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ENHANCED EPIDEMIOLOGICAL SUMMARY

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

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As of November 12, 2021, routine Variants of Concern (VOC) PCR testing of positive COVID-19 samples is no longer being conducted. All eligible positive COVID-19 samples will now be forwarded for whole genome sequencing. As of Nov. 5, 2021, the Ontario COVID-19 Genomic Network shifted to a strategy that genomic sequences all eligible positive COVID samples. This shift to a genomic sequencing strategy will allow us to identify and monitor VOCs, Variants of Interest (VOI) and other variants in a proactive and systematic way. Starting on November 17, 2021, this report will be discontinued.

Comprehensive Ontario data on variants will be found in PHO's Whole Genome Sequencing enhanced epidemiological summary. Historical data on VOCs and mutations in daily and weekly epidemiological summaries can be found on the provincial COVID-19 data webpage.

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 **November 15, 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 (99.3%) 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 0.2% of cases, while 0.2% 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] or B.1.621 [Mu]).

- 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 November 9, 2021 to November 15, 2021

Mutation Profile	Total Cases	Percentage of Cases	Reproduction Number
N501Y+ & E484K-	7	0.2%	0.85
N501Y+ & E484K+	7	0.2%	0.79
N501Y- & E484K+	14	0.3%	0.94
N501Y- & E484K-	4,139	99.3%	1.17

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.1.621 (Mu) (N501Y+ & E484K+) was first detected in Columbia. 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.[1] 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.[2] Variants of interest (VOI) are variants that may share one or more mutations common in a VOC that have clinical or public health significance but do not have sufficient evidence at this time to be categorized a VOC.

- 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.[3,4] 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.[5,6] The P.1 (Gamma) and B.1.351 (Beta) VOCs, and B.1.621 (Mu) VOI have the E484K mutation, which is of particular concern due a moderate association with reduced vaccine efficacy and increased probability of re-infection.[7,8,9] 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.[10,11]

- 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.[12]
- 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.

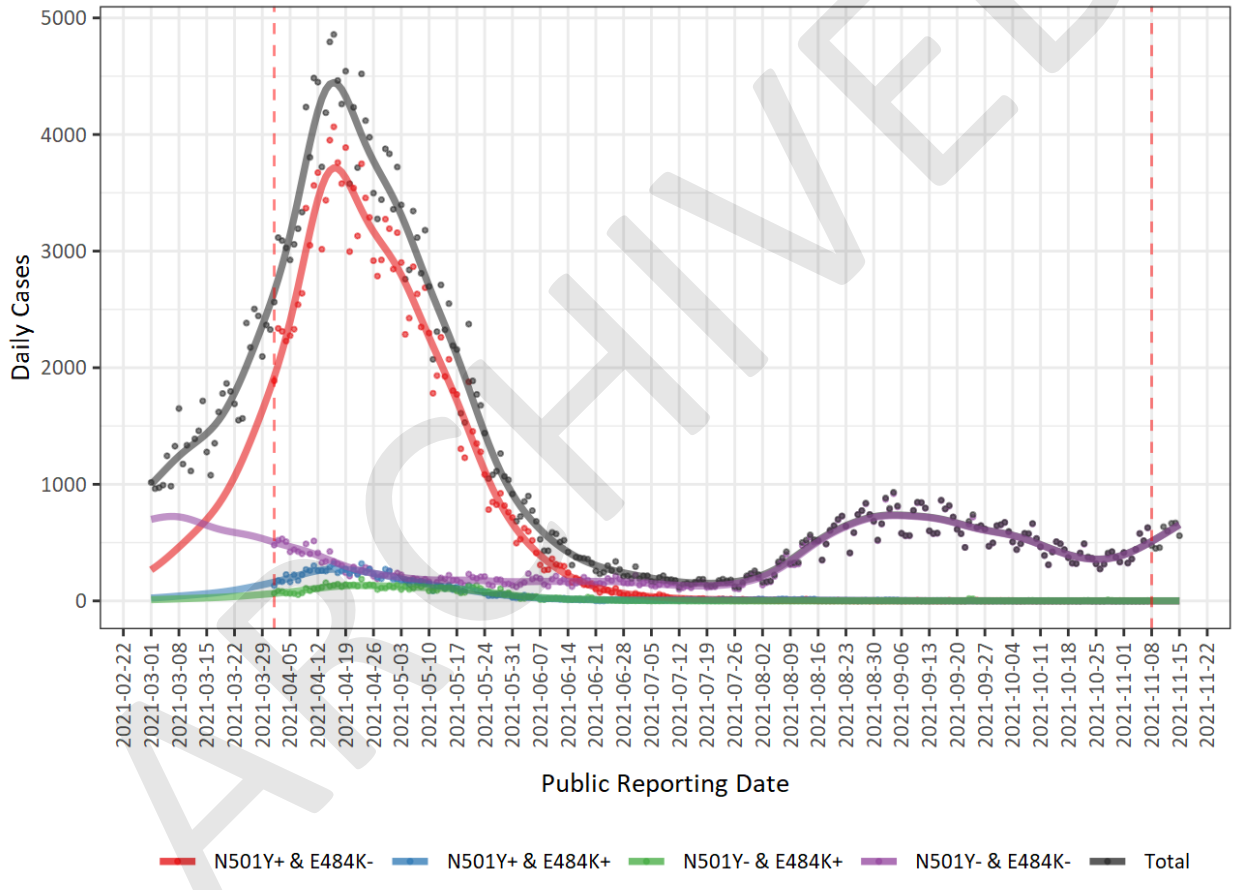
Methods

- 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], B.1.351 [Beta] or B.1.621 [Mu] 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.[13,14]

- 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

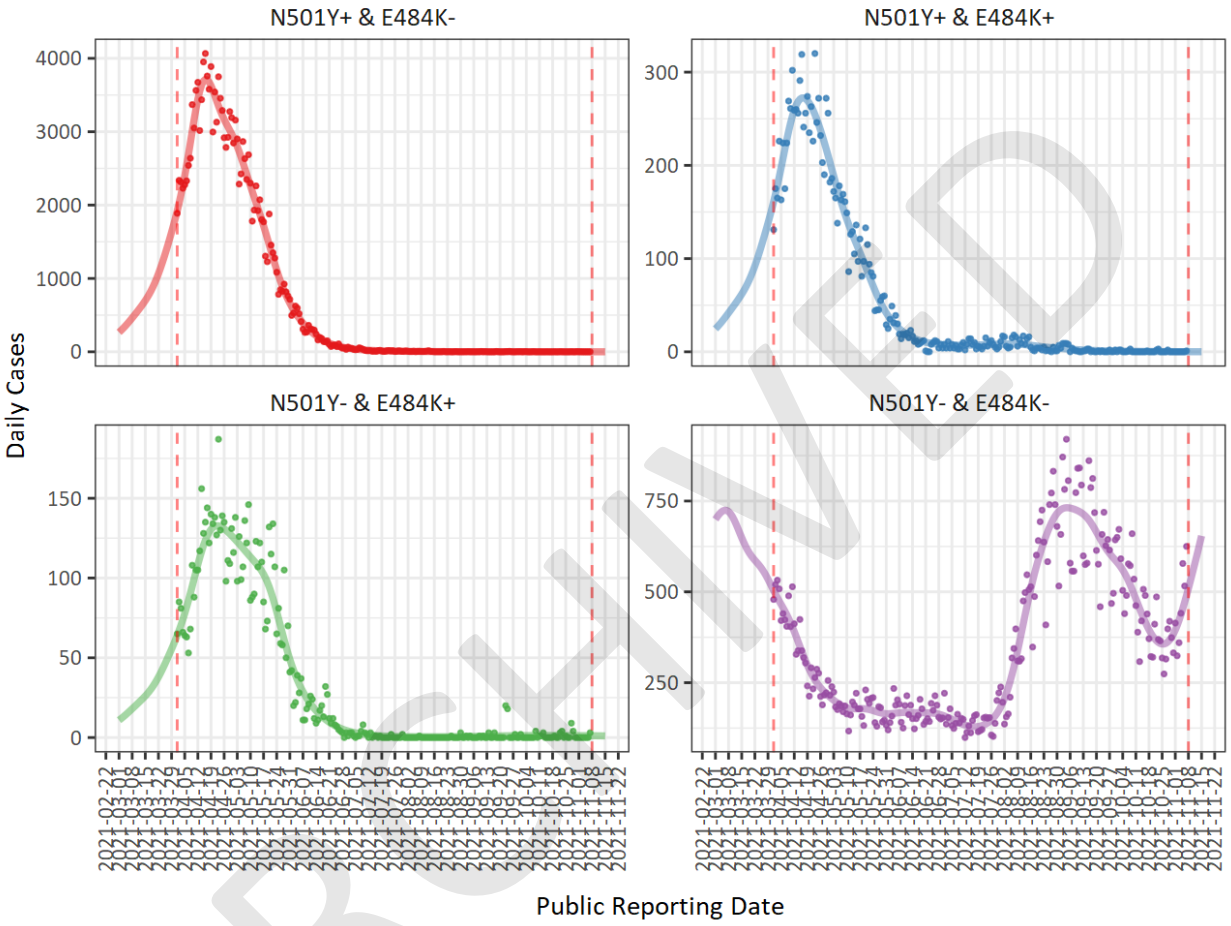
Figure 1: Estimated daily COVID-19 cases, total and mutation profiles by public reporting date in Ontario, March 1, 2021 to November 15, 2021



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 November 8, 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), B.1.351 (Beta) or B.1.621 (Mu).
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 November 15, 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.
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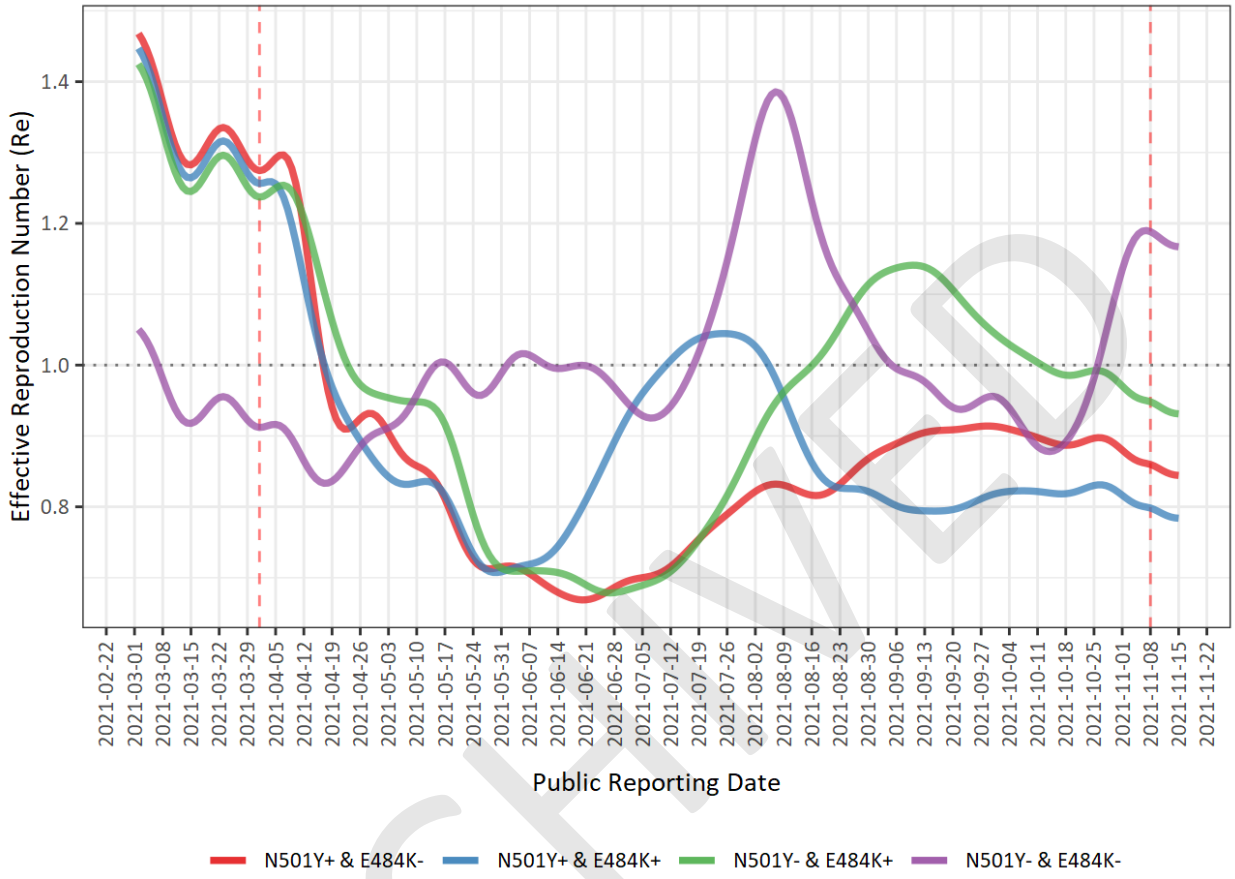
N501Y- and E484K+ (green) does not correspond to a variant of concern currently identified in Ontario.
N501Y- and E484K- (purple) are cases with neither mutation detected and includes sublineage B.1.617.2 (Delta).
Data Source: CCM

Figure 3: Effective reproduction number estimates of COVID-19 mutation profiles by public reporting date in Ontario, March 1, 2021 to November 15, 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 November 8, 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.
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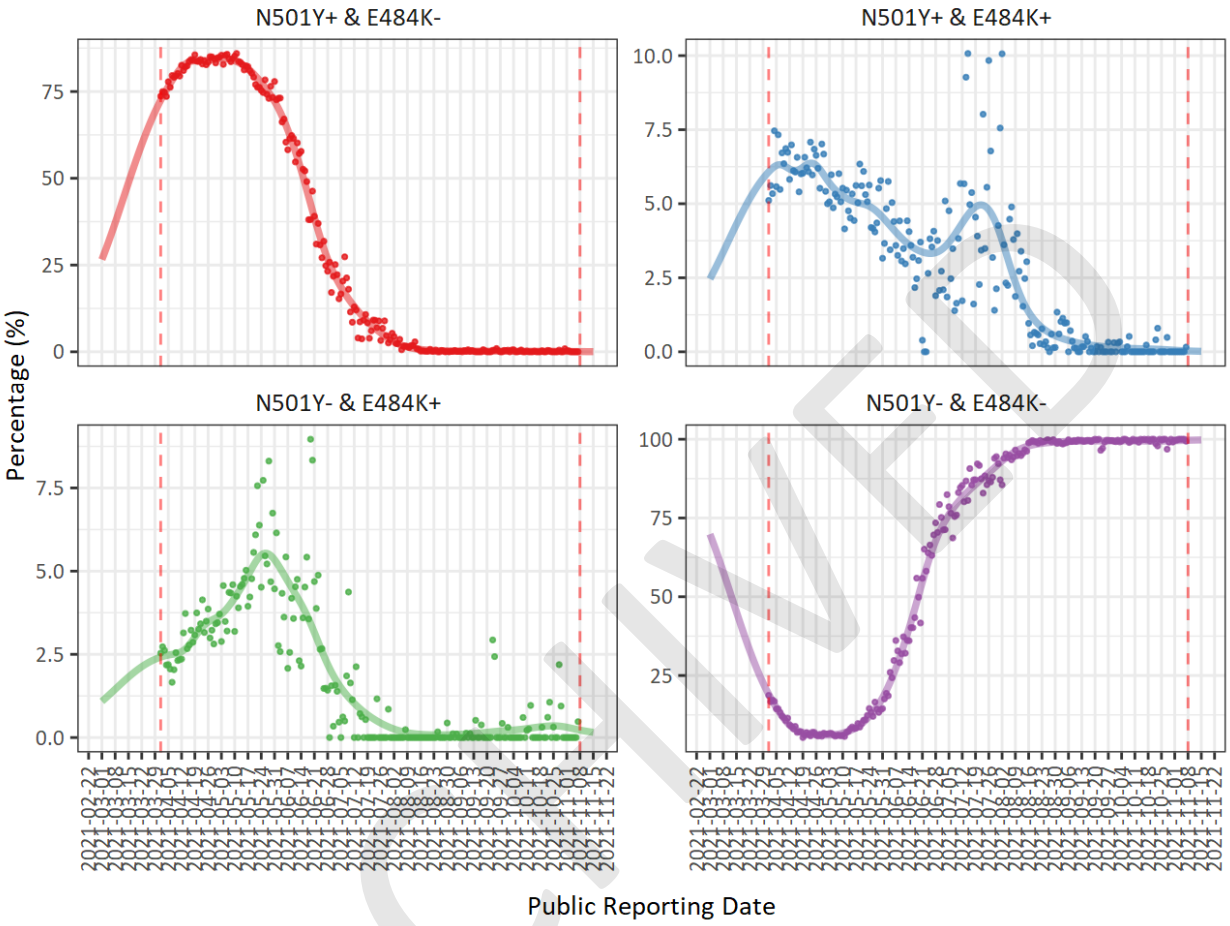
N501Y- and E484K+ (green) does not correspond to a variant of concern currently identified in Ontario.
N501Y- and E484K- (purple) are cases with neither mutation detected and includes sublineage B.1.617.2 (Delta).
Data Source: CCM

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 November 15, 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 November 8, 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.
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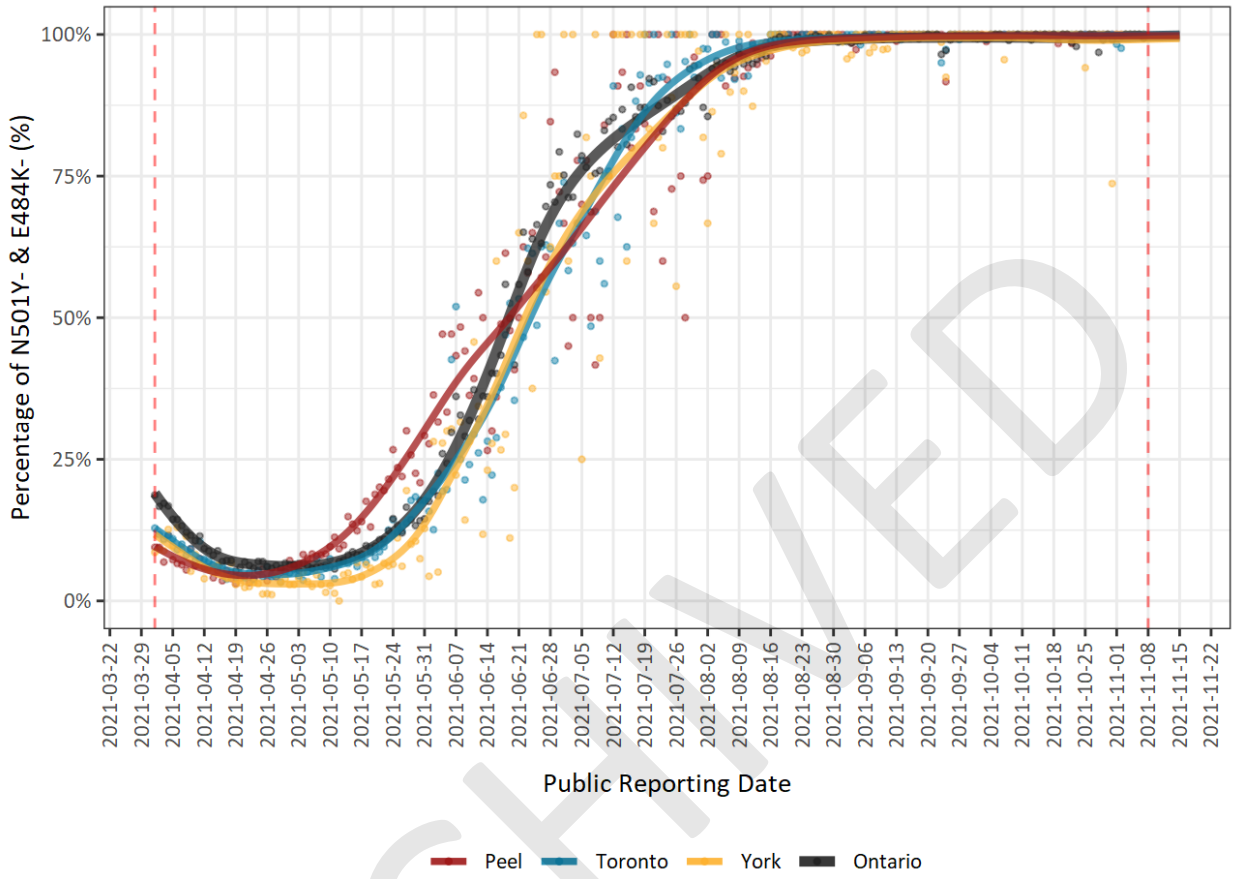
N501Y+ and E484K+ (blue) mutation detected are likely to be lineage P.1 (Gamma), B.1.351 (Beta) or B.1.621 (Mu).
N501Y- and E484K+ (green) does not correspond to a variant of concern currently identified in Ontario.
N501Y- and E484K- (purple) are cases with neither mutation detected and includes sublineage 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 November 15, 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 November 8, 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, November 2, 2021 to November 15, 2021

Public Health Unit	Number N501Y negative/E484K negative (November 2 to November 8)	Percentage N501Y negative/E484K negative (November 2 to November 8)	Number N501Y negative/E484K negative (November 9 to November 15)	Percentage N501Y negative/E484K negative (November 9 to November 15)
Algoma Public Health	16	100	1	100
Brant County Health Unit	29	100	47	100
Chatham-Kent Public Health	34	100	17	100
City of Hamilton Public Health Services	70	100	46	100
Durham Region Health Department	57	100	59	100
Eastern Ontario Health Unit	6	100	1	100
Grey Bruce Health Unit	29	100	7	100
Haldimand-Norfolk Health Unit	52	98.1	47	100
Haliburton, Kawartha, Pine Ridge District Health Unit	8	100	1	100
Halton Region Public Health	79	100	49	100
Hastings Prince Edward Public Health	9	100	1	100
Huron Perth Public Health	46	100	31	100
Kingston, Frontenac and Lennox & Addington Public Health	82	100	57	100
Lambton Public Health	55	100	15	100
Leeds, Grenville & Lanark District Health Unit	9	100	14	100
Middlesex-London Health Unit	50	100	33	100
Niagara Region Public Health	40	100	25	100
North Bay Parry Sound District Health Unit	9	100	5	100
Northwestern Health Unit	3	100	2	100
Ottawa Public Health	110	100	25	100

Public Health Unit	Number N501Y negative/E484K negative (November 2 to November 8)	Percentage N501Y negative/E484K negative (November 2 to November 8)	Number N501Y negative/E484K negative (November 9 to November 15)	Percentage N501Y negative/E484K negative (November 9 to November 15)
Peel Public Health	165	100	104	100
Peterborough Public Health	14	100	11	91.7
Porcupine Health Unit	8	100	15	93.8
Public Health Sudbury & Districts	151	100	128	100
Renfrew County and District Health Unit	4	100	0	0
Simcoe Muskoka District Health Unit	202	100	100	100
Southwestern Public Health	109	98.2	86	95.6
Thunder Bay District Health Unit	19	100	3	100
Timiskaming Health Unit	6	100	0	0
Toronto Public Health	317	99.7	127	100
Waterloo Public Health and Emergency Services	136	100	82	100
Wellington-Dufferin-Guelph Public Health	55	100	46	100
Windsor-Essex County Health Unit	131	100	116	97.5
York Region Public Health	197	100	84	100

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 **November 14, 2021 at 1 p.m**.

- VOC testing data for this report were based on information successfully extracted from CCM within the laboratory object for select Logical Observation Identifiers Names and Codes (LOINC) for cases reported between February 07, 2021 and August 17, 2021, for all PHUs by PHO as of September 29, 2021 at 1 p.m. VOC testing data for cases reported between February 07, 2021 and August 17, 2021 are supplemented with information from the Investigation lineage and Investigation mutation field. For cases reported as of August 18, 2021, VOC test value is assigned based on information solely from the Investigation lineage and Investigation mutation fields for all PHUs.

- 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), P.1 (Gamma), and B.1.621 [Mu]; or E484K—common to B.1.351 (Beta), P.1 (Gamma), and B.1.621 [Mu] 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: https://www.publichealthontario.ca/en/laboratory-services/test-information-index/covid-19-voc

References

1. Ontario Agency for Health Protection and Promotion (Public Health Ontario). Epidemiological summary: SARS-CoV-2 whole genome sequencing in Ontario, June 9, 2021 [Internet]. Toronto, ON: Queen's Printer for Ontario; 2021 [cited 2021 Jun 18]. Available from: https://www.publichealthontario.ca/-/media/documents/ncov/epi/covid-19-sars-cov2-whole-genome-sequencing-epi-summary.pdf?la=en

2. Ontario Agency for Health Protection and Promotion (Public Health Ontario). COVID-19 variants of concern (VOCs) [Internet]. Toronto, ON: Queen's Printer for Ontario; 2021 [cited 2021 Jun 18]. Available from: https://www.publichealthontario.ca/en/diseases-and-conditions/infectious-diseases/respiratory-diseases/novel-coronavirus/variants

3. Ontario Agency for Health Protection and Promotion (Public Health Ontario). Companion guide to variants of concern (VOCs) [Internet]. Toronto, ON: Queen's Printer for Ontario; 2021 [cited 2021 Jun 14]. Available from: https://www.publichealthontario.ca/-/media/documents/ncov/voc/2021/04/covid-19-companion-guide-variants.pdf?la=en

4. Public Health England. SARS-COV-2 variants of concern and variants under investigation in England: technical briefing 14 [Internet]. London: Crown Copyright; 2021 [cited 2021 Jun 10]. Available from: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/991343/Variants_of_Concern_VOC_Technical_Briefing_14.pdf

5. Davies NG, Abbott S, Barnard RC, Jarvis CI, Kucharski AJ, Munday JD, et al. Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. Science. 2021;372(6538):eabg3055. Available from: https://doi.org/10.1126/science.abg3055

6. Brown KA, Gubbay J, Hopkins J, Patel S, Buchan SA, Daneman N, et al. S-gene target failure as a marker of variant B.1.1.7 among SARS-CoV-2 isolates in the Greater Toronto Area, December 2020 to March 2021. JAMA. 2021;325(20):2115-6. Available from: https://doi.org/10.1001/jama.2021.5607

7. Sabino EC, Buss LF, Carvalho MPS, Prete CA, Crispim MAE, Fraiji NA, et al. Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. Lancet. 2021;397(10273):452-5. Available from: https://doi.org/10.1016/S0140-6736(21)00183-5

8. Jangra S, Ye C, Rathnasinghe R, Stadlbauer D, Krammer F, Simon V, et al. The E484K mutation in the SARS-CoV-2 spike protein reduces but does not abolish neutralizing activity of human convalescent and post-vaccination sera. medRxiv 21250543 [Preprint]. 2021 Jan 29 [cited 2021 Jun 14]. Available from: https://doi.org/10.1101/2021.01.26.21250543

9. Laiton-Donato K, Franco-Muñoz C, Álvarez-Díaz DA, Ruiz-Moreno HA, Usme-Ciro JA, Prada DA, et al. Characterization of the emerging B.1.621 variant of interest of SARS-CoV-2. Infect Genet Evol. 2021;105038. Available from: https://doi.org/10.1016/j.meegid.2021.105038

10. Wall EC, Wu M, Harvey R, Kelly G, Warchal S, Sawyer C, et al. Neutralising antibody activity against SARS-CoV-2 VOCs B.1.617.2 and B.1.351 by BNT162b2 vaccination. Lancet. 2021;397(10292):2331-3. Available from: https://doi.org/10.1016/S0140-6736(21)01290-3

11. Sheikh A, McMenamin J, Taylor B, Robertson C. SARS-CoV-2 Delta VOC in Scotland: demographics, risk of hospital admission, and vaccine effectiveness. Lancet. 2021;S0140-6736(21)01358-1 Available from: https://doi.org/10.1016/S0140-6736(21)01358-1

12. Sah P, Vilches TN, Shoukat A, Pandey A, Fitzpatrick MC, Moghadas SM, et al. Quantifying the potential for dominant spread of SARS-CoV-2 variant B.1.351 in the United States. medRxiv 21256996 [Preprint]. 2021 May 12 [cited 2021 Jun 14]. Available from: https://doi.org/10.1101/2021.05.10.21256996

13. Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (COVID-19) infections. Int J Infect Dis. 2020;93:284-6. Available from: https://doi.org/10.1016/j.ijid.2020.02.060

14. Du Z, Xu X, Wu Y, Wang L, Cowling BJ, Ancel Meyers L. Serial interval of COVID-19 among publicly reported confirmed cases. Emerg Infect Dis. 2020;26(6):1341-3. Available from: https://doi.org/10.3201/eid2606.200357

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