



Health Alert



City of Chicago
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Chicago Department of Public Health
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Variant B.1.1.7 SARS-CoV-2 Strain Identified in Chicago January 15, 2021

Summary and Action Items

- The first known Illinois case of the SARS-CoV-2 variant B.1.1.7 has been identified in a Chicago resident.
- The variant was identified during genomic sequencing of a specimen at a Chicago academic medical center laboratory.
- B.1.1.7 is a SARS-CoV-2 variant first detected in the UK in the fall of 2020. As of January 13, 2021, many other countries and 12 US states have also reported cases of B.1.1.7.
- Preliminary epidemiologic indicators suggest that this variant is associated with increased transmissibility.
- Currently there is no evidence to suggest that the variant impacts disease severity or vaccine efficacy.
- While efforts are being made to trace the contacts of this individual, CDPH expects that this variant and others with a transmission advantage over the current predominant strains are likely to become more established in the US, including in the Chicago region.
- Laboratories performing SARS-CoV-2 genomic sequencing are encouraged to sequence virus isolates in a timely manner and upload to public databases to identify new variant strains.
- Laboratories without sequencing capacity are encouraged to store specimens for individuals meeting certain criteria, outlined below, for possible submission to CDPH's new molecular laboratory partnership, and to notify CDPH of available specimens through the [SARS-CoV-2 Strain Surveillance Case Investigation Form](#).
- Healthcare providers should continue to reinforce the importance of everyday prevention actions that reduce the spread of all known COVID-19 variants, including wearing a mask, washing hands often, staying 6 feet away from others and avoiding crowds, avoiding non-essential travel and getting vaccinated when eligible.

Background:

The first known Illinois case of the SARS-CoV-2 variant B.1.1.7 has been identified in a Chicago resident. The variant was identified during sequencing analysis of a specimen at a Chicago academic medical center laboratory. This variant is estimated to have first emerged in the UK during September 2020. Since December 20, 2020, several countries have reported cases of the B.1.1.7 lineage, including the United States; as of January 13, 2021, [76 cases of the B.1.1.7 lineage have been identified in 12 US states](#).

Preliminary epidemiologic indicators suggest that this variant is associated with increased transmissibility (i.e., more efficient and rapid transmission) compared to other circulating strains of SARS-CoV-2. Currently there is no evidence to suggest that the variant impacts disease severity or vaccine efficacy¹. New information about the virologic, epidemiologic, and clinical characteristics of this variant is emerging. CDC maintains a [webpage](#) with more detailed information addressing the emergence of this and other SARS-CoV-2 variants².

Emergence of novel SARS-CoV-2 variants, especially those with increased transmissibility, highlights the continued need for rigorous infection prevention and control measures. **Providers should continue to counsel patients on the importance of everyday preventive actions that reduce the spread of all known variants of COVID-19, including wearing a mask, washing hands often, staying 6-feet away from others and avoiding crowds, avoiding non-essential travel, and getting vaccinated when the patient is eligible.**

National and local strain surveillance efforts are underway to increase the number and representativeness of viruses undergoing genomic characterization. CDPH is collaborating with IDPH and CDC to enhance molecular surveillance for SARS-CoV-2 in the Chicago region. In addition, CDPH is establishing flexible, advanced molecular laboratory capacity and specimen biobanking through a new Regional Innovative Public Health Laboratory (RIPHL) (see below).

To support these efforts:

- Laboratories performing genomic sequencing are encouraged to sequence virus isolates in a timely manner and upload to public databases to identify cases of the new variant.
- Laboratories without sequencing capacity are encouraged to store specimens for individuals meeting the criteria below:
 - Suspected cases of COVID-19 reinfection
 - CDPH published a Health Alert on 12/8/2020 titled Investigation and Request for Possible SARS-CoV-2 Reinfection Cases. Additional details may be found [here](#).
 - Cases with treatment failures using convalescent plasma or monoclonal antibodies
 - Cases of possible vaccination failure and breakthrough infections
 - Characteristic PCR-positive patterns observed using specific assays³

Submit reports of Chicago residents meeting criteria via the [SARS-CoV-2 Strain Surveillance Case Investigation Form](#).

Regional Innovative Public Health Laboratory (RIPHL)

In December 2020, CDPH advertised a Request for Proposals (RFP) for a Regional Innovative Public Health Laboratory to establish flexible, advanced molecular laboratory capacity and specimen biobanking for public health surveillance and response. The emergence of novel SARS-CoV-2 strains highlights the urgent, important nature of this capacity.

The RFP was awarded to Rush University Medical Center (RUMC), who will coordinate with CDPH to establish RIPHL. As RIPHL is established, staff from CDPH or RUMC may be reaching out to clinical laboratories to discuss the availability of stored historic specimens and associated clinical and epidemiologic metadata, and to consider the prospective submission of specimens to RIPHL. Although submission of specimens is not mandated, for effective molecular surveillance, RIPHL will need to build a repository of specimens from different healthcare facilities across the City and therefore collaboration with RIPHL and submission of specimens for storage and or sequencing is strongly encouraged.

References:

1. Rambaut A, Loman N, Pybus O, et al. Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations. [Virological.org](#)
European Centre for Disease Prevention and Control. Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom – 20 December 2020. [ECDC: Stockholm; 2020](#)
Volz E, Mishra S, Chand M. et al. Report 42 - Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: insights from linking epidemiological and genetic data. [Medrxiv.org](#)
2. CDC: Emerging SARS-CoV-2 Variants. URL: <https://www.cdc.gov/coronavirus/2019-ncov/more/science-and-research/scientific-brief-emerging-variants.html>
3. One of the mutations in B.1.1.7 (69-70del) is responsible for a 'dropout' in the S gene PCR target of certain assays, including the ThermoFisher TaqPath COVID-19 Combo Kit and Linea COVID-19 Assay Kit ([FDA details here](#)). Laboratories using these kits, are asked to take the following steps:
 - Review data from December 2020 to look for the following pattern: ORF1ab positive, N gene positive, S gene negative.
 - Prospectively, monitor for any occurrence of the same pattern: ORF1ab positive, N gene positive, S gene negative
 - If residual specimen is available either perform genetic sequencing or prepare to submit the specimen to public health for sequencing and further characterization. Please be sure to record and note the Ct values for detected targets, as a common reason for S gene target failure is a low copy number of the virus.
 - If the variant strain is detected, or if you have specimens for possible sequencing, notify CDPH via the [SARS-CoV-2 Strain Surveillance Case Investigation Form](#) and prepare to send residual for further characterization.