Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, April 28, 2023

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of April 26, 2023 and partner laboratories in the Ontario COVID-19 Genomics Network as of April 25, 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 (April 9 to April 15), XBB.1.5 was the most prevalent lineage (49.1%), followed XBB.1.16 (5.2%), and XBB.1.9.1 (4.5%).
- The proportion of XBB.1.5 remained stable at 50.4% (April 2 to April 8) and 49.1% (April 9 to April 15) and is projected to decrease to 26.2% (95% CI: 21.4% - 31.6%) by May 3, 2023.
- The proportion of XBB.1.16 increased from 3.6% (April 2 to April 8) to 5.2% (April 9 to April 15) and is projected to increase to 22.2% (95% CI: 14.5% - 32.2%) by May 3, 2023.
    - The weekly growth rate of XBB.1.16 is 1.88 (95% CI: 1.70 – 2.08) times that of XBB.1.5.

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

As of April 1, 2023, PHUs in Ontario will no longer be required to link cases to COVID-19 outbreaks in high risk settings. As a result, the lineage by outbreak-association table will no longer be included. Furthermore, we will no longer be able to determine if emerging lineages are overestimated in the Nowcast model due to a large outbreak.

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.

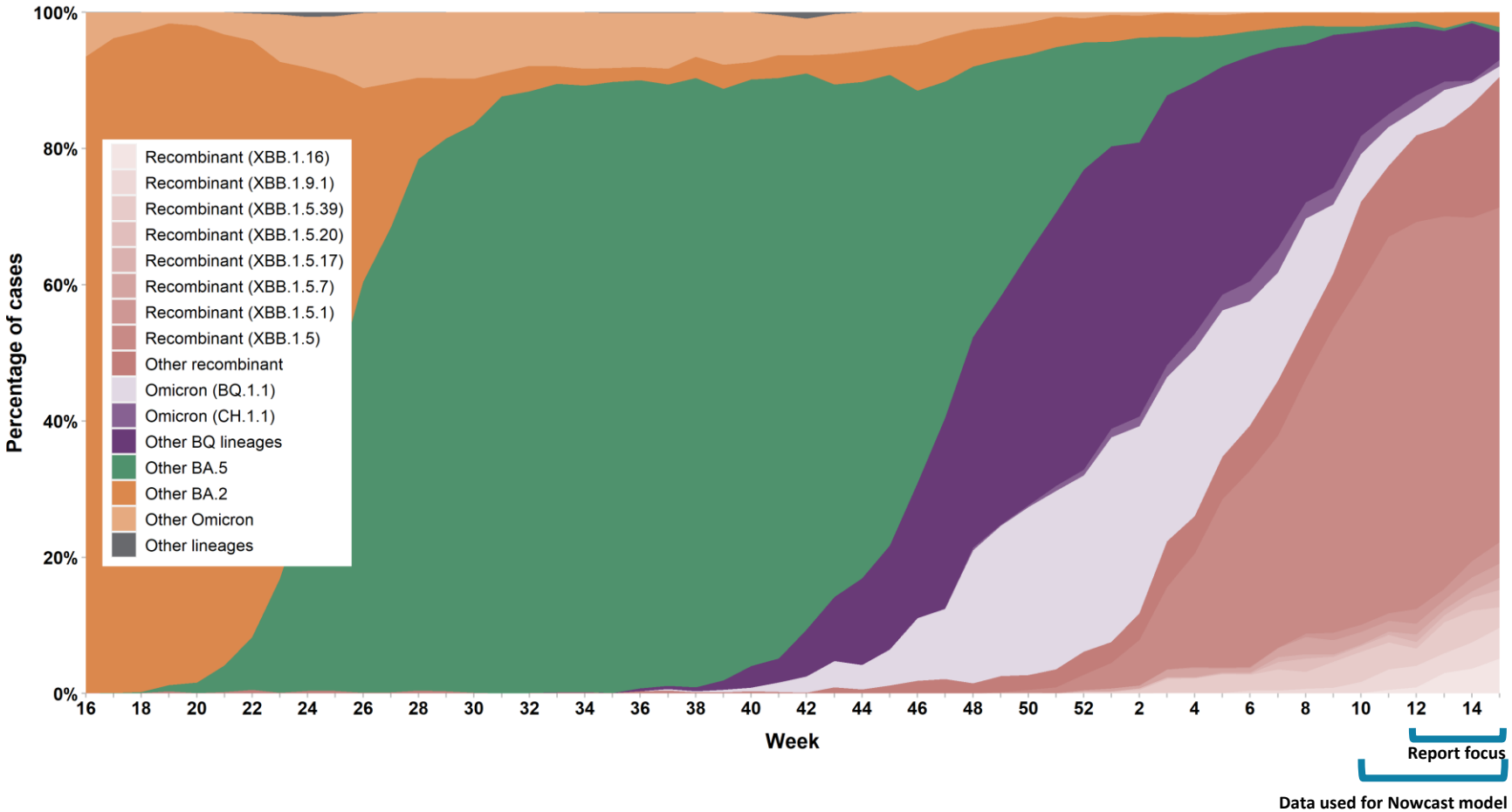
Representative Surveillance

Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, March 19 to April 15, 2023

Week	Number of cases	Number sequenced	Percentage sequenced
Week 12 (March 19 - March 25)	3,381	1,885	55.8%
Week 13 (March 26 - April 1)	2,714	1,672	61.6%
Week 14 (April 2 - April 8)	2,129	1,207	56.7%
Week 15 (April 9 - April 15)	2,198	1,262	57.4%
Total	**10,422**	**6,026**	**57.8%**

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, April 17, 2022 to April 15, 2023



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.

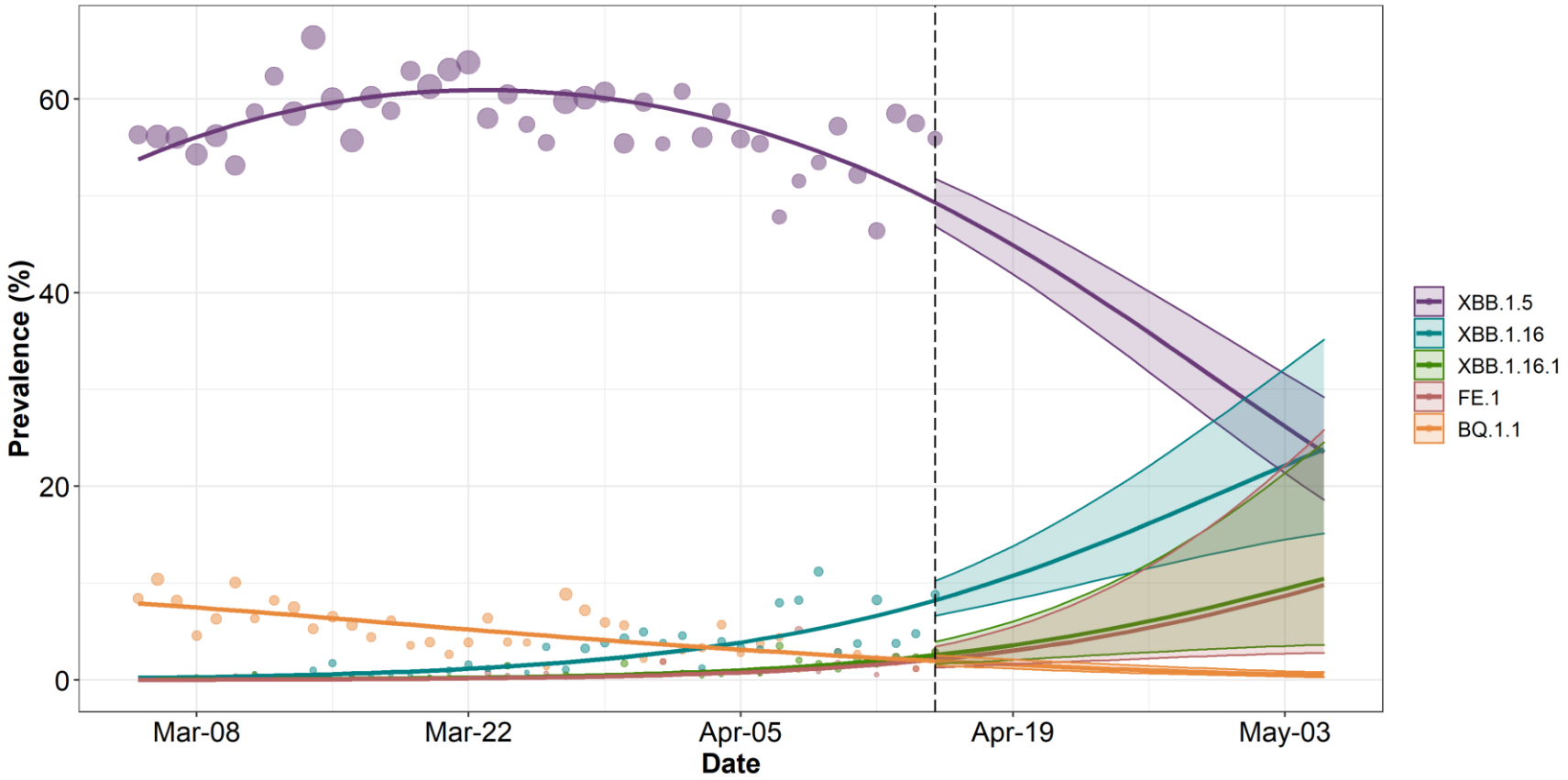
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 2. Number and percentage of cases by Pango lineage and week, representative surveillance, Ontario, March 19 to April 15, 2023

Pango lineage	Week 12 (March 19 - March 25)	Week 13 (March 26 - April 1)	Week 14 (April 2 - April 8)	Week 15 (April 9 - April 15)	Total (March 19- April 15)
XBB.1.5	1,071 (56.8%)	915 (54.7%)	608 (50.4%)	620 (49.1%)	3,214 (53.3%)
BQ.1.1	70 (3.7%)	89 (5.3%)	39 (3.2%)	20 (1.6%)	218 (3.6%)
XBB.1.5.39	48 (2.5%)	76 (4.5%)	56 (4.6%)	38 (3.0%)	218 (3.6%)
XBB.1.9.1	60 (3.2%)	48 (2.9%)	47 (3.9%)	57 (4.5%)	212 (3.5%)
XBB.1.16	17 (0.9%)	51 (3.1%)	44 (3.6%)	65 (5.2%)	177 (2.9%)
XBB.1.5.1	41 (2.2%)	27 (1.6%)	29 (2.4%)	40 (3.2%)	137 (2.3%)
XBB.1.5.7	29 (1.5%)	23 (1.4%)	25 (2.1%)	26 (2.1%)	103 (1.7%)
XBB.1.5.20	18 (1.0%)	17 (1.0%)	23 (1.9%)	32 (2.5%)	90 (1.5%)
CH.1.1	40 (2.1%)	21 (1.3%)	4 (0.3%)	12 (1.0%)	77 (1.3%)
XBB.1.5.17	21 (1.1%)	15 (0.9%)	11 (0.9%)	23 (1.8%)	70 (1.2%)
Other recombinant	240 (12.7%)	220 (13.2%)	200 (16.6%)	241 (19.1%)	901 (15.0%)
Other BQ lineages	190 (10.1%)	124 (7.4%)	102 (8.5%)	51 (4.0%)	467 (7.7%)
Other BA.5	15 (0.8%)	7 (0.4%)	4 (0.3%)	10 (0.8%)	36 (0.6%)
Other BA.2	23 (1.2%)	39 (2.3%)	15 (1.2%)	27 (2.1%)	104 (1.7%)
Other Omicron	2 (0.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (<0.1%)
Total sequenced	**1,885 (100%)**	**1,672 (100%)**	**1,207 (100%)**	**1,262 (100%)**	**6,026 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ 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, March 5, 2023 to May 6, 2023



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. 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 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: 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, March 5, 2023 to May 6, 2023

Pango lineage	Week 14 (April 5): Estimated	Week 15 (April 12): Estimated	Week 16 (April 19): Projected	Week 17 (April 26): Projected	Week 18 (May 3): Projected	Weekly relative growth rate
XBB.1.5	57.2 (55.7 - 58.7)	52.1 (50.0 - 54.3)	44.9 (41.9 - 47.9)	35.9 (31.8 - 40.1)	26.2 (21.4 - 31.6)	1.00 (reference)
XBB.1.16	3.9 (3.4 - 4.5)	6.7 (5.5 - 8.0)	10.8 (8.3 - 13.9)	16.2 (11.5 - 22.1)	22.2 (14.5 - 32.2)	1.88 (1.70 - 2.08)
XBB.1.16.1	1.0 (0.8 - 1.4)	2.0 (1.4 - 2.9)	3.6 (2.1 - 6.1)	6.1 (2.9 - 12.0)	9.4 (3.5 - 21.4)	2.11 (1.71 - 2.62)
FE.1	0.8 (0.6 - 1.1)	1.6 (1.1 - 2.4)	3.1 (1.6 - 5.5)	5.4 (2.2 - 11.7)	8.7 (2.7 - 22.1)	2.21 (1.72 - 2.83)
BQ.1.1	3.2 (2.7 - 3.7)	2.3 (1.8 - 2.9)	1.6 (1.2 - 2.1)	1.0 (0.7 - 1.5)	0.6 (0.4 - 0.9)	0.80 (0.75 - 0.85)

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 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 12 week period (six observed and six 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, March 19 to April 15, 2023

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
XBB.1.5	80 (57.6%)	9 (45.0%)	31 (50.0%)	581 (53.6%)	681 (53.7%)	777 (51.9%)	1,053 (53.9%)	3,212 (53.3%)
BQ.1.1	2 (1.4%)	1 (5.0%)	0 (0.0%)	26 (2.4%)	31 (2.4%)	67 (4.5%)	90 (4.6%)	217 (3.6%)
XBB.1.5.39	2 (1.4%)	2 (10.0%)	3 (4.8%)	37 (3.4%)	47 (3.7%)	50 (3.3%)	77 (3.9%)	218 (3.6%)
XBB.1.9.1	10 (7.2%)	1 (5.0%)	3 (4.8%)	40 (3.7%)	33 (2.6%)	56 (3.7%)	69 (3.5%)	212 (3.5%)
XBB.1.16	8 (5.8%)	0 (0.0%)	2 (3.2%)	30 (2.8%)	31 (2.4%)	54 (3.6%)	52 (2.7%)	177 (2.9%)
XBB.1.5.1	1 (0.7%)	0 (0.0%)	2 (3.2%)	29 (2.7%)	27 (2.1%)	27 (1.8%)	51 (2.6%)	137 (2.3%)
XBB.1.5.7	1 (0.7%)	0 (0.0%)	0 (0.0%)	12 (1.1%)	19 (1.5%)	31 (2.1%)	40 (2.0%)	103 (1.7%)
XBB.1.5.20	0 (0.0%)	0 (0.0%)	1 (1.6%)	21 (1.9%)	28 (2.2%)	24 (1.6%)	16 (0.8%)	90 (1.5%)
CH.1.1	1 (0.7%)	1 (5.0%)	1 (1.6%)	14 (1.3%)	20 (1.6%)	15 (1.0%)	25 (1.3%)	77 (1.3%)
XBB.1.5.17	0 (0.0%)	0 (0.0%)	0 (0.0%)	10 (0.9%)	10 (0.8%)	14 (0.9%)	36 (1.8%)	70 (1.2%)
Other recombinant	31 (22.3%)	4 (20.0%)	14 (22.6%)	186 (17.2%)	218 (17.2%)	207 (13.8%)	241 (12.3%)	901 (15.0%)
Other BQ lineages	1 (0.7%)	2 (10.0%)	4 (6.5%)	73 (6.7%)	91 (7.2%)	130 (8.7%)	166 (8.5%)	467 (7.8%)
Other BA.5	1 (0.7%)	0 (0.0%)	0 (0.0%)	7 (0.6%)	9 (0.7%)	10 (0.7%)	9 (0.5%)	36 (0.6%)
Other BA.2	1 (0.7%)	0 (0.0%)	1 (1.6%)	18 (1.7%)	23 (1.8%)	35 (2.3%)	26 (1.3%)	104 (1.7%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (0.1%)	2 (<0.1%)
Total sequenced	**139 (100%)**	**20 (100%)**	**62 (100%)**	**1,084 (100%)**	**1,268 (100%)**	**1,497 (100%)**	**1,953 (100%)**	**6,023 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ 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 XBB.1.16 cases, number identified, and total sequenced by public health unit (PHU), region, and week, representative surveillance, Ontario, March 19 to April 15, 2023

Public Health Unit	Week 12 (March 19 - March 25)	Week 13 (March 26 - April 1)	Week 14 (April 2 - April 8)	Week 15 (April 9 - April 15)	Total (March 19- April 15)
Northwestern Health Unit	0.0% (0/6)	25.0% (1/4)	0.0% (0/2)	0.0% (0/4)	6.2% (1/16)
Thunder Bay District Health Unit	0.0% (0/39)	0.0% (0/43)	0.0% (0/27)	0.0% (0/27)	0.0% (0/136)
TOTAL NORTH WEST	**0.0% (0/45)**	**2.1% (1/47)**	**0.0% (0/29)**	**0.0% (0/31)**	**0.7% (1/152)**
Algoma Public Health	0.0% (0/24)	0.0% (0/10)	0.0% (0/0)	0.0% (0/3)	0.0% (0/37)
North Bay Parry Sound District Health Unit	0.0% (0/23)	0.0% (0/14)	0.0% (0/15)	0.0% (0/1)	0.0% (0/53)
Porcupine Health Unit	0.0% (0/7)	0.0% (0/5)	0.0% (0/8)	0.0% (0/3)	0.0% (0/23)
Public Health Sudbury & Districts	0.0% (0/25)	0.0% (0/25)	0.0% (0/18)	5.3% (1/19)	1.1% (1/87)
Timiskaming Health Unit	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)
TOTAL NORTH EAST	**0.0% (0/79)**	**0.0% (0/54)**	**0.0% (0/41)**	**3.8% (1/26)**	**0.5% (1/200)**
Ottawa Public Health	0.6% (1/154)	1.3% (1/76)	2.5% (2/80)	0.0% (0/57)	1.1% (4/367)
Eastern Ontario Health Unit	0.0% (0/56)	0.0% (0/20)	0.0% (0/13)	0.0% (0/23)	0.0% (0/112)
Hastings Prince Edward Public Health	0.0% (0/17)	0.0% (0/28)	0.0% (0/20)	0.0% (0/10)	0.0% (0/75)
Kingston, Frontenac and Lennox & Addington Public Health	0.0% (0/36)	0.0% (0/45)	5.3% (3/57)	3.1% (1/32)	2.4% (4/170)
Leeds, Grenville & Lanark District Health Unit	0.0% (0/24)	0.0% (0/13)	0.0% (0/15)	7.7% (1/13)	1.5% (1/65)
Renfrew County and District Health Unit	0.0% (0/6)	0.0% (0/2)	0.0% (0/6)	0.0% (0/44)	0.0% (0/58)
TOTAL EASTERN	**0.3% (1/293)**	**0.5% (1/184)**	**2.6% (5/191)**	**1.1% (2/179)**	**1.1% (9/847)**
Durham Region Health Department	0.0% (0/72)	0.0% (0/72)	1.8% (1/56)	6.9% (5/72)	2.2% (6/272)
Haliburton, Kawartha, Pine Ridge District Health Unit	2.7% (1/37)	0.0% (0/38)	3.8% (1/26)	2.0% (1/49)	2.0% (3/150)
Peel Public Health	4.4% (6/135)	5.5% (8/146)	7.1% (6/84)	14.1% (13/92)	7.2% (33/457)
Peterborough Public Health	0.0% (0/29)	0.0% (0/38)	4.8% (1/21)	4.3% (1/23)	1.8% (2/111)
Simcoe Muskoka District Health Unit	1.3% (1/76)	23.7% (23/97)	33.3% (19/57)	16.0% (8/50)	18.2% (51/280)
York Region Public Health	0.0% (0/59)	1.4% (1/72)	0.0% (0/71)	1.0% (1/105)	0.7% (2/307)
TOTAL CENTRAL EAST	**2.0% (8/408)**	**6.9% (32/463)**	**8.9% (28/315)**	**7.4% (29/391)**	**6.2% (97/1,577)**
Toronto Public Health	1.6% (5/309)	2.6% (7/273)	1.6% (4/244)	6.2% (18/292)	3.0% (34/1,118)
TOTAL TORONTO	**1.6% (5/309)**	**2.6% (7/273)**	**1.6% (4/244)**	**6.2% (18/292)**	**3.0% (34/1,118)**
Chatham-Kent Public Health	0.0% (0/26)	0.0% (0/27)	0.0% (0/15)	0.0% (0/15)	0.0% (0/83)

Public Health Unit	Week 12 (March 19 - March 25)	Week 13 (March 26 - April 1)	Week 14 (April 2 - April 8)	Week 15 (April 9 - April 15)	Total (March 19- April 15)
Grey Bruce Health Unit	4.8% (1/21)	0.0% (0/16)	0.0% (0/16)	0.0% (0/8)	1.6% (1/61)
Huron Perth Public Health	6.7% (1/15)	5.0% (1/20)	0.0% (0/40)	0.0% (0/21)	2.1% (2/96)
Lambton Public Health	0.0% (0/23)	0.0% (0/11)	0.0% (0/13)	0.0% (0/12)	0.0% (0/59)
Middlesex-London Health Unit	1.1% (1/88)	1.2% (1/80)	4.4% (2/45)	2.2% (1/45)	1.9% (5/258)
Southwestern Public Health	0.0% (0/19)	11.8% (2/17)	7.7% (1/13)	0.0% (0/24)	4.1% (3/73)
Windsor-Essex County Health Unit	0.0% (0/145)	1.3% (1/77)	0.0% (0/49)	3.4% (1/29)	0.7% (2/300)
TOTAL SOUTH WEST	**0.9% (3/337)**	**2.0% (5/248)**	**1.6% (3/191)**	**1.3% (2/154)**	**1.4% (13/930)**
Brant County Health Unit	0.0% (0/28)	2.8% (1/36)	0.0% (0/12)	0.0% (0/13)	1.1% (1/89)
City of Hamilton Public Health Services	0.0% (0/131)	0.0% (0/111)	0.0% (0/63)	0.0% (0/34)	0.0% (0/339)
Haldimand-Norfolk Health Unit	0.0% (0/29)	0.0% (0/33)	0.0% (0/12)	0.0% (0/7)	0.0% (0/81)
Halton Region Public Health	0.0% (0/62)	1.4% (1/72)	0.0% (0/37)	6.7% (2/30)	1.5% (3/201)
Niagara Region Public Health	0.0% (0/55)	1.3% (1/77)	5.0% (2/40)	4.7% (2/43)	2.3% (5/215)
Region of Waterloo Public Health and Emergency Services	0.0% (0/46)	2.2% (1/45)	10.5% (2/19)	16.0% (8/50)	6.9% (11/160)
Wellington-Dufferin-Guelph Public Health	0.0% (0/56)	3.6% (1/28)	0.0% (0/13)	10.0% (1/10)	1.9% (2/107)
TOTAL CENTRAL WEST	**0.0% (0/407)**	**1.2% (5/402)**	**2.0% (4/196)**	**7.0% (13/187)**	**1.8% (22/1,192)**
UNKNOWN	**0.0% (0/3)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/2)**	**0.0% (0/5)**
TOTAL ONTARIO	**0.9% (17/1,885)**	**3.1% (51/1,672)**	**3.6% (44/1,207)**	**5.2% (65/1,262)**	**2.9% (177/6,026)**

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 (2.7%), 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, March 19 to April 15, 2023

Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
XBB.1.5	11 (68.8%)	91 (66.9%)	102 (67.1%)
BQ.1.1	0 (0.0%)	11 (8.1%)	11 (7.2%)
XBB.1.5.39	0 (0.0%)	0 (0.0%)	0 (0.0%)
XBB.1.9.1	0 (0.0%)	2 (1.5%)	2 (1.3%)
XBB.1.16	1 (6.2%)	0 (0.0%)	1 (0.7%)
XBB.1.5.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
XBB.1.5.7	0 (0.0%)	0 (0.0%)	0 (0.0%)
XBB.1.5.20	2 (12.5%)	0 (0.0%)	2 (1.3%)
CH.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
XBB.1.5.17	0 (0.0%)	2 (1.5%)	2 (1.3%)
Other recombinant	2 (12.5%)	26 (19.1%)	28 (18.4%)
Other BQ lineages	0 (0.0%)	4 (2.9%)	4 (2.6%)
Other BA.5	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BA.2	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**16 (100%)**	**136 (100%)**	**152 (100%)**

Note: 'Other BA.5' excludes BQ lineages. 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 (2.7%), 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, March 19 to April 15, 2023

Pango lineage	Algoma Public Health	North Bay Parry Sound District Health Unit	Porcupine Health Unit	Public Health Sudbury & Districts	Timiskaming Health Unit	Total
XBB.1.5	23 (62.2%)	44 (83.0%)	13 (56.5%)	24 (27.6%)	0 (0.0%)	104 (52.0%)
BQ.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (2.3%)	0 (0.0%)	2 (1.0%)
XBB.1.5.39	0 (0.0%)	0 (0.0%)	1 (4.3%)	0 (0.0%)	0 (0.0%)	1 (0.5%)
XBB.1.9.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.1%)	0 (0.0%)	1 (0.5%)
XBB.1.16	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.1%)	0 (0.0%)	1 (0.5%)
XBB.1.5.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
XBB.1.5.7	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.1%)	0 (0.0%)	1 (0.5%)
XBB.1.5.20	2 (5.4%)	3 (5.7%)	7 (30.4%)	12 (13.8%)	0 (0.0%)	24 (12.0%)
CH.1.1	1 (2.7%)	0 (0.0%)	0 (0.0%)	1 (1.1%)	0 (0.0%)	2 (1.0%)
XBB.1.5.17	1 (2.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)
Other recombinant	5 (13.5%)	5 (9.4%)	0 (0.0%)	23 (26.4%)	0 (0.0%)	33 (16.5%)
Other BQ lineages	5 (13.5%)	1 (1.9%)	2 (8.7%)	16 (18.4%)	0 (0.0%)	24 (12.0%)
Other BA.5	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (4.6%)	0 (0.0%)	4 (2.0%)
Other BA.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (2.3%)	0 (0.0%)	2 (1.0%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**37 (100%)**	**53 (100%)**	**23 (100%)**	**87 (100%)**	**0 (100%)**	**200 (100%)**

Note: 'Other BA.5' excludes BQ lineages. 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 (2.7%), 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, March 19 to April 15, 2023

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
XBB.1.5	97 (86.6%)	26 (34.7%)	90 (52.9%)	24 (36.9%)	193 (52.6%)	35 (60.3%)	465 (54.9%)
BQ.1.1	2 (1.8%)	9 (12.0%)	6 (3.5%)	0 (0.0%)	8 (2.2%)	1 (1.7%)	26 (3.1%)
XBB.1.5.39	4 (3.6%)	3 (4.0%)	7 (4.1%)	7 (10.8%)	40 (10.9%)	0 (0.0%)	61 (7.2%)
XBB.1.9.1	1 (0.9%)	0 (0.0%)	3 (1.8%)	0 (0.0%)	12 (3.3%)	0 (0.0%)	16 (1.9%)
XBB.1.16	0 (0.0%)	0 (0.0%)	4 (2.4%)	1 (1.5%)	4 (1.1%)	0 (0.0%)	9 (1.1%)
XBB.1.5.1	1 (0.9%)	0 (0.0%)	1 (0.6%)	0 (0.0%)	2 (0.5%)	0 (0.0%)	4 (0.5%)
XBB.1.5.7	0 (0.0%)	1 (1.3%)	0 (0.0%)	0 (0.0%)	1 (0.3%)	0 (0.0%)	2 (0.2%)
XBB.1.5.20	2 (1.8%)	1 (1.3%)	1 (0.6%)	0 (0.0%)	2 (0.5%)	2 (3.4%)	8 (0.9%)
CH.1.1	0 (0.0%)	0 (0.0%)	1 (0.6%)	0 (0.0%)	24 (6.5%)	0 (0.0%)	25 (3.0%)
XBB.1.5.17	0 (0.0%)	2 (2.7%)	0 (0.0%)	1 (1.5%)	0 (0.0%)	0 (0.0%)	3 (0.4%)
Other recombinant	4 (3.6%)	16 (21.3%)	33 (19.4%)	30 (46.2%)	44 (12.0%)	19 (32.8%)	146 (17.2%)
Other BQ lineages	0 (0.0%)	3 (4.0%)	21 (12.4%)	2 (3.1%)	33 (9.0%)	1 (1.7%)	60 (7.1%)
Other BA.5	1 (0.9%)	1 (1.3%)	1 (0.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (0.4%)
Other BA.2	0 (0.0%)	13 (17.3%)	2 (1.2%)	0 (0.0%)	4 (1.1%)	0 (0.0%)	19 (2.2%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**112 (100%)**	**75 (100%)**	**170 (100%)**	**65 (100%)**	**367 (100%)**	**58 (100%)**	**847 (100%)**

Note: 'Other BA.5' excludes BQ lineages. 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 (2.7%), 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, March 19 to April 15, 2023

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
XBB.1.5	147 (54.0%)	51 (34.0%)	202 (44.2%)	39 (35.1%)	135 (48.2%)	187 (60.9%)	761 (48.3%)
BQ.1.1	5 (1.8%)	5 (3.3%)	6 (1.3%)	21 (18.9%)	2 (0.7%)	5 (1.6%)	44 (2.8%)
XBB.1.5.39	3 (1.1%)	13 (8.7%)	19 (4.2%)	10 (9.0%)	3 (1.1%)	33 (10.7%)	81 (5.1%)
XBB.1.9.1	9 (3.3%)	1 (0.7%)	22 (4.8%)	1 (0.9%)	4 (1.4%)	11 (3.6%)	48 (3.0%)
XBB.1.16	6 (2.2%)	3 (2.0%)	33 (7.2%)	2 (1.8%)	51 (18.2%)	2 (0.7%)	97 (6.2%)
XBB.1.5.1	2 (0.7%)	2 (1.3%)	4 (0.9%)	0 (0.0%)	2 (0.7%)	4 (1.3%)	14 (0.9%)
XBB.1.5.7	15 (5.5%)	1 (0.7%)	16 (3.5%)	0 (0.0%)	7 (2.5%)	2 (0.7%)	41 (2.6%)
XBB.1.5.20	11 (4.0%)	7 (4.7%)	0 (0.0%)	7 (6.3%)	2 (0.7%)	0 (0.0%)	27 (1.7%)
CH.1.1	0 (0.0%)	0 (0.0%)	4 (0.9%)	0 (0.0%)	13 (4.6%)	2 (0.7%)	19 (1.2%)
XBB.1.5.17	11 (4.0%)	30 (20.0%)	1 (0.2%)	0 (0.0%)	0 (0.0%)	3 (1.0%)	45 (2.9%)
Other recombinant	36 (13.2%)	28 (18.7%)	70 (15.3%)	19 (17.1%)	24 (8.6%)	39 (12.7%)	216 (13.7%)
Other BQ lineages	13 (4.8%)	6 (4.0%)	72 (15.8%)	9 (8.1%)	30 (10.7%)	12 (3.9%)	142 (9.0%)
Other BA.5	1 (0.4%)	3 (2.0%)	1 (0.2%)	2 (1.8%)	5 (1.8%)	1 (0.3%)	13 (0.8%)
Other BA.2	13 (4.8%)	0 (0.0%)	6 (1.3%)	1 (0.9%)	2 (0.7%)	6 (2.0%)	28 (1.8%)
Other Omicron	0 (0.0%)	0 (0.0%)	1 (0.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.1%)
Total sequenced	**272 (100%)**	**150 (100%)**	**457 (100%)**	**111 (100%)**	**280 (100%)**	**307 (100%)**	**1,577 (100%)**

Note: 'Other BA.5' excludes BQ lineages. 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 (2.7%), 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, March 19 to April 15, 2023

Pango lineage	Toronto Public Health	Total
XBB.1.5	574 (51.3%)	574 (51.3%)
BQ.1.1	28 (2.5%)	28 (2.5%)
XBB.1.5.39	44 (3.9%)	44 (3.9%)
XBB.1.9.1	61 (5.5%)	61 (5.5%)
XBB.1.16	34 (3.0%)	34 (3.0%)
XBB.1.5.1	65 (5.8%)	65 (5.8%)
XBB.1.5.7	28 (2.5%)	28 (2.5%)
XBB.1.5.20	8 (0.7%)	8 (0.7%)
CH.1.1	12 (1.1%)	12 (1.1%)
XBB.1.5.17	6 (0.5%)	6 (0.5%)
Other recombinant	155 (13.9%)	155 (13.9%)
Other BQ lineages	83 (7.4%)	83 (7.4%)
Other BA.5	3 (0.3%)	3 (0.3%)
Other BA.2	17 (1.5%)	17 (1.5%)
Other Omicron	0 (0.0%)	0 (0.0%)
Total sequenced	**1,118 (100%)**	**1,118 (100%)**

Note: 'Other BA.5' excludes BQ lineages. 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 (2.7%), 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, March 19 to April 15, 2023

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
XBB.1.5	26 (31.3%)	35 (57.4%)	28 (29.2%)	27 (45.8%)	159 (61.6%)	40 (54.8%)	218 (72.7%)	533 (57.3%)
BQ.1.1	18 (21.7%)	4 (6.6%)	5 (5.2%)	0 (0.0%)	20 (7.8%)	3 (4.1%)	2 (0.7%)	52 (5.6%)
XBB.1.5.39	0 (0.0%)	1 (1.6%)	0 (0.0%)	1 (1.7%)	2 (0.8%)	0 (0.0%)	4 (1.3%)	8 (0.9%)
XBB.1.9.1	24 (28.9%)	2 (3.3%)	2 (2.1%)	1 (1.7%)	3 (1.2%)	0 (0.0%)	1 (0.3%)	33 (3.5%)
XBB.1.16	0 (0.0%)	1 (1.6%)	2 (2.1%)	0 (0.0%)	5 (1.9%)	3 (4.1%)	2 (0.7%)	13 (1.4%)
XBB.1.5.1	0 (0.0%)	0 (0.0%)	3 (3.1%)	3 (5.1%)	19 (7.4%)	9 (12.3%)	0 (0.0%)	34 (3.7%)
XBB.1.5.7	0 (0.0%)	1 (1.6%)	0 (0.0%)	0 (0.0%)	2 (0.8%)	0 (0.0%)	1 (0.3%)	4 (0.4%)
XBB.1.5.20	3 (3.6%)	2 (3.3%)	0 (0.0%)	1 (1.7%)	3 (1.2%)	0 (0.0%)	0 (0.0%)	9 (1.0%)
CH.1.1	0 (0.0%)	0 (0.0%)	2 (2.1%)	1 (1.7%)	0 (0.0%)	2 (2.7%)	2 (0.7%)	7 (0.8%)
XBB.1.5.17	1 (1.2%)	0 (0.0%)	2 (2.1%)	0 (0.0%)	2 (0.8%)	0 (0.0%)	1 (0.3%)	6 (0.6%)
Other recombinant	7 (8.4%)	10 (16.4%)	15 (15.6%)	18 (30.5%)	31 (12.0%)	9 (12.3%)	50 (16.7%)	140 (15.1%)
Other BQ lineages	4 (4.8%)	3 (4.9%)	37 (38.5%)	6 (10.2%)	10 (3.9%)	4 (5.5%)	18 (6.0%)	82 (8.8%)
Other BA.5	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BA.2	0 (0.0%)	2 (3.3%)	0 (0.0%)	1 (1.7%)	1 (0.4%)	3 (4.1%)	1 (0.3%)	8 (0.9%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.4%)	0 (0.0%)	0 (0.0%)	1 (0.1%)
Total sequenced	**83 (100%)**	**61 (100%)**	**96 (100%)**	**59 (100%)**	**258 (100%)**	**73 (100%)**	**300 (100%)**	**930 (100%)**

Note: 'Other BA.5' excludes BQ lineages. 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 (2.7%), 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, March 19 to April 15, 2023

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
XBB.1.5	49 (55.1%)	219 (64.6%)	27 (33.3%)	117 (58.2%)	118 (54.9%)	80 (50.0%)	61 (57.0%)	671 (56.3%)
BQ.1.1	10 (11.2%)	20 (5.9%)	1 (1.2%)	14 (7.0%)	3 (1.4%)	5 (3.1%)	0 (0.0%)	53 (4.4%)
XBB.1.5.39	0 (0.0%)	3 (0.9%)	0 (0.0%)	4 (2.0%)	10 (4.7%)	3 (1.9%)	3 (2.8%)	23 (1.9%)
XBB.1.9.1	3 (3.4%)	17 (5.0%)	0 (0.0%)	4 (2.0%)	7 (3.3%)	4 (2.5%)	16 (15.0%)	51 (4.3%)
XBB.1.16	1 (1.1%)	0 (0.0%)	0 (0.0%)	3 (1.5%)	5 (2.3%)	11 (6.9%)	2 (1.9%)	22 (1.8%)
XBB.1.5.1	0 (0.0%)	8 (2.4%)	3 (3.7%)	7 (3.5%)	0 (0.0%)	2 (1.2%)	0 (0.0%)	20 (1.7%)
XBB.1.5.7	0 (0.0%)	17 (5.0%)	1 (1.2%)	3 (1.5%)	2 (0.9%)	3 (1.9%)	1 (0.9%)	27 (2.3%)
XBB.1.5.20	0 (0.0%)	3 (0.9%)	1 (1.2%)	1 (0.5%)	5 (2.3%)	0 (0.0%)	2 (1.9%)	12 (1.0%)
CH.1.1	4 (4.5%)	5 (1.5%)	0 (0.0%)	0 (0.0%)	2 (0.9%)	1 (0.6%)	0 (0.0%)	12 (1.0%)
XBB.1.5.17	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (2.0%)	2 (0.9%)	0 (0.0%)	1 (0.9%)	7 (0.6%)
Other recombinant	17 (19.1%)	31 (9.1%)	16 (19.8%)	26 (12.9%)	48 (22.3%)	29 (18.1%)	13 (12.1%)	180 (15.1%)
Other BQ lineages	3 (3.4%)	11 (3.2%)	31 (38.3%)	7 (3.5%)	4 (1.9%)	8 (5.0%)	7 (6.5%)	71 (6.0%)
Other BA.5	1 (1.1%)	3 (0.9%)	0 (0.0%)	6 (3.0%)	1 (0.5%)	2 (1.2%)	0 (0.0%)	13 (1.1%)
Other BA.2	1 (1.1%)	2 (0.6%)	1 (1.2%)	5 (2.5%)	8 (3.7%)	12 (7.5%)	1 (0.9%)	30 (2.5%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**89 (100%)**	**339 (100%)**	**81 (100%)**	**201 (100%)**	**215 (100%)**	**160 (100%)**	**107 (100%)**	**1,192 (100%)**

Note: 'Other BA.5' excludes BQ lineages. 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 (2.7%), 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 cases admitted to hospital and deceased cases by Pango lineage, representative surveillance, Ontario, January 22, 2023 to April 15, 2023

Pango lineage	Hospital admissions	Deceased	Total cases
XBB.1.5	732 (7.7%)	92 (1.0%)	9,552 (100%)
BQ.1.1	239 (7.8%)	34 (1.1%)	3,070 (100%)
XBB.1.5.39	49 (6.4%)	11 (1.4%)	771 (100%)
XBB.1.9.1	31 (8.6%)	4 (1.1%)	359 (100%)
XBB.1.16	11 (6.1%)	2 (1.1%)	181 (100%)
XBB.1.5.1	12 (5.4%)	0 (0.0%)	223 (100%)
XBB.1.5.7	23 (6.3%)	5 (1.4%)	367 (100%)
XBB.1.5.20	7 (3.2%)	4 (1.8%)	221 (100%)
CH.1.1	38 (7.1%)	7 (1.3%)	539 (100%)
XBB.1.5.17	11 (8.3%)	1 (0.8%)	133 (100%)
Other recombinant	185 (7.9%)	21 (0.9%)	2,330 (100%)
Other BQ lineages	370 (6.9%)	68 (1.3%)	5,339 (100%)
Other BA.5	51 (8.5%)	9 (1.5%)	601 (100%)
Other BA.2	48 (8.7%)	6 (1.1%)	552 (100%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**1,810 (7.5%)**	**264 (1.1%)**	**24,269 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ lineages. Cases include only those that linked to CCM (97.5%). 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 8. Number and percentage (row %) of cases by vaccine category and Pango lineage, representative surveillance, Ontario, March 19 to April 15, 2023

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two or more booster doses	Total cases
XBB.1.5	1,064 (34.0%)	21 (0.7%)	236 (7.5%)	613 (19.6%)	1,196 (38.2%)	3,130 (100%)
BQ.1.1	43 (20.4%)	0 (0.0%)	15 (7.1%)	44 (20.9%)	109 (51.7%)	211 (100%)
XBB.1.5.39	64 (30.5%)	2 (1.0%)	11 (5.2%)	47 (22.4%)	86 (41.0%)	210 (100%)
XBB.1.9.1	59 (28.4%)	1 (0.5%)	20 (9.6%)	41 (19.7%)	87 (41.8%)	208 (100%)
XBB.1.16	57 (34.1%)	3 (1.8%)	18 (10.8%)	27 (16.2%)	62 (37.1%)	167 (100%)
XBB.1.5.1	42 (31.8%)	2 (1.5%)	14 (10.6%)	17 (12.9%)	57 (43.2%)	132 (100%)
XBB.1.5.7	24 (24.2%)	1 (1.0%)	4 (4.0%)	16 (16.2%)	54 (54.5%)	99 (100%)
XBB.1.5.20	29 (32.6%)	0 (0.0%)	14 (15.7%)	18 (20.2%)	28 (31.5%)	89 (100%)
CH.1.1	28 (37.8%)	0 (0.0%)	4 (5.4%)	10 (13.5%)	32 (43.2%)	74 (100%)
XBB.1.5.17	13 (18.8%)	1 (1.4%)	5 (7.2%)	23 (33.3%)	27 (39.1%)	69 (100%)
Other recombinant	271 (30.9%)	8 (0.9%)	77 (8.8%)	189 (21.6%)	332 (37.9%)	877 (100%)
Other BQ lineages	123 (27.2%)	2 (0.4%)	37 (8.2%)	101 (22.3%)	190 (41.9%)	453 (100%)
Other BA.5	12 (33.3%)	0 (0.0%)	2 (5.6%)	5 (13.9%)	17 (47.2%)	36 (100%)
Other BA.2	37 (36.6%)	1 (1.0%)	4 (4.0%)	18 (17.8%)	41 (40.6%)	101 (100%)
Other Omicron	1 (50.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (50.0%)	2 (100%)
Total sequenced	**1,867 (31.9%)**	**42 (0.7%)**	**461 (7.9%)**	**1,169 (20.0%)**	**2,319 (39.6%)**	**5,858 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Cases include those that linked to CCM (97.3%). Individuals with a vaccine not approved by Health Canada were excluded. Vaccine category definitions can be found in the Severe Outcomes among 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 9. Number of cases by Pango lineage, cumulative counts, Ontario, January 1, 2021 to April 15, 2023

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
Variant of Concern (VOC)			
Alpha	**11,816**	**0**	**11,816**
Beta	**1,225**	**0**	**1,225**
Gamma	**3,912**	**0**	**3,912**
Delta	**45,919**	**0**	**45,919**
Omicron	**155,956**	**904**	**156,860**
B.1.1.529	0	0	0
BA.1	6,346	0	6,346
BA.1.1	18,470	1	18,471
BA.1.1.1	42	0	42
BA.1.1.10	1,661	0	1,661
BA.1.1.12	1	0	1
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	98	0	98
BA.1.1.17	6	0	6
BA.1.1.18	204	0	204
BA.1.1.2	6	0	6
BA.1.1.5	19	0	19
BA.1.1.6	3	0	3
BA.1.1.7	7	0	7
BA.1.1.8	3	0	3
BA.1.12	1	0	1
BA.1.13	34	0	34
BA.1.13.1	1	0	1
BA.1.14	71	0	71
BA.1.14.1	1	0	1
BA.1.14.2	1	0	1
BA.1.15	1,627	0	1,627
BA.1.15.1	22	0	22
BA.1.15.2	3	0	3
BA.1.16	2	0	2
BA.1.17	719	0	719

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BA.1.17.2	1,510	0	1,510
BA.1.18	106	0	106
BA.1.19	23	0	23
BA.1.20	91	0	91
BA.1.21	2	0	2
BA.1.3	1	0	1
BA.1.4	1	0	1
BA.1.6	66	0	66
BA.1.7	1	0	1
BA.1.9	1	0	1
BA.2	16,132	2	16,134
BA.2.1	114	0	114
BA.2.10	383	0	383
BA.2.10.1	21	0	21
BA.2.10.3	1	0	1
BA.2.11	7	0	7
BA.2.12	43	0	43
BA.2.12.1	6,444	0	6,444
BA.2.12.2	2	0	2
BA.2.13	27	0	27
BA.2.13.1	44	0	44
BA.2.15	1	0	1
BA.2.16	1	0	1
BA.2.17	1	0	1
BA.2.18	69	0	69
BA.2.2	4	0	4
BA.2.20	1,451	0	1,451
BA.2.21	328	0	328
BA.2.22	5	0	5
BA.2.23	56	0	56
BA.2.24	1	0	1
BA.2.26	8	0	8
BA.2.27	2	0	2
BA.2.29	1	0	1
BA.2.3	2,371	0	2,371
BA.2.3.1	1	0	1
BA.2.3.10	81	0	81
BA.2.3.12	3	0	3
BA.2.3.14	2	0	2
BA.2.3.15	1	0	1

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BA.2.3.16	4	0	4
BA.2.3.17	3	0	3
BA.2.3.2	16	0	16
BA.2.3.20	156	0	156
BA.2.3.4	944	0	944
BA.2.3.5	1	0	1
BA.2.3.6	78	0	78
BA.2.3.7	3	0	3
BA.2.3.8	2	0	2
BA.2.31	17	0	17
BA.2.31.1	3	0	3
BA.2.32	4	0	4
BA.2.34	1	0	1
BA.2.35	5	0	5
BA.2.36	23	0	23
BA.2.37	85	0	85
BA.2.38	129	0	129
BA.2.38.1	3	0	3
BA.2.38.2	6	0	6
BA.2.40	2	0	2
BA.2.40.1	21	0	21
BA.2.41	4	0	4
BA.2.42	2	0	2
BA.2.43	1	0	1
BA.2.47	2	0	2
BA.2.48	15	0	15
BA.2.49	4	0	4
BA.2.5	40	0	40
BA.2.50	13	0	13
BA.2.51	22	0	22
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	59	0	59
BA.2.57	2	0	2
BA.2.59	1	0	1
BA.2.6	6	0	6
BA.2.62	4	0	4
BA.2.64	13	0	13

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BA.2.65	1,634	0	1,634
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	3	0	3
BA.2.74	44	0	44
BA.2.75	124	0	124
BA.2.75.1	29	0	29
BA.2.75.10	3	0	3
BA.2.75.2	236	0	236
BA.2.75.3	7	0	7
BA.2.75.4	1	0	1
BA.2.75.5	46	0	46
BA.2.75.6	4	0	4
BA.2.76	90	0	90
BA.2.78	3	0	3
BA.2.79	5	0	5
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	1,537	0	1,537
BA.2.9.2	2	0	2
BA.2.9.3	15	0	15
BA.2.9.4	1	0	1
BA.2.9.5	6	0	6
BA.2.9.7	6	0	6
BA.3.1	1	0	1
BA.4	712	0	712
BA.4.1	1,366	0	1,366
BA.4.1.1	47	0	47
BA.4.1.10	7	0	7
BA.4.1.4	2	0	2
BA.4.1.5	2	0	2
BA.4.1.6	26	0	26
BA.4.1.8	159	0	159
BA.4.1.9	6	0	6
BA.4.2	191	0	191
BA.4.3	2	0	2

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BA.4.4	83	0	83
BA.4.5	2	0	2
BA.4.6	2,464	1	2,465
BA.4.6.1	2	0	2
BA.4.6.2	64	0	64
BA.4.6.3	24	0	24
BA.4.6.4	16	0	16
BA.4.6.5	200	0	200
BA.4.7	54	0	54
BA.5	392	0	392
BA.5.1	5,981	2	5,983
BA.5.1.1	1,017	0	1,017
BA.5.1.10	252	0	252
BA.5.1.12	127	0	127
BA.5.1.15	35	0	35
BA.5.1.16	1	0	1
BA.5.1.17	12	0	12
BA.5.1.18	104	0	104
BA.5.1.19	11	0	11
BA.5.1.2	329	0	329
BA.5.1.20	30	0	30
BA.5.1.21	2	0	2
BA.5.1.22	275	0	275
BA.5.1.23	395	0	395
BA.5.1.24	122	0	122
BA.5.1.25	172	0	172
BA.5.1.27	69	0	69
BA.5.1.28	17	0	17
BA.5.1.3	70	0	70
BA.5.1.30	747	0	747
BA.5.1.33	29	0	29
BA.5.1.35	20	0	20
BA.5.1.36	12	0	12
BA.5.1.37	13	1	14
BA.5.1.4	11	0	11
BA.5.1.5	256	0	256
BA.5.1.6	60	0	60
BA.5.1.7	649	0	649
BA.5.1.9	1	0	1
BA.5.10	233	0	233

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BA.5.10.1	9	0	9
BA.5.11	4	6	10
BA.5.12	1	0	1
BA.5.2	7,224	1	7,225
BA.5.2.1	11,528	0	11,528
BA.5.2.12	3	0	3
BA.5.2.13	235	0	235
BA.5.2.14	158	0	158
BA.5.2.16	60	0	60
BA.5.2.18	48	0	48
BA.5.2.19	39	0	39
BA.5.2.2	138	0	138
BA.5.2.20	610	0	610
BA.5.2.21	339	0	339
BA.5.2.22	411	0	411
BA.5.2.23	78	0	78
BA.5.2.24	90	0	90
BA.5.2.25	126	0	126
BA.5.2.26	112	0	112
BA.5.2.27	156	0	156
BA.5.2.28	124	0	124
BA.5.2.3	191	0	191
BA.5.2.31	54	0	54
BA.5.2.32	52	0	52
BA.5.2.33	34	0	34
BA.5.2.34	251	3	254
BA.5.2.35	117	0	117
BA.5.2.36	6	0	6
BA.5.2.37	21	0	21
BA.5.2.39	1	0	1
BA.5.2.4	17	0	17
BA.5.2.44	5	0	5
BA.5.2.47	11	0	11
BA.5.2.48	9	0	9
BA.5.2.52	1	0	1
BA.5.2.53	217	0	217
BA.5.2.54	1	0	1
BA.5.2.55	1	0	1
BA.5.2.56	14	0	14
BA.5.2.57	49	0	49

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BA.5.2.58	9	0	9
BA.5.2.59	7	0	7
BA.5.2.6	289	2	291
BA.5.2.60	1	0	1
BA.5.2.61	1	0	1
BA.5.2.63	117	0	117
BA.5.2.7	11	0	11
BA.5.2.8	121	0	121
BA.5.2.9	904	0	904
BA.5.3	18	0	18
BA.5.3.1	155	1	156
BA.5.3.2	9	0	9
BA.5.3.3	39	0	39
BA.5.3.4	4	0	4
BA.5.3.5	4	0	4
BA.5.5	1,690	0	1,690
BA.5.5.1	61	0	61
BA.5.5.2	85	0	85
BA.5.5.3	22	0	22
BA.5.6	1,260	1	1,261
BA.5.6.1	14	0	14
BA.5.6.2	30	0	30
BA.5.8	198	0	198
BA.5.9	179	0	179
BB.1	1	0	1
BB.2	1	0	1
BC.2	1	0	1
BE.1	996	0	996
BE.1.1	675	0	675
BE.1.1.1	126	0	126
BE.1.1.2	61	2	63
BE.1.2	12	0	12
BE.1.2.1	612	0	612
BE.1.3	1	0	1
BE.1.4	196	0	196
BE.1.4.1	33	0	33
BE.1.4.2	10	0	10
BE.1.4.4	1	0	1
BE.10	27	0	27
BE.13	5	0	5

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BE.2	15	0	15
BE.3	187	0	187
BE.4	105	0	105
BE.4.1	21	0	21
BE.4.1.1	5	0	5
BE.4.2	2	0	2
BE.5	169	0	169
BE.6	2	0	2
BE.7	2	0	2
BE.8	1	0	1
BE.9	56	4	60
BF.1	291	0	291
BF.1.1	9	0	9
BF.10	1,814	0	1,814
BF.11	653	1	654
BF.11.1	112	0	112
BF.11.2	1	0	1
BF.11.3	225	0	225
BF.11.4	10	0	10
BF.12	48	0	48
BF.13	240	0	240
BF.14	157	0	157
BF.15	10	0	10
BF.16	59	0	59
BF.18	2	0	2
BF.19	1	0	1
BF.2	97	0	97
BF.20	4	0	4
BF.21	153	0	153
BF.23	8	0	8
BF.25	60	0	60
BF.26	551	0	551
BF.27	331	0	331
BF.28	569	0	569
BF.29	2	0	2
BF.3	44	0	44
BF.3.1	3	0	3
BF.31	5	0	5
BF.31.1	91	0	91
BF.32	5	0	5

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BF.34	40	0	40
BF.36	13	0	13
BF.38	3	0	3
BF.39	319	0	319
BF.4	217	0	217
BF.40	4	0	4
BF.41	32	0	32
BF.5	884	0	884
BF.5.5	1	0	1
BF.6	9	0	9
BF.7	1,804	0	1,804
BF.7.1	5	0	5
BF.7.10	1	0	1
BF.7.12	7	0	7
BF.7.14	11	0	11
BF.7.14.1	4	0	4
BF.7.16	43	0	43
BF.7.16.1	9	0	9
BF.7.19	19	0	19
BF.7.20	55	0	55
BF.7.21	41	0	41
BF.7.22	37	0	37
BF.7.23	178	0	178
BF.7.24	10	0	10
BF.7.26	3	0	3
BF.7.27	92	0	92
BF.7.3	1	0	1
BF.7.4	142	0	142
BF.7.4.1	135	0	135
BF.7.4.2	10	0	10
BF.7.5	92	0	92
BF.7.6	138	0	138
BF.7.7	258	0	258
BF.7.8	11	0	11
BF.8	110	0	110
BF.9	833	0	833
BG.2	86	0	86
BG.4	14	0	14
BG.5	24	0	24
BG.6	11	0	11

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BH.1	14	0	14
BK.1	229	0	229
BL.1	27	0	27
BL.1.4	1	0	1
BL.2	5	0	5
BL.3	1	0	1
BL.4	4	0	4
BL.5	2	0	2
BL.6	1	0	1
BM.1	3	0	3
BM.1.1	22	0	22
BM.1.1.1	28	0	28
BM.1.1.3	37	0	37
BM.1.1.4	1	0	1
BM.1.1.5	1	0	1
BM.2	5	0	5
BM.2.1	14	0	14
BM.4.1.1	3	0	3
BN.1	187	1	188
BN.1.1	3	0	3
BN.1.1.1	1	0	1
BN.1.10	38	0	38
BN.1.2	41	0	41
BN.1.2.1	44	0	44
BN.1.2.2	2	0	2
BN.1.2.3	30	1	31
BN.1.2.4	33	0	33
BN.1.3	146	0	146
BN.1.3.1	108	0	108
BN.1.3.3	1	0	1
BN.1.3.5	44	1	45
BN.1.3.6	3	0	3
BN.1.3.7	1	0	1
BN.1.3.8	1	0	1
BN.1.4	31	0	31
BN.1.4.2	2	0	2
BN.1.4.3	2	0	2
BN.1.5	44	1	45
BN.1.5.1	1	0	1
BN.1.5.2	21	0	21

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BN.1.7	4	0	4
BN.1.9	6	0	6
BN.2	2	0	2
BN.2.1	1	0	1
BN.3.1	41	0	41
BN.4	1	0	1
BN.5	7	0	7
BN.6	13	0	13
BQ.1	3,386	14	3,400
BQ.1.1	10,426	218	10,644
BQ.1.1.1	553	5	558
BQ.1.1.10	368	10	378
BQ.1.1.11	29	0	29
BQ.1.1.13	53	1	54
BQ.1.1.15	123	9	132
BQ.1.1.16	1	0	1
BQ.1.1.17	12	0	12
BQ.1.1.18	289	3	292
BQ.1.1.19	1	0	1
BQ.1.1.2	109	0	109
BQ.1.1.20	17	0	17
BQ.1.1.21	2	0	2
BQ.1.1.22	8	0	8
BQ.1.1.23	24	1	25
BQ.1.1.24	19	0	19
BQ.1.1.25	9	0	9
BQ.1.1.27	2	0	2
BQ.1.1.28	10	0	10
BQ.1.1.29	5	0	5
BQ.1.1.3	348	21	369
BQ.1.1.30	245	17	262
BQ.1.1.31	17	0	17
BQ.1.1.32	75	8	83
BQ.1.1.35	179	39	218
BQ.1.1.36	4	1	5
BQ.1.1.37	49	13	62
BQ.1.1.38	6	0	6
BQ.1.1.39	163	16	179
BQ.1.1.4	407	1	408
BQ.1.1.40	631	15	646

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BQ.1.1.41	154	1	155
BQ.1.1.42	8	0	8
BQ.1.1.43	10	1	11
BQ.1.1.44	69	1	70
BQ.1.1.45	57	25	82
BQ.1.1.46	85	3	88
BQ.1.1.47	80	3	83
BQ.1.1.48	61	1	62
BQ.1.1.5	357	2	359
BQ.1.1.51	159	1	160
BQ.1.1.52	119	0	119
BQ.1.1.53	0	1	1
BQ.1.1.54	23	0	23
BQ.1.1.55	49	8	57
BQ.1.1.56	3	0	3
BQ.1.1.58	6	1	7
BQ.1.1.6	93	0	93
BQ.1.1.60	5	0	5
BQ.1.1.61	44	2	46
BQ.1.1.62	1	0	1
BQ.1.1.63	4	1	5
BQ.1.1.65	97	34	131
BQ.1.1.67	137	0	137
BQ.1.1.68	66	10	76
BQ.1.1.69	122	0	122
BQ.1.1.7	366	4	370
BQ.1.1.72	2	0	2
BQ.1.1.8	107	2	109
BQ.1.1.9	41	0	41
BQ.1.10	259	19	278
BQ.1.10.1	295	0	295
BQ.1.10.2	5	0	5
BQ.1.11	320	0	320
BQ.1.12	764	0	764
BQ.1.13	750	2	752
BQ.1.13.1	173	6	179
BQ.1.14	549	10	559
BQ.1.15	11	0	11
BQ.1.15.1	37	0	37
BQ.1.16	77	0	77

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BQ.1.18	12	0	12
BQ.1.19	49	0	49
BQ.1.2	879	25	904
BQ.1.2.1	9	0	9
BQ.1.20	1	0	1
BQ.1.22	225	5	230
BQ.1.23	187	0	187
BQ.1.24	2	0	2
BQ.1.25	222	1	223
BQ.1.25.1	84	3	87
BQ.1.27	4	0	4
BQ.1.28	2	0	2
BQ.1.3	426	0	426
BQ.1.30	289	1	290
BQ.1.31	5	0	5
BQ.1.4	4	0	4
BQ.1.5	972	2	974
BQ.1.6	29	0	29
BQ.1.7	4	0	4
BQ.1.8	200	1	201
BQ.1.9	63	0	63
BR.1	4	0	4
BR.1.2	6	0	6
BR.2	7	0	7
BR.2.1	91	14	105
BR.3	7	0	7
BR.4	14	0	14
BS.1.1	4	0	4
BT.1	12	0	12
BT.2	2	0	2
BU.1	42	0	42
BU.2	9	0	9
BU.3	2	0	2
BV.2	3	0	3
BW.1	41	0	41
BW.1.1	58	1	59
BW.1.1.1	85	0	85
BW.1.1.2	50	1	51
BW.1.2	8	0	8
BY.1	91	0	91

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
BY.1.2	10	0	10
CA.1	1	0	1
CA.2	2	0	2
CA.3.1	8	0	8
CA.5	25	0	25
CA.7	57	1	58
CB.1	4	0	4
CC.1	21	0	21
CD.2	1	0	1
CE.1	32	0	32
CG.1	32	0	32
CH.1.1	720	77	797
CH.1.1.1	64	8	72
CH.1.1.10	8	8	16
CH.1.1.11	43	6	49
CH.1.1.12	1	0	1
CH.1.1.15	1	0	1
CH.1.1.16	0	4	4
CH.1.1.17	0	13	13
CH.1.1.18	1	1	2
CH.1.1.19	3	0	3
CH.1.1.2	48	10	58
CH.1.1.7	3	0	3
CJ.1	8	0	8
CJ.1.1	10	0	10
CK.1	202	5	207
CK.2	11	0	11
CK.2.1	16	0	16
CK.2.1.1	29	1	30
CK.3	33	0	33
CL.1	19	0	19
CL.1.2	2	0	2
CL.1.3	2	0	2
CM.1	55	0	55
CM.10	3	0	3
CM.12	3	0	3
CM.2	92	0	92
CM.4	2	0	2
CM.4.1	8	0	8
CM.6.1	1	0	1

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
CM.7	1	0	1
CM.8	2	0	2
CM.8.1	107	16	123
CM.8.1.2	1	0	1
CM.8.1.4	2	0	2
CM.9	10	0	10
CN.1	22	0	22
CN.2	125	0	125
CP.1	28	0	28
CP.5	1	0	1
CP.8	4	0	4
CQ.1	2	0	2
CQ.1.1	7	0	7
CQ.2	27	3	30
CR.1	7	0	7
CR.1.1	8	0	8
CR.1.2	11	0	11
CR.1.3	1	0	1
CT.1	1	0	1
CV.1	25	0	25
CV.2	1	0	1
CZ.2	294	7	301
DB.1	1	0	1
DB.3	1	0	1
DC.1	3	0	3
DE.1	79	0	79
DE.2	1	0	1
DF.1	2	0	2
DF.1.1	20	0	20
DG.1	3	0	3
DJ.1.1	18	0	18
DJ.1.1.1	4	0	4
DK.1	1	0	1
DL.1	8	0	8
DM.1	1	0	1
DN.1	2	0	2
DN.1.1	2	0	2
DN.1.1.4	1	0	1
DQ.1	1	0	1
DR.1	4	0	4

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
DR.2	14	2	16
DS.1	2	2	4
DS.2	1	0	1
DT.2	13	0	13
DU.1	25	35	60
DV.1	10	6	16
DV.1.1	29	8	37
DV.2	1	0	1
DV.3	0	1	1
DY.1	2	0	2
DY.1.1	1	0	1
DY.2	7	1	8
DY.3	1	0	1
DY.4	1	0	1
EA.1	1	0	1
EB.1	15	0	15
ED.2	76	41	117
ED.3	1	0	1
EE.1	80	1	81
EE.2	55	0	55
EE.3	159	8	167
EE.4	9	0	9
EE.5	11	0	11
EF.1	25	0	25
EF.1.1	23	0	23
EF.1.1.1	66	11	77
EF.1.2	4	0	4
EF.1.3	1	0	1
EF.2	1	0	1
EN.1	0	1	1
ES.1	227	11	238
Variant of Interest (VOI)			
Mu	**242**	**0**	**24**
Lambda	**8**	**0**	**8**
Recombinant	**11,629**	**5,122**	**16,751**
EG.1	1	17	18
EK.2.1	5	0	5
EK.3	0	1	1
EL.1	0	1	1
EM.1	1	0	1

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
EU.1.1	1	6	7
FD.1.1	8	21	29
FD.2	12	5	17
FE.1	6	35	41
FG.2	2	6	8
FG.3	2	0	2
FH.1	0	1	1
XAC	30	0	30
XAF	1	0	1
XAJ	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	69	1	70
XBB.1	391	30	421
XBB.1.1	15	0	15
XBB.1.10	3	0	3
XBB.1.11.1	1	15	16
XBB.1.15	103	1	104
XBB.1.16	15	177	192
XBB.1.16.1	5	46	51
XBB.1.17	1	0	1
XBB.1.17.1	6	2	8
XBB.1.18.1	1	3	4
XBB.1.19	1	1	2
XBB.1.19.1	4	16	20
XBB.1.2	7	0	7
XBB.1.21	2	0	2
XBB.1.22	20	9	29
XBB.1.22.1	4	3	7
XBB.1.22.2	0	2	2
XBB.1.25	1	0	1
XBB.1.26	3	0	3
XBB.1.3	1	0	1
XBB.1.30	15	0	15

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
XBB.1.4	12	0	12
XBB.1.5	7,454	3,214	10,668
XBB.1.5.1	94	137	231
XBB.1.5.10	6	12	18
XBB.1.5.11	44	9	53
XBB.1.5.12	8	34	42
XBB.1.5.13	64	47	111
XBB.1.5.14	1	8	9
XBB.1.5.15	85	36	121
XBB.1.5.16	19	7	26
XBB.1.5.17	70	70	140
XBB.1.5.18	95	42	137
XBB.1.5.19	33	4	37
XBB.1.5.2	14	8	22
XBB.1.5.20	155	90	245
XBB.1.5.21	73	5	78
XBB.1.5.23	24	20	44
XBB.1.5.24	47	14	61
XBB.1.5.25	1	2	3
XBB.1.5.26	1	2	3
XBB.1.5.28	1	0	1
XBB.1.5.3	11	31	42
XBB.1.5.30	10	14	24
XBB.1.5.31	154	47	201
XBB.1.5.32	167	49	216
XBB.1.5.33	24	7	31
XBB.1.5.34	10	11	21
XBB.1.5.35	8	24	32
XBB.1.5.36	5	20	25
XBB.1.5.37	7	31	38
XBB.1.5.39	673	218	891
XBB.1.5.4	70	46	116
XBB.1.5.5	3	0	3
XBB.1.5.6	2	0	2
XBB.1.5.7	361	103	464
XBB.1.5.8	13	10	23
XBB.1.5.9	84	35	119
XBB.1.7	1	0	1
XBB.1.9	8	2	10
XBB.1.9.1	158	212	370

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
XBB.1.9.2	28	46	74
XBB.1.9.3	2	0	2
XBB.2	74	0	74
XBB.2.3	17	30	47
XBB.2.3.2	1	3	4
XBB.2.4	5	2	7
XBB.2.5	1	0	1
XBB.2.6	30	0	30
XBB.2.7	1	0	1
XBB.2.8	2	0	2
XBB.3	18	0	18
XBB.6.1	1	0	1
XBB.8	4	0	4
XBC.1	10	1	11
XBC.1.1	2	0	2
XBC.1.3	1	1	2
XBD	2	0	2
XBE	9	0	9
XBF	182	16	198
XBF.1	1	0	1
XBF.2	2	0	2
XBF.3	15	0	15
XBF.5	1	0	1
XBF.6	1	0	1
XBF.7	2	0	2
XBF.7.1	1	0	1
XBF.9	1	0	1
XBH	1	0	1
XBJ	1	0	1
XBK	4	1	5
XBK.1	0	1	1
XBL	2	0	2
XBM	283	0	283
XBN	1	0	1
XBP	5	1	6
XBR	1	0	1
XBV	1	0	1
XE	3	0	3
XM	1	0	1
XN	1	0	1

WHO label / Pango lineage	January 1, 2021 - March 18, 2023	March 19, 2023 - April 15, 2023	Total
XQ	4	0	4
XW	7	0	7
XZ	1	0	1
Non-VOC/VOI	**6,357**	**0**	**6,357**
Total sequenced	**237,064**	**6,026**	**243,090**

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 April 26, 2023 at approximately 2:00 a.m.
- Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on April 26, 2023 at approximately 9:30 a.m.

The Hospital for Sick Children (HSC)

- Data were received by PHO on April 25, 2023 at approximately 1:10 p.m.

Kingston Health Sciences Centre (KHSC)

- Data were received by PHO on April 25, 2023 at approximately 12:25 p.m.

Shared Hospital Laboratory (SHL)

- Data were received by PHO on April 25, 2023 at approximately 5:30 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were received by PHO on April 25, 2023 at approximately 5:00 p.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on April 25, 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 April 24, 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 (2.7%), 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 hospital admission, and deceased indicators only include cases that linked to CCM (97.5% of cases).

- 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, 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, Novavax Nuvaxovid and Janssen Jcovden 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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