

SARS-CoV-2 Variants: Report for April 28, 2021

The City of New York has been conducting sequencing and analyzing epidemiologic data to characterize the spread of the SARS-CoV-2, identify emerging variants, and learn how these variants may be impacting public health.

The Health Department has identified multiple variants of interest and variants of concern, notably the **B.1.1.7** and the **B.1.526** variants:

- B.1.1.7 (first identified in the UK) is [classified by CDC as a variant of concern](#), which means that there is evidence that it increases transmissibility and the severity of disease.
 - Specifically, B.1.1.7 has been found to be 50% more transmissible and cause more severe infections.^{1,2,3}
- B.1.526 (first identified in NYC) is [classified by CDC as a variant of interest](#), because there are signs that it increases transmissibility. Studies are ongoing regarding the impact of B.1.526 on disease severity, reinfection, and vaccine effectiveness. To date, there is lab evidence that antibody therapies to the virus that causes COVID-19 may be less effective at preventing infection against this variant, but the real-world effects of this finding remain unknown.

In recent weeks, the **P.1** (first identified in Brazil) variant has also been detected in NYC. Though currently low in prevalence, this variant has been increasing.

- P.1 is [classified by CDC as a variant of concern](#), because there is evidence that it increases transmissibility, and antibodies from previous infection or from vaccination may be less effective at preventing infection against this variant.

For more information on variants of concern and variants of interest, visit [cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html](https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html).

¹ [cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html](https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html).

² Davies NG, Abbott S, Barnard RC, et al. Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. MedRxiv 2021. doi: doi.org/10.1101/2020.12.24.20248822[external icon](#).

³ Horby P, Huntley C, Davies N et al. NERVTAG note on B.1.1.7 severity. New & Emerging Threats Advisory Group, Jan. 21, 2021. Retrieved from depts.washington.edu/pandemicalliance/2021/01/25/nervtag-note-on-b-1-1-7-severity.

A lot is not yet known about the effect of some variants.

There are not enough data to draw many reliable conclusions yet. We will continue to gather and analyze data to understand the public health impact of variants and communicate when there are important updates to what we know.

What we know	What we do not yet know
<ul style="list-style-type: none">• The number of different variants of interest and of concern is increasing• B.1.526, B.1.1.7, P.1, and other variants of concern and of interest are in NYC, and the proportion of cases that are identified as these variant types is growing.• B.1.1.7 is more transmissible than some other SARS-CoV-2 variants and can cause more severe disease.• P.1 is more transmissible and there is some evidence of immunity evasion for both people who previously had COVID-19 and fully vaccinated people.• There is no evidence to date that B.1.1.7. or B.1.526 reduce effectiveness of vaccines. <i>Vaccine breakthroughs (infections among fully vaccinated people) are expected to occur in a small proportion of vaccinated people regardless of the spread of variants.</i>	<ul style="list-style-type: none">• Whether B.1.526 causes reinfection among people who previously had COVID-19 more frequently than other variant types.• Whether B.1.526 makes people sicker and increases the likelihood of hospitalization and death.• Whether B.1.526 is more likely (than other variant types of the virus) to infect people who have been fully vaccinated.

This report contains an overview of key findings on B.1.526 and B.1.1.7 from January 1, 2021 through April 17, 2021. The Health Department is continuing to investigate the prevalence of variants of concern and variants of interest that are present in NYC. Our investigations combine laboratory and epidemiologic observations to characterize each variant. Since October 2020 this has involved sequencing all specimens that the NYC Public Health Laboratory receives and which meet certain technical criteria (e.g., sufficient levels of virus). Since February 2021, the Pandemic Response Lab has been sequencing randomly selected specimens that meet certain technical criteria.

A small but increasing proportion of all confirmed cases are now being sequenced. In recent weeks, greater than 6% of specimens from confirmed cases have been sequenced by the NYC Pandemic Response Lab and the NYC Public Health Laboratory. Additional specimens are being sequenced by the New York State Wadsworth Laboratory and university and private laboratories.

We are monitoring our epidemiologic surveillance systems to assess for differences in severity, risk for reinfection, or risk for impacting vaccine effectiveness that might be associated with variants. Some of our ongoing efforts include:

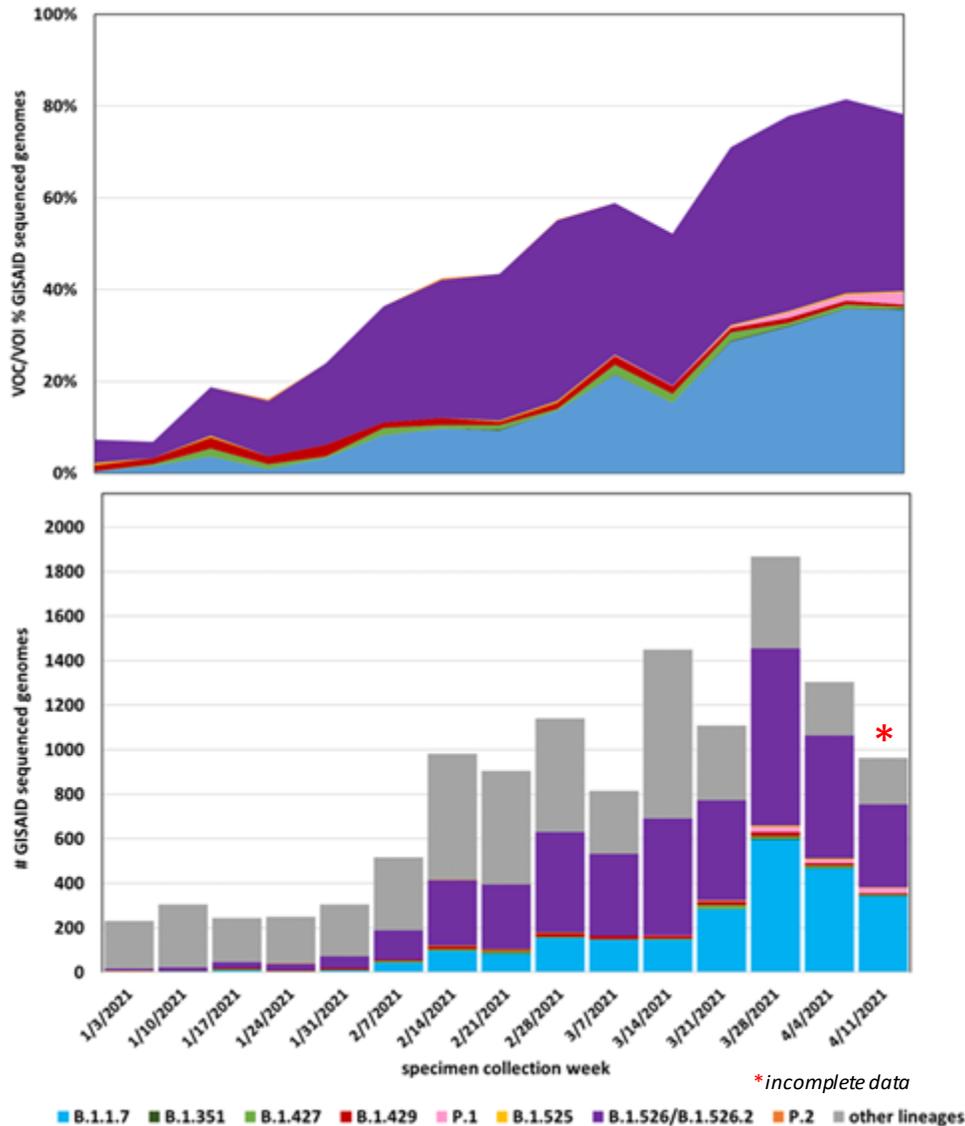
- Monitoring the number of hospitalizations and deaths that occur among patients with sequenced specimens that are caused by variants.
- Identifying cases caused by variants where the case-patient had a previous positive diagnostic test for COVID-19 more than 90 days earlier. These cases are investigated to determine if they are likely to represent a reinfection, so that we can determine if reinfection cases are more common in people that have been infected with one of the variants.
- Matching data on cases caused by variants with Citywide Immunization Registry data to identify if the person was fully immunized prior to testing positive for COVID-19.

To date, reinfection cases and cases in people who were fully vaccinated are rare. It is too early to know if either of these variants are more likely to cause reinfection or vaccine breakthrough compared to other previously circulating variants.

Key Findings of New York City Variant Cases

#1 - The proportion of variants of concern and variants of interest is increasing.

In January, variants of concern and variants of interest made up about 10% of cases reported to GISAID. By mid-March, variants of concern and variants of interest represented over 80% of cases sequenced in GISAID.

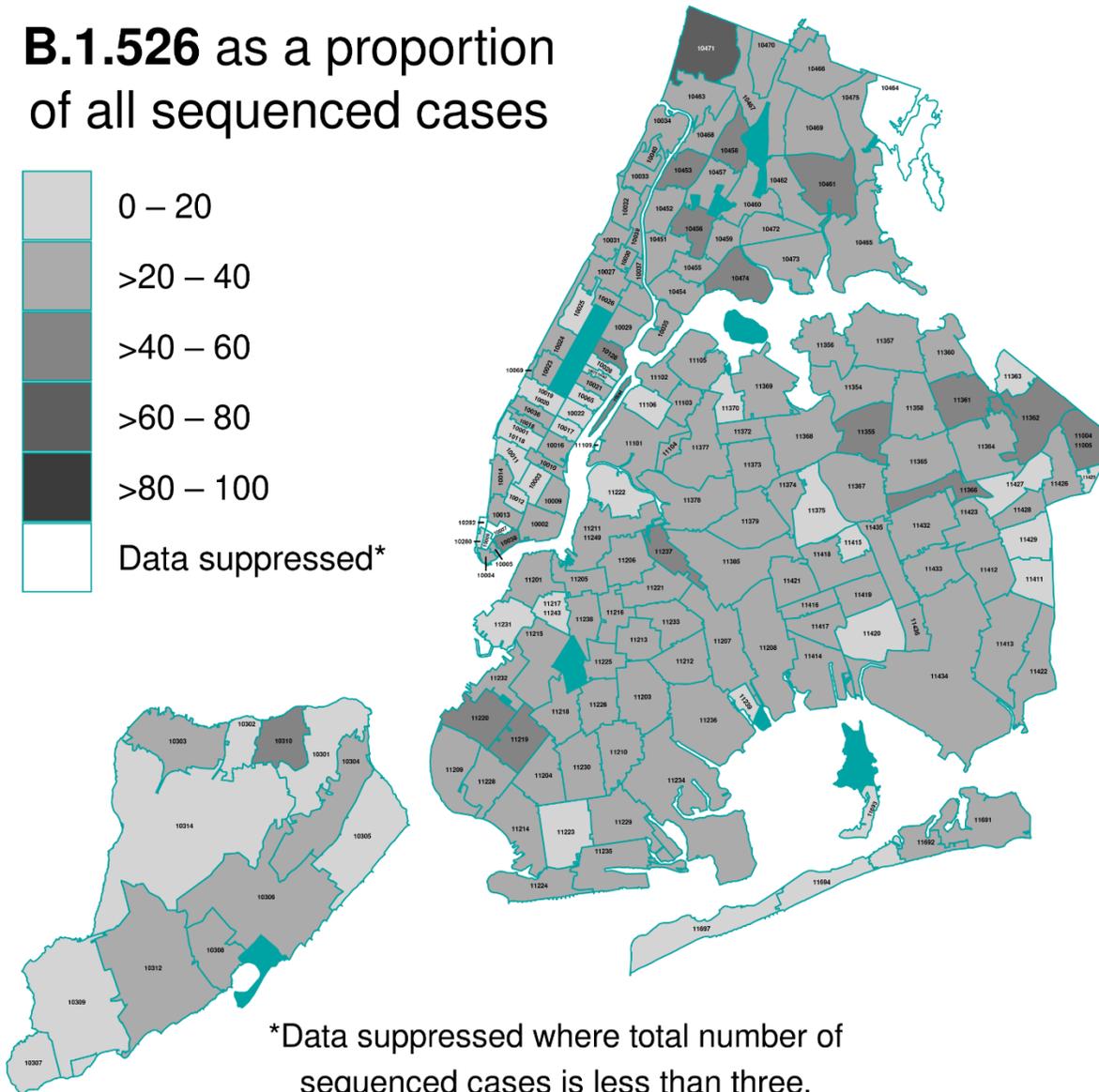
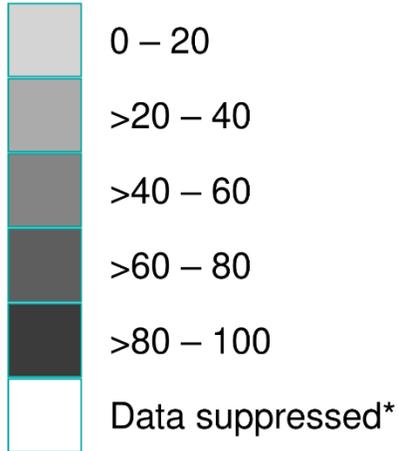


#2 - B.1.526 and B.1.1.7 variants are in all five boroughs.

These maps show the proportion of all sequenced cases that were identified by PHL and PRL as B.1.526 or B.1.1.7 by ZIP code.

B.1.526 cases are found in all five boroughs, but slightly more common in the Bronx, parts of central/eastern Queens, southwest Brooklyn, and Staten Island.

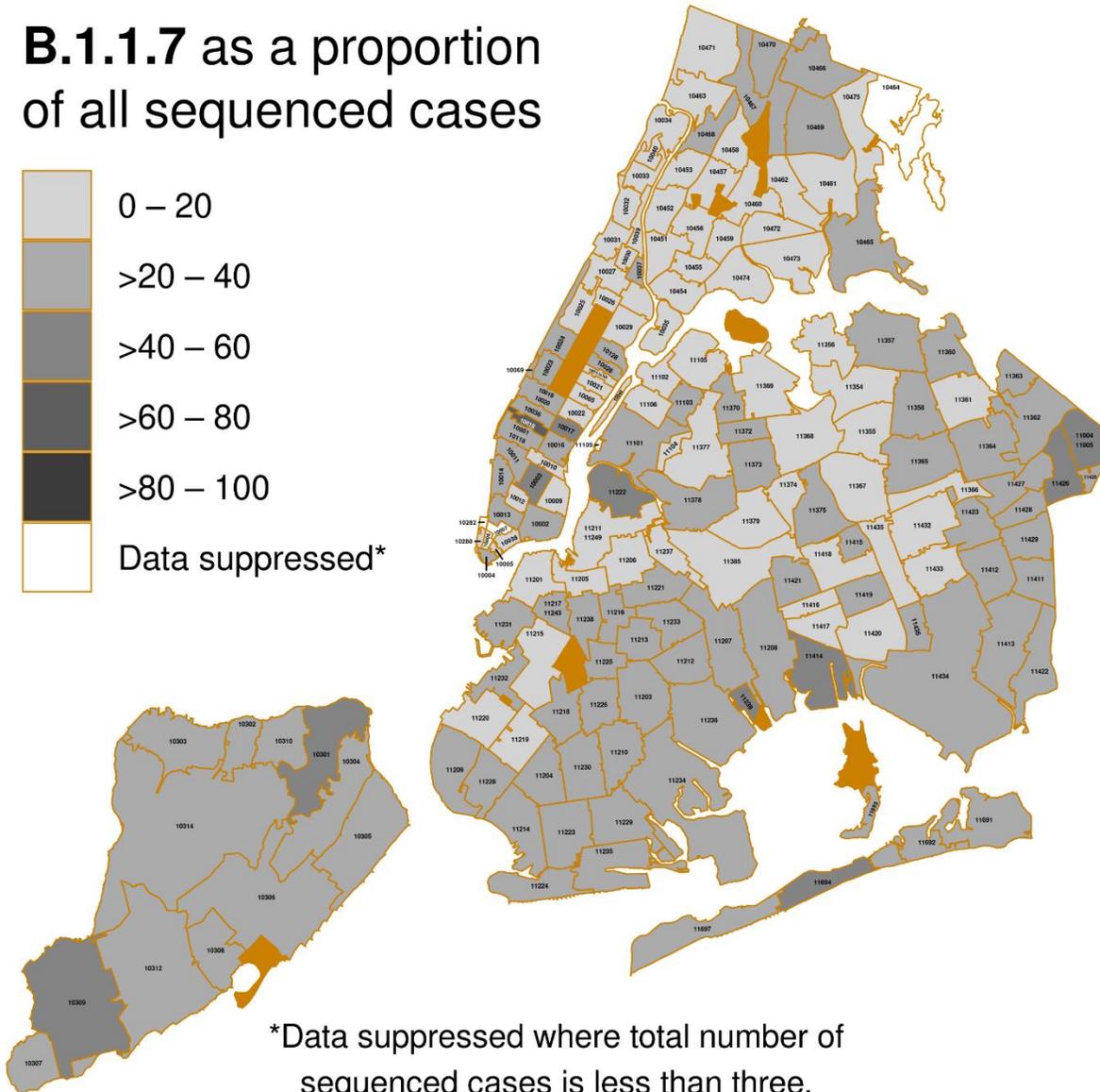
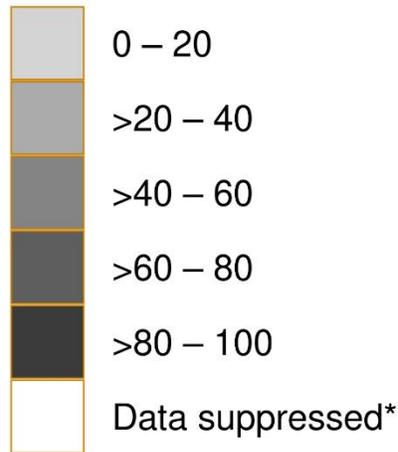
B.1.526 as a proportion of all sequenced cases



*Data suppressed where total number of sequenced cases is less than three.

B.1.1.7 cases are found in all five boroughs, but slightly more common in Staten Island, Brooklyn, most of Queens, and the southern half of Manhattan.

B.1.1.7 as a proportion of all sequenced cases



*Data suppressed where total number of sequenced cases is less than three.