

SYNOPSIS

01/07/2021

Review of “Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from Linking Epidemiological and Genetic Data”

Article citation: Volz E, Mishra S, Chand M, Barrett JC, Johnson R, Geidelberg L, et al. Transmission of SARS-CoV-2 lineage B.1.1.7 in England: insights from linking epidemiological and genetic data. medRxiv 20249034 [Preprint]. 2021 Jan 04 [cited 2021 Jan 04]. Available from:

<https://doi.org/10.1101/2020.12.30.20249034>

One-minute summary

- The severe acute respiratory syndrome coronavirus 2 (**SARS-CoV-2**) lineage **B.1.1.7** is now designated **Variant of Concern 202012/01 (VOC)** by Public Health England and is a genetic variant that **includes amino acid substitutions** with implications on **increased ACE2 binding**, and **deletions** with **impact on diagnostic assays**.
- A negative result on the S-gene component, termed S-gene target failure (SGTF), of an otherwise positive polymerase chain reaction (PCR) test for SARS-CoV-2 using the ThermoFisher TaqPath probe can be used to identify VOC in populations where VOC frequency is high. The accuracy of this approach as a proxy to genomic sequencing would decrease if the composition of the pool of circulating strains shifts towards more strains having deletions in the relevant region of the S-gene and VOC frequency is reduced.
- In this study, based on testing 35% of community coronavirus disease 2019 (COVID-19) tests using the SGTF approach, the **estimated frequency of VOC strains in London, England has increased from approximately 5% in early November 2020 to approximately 80% in mid-December**.
- **During the second English lockdown period, the real-time effective reproduction number (Rt) for VOC was 1.4 compared to 0.9 for non-VOC strains.** The authors further estimated that VOC was 1.4 to 1.8 times more transmissible than non-VOC strains. This means that, all else being equal, epidemic control would be substantially more difficult and doubling times would be faster in regions where the VOC is predominant.
- Persons under 20 years accounted for a larger proportion of cases with VOC than non-VOC strains. Such differences may be explained by other factors including increased exposure by schools remaining open during lockdown when other settings were closed, increased susceptibility of persons less than 20 years, or that symptoms are more apparent for that age group.

Additional information

- Authors adjust for diagnostic uncertainty related to use of SGTF for estimating frequency of VOC because other lineages, such as B.1.258, also have the corresponding deletion.
- Regression analysis of VOC transmissibility was conducted by a Bayesian semi-mechanistic transmission model. Based on this model, the additive reproductive advantage (difference in reproduction numbers) of VOC was 0.4-0.7 (median 0.63) and the multiplicative reproductive advantage (ratio of reproduction numbers) ranged from 1.4-1.8 (median 1.74). The authors explain that “a multiplicative transmission advantage would be expected if transmissibility had increased in all settings and individuals, while an additive advantage might reflect increases in transmissibility in specific subpopulations or contexts.”
- The findings of faster epidemic growth relating to expansion of the VOC in multiple regions of England support that increases in frequency are less likely to be due to founder effects or genetic drift.
- The transmission estimates were obtained from data during a period of increased public health measures (i.e. strict physical distancing/lockdown measures); thus, estimates may differ in other settings with different measures in place.
- Latent period or generation time were not found to be likely hypotheses to explain increased incidence growth rates.
- Limitations reported by authors include:
 - Genomic and epidemiological data, due to being part of routine surveillance data, may not be representative of SARS-CoV-2 infections in England over the time period of data used.
 - The models used did not exhaust methods to assess long-term transmission dynamics, or the spatiotemporal correlation.

PHO reviewer’s comments

- **This manuscript is a preprint** that has not been peer-reviewed and at this time should not be used to inform policy or decision-making.
- VOC has rapidly spread across England and now represents over 80% of SARS-COV-2 in certain regions. Seeding of this variant in other parts of the world has already occurred, and in the absence of vaccine-related population immunity, may lead to rapid acceleration of the pandemic in other countries, including Canada.
- Frequency of VOC strains are specific to England data and may not represent expected spread and distribution in other regions of the world with different circulating profiles of SARS-CoV-2 lineages and other measures that may affect transmission dynamics (e.g., public health measures).

Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Review of “Transmission of SARS-CoV-2 lineage B.1.1.7 in England: insights from linking epidemiological and genetic data”. Toronto, ON: Queens’s Printer for Ontario; 2020.

Disclaimer

This document was developed by Public Health Ontario (PHO). PHO provides scientific and technical advice to Ontario's government, public health organizations and health care providers. PHO's work is guided by the current best available evidence at the time of publication.

The application and use of this document is the responsibility of the user. PHO assumes no liability resulting from any such application or use.

This document may be reproduced without permission for non-commercial purposes only and provided that appropriate credit is given to PHO. No changes and/or modifications may be made to this document without express written permission from PHO.

Public Health Ontario

Public Health Ontario is a Crown corporation dedicated to protecting and promoting the health of all Ontarians and reducing inequities in health. Public Health Ontario links public health practitioners, front-line health workers and researchers to the best scientific intelligence and knowledge from around the world.

For more information about PHO, visit publichealthontario.ca.

