Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, January 27, 2023

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of January 25, 2023 and partner laboratories in the Ontario COVID-19 Genomics Network as of January 24, 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 (January 8 to 14), BQ.1.1 was the most prevalent lineage (32.7%), followed by XBB.1.5 (9.0%). For this week, 18.3% of cases were other BQ lineages and 8.8% were other BA.5 lineages (excluding BQ and BF lineages).
- The proportion of BQ.1.1 decreased from 36.1% (January 1 to 7) to 32.7% (January 8 to 14) and is projected to decline to 22.3% (95% CI: 19.5% - 25.4%) by February 1, 2023.
- The proportion of XBB.1.5 increased from 4.9% (January 1 to 7) to 9.0% (January 8 to 14) and is projected to increase to 44.2% (95% CI: 37.4% - 51.1%) by February 1, 2023.
    - The weekly growth rate of XBB.1.5 is 1.94 (95% CI: 1.82-2.07) times that of BQ.1.1.

> 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.

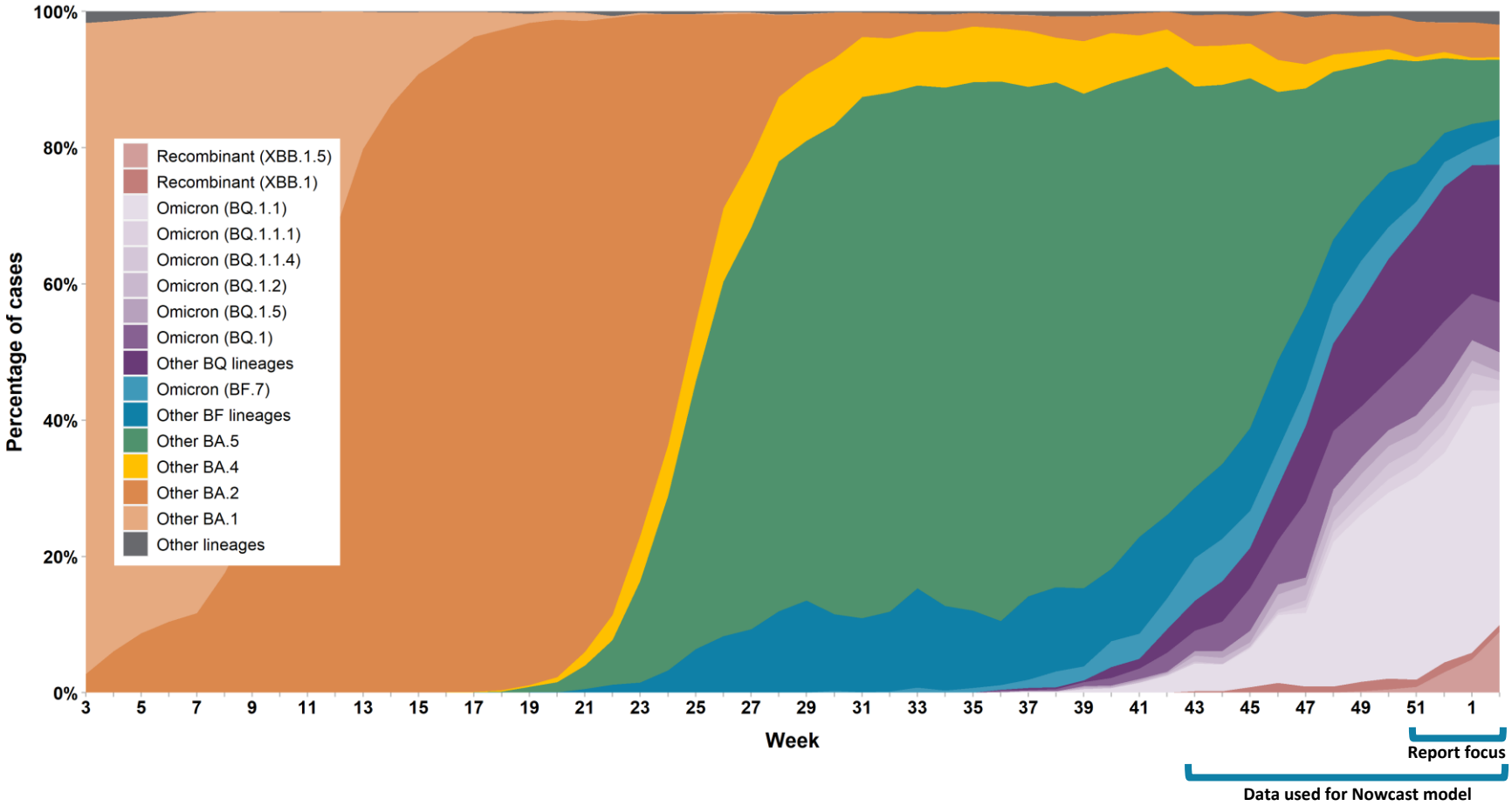
Representative Surveillance

Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, December 18, 2022 to January 14, 2023

Week	Number of cases	Number sequenced	Percentage sequenced
Week 51 (December 18 - December 24)	6,310	3,528	55.9%
Week 52 (December 25 - December 31)	6,962	3,669	52.7%
Week 1 (January 1 - January 7)	7,358	4,156	56.5%
Week 2 (January 8 - January 14)	5,636	3,339	59.2%
Total	**26,266**	**14,692**	**55.9%**

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, January 16, 2022 to January 14, 2023



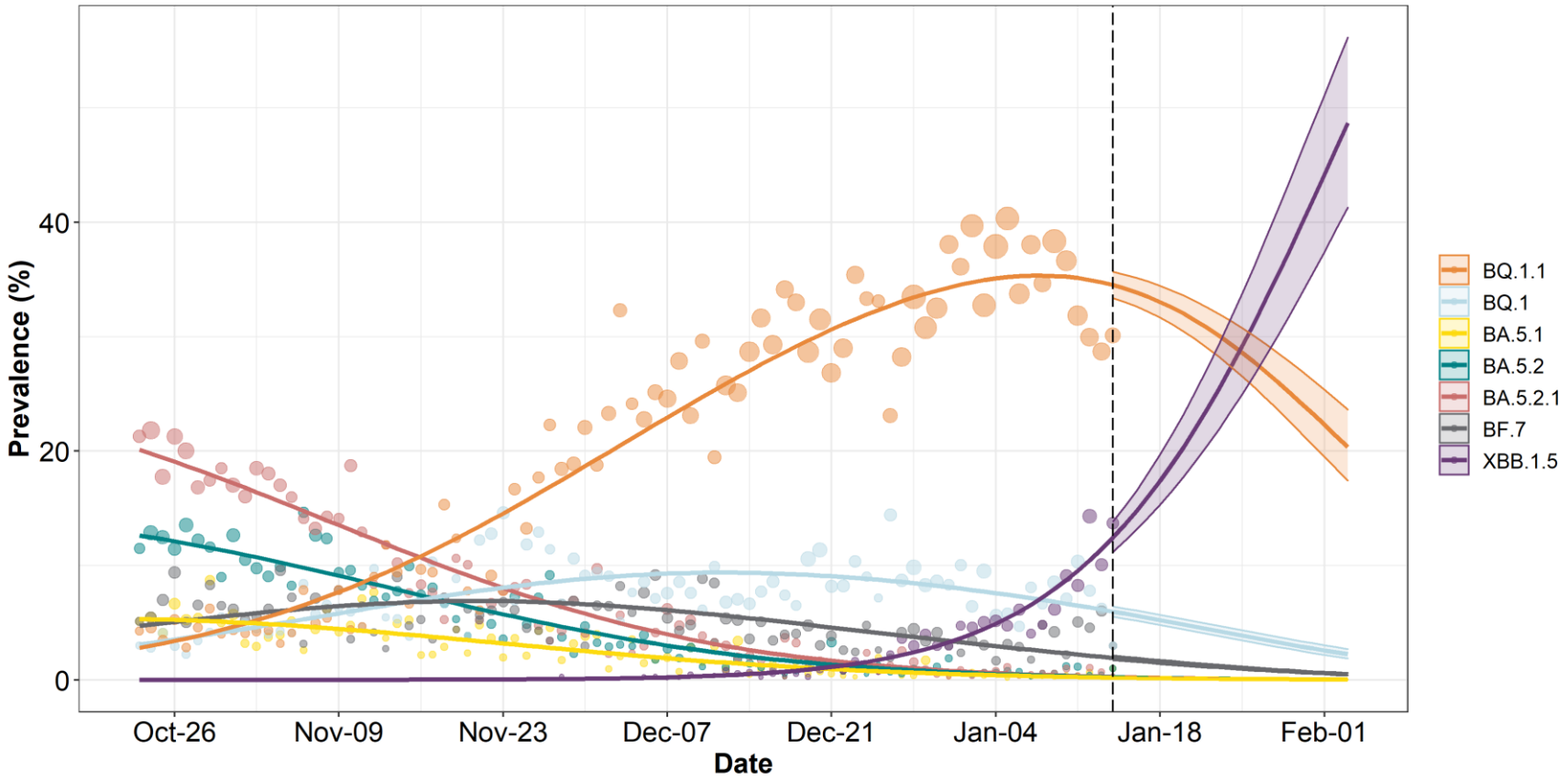
Note: Results may not be representative of Ontario overall, particularly in earlier weeks. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for 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, December 18, 2022 to January 14, 2023

WHO label/Pango lineage	Week 51 (December 18 - December 24)	Week 52 (December 25 - December 31)	Week 1 (January 1 - January 7)	Week 2 (January 8 - January 14)	Total (December 18 - January 14)
Omicron	**3,408 (96.6%)**	**3,446 (93.9%)**	**3,846 (92.5%)**	**2,943 (88.1%)**	**13,643 (92.9%)**
BQ.1.1	1,050 (29.8%)	1,130 (30.8%)	1,500 (36.1%)	1,091 (32.7%)	4,771 (32.5%)
BQ.1	325 (9.2%)	332 (9.0%)	284 (6.8%)	245 (7.3%)	1,186 (8.1%)
BF.7	125 (3.5%)	132 (3.6%)	108 (2.6%)	140 (4.2%)	505 (3.4%)
BQ.1.5	88 (2.5%)	112 (3.1%)	122 (2.9%)	97 (2.9%)	419 (2.9%)
BQ.1.1.1	77 (2.2%)	104 (2.8%)	102 (2.5%)	57 (1.7%)	340 (2.3%)
BQ.1.1.4	71 (2.0%)	80 (2.2%)	104 (2.5%)	53 (1.6%)	308 (2.1%)
BQ.1.2	82 (2.3%)	82 (2.2%)	77 (1.9%)	39 (1.2%)	280 (1.9%)
BQ.1.13	63 (1.8%)	62 (1.7%)	87 (2.1%)	65 (1.9%)	277 (1.9%)
Other BQ lineages	594 (16.8%)	662 (18.0%)	697 (16.8%)	610 (18.3%)	2,563 (17.4%)
Other BF lineages	199 (5.6%)	157 (4.3%)	143 (3.4%)	80 (2.4%)	579 (3.9%)
Other BA.5	530 (15.0%)	408 (11.1%)	392 (9.4%)	295 (8.8%)	1,625 (11.1%)
Other BA.4	21 (0.6%)	33 (0.9%)	15 (0.4%)	13 (0.4%)	82 (0.6%)
Other BA.2	183 (5.2%)	152 (4.1%)	215 (5.2%)	157 (4.7%)	707 (4.8%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (<0.1%)	1 (<0.1%)
Recombinant	**120 (3.4%)**	**223 (6.1%)**	**310 (7.5%)**	**396 (11.9%)**	**1,049 (7.1%)**
XBB.1.5	30 (0.9%)	112 (3.1%)	202 (4.9%)	301 (9.0%)	645 (4.4%)
XBB.1	38 (1.1%)	51 (1.4%)	43 (1.0%)	31 (0.9%)	163 (1.1%)
Other recombinant	52 (1.5%)	60 (1.6%)	65 (1.6%)	64 (1.9%)	241 (1.6%)
Total sequenced	**3,528 (100%)**	**3,669 (100%)**	**4,156 (100%)**	**3,339 (100%)**	**14,692 (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 23, 2022 to February 4, 2023



Note: 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 23, 2022 to February 4, 2023

WHO label/ Pango lineage	Week 1 (January 4): Estimated	Week 2 (January 11): Estimated	Week 3 (January 18): Projected	Week 4 (January 25): Projected	Week 5 (February 1): Projected	Weekly relative growth rate
BQ.1.1	35.1 (34.3 - 35.9)	35.1 (34.1 - 36.1)	33.0 (31.7 - 34.5)	28.6 (26.5 - 30.8)	22.3 (19.5 - 25.4)	1.00 (reference)
BQ.1	7.6 (7.2 - 8.0)	6.5 (6.1 - 7.0)	5.2 (4.8 - 5.7)	3.9 (3.5 - 4.3)	2.6 (2.2 - 3.0)	0.85 (0.84 - 0.87)
BA.5.1	0.4 (0.3 - 0.5)	0.3 (0.2 - 0.3)	0.1 (0.1 - 0.2)	0.1 (0.1 - 0.1)	0.0 (0.0 - 0.1)	0.61 (0.60 - 0.63)
BA.5.2	0.5 (0.4 - 0.6)	0.3 (0.2 - 0.4)	0.2 (0.1 - 0.2)	0.1 (0.1 - 0.1)	0.0 (0.0 - 0.0)	0.58 (0.56 - 0.59)
BA.5.2.1	0.6 (0.5 - 0.7)	0.3 (0.3 - 0.4)	0.2 (0.1 - 0.2)	0.1 (0.1 - 0.1)	0.0 (0.0 - 0.0)	0.56 (0.55 - 0.57)
BF.7	3.0 (2.7 - 3.2)	2.2 (2.0 - 2.5)	1.6 (1.4 - 1.8)	1.0 (0.9 - 1.2)	0.6 (0.5 - 0.7)	0.75 (0.74 - 0.76)
XBB.1.5	4.9 (4.6 - 5.3)	9.5 (8.7 - 10.5)	17.4 (15.3 - 19.7)	29.2 (25.0 - 33.8)	44.2 (37.4 - 51.1)	1.94 (1.82 - 2.07)

Note: 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, December 18, 2022 to January 14, 2023

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	**249 (88.3%)**	**43 (87.8%)**	**141 (94.6%)**	**2,895 (91.4%)**	**3,287 (92.1%)**	**3,112 (93.4%)**	**3,906 (94.5%)**	**13,633 (92.9%)**
BQ.1.1	91 (32.3%)	11 (22.4%)	56 (37.6%)	1,035 (32.7%)	1,112 (31.2%)	1,073 (32.2%)	1,391 (33.6%)	4,769 (32.5%)
BQ.1	21 (7.4%)	8 (16.3%)	10 (6.7%)	248 (7.8%)	302 (8.5%)	270 (8.1%)	327 (7.9%)	1,186 (8.1%)
BF.7	7 (2.5%)	1 (2.0%)	2 (1.3%)	82 (2.6%)	96 (2.7%)	104 (3.1%)	213 (5.2%)	505 (3.4%)
BQ.1.5	6 (2.1%)	0 (0.0%)	5 (3.4%)	89 (2.8%)	90 (2.5%)	98 (2.9%)	131 (3.2%)	419 (2.9%)
BQ.1.1.1	8 (2.8%)	1 (2.0%)	1 (0.7%)	82 (2.6%)	86 (2.4%)	77 (2.3%)	83 (2.0%)	338 (2.3%)
BQ.1.1.4	7 (2.5%)	0 (0.0%)	4 (2.7%)	83 (2.6%)	76 (2.1%)	60 (1.8%)	78 (1.9%)	308 (2.1%)
BQ.1.2	11 (3.9%)	0 (0.0%)	2 (1.3%)	71 (2.2%)	77 (2.2%)	61 (1.8%)	58 (1.4%)	280 (1.9%)
BQ.1.13	4 (1.4%)	2 (4.1%)	1 (0.7%)	50 (1.6%)	63 (1.8%)	68 (2.0%)	89 (2.2%)	277 (1.9%)
Other BQ lineages	44 (15.6%)	11 (22.4%)	24 (16.1%)	548 (17.3%)	650 (18.2%)	572 (17.2%)	711 (17.2%)	2,560 (17.4%)
Other BF lineages	8 (2.8%)	1 (2.0%)	9 (6.0%)	93 (2.9%)	122 (3.4%)	157 (4.7%)	189 (4.6%)	579 (3.9%)
Other BA.5	27 (9.6%)	6 (12.2%)	13 (8.7%)	326 (10.3%)	417 (11.7%)	375 (11.3%)	459 (11.1%)	1,623 (11.1%)
Other BA.4	2 (0.7%)	0 (0.0%)	0 (0.0%)	20 (0.6%)	21 (0.6%)	19 (0.6%)	20 (0.5%)	82 (0.6%)
Other BA.2	13 (4.6%)	2 (4.1%)	14 (9.4%)	168 (5.3%)	175 (4.9%)	177 (5.3%)	157 (3.8%)	706 (4.8%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (<0.1%)	0 (0.0%)	1 (<0.1%)
Recombinant	**33 (11.7%)**	**6 (12.2%)**	**8 (5.4%)**	**271 (8.6%)**	**282 (7.9%)**	**221 (6.6%)**	**228 (5.5%)**	**1,049 (7.1%)**
XBB.1.5	20 (7.1%)	6 (12.2%)	4 (2.7%)	174 (5.5%)	187 (5.2%)	137 (4.1%)	117 (2.8%)	645 (4.4%)
XBB.1	3 (1.1%)	0 (0.0%)	3 (2.0%)	41 (1.3%)	34 (1.0%)	35 (1.1%)	47 (1.1%)	163 (1.1%)
Other recombinant	10 (3.5%)	0 (0.0%)	1 (0.7%)	56 (1.8%)	61 (1.7%)	49 (1.5%)	64 (1.5%)	241 (1.6%)
Total sequenced	**282 (100%)**	**49 (100%)**	**149 (100%)**	**3,166 (100%)**	**3,569 (100%)**	**3,333 (100%)**	**4,134 (100%)**	**14,682 (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, December 18, 2022 to January 14, 2023

Public Health Unit	Week 51 (December 18 - December 24)	Week 52 (December 25 - December 31)	Week 1 (January 1 - January 7)	Week 2 (January 8 - January 14)	Total (December 18 - January 14)
Northwestern Health Unit	66.7% (2/3)	100% (4/4)	83.3% (10/12)	33.3% (1/3)	77.3% (17/22)
Thunder Bay District Health Unit	95.8% (23/24)	88.2% (30/34)	88.1% (59/67)	93.3% (56/60)	90.8% (168/185)
TOTAL NORTH WEST	**92.6% (25/27)**	**89.5% (34/38)**	**87.3% (69/79)**	**90.5% (57/63)**	**89.4% (185/207)**
Algoma Public Health	52.2% (12/23)	25.0% (2/8)	69.2% (9/13)	50.0% (10/20)	51.6% (33/64)
North Bay Parry Sound District Health Unit	44.4% (12/27)	59.5% (25/42)	44.0% (11/25)	75.0% (3/4)	52.0% (51/98)
Porcupine Health Unit	57.7% (15/26)	80.0% (16/20)	84.0% (21/25)	66.7% (22/33)	71.2% (74/104)
Public Health Sudbury & Districts	44.9% (22/49)	44.4% (24/54)	53.2% (25/47)	65.7% (23/35)	50.8% (94/185)
Timiskaming Health Unit	100.0% (1/1)	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)	100% (1/1)
TOTAL NORTH EAST	**49.2% (62/126)**	**54.0% (67/124)**	**60.0% (66/110)**	**63.0% (58/92)**	**56.0% (253/452)**
Ottawa Public Health	71.6% (156/218)	78.2% (147/188)	81.6% (177/217)	64.5% (127/197)	74.0% (607/820)
Eastern Ontario Health Unit	76.1% (54/71)	78.0% (46/59)	75.0% (33/44)	74.3% (26/35)	76.1% (159/209)
Hastings Prince Edward Public Health	68.8% (22/32)	70.3% (45/64)	61.3% (38/62)	66.2% (53/80)	66.4% (158/238)
Kingston, Frontenac and Lennox & Addington Public Health	77.1% (74/96)	69.0% (89/129)	80.5% (132/164)	59.9% (85/142)	71.6% (380/531)
Leeds, Grenville & Lanark District Health Unit	50.0% (26/52)	70.7% (53/75)	77.0% (67/87)	81.8% (45/55)	71.0% (191/269)
Renfrew County and District Health Unit	33.3% (3/9)	12.5% (1/8)	41.2% (7/17)	78.6% (22/28)	53.2% (33/62)
TOTAL EASTERN	**70.1% (335/478)**	**72.8% (381/523)**	**76.8% (454/591)**	**66.7% (358/537)**	**71.8% (1,528/2,129)**
Durham Region Health Department	67.1% (112/167)	74.6% (129/173)	72.5% (129/178)	81.5% (110/135)	73.5% (480/653)
Haliburton, Kawartha, Pine Ridge District Health Unit	62.7% (32/51)	62.5% (25/40)	69.6% (48/69)	68.6% (48/70)	66.5% (153/230)
Peel Public Health	70.1% (248/354)	72.9% (194/266)	66.0% (214/324)	73.1% (171/234)	70.2% (827/1,178)
Peterborough Public Health	46.3% (19/41)	51.6% (16/31)	52.9% (18/34)	66.7% (14/21)	52.8% (67/127)
Simcoe Muskoka District Health Unit	54.8% (57/104)	75.6% (118/156)	64.7% (77/119)	59.2% (71/120)	64.7% (323/499)
York Region Public Health	64.4% (172/267)	71.8% (168/234)	80.3% (184/229)	69.6% (117/168)	71.4% (641/898)

Public Health Unit	Week 51 (December 18 - December 24)	Week 52 (December 25 - December 31)	Week 1 (January 1 - January 7)	Week 2 (January 8 - January 14)	Total (December 18 - January 14)
TOTAL CENTRAL EAST	65.0% (640/984)	72.2% (650/900)	70.3% (670/953)	71.0% (531/748)	69.5% (2491/3,585)
Toronto Public Health	67.9% (546/804)	72.9% (663/910)	77.5% (749/967)	73.4% (500/681)	73.1% (2458/3,362)
TOTAL TORONTO	**67.9% (546/804)**	**72.9% (663/910)**	**77.5% (749/967)**	**73.4% (500/681)**	**73.1% (2,458/3,362)**
Chatham-Kent Public Health	22.2% (2/9)	50.0% (5/10)	34.8% (16/46)	33.3% (18/54)	34.5% (41/119)
Grey Bruce Health Unit	67.6% (25/37)	41.2% (14/34)	60.0% (18/30)	65.2% (15/23)	58.1% (72/124)
Huron Perth Public Health	90.5% (19/21)	23.1% (9/39)	57.1% (20/35)	80.6% (29/36)	58.8% (77/131)
Lambton Public Health	56.2% (9/16)	83.3% (5/6)	82.7% (43/52)	58.8% (10/17)	73.6% (67/91)
Middlesex-London Health Unit	58.6% (41/70)	59.8% (49/82)	65.4% (123/188)	55.1% (54/98)	61% (267/438)
Southwestern Public Health	47.6% (20/42)	63.6% (14/22)	56.6% (43/76)	71.4% (45/63)	60.1% (122/203)
Windsor-Essex County Health Unit	66.2% (86/130)	66.7% (112/168)	57.9% (92/159)	64.1% (100/156)	63.6% (390/613)
TOTAL SOUTH WEST	**62.2% (202/325)**	**57.6% (208/361)**	**60.6% (355/586)**	**60.6% (271/447)**	**60.3% (1,036/1,719)**
Brant County Health Unit	62.0% (31/50)	74.0% (57/77)	54.5% (30/55)	68.6% (24/35)	65.4% (142/217)
City of Hamilton Public Health Services	69.1% (132/191)	73.6% (178/242)	72.5% (222/306)	70.6% (197/279)	71.6% (729/1018)
Haldimand-Norfolk Health Unit	83.3% (60/72)	55.0% (22/40)	67.8% (40/59)	80.6% (29/36)	72.9% (151/207)
Halton Region Public Health	80.2% (77/96)	72.9% (62/85)	78.9% (86/109)	69.8% (67/96)	75.6% (292/386)
Niagara Region Public Health	66.0% (136/206)	64.4% (103/160)	62.3% (94/151)	57.1% (88/154)	62.7% (421/671)
Region of Waterloo Public Health and Emergency Services	55.4% (67/121)	63.3% (81/128)	67.6% (73/108)	40.8% (53/130)	56.3% (274/487)
Wellington-Dufferin-Guelph Public Health	77.8% (35/45)	72.2% (57/79)	78.7% (59/75)	56.8% (21/37)	72.9% (172/236)
TOTAL CENTRAL WEST	**68.9% (538/781)**	**69.1% (560/811)**	**70.0% (604/863)**	**62.5% (479/767)**	**67.7% (2,181/3,222)**
UNKNOWN	**0.0% (0/1)**	**0.0% (0/0)**	**66.7% (2/3)**	**0.0% (0/1)**	**40.0% (2/5)**
TOTAL ONTARIO	**66.6% (2,350/3,528)**	**69.9% (2,564/3,669)**	**71.5% (2,973/4,156)**	**67.6% (2,257/3,339)**	**69.0% (10,144/14,692)**

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 (2.6%), 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, December 18, 2022 to January 14, 2023

WHO label / Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
Omicron	**22 (100%)**	**181 (97.8%)**	**203 (98.1%)**
BQ.1.1	15 (68.2%)	143 (77.3%)	158 (76.3%)
BQ.1	0 (0.0%)	15 (8.1%)	15 (7.2%)
BF.7	2 (9.1%)	0 (0.0%)	2 (1.0%)
BQ.1.5	0 (0.0%)	0 (0.0%)	0 (0.0%)
BQ.1.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
BQ.1.1.4	0 (0.0%)	0 (0.0%)	0 (0.0%)
BQ.1.2	0 (0.0%)	2 (1.1%)	2 (1.0%)
BQ.1.13	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BQ lineages	2 (9.1%)	8 (4.3%)	10 (4.8%)
Other BF lineages	0 (0.0%)	8 (4.3%)	8 (3.9%)
Other BA.5	3 (13.6%)	5 (2.7%)	8 (3.9%)
Other BA.4	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BA.2	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**0 (0.0%)**	**4 (2.2%)**	**4 (1.9%)**
XBB.1.5	0 (0.0%)	3 (1.6%)	3 (1.4%)
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other recombinant	0 (0.0%)	1 (0.5%)	1 (0.5%)
Total sequenced	**22 (100%)**	**185 (100%)**	**207 (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 (2.6%), 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, December 18, 2022 to January 14, 2023

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	**63 (98.4%)**	**98 (100%)**	**102 (98.1%)**	**180 (97.3%)**	**1 (100%)**	**444 (98.2%)**
BQ.1.1	15 (23.4%)	28 (28.6%)	44 (42.3%)	36 (19.5%)	1 (100%)	124 (27.4%)
BQ.1	7 (10.9%)	5 (5.1%)	5 (4.8%)	19 (10.3%)	0 (0.0%)	36 (8.0%)
BF.7	2 (3.1%)	2 (2.0%)	4 (3.8%)	4 (2.2%)	0 (0.0%)	12 (2.7%)
BQ.1.5	0 (0.0%)	0 (0.0%)	1 (1.0%)	1 (0.5%)	0 (0.0%)	2 (0.4%)
BQ.1.1.1	1 (1.6%)	0 (0.0%)	2 (1.9%)	0 (0.0%)	0 (0.0%)	3 (0.7%)
BQ.1.1.4	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (2.7%)	0 (0.0%)	5 (1.1%)
BQ.1.2	2 (3.1%)	10 (10.2%)	4 (3.8%)	1 (0.5%)	0 (0.0%)	17 (3.8%)
BQ.1.13	0 (0.0%)	2 (2.0%)	0 (0.0%)	3 (1.6%)	0 (0.0%)	5 (1.1%)
Other BQ lineages	8 (12.5%)	6 (6.1%)	18 (17.3%)	29 (15.7%)	0 (0.0%)	61 (13.5%)
Other BF lineages	16 (25.0%)	10 (10.2%)	2 (1.9%)	37 (20.0%)	0 (0.0%)	65 (14.4%)
Other BA.5	8 (12.5%)	20 (20.4%)	19 (18.3%)	16 (8.6%)	0 (0.0%)	63 (13.9%)
Other BA.4	1 (1.6%)	4 (4.1%)	0 (0.0%)	19 (10.3%)	0 (0.0%)	24 (5.3%)
Other BA.2	3 (4.7%)	11 (11.2%)	3 (2.9%)	10 (5.4%)	0 (0.0%)	27 (6.0%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**1 (1.6%)**	**0 (0.0%)**	**2 (1.9%)**	**5 (2.7%)**	**0 (0.0%)**	**8 (1.8%)**
XBB.1.5	1 (1.6%)	0 (0.0%)	2 (1.9%)	3 (1.6%)	0 (0.0%)	6 (1.3%)
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	0 (0.0%)	1 (0.2%)
Other recombinant	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	0 (0.0%)	1 (0.2%)
Total sequenced	**64 (100%)**	**98 (100%)**	**104 (100%)**	**185 (100%)**	**1 (100%)**	**452 (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 (2.6%), 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, December 18, 2022 to January 14, 2023

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	**204 (97.6%)**	**233 (97.9%)**	**496 (93.4%)**	**244 (90.7%)**	**755 (92.1%)**	**58 (93.5%)**	**1,990 (93.5%)**
BQ.1.1	35 (16.7%)	67 (28.2%)	193 (36.3%)	74 (27.5%)	281 (34.3%)	8 (12.9%)	658 (30.9%)
BQ.1	10 (4.8%)	24 (10.1%)	46 (8.7%)	19 (7.1%)	37 (4.5%)	19 (30.6%)	155 (7.3%)
BF.7	3 (1.4%)	43 (18.1%)	27 (5.1%)	17 (6.3%)	60 (7.3%)	20 (32.3%)	170 (8.0%)
BQ.1.5	0 (0.0%)	39 (16.4%)	10 (1.9%)	1 (0.4%)	0 (0.0%)	0 (0.0%)	50 (2.3%)
BQ.1.1.1	0 (0.0%)	2 (0.8%)	5 (0.9%)	0 (0.0%)	4 (0.5%)	1 (1.6%)	12 (0.6%)
BQ.1.1.4	2 (1.0%)	3 (1.3%)	9 (1.7%)	21 (7.8%)	12 (1.5%)	4 (6.5%)	51 (2.4%)
BQ.1.2	2 (1.0%)	1 (0.4%)	14 (2.6%)	4 (1.5%)	11 (1.3%)	0 (0.0%)	32 (1.5%)
BQ.1.13	2 (1.0%)	1 (0.4%)	2 (0.4%)	1 (0.4%)	14 (1.7%)	0 (0.0%)	20 (0.9%)
Other BQ lineages	108 (51.7%)	21 (8.8%)	101 (19.0%)	71 (26.4%)	248 (30.2%)	1 (1.6%)	550 (25.8%)
Other BF lineages	2 (1.0%)	3 (1.3%)	12 (2.3%)	4 (1.5%)	9 (1.1%)	2 (3.2%)	32 (1.5%)
Other BA.5	26 (12.4%)	20 (8.4%)	44 (8.3%)	21 (7.8%)	51 (6.2%)	3 (4.8%)	165 (7.8%)
Other BA.4	3 (1.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (0.5%)	0 (0.0%)	7 (0.3%)
Other BA.2	11 (5.3%)	9 (3.8%)	33 (6.2%)	11 (4.1%)	24 (2.9%)	0 (0.0%)	88 (4.1%)
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	**5 (2.4%)**	**5 (2.1%)**	**35 (6.6%)**	**25 (9.3%)**	**65 (7.9%)**	**4 (6.5%)**	**139 (6.5%)**
XBB.1.5	5 (2.4%)	4 (1.7%)	28 (5.3%)	23 (8.6%)	65 (7.9%)	2 (3.2%)	127 (6.0%)
XBB.1	0 (0.0%)	0 (0.0%)	3 (0.6%)	0 (0.0%)	0 (0.0%)	1 (1.6%)	4 (0.2%)
Other recombinant	0 (0.0%)	1 (0.4%)	4 (0.8%)	2 (0.7%)	0 (0.0%)	1 (1.6%)	8 (0.4%)
Total sequenced	**209 (100%)**	**238 (100%)**	**531 (100%)**	**269 (100%)**	**820 (100%)**	**62 (100%)**	**2,129 (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 (2.6%), 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, December 18, 2022 to January 14, 2023

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	**623 (95.4%)**	**219 (95.2%)**	**1,061 (90.1%)**	**119 (93.7%)**	**467 (93.6%)**	**837 (93.2%)**	**3,326 (92.8%)**
BQ.1.1	271 (41.5%)	48 (20.9%)	418 (35.5%)	34 (26.8%)	141 (28.3%)	318 (35.4%)	1,230 (34.3%)
BQ.1	54 (8.3%)	31 (13.5%)	106 (9.0%)	10 (7.9%)	68 (13.6%)	69 (7.7%)	338 (9.4%)
BF.7	10 (1.5%)	4 (1.7%)	11 (0.9%)	2 (1.6%)	9 (1.8%)	8 (0.9%)	44 (1.2%)
BQ.1.5	13 (2.0%)	12 (5.2%)	17 (1.4%)	2 (1.6%)	4 (0.8%)	54 (6.0%)	102 (2.8%)
BQ.1.1.1	4 (0.6%)	9 (3.9%)	6 (0.5%)	0 (0.0%)	10 (2.0%)	17 (1.9%)	46 (1.3%)
BQ.1.1.4	15 (2.3%)	6 (2.6%)	24 (2.0%)	4 (3.1%)	3 (0.6%)	26 (2.9%)	78 (2.2%)
BQ.1.2	11 (1.7%)	3 (1.3%)	23 (2.0%)	7 (5.5%)	11 (2.2%)	20 (2.2%)	75 (2.1%)
BQ.1.13	12 (1.8%)	1 (0.4%)	18 (1.5%)	0 (0.0%)	13 (2.6%)	21 (2.3%)	65 (1.8%)
Other BQ lineages	100 (15.3%)	43 (18.7%)	215 (18.3%)	10 (7.9%)	73 (14.6%)	116 (12.9%)	557 (15.5%)
Other BF lineages	31 (4.7%)	9 (3.9%)	37 (3.1%)	13 (10.2%)	39 (7.8%)	24 (2.7%)	153 (4.3%)
Other BA.5	77 (11.8%)	40 (17.4%)	109 (9.3%)	32 (25.2%)	58 (11.6%)	118 (13.1%)	434 (12.1%)
Other BA.4	1 (0.2%)	9 (3.9%)	2 (0.2%)	1 (0.8%)	1 (0.2%)	4 (0.4%)	18 (0.5%)
Other BA.2	24 (3.7%)	3 (1.3%)	75 (6.4%)	4 (3.1%)	37 (7.4%)	42 (4.7%)	185 (5.2%)
Other BA.1	0 (0.0%)	1 (0.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (<0.1%)
Recombinant	**30 (4.6%)**	**11 (4.8%)**	**117 (9.9%)**	**8 (6.3%)**	**32 (6.4%)**	**61 (6.8%)**	**259 (7.2%)**
XBB.1.5	23 (3.5%)	7 (3.0%)	81 (6.9%)	6 (4.7%)	17 (3.4%)	38 (4.2%)	172 (4.8%)
XBB.1	5 (0.8%)	2 (0.9%)	15 (1.3%)	1 (0.8%)	10 (2.0%)	14 (1.6%)	47 (1.3%)
Other recombinant	2 (0.3%)	2 (0.9%)	21 (1.8%)	1 (0.8%)	5 (1.0%)	9 (1.0%)	40 (1.1%)
Total sequenced	**653 (100%)**	**230 (100%)**	**1,178 (100%)**	**127 (100%)**	**499 (100%)**	**898 (100%)**	**3,585 (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 (2.6%), 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, December 18, 2022 to January 14, 2023

WHO label / Pango lineage	Toronto Public Health	Total
Omicron	**3,129 (93.1%)**	**3,129 (93.1%)**
BQ.1.1	1,083 (32.2%)	1,083 (32.2%)
BQ.1	379 (11.3%)	379 (11.3%)
BF.7	95 (2.8%)	95 (2.8%)
BQ.1.5	88 (2.6%)	88 (2.6%)
BQ.1.1.1	64 (1.9%)	64 (1.9%)
BQ.1.1.4	69 (2.1%)	69 (2.1%)
BQ.1.2	65 (1.9%)	65 (1.9%)
BQ.1.13	124 (3.7%)	124 (3.7%)
Other BQ lineages	586 (17.4%)	586 (17.4%)
Other BF lineages	130 (3.9%)	130 (3.9%)
Other BA.5	301 (9.0%)	301 (9.0%)
Other BA.4	9 (0.3%)	9 (0.3%)
Other BA.2	136 (4.0%)	136 (4.0%)
Other BA.1	0 (0.0%)	0 (0.0%)
Recombinant	**233 (6.9%)**	**233 (6.9%)**
XBB.1.5	133 (4.0%)	133 (4.0%)
XBB.1	60 (1.8%)	60 (1.8%)
Other recombinant	40 (1.2%)	40 (1.2%)
Total sequenced	**3,362 (100%)**	**3,362 (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 (2.6%), 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, December 18, 2022 to January 14, 2023

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	**84 (70.6%)**	**119 (96.0%)**	**129 (98.5%)**	**81 (89.0%)**	**394 (90.0%)**	**188 (92.6%)**	**556 (90.7%)**	**1,551 (90.2%)**
BQ.1.1	24 (20.2%)	33 (26.6%)	20 (15.3%)	41 (45.1%)	156 (35.6%)	71 (35.0%)	143 (23.3%)	488 (28.4%)
BQ.1	1 (0.8%)	3 (2.4%)	5 (3.8%)	3 (3.3%)	11 (2.5%)	4 (2.0%)	14 (2.3%)	41 (2.4%)
BF.7	18 (15.1%)	7 (5.6%)	1 (0.8%)	2 (2.2%)	10 (2.3%)	3 (1.5%)	18 (2.9%)	59 (3.4%)
BQ.1.5	2 (1.7%)	22 (17.7%)	15 (11.5%)	2 (2.2%)	14 (3.2%)	5 (2.5%)	26 (4.2%)	86 (5.0%)
BQ.1.1.1	2 (1.7%)	1 (0.8%)	1 (0.8%)	1 (1.1%)	15 (3.4%)	6 (3.0%)	82 (13.4%)	108 (6.3%)
BQ.1.1.4	1 (0.8%)	4 (3.2%)	7 (5.3%)	7 (7.7%)	21 (4.8%)	6 (3.0%)	13 (2.1%)	59 (3.4%)
BQ.1.2	0 (0.0%)	5 (4.0%)	2 (1.5%)	0 (0.0%)	3 (0.7%)	0 (0.0%)	7 (1.1%)	17 (1.0%)
BQ.1.13	4 (3.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (0.5%)	4 (2.0%)	9 (1.5%)	19 (1.1%)
Other BQ lineages	7 (5.9%)	4 (3.2%)	27 (20.6%)	13 (14.3%)	45 (10.3%)	26 (12.8%)	96 (15.7%)	218 (12.7%)
Other BF lineages	7 (5.9%)	24 (19.4%)	1 (0.8%)	1 (1.1%)	8 (1.8%)	4 (2.0%)	13 (2.1%)	58 (3.4%)
Other BA.5	16 (13.4%)	12 (9.7%)	38 (29.0%)	5 (5.5%)	75 (17.1%)	24 (11.8%)	106 (17.3%)	276 (16.1%)
Other BA.4	1 (0.8%)	0 (0.0%)	0 (0.0%)	1 (1.1%)	3 (0.7%)	0 (0.0%)	3 (0.5%)	8 (0.5%)
Other BA.2	1 (0.8%)	4 (3.2%)	12 (9.2%)	5 (5.5%)	31 (7.1%)	35 (17.2%)	26 (4.2%)	114 (6.6%)
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	**35 (29.4%)**	**5 (4.0%)**	**2 (1.5%)**	**10 (11.0%)**	**44 (10.0%)**	**15 (7.4%)**	**57 (9.3%)**	**168 (9.8%)**
XBB.1.5	4 (3.4%)	4 (3.2%)	2 (1.5%)	8 (8.8%)	15 (3.4%)	13 (6.4%)	12 (2.0%)	58 (3.4%)
XBB.1	0 (0.0%)	1 (0.8%)	0 (0.0%)	0 (0.0%)	22 (5.0%)	0 (0.0%)	5 (0.8%)	28 (1.6%)
Other recombinant	31 (26.1%)	0 (0.0%)	0 (0.0%)	2 (2.2%)	7 (1.6%)	2 (1.0%)	40 (6.5%)	82 (4.8%)
Total sequenced	**119 (100%)**	**124 (100%)**	**131 (100%)**	**91 (100%)**	**438 (100%)**	**203 (100%)**	**613 (100%)**	**1,719 (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 (2.6%), 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, December 18, 2022 to January 14, 2023

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	**203 (93.5%)**	**932 (91.6%)**	**185 (89.4%)**	**366 (94.8%)**	**608 (90.6%)**	**467 (95.9%)**	**224 (94.9%)**	**2,985 (92.6%)**
BQ.1.1	51 (23.5%)	338 (33.2%)	97 (46.9%)	137 (35.5%)	207 (30.8%)	113 (23.2%)	81 (34.3%)	1,024 (31.8%)
BQ.1	9 (4.1%)	76 (7.5%)	8 (3.9%)	30 (7.8%)	53 (7.9%)	28 (5.7%)	18 (7.6%)	222 (6.9%)
BF.7	3 (1.4%)	45 (4.4%)	6 (2.9%)	19 (4.9%)	11 (1.6%)	31 (6.4%)	7 (3.0%)	122 (3.8%)
BQ.1.5	8 (3.7%)	23 (2.3%)	5 (2.4%)	6 (1.6%)	39 (5.8%)	6 (1.2%)	3 (1.3%)	90 (2.8%)
BQ.1.1.1	2 (0.9%)	50 (4.9%)	7 (3.4%)	6 (1.6%)	9 (1.3%)	9 (1.8%)	23 (9.7%)	106 (3.3%)
BQ.1.1.4	4 (1.8%)	25 (2.5%)	2 (1.0%)	7 (1.8%)	2 (0.3%)	4 (0.8%)	2 (0.8%)	46 (1.4%)
BQ.1.2	7 (3.2%)	31 (3.0%)	3 (1.4%)	11 (2.8%)	12 (1.8%)	2 (0.4%)	6 (2.5%)	72 (2.2%)
BQ.1.13	1 (0.5%)	17 (1.7%)	2 (1.0%)	3 (0.8%)	8 (1.2%)	13 (2.7%)	0 (0.0%)	44 (1.4%)
Other BQ lineages	60 (27.6%)	169 (16.6%)	27 (13.0%)	92 (23.8%)	91 (13.6%)	99 (20.3%)	39 (16.5%)	577 (17.9%)
Other BF lineages	5 (2.3%)	36 (3.5%)	5 (2.4%)	9 (2.3%)	60 (8.9%)	10 (2.1%)	7 (3.0%)	132 (4.1%)
Other BA.5	45 (20.7%)	84 (8.3%)	17 (8.2%)	30 (7.8%)	83 (12.4%)	87 (17.9%)	31 (13.1%)	377 (11.7%)
Other BA.4	1 (0.5%)	3 (0.3%)	1 (0.5%)	2 (0.5%)	3 (0.4%)	6 (1.2%)	0 (0.0%)	16 (0.5%)
Other BA.2	7 (3.2%)	35 (3.4%)	5 (2.4%)	14 (3.6%)	30 (4.5%)	59 (12.1%)	7 (3.0%)	157 (4.9%)
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	**14 (6.5%)**	**86 (8.4%)**	**22 (10.6%)**	**20 (5.2%)**	**63 (9.4%)**	**20 (4.1%)**	**12 (5.1%)**	**237 (7.4%)**
XBB.1.5	11 (5.1%)	31 (3.0%)	18 (8.7%)	9 (2.3%)	53 (7.9%)	14 (2.9%)	9 (3.8%)	145 (4.5%)
XBB.1	2 (0.9%)	9 (0.9%)	2 (1.0%)	2 (0.5%)	3 (0.4%)	4 (0.8%)	1 (0.4%)	23 (0.7%)
Other recombinant	1 (0.5%)	46 (4.5%)	2 (1.0%)	9 (2.3%)	7 (1.0%)	2 (0.4%)	2 (0.8%)	69 (2.1%)
Total sequenced	**217 (100%)**	**1,018 (100%)**	**207 (100%)**	**386 (100%)**	**671 (100%)**	**487 (100%)**	**236 (100%)**	**3,222 (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 (2.6%), 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, December 18, 2022 to January 14, 2023

WHO label / Pango lineage	Outbreak-associated	Non outbreak-associated	Total cases
Omicron	**4,549 (34.2%)**	**8,740 (65.8%)**	**13,289 (100%)**
BQ.1.1	1,661 (35.6%)	2,999 (64.4%)	4,660 (100%)
BQ.1	343 (29.6%)	816 (70.4%)	1,159 (100%)
BF.7	247 (50.5%)	242 (49.5%)	489 (100%)
BQ.1.5	151 (36.8%)	259 (63.2%)	410 (100%)
BQ.1.1.1	99 (29.7%)	234 (70.3%)	333 (100%)
BQ.1.1.4	67 (22.3%)	233 (77.7%)	300 (100%)
BQ.1.2	58 (21.2%)	216 (78.8%)	274 (100%)
BQ.1.13	99 (36.8%)	170 (63.2%)	269 (100%)
Other BQ lineages	871 (35.1%)	1,607 (64.9%)	2,478 (100%)
Other BF lineages	220 (39.3%)	340 (60.7%)	560 (100%)
Other BA.5	536 (33.8%)	1,049 (66.2%)	1,585 (100%)
Other BA.4	15 (18.8%)	65 (81.2%)	80 (100%)
Other BA.2	182 (26.3%)	509 (73.7%)	691 (100%)
Other BA.1	0 (0.0%)	1 (100%)	1 (100%)
Recombinant	**273 (26.7%)**	**751 (73.3%)**	**1,024 (100%)**
XBB.1.5	146 (23.1%)	485 (76.9%)	631 (100%)
XBB.1	39 (24.8%)	118 (75.2%)	157 (100%)
Other recombinant	88 (37.3%)	148 (62.7%)	236 (100%)
Total sequenced	**4,822 (33.7%)**	**9,491 (66.3%)**	**14,313 (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 (97.4%). '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, December 18, 2022 to January 14, 2023

WHO label / Pango lineage	Hospital admissions	Deceased	Total cases
Omicron	**825 (6.2%)**	**125 (0.9%)**	**13,289 (100%)**
BQ.1.1	286 (6.1%)	34 (0.7%)	4,660 (100%)
BQ.1	70 (6.0%)	14 (1.2%)	1,159 (100%)
BF.7	29 (5.9%)	8 (1.6%)	489 (100%)
BQ.1.5	13 (3.2%)	10 (2.4%)	410 (100%)
BQ.1.1.1	34 (10.2%)	6 (1.8%)	333 (100%)
BQ.1.1.4	13 (4.3%)	4 (1.3%)	300 (100%)
BQ.1.2	13 (4.7%)	2 (0.7%)	274 (100%)
BQ.1.13	14 (5.2%)	2 (0.7%)	269 (100%)
Other BQ lineages	135 (5.4%)	22 (0.9%)	2,478 (100%)
Other BF lineages	28 (5.0%)	4 (0.7%)	560 (100%)
Other BA.5	123 (7.8%)	13 (0.8%)	1,585 (100%)
Other BA.4	6 (7.5%)	1 (1.2%)	80 (100%)
Other BA.2	61 (8.8%)	5 (0.7%)	691 (100%)
Other BA.1	0 (0.0%)	0 (0.0%)	1 (100%)
Recombinant	**49 (4.8%)**	**6 (0.6%)**	**1,024 (100%)**
XBB.1.5	27 (4.3%)	1 (0.2%)	631 (100%)
XBB.1	10 (6.4%)	3 (1.9%)	157 (100%)
Other recombinant	12 (5.1%)	2 (0.8%)	236 (100%)
Total sequenced	**874 (6.1%)**	**131 (0.9%)**	**14,313 (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 (97.4%). 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)

Cumulative Whole Genome Sequencing Results

Table 9. Number of cases by Pango lineage, cumulative counts, Ontario, January 1, 2021 to January 14, 2023

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
Variant of Concern (VOC)			
Alpha	**11,759**	**0**	**11,759**
Beta	**1,221**	**0**	**1,221**
Gamma	**3,917**	**0**	**3,917**
Delta	**45,905**	**0**	**45,905**
Omicron	**130,829**	**13,644**	**144,473**
B.1.1.529	0	0	0
BA.1	6,384	1	6,385
BA.1.1	18,666	1	18,667
BA.1.1.1	42	0	42
BA.1.1.10	1,669	0	1,669
BA.1.1.13	3	0	3
BA.1.1.14	521	0	521
BA.1.1.15	3	0	3
BA.1.1.16	95	0	95
BA.1.1.17	6	0	6
BA.1.1.18	129	0	129
BA.1.1.2	6	0	6
BA.1.1.6	3	0	3
BA.1.1.7	11	0	11
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	70	0	70
BA.1.14.1	1	0	1
BA.1.14.2	1	0	1
BA.1.15	1,635	0	1,635
BA.1.15.1	22	0	22
BA.1.15.2	3	0	3
BA.1.16	2	0	2
BA.1.17	726	0	726
BA.1.17.2	1,500	0	1,500
BA.1.18	92	0	92

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BA.1.19	23	0	23
BA.1.20	90	0	90
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.2	16,127	5	16,132
BA.2.1	218	1	219
BA.2.10	388	0	388
BA.2.10.1	42	2	44
BA.2.10.3	1	0	1
BA.2.11	7	0	7
BA.2.12	42	0	42
BA.2.12.1	6,462	3	6,465
BA.2.12.2	2	0	2
BA.2.13	28	0	28
BA.2.13.1	44	0	44
BA.2.15	1	0	1
BA.2.16	2	0	2
BA.2.17	8	0	8
BA.2.18	70	0	70
BA.2.2	4	0	4
BA.2.20	1,496	0	1,496
BA.2.21	328	0	328
BA.2.22	5	0	5
BA.2.23	54	0	54
BA.2.24	3	0	3
BA.2.26	8	0	8
BA.2.27	1	0	1
BA.2.29	1	0	1
BA.2.3	2,367	1	2,368
BA.2.3.10	79	0	79
BA.2.3.12	3	0	3
BA.2.3.14	2	0	2
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	16	0	16
BA.2.3.20	122	26	148
BA.2.3.4	949	0	949

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
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	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	24	0	24
BA.2.37	78	0	78
BA.2.38	134	0	134
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.2.47	2	0	2
BA.2.48	15	0	15
BA.2.49	4	0	4
BA.2.5	5	0	5
BA.2.50	13	0	13
BA.2.51	19	0	19
BA.2.52	8	0	8
BA.2.53	1	0	1
BA.2.54	1	0	1
BA.2.55	1	0	1
BA.2.56	63	0	63
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
BA.2.65	1,653	0	1,653
BA.2.66	23	0	23
BA.2.68	6	0	6
BA.2.7	21	0	21
BA.2.72	6	0	6
BA.2.73	2	0	2

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BA.2.74	45	0	45
BA.2.75	124	0	124
BA.2.75.1	30	0	30
BA.2.75.10	3	0	3
BA.2.75.2	236	0	236
BA.2.75.3	5	0	5
BA.2.75.4	1	0	1
BA.2.75.5	35	10	45
BA.2.75.6	4	0	4
BA.2.76	92	0	92
BA.2.78	2	0	2
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	1,549	0	1,549
BA.2.9.2	3	0	3
BA.2.9.3	14	0	14
BA.2.9.4	1	0	1
BA.2.9.5	5	0	5
BA.2.9.7	6	0	6
BA.3.1	1	0	1
BA.4	713	0	713
BA.4.1	1,380	0	1,380
BA.4.1.1	41	0	41
BA.4.1.10	7	0	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	158	3	161
BA.4.1.9	7	0	7
BA.4.2	189	0	189
BA.4.3	2	0	2
BA.4.4	84	0	84
BA.4.5	2	0	2
BA.4.6	2,399	64	2,463
BA.4.6.1	2	0	2
BA.4.6.2	60	4	64
BA.4.6.3	8	8	16

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BA.4.6.4	20	0	20
BA.4.6.5	198	3	201
BA.4.7	55	0	55
BA.5	372	4	376
BA.5.1	6,045	76	6,121
BA.5.1.1	1,010	6	1,016
BA.5.1.10	252	1	253
BA.5.1.12	113	13	126
BA.5.1.15	32	0	32
BA.5.1.16	1	0	1
BA.5.1.17	13	0	13
BA.5.1.18	75	19	94
BA.5.1.19	11	0	11
BA.5.1.2	319	10	329
BA.5.1.20	30	4	34
BA.5.1.21	2	0	2
BA.5.1.22	267	0	267
BA.5.1.23	386	11	397
BA.5.1.24	121	0	121
BA.5.1.25	174	3	177
BA.5.1.27	31	30	61
BA.5.1.28	5	10	15
BA.5.1.3	68	0	68
BA.5.1.30	695	6	701
BA.5.1.4	11	0	11
BA.5.1.5	247	9	256
BA.5.1.6	53	4	57
BA.5.1.7	643	8	651
BA.5.1.9	1	0	1
BA.5.10	232	0	232
BA.5.10.1	6	3	9
BA.5.11	0	2	2
BA.5.2	7,531	134	7,665
BA.5.2.1	11,673	146	11,819
BA.5.2.12	2	0	2
BA.5.2.13	172	60	232
BA.5.2.14	128	27	155
BA.5.2.16	57	3	60
BA.5.2.18	45	3	48
BA.5.2.19	32	5	37

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BA.5.2.2	129	0	129
BA.5.2.20	566	2	568
BA.5.2.21	331	16	347
BA.5.2.22	412	7	419
BA.5.2.23	71	7	78
BA.5.2.24	106	54	160
BA.5.2.25	107	19	126
BA.5.2.26	102	11	113
BA.5.2.27	159	0	159
BA.5.2.28	113	20	133
BA.5.2.3	185	9	194
BA.5.2.31	52	3	55
BA.5.2.32	51	1	52
BA.5.2.33	31	3	34
BA.5.2.34	154	53	207
BA.5.2.35	54	60	114
BA.5.2.36	7	1	8
BA.5.2.37	18	3	21
BA.5.2.39	1	0	1
BA.5.2.4	13	0	13
BA.5.2.44	5	0	5
BA.5.2.47	8	0	8
BA.5.2.48	1	14	15
BA.5.2.6	242	74	316
BA.5.2.7	11	0	11
BA.5.2.8	122	0	122
BA.5.2.9	841	55	896
BA.5.3	18	0	18
BA.5.3.1	140	12	152
BA.5.3.2	9	1	10
BA.5.3.3	39	1	40
BA.5.3.4	4	0	4
BA.5.3.5	1	0	1
BA.5.5	1,691	0	1,691
BA.5.5.1	57	3	60
BA.5.5.2	84	0	84
BA.5.5.3	22	0	22
BA.5.6	1,256	6	1,262
BA.5.6.1	14	0	14
BA.5.6.2	28	2	30

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BA.5.8	197	0	197
BA.5.9	129	30	159
BB.1	1	0	1
BB.2	1	0	1
BC.2	1	0	1
BE.1	1,000	1	1,001
BE.1.1	674	21	695
BE.1.1.1	121	4	125
BE.1.1.2	61	1	62
BE.1.2	9	3	12
BE.1.2.1	459	116	575
BE.1.3	1	0	1
BE.1.4	221	1	222
BE.1.4.1	33	0	33
BE.1.4.2	3	3	6
BE.1.4.4	1	0	1
BE.10	9	7	16
BE.2	15	0	15
BE.3	187	0	187
BE.4	106	0	106
BE.4.1	21	0	21
BE.4.1.1	3	1	4
BE.4.2	2	0	2
BE.5	169	2	171
BE.6	1	1	2
BE.7	0	2	2
BE.9	5	21	26
BF.1	287	0	287
BF.1.1	9	0	9
BF.10	1,732	48	1,780
BF.11	481	153	634
BF.11.1	77	32	109
BF.11.2	0	1	1
BF.11.3	146	48	194
BF.11.4	10	0	10
BF.12	50	0	50
BF.13	221	12	233
BF.14	141	14	155
BF.15	10	0	10
BF.16	60	0	60

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BF.18	2	0	2
BF.19	1	0	1
BF.2	96	1	97
BF.20	4	0	4
BF.21	150	1	151
BF.23	8	0	8
BF.25	41	20	61
BF.26	536	17	553
BF.27	331	2	333
BF.28	559	14	573
BF.29	2	0	2
BF.3	47	2	49
BF.3.1	3	0	3
BF.31	6	0	6
BF.31.1	90	3	93
BF.32	4	1	5
BF.34	10	28	38
BF.4	217	0	217
BF.5	865	26	891
BF.6	9	0	9
BF.7	1,637	505	2,142
BF.7.1	1	5	6
BF.7.10	1	0	1
BF.7.12	7	0	7
BF.7.14	0	13	13
BF.7.3	1	0	1
BF.7.4	102	30	132
BF.7.4.1	102	20	122
BF.7.4.2	10	0	10
BF.7.5	83	7	90
BF.7.6	110	22	132
BF.7.7	164	55	219
BF.7.8	9	4	13
BF.8	110	0	110
BF.9	837	0	837
BG.2	87	0	87
BG.4	14	0	14
BG.5	24	0	24
BG.6	11	0	11
BH.1	14	0	14

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BK.1	219	9	228
BL.1	25	1	26
BL.1.4	0	1	1
BL.2	5	0	5
BL.3	1	0	1
BL.4	4	0	4
BL.5	2	0	2
BM.1	3	0	3
BM.1.1	19	5	24
BM.1.1.1	7	9	16
BM.1.1.3	30	6	36
BM.1.1.4	1	0	1
BM.1.1.5	0	1	1
BM.2	2	2	4
BM.2.1	14	0	14
BM.4.1.1	2	0	2
BN.1	84	108	192
BN.1.1	0	0	0
BN.1.1.1	0	1	1
BN.1.2	61	21	82
BN.1.2.1	10	23	33
BN.1.3	99	40	139
BN.1.3.1	49	55	104
BN.1.3.3	0	1	1
BN.1.4	14	10	24
BN.1.5	21	12	33
BN.1.5.1	1	0	1
BN.1.7	0	2	2
BN.1.9	2	0	2
BN.2	2	0	2
BN.2.1	1	0	1
BN.3.1	11	12	23
BN.4	1	0	1
BN.5	7	0	7
BN.6	11	2	13
BQ.1	1,454	1,186	2,640
BQ.1.1	2,940	4,771	7,711
BQ.1.1.1	180	340	520
BQ.1.1.10	85	206	291
BQ.1.1.11	5	5	10

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BQ.1.1.13	11	52	63
BQ.1.1.15	24	39	63
BQ.1.1.16	0	1	1
BQ.1.1.17	0	8	8
BQ.1.1.18	60	115	175
BQ.1.1.19	1	0	1
BQ.1.1.2	4	27	31
BQ.1.1.20	0	2	2
BQ.1.1.21	1	1	2
BQ.1.1.22	2	4	6
BQ.1.1.23	5	9	14
BQ.1.1.24	4	4	8
BQ.1.1.25	9	0	9
BQ.1.1.27	0	1	1
BQ.1.1.28	1	2	3
BQ.1.1.29	0	2	2
BQ.1.1.3	107	116	223
BQ.1.1.30	71	63	134
BQ.1.1.31	4	2	6
BQ.1.1.32	2	29	31
BQ.1.1.4	197	308	505
BQ.1.1.5	86	132	218
BQ.1.1.6	36	46	82
BQ.1.1.7	111	143	254
BQ.1.1.8	14	44	58
BQ.1.1.9	0	0	0
BQ.1.10	72	126	198
BQ.1.10.1	71	145	216
BQ.1.11	104	134	238
BQ.1.12	304	230	534
BQ.1.13	346	277	623
BQ.1.13.1	9	26	35
BQ.1.14	193	118	311
BQ.1.15	13	15	28
BQ.1.16	71	6	77
BQ.1.18	4	6	10
BQ.1.19	3	7	10
BQ.1.2	384	280	664
BQ.1.22	51	60	111
BQ.1.23	43	103	146

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
BQ.1.24	0	0	0
BQ.1.25	79	197	276
BQ.1.25.1	9	39	48
BQ.1.27	1	1	2
BQ.1.28	0	0	0
BQ.1.3	123	215	338
BQ.1.4	2	2	4
BQ.1.5	350	419	769
BQ.1.6	5	16	21
BQ.1.7	4	0	4
BQ.1.8	96	63	159
BQ.1.9	1	1	2
BR.1	5	0	5
BR.1.2	4	1	5
BR.2	5	5	10
BR.2.1	10	31	41
BR.3	7	0	7
BR.4	14	0	14
BS.1.1	0	2	2
BT.1	12	0	12
BT.2	1	1	2
BU.1	12	23	35
BU.2	9	0	9
BU.3	1	1	2
BV.2	2	1	3
BW.1	23	25	48
BW.1.1	19	83	102
BY.1	88	3	91
BY.1.2	10	0	10
CA.1	1	0	1
CA.2	1	0	1
CA.3	1	0	1
CA.3.1	3	1	4
CA.5	11	12	23
CA.7	13	32	45
CB.1	4	0	4
CC.1	21	0	21
CD.2	1	0	1
CE.1	31	1	32
CG.1	31	0	31

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
CH.1.1	29	181	210
CH.1.1.1	1	7	8
CH.1.1.2	1	6	7
CJ.1	3	9	12
CJ.1.1	0	1	1
CK.1	51	85	136
CK.2	4	7	11
CK.2.1	4	1	5
CK.2.1.1	18	15	33
CK.3	19	12	31
CL.1	8	8	16
CM.1	42	8	50
CM.10	2	1	3
CM.2	75	14	89
CM.4	2	0	2
CM.4.1	7	1	8
CM.6.1	1	0	1
CM.7	1	0	1
CM.8	2	0	2
CM.8.1	9	26	35
CM.9	11	0	11
CN.1	18	3	21
CN.2	61	60	121
CP.1	19	8	27
CP.5	1	0	1
CQ.1	2	0	2
CQ.1.1	7	0	7
CQ.2	4	7	11
CR.1	6	2	8
CR.1.1	2	2	4
CR.1.2	10	1	11
CR.1.3	1	0	1
CR.2	1	0	1
CT.1	1	0	1
CV.1	17	6	23
DC.1	2	0	2
DF.1	2	0	2
DF.1.1	9	10	19
DG.1	0	2	2
DJ.1.1	4	6	10

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
DK.1	0	0	0
DL.1	4	3	7
DM.1	0	1	1
Variant of Interest (VOI)			
Mu	**241**	**0**	**241**
Lambda	**8**	**0**	**8**
Recombinant	**471**	**1,049**	**1,520**
XAC	30	0	30
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	20	11	31
XBB.1	183	163	346
XBB.1.1	3	12	15
XBB.1.2	8	22	30
XBB.1.3	1	0	1
XBB.1.4	0	4	4
XBB.1.5	26	645	671
XBB.1.9	0	2	2
XBB.1.9.1	0	0	0
XBB.2	30	47	77
XBB.3	9	5	14
XBC.1	0	2	2
XBD	2	0	2
XBE	9	0	9
XBF	2	38	40
XBH	1	0	1
XBJ	0	0	0
XBM	38	98	136
XE	3	0	3
XM	1	0	1
XN	1	0	1
XQ	4	0	4
XW	7	0	7

WHO label / Pango lineage	January 1, 2021 - December 17, 2022	December 18, 2022 - January 14, 2023	Total
XZ	1	0	1
Non-VOC/VOI	**6,216**	**0**	**6,216**
Total sequenced	**200,567**	**14,693**	**215,260**

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 25, 2023 at approximately 2:00 a.m.
- Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on January 25, 2023 at approximately 9:30 a.m.

The Hospital for Sick Children (HSC)

- Data were received by PHO on January 24, 2023 at approximately 3:40 p.m.

Kingston Health Sciences Centre (KHSC)

- Data were received by PHO on January 25, 2023 at approximately 9:00 a.m.

Shared Hospital Laboratory (SHL)

- Data were received by PHO on January 24, 2023 at approximately 1:00 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were received by PHO on January 25, 2023 at approximately 2:00 a.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on January 24, 2023 at approximately 1:00 p.m.

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 (2.6%), 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 (97.4% 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'.

References

1. Public Health Agency of Canada. SARS-CoV-2 variants: national definitions, classifications and public health actions [Internet]. Ottawa, ON: Government of Canada; 2021 [modified 2021 August 26; cited 2021 August 27]. Available from: https://www.canada.ca/en/public-health/services/diseases/2019-novel-coronavirus-infection/health-professionals/testing-diagnosing-case-reporting/sars-cov-2-variants-national-definitions-classifications-public-health-actions.html

2. World Health Organization. Tracking SARS-CoV-2 variants [Internet]. Geneva, Switzerland; 2021 [modified 2021 October 29; cited 2021 November 1]. Available from: https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

3. European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern as of 28 October 2021 [Internet]. Stockholm, Sweden; 2021 [modified 2021 October 28; cited 2021 November 1]. Available from: https://www.ecdc.europa.eu/en/covid-19/variants-concern

4. Rambaut A, Holmes EC, O'Toole Á, Hill V, McCrone JT, Ruis C, et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nat Microbiol. 2020; 5(11):1403-7. Available from: https://doi.org/10.1038/s41564-020-0770-5

5. cov-lineages. pangolin [Internet]. 2020 [cited 2021 May 29]. GitHub. Available from: https://github.com/cov-lineages/pangolin

6. Davies N, Abbott S, Barnard R, Jarvis CI, Kucharski AJ, Munday JD, et al. Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. Science. 2021; 372(6538): eabg3055. Available from: https://doi.org/10.1126/science.abg3055

7. Campbell F, Archer B, Laurenson-Schafer H, Jinnai Y, Konings F, Batra N, et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. Euro Surveill. 2021; 26(24). Available from: https://doi.org/10.2807/1560-7917.ES.2021.26.24.2100509

Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Epidemiologic summary: SARS-CoV-2 whole genome sequencing in Ontario, January 27, 2023. Toronto, ON: King's Printer for Ontario; 2023.

Disclaimer

This document was developed by Public Health Ontario (PHO). PHO provides scientific and technical advice to Ontario's government, public health organizations and health care providers. PHO's work is guided by the current best available evidence at the time of publication. The application and use of this document is the responsibility of the user. PHO assumes no liability resulting from any such application or use. This document may be reproduced without permission for non-commercial purposes only and provided that appropriate credit is given to PHO. No changes and/or modifications may be made to this document without express written permission from PHO.

For Further Information

For more information, email communications@oahpp.ca.

Public Health Ontario

Public Health Ontario is an agency of the Government of Ontario dedicated to protecting and promoting the health of all Ontarians and reducing inequities in health. Public Health Ontario links public health practitioners, front-line health workers and researchers to the best scientific intelligence and knowledge from around the world.

For more information about PHO, visit publichealthontario.ca.

Ontario

©King's Printer for Ontario, 2023