Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, April 29, 2024

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by the Ontario COVID-19 Genomics Network as of April 24, 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 lineage[4] using the pangolin tool[5], allowing for the identification of lineages.

Highlights

- In the most recent week (April 7 to April 13), a total of 403 cases were sequenced. JN.1 was the most prevalent lineage (23.1%), followed by JN.1.4 (15.6%), JN.1.13.1 (14.6%), and JN.1.11.1 (10.4%).
- The proportion of JN.1 decreased from 29.1% (March 31 to April 6) to 23.1% (April 7 to April 13).
    - Based on the Nowcast model, JN.1 is projected to decrease to 9.4% (95% CI: 6.8% - 13.0%) by May 1, 2024.
- The proportion of JN.1.4 increased from 12.3% (March 31 to April 6) to 15.6% (April 7 to April 13).
    - Based on the Nowcast model, JN.1.4 is projected to decrease to 5.7% (95% CI: 3.9% - 8.4%) by May 1, 2024. The weekly growth rate of JN.1.4 is 1.00 (95% CI: 0.93 - 1.07) times that of JN.1.
- The proportion of JN.1.13.1 increased from 7.0% (March 31 to April 6) to 14.6% (April 7 to April 13).
    - Based on the Nowcast model, JN.1.13.1 is projected to increase to 28.6% (95% CI: 18.9% - 40.7%) by May 1, 2024. The weekly growth rate of JN.1.13.1 is 1.71 (95% CI: 1.52 - 1.92) 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).

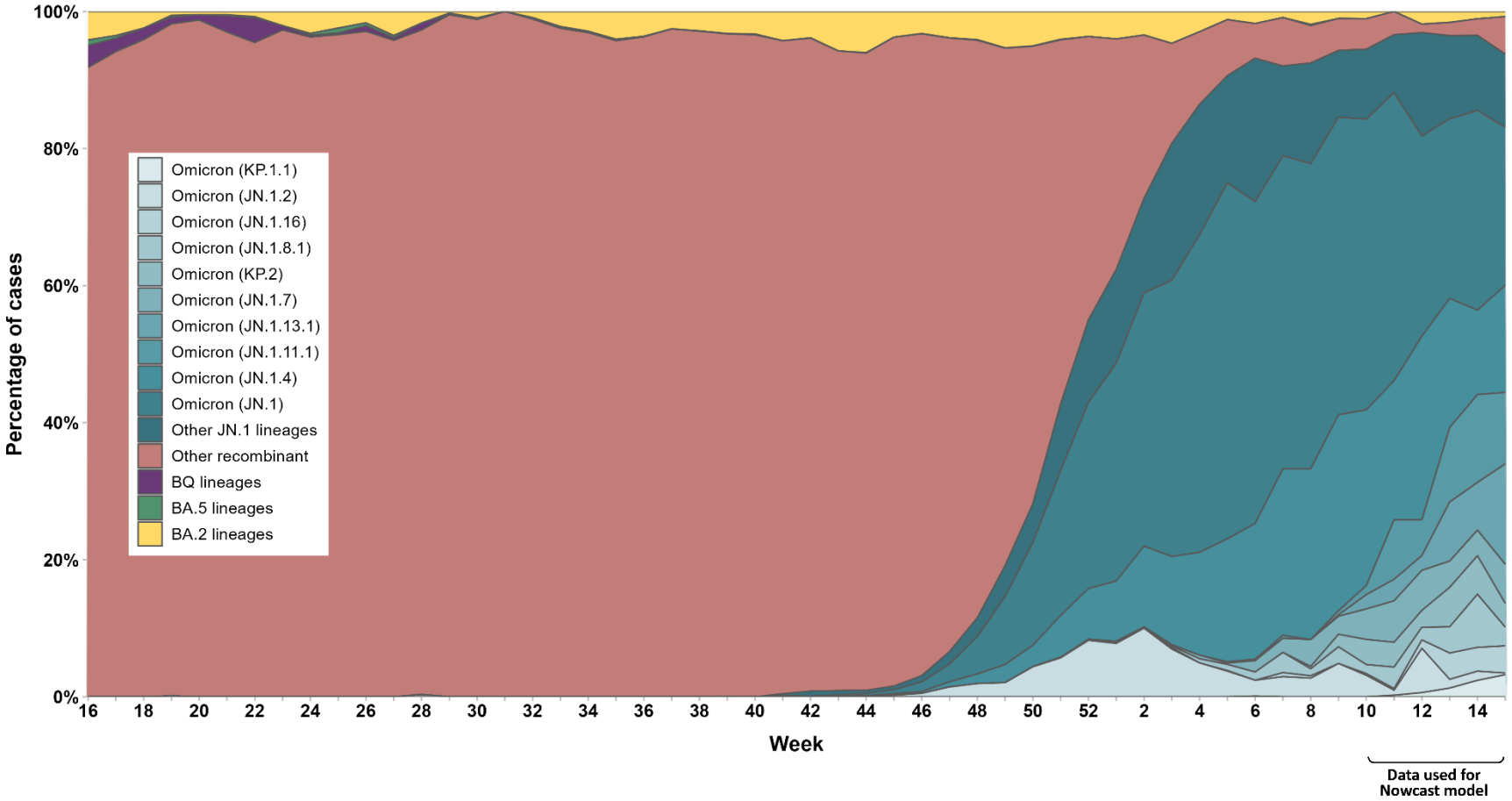
Representative Surveillance

Table 1. Number of SARS-CoV-2 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, March 17 to April 13, 2024

Week	Number of cases	Number sequenced	Percentage sequenced
Week 12 (March 17 - March 23)	582	325	55.8%
Week 13 (March 24 - March 30)	536	313	58.4%
Week 14 (March 31 - April 6)	683	374	54.8%
Week 15 (April 7 - April 13)	722	403	55.8%
Total	**2,523**	**1,415**	**56.1%**

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, April 16, 2023 to April 13, 2024



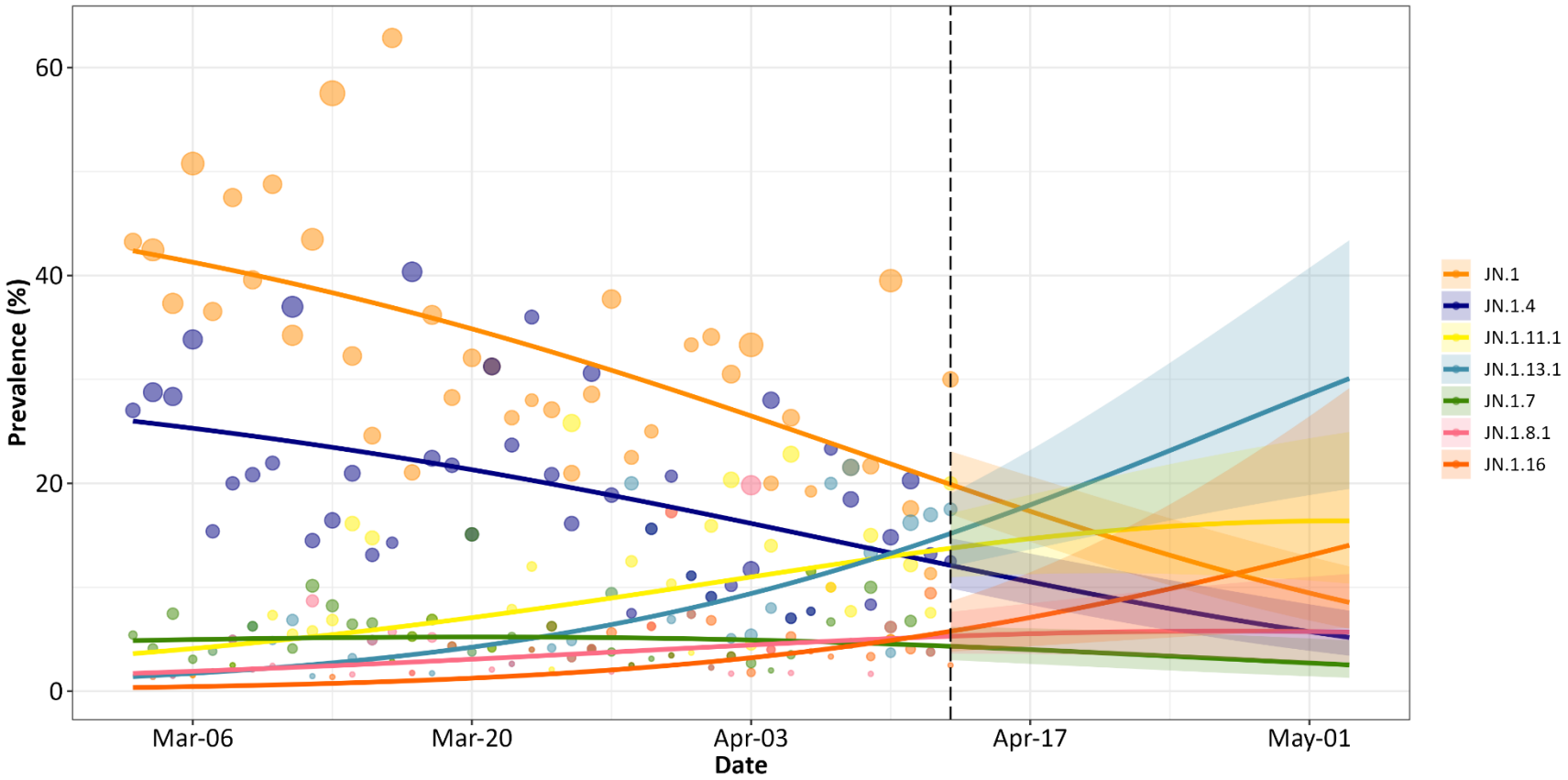
Note: Results may not be representative of Ontario overall. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for a case, the most recent sample 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, March 17 to April 13, 2024

Pango lineage	Week 12 (March 17 - March 23)	Week 13 (March 24 - March 30)	Week 14 (March 31 - April 6)	Week 15 (April 7 - April 13)	Total (March 17 - April 13)
JN.1	95 (29.2%)	82 (26.2%)	109 (29.1%)	93 (23.1%)	379 (26.8%)
JN.1.4	87 (26.8%)	59 (18.8%)	46 (12.3%)	63 (15.6%)	255 (18.0%)
JN.1.11.1	17 (5.2%)	34 (10.9%)	48 (12.8%)	42 (10.4%)	141 (10.0%)
JN.1.13.1	7 (2.2%)	27 (8.6%)	26 (7.0%)	59 (14.6%)	119 (8.4%)
JN.1.7	19 (5.8%)	12 (3.8%)	14 (3.7%)	23 (5.7%)	68 (4.8%)
KP.2	8 (2.5%)	18 (5.8%)	21 (5.6%)	14 (3.5%)	61 (4.3%)
JN.1.8.1	6 (1.8%)	12 (3.8%)	29 (7.8%)	11 (2.7%)	58 (4.1%)
JN.1.16	4 (1.2%)	12 (3.8%)	13 (3.5%)	16 (4.0%)	45 (3.2%)
JN.1.2	21 (6.5%)	4 (1.3%)	5 (1.3%)	1 (0.2%)	31 (2.2%)
KP.1.1	2 (0.6%)	4 (1.3%)	9 (2.4%)	13 (3.2%)	28 (2.0%)
Other recombinant	4 (1.2%)	6 (1.9%)	9 (2.4%)	22 (5.5%)	41 (2.9%)
Other Omicron	55 (16.9%)	43 (13.7%)	45 (12.0%)	46 (11.4%)	189 (13.4%)
Total sequenced	**325 (100%)**	**313 (100%)**	**374 (100%)**	**403 (100%)**	**1,415 (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, March 3 to May 4, 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, March 3 to May 4, 2024

Pango lineage	Week 14 (April 3): Estimated	Week 15 (April 10): Estimated	Week 16 (April 17): Projected	Week 17 (April 24): Projected	Week 18 (May 1): Projected	Weekly relative growth rate
JN.1	26.5 (24.1 - 29.0)	21.9 (19.1 - 24.9)	17.3 (14.4 - 20.7)	13.1 (10.2 - 16.6)	9.4 (6.8 - 13.0)	1.00 (reference)
JN.1.4	16.1 (14.2 - 18.3)	13.3 (11.2 - 15.8)	10.5 (8.3 - 13.2)	7.9 (5.9 - 10.7)	5.7 (3.9 - 8.4)	1.00 (0.93 - 1.07)
JN.1.11.1	11.0 (9.4 - 12.8)	13.0 (10.6 - 15.8)	14.7 (11.3 - 18.9)	15.9 (11.3 - 21.8)	16.4 (10.7 - 24.3)	1.43 (1.30 - 1.58)
JN.1.13.1	9.4 (8.0 - 11.0)	13.3 (10.8 - 16.2)	17.9 (13.6 - 23.2)	23.2 (16.4 - 31.6)	28.6 (18.9 - 40.7)	1.71 (1.52 - 1.92)
JN.1.7	4.9 (3.9 - 6.3)	4.5 (3.3 - 6.3)	4.0 (2.6 - 6.0)	3.4 (2.0 - 5.6)	2.7 (1.4 - 5.1)	1.11 (0.99 - 1.25)
JN.1.8.1	4.4 (3.5 - 5.7)	5.1 (3.6 - 7.0)	5.5 (3.6 - 8.5)	5.8 (3.3 - 9.8)	5.7 (2.9 - 11.0)	1.38 (1.20 - 1.58)
JN.1.16	3.2 (2.4 - 4.3)	4.9 (3.4 - 7.0)	7.1 (4.3 - 11.4)	9.9 (5.2 - 18.0)	13.1 (5.9 - 26.4)	1.84 (1.50 - 2.25)
Other lineages	13.2 (11.4 - 15.2)	13.4 (11.1 - 16.1)	13.0 (10.1 - 16.5)	12.1 (8.7 - 16.4)	10.7 (7.1 - 15.8)	1.23 (1.13 - 1.33)

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, March 17 to April 13, 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	13 (24.1%)	1 (20.0%)	1 (25.0%)	25 (23.1%)	40 (26.0%)	115 (27.6%)	184 (27.3%)	379 (26.8%)
JN.1.4	8 (14.8%)	0 (0.0%)	1 (25.0%)	5 (4.6%)	29 (18.8%)	77 (18.5%)	135 (20.1%)	255 (18.0%)
JN.1.11.1	4 (7.4%)	0 (0.0%)	0 (0.0%)	8 (7.4%)	14 (9.1%)	36 (8.7%)	79 (11.7%)	141 (10.0%)
JN.1.13.1	2 (3.7%)	0 (0.0%)	0 (0.0%)	17 (15.7%)	11 (7.1%)	38 (9.1%)	51 (7.6%)	119 (8.4%)
JN.1.7	3 (5.6%)	2 (40.0%)	1 (25.0%)	12 (11.1%)	6 (3.9%)	14 (3.4%)	30 (4.5%)	68 (4.8%)
KP.2	4 (7.4%)	0 (0.0%)	0 (0.0%)	5 (4.6%)	6 (3.9%)	13 (3.1%)	33 (4.9%)	61 (4.3%)
JN.1.8.1	1 (1.9%)	0 (0.0%)	0 (0.0%)	4 (3.7%)	5 (3.2%)	15 (3.6%)	33 (4.9%)	58 (4.1%)
JN.1.16	4 (7.4%)	0 (0.0%)	0 (0.0%)	6 (5.6%)	10 (6.5%)	11 (2.6%)	14 (2.1%)	45 (3.2%)
JN.1.2	2 (3.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.6%)	9 (2.2%)	19 (2.8%)	31 (2.2%)
KP.1.1	4 (7.4%)	2 (40.0%)	0 (0.0%)	6 (5.6%)	5 (3.2%)	5 (1.2%)	6 (0.9%)	28 (2.0%)
Other recombinant	2 (3.7%)	0 (0.0%)	0 (0.0%)	1 (0.9%)	2 (1.3%)	14 (3.4%)	22 (3.3%)	41 (2.9%)
Other Omicron	7 (13.0%)	0 (0.0%)	1 (25.0%)	19 (17.6%)	25 (16.2%)	69 (16.6%)	67 (10.0%)	188 (13.3%)
Total sequenced	**54 (100%)**	**5 (100%)**	**4 (100%)**	**108 (100%)**	**154 (100%)**	**416 (100%)**	**673 (100%)**	**1,414 (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 5. Number and percentage of SARS-CoV-2 cases by Pango lineage and geographic region, representative surveillance, Ontario, March 17 to April 13, 2024

Pango lineage	North West	North East	Eastern	Central East	Toronto	South West	Central West	Total
JN.1	18 (51.4%)	6 (11.3%)	144 (35.0%)	56 (16.1%)	39 (18.5%)	52 (40.3%)	64 (28.1%)	379 (26.8%)
JN.1.4	8 (22.9%)	13 (24.5%)	89 (21.6%)	80 (23.1%)	29 (13.7%)	18 (14.0%)	18 (7.9%)	255 (18.0%)
JN.1.11.1	0 (0.0%)	19 (35.8%)	50 (12.1%)	44 (12.7%)	21 (10.0%)	1 (0.8%)	6 (2.6%)	141 (10.0%)
JN.1.13.1	2 (5.7%)	1 (1.9%)	20 (4.9%)	43 (12.4%)	24 (11.4%)	20 (15.5%)	9 (3.9%)	119 (8.4%)
JN.1.7	3 (8.6%)	1 (1.9%)	18 (4.4%)	11 (3.2%)	13 (6.2%)	3 (2.3%)	19 (8.3%)	68 (4.8%)
KP.2	0 (0.0%)	0 (0.0%)	3 (0.7%)	24 (6.9%)	16 (7.6%)	3 (2.3%)	15 (6.6%)	61 (4.3%)
JN.1.8.1	2 (5.7%)	0 (0.0%)	31 (7.5%)	18 (5.2%)	4 (1.9%)	2 (1.6%)	1 (0.4%)	58 (4.1%)
JN.1.16	0 (0.0%)	2 (3.8%)	6 (1.5%)	17 (4.9%)	12 (5.7%)	3 (2.3%)	5 (2.2%)	45 (3.2%)
JN.1.2	0 (0.0%)	1 (1.9%)	3 (0.7%)	0 (0.0%)	3 (1.4%)	0 (0.0%)	24 (10.5%)	31 (2.2%)
KP.1.1	0 (0.0%)	1 (1.9%)	6 (1.5%)	7 (2.0%)	12 (5.7%)	0 (0.0%)	2 (0.9%)	28 (2.0%)
Other recombinant	2 (5.7%)	1 (1.9%)	2 (0.5%)	11 (3.2%)	6 (2.8%)	4 (3.1%)	15 (6.6%)	41 (2.9%)
Other Omicron	0 (0.0%)	8 (15.1%)	40 (9.7%)	36 (10.4%)	32 (15.2%)	23 (17.8%)	50 (21.9%)	189 (13.4%)
Total sequenced	**35 (100%)**	**53 (100%)**	**412 (100%)**	**347 (100%)**	**211 (100%)**	**129 (100%)**	**228 (100%)**	**1,415 (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. Geographic region was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (3.7%), 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, January 21 to April 13, 2024

Pango lineage	Deceased	Total cases
JN.1	40 (1.4%)	2,867 (100%)
JN.1.4	22 (1.6%)	1,383 (100%)
JN.1.11.1	6 (3.2%)	187 (100%)
JN.1.13.1	2 (1.4%)	138 (100%)
JN.1.7	2 (1.2%)	173 (100%)
KP.2	0 (0.0%)	95 (100%)
JN.1.8.1	2 (1.5%)	136 (100%)
JN.1.16	1 (2.0%)	50 (100%)
JN.1.2	2 (0.9%)	216 (100%)
KP.1.1	0 (0.0%)	27 (100%)
Other recombinant	9 (2.2%)	416 (100%)
Other Omicron	17 (1.5%)	1,104 (100%)
Total sequenced	**103 (1.5%)**	**6,792 (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, March 17 to April 13, 2024

WHO label / Pango lineage	March 17 - April 13, 2024
Omicron	**1,374**
BA.2.86.1	1
JN.1	379
JN.1.1	23
JN.1.11	3
JN.1.11.1	141
JN.1.13	1
JN.1.13.1	119
JN.1.16	45
JN.1.18	27
JN.1.19	15
JN.1.2	31
JN.1.20	2
JN.1.21	1
JN.1.22	24
JN.1.24	1
JN.1.4	255
JN.1.4.2	4
JN.1.4.3	1
JN.1.5	21
JN.1.6	2
JN.1.7	68
JN.1.7.2	11
JN.1.8	4
JN.1.8.1	58
JN.1.9	3
JN.2.1	1
JN.2.5	12
JQ.2	4
KP.1	12
KP.1.1	28
KP.2	61

WHO label / Pango lineage	March 17 - April 13, 2024
KQ.1	15
KR.1	1
Recombinant	**41**
EG.6.1	1
GJ.1.2	1
HV.1	4
HV.1.5	1
JD.1.1	1
JG.3.2	1
XDK	16
XDK.1	14
XDP	1
XDR	1
Total sequenced	**1,415**

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 April 26, 2024 at approximately 9:00 a.m.

Public Health Ontario (PHO)

- Data were submitted to the OHDP-PHAE on April 25, 2024 at approximately 9:15 a.m.

The Hospital for Sick Children (HSC)

- Data were submitted to the OHDP-PHAE on April 23, 2024 at approximately 10:45 a.m.

Kingston Health Sciences Centre (KHSC)

- Data were submitted to the OHDP-PHAE on April 23, 2024 at approximately 11:45 a.m.

Shared Hospital Laboratory (SHL)

- Data were submitted to the OHDP-PHAE on April 23, 2024 at approximately 3:30 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were submitted to the OHDP-PHAE on April 23, 2024 at approximately 4:00 p.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on April 23, 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 Ct≤ 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 1.26, pangolin assignment version 1.26, 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.

- Geographic region was assigned using diagnosing health unit in CCM. If the case did not link to CCM (3.7%), then public health unit was assigned using OCGN patient postal code or ordering provider postal code if patient postal code was missing.

- 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: 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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