Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, January 6, 2023

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of January 4, 2023 and partner laboratories in the Ontario COVID-19 Genomics Network as of January 3, 2023.

Background

The continued monitoring of global SARS-CoV-2 genomic data has identified changes in the 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. WGS has also identified a number of variants of interest (VOI), which may share one or more mutations in common with a VOC, but do not have sufficient evidence at this time to be categorized as a VOC (i.e. evidence of increased transmissibility, disease severity, or immune escape). These variants are also characterized and monitored through genomic surveillance. A VOI may be re-classified as a VOC where there is sufficient scientific evidence to support this designation. The VOC/VOI categories used in this report were derived from the Public Health Agency of Canada (PHAC)[1], the World Health Organization (WHO)[2], and the European Centre for Disease Prevention and Control (ECDC).[3]

As SARS-CoV-2 continues to evolve, lineages will naturally divide into descendant sub-lineages – 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.1 [alias for B.1.1.529.1], BA.5 [alias for B.1.1.529.5]), and BA.5 sublineages (e.g., BQ.1, BF.7). The designation of a descendant lineage does not necessarily imply a biological difference from the parent lineage. Rather, the new designation represents a refined genetic group that can be tracked separately. As more research is conducted, there may be evidence of a difference, at which time a new WHO Greek letter classification may be assigned to a newly emerged variant.

The Ontario COVID-19 Genomics Network (OCGN) performs WGS on samples received for SARS-CoV-2 diagnostic testing or VOC PCR testing. Sequences are processed using bioinformatics analyses and assigned a Pango lineage[4] using the pangolin tool[5], allowing for the identification of VOC, VOI and other lineages.

Highlights

- In the most recent week (December 18 to 24), BQ.1.1 was the most prevalent lineage (31.7%), followed by BQ.1 (10.6%), and BF.7 (3.8%). For this week, 16.0% of cases were other BQ lineages, 11.6% were other BA.5 lineages (excluding BQ and BF lineages), and 5.4% were other BF lineages.
- The proportion of BQ.1.1 increased from 28.0% (December 11 to 17) to 31.7% (December 18 to 24) and is projected to increase to 32.5% (95% CI: 28.1% - 37.2%) by January 11, 2023.
- The proportion of BQ.1 increased from 8.5% (December 11 to 17) to 10.6% (December 18 to 24) and is projected to decline to 5.7% (95% CI: 4.8% - 6.7%) by January 11, 2023.
- The proportion of XBB.1 (including XBB.1.5) remained stable at 2.2% (December 11 to 17) and 2.0% (December 18 to 24).

OCGN labs are in the process of updating Pango version and will be able to identify XBB.1.5 specifically in the next report.

Lineage counts may change between reports as the Pango lineage assignment models are updated.

As of December 31, 2021, diagnostic PCR testing was restricted to high-risk populations. Testing eligibility was expanded on April 11, 2022 to include additional high-risk groups (see technical notes for details). As such, representative surveillance only pertains to tested populations.

The OCGN moved from sequencing 75% to 100% of eligible samples on December 9, 2022.

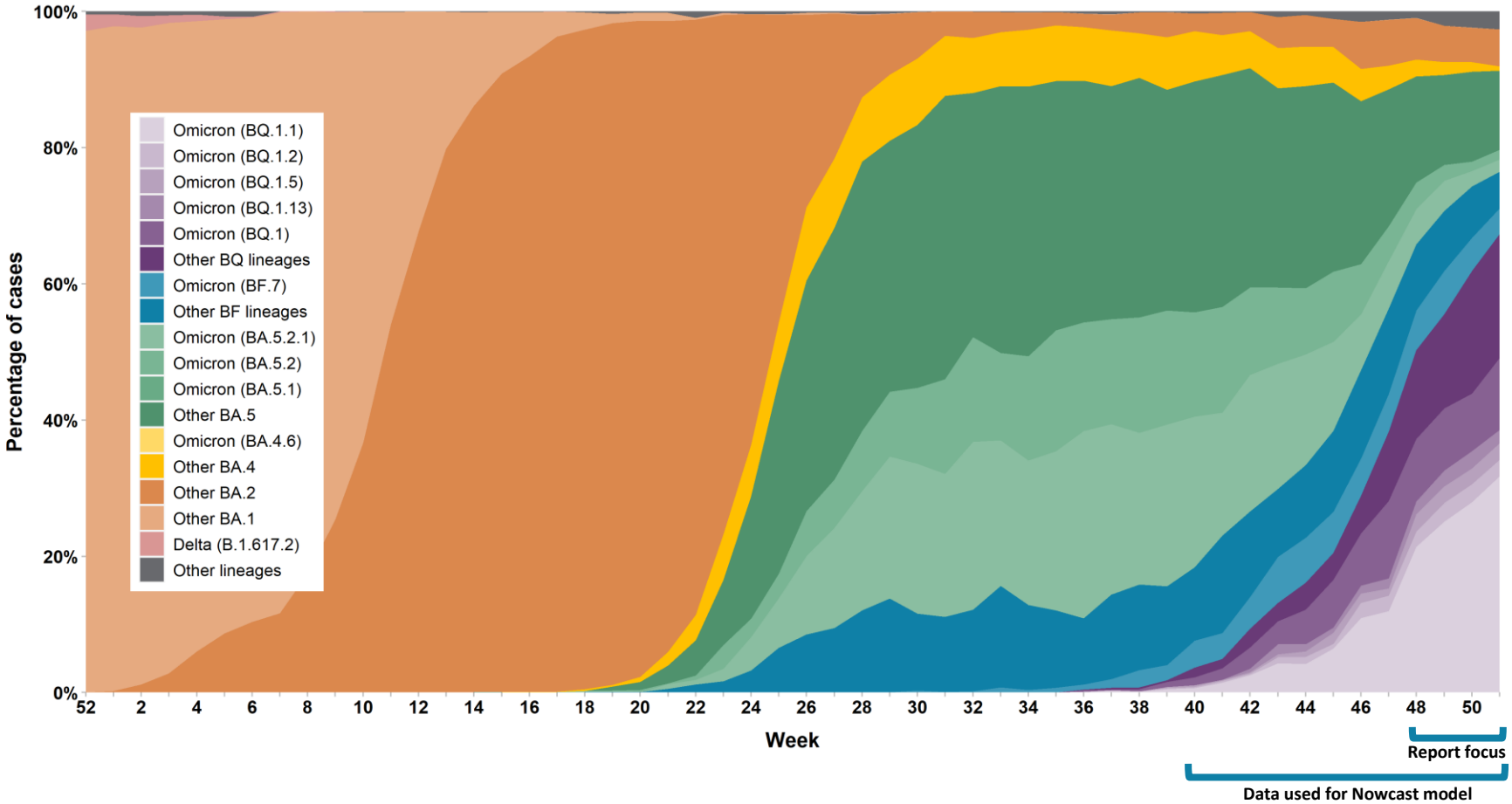
Representative Surveillance

Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, November 27 to December 24, 2022

Week	Number of cases	Number sequenced	Percentage sequenced
Week 48 (November 27 - December 3)	4,860	2,028	41.7%
Week 49 (December 4 - December 10)	5,271	2,559	48.5%
Week 50 (December 11 - December 17)	6,153	3,132	50.9%
Week 51 (December 18 - December 24)	6,035	2,670	44.2%
Total	**22,319**	**10,389**	**46.5%**

Note: 'Number of cases' is the number of confirmed positive cases of COVID-19 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, and do not include all samples tested for other reasons including travel, outbreak investigation, coroner's cases, reinfection or possible vaccine escape. '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. Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction and will be included in subsequent reports.
Data sources: CCM, PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Figure 1. Percentage of COVID-19 cases by the most prevalent lineages and week, representative surveillance, Ontario, December 26, 2021 to December 24, 2022



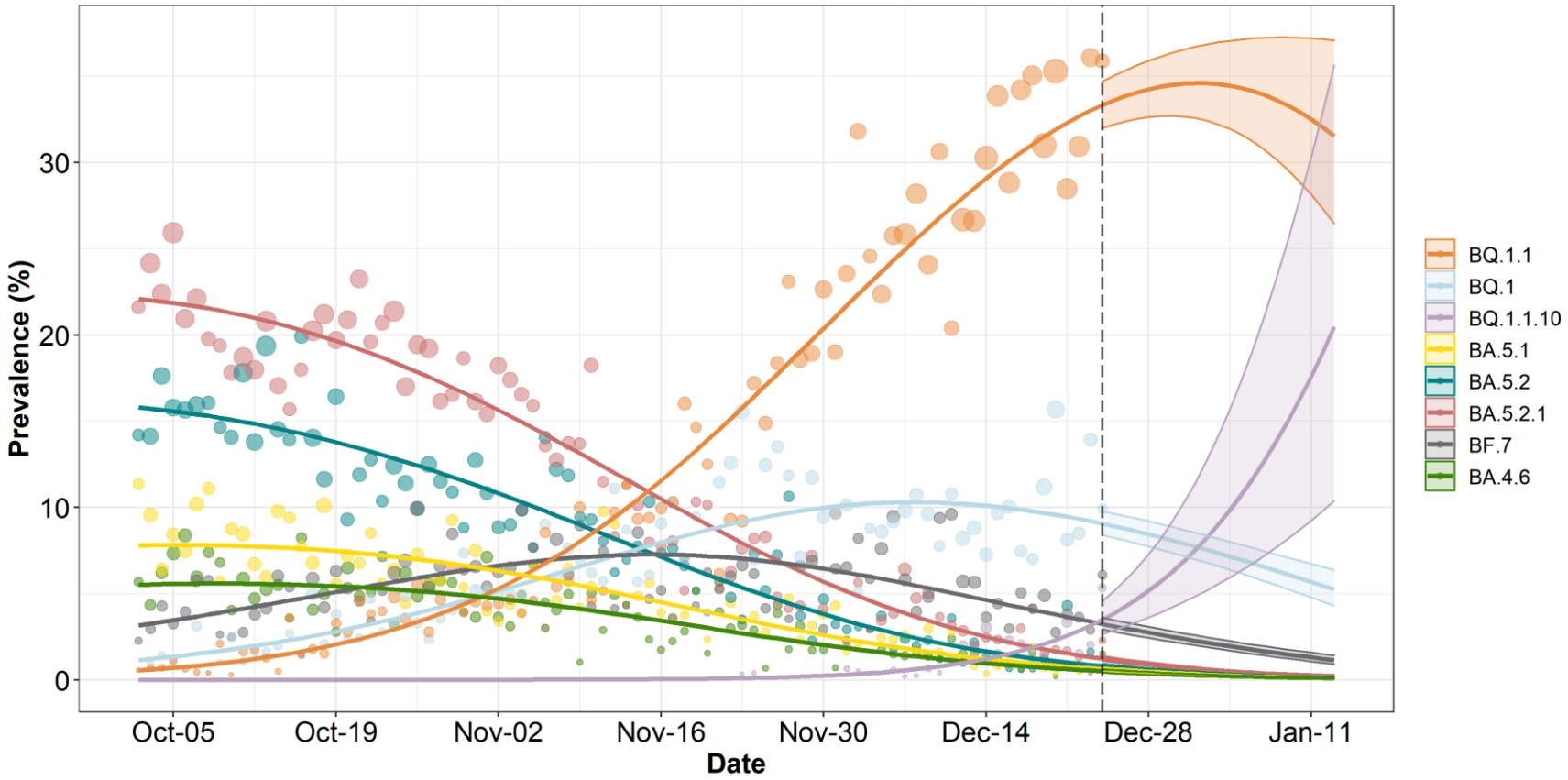
Note: Results may not be representative of Ontario overall, particularly in earlier weeks. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for a case, the most recent sample was included. Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction and will be included in subsequent reports.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 2. Number and percentage of cases by Pango lineage and week, representative surveillance, Ontario, November 27 to December 24, 2022

WHO label/Pango lineage	Week 48 (November 27 - December 3)	Week 49 (December 4 - December 10)	Week 50 (December 11- December 17)	Week 51 (December 18 - December 24)	Total (November 27- December 24)
Omicron	**2,009 (99.1%)**	**2,505 (97.9%)**	**3,058 (97.6%)**	**2,600 (97.4%)**	**10,172 (97.9%)**
BQ.1.1	434 (21.4%)	642 (25.1%)	876 (28.0%)	847 (31.7%)	2,799 (26.9%)
BQ.1	186 (9.2%)	234 (9.1%)	265 (8.5%)	282 (10.6%)	967 (9.3%)
BF.7	117 (5.8%)	162 (6.3%)	153 (4.9%)	101 (3.8%)	533 (5.1%)
BA.5.2.1	105 (5.2%)	114 (4.5%)	71 (2.3%)	47 (1.8%)	337 (3.2%)
BQ.1.2	45 (2.2%)	70 (2.7%)	82 (2.6%)	65 (2.4%)	262 (2.5%)
BQ.1.5	52 (2.6%)	63 (2.5%)	73 (2.3%)	65 (2.4%)	253 (2.4%)
BQ.1.13	38 (1.9%)	59 (2.3%)	79 (2.5%)	52 (1.9%)	228 (2.2%)
BA.5.2	79 (3.9%)	59 (2.3%)	43 (1.4%)	39 (1.5%)	220 (2.1%)
BQ.1.1.4	30 (1.5%)	43 (1.7%)	75 (2.4%)	60 (2.2%)	208 (2.0%)
Other BQ lineages	235 (11.6%)	311 (12.2%)	488 (15.6%)	426 (16.0%)	1,460 (14.1%)
Other BF lineages	197 (9.7%)	225 (8.8%)	236 (7.5%)	144 (5.4%)	802 (7.7%)
Other BA.5	319 (15.7%)	352 (13.8%)	419 (13.4%)	311 (11.6%)	1,401 (13.5%)
Other BA.4	51 (2.5%)	49 (1.9%)	44 (1.4%)	17 (0.6%)	161 (1.5%)
Other BA.2	120 (5.9%)	122 (4.8%)	153 (4.9%)	144 (5.4%)	539 (5.2%)
Other BA.1	1 (<0.1%)	0 (0.0%)	1 (<0.1%)	0 (0.0%)	2 (<0.1%)
Recombinant	**19 (0.9%)**	**54 (2.1%)**	**74 (2.4%)**	**70 (2.6%)**	**217 (2.1%)**
XBB.1	19 (0.9%)	42 (1.6%)	68 (2.2%)	54 (2.0%)	183 (1.8%)
Other recombinant	0 (0.0%)	12 (0.5%)	6 (0.2%)	16 (0.6%)	34 (0.3%)
Total sequenced	**2,028 (100%)**	**2,559 (100%)**	**3,132 (100%)**	**2,670 (100%)**	**10,389 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Figure 2. Estimated daily prevalence (%) by Pango lineage, using Nowcast model, Ontario, October 5, 2022 to January 14, 2023



Note: The prevalence projections for BQ.1.1.10 may be an overestimate due to two outbreaks (>15 cases) in week 50 (December 14) and because it is an emerging lineage. Each curve represents the estimated prevalence of a given lineage from Nowcast modelling, which uses 12 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. Only lineages with at least 14 days of non-zero case counts were included in the model. Figure includes all lineages with at least one day of an estimated prevalence of 5% or greater during the 18 week period (12 observed and 6 projected). Only three weeks of projected data are shown. Prevalence projections may be overestimated for emerging lineages.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 3. Estimated prevalence (%), projected prevalence (%), and weekly relative growth rate (with 95% confidence intervals) by Pango lineage, using Nowcast model, Ontario, October 5, 2022 to January 14, 2023

WHO label/ Pango lineage	Week 50 (December 14): Estimated	Week 51 (December 21): Estimated	Week 52 (December 28): Projected	Week 1 (January 4): Projected	Week 2 (January 11): Projected	Weekly relative growth rate
BQ.1.1	29.1 (28.2 - 30.0)	32.3 (31.1 - 33.5)	34.2 (32.6 - 35.9)	34.5 (31.9 - 37.1)	32.5 (28.1 - 37.2)	1.00 (reference)
BQ.1	10.1 (9.5 - 10.7)	9.5 (8.8 - 10.1)	8.4 (7.7 - 9.2)	7.2 (6.4 - 8.0)	5.7 (4.8 - 6.7)	0.84 (0.83 - 0.86)
BQ.1.1.10	1.2 (1.0 - 1.5)	2.6 (2.1 - 3.2)	5.2 (3.6 - 7.3)	9.9 (5.9 - 15.7)	17.6 (9.2 - 30.3)	1.89 (1.59 - 2.25)
BA.5.1	1.2 (1.1 - 1.4)	0.8 (0.7 - 0.9)	0.5 (0.4 - 0.6)	0.3 (0.2 - 0.3)	0.1 (0.1 - 0.2)	0.57 (0.56 - 0.59)
BA.5.2	1.6 (1.5 - 1.9)	1.0 (0.9 - 1.2)	0.6 (0.5 - 0.7)	0.3 (0.3 - 0.4)	0.2 (0.1 - 0.2)	0.55 (0.54 - 0.56)
BA.5.2.1	2.5 (2.3 - 2.8)	1.5 (1.4 - 1.7)	0.9 (0.8 - 1.0)	0.5 (0.4 - 0.6)	0.3 (0.2 - 0.3)	0.55 (0.54 - 0.57)
BF.7	4.6 (4.3 - 5.0)	3.7 (3.3 - 4.0)	2.7 (2.4 - 3.1)	2.0 (1.7 - 2.3)	1.3 (1.1 - 1.6)	0.71 (0.69 - 0.72)
BA.4.6	1.0 (0.8 - 1.1)	0.6 (0.5 - 0.7)	0.4 (0.3 - 0.5)	0.2 (0.2 - 0.3)	0.1 (0.1 - 0.2)	0.58 (0.56 - 0.59)

Note: The prevalence projections and growth rate for BQ.1.1.10 may be an overestimate due to two outbreaks (>15 cases) in week 50 (December 14) and because it is an emerging lineage. The Nowcast model uses 12 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 14 days of non-zero case counts were included in the model. Lineages that had at least one day with a prevalence of 5% or greater in the 18 week period (12 observed and 6 projected) were included in the table. Only 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: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 4. Number and percentage of cases by Pango lineage and age group, representative surveillance, Ontario, November 27 to December 24, 2022

WHO label/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
Omicron	**185 (96.4%)**	**38 (95.0%)**	**104 (98.1%)**	**2,050 (97.0%)**	**2,587 (97.2%)**	**2,383 (98.1%)**	**2,814 (99.2%)**	**10,161 (97.9%)**
BQ.1.1	52 (27.1%)	10 (25.0%)	35 (33.0%)	559 (26.5%)	696 (26.2%)	650 (26.8%)	795 (28.0%)	2,797 (27.0%)
BQ.1	17 (8.9%)	5 (12.5%)	5 (4.7%)	225 (10.6%)	271 (10.2%)	198 (8.2%)	245 (8.6%)	966 (9.3%)
BF.7	9 (4.7%)	0 (0.0%)	3 (2.8%)	95 (4.5%)	135 (5.1%)	134 (5.5%)	157 (5.5%)	533 (5.1%)
BA.5.2.1	9 (4.7%)	5 (12.5%)	1 (0.9%)	47 (2.2%)	75 (2.8%)	82 (3.4%)	118 (4.2%)	337 (3.2%)
BQ.1.2	5 (2.6%)	0 (0.0%)	5 (4.7%)	51 (2.4%)	85 (3.2%)	60 (2.5%)	56 (2.0%)	262 (2.5%)
BQ.1.5	8 (4.2%)	1 (2.5%)	5 (4.7%)	62 (2.9%)	61 (2.3%)	59 (2.4%)	57 (2.0%)	253 (2.4%)
BQ.1.13	2 (1.0%)	2 (5.0%)	1 (0.9%)	47 (2.2%)	58 (2.2%)	48 (2.0%)	69 (2.4%)	227 (2.2%)
BA.5.2	5 (2.6%)	0 (0.0%)	2 (1.9%)	27 (1.3%)	49 (1.8%)	55 (2.3%)	82 (2.9%)	220 (2.1%)
BQ.1.1.4	5 (2.6%)	1 (2.5%)	3 (2.8%)	53 (2.5%)	53 (2.0%)	47 (1.9%)	45 (1.6%)	207 (2.0%)
Other BQ lineages	24 (12.5%)	7 (17.5%)	13 (12.3%)	332 (15.7%)	410 (15.4%)	312 (12.9%)	359 (12.6%)	1,457 (14.0%)
Other BF lineages	7 (3.6%)	1 (2.5%)	8 (7.5%)	134 (6.3%)	177 (6.7%)	223 (9.2%)	252 (8.9%)	802 (7.7%)
Other BA.5	24 (12.5%)	4 (10.0%)	14 (13.2%)	279 (13.2%)	327 (12.3%)	359 (14.8%)	391 (13.8%)	1,398 (13.5%)
Other BA.4	7 (3.6%)	0 (0.0%)	3 (2.8%)	34 (1.6%)	40 (1.5%)	25 (1.0%)	52 (1.8%)	161 (1.6%)
Other BA.2	11 (5.7%)	2 (5.0%)	6 (5.7%)	105 (5.0%)	149 (5.6%)	130 (5.4%)	136 (4.8%)	539 (5.2%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (<0.1%)	1 (<0.1%)	0 (0.0%)	2 (<0.1%)
Recombinant	**7 (3.6%)**	**2 (5.0%)**	**2 (1.9%)**	**63 (3.0%)**	**74 (2.8%)**	**45 (1.9%)**	**24 (0.8%)**	**217 (2.1%)**
XBB.1	4 (2.1%)	2 (5.0%)	2 (1.9%)	55 (2.6%)	61 (2.3%)	38 (1.6%)	21 (0.7%)	183 (1.8%)
Other recombinant	3 (1.6%)	0 (0.0%)	0 (0.0%)	8 (0.4%)	13 (0.5%)	7 (0.3%)	3 (0.1%)	34 (0.3%)
Total sequenced	**192 (100%)**	**40 (100%)**	**106 (100%)**	**2,113 (100%)**	**2,661 (100%)**	**2,428 (100%)**	**2,838 (100%)**	**10,378 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 5. Percentage of BQ.1 cases (including all BQ.1 sub-lineages), number identified, and total sequenced by public health unit (PHU), region, and week, representative surveillance, Ontario, November 27 to December 24, 2022

Public Health Unit	Week 48 (November 27 - December 3)	Week 49 (December 4 - December 10)	Week 50 (December 11- December 17)	Week 51 (December 18 - December 24)	Total (November 27- December 24)
Northwestern Health Unit	40.0% (2/5)	16.7% (1/6)	28.6% (2/7)	0.0% (0/0)	27.8% (5/18)
Thunder Bay District Health Unit	31.0% (9/29)	8.7% (2/23)	76.2% (16/21)	100.0% (8/8)	43.2% (35/81)
TOTAL NORTH WEST	**32.4% (11/34)**	**10.3% (3/29)**	**64.3% (18/28)**	**100.0% (8/8)**	**40.4% (40/99)**
Algoma Public Health	20.0% (1/5)	14.3% (1/7)	38.5% (5/13)	37.5% (6/16)	31.7% (13/41)
North Bay Parry Sound District Health Unit	22.2% (2/9)	60.0% (6/10)	44.0% (11/25)	26.7% (4/15)	39% (23/59)
Porcupine Health Unit	53.8% (7/13)	42.9% (3/7)	71.4% (10/14)	60.0% (6/10)	59.1% (26/44)
Public Health Sudbury & Districts	38.5% (15/39)	48.0% (24/50)	47.9% (34/71)	54.2% (13/24)	46.7% (86/184)
Timiskaming Health Unit	0.0% (0/0)	100.0% (2/2)	0.0% (0/0)	100.0% (1/1)	100% (3/3)
TOTAL NORTH EAST	**37.9% (25/66)**	**47.4% (36/76)**	**48.8% (60/123)**	**45.5% (30/66)**	**45.6% (151/331)**
Ottawa Public Health	36.2% (34/94)	43.1% (75/174)	65.8% (129/196)	71.9% (156/217)	57.9% (394/681)
Eastern Ontario Health Unit	71.4% (30/42)	56.7% (17/30)	51.2% (22/43)	76.1% (51/67)	65.9% (120/182)
Hastings Prince Edward Public Health	30.4% (7/23)	31.0% (9/29)	40.9% (9/22)	67.7% (21/31)	43.8% (46/105)
Kingston, Frontenac and Lennox & Addington Public Health	45.9% (17/37)	54.8% (40/73)	62.8% (59/94)	74.5% (70/94)	62.4% (186/298)
Leeds, Grenville & Lanark District Health Unit	68.2% (30/44)	18.0% (11/61)	24.4% (22/90)	52.9% (27/51)	36.6% (90/246)
Renfrew County and District Health Unit	0.0% (0/7)	36.8% (7/19)	42.9% (3/7)	27.3% (3/11)	29.5% (13/44)
TOTAL EASTERN	**47.8% (118/247)**	**41.2% (159/386)**	**54.0% (244/452)**	**69.6% (328/471)**	**54.6% (849/1,556)**
Durham Region Health Department	45.7% (37/81)	52.4% (76/145)	65.2% (88/135)	66.9% (93/139)	58.8% (294/500)
Haliburton, Kawartha, Pine Ridge District Health Unit	64.0% (16/25)	38.9% (7/18)	72.9% (43/59)	60.7% (17/28)	63.8% (83/130)
Peel Public Health	57.9% (92/159)	64.2% (131/204)	68.1% (169/248)	71.2% (208/292)	66.4% (600/903)
Peterborough Public Health	18.2% (2/11)	40.0% (4/10)	64.7% (11/17)	50.0% (2/4)	45.2% (19/42)
Simcoe Muskoka District Health Unit	67.0% (71/106)	55.8% (63/113)	57.5% (77/134)	53.8% (50/93)	58.5% (261/446)
York Region Public Health	60.8% (104/171)	64.9% (113/174)	67.3% (150/223)	61.0% (125/205)	63.6% (492/773)
TOTAL CENTRAL EAST	**58.2% (322/553)**	**59.3% (394/664)**	**65.9% (538/816)**	**65.0% (495/761)**	**62.6% (1,749/2,794)**
Toronto Public Health	52.6% (281/534)	67.7% (441/651)	67.4% (541/803)	67.1% (466/694)	64.5% (1729/2682)
TOTAL TORONTO	**52.6% (281/534)**	**67.7% (441/651)**	**67.4% (541/803)**	**67.1% (466/694)**	**64.5% (1,729/2,682)**

Public Health Unit	Week 48 (November 27 - December 3)	Week 49 (December 4 - December 10)	Week 50 (December 11- December 17)	Week 51 (December 18 - December 24)	Total (November 27- December 24)
Chatham-Kent Public Health	15.0% (3/20)	61.0% (25/41)	60.0% (6/10)	33.3% (2/6)	46.8% (36/77)
Grey Bruce Health Unit	0.0% (0/8)	20.0% (2/10)	68.2% (15/22)	75.0% (24/32)	56.9% (41/72)
Huron Perth Public Health	15.0% (3/20)	35.0% (7/20)	57.9% (11/19)	91.7% (22/24)	51.8% (43/83)
Lambton Public Health	26.7% (8/30)	52.4% (11/21)	59.1% (13/22)	50.0% (5/10)	44.6% (37/83)
Middlesex-London Health Unit	39.4% (26/66)	67.3% (66/98)	61.8% (34/55)	59.7% (37/62)	58% (163/281)
Southwestern Public Health	60.7% (17/28)	38.5% (10/26)	65.9% (29/44)	54.3% (19/35)	56.4% (75/133)
Windsor-Essex County Health Unit	40.7% (22/54)	52.8% (38/72)	70.0% (35/50)	63.0% (29/46)	55.9% (124/222)
TOTAL SOUTH WEST	**35.0% (79/226)**	**55.2% (159/288)**	**64.4% (143/222)**	**64.2% (138/215)**	**54.6% (519/951)**
Brant County Health Unit	46.2% (6/13)	42.9% (6/14)	53.8% (7/13)	86.7% (13/15)	58.2% (32/55)
City of Hamilton Public Health Services	58.9% (56/95)	51.2% (62/121)	64.6% (128/198)	72.0% (85/118)	62.2% (331/532)
Haldimand-Norfolk Health Unit	40.0% (6/15)	66.7% (18/27)	66.7% (18/27)	87.9% (51/58)	73.2% (93/127)
Halton Region Public Health	68.8% (33/48)	50.5% (47/93)	57.5% (61/106)	79.7% (63/79)	62.6% (204/326)
Niagara Region Public Health	31.3% (21/67)	38.7% (29/75)	55.9% (100/179)	64.4% (65/101)	50.9% (215/422)
Region of Waterloo Public Health and Emergency Services	41.3% (43/104)	38.5% (37/96)	35.3% (42/119)	60.5% (26/43)	40.9% (148/362)
Wellington-Dufferin-Guelph Public Health	72.0% (18/25)	79.5% (31/39)	82.6% (38/46)	76.3% (29/38)	78.4% (116/148)
TOTAL CENTRAL WEST	**49.9% (183/367)**	**49.5% (230/465)**	**57.3% (394/688)**	**73.5% (332/452)**	**57.8% (1,139/1,972)**
UNKNOWN	**100.0% (1/1)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/3)**	**25% (1/4)**
TOTAL ONTARIO	**50.3% (1,020/2,028)**	**55.6% (1,422/2,559)**	**61.9% (1,938/3,132)**	**67.3% (1,797/2,670)**	**59.5% (6,177/10,389)**

Note: 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 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 6a. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North West Region, November 27 to December 24, 2022

WHO label / Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
Omicron	**18 (100%)**	**81 (100%)**	**99 (100%)**
BQ.1.1	1 (5.6%)	21 (25.9%)	22 (22.2%)
BQ.1	1 (5.6%)	9 (11.1%)	10 (10.1%)
BF.7	4 (22.2%)	1 (1.2%)	5 (5.1%)
BA.5.2.1	1 (5.6%)	16 (19.8%)	17 (17.2%)
BQ.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)
BQ.1.5	0 (0.0%)	0 (0.0%)	0 (0.0%)
BQ.1.13	0 (0.0%)	0 (0.0%)	0 (0.0%)
BA.5.2	0 (0.0%)	2 (2.5%)	2 (2.0%)
BQ.1.1.4	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BQ lineages	3 (16.7%)	5 (6.2%)	8 (8.1%)
Other BF lineages	8 (44.4%)	22 (27.2%)	30 (30.3%)
Other BA.5	0 (0.0%)	2 (2.5%)	2 (2.0%)
Other BA.4	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BA.2	0 (0.0%)	3 (3.7%)	3 (3.0%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other recombinant	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**18 (100%)**	**81 (100%)**	**99 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6b. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North East Region, November 27 to December 24, 2022

WHO label / Pango lineage	Algoma Public Health	North Bay Parry Sound District Health Unit	Porcupine Health Unit	Public Health Sudbury & Districts	Timiskaming Health Unit	Total
Omicron	**41 (100%)**	**59 (100%)**	**44 (100%)**	**182 (98.9%)**	**3 (100%)**	**329 (99.4%)**
BQ.1.1	11 (26.8%)	15 (25.4%)	14 (31.8%)	57 (31.0%)	2 (66.7%)	99 (29.9%)
BQ.1	2 (4.9%)	3 (5.1%)	6 (13.6%)	15 (8.2%)	0 (0.0%)	26 (7.9%)
BF.7	0 (0.0%)	3 (5.1%)	3 (6.8%)	1 (0.5%)	0 (0.0%)	7 (2.1%)
BA.5.2.1	1 (2.4%)	4 (6.8%)	2 (4.5%)	7 (3.8%)	0 (0.0%)	14 (4.2%)
BQ.1.2	0 (0.0%)	1 (1.7%)	2 (4.5%)	1 (0.5%)	0 (0.0%)	4 (1.2%)
BQ.1.5	0 (0.0%)	1 (1.7%)	2 (4.5%)	1 (0.5%)	0 (0.0%)	4 (1.2%)
BQ.1.13	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (2.2%)	0 (0.0%)	4 (1.2%)
BA.5.2	2 (4.9%)	0 (0.0%)	1 (2.3%)	4 (2.2%)	0 (0.0%)	7 (2.1%)
BQ.1.1.4	0 (0.0%)	0 (0.0%)	1 (2.3%)	1 (0.5%)	0 (0.0%)	2 (0.6%)
Other BQ lineages	0 (0.0%)	3 (5.1%)	1 (2.3%)	7 (3.8%)	1 (33.3%)	12 (3.6%)
Other BF lineages	20 (48.8%)	2 (3.4%)	4 (9.1%)	48 (26.1%)	0 (0.0%)	74 (22.4%)
Other BA.5	4 (9.8%)	4 (6.8%)	7 (15.9%)	15 (8.2%)	0 (0.0%)	30 (9.1%)
Other BA.4	1 (2.4%)	3 (5.1%)	1 (2.3%)	18 (9.8%)	0 (0.0%)	23 (6.9%)
Other BA.2	0 (0.0%)	20 (33.9%)	0 (0.0%)	3 (1.6%)	0 (0.0%)	23 (6.9%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**2 (1.1%)**	**0 (0.0%)**	**2 (0.6%)**
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.1%)	0 (0.0%)	2 (0.6%)
Other recombinant	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**41 (100%)**	**59 (100%)**	**44 (100%)**	**184 (100%)**	**3 (100%)**	**331 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6c. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Eastern Region, November 27 to December 24, 2022

WHO label / 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
Omicron	**182 (100%)**	**103 (98.1%)**	**292 (98.0%)**	**242 (98.4%)**	**673 (98.8%)**	**42 (95.5%)**	**1,534 (98.6%)**
BQ.1.1	24 (13.2%)	17 (16.2%)	64 (21.5%)	36 (14.6%)	154 (22.6%)	9 (20.5%)	304 (19.5%)
BQ.1	24 (13.2%)	11 (10.5%)	47 (15.8%)	11 (4.5%)	36 (5.3%)	0 (0.0%)	129 (8.3%)
BF.7	4 (2.2%)	6 (5.7%)	20 (6.7%)	77 (31.3%)	142 (20.9%)	8 (18.2%)	257 (16.5%)
BA.5.2.1	1 (0.5%)	8 (7.6%)	7 (2.3%)	15 (6.1%)	12 (1.8%)	7 (15.9%)	50 (3.2%)
BQ.1.2	0 (0.0%)	6 (5.7%)	7 (2.3%)	4 (1.6%)	11 (1.6%)	0 (0.0%)	28 (1.8%)
BQ.1.5	0 (0.0%)	0 (0.0%)	2 (0.7%)	1 (0.4%)	5 (0.7%)	0 (0.0%)	8 (0.5%)
BQ.1.13	10 (5.5%)	1 (1.0%)	7 (2.3%)	0 (0.0%)	14 (2.1%)	0 (0.0%)	32 (2.1%)
BA.5.2	19 (10.4%)	1 (1.0%)	7 (2.3%)	2 (0.8%)	7 (1.0%)	0 (0.0%)	36 (2.3%)
BQ.1.1.4	2 (1.1%)	0 (0.0%)	3 (1.0%)	3 (1.2%)	7 (1.0%)	0 (0.0%)	15 (1.0%)
Other BQ lineages	60 (33.0%)	11 (10.5%)	56 (18.8%)	35 (14.2%)	167 (24.5%)	4 (9.1%)	333 (21.4%)
Other BF lineages	0 (0.0%)	3 (2.9%)	8 (2.7%)	4 (1.6%)	10 (1.5%)	3 (6.8%)	28 (1.8%)
Other BA.5	32 (17.6%)	35 (33.3%)	46 (15.4%)	41 (16.7%)	85 (12.5%)	8 (18.2%)	247 (15.9%)
Other BA.4	5 (2.7%)	0 (0.0%)	9 (3.0%)	3 (1.2%)	10 (1.5%)	3 (6.8%)	30 (1.9%)
Other BA.2	1 (0.5%)	4 (3.8%)	9 (3.0%)	10 (4.1%)	13 (1.9%)	0 (0.0%)	37 (2.4%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**0 (0.0%)**	**2 (1.9%)**	**6 (2.0%)**	**4 (1.6%)**	**8 (1.2%)**	**2 (4.5%)**	**22 (1.4%)**
XBB.1	0 (0.0%)	1 (1.0%)	6 (2.0%)	2 (0.8%)	8 (1.2%)	2 (4.5%)	19 (1.2%)
Other recombinant	0 (0.0%)	1 (1.0%)	0 (0.0%)	2 (0.8%)	0 (0.0%)	0 (0.0%)	3 (0.2%)
Total sequenced	**182 (100%)**	**105 (100%)**	**298 (100%)**	**246 (100%)**	**681 (100%)**	**44 (100%)**	**1,556 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6d. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central East Region, November 27 to December 24, 2022

WHO label / 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
Omicron	**490 (98.0%)**	**127 (97.7%)**	**879 (97.3%)**	**41 (97.6%)**	**439 (98.4%)**	**756 (97.8%)**	**2,732 (97.8%)**
BQ.1.1	118 (23.6%)	52 (40.0%)	313 (34.7%)	5 (11.9%)	134 (30.0%)	253 (32.7%)	875 (31.3%)
BQ.1	66 (13.2%)	10 (7.7%)	86 (9.5%)	9 (21.4%)	42 (9.4%)	43 (5.6%)	256 (9.2%)
BF.7	25 (5.0%)	2 (1.5%)	17 (1.9%)	1 (2.4%)	13 (2.9%)	12 (1.6%)	70 (2.5%)
BA.5.2.1	22 (4.4%)	7 (5.4%)	22 (2.4%)	10 (23.8%)	28 (6.3%)	32 (4.1%)	121 (4.3%)
BQ.1.2	11 (2.2%)	0 (0.0%)	29 (3.2%)	0 (0.0%)	8 (1.8%)	16 (2.1%)	64 (2.3%)
BQ.1.5	22 (4.4%)	2 (1.5%)	6 (0.7%)	0 (0.0%)	12 (2.7%)	28 (3.6%)	70 (2.5%)
BQ.1.13	6 (1.2%)	1 (0.8%)	19 (2.1%)	0 (0.0%)	11 (2.5%)	36 (4.7%)	73 (2.6%)
BA.5.2	15 (3.0%)	0 (0.0%)	11 (1.2%)	2 (4.8%)	3 (0.7%)	20 (2.6%)	51 (1.8%)
BQ.1.1.4	7 (1.4%)	2 (1.5%)	14 (1.6%)	0 (0.0%)	5 (1.1%)	17 (2.2%)	45 (1.6%)
Other BQ lineages	64 (12.8%)	16 (12.3%)	133 (14.7%)	5 (11.9%)	49 (11.0%)	99 (12.8%)	366 (13.1%)
Other BF lineages	45 (9.0%)	9 (6.9%)	57 (6.3%)	1 (2.4%)	51 (11.4%)	31 (4.0%)	194 (6.9%)
Other BA.5	61 (12.2%)	24 (18.5%)	99 (11.0%)	6 (14.3%)	49 (11.0%)	123 (15.9%)	362 (13.0%)
Other BA.4	5 (1.0%)	2 (1.5%)	4 (0.4%)	2 (4.8%)	4 (0.9%)	5 (0.6%)	22 (0.8%)
Other BA.2	23 (4.6%)	0 (0.0%)	69 (7.6%)	0 (0.0%)	30 (6.7%)	41 (5.3%)	163 (5.8%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**10 (2.0%)**	**3 (2.3%)**	**24 (2.7%)**	**1 (2.4%)**	**7 (1.6%)**	**17 (2.2%)**	**62 (2.2%)**
XBB.1	7 (1.4%)	3 (2.3%)	16 (1.8%)	1 (2.4%)	6 (1.3%)	15 (1.9%)	48 (1.7%)
Other recombinant	3 (0.6%)	0 (0.0%)	8 (0.9%)	0 (0.0%)	1 (0.2%)	2 (0.3%)	14 (0.5%)
Total sequenced	**500 (100%)**	**130 (100%)**	**903 (100%)**	**42 (100%)**	**446 (100%)**	**773 (100%)**	**2,794 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6e. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Toronto Region, November 27 to December 24, 2022

WHO label / Pango lineage	Toronto Public Health	Total
Omicron	**2,612 (97.4%)**	**2,612 (97.4%)**
BQ.1.1	699 (26.1%)	699 (26.1%)
BQ.1	303 (11.3%)	303 (11.3%)
BF.7	66 (2.5%)	66 (2.5%)
BA.5.2.1	58 (2.2%)	58 (2.2%)
BQ.1.2	91 (3.4%)	91 (3.4%)
BQ.1.5	98 (3.7%)	98 (3.7%)
BQ.1.13	84 (3.1%)	84 (3.1%)
BA.5.2	40 (1.5%)	40 (1.5%)
BQ.1.1.4	76 (2.8%)	76 (2.8%)
Other BQ lineages	378 (14.1%)	378 (14.1%)
Other BF lineages	207 (7.7%)	207 (7.7%)
Other BA.5	337 (12.6%)	337 (12.6%)
Other BA.4	15 (0.6%)	15 (0.6%)
Other BA.2	159 (5.9%)	159 (5.9%)
Other BA.1	1 (<0.1%)	1 (<0.1%)
Recombinant	**70 (2.6%)**	**70 (2.6%)**
XBB.1	62 (2.3%)	62 (2.3%)
Other recombinant	8 (0.3%)	8 (0.3%)
Total sequenced	**2,682 (100%)**	**2,682 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6f. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, South West Region, November 27 to December 24, 2022

WHO label / 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
Omicron	**77 (100%)**	**72 (100%)**	**83 (100%)**	**83 (100%)**	**278 (98.9%)**	**127 (95.5%)**	**222 (100%)**	**942 (99.1%)**
BQ.1.1	24 (31.2%)	9 (12.5%)	9 (10.8%)	22 (26.5%)	113 (40.2%)	47 (35.3%)	63 (28.4%)	287 (30.2%)
BQ.1	2 (2.6%)	4 (5.6%)	19 (22.9%)	4 (4.8%)	12 (4.3%)	6 (4.5%)	7 (3.2%)	54 (5.7%)
BF.7	3 (3.9%)	7 (9.7%)	1 (1.2%)	19 (22.9%)	11 (3.9%)	5 (3.8%)	2 (0.9%)	48 (5.0%)
BA.5.2.1	1 (1.3%)	2 (2.8%)	1 (1.2%)	4 (4.8%)	8 (2.8%)	2 (1.5%)	7 (3.2%)	25 (2.6%)
BQ.1.2	0 (0.0%)	2 (2.8%)	2 (2.4%)	1 (1.2%)	4 (1.4%)	1 (0.8%)	4 (1.8%)	14 (1.5%)
BQ.1.5	2 (2.6%)	23 (31.9%)	1 (1.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	15 (6.8%)	41 (4.3%)
BQ.1.13	2 (2.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (1.1%)	2 (1.5%)	6 (2.7%)	13 (1.4%)
BA.5.2	2 (2.6%)	8 (11.1%)	2 (2.4%)	4 (4.8%)	8 (2.8%)	3 (2.3%)	5 (2.3%)	32 (3.4%)
BQ.1.1.4	1 (1.3%)	1 (1.4%)	2 (2.4%)	2 (2.4%)	12 (4.3%)	10 (7.5%)	3 (1.4%)	31 (3.3%)
Other BQ lineages	5 (6.5%)	2 (2.8%)	10 (12.0%)	8 (9.6%)	19 (6.8%)	9 (6.8%)	26 (11.7%)	79 (8.3%)
Other BF lineages	12 (15.6%)	5 (6.9%)	16 (19.3%)	8 (9.6%)	21 (7.5%)	7 (5.3%)	27 (12.2%)	96 (10.1%)
Other BA.5	19 (24.7%)	7 (9.7%)	18 (21.7%)	10 (12.0%)	35 (12.5%)	21 (15.8%)	18 (8.1%)	128 (13.5%)
Other BA.4	4 (5.2%)	0 (0.0%)	1 (1.2%)	1 (1.2%)	20 (7.1%)	1 (0.8%)	13 (5.9%)	40 (4.2%)
Other BA.2	0 (0.0%)	2 (2.8%)	1 (1.2%)	0 (0.0%)	12 (4.3%)	13 (9.8%)	26 (11.7%)	54 (5.7%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**3 (1.1%)**	**6 (4.5%)**	**0 (0.0%)**	**9 (0.9%)**
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.4%)	5 (3.8%)	0 (0.0%)	6 (0.6%)
Other recombinant	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (0.7%)	1 (0.8%)	0 (0.0%)	3 (0.3%)
Total sequenced	**77 (100%)**	**72 (100%)**	**83 (100%)**	**83 (100%)**	**281 (100%)**	**133 (100%)**	**222 (100%)**	**951 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6g. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central West Region, November 27 to December 24, 2022

WHO label / 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
Omicron	**53 (96.4%)**	**518 (97.4%)**	**120 (94.5%)**	**315 (96.6%)**	**410 (97.2%)**	**358 (98.9%)**	**146 (98.6%)**	**1,920 (97.4%)**
BQ.1.1	10 (18.2%)	124 (23.3%)	66 (52.0%)	98 (30.1%)	110 (26.1%)	56 (15.5%)	49 (33.1%)	513 (26.0%)
BQ.1	1 (1.8%)	24 (4.5%)	4 (3.1%)	50 (15.3%)	39 (9.2%)	44 (12.2%)	26 (17.6%)	188 (9.5%)
BF.7	5 (9.1%)	15 (2.8%)	2 (1.6%)	5 (1.5%)	14 (3.3%)	36 (9.9%)	3 (2.0%)	80 (4.1%)
BA.5.2.1	0 (0.0%)	16 (3.0%)	4 (3.1%)	14 (4.3%)	12 (2.8%)	5 (1.4%)	1 (0.7%)	52 (2.6%)
BQ.1.2	2 (3.6%)	25 (4.7%)	1 (0.8%)	15 (4.6%)	5 (1.2%)	6 (1.7%)	7 (4.7%)	61 (3.1%)
BQ.1.5	2 (3.6%)	9 (1.7%)	0 (0.0%)	2 (0.6%)	14 (3.3%)	5 (1.4%)	0 (0.0%)	32 (1.6%)
BQ.1.13	3 (5.5%)	8 (1.5%)	1 (0.8%)	2 (0.6%)	6 (1.4%)	0 (0.0%)	2 (1.4%)	22 (1.1%)
BA.5.2	4 (7.3%)	24 (4.5%)	1 (0.8%)	6 (1.8%)	3 (0.7%)	13 (3.6%)	1 (0.7%)	52 (2.6%)
BQ.1.1.4	0 (0.0%)	16 (3.0%)	4 (3.1%)	8 (2.5%)	4 (0.9%)	5 (1.4%)	2 (1.4%)	39 (2.0%)
Other BQ lineages	14 (25.5%)	125 (23.5%)	17 (13.4%)	29 (8.9%)	37 (8.8%)	32 (8.8%)	30 (20.3%)	284 (14.4%)
Other BF lineages	4 (7.3%)	47 (8.8%)	4 (3.1%)	25 (7.7%)	57 (13.5%)	30 (8.3%)	5 (3.4%)	172 (8.7%)
Other BA.5	7 (12.7%)	61 (11.5%)	11 (8.7%)	40 (12.3%)	89 (21.1%)	73 (20.2%)	12 (8.1%)	293 (14.9%)
Other BA.4	0 (0.0%)	5 (0.9%)	2 (1.6%)	4 (1.2%)	8 (1.9%)	12 (3.3%)	0 (0.0%)	31 (1.6%)
Other BA.2	1 (1.8%)	18 (3.4%)	3 (2.4%)	17 (5.2%)	12 (2.8%)	41 (11.3%)	8 (5.4%)	100 (5.1%)
Other BA.1	0 (0.0%)	1 (0.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.1%)
Recombinant	**2 (3.6%)**	**14 (2.6%)**	**7 (5.5%)**	**11 (3.4%)**	**12 (2.8%)**	**4 (1.1%)**	**2 (1.4%)**	**52 (2.6%)**
XBB.1	2 (3.6%)	12 (2.3%)	5 (3.9%)	10 (3.1%)	12 (2.8%)	3 (0.8%)	2 (1.4%)	46 (2.3%)
Other recombinant	0 (0.0%)	2 (0.4%)	2 (1.6%)	1 (0.3%)	0 (0.0%)	1 (0.3%)	0 (0.0%)	6 (0.3%)
Total sequenced	**55 (100%)**	**532 (100%)**	**127 (100%)**	**326 (100%)**	**422 (100%)**	**362 (100%)**	**148 (100%)**	**1,972 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. 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 recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 7. Number and percentage (row %) of outbreak-associated and non outbreak-associated cases by Pango lineage, representative surveillance, Ontario, November 27 to December 24, 2022

WHO label / Pango lineage	Outbreak-associated	Non outbreak-associated	Total cases
Omicron	**3,457 (35.0%)**	**6,430 (65.0%)**	**9,887 (100%)**
BQ.1.1	1,026 (37.8%)	1,688 (62.2%)	2,714 (100%)
BQ.1	309 (32.9%)	630 (67.1%)	939 (100%)
BF.7	212 (40.8%)	307 (59.2%)	519 (100%)
BA.5.2.1	139 (42.1%)	191 (57.9%)	330 (100%)
BQ.1.2	55 (21.7%)	199 (78.3%)	254 (100%)
BQ.1.5	66 (26.9%)	179 (73.1%)	245 (100%)
BQ.1.13	84 (38.7%)	133 (61.3%)	217 (100%)
BA.5.2	96 (45.3%)	116 (54.7%)	212 (100%)
BQ.1.1.4	24 (11.7%)	182 (88.3%)	206 (100%)
Other BQ lineages	465 (32.8%)	952 (67.2%)	1,417 (100%)
Other BF lineages	322 (41.0%)	464 (59.0%)	786 (100%)
Other BA.5	454 (33.3%)	910 (66.7%)	1,364 (100%)
Other BA.4	54 (34.2%)	104 (65.8%)	158 (100%)
Other BA.2	150 (28.6%)	374 (71.4%)	524 (100%)
Other BA.1	1 (50.0%)	1 (50.0%)	2 (100%)
Recombinant	**16 (7.8%)**	**190 (92.2%)**	**206 (100%)**
XBB.1	15 (8.5%)	161 (91.5%)	176 (100%)
Other recombinant	1 (3.3%)	29 (96.7%)	30 (100%)
Total sequenced	**3,473 (34.4%)**	**6,620 (65.6%)**	**10,093 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. Cases include only those that linked to CCM (97.2%). 'Outbreak-associated cases' include cases linked to a confirmed outbreak as declared by the local medical officer of health or their designate. 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 recent weeks were complete at the time of data extraction.

Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Hamilton Regional Laboratory Medicine Program, The Shared Hospital Laboratory, CCM (outbreak Indicator)

Table 8. Number and percentage (row %) of cases admitted to hospital and deceased cases by Pango lineage, representative surveillance, Ontario, November 27 to December 24, 2022

WHO label / Pango lineage	Hospital admissions	Deceased	Total cases
Omicron	**534 (5.4%)**	**80 (0.8%)**	**9,887 (100%)**
BQ.1.1	129 (4.8%)	24 (0.9%)	2,714 (100%)
BQ.1	48 (5.1%)	9 (1.0%)	939 (100%)
BF.7	23 (4.4%)	8 (1.5%)	519 (100%)
BA.5.2.1	26 (7.9%)	2 (0.6%)	330 (100%)
BQ.1.2	16 (6.3%)	1 (0.4%)	254 (100%)
BQ.1.5	8 (3.3%)	1 (0.4%)	245 (100%)
BQ.1.13	10 (4.6%)	2 (0.9%)	217 (100%)
BA.5.2	13 (6.1%)	4 (1.9%)	212 (100%)
BQ.1.1.4	13 (6.3%)	1 (0.5%)	206 (100%)
Other BQ lineages	65 (4.6%)	8 (0.6%)	1,417 (100%)
Other BF lineages	43 (5.5%)	5 (0.6%)	786 (100%)
Other BA.5	95 (7.0%)	14 (1.0%)	1,364 (100%)
Other BA.4	4 (2.5%)	0 (0.0%)	158 (100%)
Other BA.2	41 (7.8%)	1 (0.2%)	524 (100%)
Other BA.1	0 (0.0%)	0 (0.0%)	2 (100%)
Recombinant	**6 (2.9%)**	**0 (0.0%)**	**206 (100%)**
XBB.1	5 (2.8%)	0 (0.0%)	176 (100%)
Other recombinant	1 (3.3%)	0 (0.0%)	30 (100%)
Total sequenced	**540 (5.4%)**	**80 (0.8%)**	**10,093 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. Cases include only those that linked to CCM (97.2%). Hospital admissions include all cases admitted to hospital (or had their hospital stay extended) because of COVID-19 at time of data extraction. 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 COVID-19 hospital admission and 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 recent weeks were complete at the time of data extraction.

Data Sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Hamilton Regional Laboratory Medicine Program, The Shared Hospital Laboratory, CCM (hospital admission and death indicators)

Table 9. Number and percentage (row %) of cases by vaccine category and Pango lineage, representative surveillance, Ontario, November 27 to December 24, 2022

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two or more booster doses	Total cases
Omicron	**2,646 (26.8%)**	**62 (0.6%)**	**873 (8.8%)**	**2,594 (26.2%)**	**3,707 (37.5%)**	**9,882 (100%)**
BQ.1.1	761 (28.0%)	13 (0.5%)	235 (8.7%)	690 (25.4%)	1,015 (37.4%)	2,714 (100%)
BQ.1	288 (30.7%)	9 (1.0%)	81 (8.6%)	253 (26.9%)	308 (32.8%)	939 (100%)
BF.7	104 (20.1%)	3 (0.6%)	50 (9.7%)	156 (30.1%)	205 (39.6%)	518 (100%)
BA.5.2.1	65 (19.7%)	5 (1.5%)	29 (8.8%)	81 (24.5%)	150 (45.5%)	330 (100%)
BQ.1.2	86 (33.9%)	1 (0.4%)	20 (7.9%)	72 (28.3%)	75 (29.5%)	254 (100%)
BQ.1.5	75 (30.6%)	2 (0.8%)	20 (8.2%)	61 (24.9%)	87 (35.5%)	245 (100%)
BQ.1.13	58 (26.7%)	0 (0.0%)	17 (7.8%)	60 (27.6%)	82 (37.8%)	217 (100%)
BA.5.2	37 (17.5%)	0 (0.0%)	28 (13.2%)	49 (23.1%)	98 (46.2%)	212 (100%)
BQ.1.1.4	63 (30.6%)	0 (0.0%)	19 (9.2%)	62 (30.1%)	62 (30.1%)	206 (100%)
Other BQ lineages	428 (30.2%)	7 (0.5%)	123 (8.7%)	353 (24.9%)	504 (35.6%)	1,415 (100%)
Other BF lineages	180 (22.9%)	5 (0.6%)	70 (8.9%)	220 (28.0%)	311 (39.6%)	786 (100%)
Other BA.5	319 (23.4%)	11 (0.8%)	119 (8.7%)	361 (26.5%)	554 (40.6%)	1,364 (100%)
Other BA.4	42 (26.6%)	1 (0.6%)	14 (8.9%)	38 (24.1%)	63 (39.9%)	158 (100%)
Other BA.2	138 (26.4%)	5 (1.0%)	48 (9.2%)	138 (26.4%)	193 (37.0%)	522 (100%)
Other BA.1	2 (100%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (100%)
Recombinant	**76 (36.9%)**	**1 (0.5%)**	**15 (7.3%)**	**51 (24.8%)**	**63 (30.6%)**	**206 (100%)**
XBB.1	66 (37.5%)	1 (0.6%)	14 (8.0%)	42 (23.9%)	53 (30.1%)	176 (100%)
Other recombinant	10 (33.3%)	0 (0.0%)	1 (3.3%)	9 (30.0%)	10 (33.3%)	30 (100%)
Total sequenced	**2,722 (27.0%)**	**63 (0.6%)**	**888 (8.8%)**	**2,645 (26.2%)**	**3,770 (37.4%)**	**10,088 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Cases include those that linked to CCM (97.2%). Individuals with a vaccine not approved by Health Canada were excluded. Vaccine category definitions can be found in the Confirmed Cases of COVID-19 Following Vaccination in Ontario report. A higher proportion of cases reported among more vaccinated cases is a reflection of both trends in vaccine administration (increasing number of doses administered over time) and trends in COVID-19 incidence. 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 recent weeks were complete at the time of data extraction.

Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Hamilton Regional Laboratory Medicine Program, Shared Hospital Laboratory, CCM, COVaxON

Cumulative Whole Genome Sequencing Results

Table 10. Number of cases by Pango lineage, cumulative counts, Ontario, January 1, 2021 to December 24, 2022

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
Variant of Concern (VOC)			
Alpha	**11,771**	**0**	**11,771**
Beta	**1,224**	**0**	**1,224**
Gamma	**3,918**	**0**	**3,918**
Delta	**45,947**	**0**	**45,947**
Omicron	**122,944**	**11,112**	**134,056**
B.1.1.529	0	0	0
BA.1	6,345	0	6,345
BA.1.1	18,757	1	18,758
BA.1.1.1	44	0	44
BA.1.1.10	1,676	0	1,676
BA.1.1.13	4	0	4
BA.1.1.14	514	0	514
BA.1.1.15	3	0	3
BA.1.1.16	111	0	111
BA.1.1.17	6	0	6
BA.1.1.18	130	0	130
BA.1.1.2	8	0	8
BA.1.1.5	1	0	1
BA.1.1.6	3	0	3
BA.1.1.7	6	0	6
BA.1.1.8	3	0	3
BA.1.1.9	5	0	5
BA.1.12	2	0	2
BA.1.13	34	0	34
BA.1.13.1	1	0	1
BA.1.14	70	0	70
BA.1.14.1	1	0	1
BA.1.14.2	1	0	1
BA.1.15	1,638	1	1,639
BA.1.15.1	22	0	22
BA.1.15.2	3	0	3
BA.1.16	2	0	2

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BA.1.17	715	0	715
BA.1.17.2	1,521	0	1,521
BA.1.18	92	0	92
BA.1.19	24	0	24
BA.1.20	91	0	91
BA.1.21	5	0	5
BA.1.3	1	0	1
BA.1.4	1	0	1
BA.1.6	66	0	66
BA.1.7	2	0	2
BA.1.9	25	0	25
BA.2	15,427	2	15,429
BA.2.1	122	0	122
BA.2.10	390	0	390
BA.2.10.1	34	20	54
BA.2.10.3	1	0	1
BA.2.11	7	0	7
BA.2.12	63	0	63
BA.2.12.1	6,468	2	6,470
BA.2.12.2	2	0	2
BA.2.13	26	0	26
BA.2.13.1	45	0	45
BA.2.15	1	0	1
BA.2.16	11	0	11
BA.2.17	25	0	25
BA.2.18	70	0	70
BA.2.2	4	0	4
BA.2.20	1,678	0	1,678
BA.2.21	328	0	328
BA.2.22	5	0	5
BA.2.23	51	0	51
BA.2.24	29	0	29
BA.2.25	1	0	1
BA.2.26	8	0	8
BA.2.27	2	0	2
BA.2.29	2	0	2
BA.2.3	2,371	0	2,371
BA.2.3.10	79	0	79
BA.2.3.12	3	0	3
BA.2.3.14	2	0	2

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BA.2.3.15	1	0	1
BA.2.3.16	4	0	4
BA.2.3.17	3	0	3
BA.2.3.2	19	0	19
BA.2.3.20	93	76	169
BA.2.3.4	952	0	952
BA.2.3.5	1	0	1
BA.2.3.6	79	0	79
BA.2.3.7	3	0	3
BA.2.3.8	2	0	2
BA.2.31	18	0	18
BA.2.31.1	3	0	3
BA.2.32	4	0	4
BA.2.33	1	0	1
BA.2.34	1	0	1
BA.2.35	5	0	5
BA.2.36	26	0	26
BA.2.37	84	0	84
BA.2.38	712	1	713
BA.2.38.1	3	0	3
BA.2.38.2	6	0	6
BA.2.40.1	24	0	24
BA.2.41	4	0	4
BA.2.42	2	0	2
BA.2.43	1	0	1
BA.2.45	3	0	3
BA.2.47	2	0	2
BA.2.48	15	0	15
BA.2.49	4	0	4
BA.2.5	5	0	5
BA.2.50	11	0	11
BA.2.51	19	0	19
BA.2.52	9	0	9
BA.2.53	1	0	1
BA.2.54	1	0	1
BA.2.55	1	0	1
BA.2.56	40	0	40
BA.2.57	2	0	2
BA.2.59	1	0	1
BA.2.6	6	0	6

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BA.2.62	4	0	4
BA.2.64	13	0	13
BA.2.65	1,658	0	1,658
BA.2.66	23	0	23
BA.2.68	6	0	6
BA.2.7	15	0	15
BA.2.72	5	0	5
BA.2.73	2	0	2
BA.2.74	45	0	45
BA.2.75	124	0	124
BA.2.75.1	24	0	24
BA.2.75.10	4	0	4
BA.2.75.2	234	5	239
BA.2.75.3	11	0	11
BA.2.75.4	1	0	1
BA.2.75.5	27	6	33
BA.2.75.6	4	1	5
BA.2.76	94	0	94
BA.2.78	3	0	3
BA.2.79	6	0	6
BA.2.79.1	1	0	1
BA.2.8	9	0	9
BA.2.81	10	0	10
BA.2.82	1	0	1
BA.2.9	1,551	0	1,551
BA.2.9.2	2	0	2
BA.2.9.3	16	0	16
BA.2.9.4	1	0	1
BA.2.9.5	9	0	9
BA.2.9.7	6	0	6
BA.3.1	1	0	1
BA.4	717	1	718
BA.4.1	1,382	0	1,382
BA.4.1.1	42	1	43
BA.4.1.10	6	1	7
BA.4.1.4	3	0	3
BA.4.1.5	2	0	2
BA.4.1.6	26	0	26
BA.4.1.8	148	11	159
BA.4.1.9	7	0	7

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BA.4.2	177	0	177
BA.4.3	10	0	10
BA.4.4	83	0	83
BA.4.5	2	0	2
BA.4.6	2,487	156	2,643
BA.4.6.1	2	0	2
BA.4.6.2	33	11	44
BA.4.6.3	0	7	7
BA.4.6.4	15	0	15
BA.4.7	55	0	55
BA.5	430	16	446
BA.5.1	6,437	180	6,617
BA.5.1.1	987	32	1,019
BA.5.1.10	216	14	230
BA.5.1.12	85	60	145
BA.5.1.14	1	0	1
BA.5.1.15	26	0	26
BA.5.1.16	1	0	1
BA.5.1.17	14	0	14
BA.5.1.18	62	14	76
BA.5.1.19	11	0	11
BA.5.1.2	318	4	322
BA.5.1.20	27	6	33
BA.5.1.21	3	0	3
BA.5.1.22	260	7	267
BA.5.1.23	455	15	470
BA.5.1.24	123	0	123
BA.5.1.25	172	7	179
BA.5.1.27	11	35	46
BA.5.1.28	5	5	10
BA.5.1.3	87	1	88
BA.5.1.30	71	0	71
BA.5.1.4	11	0	11
BA.5.1.5	224	25	249
BA.5.1.6	51	6	57
BA.5.1.7	637	9	646
BA.5.1.8	1	0	1
BA.5.1.9	1	0	1
BA.5.10	232	1	233
BA.5.10.1	10	10	20

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BA.5.2	7,175	248	7,423
BA.5.2.1	11,268	359	11,627
BA.5.2.12	3	0	3
BA.5.2.13	124	53	177
BA.5.2.14	111	27	138
BA.5.2.16	55	5	60
BA.5.2.18	34	1	35
BA.5.2.19	33	0	33
BA.5.2.2	140	0	140
BA.5.2.20	648	31	679
BA.5.2.21	304	51	355
BA.5.2.22	403	16	419
BA.5.2.23	66	8	74
BA.5.2.24	67	75	142
BA.5.2.25	94	22	116
BA.5.2.26	92	15	107
BA.5.2.27	154	2	156
BA.5.2.28	100	15	115
BA.5.2.3	153	36	189
BA.5.2.31	51	2	53
BA.5.2.32	37	14	51
BA.5.2.33	21	12	33
BA.5.2.34	123	28	151
BA.5.2.35	25	33	58
BA.5.2.36	8	0	8
BA.5.2.37	16	0	16
BA.5.2.4	13	0	13
BA.5.2.6	192	155	347
BA.5.2.7	10	1	11
BA.5.2.8	122	0	122
BA.5.2.9	833	28	861
BA.5.3	17	0	17
BA.5.3.1	151	30	181
BA.5.3.2	9	0	9
BA.5.3.3	44	1	45
BA.5.3.4	4	0	4
BA.5.3.5	0	1	1
BA.5.5	1,686	2	1,688
BA.5.5.1	52	7	59
BA.5.5.2	86	0	86

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BA.5.5.3	22	0	22
BA.5.6	1,249	8	1,257
BA.5.6.1	14	0	14
BA.5.6.2	25	0	25
BA.5.8	199	0	199
BA.5.9	104	32	136
BB.1	1	0	1
BB.2	1	0	1
BC.2	1	0	1
BE.1	996	4	1,000
BE.1.1	675	20	695
BE.1.1.1	107	16	123
BE.1.1.2	61	0	61
BE.1.2	9	1	10
BE.1.2.1	383	114	497
BE.1.3	1	0	1
BE.1.4	207	0	207
BE.1.4.1	33	0	33
BE.1.4.2	3	0	3
BE.1.4.4	1	0	1
BE.2	15	0	15
BE.3	187	0	187
BE.4	105	0	105
BE.4.1	22	0	22
BE.4.1.1	0	2	2
BE.4.2	1	1	2
BE.5	151	1	152
BF.1	297	0	297
BF.1.1	9	0	9
BF.10	1,745	26	1,771
BF.11	367	195	562
BF.11.1	26	60	86
BF.11.3	81	45	126
BF.11.4	7	3	10
BF.12	50	0	50
BF.13	195	27	222
BF.14	79	67	146
BF.15	10	0	10
BF.16	60	0	60
BF.18	7	0	7

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BF.19	1	0	1
BF.2	93	4	97
BF.20	4	0	4
BF.21	148	3	151
BF.23	8	0	8
BF.25	37	14	51
BF.26	515	29	544
BF.27	322	9	331
BF.28	501	60	561
BF.29	3	0	3
BF.3	55	43	98
BF.3.1	3	0	3
BF.31	30	2	32
BF.31.1	79	5	84
BF.32	2	1	3
BF.4	252	1	253
BF.5	834	40	874
BF.6	10	1	11
BF.7	1,247	566	1,813
BF.7.1	2	4	6
BF.7.12	6	1	7
BF.7.3	1	0	1
BF.7.4	53	54	107
BF.7.4.1	59	32	91
BF.7.4.2	6	1	7
BF.7.5	40	40	80
BF.7.6	50	68	118
BF.7.7	114	54	168
BF.7.8	6	3	9
BF.8	111	0	111
BF.9	839	0	839
BG.2	88	0	88
BG.4	14	0	14
BG.5	24	0	24
BG.6	11	0	11
BH.1	14	0	14
BK.1	225	24	249
BL.1	30	4	34
BL.1.4	0	1	1
BL.2	4	0	4

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BL.3	1	0	1
BL.4	4	0	4
BM.1	3	0	3
BM.1.1	21	1	22
BM.1.1.1	1	14	15
BM.1.1.3	27	1	28
BM.2	1	0	1
BM.2.1	11	0	11
BM.4.1.1	2	1	3
BN.1	45	84	129
BN.1.2	10	60	70
BN.1.2.1	1	10	11
BN.1.3	48	65	113
BN.1.3.1	4	52	56
BN.1.4	5	7	12
BN.1.5	6	15	21
BN.2	2	0	2
BN.2.1	1	0	1
BN.3.1	9	4	13
BN.4	1	0	1
BN.5	7	0	7
BN.6	6	6	12
BQ.1	882	1,052	1,934
BQ.1.1	923	3,039	3,962
BQ.1.1.1	36	209	245
BQ.1.1.10	2	148	150
BQ.1.1.13	1	18	19
BQ.1.1.15	3	26	29
BQ.1.1.17	0	2	2
BQ.1.1.18	27	43	70
BQ.1.1.2	0	6	6
BQ.1.1.3	18	125	143
BQ.1.1.4	36	218	254
BQ.1.1.5	15	84	99
BQ.1.1.6	14	37	51
BQ.1.1.7	28	98	126
BQ.1.1.8	4	15	19
BQ.1.10	37	48	85
BQ.1.10.1	27	78	105
BQ.1.11	36	106	142

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
BQ.1.12	136	199	335
BQ.1.13	155	249	404
BQ.1.14	87	133	220
BQ.1.15	0	19	19
BQ.1.16	67	4	71
BQ.1.18	0	10	10
BQ.1.19	3	26	29
BQ.1.2	175	285	460
BQ.1.22	32	28	60
BQ.1.3	47	114	161
BQ.1.4	1	1	2
BQ.1.5	129	273	402
BQ.1.6	1	6	7
BQ.1.7	3	1	4
BQ.1.8	61	42	103
BQ.1.9	1	0	1
BR.1	5	0	5
BR.1.2	3	1	4
BR.2	3	22	25
BR.3	6	1	7
BR.4	13	0	13
BT.1	12	0	12
BU.1	7	11	18
BU.2	8	0	8
BU.3	0	2	2
BV.2	2	0	2
BW.1	10	52	62
BY.1	86	1	87
BY.1.2	10	0	10
CA.1	1	0	1
CA.2	1	0	1
CA.3	0	3	3
CA.5	3	14	17
CA.7	5	10	15
CB.1	4	0	4
CC.1	22	0	22
CD.2	1	0	1
CE.1	29	2	31
CG.1	27	5	32
CH.1.1	4	52	56

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
CJ.1	3	0	3
CK.1	11	56	67
CK.2	1	4	5
CK.2.1	0	2	2
CK.2.1.1	3	20	23
CL.1	2	7	9
CM.1	34	9	43
CM.2	56	13	69
CM.4	4	5	9
CM.6	0	1	1
CN.1	8	8	16
CP.1	9	15	24
CP.5	1	0	1
CP.6	1	0	1
CQ.1	7	2	9
CQ.2	2	2	4
CR.1	11	4	15
CR.1.1	1	1	2
CR.2	12	0	12
CT.1	0	1	1
CV.1	7	10	17
Variant of Interest (VOI)			
Mu	**241**	**0**	**241**
Lambda	**8**	**0**	**8**
Recombinant	**274**	**235**	**509**
XAC	31	0	31
XAF	1	0	1
XAM	5	0	5
XAN	5	0	5
XAP	3	0	3
XAQ	1	0	1
XAS	16	0	16
XAV	8	0	8
XAZ	52	0	52
XB	1	0	1
XBB	17	6	23
XBB.1	73	196	269
XBB.1.1	2	4	6
XBB.1.3	1	0	1
XBB.2	17	24	41

WHO label / Pango lineage	January 1, 2021 - November 26, 2022	November 27, 2022 - December 24, 2022	Total
XBB.3	6	5	11
XBD	2	0	2
XBE	9	0	9
XE	3	0	3
XM	1	0	1
XN	1	0	1
XQ	4	0	4
XW	14	0	14
XZ	1	0	1
Non-VOC/VOI	**6,261**	**0**	**6,261**
Total sequenced	**192,588**	**11,347**	**203,935**

Note: Results do not represent all Ontario cases. Includes results from PHO since January 1, 2021, The Hospital for Sick Children since April 21, 2021, Kingston Health Sciences Centre since January 1, 2021, Shared Hospital Laboratory since March 26, 2021, and Hamilton Regional Laboratory Medicine Program since April 11, 2021. Past testing algorithms have led to preferential sequencing of samples with N501Y and/or E484K mutations detected by PCR, which has biased the results toward lineages with these mutations. 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: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Technical Notes

Data Sources

Public Health Ontario (PHO)

- Data were extracted from the PHO Laboratory Information Management System on January 4, 2023 at approximately 2:00 a.m.
- Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on January 4, 2023 at approximately 9:30 a.m.

The Hospital for Sick Children (HSC)

- Data were received by PHO on January 3, 2023 at approximately 3:00 p.m.

Kingston Health Sciences Centre (KHSC)

- Data were received by PHO on January 3, 2023 at approximately 1:00 p.m.

Shared Hospital Laboratory (SHL)

- Data were received by PHO on January 3, 2023 at approximately 10:40 a.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were received by PHO on January 3, 2023 at approximately 8:00 p.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on January 3 2023 at approximately 1:00 p.m.

Ontario Ministry of Health's COVaxON application (COVaxON)

- COVID-19 vaccination data were based on information successfully extracted from the Ontario Ministry of Health's COVaxON application as of January 3 2023 at approximately 7:00 a.m.
- COVaxON data was linked to COVID-19 case data from CCM.

Ontario SARS-CoV-2 Whole Genome Sequencing Strategy

- At the beginning of 2021, Ontario's whole genome sequencing strategy was to sequence samples with specific mutations identified from VOC PCR testing to confirm they were variants of concern. From February 3, 2021 this included sequencing samples with the N501Y mutation detected (initially associated with the B.1.1.7 [Alpha] lineage) and from March 22, 2021, samples with the E484K mutation detected (initially associated with the P.1 [Gamma] and B.1.351 [Beta] lineages).

- As of May 2, 2021, Ontario's strategy shifted to representative surveillance with VOC PCR testing laboratories being asked to send a proportion of eligible samples (Ct ≤ 30 and sufficient volume remaining) to Ontario COVID-19 Genomics Network (OCGN) sequencing laboratories. PHO began sequencing a 10% systematic sample of eligible samples on May 2 and 50% on May 30. Other VOC PCR testing laboratories were asked to begin submitting a 10% systematic or random sample of eligible samples to OCGN laboratories on May 26 and 50% on June 2. All VOC PCR/diagnostic testing laboratories shifted to submitting 100% of eligible samples to the OCGN on June 14; 50% on August 27; 10% on September 10; 25% on October 8; 100% on November 5; 50% on December 7; 10% on December 20; 5% on December 30; 20% on February 16; 50% on March 9; 25% on March 30; 10% on April 13; 25% on May 12; 100% on June 10; 50% on July 8; 20% on July 22; 50% on August 24; 75% on November 23; and 100% on December 9, 2022. The proportion of samples sequenced may change over time with changes in provincial case trends. Due to logistics, not all laboratories may have implemented sampling proportion changes at the same time.

- As of November 12, 2021, VOC PCR testing has been discontinued. The 73 diagnostic testing laboratories were asked to 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 6, 2021, VOC PCR testing for S gene target failure (SGTF) was implemented across Ontario to screen for Omicron. Diagnostic testing laboratories were asked to send all eligible samples (diagnostic PCR Ct≤35 and sufficient volume remaining) to one of eight SGTF testing laboratories. The SGTF testing laboratories will then submit a proportion of eligible samples (SGTF PCR Ct≤30 and sufficient volume remaining) for WGS according to the representative surveillance strategy.

    - Due to logistics, not all laboratories may have implemented SGTF testing at the same time.

- As of December 30, 2021, SGTF testing of all eligible samples was discontinued in Ontario. The 73 diagnostic testing laboratories were asked to send a proportion of eligible samples (diagnostic PCR Ct≤ 30 and sufficient volume remaining) to one of the five OCGN laboratories for whole genome sequencing, according to the representative surveillance strategy.

- As of December 31, 2021, diagnostic PCR testing was restricted to high-risk populations. Since then, the Ministry of Health continues to update its guidance on testing. As such, representative surveillance only pertains to tested populations.

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

- Lineage nomenclature is dynamic. Pango lineage naming and assignment may change as more samples are sequenced and analyzed globally. Similarly, VOC and VOI classifications may change.
- Whole genome sequencing sample logistics are complex and require samples to be transferred across a large network of laboratories. Samples are initially sent to one of 73 diagnostic testing laboratories. If the diagnostic PCR cycle threshold is ≤ 35 and there is sufficient volume remaining, samples are submitted for testing at one of 11 VOC PCR testing laboratories. If the VOC PCR cycle threshold is ≤ 30 and there is sufficient volume remaining, VOC PCR testing laboratories have been asked to submit a proportion of their eligible samples to one of five OCGN laboratories for sequencing according to the surveillance strategy. As of November 12, VOC PCR has been discontinued. Diagnostic testing laboratories now send eligible samples (Ct ≤ 30 and sufficient volume remaining) directly to one of the five OCGN laboratories for whole genome sequencing.
    - PHO is unable to confirm whether VOC PCR testing laboratories or diagnostic testing laboratories (November 12, 2021 onwards) have submitted eligible samples.
- Data submitted to PHO 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 (2.8%), 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. Individual VOC PCR laboratories may have implemented the strategy and/or increased the proportion of samples selected on different dates. Cumulative data included do not reflect all whole genome sequencing conducted in Ontario.
    - 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.
    - Past testing algorithms have led to preferential sequencing of samples with N501Y and/or E484K mutations detected by VOC PCR. This has created a sampling bias reflected in the distribution of lineage results prior to May 2, 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 twelve 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 fourteen 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 ($\Delta r = r_{lineage} - r_{reference}$), and can be derived from a logistic regression model where the outcome is the relative frequency of a lineage and the predictor is 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 COVID-19 Data Tool.

- Data corrections or updates can result in case records being removed and/or updated from past reports.

- Dates associated with COVID-19 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).

- Tables for outbreak, hospital admission, and deceased indicators only include cases that linked to CCM (97.2% of cases).

- 'Outbreak-associated cases' include cases linked to a confirmed outbreak as declared by the local medical officer of health or their designate in accordance to the Health Protection and Promotion Act and criteria outlined in Ministry guidance documents.

- Outbreaks in settings outside of Ontario are excluded from all outbreak counts.

- Data on hospital admissions and deaths are likely under-reported as these events may occur after the completion of public health follow up of cases. Cases that were admitted to hospital or died after follow-up was completed may not be captured in CCM.

- Hospital admission includes all cases ever admitted to a hospital (or that had their hospital stay extended) because of COVID-19. It includes cases that have been discharged from hospital as well as cases that are currently hospitalized. Includes cases in an Intensive Care Unit (ICU) but not emergency room visits. Hospital admissions were identified by a reported hospital admission date or reported 'Yes' for hospitalization/ICU.

- For surveillance purposes, a COVID-19 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 COVID-19 (e.g., trauma, medically assisted death). There should be no period of complete recovery from COVID-19 between illness and reported death.

- Deaths are determined by using the outcome and Type of Death fields in CCM. COVID-19 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'.

Data Caveats and Methods: COVaxON

- In order to identify cases post-vaccination, vaccine uptake data extracted from the Ontario Ministry of Health's (MOH) COVaxON application was linked to case data extracted from the MOH's Public Health Case and Contact Management Solution (CCM).

    - Clients in COVaxON and CCM were linked using health card number as well as other personal identifiers, including name, date of birth, gender, and postal code.

- Linkage was done using processed COVaxON and CCM data. Methods for processing COVaxON vaccine uptake data are described in the Technical Notes of the COVID-19 Vaccine Uptake Report and methods for processing post-vaccination cases are described in the Technical Notes of the Confirmed Cases of COVID-19 Post Vaccination Report.

- Only cases that have received Health Canada authorized vaccines including, Pfizer-BioNTech Comirnaty™, Moderna Spikevax™, AstraZeneca Vaxzevria™/COVISHIELD, and Janssen are included. Cases that received one or more doses of a non-Health Canada authorized vaccine are excluded.

- A higher proportion of cases reported in post-series initiation and post-series completion is a reflection of both trends in vaccine administration (increasing number of doses administered over time) and trends in COVID-19 incidence. Further details on vaccine administration trends in Ontario are described in the COVID-19 Vaccine Uptake Report.

- Factors, such as age, that may affect the risk of COVID-19 hospitalization and death are not accounted for in these analyses. As a result, the proportion of severe outcomes following booster doses may be higher compared to other vaccination statuses since booster eligibility was initially restricted to older adults who are more likely to have severe outcomes and who also have the highest uptake for booster doses.

- For vaccine category definitions, please refer to Confirmed Cases of COVID-19 Following Vaccination in Ontario.

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