Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, January 13, 2025

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by the Ontario COVID-19 Genomics Network as of January 8, 2025.

Background

The continued monitoring of global SARS-CoV-2 genomic data has identified changes in the virus' genome as it spreads through populations. These random changes or mutations arise as a virus evolves over time. The accumulation of these mutations can result in a new lineage of the virus, which is a common occurrence. These new lineages will differ slightly in genome sequence and are termed variants. Although many variants will have no difference in the ability to spread or cause disease, some variants have mutations which may enhance virulence, transmissibility, and/or allow the virus to escape natural or vaccine-induced immunity.

The identification of variants and mutations occurs through whole genome sequencing (WGS) of select samples. Through global surveillance of SARS-CoV-2 genomes, a number of variants have been identified with evidence of clinical and/or public health significance, termed variants of concern (VOC). Variants designated as VOCs include B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta), and B.1.1.529 (Omicron), some of which have been de-escalated due to their diminishing prevalence globally.[1-3]

As SARS-CoV-2 continues to evolve, lineages will naturally divide into descendant sublineages - a genetically closely related group derived from a common ancestor. The descendant branches are given new lineage aliases, such as for B.1.1.529 (Omicron) lineages (e.g., BA.2 [alias for B.1.1.529.2] and JN.1 [alias for B.1.1.529.2.86.1.1]). When a host is infected with two or more descendant lineages, lineages can recombine to form a new recombinant lineage (e.g., KP.3.3 and KS.1.1 to form XEC). New designations represent refined genetic groups that can be tracked separately. As more research is conducted, there may be evidence of an important difference in terms of transmissibility, severity, or immune escape, at which time WHO may assign a new Greek letter classification to a lineage.

The Ontario COVID-19 Genomics Network (OCGN) performs WGS on all eligible positive SARS-CoV-2 samples (see Technical Notes for details). Sequences are processed using bioinformatics analyses and assigned a Pango lineage[4] using the pangolin tool[5], allowing for the identification of lineages.

Highlights

- In the most recent week (December 22 to December 28), a total of 784 cases were sequenced. XEC was the most prevalent lineage (31.5%), followed by KP.3.1.1 (17.5%), and MC.1 (10.5%).
- The proportion of XEC increased from 25.7% (December 15 to December 21) to 31.5% (December 22 to December 28).
    - Based on the Nowcast model, XEC is projected to decrease to 23.5% (95% CI: 19.7% - 27.8%) by January 15, 2025. The weekly relative growth rate of XEC is 1.12 (95% CI: 1.07 - 1.17) times that of KP.3.1.1.
- The proportion of KP.3.1.1 decreased from 22.2% (December 15 to December 21) to 17.5% (December 22 to December 28).
    - Based on the Nowcast model, KP.3.1.1 is projected to decrease to 9.7% (95% CI: 7.7% - 12.0%) by January 15, 2025.

> Lineage counts and designations may change between reports as components of the Pango lineage assignment models are updated (see Technical Notes for details).
>
> Due to technical and logistical issues, data from Kingston Health Sciences Centre are incomplete for weeks 50 to 52 (December 8 to December 28) and data from The Hospital for Sick Children is incomplete for week 52 (December 22 to December 28). As a result, counts, proportions, and Nowcast projections may change compared to previous and subsequent reports.

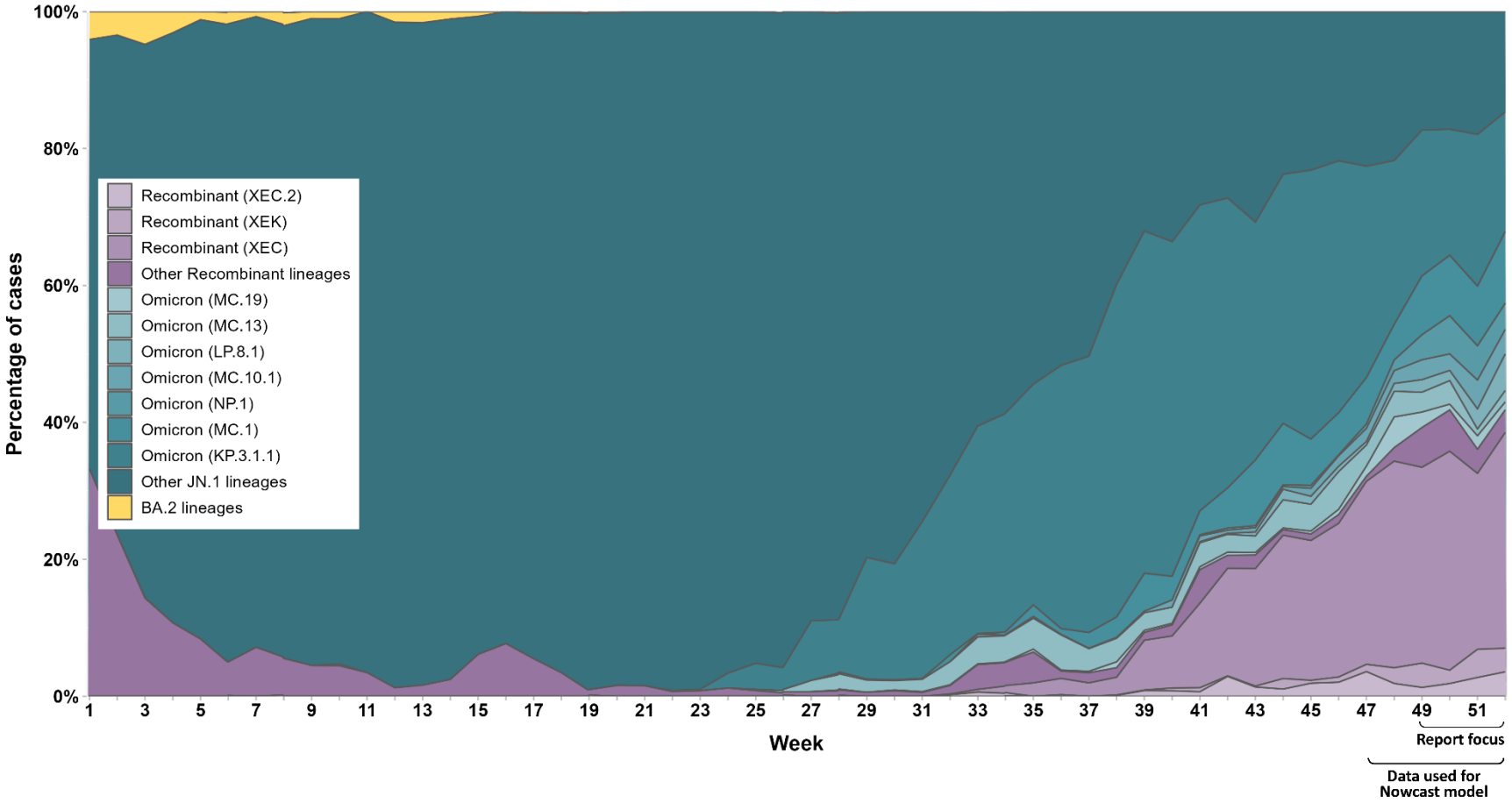
Representative Surveillance

Table 1: Number of SARS-CoV-2 positive specimens, number and percentage of specimens sequenced for representative surveillance by week, Ontario, December 1 to December 28, 2024

Week	Number of Positive Specimens	Number of Specimens Sequenced	Percentage of Specimens Sequenced
Week 49 (December 1 - December 7)	1,523	961	63.1%
Week 50 (December 8 - December 14)	1,682	1,104	65.6%
Week 51 (December 15 - December 21)	1,789	1,036	57.9%
Week 52 (December 22 - December 28)	1,865	803	43.1%
Total	**6,859**	**3,904**	**56.9%**

Note: The 3,904 specimens sequenced were associated with 3,810 unique cases; in the most recent week, 803 specimens sequenced were associated with 784 unique cases. Unique cases are the denominator for tables throughout the report. 'Number of positive specimens' is the number of tests positive for SARS-CoV-2 in Ontario. Date was assigned to best align with sample collection date, which may differ from other PHO products. 'Number of specimens sequenced' is the number of specimens sequenced for representative surveillance. 'Percentage sequenced' may be lower than the sampling proportion because not all specimens are eligible to be sequenced (i.e. excludes samples with cycle threshold >30 or insufficient volume). Results may not be representative of Ontario overall. For representative surveillance: details on the proportion of eligible samples sequenced by the OCGN can be found in the Technical Notes. Week was assigned based on earliest date available for a sample. Not all sequencing and bioinformatics analyses for the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data sources: Ontario Laboratories Information System (OLIS) from the Ontario Respiratory Virus Tool (ORVT), Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Figure 1: Percentage of SARS-CoV-2 cases by the most prevalent lineages and week, representative surveillance, Ontario, December 31, 2023 to December 28, 2024



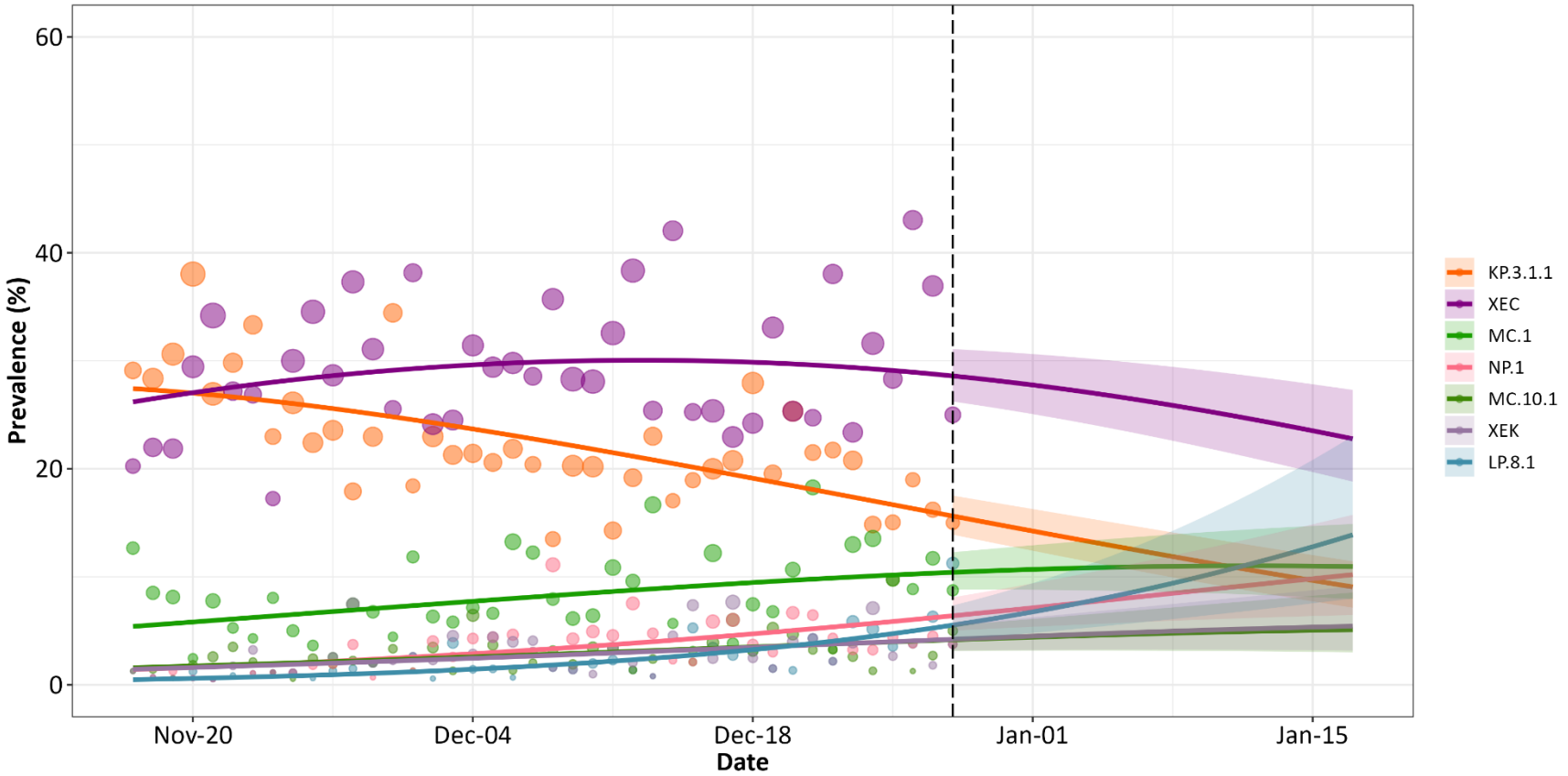
Note: Results may not be representative of Ontario overall. Details on the proportion of eligible samples sequenced by the OCGN can be found in the Technical Notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for a case, the most recent sample was included. Not all sequencing and bioinformatics analyses for the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 2: Number and percentage of SARS-CoV-2 cases by Pango lineage and week, representative surveillance, Ontario, December 1 to December 28, 2024

Pango Lineage	Week 49 (December 1 - December 7)	Week 50 (December 8 - December 14)	Week 51 (December 15 - December 21)	Week 52 (December 22 - December 28)	Total (December 1 - December 28)
XEC	266 (28.6%)	344 (32.0%)	262 (25.7%)	247 (31.5%)	1,119 (29.4%)
KP.3.1.1	198 (21.3%)	198 (18.4%)	226 (22.2%)	137 (17.5%)	759 (19.9%)
MC.1	80 (8.6%)	95 (8.8%)	89 (8.7%)	82 (10.5%)	346 (9.1%)
NP.1	34 (3.7%)	60 (5.6%)	51 (5.0%)	30 (3.8%)	175 (4.6%)
MC.10.1	27 (2.9%)	26 (2.4%)	43 (4.2%)	28 (3.6%)	124 (3.3%)
XEK	33 (3.5%)	21 (2.0%)	42 (4.1%)	27 (3.4%)	123 (3.2%)
LP.8.1	17 (1.8%)	16 (1.5%)	30 (2.9%)	42 (5.4%)	105 (2.8%)
XEC.2	12 (1.3%)	20 (1.9%)	28 (2.7%)	28 (3.6%)	88 (2.3%)
MC.13	27 (2.9%)	37 (3.4%)	10 (1.0%)	13 (1.7%)	87 (2.3%)
MC.19	21 (2.3%)	9 (0.8%)	20 (2.0%)	9 (1.1%)	59 (1.5%)
Other recombinant	54 (5.8%)	65 (6.0%)	36 (3.5%)	26 (3.3%)	181 (4.8%)
Other Omicron	161 (17.3%)	185 (17.2%)	183 (17.9%)	115 (14.7%)	644 (16.9%)
Total sequenced	**930 (100%)**	**1,076 (100%)**	**1,020 (100%)**	**784 (100%)**	**3,810 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the Technical Notes. Week was assigned based on the earliest date available for the sample. Not all sequencing and bioinformatics analyses for the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Figure 2: Estimated daily SARS-CoV-2 prevalence (%) by Pango lineage, using Nowcast model, Ontario, November 17, 2024 to January 18, 2025



Note: Each curve represents the estimated prevalence of a given lineage from Nowcast modelling, which uses six weeks of daily representative surveillance data in a multinomial logistic regression. Each set of dots represents the observed daily prevalence of a given lineage, while their size represents the relative number of samples. The vertical dashed line indicates the most recent day of data, after which projected Nowcast prevalence estimates are presented with their 95% confidence intervals. The vertical grey lines indicate the mid-point of the week. Lineages with at least 21 days of non-zero case counts were included in the model and lineages that did not have at least 21 days of non-zero case counts were included but not shown. Figure includes all lineages with at least one day of an estimated prevalence of 5% or greater during the 12 week period (six observed and six projected). Only three weeks of projected data are shown. Prevalence projections may be overestimated for emerging lineages.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 3: Estimated SARS-CoV-2 prevalence (%), projected prevalence (%), and weekly relative growth rate (with 95% confidence intervals) by Pango lineage, using Nowcast model, Ontario, November 17, 2024 to January 18, 2025

Pango Lineage	Week 51 (December 18): Estimated	Week 52 (December 25): Estimated	Week 1 (January 1): Projected	Week 2 (January 8): Projected	Week 2 (January 15): Projected	Weekly Relative Growth Rate
KP.3.1.1	19.1 (17.8 - 20.6)	16.7 (15.1 - 18.4)	14.2 (12.4 - 16.3)	11.9 (10.0 - 14.1)	9.7 (7.7 - 12.0)	1.00 (reference)
XEC	29.9 (28.3 - 31.5)	29.1 (27.0 - 31.3)	27.8 (25.1 - 30.6)	25.9 (22.6 - 29.4)	23.5 (19.7 - 27.8)	1.12 (1.07 - 1.17)
MC.1	9.5 (8.5 - 10.6)	10.2 (8.8 - 11.8)	10.7 (8.8 - 12.9)	11.0 (8.6 - 13.9)	11.0 (8.1 - 14.7)	1.23 (1.15 - 1.31)
NP.1	4.7 (4.0 - 5.5)	5.9 (4.7 - 7.2)	7.1 (5.4 - 9.4)	8.5 (5.9 - 12.0)	9.8 (6.4 - 14.9)	1.43 (1.29 - 1.57)
MC.10.1	3.5 (2.9 - 4.2)	4.0 (3.1 - 5.1)	4.4 (3.2 - 6.1)	4.8 (3.2 - 7.2)	5.0 (3.0 - 8.2)	1.30 (1.17 - 1.44)
XEK	3.5 (2.9 - 4.2)	4.0 (3.1 - 5.1)	4.5 (3.2 - 6.2)	5.0 (3.3 - 7.5)	5.3 (3.2 - 8.7)	1.32 (1.19 - 1.47)
LP.8.1	3.2 (2.7 - 3.9)	4.7 (3.7 - 6.1)	6.7 (4.8 - 9.4)	9.4 (6.1 - 14.3)	12.8 (7.5 - 20.8)	1.67 (1.47 - 1.90)
Other lineages	11.4 (10.3 - 12.6)	10.2 (8.9 - 11.7)	8.9 (7.5 - 10.7)	7.7 (6.1 - 9.5)	6.4 (4.8 - 8.4)	1.03 (0.97 - 1.08)

Note: The Nowcast model uses six weeks of daily representative surveillance data in a multinomial logistic regression that estimates and projects the prevalence of SARS-CoV-2 lineages. The weekly relative growth rate is a measure of a lineage's growth rate relative to the reference lineage and is estimated in the Nowcast model. The weekly relative growth rate and projections may be overestimated for emerging lineages. The prevalence estimates and projections presented are from the Wednesday (mid-point) of the specified week. Lineages with at least 21 days of non-zero case counts were included in the model separately. 'Other lineages' includes all other lineages combined that did not individually have at least 21 days of non-zero case counts. Lineages that had at least one day with a prevalence of 5% or greater in the 12 week period (six observed and six projected) were included in the table. Only two weeks of observed and three weeks of projected data are shown. Prevalence estimates are based on the model and are not expected to be the same as the observed data (e.g. Table 2). Details on the methodology used to calculate Nowcast prevalence estimates, projections, and the weekly relative growth rates can be found in the Technical Notes.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 4: Number and percentage of SARS-CoV-2 cases by Pango lineage and age group, representative surveillance, Ontario, December 1 to December 28, 2024

Pango Lineage	Ages: 0-4	Ages: 5-11	Ages: 12-19	Ages: 20-39	Ages: 40-59	Ages: 60-79	Ages: 80 and over	Total
XEC	51 (39.5%)	4 (30.8%)	9 (42.9%)	46 (26.0%)	101 (32.8%)	326 (29.2%)	580 (28.4%)	1,117 (29.3%)
KP.3.1.1	27 (20.9%)	1 (7.7%)	0 (0.0%)	38 (21.5%)	54 (17.5%)	238 (21.3%)	401 (19.6%)	759 (19.9%)
MC.1	6 (4.7%)	1 (7.7%)	3 (14.3%)	11 (6.2%)	25 (8.1%)	105 (9.4%)	195 (9.5%)	346 (9.1%)
NP.1	2 (1.6%)	2 (15.4%)	0 (0.0%)	10 (5.6%)	9 (2.9%)	45 (4.0%)	107 (5.2%)	175 (4.6%)
MC.10.1	4 (3.1%)	1 (7.7%)	1 (4.8%)	4 (2.3%)	10 (3.2%)	33 (3.0%)	71 (3.5%)	124 (3.3%)
XEK	3 (2.3%)	0 (0.0%)	1 (4.8%)	8 (4.5%)	15 (4.9%)	32 (2.9%)	64 (3.1%)	123 (3.2%)
LP.8.1	2 (1.6%)	0 (0.0%)	1 (4.8%)	9 (5.1%)	16 (5.2%)	29 (2.6%)	48 (2.3%)	105 (2.8%)
XEC.2	4 (3.1%)	0 (0.0%)	0 (0.0%)	9 (5.1%)	6 (1.9%)	20 (1.8%)	49 (2.4%)	88 (2.3%)
MC.13	3 (2.3%)	1 (7.7%)	1 (4.8%)	5 (2.8%)	8 (2.6%)	19 (1.7%)	50 (2.4%)	87 (2.3%)
MC.19	1 (0.8%)	1 (7.7%)	1 (4.8%)	3 (1.7%)	3 (1.0%)	20 (1.8%)	30 (1.5%)	59 (1.5%)
Other recombinant	7 (5.4%)	0 (0.0%)	0 (0.0%)	5 (2.8%)	15 (4.9%)	44 (3.9%)	110 (5.4%)	181 (4.8%)
Other Omicron	19 (14.7%)	2 (15.4%)	4 (19.0%)	29 (16.4%)	46 (14.9%)	206 (18.4%)	338 (16.5%)	644 (16.9%)
Total sequenced	**129 (100%)**	**13 (100%)**	**21 (100%)**	**177 (100%)**	**308 (100%)**	**1,117 (100%)**	**2,043 (100%)**	**3,808 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Age was assigned based on the birth date provided in OCGN; excludes cases with missing birth dates.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 5: Number and percentage of SARS-CoV-2 cases by Pango lineage and geographic region, representative surveillance, Ontario, December 1 to December 28, 2024

Pango Lineage	North West	North East	Eastern	Central East	Toronto	South West	Central West	Unknown	Total
XEC	10 (21.7%)	19 (21.1%)	79 (23.7%)	271 (26.3%)	137 (21.3%)	132 (40.4%)	240 (33.9%)	231 (36.5%)	1,119 (29.4%)
KP.3.1.1	4 (8.7%)	26 (28.9%)	51 (15.3%)	199 (19.3%)	158 (24.5%)	74 (22.6%)	128 (18.1%)	119 (18.8%)	759 (19.9%)
MC.1	0 (0.0%)	27 (30.0%)	60 (18.0%)	124 (12.1%)	31 (4.8%)	9 (2.8%)	44 (6.2%)	51 (8.1%)	346 (9.1%)
NP.1	7 (15.2%)	6 (6.7%)	12 (3.6%)	58 (5.6%)	49 (7.6%)	4 (1.2%)	12 (1.7%)	27 (4.3%)	175 (4.6%)
MC.10.1	0 (0.0%)	0 (0.0%)	7 (2.1%)	42 (4.1%)	20 (3.1%)	11 (3.4%)	21 (3.0%)	23 (3.6%)	124 (3.3%)
XEK	0 (0.0%)	2 (2.2%)	19 (5.7%)	18 (1.7%)	29 (4.5%)	2 (0.6%)	35 (4.9%)	18 (2.8%)	123 (3.2%)
LP.8.1	0 (0.0%)	1 (1.1%)	15 (4.5%)	21 (2.0%)	34 (5.3%)	2 (0.6%)	17 (2.4%)	15 (2.4%)	105 (2.8%)
XEC.2	0 (0.0%)	1 (1.1%)	3 (0.9%)	25 (2.4%)	31 (4.8%)	3 (0.9%)	6 (0.8%)	19 (3.0%)	88 (2.3%)
MC.13	2 (4.3%)	0 (0.0%)	11 (3.3%)	15 (1.5%)	3 (0.5%)	23 (7.0%)	28 (4.0%)	5 (0.8%)	87 (2.3%)
MC.19	0 (0.0%)	0 (0.0%)	4 (1.2%)	19 (1.8%)	15 (2.3%)	0 (0.0%)	11 (1.6%)	10 (1.6%)	59 (1.5%)
Other recombinant	0 (0.0%)	1 (1.1%)	7 (2.1%)	72 (7.0%)	15 (2.3%)	11 (3.4%)	55 (7.8%)	20 (3.2%)	181 (4.8%)
Other Omicron	23 (50.0%)	7 (7.8%)	65 (19.5%)	165 (16.0%)	122 (18.9%)	56 (17.1%)	111 (15.7%)	95 (15.0%)	644 (16.9%)
Total sequenced	46 (100%)	90 (100%)	333 (100%)	1,029 (100%)	644 (100%)	327 (100%)	708 (100%)	633 (100%)	3,810 (100%)

Note: Cases with missing/unassigned patient postal code (16.5%) or out of province postal codes (0.1%) were included in the "Unknown" category. Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports. Geographic region was assigned based on OCGN patient postal code.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Cumulative Whole Genome Sequencing Results

Table 6: Number of SARS-CoV-2 cases by Pango lineage, cumulative counts, Ontario, December 1 to December 28, 2024

WHO Label / Pango Lineage	December 1 - December 28, 2024
Omicron	**2,299**
JN.1	1
JN.1.16.5	8
KP.1.1.3	1
KP.2.14	1
KP.2.3	2
KP.2.3.4	24
KP.2.6	1
KP.3	16
KP.3.1	1
KP.3.1.1	759
KP.3.1.4	2
KP.3.2.3	7
KP.3.2.6	8
KP.3.3	13
KP.3.3.1	21
KP.3.3.2	2
KP.3.3.4	1
KP.3.5	15
KP.3.7	6
KP.4.2	17
KP.4.2.5	1
LB.1.3.1	18
LB.1.7	2
LF.7	3

WHO Label / Pango Lineage	December 1 - December 28, 2024
LF.7.1	22
LF.7.1.2	2
LF.7.2	6
LF.7.2.1	5
LF.7.3	4
LP.7	25
LP.8.1	105
MA.1	3
MC.1	346
MC.1.1	4
MC.10	49
MC.10.1	124
MC.10.2	47
MC.11	41
MC.13	87
MC.13.1	10
MC.13.2	12
MC.14	3
MC.16	37
MC.17	9
MC.19	59
MC.2	24
MC.21	3
MC.21.1	2
MC.22	7
MC.4	2
MC.6	16
MC.8	24
MC.8.1	34

WHO Label / Pango Lineage	December 1 - December 28, 2024
MC.9	6
MY.1	4
NC.1	7
ND.1.1	1
NF.1	8
NL.1	1
NL.3	52
NL.4	3
NP.1	175
Recombinant	**1,511**
GB.1	1
XDY.1	1
XEC	1,119
XEC.1	12
XEC.2	88
XEC.3	20
XEC.4	21
XEC.5	19
XEC.6	4
XEF	39
XEK	123
XEL	14
XEM	47
XEN	3
Total Sequenced	**3,810**

Note: Results do not represent all Ontario cases. Includes results from the OHDP-PHAE from the past month. Pango lineage assignments may change over time, which may impact cumulative totals. Results should be interpreted with caution as frequencies do not reflect prevalence. Sample date represents the earliest date available for the sample. If more than one sample was sequenced for a case, the most recent sample was included.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Technical Notes

Data Sources

Ontario Health Data Platform – Public Health Analytic Environment (OHDP-PHAE)

- Ontario COVID-19 Genomics Network (OCGN) data were extracted from the Ontario Health Data Platform – Public Health Analytic Environment on January 9, 2025 at approximately 9:00 a.m.

Public Health Ontario (PHO)

- Data were submitted to the OHDP-PHAE on January 7, 2025 at approximately 2:00 p.m.

The Hospital for Sick Children (HSC)

- Data were submitted to the OHDP-PHAE on January 7, 2025 at approximately 11:15 a.m.

Kingston Health Sciences Centre (KHSC)

- Data were submitted to the OHDP-PHAE on December 10, 2024 at approximately 1:45 p.m.

Shared Hospital Laboratory (SHL)

- Data were submitted to the OHDP-PHAE on January 7, 2025 at approximately 9:35 a.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were submitted to the OHDP-PHAE on January 8, 2025 at approximately 4:45 p.m.

Ontario Laboratories Information System (OLIS) data – Ontario Respiratory Virus Tool (ORVT)

- OLIS data were extracted from Public Health Ontario's ORVT on January 10, 2025 at approximately 11:30 a.m.

Ontario SARS-CoV-2 Whole Genome Sequencing Strategy

- Ontario's whole genome sequencing strategy began early 2021 to confirm the identification of VOCs from PCR testing. Since then, the strategy has shifted to representative surveillance as of May 2, 2021. Diagnostic testing laboratories currently send all eligible samples (diagnostic PCR Ct≤ 30 and sufficient volume remaining) to one of the five OCGN laboratories for whole genome sequencing.
- The Ministry of Health continues to update its guidance on testing and as such, representative surveillance only pertains to tested populations.

Data Caveats and Methods: Ontario COVID-19 Genomics Network (OCGN)

- Lineage is assigned using the Phylogenetic Assignment of Named Global Outbreak Lineages (pangolin) tool, a software package for predicting SARS-CoV-2 lineages from genome sequences and global lineages. Lineages were reported using pangolin version 4.3.1, pangolin data version 1.31, pangolin assignment version 1.31, scorpio version 0.3.19, and constellations version 0.1.12.
- Lineage nomenclature is dynamic. Pango lineage naming and assignment may change as more samples are sequenced and analyzed globally.
- Whole genome sequencing sample logistics are complex and require samples to be transferred across a large network of laboratories. We are unable to verify all eligible samples are sent to the OCGN laboratories for sequencing.

- Data submitted to the OHDP-PHAE from OCGN laboratories have not been independently verified.
- The dates associated with samples submitted by network laboratories vary due to sample logistics and different laboratory information systems. Dates associated with WGS samples were assigned based on a hierarchy: sample collection date > SARS-CoV-2 diagnostic received date > SARS-CoV-2 diagnostic reported date > WGS received date > WGS reported date. Weeks were created to align with surveillance weeks used by the Public Health Agency of Canada for influenza reporting.
- Samples from the same case were linked if they had the same health card number or if they had the same first name, last name, and date of birth. If more than one sample was sequenced for a case, the most recent sample was used. This may shift a case to a more recent week if a subsequent sample was sequenced from the same case. A small proportion of cases may have samples that were not linked due to inconsistencies or data entry errors.
- Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction.
- Geographic region was assigned based on OCGN patient postal code. 16.5% of cases had missing/unassigned patient postal code, and 0.1% of cases had out of province postal codes.
- North West region includes Northwestern Health Unit and Thunder Bay District Health Unit; North East region includes Algoma Public Health, North Bay Parry Sound District Health Unit, Porcupine Health Unit, Public Health Sudbury & Districts and Timiskaming Health Unit; Eastern region includes Eastern Ontario Health Unit, Hastings Prince Edward Public Health, Kingston, Frontenac and Lennox & Addington (KFLA) Public Health, Leeds, Grenville & Lanark District Health Unit, Ottawa Public Health and Renfrew County and District Health Unit; Central East region includes Durham Region Health Department, Haliburton, Kawartha, Pine Ridge (HKPR) District Health Unit, Peel Public Health, Peterborough Public Health, Simcoe Muskoka District Health Unit, and York Region Public Health; Toronto region includes Toronto Public Health; South West region includes Chatham-Kent Public Health, Grey Bruce Health Unit, Huron Perth Public Health, Lambton Public Health, Middlesex-London Health Unit, Southwestern Public Health, and Windsor-Essex County Health Unit; Central West region includes Brant County Health Unit, City of Hamilton Public Health Services, Haldimand-Norfolk Health Unit, Halton Region Public Health, Niagara Region Public Health, Region of Waterloo Public Health and Emergency Services, and Wellington-Dufferin-Guelph Public Health.
- For representative surveillance, results may not be representative of Ontario overall. Samples selected include a proportion of eligible samples received by OCGN laboratories according to the whole genome sequencing strategy.
    - Data from the OCGN laboratories cover different time periods: PHO since January 1, 2021, HSC since April 21, 2021, KHSC since January 1, 2021, SHL since March 26, 2021, and HRLMP since April 11, 2021.

Methods: Nowcast Estimates, Projections and Weekly Relative Growth Rate

- Nowcast estimates and projections are generated using a multinomial logistic regression model. The Nowcast model uses six weeks of daily representative surveillance data up to the most recent date, with date as the univariate model predictor. Lineages that had at least one day with an estimated or projected prevalence of 5% or greater were included in the table and figure. Lineages with at least 21 days of non-zero case counts were included in the model.
- Projected Nowcast estimates are future predictions of prevalence after the most recent date of observed data.

- Weekly relative growth rate is a measure of a lineage's growth relative to a reference lineage, over a seven day period.[6] Relative growth rates greater than one suggest an increased growth rate compared to the reference; relative growth rates less than one suggest a decreased growth rate compared to the reference.
- These weekly relative growth rates can be calculated by exponentiating the weekly selection rate coefficient from the Nowcast model.
    - The selection rate coefficient is the difference in growth rate between two lineages ($\Delta r = r_{lineage} - r_{reference}$), and can be derived from a logistic regression model where the outcome is the relative frequency of a lineage and the predictor is the date, measured in weeks.[6,7]
- The weekly relative growth rate and projections may be overestimated for emerging lineages.

Data Caveats and Methods: Ontario Laboratories Information System Data – Ontario Respiratory Virus Tool

- Sample collection date is used to assign the date of the test.
- 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 number of positive tests does not necessarily translate to the number of specimens or persons testing positive. For more information about this data source, see ORVT Technical Notes.

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