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SUMMARY REPORT

# SARS-CoV-2 Variants of Concern: Results of Point Prevalence Study

February 12, 2021

This report provides results of a single day point prevalence study of SARS-CoV-2 variants of concern (VOC), consisting of SARS-CoV-2-positive samples from January 20, 2021 in Ontario that were submitted to Public Health Ontario (PHO). These results identify samples that have the spike (S) gene N501Y mutation, which is found in the three VOCs:

- PANGO lineage B.1.1.7 (also known as 202012/01, first detected in the United Kingdom);
- PANGO lineage B.1.351 (also known as 501Y.V2, first detected in South Africa);
- PANGO lineage P.1 (also known as 501Y.V3, first detected in Brazil)

Experts believe these variants likely have clinical and public health significance, which may include increased transmissibility, virulence and/or decreased vaccine efficacy.1-3 This report describes the results of an N501Y screening test and whole genome sequencing for VOC confirmation and lineage identification. Results include the most current information available from PHO's Laboratory Information Management System as of February 6, 2021.

## Highlights

- A total of 2,756 samples were received by PHO Laboratory out of an estimated 3,003 samples with SARS-CoV-2 reported in Ontario on January 20, 2021; screening for the N501Y mutation was completed for 2,570 samples and could not be completed for 186 samples, likely due to low viral quantity in the sample
- Overall, 113 of 2,570 samples (4.4%) screened had the N501Y mutation detected; the majority, 91/113 (80.5%) were detected in Simcoe Muskoka District Health Unit
- Of the 113 samples with N501Y detected, 88 samples have been confirmed by whole genome sequencing; 87 belong to PANGO lineage B.1.1.7 and one belongs to PANGO lineage B.1.351 (from Peel Public Health)
- A total of 3 (2.7%) samples with N501Y detected were from individuals with recent international travel prior to SARS-CoV-2 diagnosis; none of these were associated with an outbreak
- Prevalence of the N501Y mutation was 1.1% for samples not associated with an outbreak and
- 13.2% for samples associated with an outbreak (detected among 2.0% of the different outbreaks tested)

- Prevalence was higher in females for samples associated with an outbreak, and similar for males and females for samples not associated with an outbreak
- Prevalence was higher in older age groups (> 60 years old) for samples associated with an outbreak, and similar across age groups for samples not associated with an outbreak
- The N501Y mutation was detected in samples associated with six outbreaks; three outbreaks in Simcoe Muskoka District Health Unit, two in Peel Public Health, and one in Toronto Public Health
- For samples not associated with an outbreak, the N501Y mutation was detected in samples from Toronto Public Health (n=7), Peel Public Health (n=5), York Region Public Health (n=3), Simcoe Muskoka District Health Unit (n=3), Durham Region Health Department (n=2) and Region of Waterloo Public Health and Emergency Services (n=1)

# Methods

PHO requested all samples reported on January 20, 2021 as positive for SARS-CoV-2 across the Ontario Provincial COVID-19 Diagnostic Network be sent to PHO Laboratory for VOC screening. For each sample the genetic material of the virus (RNA) was extracted. Next, a single nucleotide polymorphism (SNP) real-time reverse transcription polymerase chain reaction (rRT-PCR) assay, developed by researchers at PHO Laboratory, was used for specific detection of the N501Y mutation.

Samples for which the N501Y mutation was detected were whole genome sequenced or are currently in the process of being sequenced to confirm the N501Y mutation, determine PANGO lineage and investigate other possible mutations of interest.

# Prevalence of N501Y mutation by outbreak status, age, gender and public health unit

**Table 1. Number and proportion of SARS-CoV-2 positive samples with the spike (S) gene N501Y mutation by outbreak status, January 20, 2021**

| | Detected | Not detected | Total |
|---|---|---|---|
| Outbreak | 92 (13.2%) | 606 (86.8%) | 698 |
| Non-outbreak | 21 (1.1%) | 1,851 (98.9%) | 1,872 |
| Total | 113 (4.4%) | 2,457 (95.6%) | 2,570 |

**Note**: Excludes samples where the N501Y screen test could not be completed, likely due to low viral quantity in the sample (n=186). There were six outbreaks with N501Y mutation detected. In total, 300 different outbreaks had samples submitted for screening. Laboratory records for 47 samples were unable to be matched to confirmed cases in CCM, none of these had N501Y mutation detected. These were included as non-outbreak samples. As a result, the number tested may be an underestimate for outbreaks, and an overestimate for non-outbreaks.

Information on how samples are identified as outbreak associated is available in the technical notes.
**Data source:** PHO Laboratory Information System and CCM

### Table 2. Proportion (%) of SARS-CoV-2 positive samples with the spike (S) gene N501Y mutation (detected/tested) by gender and outbreak status, January 20, 2021

| Gender | Outbreak | Non-outbreak | Total |
|---|---|---|---|
| Male | 8.7% (27/310) | 1.1% (11/958) | 3.0% (38/1,268) |
| Female | 18.2% (65/357) | 1.2% (10/853) | 6.2% (75/1,210) |
| Unknown | 0.0% (0/31) | 0.0% (0/61) | 0.0% (0/92) |

**Note**: Excludes samples where the N501Y screen test could not be completed, likely due to low viral quantity in the sample (n=186). Not all samples have gender reported. These samples have been included as unknown. Laboratory records for 47 samples were unable to be matched to confirmed cases in CCM, none of these had N501Y mutation detected. These were included as non-outbreak samples. As a result, the number tested may be an underestimate for outbreaks, and an overestimate for non-outbreaks. Information on how samples are identified as outbreak associated is available in the technical notes.
**Data source:** PHO Laboratory Information System and CCM

### Table 3. Proportion (%) of SARS-CoV-2 positive samples with the spike (S) gene N501Y mutation (detected/tested) by age group and outbreak status, January 20, 2021

| Age group[ | Outbreak | Non-outbreak | Total |
|---|---|---|---|
| Ages: 19 and under | 7.1% (2/28) | 1.9% (5/259) | 2.4% (7/287) |
| Ages: 20-39 | 7.2% (14/194) | 0.7% (5/680) | 2.2% (19/874) |
| Ages: 40-59 | 5.5% (10/183) | 1.6%(9/560) | 2.6% (19/743) |
| Ages: 60-79 | 20.5% (27/132) | 0.7% (2/305) | 6.6% (29/437) |
| Ages: 80 and over | 24.2% (39/161) | 0.0% (0/47) | 18.8% (39/208) |
| Unknown Age | 0.0% (0/0) | 0.0% (0/21) | 0.0% (0/21) |

**Note**: Excludes samples where the N501Y screen test could not be completed, likely due to low viral quantity in the sample (n=186). Not all samples have an age reported. These samples have been included as unknown. Laboratory records for 47 samples were unable to be matched to confirmed cases in CCM, none of these had N501Y mutation detected. These were included as non-outbreak samples. As a result, the number tested may be an underestimate for outbreaks, and an overestimate for non-outbreaks. Information on how samples are identified as outbreak associated is available in the technical notes.
**Data source:** PHO Laboratory Information System and CCM

**Table 4. Proportion (%) of SARS-CoV-2 positive samples with the spike (S) gene N501Y mutation (detected/tested) by public health unit and outbreak status, January 20, 2021**

| Public Health Unit | Outbreak | Non-outbreak | Total |
|---|---|---|---|
| Algoma Public Health | 0.0% (0/1) | 0.0% (0/3) | 0.0% (0/4) |
| Brant County Health Unit | 0.0% (0/0) | 0.0% (0/12) | 0.0% (0/12) |
| Chatham-Kent Public Health | 0.0% (0/1) | 0.0% (0/4) | 0.0% (0/5) |
| City of Hamilton Public Health Services | 0.0% (0/28) | 0.0% (0/7) | 0.0% (0/35) |
| Durham Region Health Department | 0.0% (0/17) | 2.6% (2/76) | 2.2% (2/93) |
| Eastern Ontario Health Unit | 0.0% (0/3) | 0.0% (0/14) | 0.0% (0/17) |
| Grey Bruce Health Unit | 0.0% (0/2) | 0.0% (0/2) | 0.0% (0/4) |
| Haldimand-Norfolk Health Unit | 0.0% (0/0) | 0.0% (0/5) | 0.0% (0/5) |
| Haliburton, Kawartha, Pine Ridge District Health Unit | 0.0% (0/12) | 0.0% (0/10) | 0.0% (0/22) |
| Halton Region Public Health | 0.0% (0/16) | 0.0% (0/43) | 0.0% (0/59) |
| Hastings Prince Edward Public Health | 0.0% (0/0) | 0.0% (0/2) | 0.0% (0/2) |
| Huron Perth Public Health | 0.0% (0/6) | 0.0% (0/15) | 0.0% (0/21) |
| Kingston, Frontenac and Lennox & Addington Public Health | 0.0% (0/0) | 0.0% (0/5) | 0.0% (0/5) |
| Lambton Public Health | 0.0% (0/4) | 0.0% (0/21) | 0.0% (0/25) |
| Leeds, Grenville & Lanark District Health Unit | 0.0% (0/1) | 0.0% (0/4) | 0.0% (0/5) |
| Middlesex-London Health Unit | 0.0% (0/13) | 0.0% (0/39) | 0.0% (0/52) |
| Niagara Region Public Health | 0.0% (0/46) | 0.0% (0/57) | 0.0% (0/103) |
| North Bay Parry Sound District Health Unit | 0.0% (0/1) | 0.0% (0/0) | 0.0% (0/1) |
| Northwestern Health Unit | 0.0% (0/0) | 0.0% (0/0) | 0.0% (0/0) |

| Public Health Unit | Outbreak | Non-outbreak | Total |
|---|---|---|---|
| Ottawa Public Health | 0.0% (0/5) | 0.0% (0/47) | 0.0% (0/52) |
| Peel Public Health | 1.9% (2/103) | 1.2% (5/427) | 1.3% (7/530) |
| Peterborough Public Health | 0.0% (0/2) | 0.0% (0/7) | 0.0% (0/9) |
| Porcupine Health Unit | 0.0% (0/0) | 0.0% (0/0) | 0.0% (0/0) |
| Public Health Sudbury & Districts | 0.0% (0/6) | 0.0% (0/7) | 0.0% (0/13) |
| Region of Waterloo Public Health and Emergency Services | 0.0% (0/40) | 1.6% (1/64) | 1.0% (1/104) |
| Renfrew County and District Health Unit | 0.0% (0/0) | 0.0% (0/0) | 0.0% (0/0) |
| Simcoe Muskoka District Health Unit | 73.9% (88/119) | 12.0% (3/25) | 63.2% (91/144) |
| Southwestern Public Health | 0.0% (0/3) | 0.0% (0/9) | 0.0% (0/12) |
| Thunder Bay District Health Unit | 0.0% (0/50) | 0.0% (0/3) | 0.0% (0/53) |
| Timiskaming Health Unit | 0.0% (0/0) | 0.0% (0/0) | 0.0% (0/0) |
| Toronto Public Health | 1.8% (2/109) | 1.2% (7/572) | 1.3% (9/681) |
| Wellington-Dufferin-Guelph Public Health | 0.0% (0/21) | 0.0% (0/27) | 0.0% (0/48) |
| Windsor-Essex County Health Unit | 0.0% (0/34) | 0.0% (0/111) | 0.0% (0/145) |
| York Region Public Health | 0.0% (0/55) | 1.4% (3/207) | 1.1% (3/262) |
| Unknown | 0.0% (0/0) | 0.0% (0/47) | 0.0% (0/47) |

**Note**: Excludes samples where the N501Y screen test could not be completed, likely due to low viral quantity in the sample (n=186). PHO has not received all samples reported on January 20, 2021. As such, some public health units may have a small proportion of SARS-CoV-2 positive samples screened for the N501Y mutation at the time of this report. Laboratory records for 47 samples were unable to be matched to confirmed cases in CCM, none of these had N501Y mutation detected. These were included as non-outbreak samples. As a result, the number tested may be an underestimate for outbreaks, and an overestimate for non-outbreaks. Information on how samples are identified as outbreak associated is available in the technical notes.
**Data source:** PHO Laboratory Information System and CCM

# Confirmatory Results by Whole Genome Sequencing

**Table 5. Number and proportion of samples with N501Y mutation detected confirmed by whole genome sequencing (PANGO lineage), January 20, 2021**

| Lineage | Number (%) |
|---|---|
| B.1.1.7 (first detected in the United Kingdom) | 87 (77.0%) |
| B.1.351 (first detected in South Africa) | 1 (0.9%) |
| Confirmation pending | 22 (19.4%) |
| Unable to confirm – likely due to low viral quantity | 3 (2.7%) |
| Total | 113 (100.0%) |

**Note**: The sample confirmed as B.1.351 was from an individual residing in Peel Public Health.
**Data source:** PHO SARS-CoV-2 whole genome sequencing database

# Technical Notes and Data Caveats

## Data sources

Patient information and N501Y PCR results were extracted from PHO Laboratory Information Management System, **February 4, 2021 at 2 p.m.** (patient information) and **February 6, 2021 at 1 p.m.** (N501Y PCR results).

Whole genome sequencing confirmatory results were extracted from PHO SARS-CoV-2 whole genome sequencing database on **February 7, 2021 at 4 p.m.**

The total number of SARS-CoV-2 positive samples reported on January 20, 2021 was obtained from the COVID-19 Provincial Diagnostic Testing Network.

Information on outbreaks, public health unit, and travel history was extracted from the Public Health Case and Contact Management Solution (CCM) by PHO as of **February 4, 2021 at 1 p.m.**

- Information successfully extracted from the Public Health Case and Contact Management Solution (CCM) by PHO as of **February 4, 2021 at 1 p.m.**
- CCM is a dynamic disease reporting systems, which allow ongoing updates to data previously entered. As a result, data extracted from CCM represent a snapshot at the time of extraction and may differ from previous or subsequent reports.

## Data caveats: patient information and test results (PHO Laboratory Information Management System)

- The results in this report reflect the single-day prevalence among samples received by PHO Laboratory by February 4, 2021 and should be interpreted with caution.
- Approximately 91.8% (2,756/3,003) of SARS-CoV-2 positive samples reported in Ontario on January 20, 2021 were received and tested by Public Health Ontario Laboratory as of February 4, 2021. The remaining samples were either not received or were ineligible/not sent due to low viral quantity in the sample (i.e. high rRT-PCR cycle threshold [Ct] values [>35] or low volumes [< 500µl]). As a result, the number of samples screened for the N501Y mutation in a specific public health unit may be lower than the number of SARS-CoV-2 positives reported on January 20, 2021.
- Samples for which the N501Y screen assay could not be completed (n=186) were excluded from the analysis. Some laboratories sent all samples positive for SARS-CoV-2 to PHO regardless of viral quantity in the sample. Therefore, it is likely that samples for which the N501Y screen assay could not be completed were due to low viral quantities (i.e. high Ct values).
- Counts reported throughout the summary are sample-based and not person-based. As such, it is possible that more than one sample was tested per individual. However, no individual had more than one sample with the N501Y mutation detected.

## Data caveats: information on outbreaks, public health unit, and travel (CCM)

- A total of 47 samples submitted to PHO Laboratory for VOC screening were unable to be linked to confirmed cases in CCM. As a result, information on outbreaks, public health unit, and travel history were not reported for these cases.
- Orientation of case counts by geography is based on the permanent health unit (PHU). PHU refers to the case's public health unit of residence at the time of illness onset and not necessarily the location of exposure. Cases for which the PHU was reported as MOH-PHO (to signify a case that is not a resident of Ontario) have been excluded from the analyses.
- Outbreak-associated cases were defined as cases with a link to a confirmed local outbreak.
- Due to reporting delays and potential variations in data entry processes across public health units, there may be additional outbreak associated cases that have not yet been entered in CCM, or have not been linked to an outbreak.
- Outbreaks are declared by the local medical officer of health or their designate in accordance to the Health Protection and Promotion Act and criteria outlined in Ministry guidance documents.
- Travel-related cases were defined as any case classified as ‘travel’ as their likely source of acquisition. Likely source of acquisition which is determined by examining the epidemiologic link and epidemiologic link status fields in CCM. If no epidemiologic link is identified in those fields the risk factor fields are examined to determine whether a case travelled, was associated with a confirmed outbreak, was a contact of a case, had no known epidemiological link (sporadic community transmission) or was reported to have an unknown source/no information was reported. Some cases may have no information reported if the case is untraceable, was lost to follow-up or referred to FNIHB. Cases with multiple risk factors were assigned to a single likely acquisition source group which was determined hierarchically in the following order: Outbreak-associated > close contact of a confirmed case > travel > no known epidemiological link > information missing or unknown.
- Travel risk factor and exposure information was examined to determine if cases traveled outside of Canada during the incubation period.

# References


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