

# **Enhanced Epidemiological Summary**

# COVID-19 Variants of Concern in Ontario: December 1, 2020 to May 9, 2021

This report includes the most current information available from Public Health Case and Contact Management Solution (CCM) for all public health units (PHUs) in Ontario as of **May 9, 2021.** 

Please visit the interactive Ontario COVID-19 Data Tool to explore other recent COVID-19 data by public health unit, age group, gender, and trends over time. A Daily Epidemiological Summary, a Weekly Epidemiological Summary, as well as additional Enhanced Epidemiological Reports are available on the Public Health Ontario website.

## **Purpose**

This report provides a focused analysis on confirmed COVID-19 cases with the VOCs lineages B.1.1.7, B.1.315, P.1 or VOC associated mutations. Further details on these COVID-19 VOCs can be found in the <u>Technical</u> Notes.

Changes to the VOC testing algorithm may occur over time and trends should be interpreted with caution. Details on PHO's VOC testing can be found here.

# **Highlights**

- As of May 9, 2021, Ontario has confirmed a total of 127,704 COVID-19 cases with a known VOC or VOC-associated mutation detected.
  - Of these, 73.0% (93,236/127,704) are confirmed or presumed to be lineage B.1.1.7, which continues to be the dominant strain circulating in Ontario.
- Just over half (50.1%; 64,704/127,704) of COVID-19 cases with a known VOC or VOC-associated mutation are males and two-thirds (67.4%; 86,029/127,704) are between 20 to 59 years of age.
- COVID-19 VOCs or VOC-associated mutations have been confirmed in all 34 public health units and seven geographic regions in the province.
  - Almost three-quarters (74.3%; 94,876/127,704) of confirmed COVID-19 VOC or VOC-associated mutations have been reported in the regions of Central East (54,376; 42.6%) and Toronto (40,500; 31.7%).
- Close to half (47.2%; 60,244/127,704) of COVID-19 VOCs or VOC-associated mutations are linked to close contact with a confirmed case.
- A total of 871 fatalities have been reported among cases with a known VOC or VOC-associated mutation (case fatality: 0.7%); 749/871 (86.0%) have occurred among those 60 years of age or older.

#### **Cases Over Time**

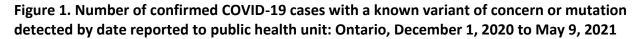
Table 1. Number of confirmed COVID-19 cases with a known variant of concern or mutation detected: Ontario, December 1, 2020 to May 9, 2021

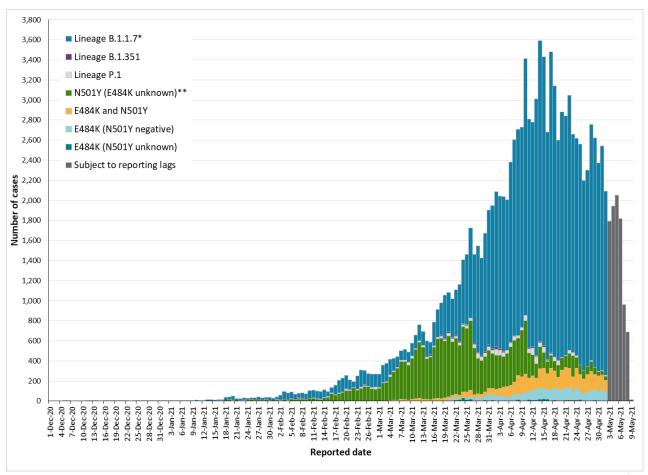
	Total (%)
Variants of concern	
Lineage B.1.1.7*	93,236 (97.8)
Lineage B.1.351	511 (0.5)
Lineage P.1	1,557 (1.6)
Mutations (lineage not determined)	
N501Y positive (E484K unknown)**	22,109 (68.2)
E484K positive and N501Y positive <sup>†</sup>	6,212 (19.2)
E484K positive and N501Y negative	3,577 (11.0)
E484K positive (N501Y unknown)	502 (1.6)
Total	127,704 (100.0)

**Note:** Interpret the VOC and mutation data with caution due to the varying time required to complete VOC testing and/or genomic analysis following the initial positive test for SARS-CoV-2. Due to the nature of the genomic analysis, test results may be completed in batches. Data corrections or updates can result in case records being removed and/or updated and may result in totals differing from past publicly reported case counts. Data for calculating the change in cases and the cumulative case counts uses data from the Investigation Subtype field only. Changes to the VOC testing algorithm may impact counts and trends. Further details can be found in the data caveats section.

<sup>\*</sup>Includes all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation in the Investigation Subtype field.

<sup>\*\*</sup>The category 'N501Y (E484K unknown)' mainly consists of results from before the introduction of the E484K test. Counts will shift from this category into a VOC lineage category as E484K tests or genomic analysis are completed. †Confirmed COVID-19 cases that are positive for both the E484K and N501Y mutations are likely to be lineage B.1.351 or P.1 based on current epidemiology.



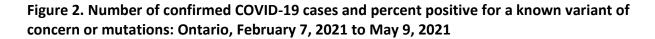


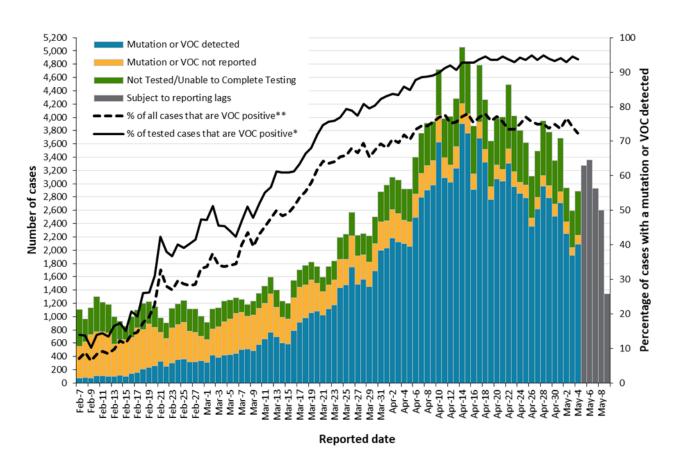
**Note:** Reported date is based on the date the case was reported, not the date that the VOC or mutation was identified. Further details on testing for variants of concern can be found in the technical notes. Interpret the VOC and mutation trends with caution due to the varying time required to complete testing and/or genomic analysis following the initial positive test for SARS-CoV-2. Data for cases with a B.1.1.7, B.1.351, and P.1 lineage detected or any of the mutations listed above are determined using the Investigation Subtype field only. Changes to the VOC testing algorithm may impact counts and trends. Further details can be found in the data caveats section.

\*Includes all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation in the Investigation Subtype field. Starting March 22, 2021, specimens tested for the both the N501Y and E484K mutation, and found to be positive for the N501Y mutation only, are not forwarded for further genomic analysis and are presumed to be B.1.1.7.

\*\*The category 'N501Y (E484K unknown)' mainly consists of results from before the introduction of the E484K test. Counts will shift from this category into a VOC lineage category as E484K tests or genomic analysis are completed.

Data Source: CCM





**Note**: Data used to calculate the number of cases tested for mutations common to VOCs or lineages using genomic analyses are obtained using information from the Laboratory object in CCM in addition to the data from the Investigation Subtype field. Therefore, comparisons to counts using only information from the Investigation Subtype field may not align. The percent of cases due to a VOC may be higher than described in this report.

<sup>\*</sup>The denominator includes only confirmed COVID-19 cases that were able to be tested for VOCs (e.g. those identified as 'Detected' or 'Not Detected'.

<sup>\*\*</sup>The denominator includes all confirmed COVID-19 cases, including those that were unable to be tested for VOCs (e.g. those identified as 'Detected', 'Not Detected' and 'Not Tested/Unable to Complete Testing'.

### **Case Characteristics**

Table 2a. Number of confirmed COVID-19 cases with a known variant of concern by gender and age group: Ontario, December 1, 2020 to May 9, 2021

Gender and Age Group (Years)	Lineage B.1.1.7*	Lineage B.1.351	Lineage P.1	Total VOCs (%)
Gender: Male	47,090 (50.5)	257 (50.3)	824 (52.9)	48,171 (50.5)
Gender: Female	45,384 (48.7)	252 (49.3)	722 (46.4)	46,358 (48.6)
Ages: 19 and under	16,673 (17.9)	81 (15.8)	277 (17.8)	17,031 (17.8)
Ages: 20-39	34,686 (37.2)	176 (34.4)	530 (34.0)	35,392 (37.1)
Ages: 40-59	28,507 (30.6)	161 (31.5)	492 (31.6)	29,160 (30.6)
Ages: 60-79	11,658 (12.5)	78 (15.3)	251 (13.8)	11,951 (12.5)
Ages: 80 and over	1,703 (1.8)	15 (2.9)	43 (2.8)	1,761 (1.8)
Total	93,236 (97.8)	511 (0.5)	1,557 (1.6)	95,304 (100.0)

**Note:** Not all cases have a reported gender or age. Data corrections or updates can result in case records being removed and/or updated from past reports and may result in subset totals (i.e., gender, age group) differing from past publicly reported case counts.

<sup>\*</sup>Includes all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation in the Investigation Subtype field. Starting March 22, 2021, specimens tested for the both the N501Y and E484K mutation, and found to be positive for the N501Y mutation only, are not forwarded for further genomic analysis and are presumed to be B.1.1.7.

Table 2b. Number of confirmed COVID-19 cases with a known mutation by gender and age group: Ontario, December 1, 2020 to May 9, 2021

Gender and Age Group (Years)	N501Y positive / E484K unknown*	E484K positive / N501Y positive	E484K positive / N501Y negative	E484K positive / N501Y unknown	Total Mutations (%)
Gender: Male	11,300 (51.1)	3,136 (50.5)	1,824 (51.0)	273 (54.4)	16,533 (51.0)
Gender: Female	10,590 (47.9)	3,025 (48.7)	1,734 (48.5)	221 (44.0)	15,570 (48.1)
Ages: 19 and under	4,462 (20.2)	1,062 (17.1)	635 (17.7)	94 (18.7)	6,253 (19.3)
Ages: 20-39	8,320 (37.6)	2,218 (35.7)	1,431 (40.0)	183 (36.4)	12,152 (37.5)
Ages: 40-59	6,201 (28.0)	1,932 (31.1)	1,043 (29.2)	149 (29.7)	9,325 (28.8)
Ages: 60-79	2,655 (12.0)	849 (13.7)	401 (11.2)	61 (12.1)	3,966 (12.2)
Ages: 80 and over	468 (2.1)	151 (2.4)	67 (1.9)	15 (3.0)	701 (2.2)
Total	22,109 (68.2)	6,212 (19.2)	3,577 (11.0)	502 (1.6)	32,400 (100.0)

**Note:** Not all cases have a reported gender or age. Data corrections or updates can result in case records being removed and/or updated from past reports and may result in subset totals (i.e., gender, age group) differing from past publicly reported case counts.

<sup>\*</sup>The category 'N501Y positive/E484K unknown' consists mainly of results from before the introduction of the E484K test. Counts will shift from this category into a VOC lineage category as E484K tests or genomic analysis are completed. **Data Source**: CCM

# Geography

Table 3. Number of confirmed COVID-19 cases with a known variant of concern or mutation detected by public health unit and region: Ontario, December 1, 2020 to May 9, 2021

Public Health Unit and Region	Lineage B.1.1.7*	Lineage B.1.351	Lineage P.1	Mutation detected**	Total (%)
Northwestern Health Unit	32 (0.0)	0 (0.0)	1 (0.1)	26 (0.1)	59 (0.0)
Thunder Bay District Health Unit	16 (0.0)	0 (0.0)	0 (0.0)	42 (0.1)	58 (0.0)
TOTAL NORTH WEST	48 (0.0)	0 (0.0)	1 (0.1)	68 (0.2)	117 (0.1)
Algoma Public Health	45 (0.0)	0 (0.0)	0 (0.0)	20 (0.1)	65 (0.0)
North Bay Parry Sound District Health Unit	87 (0.1)	27 (5.3)	0 (0.0)	15 (0.0)	129 (0.1)
Porcupine Health Unit	141 (0.1)	2 (0.4)	0 (0.0)	9 (0.0)	152 (0.1)
Public Health Sudbury & Districts	429 (0.5)	1 (0.2)	0 (0.0)	416 (1.3)	846 (0.7)
Timiskaming Health Unit	70 (0.1)	1 (0.2)	0 (0.0)	0 (0.0)	71 (0.1)
TOTAL NORTH EAST	772 (0.8)	31 (6.1)	0 (0.0)	460 (1.4)	1,263 (1.0)
Ottawa Public Health	4,476 (4.8)	96 (18.8)	8 (0.5)	719 (2.2)	5,299 (4.1)
Eastern Ontario Health Unit	562 (0.6)	23 (4.5)	2 (0.1)	294 (0.9)	881 (0.7)
Hastings Prince Edward Public Health	15 (0.0)	0 (0.0)	1 (0.1)	342 (1.1)	358 (0.3)
Kingston, Frontenac and Lennox & Addington Public Health	315 (0.3)	0 (0.0)	21 (1.3)	132 (0.4)	468 (0.4)
Leeds, Grenville & Lanark District Health Unit	255 (0.3)	9 (1.8)	0 (0.0)	37 (0.1)	301 (0.2)
Renfrew County and District Health Unit	142 (0.1)	2 (0.4)	0 (0.0)	23 (0.1)	167 (0.1)

Public Health Unit and Region	Lineage B.1.1.7*	Lineage B.1.351	Lineage P.1	Mutation detected**	Total (%)
TOTAL EASTERN	5,765 (6.2)	130 (25.4)	32 (2.1)	1,547 (4.8)	7,474 (5.8)
Durham Region Health Department	7,475 (8.0)	18 (3.5)	78 (5.0)	1,072 (3.3)	8,643 (6.8)
Haliburton, Kawartha, Pine Ridge District Health Unit	248 (0.3)	0 (0.0)	7 (0.4)	202 (0.6)	457 (0.4)
Peel Public Health	20,455 (21.9)	62 (12.1)	466 (29.9)	5,178 (16.0)	26,161 (20.5)
Peterborough Public Health	321 (0.3)	0 (0.0)	1 (0.1)	165 (0.5)	487 (0.4)
Simcoe Muskoka District Health Unit	2,748 (2.9)	16 (3.1)	68 (4.4)	858 (2.6)	3,690 (2.9)
York Region Public Health	12,062 (12.9)	21 (4.1)	165 (10.6)	2,690 (8.3)	14,938 (11.7)
TOTAL CENTRAL EAST	43,309 (46.4)	117 (22.9)	785 (50.4)	10,165 (31.4)	54,376 (42.6)
Toronto Public Health	24,065 (25.8)	197 (38.5)	583 (37.4)	15,655 (48.3)	40,500 (31.7)
TOTAL TORONTO	24,065 (25.8)	197 (38.5)	583 (37.4)	15,655 (48.3)	40,500 (31.7)
Chatham-Kent Public Health	68 (0.1)	4 (0.8)	3 (0.2)	112 (0.3)	187 (0.1)
Grey Bruce Health Unit	238 (0.3)	0 (0.0)	3 (0.2)	42 (0.1)	283 (0.2)
Huron Perth Public Health	83 (0.1)	0 (0.0)	0 (0.0)	69 (0.2)	152 (0.1)
Lambton Public Health	316 (0.3)	0 (0.0)	4 (0.3)	81 (0.2)	401 (0.3)
Middlesex-London Health Unit	1,942 (2.1)	0 (0.0)	16 (1.0)	279 (0.9)	2,237 (1.7)
Southwestern Public Health	497 (0.5)	0 (0.0)	2 (0.1)	77 (0.2)	576 (0.4)
Windsor-Essex County Health Unit	1,069 (1.1)	4 (0.8)	5 (0.3)	90 (0.3)	1,168 (0.9)
TOTAL SOUTH WEST	4,213 (4.5)	8 (1.6)	33 (2.1)	750 (2.3)	5,004 (3.9)

Public Health Unit and Region	Lineage B.1.1.7*	Lineage B.1.351	Lineage P.1	Mutation detected**	Total (%)
Brant County Health Unit	426 (0.5)	0 (0.0)	15 (1.0)	418 (1.3)	859 (0.7)
City of Hamilton Public Health Services	3,870 (4.1)	10 (2.0)	17 (1.1)	1,044 (3.2)	4,941 (3.9)
Haldimand-Norfolk Health Unit	283 (0.3)	0 (0.0)	3 (0.2)	322 (1.0)	608 (0.5)
Halton Region Public Health	3,962 (4.2)	16 (3.1)	51 (3.3)	559 (1.7)	4,588 (3.6)
Niagara Region Public Health	2,813 (3.0)	0 (0.0)	3 (0.2)	949 (2.9)	3,765 (2.9)
Region of Waterloo Public Health and Emergency Services	2,093 (2.2)	2 (0.4)	17 (1.1)	276 (0.8)	2,388 (1.9)
Wellington-Dufferin- Guelph Public Health	1,617 (1.7)	0 (0.0)	17 (1.1)	187 (0.6)	1,821 (1.4)
TOTAL CENTRAL WEST	15,064 (16.2)	28 (5.5)	123 (7.9)	3,755 (11.6)	18,970 (14.8)
TOTAL ONTARIO	93,236 (73.0)	511 (0.4)	1,557 (1.2)	32,400 (25.4)	127,704 (100.0)

<sup>\*</sup>Includes all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation in the Investigation Subtype field. Starting March 22, 2021, specimens tested for the both the N501Y and E484K mutation, and found to be positive for the N501Y mutation only, are not forwarded for further genomic analysis and are presumed to be B.1.1.7.

<sup>\*\*</sup>Includes all confirmed COVID-19 cases where a mutation was detected (i.e., N501Y positive/E484K unknown, E484K positive and N501Y positive, E484K positive and N501Y negative, and E484K positive and N501Y unknown) but the lineage has not been determined.

# Severity and Outcome

Table 4a. Number of confirmed COVID-19 cases with a known variant of concern detected by severity and outcome: Ontario, December 1, 2020 to May 9, 2021

Severity and outcome	Lineage B.1.1.7*	Lineage B.1.351	Lineage P.1	Total VOCs (%)
Ever hospitalized	4,610 (4.9)	58 (11.4)	128 (8.2)	4,796 (5.0)
Ever in intensive care unit	912 (1.0)	23 (4.5)	27 (1.7)	962 (1.0)
Fatal outcome	550 (0.6)	14 (2.7)	25 (1.6)	589 (0.6)

**Note:** The determination of severity and outcome indicators are described in the <u>Technical Notes</u>.

Data Source: CCM

Table 4b. Number of confirmed COVID-19 cases with a known mutation detected by severity and outcome: Ontario, December 1, 2020 to May 9, 2021

Severity and outcome	N501Y positive / E484K unknown*	E484K positive / N501Y positive	E484K positive / N501Y negative	E484K positive / N501Y unknown	Total Mutations (%)
Ever hospitalized	1,080 (4.9)	426 (6.9)	134 (3.7)	14 (2.8)	1,654 (5.1)
Ever in intensive care unit	201 (0.9)	95 (1.5)	25 (0.7)	2 (0.4)	323 (1.0)
Fatal outcome	203 (0.9)	61 (1.0)	14 (0.4)	4 (0.8)	282 (0.9)

Note: The determination of severity and outcome indicators are described in the Technical Notes.

<sup>\*</sup>Includes all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation in the Investigation Subtype field. Starting March 22, 2021, specimens tested for the both the N501Y and E484K mutation, and found to be positive for the N501Y mutation only, are not forwarded for further genomic analysis and are presumed to be B.1.1.7.

<sup>\*</sup>The category 'N501Y (E484K unknown)' mainly consists of results from before the introduction of the E484K test. Counts will shift from this category into a VOC lineage category as E484K tests or genomic analysis are completed.

Table 5a. Number of fatalities among confirmed COVID-19 cases with a known variant of concern detected by age group: Ontario, December 1, 2020 to May 9, 2021

Age Group (Years)	Lineage B.1.1.7*	Lineage B.1.351	Lineage P.1	Total fatalities by age group (%)	Case fatality by age group (%)
Ages: 19 and under	1 (0.2)	0 (0.0)	0 (0.0)	1 (0.2)	<0.1
Ages: 20-39	13 (2.4)	0 (0.0)	0 (0.0)	13 (2.2)	<0.1
Ages: 40-59	70 (12.7)	2 (14.3)	3 (12.0)	75 (12.7)	0.3
Ages: 60-79	234 (42.5)	6 (42.9)	12 (48.0)	252 (42.8)	2.1
Ages: 80 and over	232 (42.2)	6 (42.9)	10 (40.0)	248 (42.1)	14.1
Total	550 (93.4)	14 (2.4)	25 (4.2)	589 (100.0)	0.6

**Note:** Not all cases have a reported age. Data corrections or updates can result in case records being removed and/or updated from past reports and may result in subset totals (i.e., gender, age group) differing from past publicly reported case counts.

Table 5b. Number of fatalities among confirmed COVID-19 cases with a known mutation detected by age group: Ontario, December 1, 2020 to May 9, 2021

Age Group (Years)	N501Y positive / E484K unknown*	E484K positive / N501Y positive	E484K positive / N501Y negative	E484K positive / N501Y unknown	Total fatalities by age group (%)	Case fatality by age group (%)
Ages: 19 and under	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0.0
Ages: 20-39	4 (2.0)	1 (1.6)	1 (7.1)	0 (0.0)	6 (2.1)	<0.1
Ages: 40-59	17 (8.4)	9 (14.7)	0 (0.0)	1 (25.0)	27 (9.6)	0.3
Ages: 60-79	85 (41.9)	37 (60.7)	7 (50.0)	2 (50.0)	131 (46.4)	3.3
Ages: 80 and over	97 (47.8)	14 (22.9)	6 (42.9)	1 (25.0)	118 (41.8)	16.8
Total	203 (72.0)	61 (21.6)	14 (5.0)	4 (1.4)	282 (100.0)	0.9

<sup>\*</sup>Includes all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation in the Investigation Subtype field. Starting March 22, 2021, specimens tested for the both the N501Y and E484K mutation, and found to be positive for the N501Y mutation only, are not forwarded for further genomic analysis and are presumed to be B.1.1.7.

**Note:** Not all cases have a reported age. Data corrections or updates can result in case records being removed and/or updated from past reports and may result in subset totals (i.e., gender, age group) differing from past publicly reported case counts

\*The category 'N501Y (E484K unknown)' mainly consists of results from before the introduction of the E484K test. Counts will shift from this category into a VOC lineage category as E484K tests or genomic analysis are completed. **Data Source**: CCM

# Likely Source of Acquisition

Table 6a. Number of confirmed COVID-19 cases with a known variant of concern detected by likely source of acquisition: Ontario, December 1, 2020 to May 9, 2021

Likely Acquisition	Lineage B.1.1.7*	Lineage B.1.351	Lineage P.1	Total (%)
Close contact of a confirmed case	43,324 (46.5)	246 (48.1)	855 (54.9)	44,425 (46.6)
No known epidemiological link	33,061 (35.5)	136 (26.6)	456 (29.3)	33,653 (35.3)
Outbreak	7,533 (8.1)	82 (16.0)	158 (10.1)	7,773 (8.2)
Travel related	514 (0.5)	15 (2.9)	13 (0.8)	542 (0.6)
Information missing or unknown	8,804 (9.4)	32 (6.3)	75 (4.8)	8,911 (9.3)
Total	93,236 (97.8)	511 (0.5)	1,557 (1.6)	95,304 (100.0)

**Note:** The determination of the likely source of acquisition is described in the Technical Notes.

<sup>\*</sup>Includes all confirmed COVID-19 cases where lineage B.1.1.7 was identified by genomic analysis and those presumed to be B.1.1.7 based on positive N501Y and negative E484K mutation in the Investigation Subtype field. Starting March 22, 2021, specimens tested for the both the N501Y and E484K mutation, and found to be positive for the N501Y mutation only, are not forwarded for further genomic analysis and are presumed to be B.1.1.7.

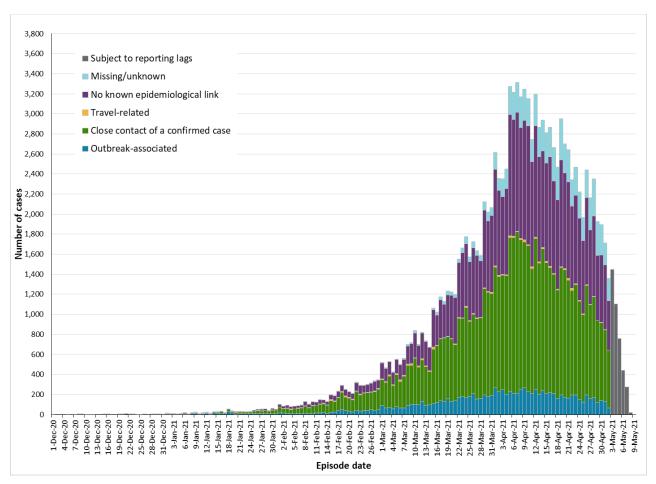
Table 6b. Number of confirmed COVID-19 cases with a known mutation detected by likely source of acquisition: Ontario, December 1, 2020 to May 9, 2021

Likely Acquisition	N501Y positive / E484K unknown*	E484K positive / N501Y positive	E484K positive / N501Y negative	E484K positive / N501Y unknown	Total (%)
Close contact of a confirmed case	10,430 (47.2)	3,290 (53.0)	1,857 (51.9)	242 (48.2)	15,819 (48.8)
No known epidemiological link	7,272 (32.9)	1,827 (29.4)	1,150 (32.1)	150 (29.9)	10,399 (32.1)
Outbreak	2,698 (12.2)	561 (9.0)	262 (7.3)	50 (10.0)	3,571 (11.0)
Travel related	264 (1.2)	62 (1.0)	24 (0.7)	6 (1.2)	356 (1.1)
Information missing or unknown	1,445 (6.5)	472 (7.6)	284 (7.9)	54 (10.8)	2,255 (7.0)
Total	22,109 (68.2)	6,212 (19.2)	3,577 (11.0)	402 (1.5)	32,400 (100.0)

**Note:** The determination of the likely source of acquisition is described in the <u>Technical Notes</u>.

<sup>\*</sup>The category 'N501Y (E484K unknown)' mainly consists of results from before the introduction of the E484K test. Counts will shift from this category into a VOC lineage category as E484K tests or genomic analysis are completed.

Figure 3. Number of confirmed COVID-19 cases with a known variant of concern or mutation detected by likely source of acquisition and approximation of symptom onset: Ontario, December 1, 2021 to May 9, 2021



**Note:** Episode date and likely source of acquisition are defined in the <u>Technical Notes</u>.

# Outbreaks and associated cases

Table 7. Number of confirmed outbreak-associated COVID-19 cases with a confirmed variant of concern of mutation detected by outbreak setting: Ontario, January 1, 2021 to May 9, 2021

Outbreak setting	Total number of reported outbreaks <sup>1</sup>	Total number of outbreaks- associated cases <sup>2,3</sup>	Number (%) of outbreaks with at least one confirmed VOC or mutation case	Of outbreaks with at least one confirmed VOC or mutation case: Total number of outbreak associated cases <sup>2,3</sup>	Of outbreaks with at least one confirmed VOC or mutation case: Number (%) of outbreak- associated confirmed VOC cases <sup>2,3</sup>
Congregate Care	1,049	8,504	209 (19.9)	1,810	1,055 (58.3)
Long term care homes	454	3,692	84 (18.5)	738	382 (51.8)
Retirement homes	319	1,930	44 (13.8)	249	182 (73.1)
Hospitals	276	2,882	81 (29.3)	823	491 (59.7)
Congregate Living	630	5,580	192 (30.5)	2,058	1,429 (69.4)
Correctional facility	33	1,060	8 (24.2)	155	90 (58.1)
Shelter	142	1,712	57 (40.1)	943	565 (59.9)
Group home/ supportive housing	341	1,716	92 (27.0)	473	364 (77.0)
Short-term accommodations	21	146	7 (33.3)	69	62 (89.9)
Congregate other	93	946	28 (30.1)	418	348 (83.3)
Education	1,344	6,055	669 (49.8)	3,113	2,406 (77.3)
Child care	509	2,470	243 (47.7)	1,367	1,088 (79.6)

Outbreak setting	Total number of reported outbreaks <sup>1</sup>	Total number of outbreaks- associated cases <sup>2,3</sup>	Number (%) of outbreaks with at least one confirmed VOC or mutation case	Of outbreaks with at least one confirmed VOC or mutation case: Total number of outbreak associated cases <sup>2,3</sup>	Of outbreaks with at least one confirmed VOC or mutation case: Number (%) of outbreak- associated confirmed VOC cases <sup>2,3</sup>
School - elementary	640	2,623	341 (53.3)	1,409	1,056 (74.9)
School – elementary/ secondary	36	129	17 (47.2)	63	48 (76.2)
School – secondary	134	494	57 (42.5)	210	164 (78.1)
School – post- secondary	25	339	11 (44.0)	64	50 (78.1)
Other Settings	1,930	15,313	739 (38.3)	6,752	5,011 (74.2)
Bar/restaurant/ nightclub	125	579	55 (44.0)	281	225 (80.1)
Medical/health services	70	355	18 (25.7)	93	83 (89.2)
Personal service settings	17	69	7 (41.2)	34	31 (91.2)
Recreational fitness	30	234	11 (36.7)	58	50 (86.2)
Retail	202	1,150	76 (37.6)	457	363 (79.4)
Other recreation/ community	108	1,495	51 (47.2)	462	376 (81.4)
Workplace – farm	124	745	19 (15.3)	128	56 (43.8)
Workplace – food processing	91	1,442	39 (42.9)	872	471 (54.0)

Outbreak setting	Total number of reported outbreaks <sup>1</sup>	Total number of outbreaks- associated cases <sup>2,3</sup>	Number (%) of outbreaks with at least one confirmed VOC or mutation case	Of outbreaks with at least one confirmed VOC or mutation case: Total number of outbreak associated cases <sup>2,3</sup>	Of outbreaks with at least one confirmed VOC or mutation case: Number (%) of outbreak- associated confirmed VOC cases <sup>2,3</sup>
Other types of workplaces	1,145	9,127	454 (39.7)	4,306	3,309 (76.8)
Other/unknown	18	117	9 (50.0)	61	47 (77.0)
Total	4,953	35,452	1,809 (36.5)	13,733	9,901 (72.1)

**Note:** Due to the timing of the first confirmed cases of COVID-19 VOCs in Ontario, this table includes only those outbreaks with a reported date on or after January 1, 2021. Outbreak categories are mutually exclusive. Retail includes settings such as grocery stores, pharmacies, malls, etc. Other types of workplaces include settings such as offices as well as warehousing, shipping and distribution, construction, etc. Other recreation includes settings such as entertainment and event venues, gatherings (e.g., weddings), religious facilities, etc. Medical/health services refer to settings such as doctor's office or clinic, wellness clinics, etc., and excludes categories listed in the congregate care setting group. Ongoing re-classification of settings for reported outbreaks can result in outbreak counts that may differ from previously reported counts.

<sup>&</sup>lt;sup>1</sup>The definition of what constitutes an outbreak varies by setting. Outbreak definitions for a number of settings may be found on the Ministry of Health's <u>COVID-19 guidance for the health sector</u> website.

<sup>&</sup>lt;sup>2</sup>Outbreak-associated cases include all cases that are linked to a confirmed outbreak in CCM. Although these cases are associated with an outbreak, it may not be considered to be their most likely source of acquisition. For this reason, the number of outbreak-associated cases in this table may differ from the number of cases with a likely acquisition of outbreak (Table 6a/Table 6b).

<sup>&</sup>lt;sup>3</sup>In most outbreaks under investigation, typically only a fixed number of specimens are to be submitted for laboratory testing; thus, although it is likely that cases epidemiologically linked to an outbreak with at least one VOC case would also be VOCs, this may not always be the case.

#### **Technical Notes**

#### **Data Sources**

- The data for this report were based on information successfully extracted from the Public Health Case and Contact Management Solution (CCM) for all PHUs by PHO as of May 9, 2021 at 1:00 p.m.
- CCM is a dynamic disease reporting system, which allows 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.
- COVID-19 test data were based on information from the Provincial COVID-19 Diagnostics Network, reported by member microbiology laboratories.

#### **Data Caveats**

- These data only represent cases reported to public health units and recorded in CCM. As a result, all counts will be subject to varying degrees of underreporting due to a variety of factors, such as disease awareness and medical care seeking behaviours, which may depend on severity of illness, clinical practice, changes in laboratory testing, and reporting behaviours.
- Lags in CCM data entry due to weekend staffing may result in lower case counts than would otherwise be recorded.
- Only cases meeting the confirmed case classification as listed in the MOH <u>COVID-19 case definition</u> are included.
- Cases of confirmed reinfection, as defined in the provincial case definitions, are counted as unique investigations.
- Case classification information may be updated for individuals with a positive result issued from a point-of-care assay.
- The number of tests performed does not reflect the number of specimens or persons tested. More than one test may be performed per specimen or per person. As such, the percentage of tests that were positive does not necessarily translate to the number of specimens or persons testing positive.
- Reported date is the date the case was reported to the public health unit.
- Episode date is based on an estimate of the date that best approximates the date of disease onset. This date is calculated based on either the date of symptom onset, specimen collection/test date, or the date reported to the public health unit.
- Resolved cases are determined only for COVID-19 cases that have not died. Cases that have died are considered fatal and not resolved. The following cases are classified as resolved:
  - Cases that are reported as 'recovered' in CCM
  - Cases that are not hospitalized and are 14 days past their episode date

- Cases that are currently hospitalized (no hospital end date entered) and have a status of 'closed' in CCM (indicating public health unit follow-up is complete) and are 14 days past their symptom onset date or specimen collection date
- Hospitalization includes all cases for which a hospital admission date was reported at the time of
  data extraction. It includes cases that have been discharged from hospital as well as cases that are
  currently hospitalized. Emergency room visits are not included in the number of reported
  hospitalizations.
- Intensive care unit (ICU) admission includes all cases for which an ICU admission date was reported at the time of data extraction. It is a subset of the count of hospitalized cases. It includes cases that have been treated or that are currently being treated in an ICU.
- Case counts by geography are based on the diagnosing health unit which 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 DHU was reported as MOH (to signify a case that is not a resident of Ontario)
  have been excluded from the analyses.
- Likely source of acquisition 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:
  - For cases with an episode date *on or after* April 1, 2020: Outbreak-associated > close contact of a confirmed case > travel > no known epidemiological link > information missing or unknown
  - For cases with an episode date before April 1, 2020: Travel > outbreak-associated > close contact of a confirmed case > no known epidemiological link > information missing or unknown
- Deaths are determined by using the outcome field in CCM. Any case marked 'Fatal' is included in the deaths data. The CCM field Type of Death is not used to further categorize the data.
  - The date of death is determined using the outcome date field for cases marked as 'Fatal' in the outcome field.
- COVID-19 cases from CCM for which the Classification and/or Disposition was reported as ENTERED
  IN ERROR, DOES NOT MEET DEFINITION, IGNORE, DUPLICATE, or any variation on these values have
  been excluded. The provincial case count for COVID-19 includes cases that are counted once across
  all systems from which the case data are obtained. Duplicate records may exist if these records were
  not identified and resolved prior to data upload to the Ministry.
- PANGO lineage B.1.1.7: This lineage was first detected in England in September, 2020. Early evidence suggests that the N501Y mutation may increase SARS-CoV-2 transmissibility. The PANGO lineage B.1.1.7 is assigned to genome sequences with at least 5 of the 17 defining B.1.1.7 single nucleotide polymorphisms (SNPs).

- PANGO lineage B.1.351 (also known as 501Y.V2): This lineage was first detected October, 2020 in South Africa and has several mutations of concern, including spike (S) gene: N501Y, K417N, and E484K. Early evidence suggests that these mutations may increase SARS-CoV-2 transmissibility and decrease vaccine efficacy. The PANGO lineage B.1.351 will be assigned to genome sequences at least 5 of the 9 defining B.1.351 SNPs.
- PANGO lineage P.1 (also known as 501Y.V3): This lineage was first detected January, 2021 in Brazil
  and has several mutations of concern, including spike (S) gene N501Y, K417T, and E484K. Early
  evidence suggests that these mutations may increase SARS-CoV-2 transmissibility and decrease
  vaccine efficacy. The PANGO lineage P.1 is assigned to genome sequences with more than 10 of the
  17 defining P.1 SNPs.
- Public Health Ontario conducts testing and genomic analyses for SARS-CoV-2 positive specimens
  using the criteria outlined here: <a href="https://www.publichealthontario.ca/en/laboratory-services/test-information-index/covid-19-voc">https://www.publichealthontario.ca/en/laboratory-services/test-information-index/covid-19-voc</a>
- Changes to the VOC testing algorithm may occur over time and trends should be interpreted with
  caution. Since February 3, 2021 all PCR positive SARS-Co-V-2 specimens with CT values ≤ 35 are
  tested for a N501Y mutation. Starting March 22, 2021, these specimens are tested for the E484K
  mutations as well. Specimens that are positive for the N501Y mutation only are not being forwarded
  for further genomic analysis. Specimens that are E484K positive (with or without N501Y) are
  forwarded for genomic analysis.
- Laboratory detection of a variant of concern is a multi-step process. Samples that test positive for SARS-CoV-2 and have a cycle threshold (Ct) value ≤ 35 can be tested for mutations common to variants of concern. If positive for the mutation of interest these samples may then undergo genomic analyses to identify the VOC. VOC lineages may still be confirmed using genomic analysis despite specific S gene mutation(s) being documented as 'unable to complete' due to poor sequence quality at the genome position.
- VOC testing data are analyzed for cases with a reported date on or after February 7, 2021. VOC
  testing data are based on CCM information reported within the laboratory object for select Logical
  Observation Identifiers Names and Codes (LOINC) and supplemented with information from the
  Investigation Subtype field. A confirmed Case Investigation is assigned a VOC test value (e.g., VOC
  test detected, VOC test not detected) based on the following hierarchy:
  - If multiple laboratory results are identified, a VOC test value is assigned based on the following hierarchy: Detected > Not Detected > Unable to complete
  - If a laboratory result is 'Not Detected' or 'Unable to complete', but data on the Investigation Subtype field is listed as a lineage or mutation common to a VOC, then the VOC test value is set to 'Detected'
- If a VOC is identified through genomic analysis cases initially classified as a mutation may be updated and moved to the appropriate lineage (B.1.1.7, B.1.351 and P.1).
- LOINCs are a set of internationally used result description codes. In the absence of a standard LOINC,
  Ontario Health can create local result codes, which are identified with an 'XON' prefix. LOINCs
  incorporate details of the result value (e.g. test method, target detected such as IgG, DNA, isolate
  etc.) and are unique to each result.

- VOC testing data in this report are assigned on a per case basis. Multiple laboratory results may be associated to a single case investigation, but for analysis purposes are only counted once.
  - The percent of cases that test VOC positive is calculated by taking the number of VOC test positive, divided by the total number of confirmed COVID-19 cases for a given reported date.
- The VOC percent positive may be higher than described in this report. While all confirmed COVID-19
  cases are included in the denominator, not all cases were able to be tested for VOCs. As testing
  algorithms change, the VOC percent positivity may not be reflective of the exact number of COVID19 cases due to VOCs

### 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.

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# For Further Information

For more information, email cd@oahpp.ca.

## **Public Health Ontario**

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