

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario,
March 11, 2024

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by the Ontario COVID-19 Genomics Network as of March 6, 2024.

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., BJ.1 and BM.1.1.1 recombine to form XBB). Sublineages of the XBB lineage include XBB.1.16, and HV.1 [alias for XBB.1.9.2.5.1.6.1]. 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 a new WHO Greek letter classification may be assigned 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 lineage⁴ using the pangolin tool⁵, allowing for the identification of lineages.

Highlights

- In the most recent week (February 18 to February 24), a total of 579 cases were sequenced. JN.1 was the most prevalent lineage (44.6%), followed by JN.1.4 (24.9%), and JN.1.7 (4.0%).
- The proportion of JN.1 decreased from 45.7% (February 11 to February 17) to 44.6% (February 18 to February 24).
 - Based on the Nowcast model, JN.1 is projected to decrease to 36.8% (95% CI: 31.0% - 43.1%) by March 13, 2024.
- The proportion of JN.1.4 remained stable at 24.0% (February 11 to February 17) and 24.9% (February 18 to February 24).
 - Based on the Nowcast model, JN.1.4 is projected to increase to 29.8% (95% CI: 24.2% - 36.0%) by March 13, 2024. The weekly growth rate of JN.1.4 is 1.13 (95% CI: 1.09 - 1.18) times that of JN.1.

Lineage counts and designations may change between reports as the Pango lineage assignment models are updated (see Technical Notes for details).

Representative Surveillance

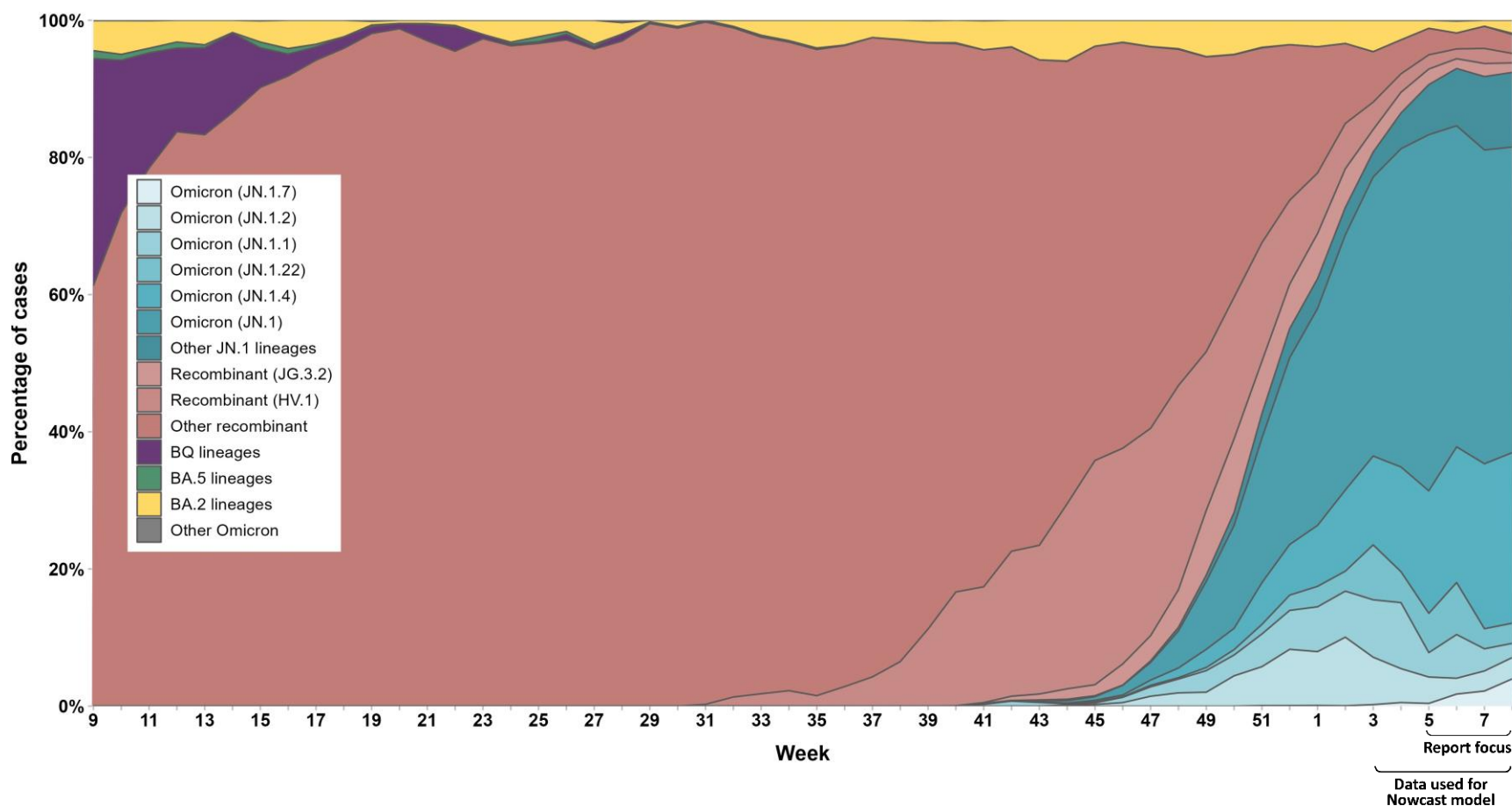
Table 1. Number of SARS-CoV-2 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, January 28 to February 24, 2024

Week	Number of cases	Number sequenced	Percentage sequenced
Week 5 (January 28 - February 3)	1,607	1,013	63.0%
Week 6 (February 4 - February 10)	1,322	910	68.8%
Week 7 (February 11 - February 17)	1,152	682	59.2%
Week 8 (February 18 - February 24)	1,006	579	57.6%
Total	5,087	3,184	62.6%

Note: 'Number of cases' is the number of confirmed positive cases of SARS-CoV-2 in Ontario. Date was assigned to best align with sample collection date, which may differ from other PHO products. 'Number sequenced' is the number of cases sequenced for representative surveillance. Results may not be representative of Ontario overall. 'Percentage sequenced' may be lower than the sampling proportion because not all cases are eligible to be sequenced (i.e. excludes samples with cycle threshold >30 or insufficient volume). 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: Public Health Case and Contact Management Solution (CCM), 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, February 26, 2023 to February 24, 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)

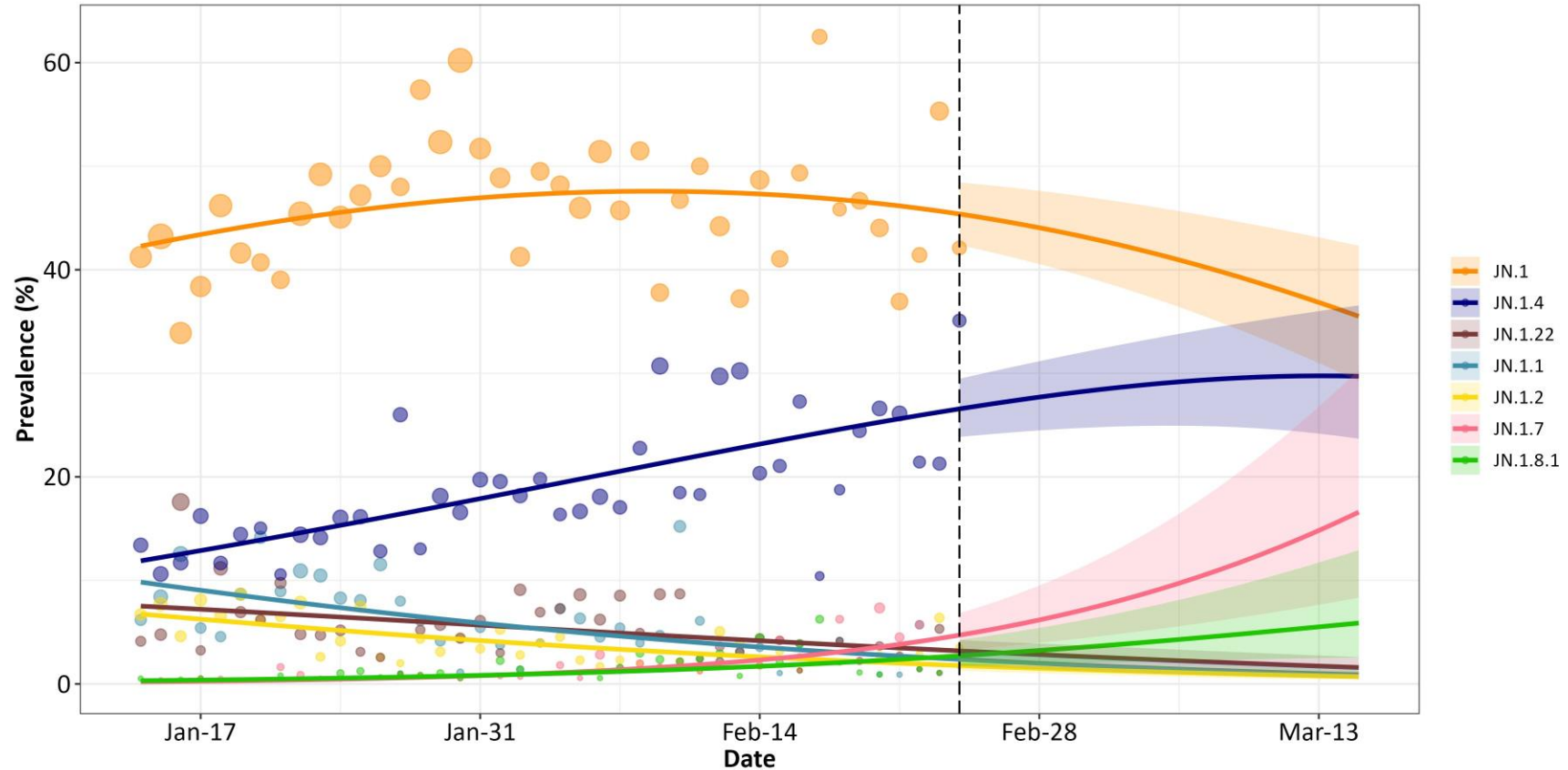
Table 2. Number and percentage of SARS-CoV-2 cases by Pango lineage and week, representative surveillance, Ontario, January 28 to February 24, 2024

Pango lineage	Week 5 (January 28- February 3)	Week 6 (February 4- February 10)	Week 7 (February 11- February 17)	Week 8 (February 18- February 24)	Total (January 28 - February 24)
JN.1	526 (51.9%)	426 (46.8%)	312 (45.7%)	258 (44.6%)	1,522 (47.8%)
JN.1.4	181 (17.9%)	180 (19.8%)	164 (24.0%)	144 (24.9%)	669 (21.0%)
JN.1.22	58 (5.7%)	69 (7.6%)	20 (2.9%)	17 (2.9%)	164 (5.2%)
JN.1.1	36 (3.6%)	58 (6.4%)	22 (3.2%)	12 (2.1%)	128 (4.0%)
JN.1.2	39 (3.8%)	21 (2.3%)	20 (2.9%)	18 (3.1%)	98 (3.1%)
JN.1.7	4 (0.4%)	16 (1.8%)	15 (2.2%)	23 (4.0%)	58 (1.8%)
HV.1	21 (2.1%)	13 (1.4%)	15 (2.2%)	8 (1.4%)	57 (1.8%)
JG.3.2	23 (2.3%)	13 (1.4%)	13 (1.9%)	8 (1.4%)	57 (1.8%)
Other recombinant	39 (3.8%)	21 (2.3%)	22 (3.2%)	16 (2.8%)	98 (3.1%)
Other Omicron	86 (8.5%)	93 (10.2%)	79 (11.6%)	75 (13.0%)	333 (10.5%)
Total sequenced	1,013 (100%)	910 (100%)	682 (100%)	579 (100%)	3,184 (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, January 14 to March 16, 2024



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, January 14 to March 16, 2024

Pango lineage	Week 7 (February 14): Estimated	Week 8 (February 21): Estimated	Week 9 (February 28): Projected	Week 10 (March 6): Projected	Week 11 (March 13): Projected	Weekly relative growth rate
JN.1	47.3 (45.3 - 49.3)	46.2 (43.5 - 48.9)	44.1 (40.6 - 47.6)	40.9 (36.4 - 45.7)	36.8 (31.0 - 43.1)	1.00 (reference)
JN.1.4	23.2 (21.5 - 24.9)	25.6 (23.2 - 28.1)	27.7 (24.5 - 31.2)	29.2 (24.9 - 33.8)	29.8 (24.2 - 36.0)	1.13 (1.09 - 1.18)
JN.1.22	4.2 (3.4 - 5.1)	3.5 (2.7 - 4.5)	2.8 (2.1 - 3.9)	2.2 (1.5 - 3.3)	1.7 (1.1 - 2.7)	0.85 (0.79 - 0.92)
JN.1.1	3.6 (2.9 - 4.4)	2.7 (2.1 - 3.5)	2.0 (1.4 - 2.8)	1.4 (1.0 - 2.2)	1.0 (0.6 - 1.6)	0.78 (0.72 - 0.83)
JN.1.2	2.6 (2.1 - 3.3)	2.0 (1.5 - 2.8)	1.5 (1.0 - 2.2)	1.1 (0.7 - 1.8)	0.8 (0.4 - 1.4)	0.79 (0.72 - 0.86)
JN.1.7	2.3 (1.8 - 3.0)	3.8 (2.7 - 5.3)	6.2 (4.0 - 9.5)	9.7 (5.6 - 16.4)	14.8 (7.6 - 26.8)	1.69 (1.44 - 1.98)
JN.1.8.1	1.7 (1.3 - 2.3)	2.4 (1.6 - 3.5)	3.2 (1.9 - 5.4)	4.3 (2.2 - 8.1)	5.5 (2.5 - 11.7)	1.43 (1.22 - 1.68)
Other lineages	9.6 (8.5 - 10.9)	9.4 (7.9 - 11.0)	8.9 (7.2 - 11.0)	8.3 (6.3 - 10.7)	7.4 (5.3 - 10.2)	1.00 (0.94 - 1.05)

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, January 28 to February 24, 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
JN.1	76 (46.3%)	12 (46.2%)	12 (54.5%)	130 (48.0%)	168 (46.2%)	441 (48.2%)	680 (47.9%)	1,519 (47.8%)
JN.1.4	32 (19.5%)	6 (23.1%)	3 (13.6%)	41 (15.1%)	80 (22.0%)	175 (19.1%)	332 (23.4%)	669 (21.0%)
JN.1.22	4 (2.4%)	1 (3.8%)	0 (0.0%)	12 (4.4%)	20 (5.5%)	47 (5.1%)	80 (5.6%)	164 (5.2%)
JN.1.1	8 (4.9%)	1 (3.8%)	1 (4.5%)	22 (8.1%)	20 (5.5%)	29 (3.2%)	47 (3.3%)	128 (4.0%)
JN.1.2	8 (4.9%)	1 (3.8%)	1 (4.5%)	13 (4.8%)	8 (2.2%)	27 (3.0%)	40 (2.8%)	98 (3.1%)
JN.1.7	3 (1.8%)	0 (0.0%)	0 (0.0%)	5 (1.8%)	8 (2.2%)	14 (1.5%)	28 (2.0%)	58 (1.8%)
HV.1	4 (2.4%)	1 (3.8%)	1 (4.5%)	1 (0.4%)	6 (1.6%)	12 (1.3%)	32 (2.3%)	57 (1.8%)
JG.3.2	2 (1.2%)	1 (3.8%)	1 (4.5%)	4 (1.5%)	11 (3.0%)	21 (2.3%)	17 (1.2%)	57 (1.8%)
Other recombinant	7 (4.3%)	1 (3.8%)	1 (4.5%)	5 (1.8%)	10 (2.7%)	48 (5.2%)	26 (1.8%)	98 (3.1%)
Other Omicron	20 (12.2%)	2 (7.7%)	2 (9.1%)	38 (14.0%)	33 (9.1%)	101 (11.0%)	137 (9.7%)	333 (10.5%)
Total sequenced	164 (100%)	26 (100%)	22 (100%)	271 (100%)	364 (100%)	915 (100%)	1,419 (100%)	3,181 (100%)

Note: Includes the most prevalent lineages detected in the past month. Age was assigned based on the birth date provided in OCGN, and if missing, based on the birth date from CCM; excludes cases with missing birth dates.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5a. Number and percentage of SARS-CoV-2 cases by Pango lineage and public health unit (PHU), representative surveillance, North West Region, January 28 to February 24, 2024

Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
JN.1	2 (50.0%)	30 (45.5%)	32 (45.7%)
JN.1.4	0 (0.0%)	22 (33.3%)	22 (31.4%)
JN.1.22	0 (0.0%)	2 (3.0%)	2 (2.9%)
JN.1.1	1 (25.0%)	2 (3.0%)	3 (4.3%)
JN.1.2	0 (0.0%)	1 (1.5%)	1 (1.4%)
JN.1.7	0 (0.0%)	1 (1.5%)	1 (1.4%)
HV.1	1 (25.0%)	3 (4.5%)	4 (5.7%)
JG.3.2	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other recombinant	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other Omicron	0 (0.0%)	5 (7.6%)	5 (7.1%)
Total sequenced	4 (100%)	66 (100%)	70 (100%)

Note: 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5b. Number and percentage of SARS-CoV-2 cases by Pango lineage and public health unit (PHU), representative surveillance, North East Region, January 28 to February 24, 2024

Pango lineage	Algoma Public Health	North Bay Parry Sound District Health Unit	Porcupine Health Unit	Public Health Sudbury & Districts	Timiskaming Health Unit	Total
JN.1	7 (41.2%)	7 (43.8%)	7 (30.4%)	13 (16.5%)	1 (6.2%)	35 (23.2%)
JN.1.4	8 (47.1%)	2 (12.5%)	9 (39.1%)	46 (58.2%)	15 (93.8%)	80 (53.0%)
JN.1.22	0 (0.0%)	0 (0.0%)	1 (4.3%)	1 (1.3%)	0 (0.0%)	2 (1.3%)
JN.1.1	0 (0.0%)	1 (6.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.7%)
JN.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
JN.1.7	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
HV.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.3%)	0 (0.0%)	1 (0.7%)
JG.3.2	0 (0.0%)	1 (6.2%)	4 (17.4%)	0 (0.0%)	0 (0.0%)	5 (3.3%)
Other recombinant	1 (5.9%)	5 (31.2%)	0 (0.0%)	18 (22.8%)	0 (0.0%)	24 (15.9%)
Other Omicron	1 (5.9%)	0 (0.0%)	2 (8.7%)	0 (0.0%)	0 (0.0%)	3 (2.0%)
Total sequenced	17 (100%)	16 (100%)	23 (100%)	79 (100%)	16 (100%)	151 (100%)

Note: 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5c. Number and percentage of SARS-CoV-2 cases by Pango lineage and public health unit (PHU), representative surveillance, Eastern Region, January 28 to February 24, 2024

Pango lineage	Eastern Ontario Health Unit	Hastings Prince Edward Public Health	Kingston, Frontenac and Lennox & Addington Public Health	Leeds, Grenville & Lanark District Health Unit	Ottawa Public Health	Renfrew County and District Health Unit	Total
JN.1	21 (50.0%)	18 (69.2%)	39 (43.8%)	4 (13.3%)	151 (43.3%)	9 (20.9%)	242 (41.8%)
JN.1.4	10 (23.8%)	2 (7.7%)	6 (6.7%)	9 (30.0%)	60 (17.2%)	20 (46.5%)	107 (18.5%)
JN.1.22	2 (4.8%)	1 (3.8%)	4 (4.5%)	4 (13.3%)	78 (22.3%)	1 (2.3%)	90 (15.5%)
JN.1.1	3 (7.1%)	0 (0.0%)	22 (24.7%)	2 (6.7%)	10 (2.9%)	0 (0.0%)	37 (6.4%)
JN.1.2	0 (0.0%)	1 (3.8%)	7 (7.9%)	3 (10.0%)	3 (0.9%)	0 (0.0%)	14 (2.4%)
JN.1.7	1 (2.4%)	1 (3.8%)	0 (0.0%)	1 (3.3%)	17 (4.9%)	0 (0.0%)	20 (3.5%)
HV.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (0.9%)	1 (2.3%)	4 (0.7%)
JG.3.2	0 (0.0%)	0 (0.0%)	2 (2.2%)	0 (0.0%)	1 (0.3%)	1 (2.3%)	4 (0.7%)
Other recombinant	0 (0.0%)	0 (0.0%)	4 (4.5%)	4 (13.3%)	5 (1.4%)	0 (0.0%)	13 (2.2%)
Other Omicron	5 (11.9%)	3 (11.5%)	5 (5.6%)	3 (10.0%)	21 (6.0%)	11 (25.6%)	48 (8.3%)
Total sequenced	42 (100%)	26 (100%)	89 (100%)	30 (100%)	349 (100%)	43 (100%)	579 (100%)

Note: 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5d. Number and percentage of SARS-CoV-2 cases by Pango lineage health unit and public (PHU), representative surveillance, Central East Region, January 28 to February 24, 2024

Pango lineage	Durham Region Health Department	Haliburton, Kawartha, Pine Ridge District Health Unit	Peel Public Health	Peterborough Public Health	Simcoe Muskoka District Health Unit	York Region Public Health	Total
JN.1	86 (62.3%)	13 (48.1%)	112 (55.7%)	27 (62.8%)	35 (31.2%)	90 (52.6%)	363 (52.5%)
JN.1.4	19 (13.8%)	1 (3.7%)	19 (9.5%)	6 (14.0%)	54 (48.2%)	42 (24.6%)	141 (20.4%)
JN.1.22	9 (6.5%)	0 (0.0%)	2 (1.0%)	0 (0.0%)	8 (7.1%)	7 (4.1%)	26 (3.8%)
JN.1.1	3 (2.2%)	2 (7.4%)	10 (5.0%)	1 (2.3%)	0 (0.0%)	6 (3.5%)	22 (3.2%)
JN.1.2	4 (2.9%)	1 (3.7%)	7 (3.5%)	1 (2.3%)	0 (0.0%)	5 (2.9%)	18 (2.6%)
JN.1.7	1 (0.7%)	0 (0.0%)	10 (5.0%)	0 (0.0%)	2 (1.8%)	2 (1.2%)	15 (2.2%)
HV.1	4 (2.9%)	1 (3.7%)	2 (1.0%)	0 (0.0%)	1 (0.9%)	1 (0.6%)	9 (1.3%)
JG.3.2	1 (0.7%)	1 (3.7%)	3 (1.5%)	1 (2.3%)	2 (1.8%)	1 (0.6%)	9 (1.3%)
Other recombinant	3 (2.2%)	4 (14.8%)	4 (2.0%)	4 (9.3%)	2 (1.8%)	2 (1.2%)	19 (2.7%)
Other Omicron	8 (5.8%)	4 (14.8%)	32 (15.9%)	3 (7.0%)	8 (7.1%)	15 (8.8%)	70 (10.1%)
Total sequenced	138 (100%)	27 (100%)	201 (100%)	43 (100%)	112 (100%)	171 (100%)	692 (100%)

Note: 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5e. Number and percentage of SARS-CoV-2 cases by Pango lineage and public health unit (PHU), representative surveillance, Toronto Region, January 28 to February 24, 2024

Pango lineage	Toronto Public Health	Total
JN.1	284 (49.7%)	284 (49.7%)
JN.1.4	106 (18.6%)	106 (18.6%)
JN.1.22	12 (2.1%)	12 (2.1%)
JN.1.1	29 (5.1%)	29 (5.1%)
JN.1.2	23 (4.0%)	23 (4.0%)
JN.1.7	6 (1.1%)	6 (1.1%)
HV.1	14 (2.5%)	14 (2.5%)
JG.3.2	8 (1.4%)	8 (1.4%)
Other recombinant	7 (1.2%)	7 (1.2%)
Other Omicron	82 (14.4%)	82 (14.4%)
Total sequenced	571 (100%)	571 (100%)

Note: 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5f. Number and percentage of SARS-CoV-2 cases by Pango lineage and public health unit (PHU), representative surveillance, South West Region, January 28 to February 24, 2024

Pango lineage	Chatham-Kent Public Health	Grey Bruce Health Unit	Huron Perth Public Health	Lambton Public Health	Middlesex-London Health Unit	Southwestern Public Health	Windsor-Essex County Health Unit	Total
JN.1	17 (60.7%)	16 (48.5%)	24 (38.7%)	12 (70.6%)	51 (47.2%)	15 (34.9%)	66 (61.7%)	201 (50.5%)
JN.1.4	2 (7.1%)	4 (12.1%)	24 (38.7%)	2 (11.8%)	9 (8.3%)	18 (41.9%)	15 (14.0%)	74 (18.6%)
JN.1.22	0 (0.0%)	4 (12.1%)	0 (0.0%)	0 (0.0%)	5 (4.6%)	0 (0.0%)	1 (0.9%)	10 (2.5%)
JN.1.1	0 (0.0%)	0 (0.0%)	7 (11.3%)	0 (0.0%)	2 (1.9%)	2 (4.7%)	1 (0.9%)	12 (3.0%)
JN.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (11.8%)	5 (4.6%)	2 (4.7%)	5 (4.7%)	14 (3.5%)
JN.1.7	7 (25.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (2.8%)	10 (2.5%)
HV.1	2 (7.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (3.7%)	0 (0.0%)	1 (0.9%)	7 (1.8%)
JG.3.2	0 (0.0%)	1 (3.0%)	2 (3.2%)	0 (0.0%)	2 (1.9%)	0 (0.0%)	0 (0.0%)	5 (1.3%)
Other recombinant	0 (0.0%)	1 (3.0%)	0 (0.0%)	0 (0.0%)	4 (3.7%)	0 (0.0%)	6 (5.6%)	11 (2.8%)
Other Omicron	0 (0.0%)	7 (21.2%)	5 (8.1%)	1 (5.9%)	26 (24.1%)	6 (14.0%)	9 (8.4%)	54 (13.6%)
Total sequenced	28 (100%)	33 (100%)	62 (100%)	17 (100%)	108 (100%)	43 (100%)	107 (100%)	398 (100%)

Note: 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5g. Number and percentage of SARS-CoV-2 cases by Pango lineage and public health unit (PHU), representative surveillance, Central West Region, January 28 to February 24, 2024

Pango lineage	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	Wellington-Dufferin-Guelph Public Health	Total
JN.1	15 (46.9%)	95 (46.8%)	15 (37.5%)	67 (60.9%)	79 (51.3%)	47 (42.0%)	46 (65.7%)	364 (50.5%)
JN.1.4	1 (3.1%)	31 (15.3%)	15 (37.5%)	15 (13.6%)	41 (26.6%)	23 (20.5%)	12 (17.1%)	138 (19.1%)
JN.1.22	6 (18.8%)	4 (2.0%)	0 (0.0%)	1 (0.9%)	0 (0.0%)	5 (4.5%)	6 (8.6%)	22 (3.1%)
JN.1.1	2 (6.2%)	10 (4.9%)	1 (2.5%)	0 (0.0%)	6 (3.9%)	5 (4.5%)	0 (0.0%)	24 (3.3%)
JN.1.2	3 (9.4%)	5 (2.5%)	3 (7.5%)	5 (4.5%)	4 (2.6%)	7 (6.2%)	1 (1.4%)	28 (3.9%)
JN.1.7	1 (3.1%)	3 (1.5%)	0 (0.0%)	2 (1.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	6 (0.8%)
HV.1	0 (0.0%)	1 (0.5%)	0 (0.0%)	14 (12.7%)	2 (1.3%)	0 (0.0%)	1 (1.4%)	18 (2.5%)
JG.3.2	0 (0.0%)	14 (6.9%)	0 (0.0%)	0 (0.0%)	10 (6.5%)	2 (1.8%)	0 (0.0%)	26 (3.6%)
Other recombinant	0 (0.0%)	8 (3.9%)	5 (12.5%)	2 (1.8%)	3 (1.9%)	4 (3.6%)	2 (2.9%)	24 (3.3%)
Other Omicron	4 (12.5%)	32 (15.8%)	1 (2.5%)	4 (3.6%)	9 (5.8%)	19 (17.0%)	2 (2.9%)	71 (9.8%)
Total sequenced	32 (100%)	203 (100%)	40 (100%)	110 (100%)	154 (100%)	112 (100%)	70 (100%)	721 (100%)

Note: 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 6. Number and percentage (row %) of deceased SARS-CoV-2 cases by Pango lineage, representative surveillance, Ontario, December 3, 2023 to February 24, 2024

Pango lineage	Deceased	Total cases
JN.1	69 (1.3%)	5,374 (100%)
JN.1.4	29 (1.6%)	1,791 (100%)
JN.1.22	8 (1.5%)	520 (100%)
JN.1.1	16 (1.7%)	963 (100%)
JN.1.2	12 (1.2%)	1,028 (100%)
JN.1.7	1 (1.4%)	72 (100%)
HV.1	26 (1.2%)	2,164 (100%)
JG.3.2	18 (1.5%)	1,179 (100%)
Other recombinant	52 (1.3%)	3,923 (100%)
Other Omicron	16 (1.1%)	1,455 (100%)
Total sequenced	247 (1.3%)	18,469 (100%)

Note: Includes the most prevalent lineages detected in the past month. Cases include only those that linked to CCM (96.4%). Deceased cases include cases that reported a “Fatal” outcome and the type of death value in CCM was not ‘DOPHS was unrelated to cause of death’ or ‘Under PHU Review’ at the time of data extraction. Factors, such as age, that may affect the risk of SARS-CoV-2 death are not accounted for in these analyses. 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. 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.

Data Sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM) - death indicators

Cumulative Whole Genome Sequencing Results

Table 7. Number of SARS-CoV-2 cases by Pango lineage, cumulative counts, Ontario, January 28 to February 24, 2024

WHO label / Pango lineage	January 28 - February 24, 2024
Omicron	2,972
BA.1.1.14	1
BA.2.86	1
BA.2.86.1	11
BA.2.86.3	7
BA.5.2.1	1
JN.1	1,522
JN.1.1	128
JN.1.10	10
JN.1.11.1	29
JN.1.13	3
JN.1.15	6
JN.1.16	6
JN.1.17	2
JN.1.18	16
JN.1.19	8
JN.1.2	98
JN.1.20	11
JN.1.21	1
JN.1.22	164
JN.1.3	39
JN.1.4	669
JN.1.4.2	16
JN.1.5	27
JN.1.6	10
JN.1.6.1	1
JN.1.7	58
JN.1.8	15
JN.1.8.1	46
JN.1.9	39
JN.10	1
JN.2	3
JN.2.1	2
JN.2.2	1
JN.2.5	18
JN.3	1
JN.5	1
Recombinant	212

WHO label / Pango lineage	January 28 - February 24, 2024
EG.5.1.1	2
EG.5.1.6	1
EG.5.1.8	2
GE.1.2	1
GK.1.1	1
GK.1.8	2
HK.3	7
HK.3.2	4
HK.3.2.1	2
HK.8.1	1
HV.1	57
HV.1.6	1
HV.1.6.1	1
JD.1.1	1
JD.1.1.1	3
JD.1.1.5	1
JD.1.1.7	1
JD.1.1.8	1
JG.3	5
JG.3.2	57
KC.1	14
KL.1	23
KL.1.1	3
XBB.1.16	2
XBB.1.16.6	1
XDA	1
XDD	2
XDK	11
XDP	4
Total sequenced	3,184

Note: Results do not represent all Ontario cases. Includes results from the OHDP-PHAE from the past year. 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 March 7, 2024 at approximately 9:00 a.m.

Public Health Ontario (PHO)

- Data were submitted to the OHDP-PHAE on March 6, 2024 at approximately 11:15 a.m.

The Hospital for Sick Children (HSC)

- Data were submitted to the OHDP-PHAE on March 5, 2024 at approximately 12:45 p.m.

Kingston Health Sciences Centre (KHSC)

- Data were submitted to the OHDP-PHAE on March 5, 2024 at approximately 12:45 p.m.

Shared Hospital Laboratory (SHL)

- Data were submitted to the OHDP-PHAE on March 5, 2024 at approximately 5:15 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were submitted to the OHDP-PHAE on March 6, 2024 at approximately 11:00 a.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on March 5, 2024 at approximately 1:00 p.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 $C_t \leq 30$ and sufficient volume remaining) to one of the five OCGN laboratories for whole genome sequencing.
- As of December 31, 2021, diagnostic PCR testing was restricted to high-risk populations. 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 1.25.1, pangolin assignment version 1.25.1, 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 > VOC PCR received date > VOC PCR 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.
- Public health unit was assigned using diagnosing health unit in CCM. If the case did not link to CCM (3.5%), then public health unit was assigned using OCGN patient postal code or ordering provider postal code if patient postal code was missing.
- 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.
- Relative growth rate is a measure of a lineage's growth relative to a reference lineage.⁶ Relative growth rates greater than 1 suggest an increased growth rate compared to the reference; relative growth rates less than 1 suggest a decreased growth rate compared to the reference.
- These relativized growth rates can be calculated by exponentiating the selection rate coefficient from the Nowcast model.
 - The selection rate coefficient is the difference in growth rate between two lineages ($\Delta r = r_{\text{lineage}} - r_{\text{reference}}$), and can be derived from a logistic regression model where the outcome is the relative frequency of a lineage and the predictor is time.^{6,7}
- The weekly relative growth rate and projections may be overestimated for emerging lineages.

Data Caveats and Methods: Public Health Case and Contact Management Solution (CCM)

- 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.
- Methods for processing the CCM case data are described in the [Technical Notes](#) of the Ontario Respiratory Virus Tool.
- Data corrections or updates can result in case records being removed and/or updated from past reports.
- Dates associated with SARS-CoV-2 cases in Ontario were assigned using a hierarchy to best align with the sample date used for representative surveillance: sample collection date > test reported date > case reported date. As a result, the number of cases may differ from other reports which use different dates.
- Cases were linked to CCM if they had the same health card number or if they had the same first name, last name, and date of birth. Cases may not have linked to CCM due to discrepancies in patient identifiers or if they were not residents of Ontario (diagnosing health unit was reported as MOH).
- Table for deceased indicators only include cases that linked to CCM (96.4% of cases).
- Data on deaths are likely under-reported as these events may occur after the completion of public health follow up of cases. Cases that died after follow-up was completed may not be captured in CCM.

- For surveillance purposes, a SARS-CoV-2 death is defined as a death resulting from a clinically compatible illness unless there is a clear alternative cause of death that cannot be related to SARS-CoV-2 (e.g., trauma, medically assisted death). There should be no period of complete recovery from SARS-CoV-2 between illness and reported death.
- Deaths are determined by using the outcome and Type of Death fields in CCM. SARS-CoV-2 deaths are counted where the Outcome value is 'Fatal' and the Type of Death value is not 'DOPHS was unrelated to cause of death' or 'Under PHU Review'.

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Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Epidemiologic summary: SARS-CoV-2 whole genome sequencing in Ontario, March 11, 2024. Toronto, ON: King's Printer for Ontario; 2024.

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