ENHANCED EPIDEMIOLOGICAL SUMMARY

Estimating the Prevalence and Growth of SARS-CoV-2 Variants in Ontario using Mutation Profiles

Purpose

This report provides a description of the incidence, prevalence, and growth of SARS-CoV-2 variants based on mutation profiles in Ontario. This report reflects cases that have been publicly reported up to August 24, 2021 and includes the most current information available from CCM.

For more information on variants confirmed by whole genome sequencing, refer to the SARS-CoV-2 Whole Genome Sequencing weekly report.

Highlights

• We estimate that currently, the majority (95.9%) of COVID-19 cases in Ontario are infected with a SARS-CoV-2 variant having the N501Y- & E484K- mutation profile, which includes cases of the B.1.617.2 (Delta) variant. Cases with the N501Y+ & E484K- mutation profile (likely B.1.1.7 [Alpha]), represent 0.7% of cases, while 3.2% of cases are infected with a SARS-CoV-2 variant having the N501Y+ & E484K+ mutation profile (likely P.1 [Gamma] or B.1.351 [Beta]).

• The incidence of the N501Y- & E484K- mutation profile in Table 1 is currently increasing, shown by the effective reproduction number above one. Incidence for all other mutation profiles is currently decreasing, as demonstrated by the effective reproduction numbers below one.

Table 1: Cumulative estimated cases, percentage of cases, and effective reproduction numbers by mutation profile in Ontario from August 18, 2021 to August 24, 2021

<table>
<thead>
<tr>
<th>Mutation Profile</th>
<th>Total Cases</th>
<th>Percentage of Cases</th>
<th>Reproduction Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>N501Y+ &amp; E484K-</td>
<td>31</td>
<td>0.7%</td>
<td>0.74</td>
</tr>
<tr>
<td>N501Y+ &amp; E484K+</td>
<td>137</td>
<td>3.2%</td>
<td>0.97</td>
</tr>
<tr>
<td>N501Y- &amp; E484K+</td>
<td>7</td>
<td>0.2%</td>
<td>0.74</td>
</tr>
<tr>
<td>N501Y- &amp; E484K-</td>
<td>4,107</td>
<td>95.9%</td>
<td>1.14</td>
</tr>
</tbody>
</table>
Estimating the Prevalence and Growth of SARS-CoV-2 Variants in Ontario using Mutation Profiles

Note: B.1.1.7 (Alpha) (N501Y+ & E484K-) was first detected in the United Kingdom; P.1 (Gamma) (N501Y+ & E484K+) was first detected in Brazil; B.1.351 (Beta) (N501Y+ & E484K+) was first detected in South Africa. B.1.617.2 (Delta) (included in N501Y- & E484K-) was first detected in India. The reproduction number is the average number of secondary cases of infection generated by each person infected with COVID-19. Lower total daily case counts may result in less stable reproduction number estimates for each mutation profile.

Data Source: CCM

Background

- Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) mutations occur regularly and the accumulation of these mutations can result in a new lineage of the virus. These new lineages will differ slightly in genome sequence and are termed variants. Variants of concern (VOC) are variants that have clinical or public health significance that affect the spread, severity of disease, vaccine effectiveness or diagnostic testing.

- Four SARS-CoV-2 VOCs that cause COVID-19 identified globally and in Ontario include: B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta). Evidence shows that these VOCs are more transmissible and/or may cause more severe illness than the previously circulating strains, in addition to reduced antibody neutralization. The B.1.1.7 variant (Alpha) harbours the N501Y mutation which is thought to provide a substantial transmission advantage over variants without this mutation. The P.1 (Gamma) and B.1.351 (Beta) variants have the E484K mutation, which is of particular concern due to a moderate association with reduced vaccine efficacy and increased probability of re-infection. The B.1.617.2 variant (Delta), does not have either N501Y or E484K mutation but early evidence suggests potential reduced antibody neutralization and increased severity.

- Surveillance of the relative growth rates of variants with notable mutations of interest is necessary to ensure the continued suppression of COVID-19 in Ontario.

- In this report, SARS-CoV-2 variants are examined based on their mutation profile instead of their lineage classification due to more timely mutation data availability compared to Whole Genome Sequencing (WGS) results required to determine the variant’s lineage.

Methods

- COVID-19 cases were categorized into four fully specified mutation profiles: (1) cases with the N501Y mutation (N501Y+ & E484K-), (2) cases with the E484K mutation (N501Y- & E484K+), (3) cases with both the N501Y and the E484K mutation (N501Y+ & E484K+), and (4) cases with neither mutation based on laboratory screening and testing (N501Y- & E484K-). COVID-19 cases with reported lineage information from WGS that matched a specific mutation profile were also included in these groups (B.1.1.7 [Alpha] to N501Y+ & E484K-; P.1 [Gamma] or B.1.351 [Beta] to N501Y+ & E484K+; B.1.617 lineages, including sublineage B.1.617.2 [Delta], to N501Y- & E484K-).

- The percentages of each fully specified mutation profile were calculated by taking the number of cases in each mutation profile divided by all cases with fully specified mutation profiles for a
given public reporting date. These percentages were then multiplied by percentage of cases that screened positive for a mutation common to VOCs and the total number of confirmed COVID-19 cases for a given public reporting date to extrapolate the number of cases in each mutation profile.

- Generalized additive models were used to estimate daily counts for each mutation profile including time periods identified to have surveillance biases due to changes in laboratory testing and reporting lags (prior to April 1, 2021 and in the most recent 7 days). Estimates were modeled from March 1, 2021 to March 31, 2021 when less than 50% of samples sent for VOC testing were being tested by the multiplex real-time PCR assay and for the most recent 7 days due to reporting lags of mutation and variant information in CCM. The model accounted for temporal autocorrelation with an auto regressive term of order 1 and moving average term of order 1.

- The effective reproduction number (Re) was estimated for each mutation profile by estimating the daily growth rates from the model, and then scaling to the serial interval of 4.5 days.\textsuperscript{12,13}

- The percentage of N501Y- and E484K- in Table 2 is calculated by the number of cases reported to have the N501Y- and E484K- mutation profile divided by the number of cases screened for mutations common to VOCs for a given public reporting date, then aggregated to the 7 day period. The percentage of N501Y- and E484K- is impacted by reporting lags and should be interpreted within the context of total case numbers and percentage screened for mutations common to VOCs.
Results

Figure 1: Estimated daily COVID-19 cases, total and mutation profiles by public reporting date in Ontario, March 1, 2021 to August 24, 2021

Note: Public reporting date is the date the public health unit reported the case to Public Health Ontario plus one day to account for the delay in public reporting. This is not the date on which a variant or mutation was identified. Data in the time period between the vertical dashed red lines (April 1, 2021 to August 17, 2021) were used to estimate daily cases before April 1, 2021 and in the most recent 7 days to account for surveillance biases and reporting lags.
N501Y+ and E484K- (red) mutation detected are likely to be lineage B.1.1.7 (Alpha).
N501Y+ and E484K+ (blue) mutation detected are likely to be lineage P.1 (Gamma) or B.1.351 (Beta).
N501Y- and E484K+ (green) does not correspond to a variant of concern currently identified in Ontario.
N501Y- and E484K- (purple) are cases with neither mutation detected and includes sublineage B.1.617.2 (Delta).

Data Source: CCM
Figure 2: Estimated daily COVID-19 cases for each mutation profile by public reporting date in Ontario, March 1, 2021 to August 24, 2021

**Note:** The daily cases scale (y-axis) differ among the different panels of this figure.
Public reporting date is the date the public health unit reported the case to Public Health Ontario plus one day to account for the delay in public reporting. This is not the date on which a variant or mutation was identified.
Data in the time period between the vertical dashed red lines (April 1, 2021 to August 17, 2021) were used to estimate daily cases before April 1, 2021 and in the most recent 7 days to account for surveillance biases and reporting lags.
N501Y+ and E484K- (red) mutation detected are likely to be lineage B.1.1.7 (Alpha).
N501Y+ and E484K+ (blue) mutation detected are likely to be lineage P.1 (Gamma) or B.1.351 (Beta).
N501Y- and E484K+ (green) does not correspond to a variant of concern currently identified in Ontario.
N501Y- and E484K- (purple) are cases with neither mutation detected and includes sublineage B.1.617.2 (Delta).
**Data Source:** CCM
Figure 3: Effective reproduction number estimates of COVID-19 mutation profiles by public reporting date in Ontario, March 1, 2021 to August 24, 2021

Note: Public reporting date is the date the public health unit reported the case to Public Health Ontario plus one day to account for the delay in public reporting. This is not the date on which a variant or mutation was identified. Data in the time period between the vertical dashed red lines (April 1, 2021 to August 17, 2021) were used to estimate daily cases before April 1, 2021 and in the most recent 7 days to account for surveillance biases and reporting lags.

N501Y+ and E484K- (red) mutation detected are likely to be lineage B.1.1.7 (Alpha).
N501Y+ and E484K+ (blue) mutation detected are likely to be lineage P.1 (Gamma) or B.1.351 (Beta).
N501Y- and E484K+ (green) does not correspond to a variant of concern currently identified in Ontario.
N501Y- and E484K- (purple) are cases with neither mutation detected and includes sublineage B.1.617.2 (Delta).

Data Source: CCM

The reproduction number is the average number of secondary cases of infection generated by each person infected with COVID-19. A reproduction number greater than one means that the overall number of new cases is growing, while a reproduction number less than one means the overall number of new cases is decreasing and suggests that COVID-19 is coming under control. Lower total daily case counts may result in less stable reproduction number estimates for each mutation profile.
Figure 4: Percentage of COVID-19 cases by mutation profile and public reporting date in Ontario, March 1, 2021 to August 24, 2021

Note: The percentage scale (y-axis) differ among the different panels of this figure.
Public reporting date is the date the public health unit reported the case to Public Health Ontario plus one day to account for the delay in public reporting. This is not the date on which a variant or mutation was identified.
Data in the time period between the vertical dashed red lines (April 1, 2021 to August 17, 2021) were used to estimate daily cases before April 1, 2021 and in the most recent 7 days to account for surveillance biases and reporting lags.
N501Y+ and E484K- (red) mutation detected are likely to be lineage B.1.1.7 (Alpha).
N501Y+ and E484K+ (blue) mutation detected are likely to be lineage P.1 (Gamma) or B.1.351 (Beta).
N501Y- and E484K+ (green) does not correspond to a variant of concern currently identified in Ontario.
N501Y- and E484K- (purple) are cases with neither mutation detected and includes sublineage B.1.617.2 (Delta).
Data Source: CCM
Figure 5: Percentage of COVID-19 cases that are N501Y- and E484K-, Ontario and selected PHUs, April 1, 2021 to August 24, 2021

Note: Public reporting date is the date the public health unit reported the case to Public Health Ontario plus one day to account for the delay in public reporting. This is not the date on which a variant or mutation was identified. Data in the time period between the vertical dashed red lines (April 1, 2021 to August 17, 2021) were used to estimate daily cases in the most recent 7 days to account for surveillance biases and reporting lags. N501Y- and E484K- are cases with neither mutation detected and includes sublineage B.1.617.2 (Delta). Percentages presented by public health unit (PHU) are based on the diagnosing health unit.

Data Source: CCM
Table 2: Number and percentage of N501Y- and E484K- cases by public health unit, August 11, 2021 to August 24, 2021

<table>
<thead>
<tr>
<th>Public Health Unit</th>
<th>Number N501Y negative/E484K negative (August 11 to August 17)</th>
<th>Percentage N501Y negative/E484K negative (August 11 to August 17)</th>
<th>Number N501Y negative/E484K negative (August 18 to August 24)</th>
<th>Percentage N501Y negative/E484K negative (August 18 to August 24)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Algoma Public Health</td>
<td>1</td>
<td>100</td>
<td>4</td>
<td>100</td>
</tr>
<tr>
<td>Brant County Health Unit</td>
<td>29</td>
<td>100</td>
<td>29</td>
<td>100</td>
</tr>
<tr>
<td>Chatham-Kent Public Health</td>
<td>25</td>
<td>96.2</td>
<td>26</td>
<td>100</td>
</tr>
<tr>
<td>City of Hamilton Public Health Services</td>
<td>244</td>
<td>98</td>
<td>304</td>
<td>99.3</td>
</tr>
<tr>
<td>Durham Region Health Department</td>
<td>103</td>
<td>97.2</td>
<td>77</td>
<td>96.2</td>
</tr>
<tr>
<td>Eastern Ontario Health Unit</td>
<td>1</td>
<td>9.1</td>
<td>4</td>
<td>100</td>
</tr>
<tr>
<td>Grey Bruce Health Unit</td>
<td>16</td>
<td>94.1</td>
<td>16</td>
<td>100</td>
</tr>
<tr>
<td>Haldimand-Norfolk Health Unit</td>
<td>8</td>
<td>88.9</td>
<td>20</td>
<td>100</td>
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<tr>
<td>Haliburton, Kawartha, Pine Ridge District Health Unit</td>
<td>9</td>
<td>100</td>
<td>18</td>
<td>100</td>
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<tr>
<td>Halton Region Public Health</td>
<td>87</td>
<td>91.6</td>
<td>82</td>
<td>98.8</td>
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<td>Hastings Prince Edward Public Health</td>
<td>7</td>
<td>100</td>
<td>14</td>
<td>100</td>
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<tr>
<td>Huron Perth Public Health</td>
<td>19</td>
<td>100</td>
<td>18</td>
<td>94.7</td>
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<tr>
<td>Kingston, Frontenac and Lennox &amp; Addington Public Health</td>
<td>3</td>
<td>75</td>
<td>11</td>
<td>100</td>
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<tr>
<td>Lambton Public Health</td>
<td>9</td>
<td>100</td>
<td>14</td>
<td>100</td>
</tr>
<tr>
<td>Leeds, Grenville &amp; Lanark District Health Unit</td>
<td>12</td>
<td>80</td>
<td>4</td>
<td>100</td>
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<tr>
<td>Middlesex-London Health Unit</td>
<td>88</td>
<td>97.8</td>
<td>168</td>
<td>96</td>
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<tr>
<td>Niagara Region Public Health</td>
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<td>87.5</td>
<td>19</td>
<td>100</td>
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<tr>
<td>North Bay Parry Sound District Health Unit</td>
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<td>Northwestern Health Unit</td>
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<td>1</td>
<td>100</td>
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<tr>
<td>Ottawa Public Health</td>
<td>85</td>
<td>95.5</td>
<td>7</td>
<td>87.5</td>
</tr>
<tr>
<td>Public Health Unit</td>
<td>Number N501Y negative/E484K negative (August 11 to August 17)</td>
<td>Percentage N501Y negative/E484K negative (August 11 to August 17)</td>
<td>Number N501Y negative/E484K negative (August 18 to August 24)</td>
<td>Percentage N501Y negative/E484K negative (August 18 to August 24)</td>
</tr>
<tr>
<td>-------------------------------------------</td>
<td>---------------------------------------------------------------</td>
<td>-----------------------------------------------------------------</td>
<td>---------------------------------------------------------------</td>
<td>-----------------------------------------------------------------</td>
</tr>
<tr>
<td>Peel Public Health</td>
<td>310</td>
<td>94.5</td>
<td>340</td>
<td>97.7</td>
</tr>
<tr>
<td>Peterborough Public Health</td>
<td>4</td>
<td>100</td>
<td>14</td>
<td>100</td>
</tr>
<tr>
<td>Porcupine Health Unit</td>
<td>1</td>
<td>100</td>
<td>4</td>
<td>100</td>
</tr>
<tr>
<td>Public Health Sudbury &amp; Districts</td>
<td>17</td>
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<td>21</td>
<td>100</td>
</tr>
<tr>
<td>Renfrew County and District Health Unit</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
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<tr>
<td>Simcoe Muskoka District Health Unit</td>
<td>89</td>
<td>97.8</td>
<td>49</td>
<td>96.1</td>
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<tr>
<td>Southwestern Public Health</td>
<td>22</td>
<td>81.5</td>
<td>20</td>
<td>100</td>
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<tr>
<td>Thunder Bay District Health Unit</td>
<td>1</td>
<td>100</td>
<td>3</td>
<td>100</td>
</tr>
<tr>
<td>Timiskaming Health Unit</td>
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<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Toronto Public Health</td>
<td>595</td>
<td>91.8</td>
<td>257</td>
<td>87.4</td>
</tr>
<tr>
<td>Waterloo Public Health and Emergency Services</td>
<td>97</td>
<td>96</td>
<td>75</td>
<td>97.4</td>
</tr>
<tr>
<td>Wellington-Dufferin-Guelph Public Health</td>
<td>17</td>
<td>73.9</td>
<td>25</td>
<td>89.3</td>
</tr>
<tr>
<td>Windsor-Essex County Health Unit</td>
<td>210</td>
<td>99.5</td>
<td>192</td>
<td>96.5</td>
</tr>
<tr>
<td>York Region Public Health</td>
<td>278</td>
<td>95.2</td>
<td>245</td>
<td>96.8</td>
</tr>
</tbody>
</table>

**Note:** Public reporting date is the date the public health unit reported the case to Public Health Ontario plus one day to account for the delay in public reporting. This is not the date on which a variant or mutation was identified. Cases and percentages presented by public health unit (PHU) are based on the diagnosing health unit. The percentage of N501Y- and E484K- (includes sublineage B.1.617.2 [Delta]) is subject to reporting delays that may vary by geography and should be interpreted within the context of total case numbers and percentage screened for mutations common to VOCs.

**Data Source:** CCM
Data Notes and Limitations

- 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 August 23, 2021 at 1 p.m.

- VOC Data for this report were based on information successfully extracted from CCM for all PHUs by PHO as of August 23, 2021 at 1 p.m for cases reported from April 1, 2021 onwards and as of August 20, 2021 at 9 a.m. for cases reported up to March 31, 2021.

- CCM is a dynamic 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.

- The 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.

- The date variable used in the figures for the epidemic curves and the reproduction numbers throughout this report refers to the date that a case first appeared in the compiled data set + 1 additional day. This corresponds to the “public reporting date” of each case at the provincial level.

  - In order to account for certain instances when there were long lags between when a case’s specimen was collected and when their data was entered into CCM, we replaced the public reporting date with the specimen collection date + 3 days (the mode of the distribution from specimen collection to public reporting date). This replacement was made for cases whose delay between specimen collection and case creation was between 7 and 90 days.

  - In rare circumstances when this delay was more than 90 days, we did not make the date replacement.

- Orientation of case counts by geography is based on the diagnosing health unit (DHU). DHU refers to the case’s public health unit of residence at the time of illness onset and not necessarily the location of exposure.

- The 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 VOCs (i.e., N501Y—common to B.1.1.7 (Alpha), B.1.351 (Beta), and P.1 (Gamma); or E484K—common to B.1.351 (Beta) and P.1 (Gamma) only). If positive for the mutations common to VOCs with a Ct value of ≤30, these samples may then undergo genomic analyses to identify the VOC lineage.

- Estimates of the effective reproduction numbers for each mutation profile may be less stable when the total number of reported cases is low. Estimates of daily cases, percentages, and
effective reproduction numbers may also be impacted due to changes in the proportion of samples that are screened for mutations common to VOCs.

- The variant testing algorithm has changed over time in Ontario. Since February 3, 2021 all PCR positive SARS-CoV-2 specimens with Ct values ≤ 35 are tested for a N501Y mutation. Starting March 22, 2021, these specimens are tested for the E484K mutation as well. As of May 26, 2021, cases where a E484K mutation is detected will no longer be reflexed for sequencing as VOC testing labs switched to a representative sampling method where only a proportion of all positives with a Ct ≤ 30 are forwarded for further genomic analysis.

- Public Health Ontario conducts testing and genomic analyses for SARS-CoV-2 positive specimens using the criteria outlined here:
References


Citation


Disclaimer

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