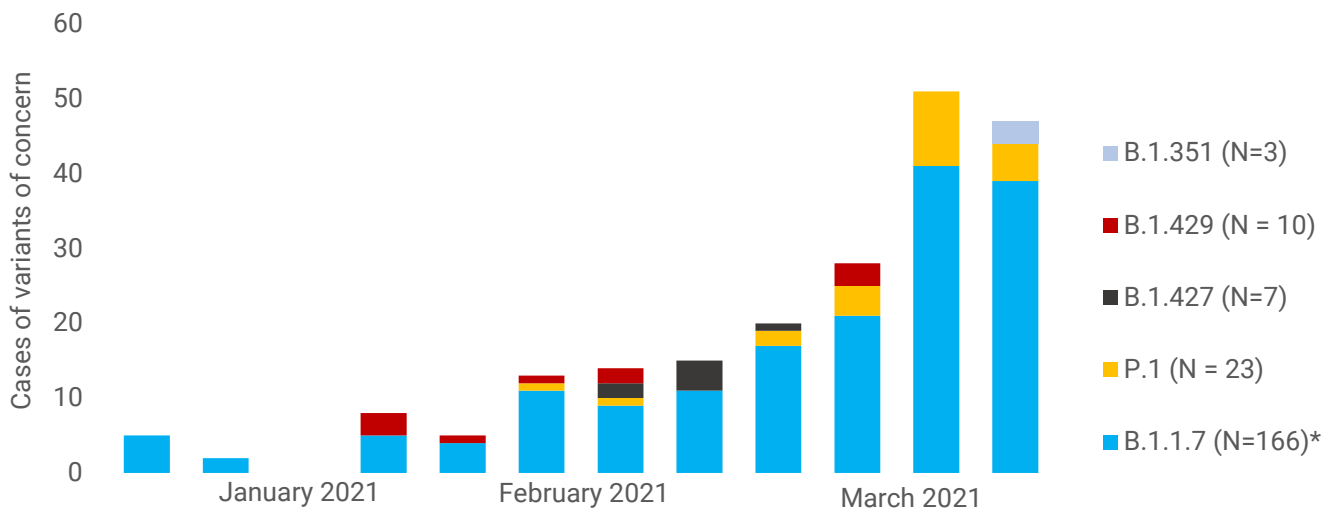
Variants of concern in Chicago

The majority of specimens that have undergone genome sequencing from Illinois are not VOCs. The most commonly detected VOCs in Illinois have been B.1.1.7, B.1.427 and B.1.429.

In Chicago, as of April 12, 2021, 209 cases caused by one of the VOCs have been identified. This is likely a significant underestimate of the number of cases caused by VOCs because, as explained above, only a minority of specimens can undergo genomic sequencing.

All five VOCs have been identified in Chicago, but at different levels. Overall, more VOCs have been detected in recent weeks, though this is likely partly due to an increase in the amount of genomic sequencing occurring, and an increase in the number of COVID-19 cases detected in Chicago.

Figure: Cases of SARS-CoV-2 variants of concern detected in Chicago residents – Jan-March 2021



*One case of B.1.1.7 was detected in December 2020.

B.1.1.7 has been the most commonly-detected VOC in Chicago, accounting for 80% of VOCs, though it is notable P1 has also been detected more frequently in recent weeks. Of note, B.1.1.7 is the only VOC which shows a characteristic pattern with some diagnostic PCR tests. Because of this pattern, it is possible to 'pre-screen' specimens and sequence those that are more likely to be B.1.1.7. This pre-screening was widely implemented in Chicago to detect the first few B.1.1.7 cases; it is therefore likely the proportion of B.1.1.7s detected is overrepresented. Each week, the CDC reports [updated estimates of the proportion of different SARS-CoV-2 variants circulating nationally](#) – these data are drawn from a more random sample, and might provide a more representative picture.

Given these VOCs spread more easily from person-to-person, it is expected that more cases of VOCs will be observed. CDC had expected B.1.1.7 to become the predominant variant in the US in March 2021¹ – CDPH expects B.1.1.7 or other, more transmissible VOCs, to become the predominant SARS-CoV-2 strains in Chicago in the near future.

What CDPH is doing

In addition to genomic surveillance, CDPH identifies and investigates cases of COVID-19 in people who are fully vaccinated, or cases of reinfection, to investigate if these are more likely to be caused by variants of concern. It is still too early to know if VOCs are more likely to cause vaccine breakthrough cases or reinfection cases.

What the public can do

Variants of concern pose a threat to the progress made in reducing the number of COVID-19 hospitalizations and deaths in Chicago and they are likely one factor contributing to the recent increases in cases in Spring 2021.

Variants of concern can be prevented in exactly the same ways as every other SARS-CoV-2 virus. In addition, reducing the amount of circulating virus will reduce the chances of novel concerning variants from emerging.

Wash your hands. Wear a mask. Stay 6 feet from people who are not from your household. Participate in contact tracing if you are contacted. Get vaccinated as soon as you are eligible, and get both doses if you are offered a vaccine that requires two doses.

¹ Galloway, S et al. Emergence of SARS-CoV-2 B.1.1.7 Lineage – United States, December 29, 2020-January 12, 2021. *MMWR*. URL: <https://www.cdc.gov/mmwr/volumes/70/wr/mm7003e2.htm>