Spatiotemporal analyses of two co-circulating SARS-CoV-2 variants within New York State

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Background

- The emergence of SARS-CoV-2 variants of concern and variants of interest raised alarm, because of their potential for increased transmission and immune evasion (1,2).
- We describe the interplay between B.1.1.7 (Alpha) and B.1.526 (Iota) in New York State (NYS) from December 2020–April 2021 through phylogeographic analyses, space-time scan statistics, and cartographic visualization, providing an opportunity to compare the dynamics of competing variants.
- Elucidating the evolutionary and epidemiologic dynamics among novel SARS-CoV-2 variants is essential for understanding the trajectory of the COVID-19 pandemic.

Methods

- The NYSDOH Wadsworth Center coordinated with >30 clinical labs throughout NYS to submit SARS-CoV-2-positive respiratory swabs for whole-genome sequencing (WGS).
- Specimens collected between Dec 2020 – Apr 2021 were included in this study. Where multiple specimens had been collected from a patient, only the earliest was included.
- Total nucleic acid was extracted on a MagNAPure 96 and processed for WGS with a modified ARTIC V3 protocol.
- Illumina libraries were processed with the ARTIC nextflow pipeline.
- COVID-19 incidence was multiplied by the proportion of B.1.526 and B.1.1.7 to estimate the number of COVID-19 cases attributable to each variant at the ZIP code level.
- Inverse distance weighted interpolation was used to visualize the spatiotemporal variation in the proportion of COVID-19 cases attributable to each variant, and to provide estimates for these proportions in areas where data was missing.
- Retrospective multinomial space-time scan statistic in SaTScan was used to identify statistically-significant geographic clusters of COVID-19 cases attributable to each variant.
- Maximum-likelihood time-calibrated phylogenetic trees were constructed for both lineages incorporating all B.1.526 or B.1.1.7 NYS genomes and a representative subset of genomes from other states.
- Phylogeny was assessed by NYS economic region, including number of introductions between regions.

Results

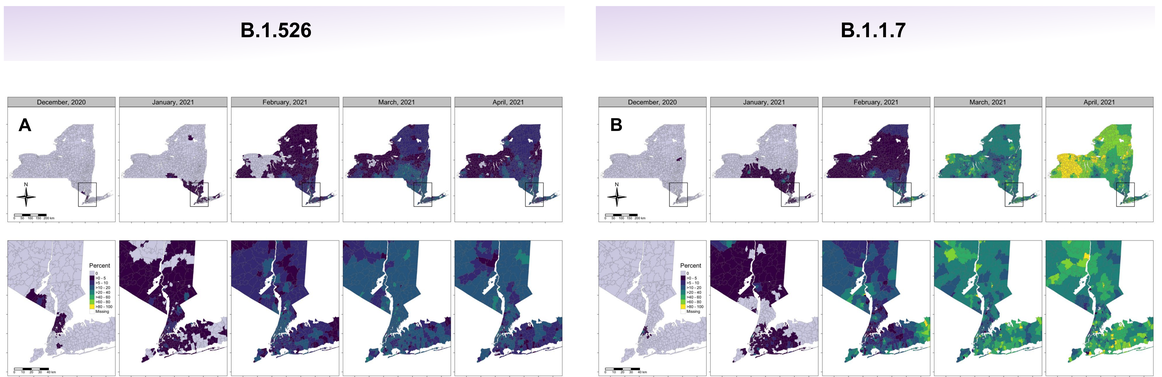

Figure 1: Inverse distance weighted interpolations of percentage of total COVID-19 cases attributable to B.1.526 (**A**) and B.1.1.7 (**B**) variants by ZIP code tabulation area, New York, December 2020 – April 2021.

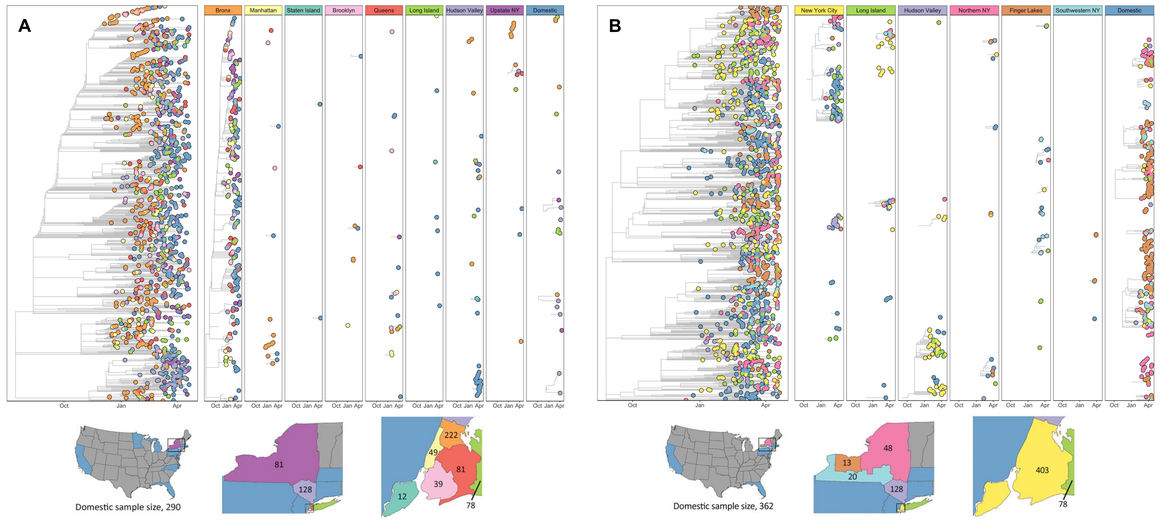

Figure 2: Time-calibrated phylogeny of B.1.526 (**A**) and B.1.1.7 (**B**), New York and other states, December 2020 – April 2021. Left panels represent a maximum-likelihood phylogeny of genomes from New York and other states generated in IQTree with timescale inferred by TreeTime and ancestral state reconstruction performed in BEAST. Faceted panels indicate the source of introductions into different New York regions and other states ("Domestic"). Introductions supported by an ancestral state probability >0.7 are shown. Bottom panels show locations sampled and sample sizes.

Results

- B.1.526 exhibited constricted initial spread focused in the NYC metro area in January 2021, and while it eventually spread statewide, never reached clear dominance in any region (Fig 1A).
- B.1.526 showed significant clustering in the NYC region in March, but no significant clustering in April.
- B.1.526 likely evolved within NYC, with many introductions originating from the Bronx and spreading to other NYS regions and states (Fig 2A).
- B.1.1.7 spread through southern NYS beginning in January 2021, reaching sustained high proportion throughout the state by April, with strong dominance in the western region (Fig 1B). This was supported by a large cluster of significantly elevated B.1.1.7 risk in the western/Finger Lakes region in April.
- B.1.1.7 was repeatedly introduced from other states into NYS.
- NYC and the surrounding metro region also played a role in spreading B.1.1.7 to other parts of NYS.

Conclusions

- Despite a homegrown advantage, the spread of B.1.526 appears to have been limited by the repeated introduction and transmission of B.1.1.7 throughout the rest of NYS.
- This finding is consistent with the enhanced transmissibility of B.1.1.7 in comparison to prior circulating lineages.
- Spatiotemporal and phylogeographic methodologies can be paired to reveal a more in-depth history of the emergence of novel SARS-CoV-2 variants.

References

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