Chicago Department of Public Health

Health Alert

CDPH Chicago Department of Public Health

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Chicago Department of Public Health
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Variant P.1 SARS-CoV-2 Strain Identified in Chicago

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Summary and Action Items

- The first known Illinois case of the SARS-CoV-2 variant P.1 has been identified in a Chicago resident.
- The variant was identified during genomic sequencing of a specimen at a Chicago academic medical center laboratory.
- The P.1 variant was first identified in travelers from Brazil during routine airport screening in Tokyo, Japan, in early January 2021. As of March 2, 2021, many other countries and 5 US states have also reported cases of P.1.
- 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 public health laboratories and to notify CDPH of available specimens through the SARS-CoV-2 Strain Surveillance Case Investigation Form.
- Laboratories storing specimens for individuals meeting the vaccine breakthrough criteria, outlined below, should notify CDPH of available specimen through the separate Vaccine Breakthrough 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 well-fitting 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 P.1 has been identified in a Chicago resident. The variant was identified during sequencing analysis of a specimen at a Chicago academic medical center laboratory. The P.1 variant was first identified in travelers from Brazil during routine airport screening in Tokyo, Japan, in early January 2021. As of March 2, 2021, many other countries have also reported cases of P.1 and 10 cases of the P.1 variant have been identified in 5 US states.

There is evidence to suggest that some of the mutations in the P.1 variant may increase its transmissibility. In addition, there is some evidence the antigenic profile may affect the ability of antibodies generated through a previous natural infection or through vaccination to recognize and neutralize the virus. 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 variants[1].

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 well-fitting mask, washing hands often, staying 6-feet away from others and avoiding crowds, avoiding non-essential travel, and getting vaccinated when 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).

Consistent with previous CDPH guidance and recent IDPH guidance:

- All laboratories performing RT-PCR for SARS-CoV-2 are encouraged to retain specimens for at least 30 days.
- Laboratories performing genomic sequencing are encouraged to sequence SARS-CoV-2 isolates in a timely manner and upload promptly to public databases, e.g. GISAID, to identify cases of new variants.
- Laboratories performing RT-PCR but without sequencing capacity are encouraged to contact CDPH by submitting information to the SARS-CoV-2 Strain Surveillance Case Investigation Form about samples meeting the below criteria, for possible submission to a reference laboratory for sequencing:
    1. S-gene target failures (or S-gene "dropouts"): if using TaqPath assay and Ct $\leq$ 25 in other targets
    2. COVID-19 reinfection: COVID-19 positive samples from suspected reinfection in patients that have had a positive confirmed test at least 90 days apart, as outlined in previous CDPH guidance.
    3. Specimens with a Ct <30 from cases linked to a variant case through contact tracing investigations.
    4. Atypical clinical presentations or cases with treatment failure. Please note, since sequencing is considered a surveillance test without CLIA certification, results will not be provided outside of public health.
    5. For vaccine breakthroughs, **a separate Vaccine Breakthrough Investigation Form is used:**
        a. COVID-19 positive PCR samples from patients fully vaccinated (14 days after second dose of FDA-authorized vaccination series)
        b. Patient does not have a history of a positive COVID-19 test less than 45 days prior to the current test.

Establishing SARS-CoV-2 strain surveillance locally

As reported previously, CDPH's Regional Innovative Public Health Laboratory (RIPHL) is establishing local sequencing capacity for public health through a partnership with Rush University Medical Center. In the coming weeks, we anticipate RIPHL will begin to accept SARS-CoV-2 specimens from across Chicago for molecular characterization, and CDPH will issue guidance about the submission of surveillance specimens at that time.