Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, February 17, 2023

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of February 15, 2023 and partner laboratories in the Ontario COVID-19 Genomics Network as of February 14, 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 29 to February 4), XBB.1.5 was the most prevalent lineage (31.1%), followed by BQ.1.1 (28.2%), and BQ.1 (3.6%).
- The proportion of BQ.1.1 decreased from 33.1% (January 22 to 28) to 28.2% (January 29 to February 4) and is projected to decline to 11.1% (95% CI: 10.1% - 12.3%) by February 22, 2023.
- The proportion of XBB.1.5 increased from 22.5% (January 22 to 28) to 31.1% (January 29 to February 4) and is projected to increase to 69.9% (95% CI: 67.0% - 72.6%) by February 22, 2023.
    - The weekly growth rate of XBB.1.5 is 1.71 (95% CI: 1.67-1.76) times that of BQ.1.1.
    - In the most recent week, Brant County Health Unit reported the highest proportion of XBB.1.5 cases (53.3%), followed by Kingston, Frontenac and Lennox & Addington Public Health (51.6%), and Niagara Region Public Health (47.7%); excluding public health units with fewer than 25 cases sequenced.

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.

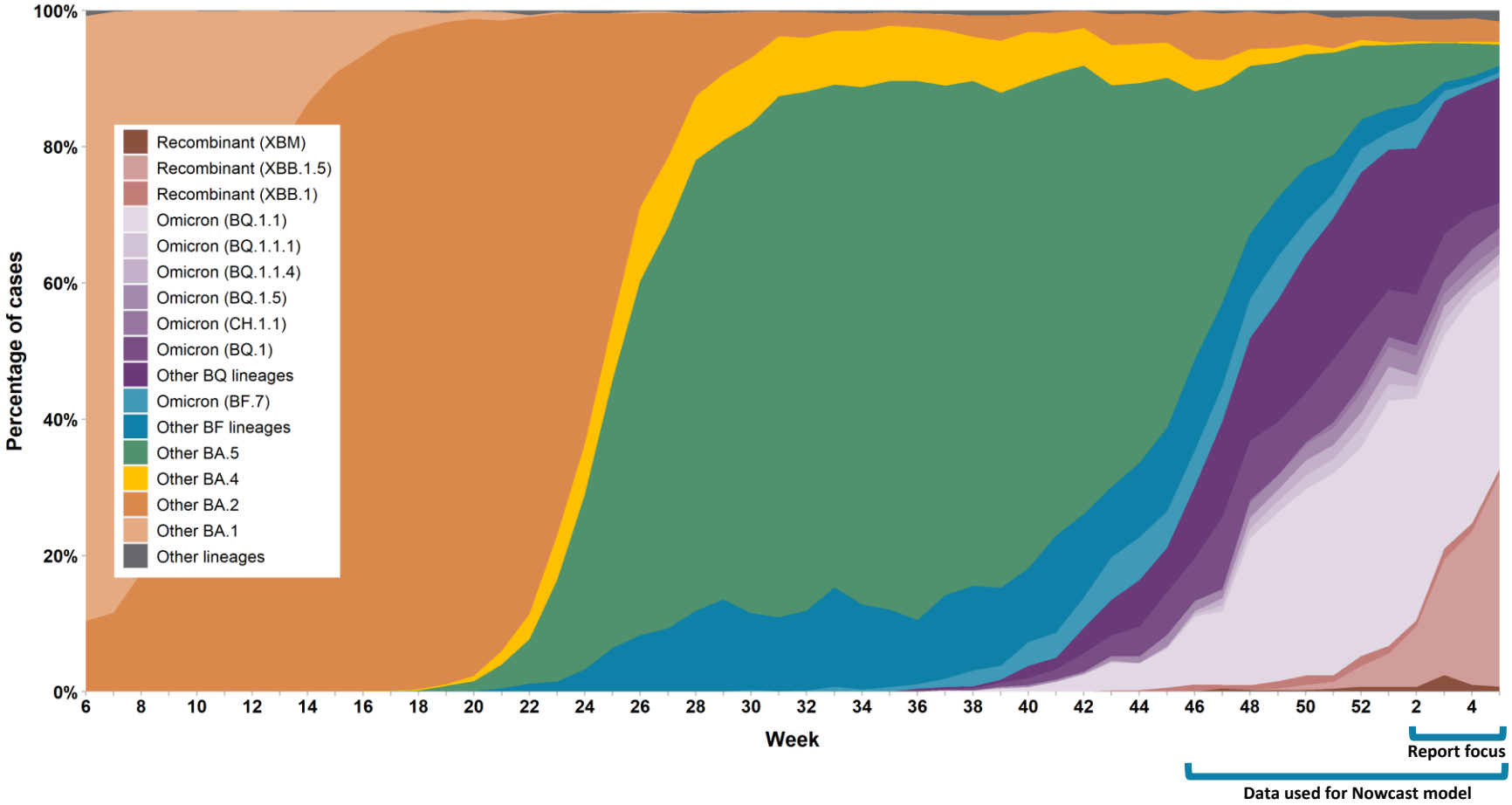
Representative Surveillance

Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, January 8 to February 4, 2023

Week	Number of cases	Number sequenced	Percentage sequenced
Week 2 (January 8 - January 14)	5,699	3,394	59.6%
Week 3 (January 15 - January 21)	5,233	3,045	58.2%
Week 4 (January 22 - January 28)	4,884	2,646	54.2%
Week 5 (January 29 - February 4)	4,539	2,613	57.6%
Total	**20,355**	**11,698**	**57.5%**

Note: 'Number of cases' is the number of confirmed positive cases of COVID-19 in Ontario. Date was assigned to best align with sample collection date, which may differ from other PHO products. 'Number sequenced' is the number of cases sequenced for representative surveillance. Results may not be representative of Ontario overall, and do not include all samples tested for other reasons including travel, outbreak investigation, coroner's cases, reinfection or possible vaccine escape. 'Percentage sequenced' may be lower than the sampling proportion because not all cases are eligible to be sequenced (i.e. excludes samples with cycle threshold >30 or insufficient volume). For representative surveillance: details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction and will be included in subsequent reports.
Data sources: CCM, PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Figure 1. Percentage of COVID-19 cases by the most prevalent lineages and week, representative surveillance, Ontario, February 6, 2022 to February 4, 2023



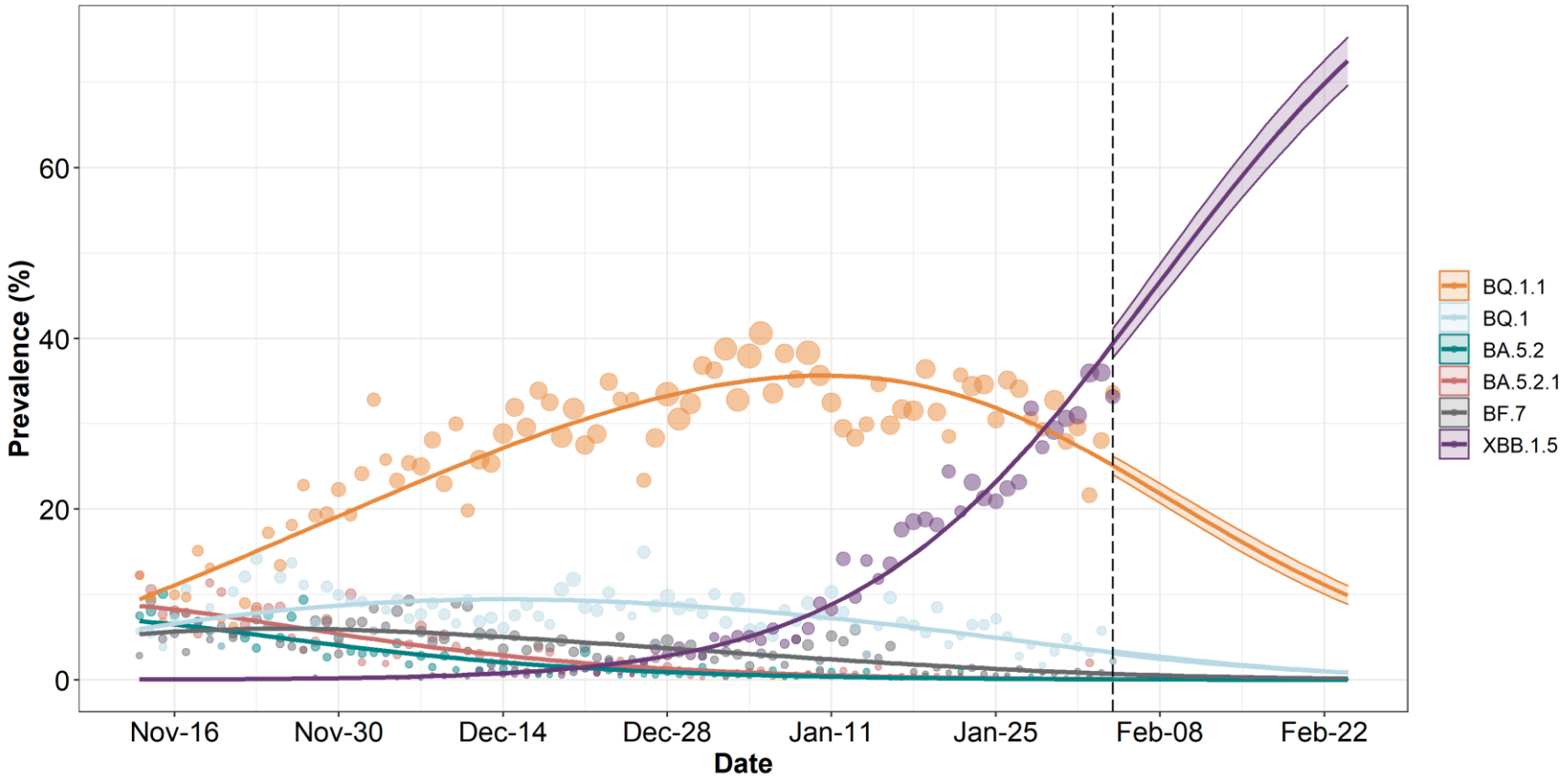
Note: Results may not be representative of Ontario overall, particularly in earlier weeks. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for 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, January 8 to February 4, 2023

WHO label/Pango lineage	Week 2 (January 8 - January 14)	Week 3 (January 15 - January 21)	Week 4 (January 22 - January 28)	Week 5 (January 29 - February 4)	Total (January 8- February 4)
Omicron	**2,996 (88.3%)**	**2,367 (77.7%)**	**1,964 (74.2%)**	**1,717 (65.7%)**	**9,044 (77.3%)**
BQ.1.1	1,107 (32.6%)	955 (31.4%)	876 (33.1%)	736 (28.2%)	3,674 (31.4%)
BQ.1	255 (7.5%)	209 (6.9%)	142 (5.4%)	95 (3.6%)	701 (6.0%)
BQ.1.5	97 (2.9%)	58 (1.9%)	51 (1.9%)	35 (1.3%)	241 (2.1%)
CH.1.1	52 (1.5%)	57 (1.9%)	64 (2.4%)	64 (2.4%)	237 (2.0%)
BF.7	140 (4.1%)	46 (1.5%)	20 (0.8%)	20 (0.8%)	226 (1.9%)
BQ.1.1.1	58 (1.7%)	63 (2.1%)	42 (1.6%)	53 (2.0%)	216 (1.8%)
BQ.1.1.4	57 (1.7%)	66 (2.2%)	32 (1.2%)	37 (1.4%)	192 (1.6%)
BQ.1.25	57 (1.7%)	47 (1.5%)	48 (1.8%)	32 (1.2%)	184 (1.6%)
Other BQ lineages	670 (19.7%)	544 (17.9%)	434 (16.4%)	450 (17.2%)	2,098 (17.9%)
Other BF lineages	82 (2.4%)	39 (1.3%)	27 (1.0%)	25 (1.0%)	173 (1.5%)
Other BA.5	301 (8.9%)	178 (5.8%)	128 (4.8%)	81 (3.1%)	688 (5.9%)
Other BA.4	13 (0.4%)	3 (0.1%)	9 (0.3%)	11 (0.4%)	36 (0.3%)
Other BA.2	106 (3.1%)	102 (3.3%)	91 (3.4%)	78 (3.0%)	377 (3.2%)
Other BA.1	1 (<0.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (<0.1%)
Recombinant	**398 (11.7%)**	**678 (22.3%)**	**682 (25.8%)**	**896 (34.3%)**	**2,654 (22.7%)**
XBB.1.5	301 (8.9%)	517 (17.0%)	596 (22.5%)	813 (31.1%)	2,227 (19.0%)
XBB.1	24 (0.7%)	75 (2.5%)	27 (1.0%)	20 (0.8%)	146 (1.2%)
XBM	30 (0.9%)	49 (1.6%)	31 (1.2%)	22 (0.8%)	132 (1.1%)
Other recombinant	43 (1.3%)	37 (1.2%)	28 (1.1%)	41 (1.6%)	149 (1.3%)
Total sequenced	**3,394 (100%)**	**3,045 (100%)**	**2,646 (100%)**	**2,613 (100%)**	**11,698 (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, November 13, 2022 to February 25, 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, November 13, 2022 to February 25, 2023

WHO label/ Pango lineage	Week 4 (January 25): Estimated	Week 5 (February 1): Estimated	Week 6 (February 8): Projected	Week 7 (February 15): Projected	Week 8 (February 22): Projected	Weekly relative growth rate
BQ.1.1	31.9 (31.0 - 32.7)	27.4 (26.4 - 28.4)	21.8 (20.7 - 23.0)	16.1 (15.0 - 17.4)	11.1 (10.1 - 12.3)	1.00 (reference)
BQ.1	4.9 (4.6 - 5.3)	3.7 (3.4 - 4.1)	2.6 (2.3 - 2.9)	1.7 (1.5 - 1.9)	1.0 (0.9 - 1.2)	0.87 (0.86 - 0.89)
BA.5.2	0.1 (0.1 - 0.2)	0.1 (0.0 - 0.1)	0.0 (0.0 - 0.0)	0.0 (0.0 - 0.0)	0.0 (0.0 - 0.0)	0.60 (0.58 - 0.62)
BA.5.2.1	0.2 (0.1 - 0.2)	0.1 (0.1 - 0.1)	0.0 (0.0 - 0.1)	0.0 (0.0 - 0.0)	0.0 (0.0 - 0.0)	0.61 (0.59 - 0.63)
BF.7	1.3 (1.1 - 1.5)	0.9 (0.7 - 1.0)	0.5 (0.4 - 0.6)	0.3 (0.3 - 0.4)	0.2 (0.1 - 0.2)	0.78 (0.76 - 0.79)
XBB.1.5	23.2 (22.4 - 24.1)	34.2 (32.8 - 35.6)	46.7 (44.7 - 48.8)	59.1 (56.5 - 61.6)	69.9 (67.0 - 72.6)	1.71 (1.67 - 1.76)

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, January 8 to February 4, 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	**166 (72.8%)**	**49 (66.2%)**	**111 (68.9%)**	**1,957 (73.5%)**	**2,205 (74.8%)**	**2,024 (78.2%)**	**2,526 (83.5%)**	**9,038 (77.3%)**
BQ.1.1	63 (27.6%)	23 (31.1%)	43 (26.7%)	783 (29.4%)	946 (32.1%)	788 (30.4%)	1,025 (33.9%)	3,671 (31.4%)
BQ.1	8 (3.5%)	5 (6.8%)	6 (3.7%)	133 (5.0%)	186 (6.3%)	167 (6.5%)	196 (6.5%)	701 (6.0%)
BQ.1.5	2 (0.9%)	2 (2.7%)	4 (2.5%)	41 (1.5%)	63 (2.1%)	60 (2.3%)	69 (2.3%)	241 (2.1%)
CH.1.1	3 (1.3%)	1 (1.4%)	3 (1.9%)	75 (2.8%)	61 (2.1%)	48 (1.9%)	45 (1.5%)	236 (2.0%)
BF.7	3 (1.3%)	0 (0.0%)	1 (0.6%)	33 (1.2%)	30 (1.0%)	47 (1.8%)	112 (3.7%)	226 (1.9%)
BQ.1.1.1	11 (4.8%)	2 (2.7%)	3 (1.9%)	60 (2.3%)	53 (1.8%)	33 (1.3%)	54 (1.8%)	216 (1.8%)
BQ.1.1.4	3 (1.3%)	1 (1.4%)	3 (1.9%)	56 (2.1%)	49 (1.7%)	34 (1.3%)	46 (1.5%)	192 (1.6%)
BQ.1.25	1 (0.4%)	1 (1.4%)	2 (1.2%)	44 (1.7%)	43 (1.5%)	39 (1.5%)	53 (1.8%)	183 (1.6%)
Other BQ lineages	51 (22.4%)	9 (12.2%)	29 (18.0%)	458 (17.2%)	474 (16.1%)	510 (19.7%)	566 (18.7%)	2,097 (17.9%)
Other BF lineages	4 (1.8%)	0 (0.0%)	3 (1.9%)	31 (1.2%)	35 (1.2%)	48 (1.9%)	52 (1.7%)	173 (1.5%)
Other BA.5	10 (4.4%)	2 (2.7%)	9 (5.6%)	141 (5.3%)	165 (5.6%)	164 (6.3%)	197 (6.5%)	688 (5.9%)
Other BA.4	0 (0.0%)	0 (0.0%)	1 (0.6%)	10 (0.4%)	6 (0.2%)	11 (0.4%)	8 (0.3%)	36 (0.3%)
Other BA.2	7 (3.1%)	3 (4.1%)	4 (2.5%)	92 (3.5%)	94 (3.2%)	74 (2.9%)	103 (3.4%)	377 (3.2%)
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	**62 (27.2%)**	**25 (33.8%)**	**50 (31.1%)**	**707 (26.5%)**	**744 (25.2%)**	**564 (21.8%)**	**498 (16.5%)**	**2,650 (22.7%)**
XBB.1.5	56 (24.6%)	24 (32.4%)	44 (27.3%)	601 (22.6%)	647 (21.9%)	459 (17.7%)	392 (13.0%)	2,223 (19.0%)
XBB.1	2 (0.9%)	0 (0.0%)	1 (0.6%)	27 (1.0%)	30 (1.0%)	47 (1.8%)	39 (1.3%)	146 (1.2%)
XBM	1 (0.4%)	1 (1.4%)	1 (0.6%)	33 (1.2%)	31 (1.1%)	26 (1.0%)	39 (1.3%)	132 (1.1%)
Other recombinant	3 (1.3%)	0 (0.0%)	4 (2.5%)	46 (1.7%)	36 (1.2%)	32 (1.2%)	28 (0.9%)	149 (1.3%)
Total sequenced	**228 (100%)**	**74 (100%)**	**161 (100%)**	**2,664 (100%)**	**2,949 (100%)**	**2,588 (100%)**	**3,024 (100%)**	**11,688 (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 XBB.1.5 cases, number identified, and total sequenced by public health unit (PHU), region, and week, representative surveillance, Ontario, January 8 to February 4, 2023

Public Health Unit	Week 2 (January 8 - January 14)	Week 3 (January 15 - January 21)	Week 4 (January 22 - January 28)	Week 5 (January 29 - February 4)	Total (January 8- February 4)
Northwestern Health Unit	0.0% (0/4)	0.0% (0/2)	50.0% (3/6)	85.7% (6/7)	47.4% (9/19)
Thunder Bay District Health Unit	3.3% (2/60)	1.8% (1/57)	15.4% (8/52)	25.7% (9/35)	9.8% (20/204)
TOTAL NORTH WEST	**3.1% (2/64)**	**1.7% (1/59)**	**19.0% (11/58)**	**35.7% (15/42)**	**13.0% (29/223)**
Algoma Public Health	0.0% (0/20)	0.0% (0/13)	10.0% (2/20)	5.7% (2/35)	4.5% (4/88)
North Bay Parry Sound District Health Unit	0.0% (0/15)	11.1% (3/27)	34.8% (8/23)	37.5% (12/32)	23.7% (23/97)
Porcupine Health Unit	0.0% (0/33)	3.8% (1/26)	0.0% (0/9)	10.0% (1/10)	2.6% (2/78)
Public Health Sudbury & Districts	2.9% (1/35)	13.5% (5/37)	1.6% (1/61)	3.9% (2/51)	4.9% (9/184)
Timiskaming Health Unit	0.0% (0/0)	0.0% (0/0)	100% (1/1)	0.0% (0/1)	50.0% (1/2)
TOTAL NORTH EAST	**1.0% (1/103)**	**8.7% (9/103)**	**10.5% (12/114)**	**13.2% (17/129)**	**8.7% (39/449)**
Ottawa Public Health	24.2% (48/198)	12.0% (26/216)	19.8% (26/131)	27.8% (35/126)	20.1% (135/671)
Eastern Ontario Health Unit	8.6% (3/35)	5.7% (2/35)	16.7% (3/18)	32.1% (9/28)	14.7% (17/116)
Hastings Prince Edward Public Health	3.8% (3/79)	6.2% (3/48)	5.9% (3/51)	28.8% (17/59)	11.0% (26/237)
Kingston, Frontenac and Lennox & Addington Public Health	16.3% (23/141)	26.8% (41/153)	38.4% (48/125)	51.6% (80/155)	33.4% (192/574)
Leeds, Grenville & Lanark District Health Unit	7.4% (4/54)	13.6% (8/59)	21.6% (16/74)	36.7% (11/30)	18.0% (39/217)
Renfrew County and District Health Unit	0.0% (0/28)	11.1% (1/9)	10.0% (1/10)	18.2% (2/11)	6.9% (4/58)
TOTAL EASTERN	**15.1% (81/535)**	**15.6% (81/520)**	**23.7% (97/409)**	**37.7% (154/409)**	**22.1% (413/1,873)**
Durham Region Health Department	6.8% (9/133)	41.1% (53/129)	30.8% (36/117)	36.3% (49/135)	28.6% (147/514)
Haliburton, Kawartha, Pine Ridge District Health Unit	8.5% (6/71)	0.0% (0/49)	25.0% (14/56)	22.4% (13/58)	14.1% (33/234)
Peel Public Health	8.7% (20/229)	21.1% (47/223)	29.1% (46/158)	30.0% (48/160)	20.9% (161/770)
Peterborough Public Health	19.0% (4/21)	16.0% (4/25)	10.7% (3/28)	16.3% (7/43)	15.4% (18/117)
Simcoe Muskoka District Health Unit	7.6% (9/119)	11.1% (10/90)	9.2% (12/131)	14.9% (18/121)	10.6% (49/461)
York Region Public Health	10.1% (17/168)	19.8% (23/116)	20.3% (27/133)	24.4% (33/135)	18.1% (100/552)
TOTAL CENTRAL EAST	**8.8% (65/741)**	**21.7% (137/632)**	**22.2% (138/623)**	**25.8% (168/652)**	**19.2% (508/2,648)**
Toronto Public Health	9.9% (67/679)	23.0% (130/564)	24.6% (130/529)	36.1% (172/476)	22.2% (499/2,248)
TOTAL TORONTO	**9.9% (67/679)**	**23.0% (130/564)**	**24.6% (130/529)**	**36.1% (172/476)**	**22.2% (499/2,248)**

Public Health Unit	Week 2 (January 8 - January 14)	Week 3 (January 15 - January 21)	Week 4 (January 22 - January 28)	Week 5 (January 29 - February 4)	Total (January 8- February 4)
Chatham-Kent Public Health	3.7% (2/54)	11.9% (7/59)	7.7% (2/26)	6.8% (3/44)	7.7% (14/183)
Grey Bruce Health Unit	8.7% (2/23)	3.8% (1/26)	11.1% (2/18)	20.0% (3/15)	9.8% (8/82)
Huron Perth Public Health	5.7% (2/35)	3.8% (2/52)	14.3% (3/21)	7.1% (1/14)	6.6% (8/122)
Lambton Public Health	17.6% (3/17)	19.4% (6/31)	46.2% (6/13)	39.3% (11/28)	29.2% (26/89)
Middlesex-London Health Unit	8.3% (8/96)	4.5% (7/155)	19.2% (20/104)	33.7% (31/92)	14.8% (66/447)
Southwestern Public Health	6.3% (4/63)	4.3% (3/70)	15.2% (7/46)	40.9% (9/22)	11.4% (23/201)
Windsor-Essex County Health Unit	4.5% (7/155)	15.4% (23/149)	35.6% (36/101)	29.2% (21/72)	18.2% (87/477)
TOTAL SOUTH WEST	**6.3% (28/443)**	**9.0% (49/542)**	**23.1% (76/329)**	**27.5% (79/287)**	**14.5% (232/1,601)**
Brant County Health Unit	5.6% (2/36)	24.2% (8/33)	30.8% (8/26)	53.3% (16/30)	27.2% (34/125)
City of Hamilton Public Health Services	5.7% (18/316)	10.6% (15/141)	19.4% (31/160)	25.4% (46/181)	13.8% (110/798)
Haldimand-Norfolk Health Unit	5.4% (2/37)	7.7% (5/65)	2.9% (1/35)	10.3% (3/29)	6.6% (11/166)
Halton Region Public Health	0.0% (0/100)	12.5% (8/64)	20.3% (13/64)	19.7% (12/61)	11.4% (33/289)
Niagara Region Public Health	13.2% (22/167)	28.0% (49/175)	31.0% (54/174)	47.7% (71/149)	29.5% (196/665)
Region of Waterloo Public Health and Emergency Services	6.0% (8/133)	10.2% (10/98)	18.1% (15/83)	39.3% (48/122)	18.6% (81/436)
Wellington-Dufferin-Guelph Public Health	13.5% (5/37)	33.3% (14/42)	23.8% (10/42)	26.1% (12/46)	24.6% (41/167)
TOTAL CENTRAL WEST	**6.9% (57/826)**	**17.6% (109/618)**	**22.6% (132/584)**	**33.7% (208/618)**	**19.1% (506/2,646)**
UNKNOWN	**0.0% (0/1)**	**0.0% (0/2)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/3)**
TOTAL ONTARIO	**8.9% (301/3,394)**	**17.0% (517/3,045)**	**22.5% (596/2,646)**	**31.1% (813/2,613)**	**19.0% (2,227/11,698)**

Note: Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 6a. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North West Region, January 8 to February 4, 2023

WHO label / Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
Omicron	**10 (52.6%)**	**183 (89.7%)**	**193 (86.5%)**
BQ.1.1	5 (26.3%)	150 (73.5%)	155 (69.5%)
BQ.1	0 (0.0%)	4 (2.0%)	4 (1.8%)
BQ.1.5	0 (0.0%)	0 (0.0%)	0 (0.0%)
CH.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
BF.7	1 (5.3%)	3 (1.5%)	4 (1.8%)
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.1.25	0 (0.0%)	1 (0.5%)	1 (0.4%)
Other BQ lineages	0 (0.0%)	16 (7.8%)	16 (7.2%)
Other BF lineages	0 (0.0%)	3 (1.5%)	3 (1.3%)
Other BA.5	3 (15.8%)	5 (2.5%)	8 (3.6%)
Other BA.4	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BA.2	1 (5.3%)	1 (0.5%)	2 (0.9%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**9 (47.4%)**	**21 (10.3%)**	**30 (13.5%)**
XBB.1.5	9 (47.4%)	20 (9.8%)	29 (13.0%)
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
XBM	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other recombinant	0 (0.0%)	1 (0.5%)	1 (0.4%)
Total sequenced	**19 (100%)**	**204 (100%)**	**223 (100%)**

Note: 'Other BA.5' excludes BQ and BF 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6b. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North East Region, January 8 to February 4, 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	**84 (95.5%)**	**74 (76.3%)**	**76 (97.4%)**	**173 (94.0%)**	**1 (50.0%)**	**408 (90.9%)**
BQ.1.1	30 (34.1%)	29 (29.9%)	21 (26.9%)	78 (42.4%)	0 (0.0%)	158 (35.2%)
BQ.1	1 (1.1%)	5 (5.2%)	1 (1.3%)	8 (4.3%)	1 (50.0%)	16 (3.6%)
BQ.1.5	0 (0.0%)	1 (1.0%)	0 (0.0%)	1 (0.5%)	0 (0.0%)	2 (0.4%)
CH.1.1	10 (11.4%)	1 (1.0%)	1 (1.3%)	2 (1.1%)	0 (0.0%)	14 (3.1%)
BF.7	10 (11.4%)	2 (2.1%)	0 (0.0%)	3 (1.6%)	0 (0.0%)	15 (3.3%)
BQ.1.1.1	0 (0.0%)	1 (1.0%)	2 (2.6%)	3 (1.6%)	0 (0.0%)	6 (1.3%)
BQ.1.1.4	0 (0.0%)	3 (3.1%)	0 (0.0%)	3 (1.6%)	0 (0.0%)	6 (1.3%)
BQ.1.25	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other BQ lineages	8 (9.1%)	10 (10.3%)	38 (48.7%)	52 (28.3%)	0 (0.0%)	108 (24.1%)
Other BF lineages	10 (11.4%)	6 (6.2%)	2 (2.6%)	5 (2.7%)	0 (0.0%)	23 (5.1%)
Other BA.5	8 (9.1%)	6 (6.2%)	7 (9.0%)	5 (2.7%)	0 (0.0%)	26 (5.8%)
Other BA.4	6 (6.8%)	0 (0.0%)	0 (0.0%)	4 (2.2%)	0 (0.0%)	10 (2.2%)
Other BA.2	1 (1.1%)	10 (10.3%)	4 (5.1%)	9 (4.9%)	0 (0.0%)	24 (5.3%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**4 (4.5%)**	**23 (23.7%)**	**2 (2.6%)**	**11 (6.0%)**	**1 (50.0%)**	**41 (9.1%)**
XBB.1.5	4 (4.5%)	23 (23.7%)	2 (2.6%)	9 (4.9%)	1 (50.0%)	39 (8.7%)
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
XBM	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	**88 (100%)**	**97 (100%)**	**78 (100%)**	**184 (100%)**	**2 (100%)**	**449 (100%)**

Note: 'Other BA.5' excludes BQ and BF 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6c. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Eastern Region, January 8 to February 4, 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	**99 (85.3%)**	**208 (87.8%)**	**372 (64.8%)**	**176 (81.1%)**	**528 (78.7%)**	**51 (87.9%)**	**1,434 (76.6%)**
BQ.1.1	33 (28.4%)	53 (22.4%)	135 (23.5%)	95 (43.8%)	216 (32.2%)	15 (25.9%)	547 (29.2%)
BQ.1	10 (8.6%)	4 (1.7%)	19 (3.3%)	4 (1.8%)	21 (3.1%)	20 (34.5%)	78 (4.2%)
BQ.1.5	1 (0.9%)	52 (21.9%)	5 (0.9%)	1 (0.5%)	3 (0.4%)	1 (1.7%)	63 (3.4%)
CH.1.1	0 (0.0%)	0 (0.0%)	1 (0.2%)	0 (0.0%)	9 (1.3%)	0 (0.0%)	10 (0.5%)
BF.7	3 (2.6%)	24 (10.1%)	12 (2.1%)	3 (1.4%)	18 (2.7%)	7 (12.1%)	67 (3.6%)
BQ.1.1.1	1 (0.9%)	1 (0.4%)	3 (0.5%)	6 (2.8%)	9 (1.3%)	1 (1.7%)	21 (1.1%)
BQ.1.1.4	1 (0.9%)	1 (0.4%)	4 (0.7%)	8 (3.7%)	6 (0.9%)	3 (5.2%)	23 (1.2%)
BQ.1.25	0 (0.0%)	1 (0.4%)	10 (1.7%)	0 (0.0%)	5 (0.7%)	0 (0.0%)	16 (0.9%)
Other BQ lineages	42 (36.2%)	56 (23.6%)	85 (14.8%)	45 (20.7%)	182 (27.1%)	2 (3.4%)	412 (22.0%)
Other BF lineages	2 (1.7%)	0 (0.0%)	4 (0.7%)	2 (0.9%)	2 (0.3%)	0 (0.0%)	10 (0.5%)
Other BA.5	2 (1.7%)	8 (3.4%)	35 (6.1%)	7 (3.2%)	36 (5.4%)	2 (3.4%)	90 (4.8%)
Other BA.4	1 (0.9%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.1%)
Other BA.2	3 (2.6%)	8 (3.4%)	59 (10.3%)	5 (2.3%)	21 (3.1%)	0 (0.0%)	96 (5.1%)
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	**17 (14.7%)**	**29 (12.2%)**	**202 (35.2%)**	**41 (18.9%)**	**143 (21.3%)**	**7 (12.1%)**	**439 (23.4%)**
XBB.1.5	17 (14.7%)	26 (11.0%)	192 (33.4%)	39 (18.0%)	135 (20.1%)	4 (6.9%)	413 (22.1%)
XBB.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	1 (0.1%)	1 (1.7%)	3 (0.2%)
XBM	0 (0.0%)	1 (0.4%)	2 (0.3%)	1 (0.5%)	1 (0.1%)	2 (3.4%)	7 (0.4%)
Other recombinant	0 (0.0%)	2 (0.8%)	8 (1.4%)	0 (0.0%)	6 (0.9%)	0 (0.0%)	16 (0.9%)
Total sequenced	**116 (100%)**	**237 (100%)**	**574 (100%)**	**217 (100%)**	**671 (100%)**	**58 (100%)**	**1,873 (100%)**

Note: 'Other BA.5' excludes BQ and BF 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6d. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central East Region, January 8 to February 4, 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	**357 (69.5%)**	**196 (83.8%)**	**578 (75.1%)**	**92 (78.6%)**	**389 (84.4%)**	**431 (78.1%)**	**2,043 (77.2%)**
BQ.1.1	183 (35.6%)	75 (32.1%)	254 (33.0%)	49 (41.9%)	193 (41.9%)	170 (30.8%)	924 (34.9%)
BQ.1	17 (3.3%)	26 (11.1%)	59 (7.7%)	7 (6.0%)	22 (4.8%)	34 (6.2%)	165 (6.2%)
BQ.1.5	6 (1.2%)	5 (2.1%)	7 (0.9%)	0 (0.0%)	5 (1.1%)	17 (3.1%)	40 (1.5%)
CH.1.1	2 (0.4%)	1 (0.4%)	17 (2.2%)	2 (1.7%)	9 (2.0%)	3 (0.5%)	34 (1.3%)
BF.7	1 (0.2%)	3 (1.3%)	5 (0.6%)	1 (0.9%)	1 (0.2%)	1 (0.2%)	12 (0.5%)
BQ.1.1.1	4 (0.8%)	0 (0.0%)	8 (1.0%)	1 (0.9%)	2 (0.4%)	8 (1.4%)	23 (0.9%)
BQ.1.1.4	6 (1.2%)	5 (2.1%)	15 (1.9%)	2 (1.7%)	5 (1.1%)	9 (1.6%)	42 (1.6%)
BQ.1.25	23 (4.5%)	2 (0.9%)	10 (1.3%)	8 (6.8%)	1 (0.2%)	3 (0.5%)	47 (1.8%)
Other BQ lineages	73 (14.2%)	40 (17.1%)	151 (19.6%)	10 (8.5%)	75 (16.3%)	102 (18.5%)	451 (17.0%)
Other BF lineages	5 (1.0%)	4 (1.7%)	4 (0.5%)	1 (0.9%)	32 (6.9%)	8 (1.4%)	54 (2.0%)
Other BA.5	30 (5.8%)	32 (13.7%)	30 (3.9%)	8 (6.8%)	33 (7.2%)	26 (4.7%)	159 (6.0%)
Other BA.4	1 (0.2%)	0 (0.0%)	2 (0.3%)	0 (0.0%)	1 (0.2%)	2 (0.4%)	6 (0.2%)
Other BA.2	6 (1.2%)	2 (0.9%)	16 (2.1%)	3 (2.6%)	10 (2.2%)	48 (8.7%)	85 (3.2%)
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	**157 (30.5%)**	**38 (16.2%)**	**192 (24.9%)**	**25 (21.4%)**	**72 (15.6%)**	**121 (21.9%)**	**605 (22.8%)**
XBB.1.5	147 (28.6%)	33 (14.1%)	161 (20.9%)	18 (15.4%)	49 (10.6%)	100 (18.1%)	508 (19.2%)
XBB.1	1 (0.2%)	0 (0.0%)	1 (0.1%)	0 (0.0%)	1 (0.2%)	2 (0.4%)	5 (0.2%)
XBM	3 (0.6%)	3 (1.3%)	21 (2.7%)	3 (2.6%)	18 (3.9%)	6 (1.1%)	54 (2.0%)
Other recombinant	6 (1.2%)	2 (0.9%)	9 (1.2%)	4 (3.4%)	4 (0.9%)	13 (2.4%)	38 (1.4%)
Total sequenced	**514 (100%)**	**234 (100%)**	**770 (100%)**	**117 (100%)**	**461 (100%)**	**552 (100%)**	**2,648 (100%)**

Note: 'Other BA.5' excludes BQ and BF 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6e. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Toronto Region, January 8 to February 4, 2023

WHO label / Pango lineage	Toronto Public Health	Total
Omicron	**1,681 (74.8%)**	**1,681 (74.8%)**
BQ.1.1	712 (31.7%)	712 (31.7%)
BQ.1	163 (7.3%)	163 (7.3%)
BQ.1.5	42 (1.9%)	42 (1.9%)
CH.1.1	37 (1.6%)	37 (1.6%)
BF.7	20 (0.9%)	20 (0.9%)
BQ.1.1.1	30 (1.3%)	30 (1.3%)
BQ.1.1.4	24 (1.1%)	24 (1.1%)
BQ.1.25	57 (2.5%)	57 (2.5%)
Other BQ lineages	438 (19.5%)	438 (19.5%)
Other BF lineages	29 (1.3%)	29 (1.3%)
Other BA.5	72 (3.2%)	72 (3.2%)
Other BA.4	6 (0.3%)	6 (0.3%)
Other BA.2	51 (2.3%)	51 (2.3%)
Other BA.1	0 (0.0%)	0 (0.0%)
Recombinant	**567 (25.2%)**	**567 (25.2%)**
XBB.1.5	499 (22.2%)	499 (22.2%)
XBB.1	0 (0.0%)	0 (0.0%)
XBM	46 (2.0%)	46 (2.0%)
Other recombinant	22 (1.0%)	22 (1.0%)
Total sequenced	**2,248 (100%)**	**2,248 (100%)**

Note: 'Other BA.5' excludes BQ and BF 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6f. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, South West Region, January 8 to February 4, 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	**144 (78.7%)**	**74 (90.2%)**	**111 (91.0%)**	**62 (69.7%)**	**301 (67.3%)**	**173 (86.1%)**	**360 (75.5%)**	**1,225 (76.5%)**
BQ.1.1	61 (33.3%)	26 (31.7%)	34 (27.9%)	27 (30.3%)	133 (29.8%)	68 (33.8%)	116 (24.3%)	465 (29.0%)
BQ.1	4 (2.2%)	4 (4.9%)	3 (2.5%)	1 (1.1%)	10 (2.2%)	9 (4.5%)	11 (2.3%)	42 (2.6%)
BQ.1.5	5 (2.7%)	8 (9.8%)	13 (10.7%)	0 (0.0%)	5 (1.1%)	1 (0.5%)	6 (1.3%)	38 (2.4%)
CH.1.1	1 (0.5%)	7 (8.5%)	7 (5.7%)	6 (6.7%)	4 (0.9%)	35 (17.4%)	8 (1.7%)	68 (4.2%)
BF.7	20 (10.9%)	1 (1.2%)	1 (0.8%)	0 (0.0%)	3 (0.7%)	1 (0.5%)	14 (2.9%)	40 (2.5%)
BQ.1.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.1%)	19 (4.3%)	2 (1.0%)	25 (5.2%)	47 (2.9%)
BQ.1.1.4	3 (1.6%)	0 (0.0%)	33 (27.0%)	5 (5.6%)	8 (1.8%)	6 (3.0%)	6 (1.3%)	61 (3.8%)
BQ.1.25	0 (0.0%)	0 (0.0%)	1 (0.8%)	0 (0.0%)	1 (0.2%)	0 (0.0%)	0 (0.0%)	2 (0.1%)
Other BQ lineages	23 (12.6%)	9 (11.0%)	11 (9.0%)	9 (10.1%)	55 (12.3%)	30 (14.9%)	119 (24.9%)	256 (16.0%)
Other BF lineages	2 (1.1%)	3 (3.7%)	0 (0.0%)	3 (3.4%)	2 (0.4%)	1 (0.5%)	7 (1.5%)	18 (1.1%)
Other BA.5	21 (11.5%)	15 (18.3%)	5 (4.1%)	5 (5.6%)	45 (10.1%)	15 (7.5%)	39 (8.2%)	145 (9.1%)
Other BA.4	2 (1.1%)	0 (0.0%)	2 (1.6%)	0 (0.0%)	1 (0.2%)	0 (0.0%)	1 (0.2%)	6 (0.4%)
Other BA.2	2 (1.1%)	1 (1.2%)	1 (0.8%)	5 (5.6%)	15 (3.4%)	5 (2.5%)	8 (1.7%)	37 (2.3%)
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	**39 (21.3%)**	**8 (9.8%)**	**11 (9.0%)**	**27 (30.3%)**	**146 (32.7%)**	**28 (13.9%)**	**117 (24.5%)**	**376 (23.5%)**
XBB.1.5	14 (7.7%)	8 (9.8%)	8 (6.6%)	26 (29.2%)	66 (14.8%)	23 (11.4%)	87 (18.2%)	232 (14.5%)
XBB.1	25 (13.7%)	0 (0.0%)	2 (1.6%)	1 (1.1%)	67 (15.0%)	1 (0.5%)	24 (5.0%)	120 (7.5%)
XBM	0 (0.0%)	0 (0.0%)	1 (0.8%)	0 (0.0%)	10 (2.2%)	1 (0.5%)	3 (0.6%)	15 (0.9%)
Other recombinant	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (0.7%)	3 (1.5%)	3 (0.6%)	9 (0.6%)
Total sequenced	**183 (100%)**	**82 (100%)**	**122 (100%)**	**89 (100%)**	**447 (100%)**	**201 (100%)**	**477 (100%)**	**1,601 (100%)**

Note: 'Other BA.5' excludes BQ and BF 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 6g. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central West Region, January 8 to February 4, 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	**87 (69.6%)**	**647 (81.1%)**	**154 (92.8%)**	**245 (84.8%)**	**458 (68.9%)**	**344 (78.9%)**	**116 (69.5%)**	**2,051 (77.5%)**
BQ.1.1	26 (20.8%)	205 (25.7%)	33 (19.9%)	81 (28.0%)	238 (35.8%)	84 (19.3%)	43 (25.7%)	710 (26.8%)
BQ.1	14 (11.2%)	62 (7.8%)	66 (39.8%)	27 (9.3%)	37 (5.6%)	24 (5.5%)	2 (1.2%)	232 (8.8%)
BQ.1.5	2 (1.6%)	17 (2.1%)	3 (1.8%)	6 (2.1%)	19 (2.9%)	6 (1.4%)	3 (1.8%)	56 (2.1%)
CH.1.1	1 (0.8%)	19 (2.4%)	0 (0.0%)	9 (3.1%)	11 (1.7%)	28 (6.4%)	6 (3.6%)	74 (2.8%)
BF.7	1 (0.8%)	25 (3.1%)	1 (0.6%)	23 (8.0%)	6 (0.9%)	5 (1.1%)	7 (4.2%)	68 (2.6%)
BQ.1.1.1	1 (0.8%)	62 (7.8%)	2 (1.2%)	9 (3.1%)	5 (0.8%)	9 (2.1%)	1 (0.6%)	89 (3.4%)
BQ.1.1.4	4 (3.2%)	8 (1.0%)	4 (2.4%)	4 (1.4%)	4 (0.6%)	7 (1.6%)	4 (2.4%)	35 (1.3%)
BQ.1.25	5 (4.0%)	15 (1.9%)	22 (13.3%)	2 (0.7%)	3 (0.5%)	7 (1.6%)	7 (4.2%)	61 (2.3%)
Other BQ lineages	16 (12.8%)	167 (20.9%)	10 (6.0%)	45 (15.6%)	63 (9.5%)	91 (20.9%)	23 (13.8%)	415 (15.7%)
Other BF lineages	2 (1.6%)	9 (1.1%)	0 (0.0%)	1 (0.3%)	19 (2.9%)	2 (0.5%)	2 (1.2%)	35 (1.3%)
Other BA.5	11 (8.8%)	33 (4.1%)	7 (4.2%)	24 (8.3%)	43 (6.5%)	61 (14.0%)	8 (4.8%)	187 (7.1%)
Other BA.4	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.3%)	1 (0.2%)	4 (0.9%)	1 (0.6%)	7 (0.3%)
Other BA.2	4 (3.2%)	25 (3.1%)	6 (3.6%)	13 (4.5%)	9 (1.4%)	16 (3.7%)	9 (5.4%)	82 (3.1%)
Other BA.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Recombinant	**38 (30.4%)**	**151 (18.9%)**	**12 (7.2%)**	**44 (15.2%)**	**207 (31.1%)**	**92 (21.1%)**	**51 (30.5%)**	**595 (22.5%)**
XBB.1.5	34 (27.2%)	110 (13.8%)	11 (6.6%)	33 (11.4%)	196 (29.5%)	81 (18.6%)	41 (24.6%)	506 (19.1%)
XBB.1	1 (0.8%)	9 (1.1%)	0 (0.0%)	1 (0.3%)	4 (0.6%)	3 (0.7%)	0 (0.0%)	18 (0.7%)
XBM	1 (0.8%)	1 (0.1%)	0 (0.0%)	1 (0.3%)	2 (0.3%)	2 (0.5%)	2 (1.2%)	9 (0.3%)
Other recombinant	2 (1.6%)	31 (3.9%)	1 (0.6%)	9 (3.1%)	5 (0.8%)	6 (1.4%)	8 (4.8%)	62 (2.3%)
Total sequenced	**125 (100%)**	**798 (100%)**	**166 (100%)**	**289 (100%)**	**665 (100%)**	**436 (100%)**	**167 (100%)**	**2,646 (100%)**

Note: 'Other BA.5' excludes BQ and BF 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 (2.8%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 7. Number and percentage (row %) of outbreak-associated and non outbreak-associated cases by Pango lineage, representative surveillance, Ontario, January 8 to February 4, 2023

WHO label / Pango lineage	Outbreak-associated	Non outbreak-associated	Total cases
Omicron	**2,958 (33.7%)**	**5,826 (66.3%)**	**8,784 (100%)**
BQ.1.1	1,151 (32.2%)	2,418 (67.8%)	3,569 (100%)
BQ.1	212 (30.9%)	473 (69.1%)	685 (100%)
BQ.1.5	89 (37.9%)	146 (62.1%)	235 (100%)
CH.1.1	85 (37.1%)	144 (62.9%)	229 (100%)
BF.7	129 (58.9%)	90 (41.1%)	219 (100%)
BQ.1.1.1	60 (28.7%)	149 (71.3%)	209 (100%)
BQ.1.1.4	50 (27.0%)	135 (73.0%)	185 (100%)
BQ.1.25	74 (41.1%)	106 (58.9%)	180 (100%)
Other BQ lineages	726 (35.6%)	1,311 (64.4%)	2,037 (100%)
Other BF lineages	56 (33.5%)	111 (66.5%)	167 (100%)
Other BA.5	220 (33.1%)	445 (66.9%)	665 (100%)
Other BA.4	4 (11.1%)	32 (88.9%)	36 (100%)
Other BA.2	102 (27.8%)	265 (72.2%)	367 (100%)
Other BA.1	0 (0.0%)	1 (100%)	1 (100%)
Recombinant	**612 (23.7%)**	**1,969 (76.3%)**	**2,581 (100%)**
XBB.1.5	442 (20.4%)	1,725 (79.6%)	2,167 (100%)
XBB.1	79 (55.2%)	64 (44.8%)	143 (100%)
XBM	54 (43.2%)	71 (56.8%)	125 (100%)
Other recombinant	37 (25.3%)	109 (74.7%)	146 (100%)
Total sequenced	**3,570 (31.4%)**	**7,795 (68.6%)**	**11,365 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. Cases include only those that linked to CCM (97.2%). 'Outbreak-associated cases' include cases linked to a confirmed outbreak as declared by the local medical officer of health or their designate. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction.

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

Table 8. Number and percentage (row %) of cases admitted to hospital and deceased cases by Pango lineage, representative surveillance, Ontario, January 8 to February 4, 2023

WHO label / Pango lineage	Hospital admissions	Deceased	Total cases
Omicron	**554 (6.3%)**	**94 (1.1%)**	**8,784 (100%)**
BQ.1.1	208 (5.8%)	22 (0.6%)	3,569 (100%)
BQ.1	42 (6.1%)	7 (1.0%)	685 (100%)
BQ.1.5	14 (6.0%)	6 (2.6%)	235 (100%)
CH.1.1	11 (4.8%)	1 (0.4%)	229 (100%)
BF.7	15 (6.8%)	3 (1.4%)	219 (100%)
BQ.1.1.1	9 (4.3%)	1 (0.5%)	209 (100%)
BQ.1.1.4	11 (5.9%)	4 (2.2%)	185 (100%)
BQ.1.25	12 (6.7%)	2 (1.1%)	180 (100%)
Other BQ lineages	126 (6.2%)	28 (1.4%)	2,037 (100%)
Other BF lineages	13 (7.8%)	3 (1.8%)	167 (100%)
Other BA.5	58 (8.7%)	12 (1.8%)	665 (100%)
Other BA.4	2 (5.6%)	0 (0.0%)	36 (100%)
Other BA.2	33 (9.0%)	5 (1.4%)	367 (100%)
Other BA.1	0 (0.0%)	0 (0.0%)	1 (100%)
Recombinant	**140 (5.4%)**	**10 (0.4%)**	**2,581 (100%)**
XBB.1.5	122 (5.6%)	8 (0.4%)	2,167 (100%)
XBB.1	3 (2.1%)	1 (0.7%)	143 (100%)
XBM	8 (6.4%)	1 (0.8%)	125 (100%)
Other recombinant	7 (4.8%)	0 (0.0%)	146 (100%)
Total sequenced	**694 (6.1%)**	**104 (0.9%)**	**11,365 (100%)**

Note: Includes the most prevalent lineages detected in the past month. 'Other BA.5' excludes BQ and BF lineages. Cases include only those that linked to CCM (97.2%). Hospital admissions include all cases admitted to hospital (or had their hospital stay extended) because of COVID-19 at time of data extraction. Deceased cases include cases that reported a "Fatal" outcome and the type of death value in CCM was not 'DOPHS was unrelated to cause of death' or 'Under PHU Review' at the time of data extraction. Factors, such as age, that may affect the risk of COVID-19 hospital admission and death are not accounted for in these analyses. Results may not be representative of Ontario overall. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction.
Data Sources: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Hamilton Regional Laboratory Medicine Program, The Shared Hospital Laboratory, CCM (hospital admission and death indicators)

Cumulative Whole Genome Sequencing Results

Table 9. Number of cases by Pango lineage, cumulative counts, Ontario, January 1, 2021 to February 4, 2023

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
Variant of Concern (VOC)			
Alpha	**11,756**	**0**	**11,756**
Beta	**1,221**	**0**	**1,221**
Gamma	**3,913**	**0**	**3,913**
Delta	**45,889**	**0**	**45,889**
Omicron	**141,461**	**9,044**	**150,505**
B.1.1.529	0	0	0
BA.1	6,380	0	6,380
BA.1.1	18,618	1	18,619
BA.1.1.1	42	0	42
BA.1.1.10	1,667	0	1,667
BA.1.1.13	3	0	3
BA.1.1.14	520	0	520
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	128	0	128
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	1,633	0	1,633
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	1,498	0	1,498
BA.1.18	92	0	92

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 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	16,098	1	16,099
BA.2.1	217	0	217
BA.2.10	387	0	387
BA.2.10.1	47	1	48
BA.2.10.3	1	0	1
BA.2.11	7	0	7
BA.2.12	42	0	42
BA.2.12.1	6,455	2	6,457
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	1,493	0	1,493
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	2,366	0	2,366
BA.2.3.10	80	0	80
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	140	16	156
BA.2.3.4	946	0	946

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 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	1,647	0	1,647
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	1	3

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 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	45	1	46
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	1,546	0	1,546
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	1	714
BA.4.1	1,379	0	1,379
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	161	0	161
BA.4.1.9	7	0	7
BA.4.2	188	0	188
BA.4.3	2	0	2
BA.4.4	83	0	83
BA.4.5	2	0	2
BA.4.6	2,450	19	2,469
BA.4.6.1	2	0	2
BA.4.6.2	60	5	65
BA.4.6.3	13	9	22

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
BA.4.6.4	20	0	20
BA.4.6.5	199	2	201
BA.4.7	55	0	55
BA.5	380	0	380
BA.5.1	6,096	40	6,136
BA.5.1.1	1,015	1	1,016
BA.5.1.10	252	0	252
BA.5.1.12	122	4	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	90	8	98
BA.5.1.19	11	0	11
BA.5.1.2	328	1	329
BA.5.1.20	33	2	35
BA.5.1.21	2	0	2
BA.5.1.22	267	0	267
BA.5.1.23	396	1	397
BA.5.1.24	121	0	121
BA.5.1.25	175	0	175
BA.5.1.27	58	13	71
BA.5.1.28	15	2	17
BA.5.1.3	68	0	68
BA.5.1.30	703	2	705
BA.5.1.4	11	0	11
BA.5.1.5	254	2	256
BA.5.1.6	57	0	57
BA.5.1.7	646	6	652
BA.5.1.9	1	0	1
BA.5.10	232	1	233
BA.5.10.1	9	0	9
BA.5.11	2	2	4
BA.5.2	7,623	37	7,660
BA.5.2.1	11,786	51	11,837
BA.5.2.12	2	0	2
BA.5.2.13	220	17	237
BA.5.2.14	154	3	157
BA.5.2.16	60	0	60
BA.5.2.18	48	0	48
BA.5.2.19	32	7	39

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
BA.5.2.2	129	0	129
BA.5.2.20	566	1	567
BA.5.2.21	343	1	344
BA.5.2.22	416	0	416
BA.5.2.23	75	4	79
BA.5.2.24	153	51	204
BA.5.2.25	121	5	126
BA.5.2.26	113	0	113
BA.5.2.27	160	0	160
BA.5.2.28	130	5	135
BA.5.2.3	194	0	194
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	191	45	236
BA.5.2.35	107	9	116
BA.5.2.36	8	0	8
BA.5.2.37	21	0	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	9	0	9
BA.5.2.48	20	1	21
BA.5.2.6	303	18	321
BA.5.2.7	11	0	11
BA.5.2.8	122	0	122
BA.5.2.9	882	21	903
BA.5.3	18	0	18
BA.5.3.1	152	3	155
BA.5.3.2	9	0	9
BA.5.3.3	40	0	40
BA.5.3.4	4	0	4
BA.5.3.5	1	2	3
BA.5.5	1,691	1	1,692
BA.5.5.1	59	1	60
BA.5.5.2	84	0	84
BA.5.5.3	22	0	22
BA.5.6	1,260	0	1,260
BA.5.6.1	14	0	14
BA.5.6.2	29	1	30

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
BA.5.8	197	0	197
BA.5.9	150	14	164
BB.1	1	0	1
BB.2	1	0	1
BC.2	1	0	1
BE.1	1,001	0	1,001
BE.1.1	683	11	694
BE.1.1.1	122	2	124
BE.1.1.2	62	1	63
BE.1.2	12	0	12
BE.1.2.1	563	44	607
BE.1.3	1	0	1
BE.1.4	222	1	223
BE.1.4.1	33	0	33
BE.1.4.2	5	4	9
BE.1.4.4	1	0	1
BE.10	16	4	20
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	4	1	5
BE.4.2	2	0	2
BE.5	171	0	171
BE.6	2	0	2
BE.7	2	0	2
BE.8	1	0	1
BE.9	22	15	37
BF.1	287	0	287
BF.1.1	9	0	9
BF.10	1,756	28	1,784
BF.11	607	37	644
BF.11.1	108	5	113
BF.11.2	1	0	1
BF.11.3	186	35	221
BF.11.4	10	0	10
BF.12	50	0	50
BF.13	233	5	238
BF.14	153	2	155
BF.15	10	0	10

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
BF.16	60	0	60
BF.18	2	0	2
BF.19	1	0	1
BF.2	96	0	96
BF.20	4	0	4
BF.21	151	1	152
BF.23	8	0	8
BF.25	61	0	61
BF.26	550	5	555
BF.27	331	0	331
BF.28	570	1	571
BF.29	2	0	2
BF.3	45	0	45
BF.3.1	3	0	3
BF.31	6	0	6
BF.31.1	92	0	92
BF.32	5	0	5
BF.34	37	3	40
BF.4	217	0	217
BF.5	887	3	890
BF.6	9	0	9
BF.7	1,991	226	2,217
BF.7.1	3	2	5
BF.7.10	1	0	1
BF.7.12	7	0	7
BF.7.14	13	2	15
BF.7.3	1	0	1
BF.7.4	125	16	141
BF.7.4.1	119	10	129
BF.7.4.2	10	0	10
BF.7.5	89	2	91
BF.7.6	135	0	135
BF.7.7	219	10	229
BF.7.8	13	6	19
BF.8	109	0	109
BF.9	836	0	836
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 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
BH.1	14	0	14
BK.1	228	1	229
BL.1	26	0	26
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	0	1	1
BM.1	3	0	3
BM.1.1	20	3	23
BM.1.1.1	13	9	22
BM.1.1.3	32	4	36
BM.1.1.4	1	0	1
BM.1.1.5	1	0	1
BM.2	3	1	4
BM.2.1	14	0	14
BM.4.1.1	2	0	2
BN.1	172	39	211
BN.1.1	0	2	2
BN.1.1.1	0	1	1
BN.1.2	78	15	93
BN.1.2.1	33	9	42
BN.1.3	139	42	181
BN.1.3.1	98	11	109
BN.1.3.3	0	1	1
BN.1.4	22	10	32
BN.1.5	30	15	45
BN.1.5.1	1	0	1
BN.1.7	1	2	3
BN.1.9	4	2	6
BN.2	2	0	2
BN.2.1	1	0	1
BN.3.1	22	13	35
BN.4	1	0	1
BN.5	7	0	7
BN.6	13	0	13
BQ.1	2,398	701	3,099
BQ.1.1	6,634	3,674	10,308
BQ.1.1.1	469	216	685

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
BQ.1.1.10	257	72	329
BQ.1.1.11	13	7	20
BQ.1.1.13	65	26	91
BQ.1.1.15	55	29	84
BQ.1.1.16	0	2	2
BQ.1.1.17	6	4	10
BQ.1.1.18	133	137	270
BQ.1.1.19	1	0	1
BQ.1.1.2	20	55	75
BQ.1.1.20	2	11	13
BQ.1.1.21	1	1	2
BQ.1.1.22	6	2	8
BQ.1.1.23	13	8	21
BQ.1.1.24	10	7	17
BQ.1.1.25	9	0	9
BQ.1.1.27	1	0	1
BQ.1.1.28	3	3	6
BQ.1.1.29	2	3	5
BQ.1.1.3	193	80	273
BQ.1.1.30	128	57	185
BQ.1.1.31	7	4	11
BQ.1.1.32	22	48	70
BQ.1.1.4	456	192	648
BQ.1.1.5	185	114	299
BQ.1.1.6	72	17	89
BQ.1.1.7	224	97	321
BQ.1.1.8	51	32	83
BQ.1.1.9	0	22	22
BQ.1.10	146	99	245
BQ.1.10.1	203	77	280
BQ.1.11	227	50	277
BQ.1.12	491	175	666
BQ.1.13	556	153	709
BQ.1.13.1	27	95	122
BQ.1.14	292	110	402
BQ.1.15	25	17	42
BQ.1.16	77	0	77
BQ.1.18	8	6	14
BQ.1.19	7	5	12
BQ.1.2	598	100	698

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
BQ.1.20	0	1	1
BQ.1.22	98	70	168
BQ.1.23	121	64	185
BQ.1.24	0	2	2
BQ.1.25	230	184	414
BQ.1.25.1	43	19	62
BQ.1.27	1	2	3
BQ.1.28	0	1	1
BQ.1.3	254	159	413
BQ.1.4	4	0	4
BQ.1.5	675	241	916
BQ.1.6	21	6	27
BQ.1.7	4	0	4
BQ.1.8	149	38	187
BQ.1.9	1	11	12
BR.1	4	0	4
BR.1.2	6	0	6
BR.2	7	0	7
BR.2.1	37	26	63
BR.3	7	0	7
BR.4	14	0	14
BS.1.1	1	3	4
BT.1	12	0	12
BT.2	2	0	2
BU.1	31	10	41
BU.2	9	0	9
BU.3	2	0	2
BV.2	3	0	3
BW.1	42	5	47
BW.1.1	67	74	141
BY.1	91	0	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	4	3	7
CA.5	22	3	25
CA.7	37	14	51
CB.1	4	0	4
CC.1	21	0	21

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
CD.2	1	0	1
CE.1	31	0	31
CG.1	31	0	31
CH.1.1	157	237	394
CH.1.1.1	4	29	33
CH.1.1.2	7	6	13
CJ.1	4	17	21
CJ.1.1	0	3	3
CK.1	109	78	187
CK.2	11	0	11
CK.2.1	5	0	5
CK.2.1.1	31	7	38
CK.3	30	3	33
CL.1	15	4	19
CM.1	50	5	55
CM.10	3	0	3
CM.12	1	1	2
CM.2	87	4	91
CM.4	2	0	2
CM.4.1	8	0	8
CM.6.1	1	0	1
CM.7	1	0	1
CM.8	2	0	2
CM.8.1	20	60	80
CM.9	11	0	11
CN.1	19	5	24
CN.2	120	4	124
CP.1	26	2	28
CP.5	1	0	1
CQ.1	2	0	2
CQ.1.1	7	0	7
CQ.2	10	2	12
CR.1	7	1	8
CR.1.1	2	5	7
CR.1.2	10	1	11
CR.1.3	1	0	1
CR.2	1	0	1
CT.1	1	0	1
CV.1	23	1	24
CV.2	1	0	1

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
DC.1	3	0	3
DE.1	79	0	79
DE.2	0	1	1
DF.1	2	0	2
DF.1.1	14	6	20
DG.1	2	1	3
DJ.1.1	11	8	19
DK.1	0	1	1
DL.1	8	0	8
DM.1	1	0	1
DQ.1	0	1	1
DR.1	0	2	2
Variant of Interest (VOI)			
Mu	**241**	**0**	**241**
Lambda	**8**	**0**	**8**
Recombinant	**1,146**	**2,654**	**3,800**
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	32	3	35
XBB.1	311	132	443
XBB.1.1	15	0	15
XBB.1.2	15	40	55
XBB.1.3	1	0	1
XBB.1.4	3	8	11
XBB.1.5	388	2,227	2,615
XBB.1.9	1	4	5
XBB.1.9.1	0	9	9
XBB.2	69	30	99
XBB.3	13	2	15
XBB.6.1	0	1	1
XBC.1	0	4	4
XBC.1.1	1	1	2

WHO label / Pango lineage	January 1, 2021 - January 7, 2023	January 8, 2023 – February 4, 2023	Total
XBD	2	0	2
XBE	9	0	9
XBF	30	46	76
XBH	1	0	1
XBJ	0	1	1
XBM	116	146	262
XE	3	0	3
XM	1	0	1
XN	1	0	1
XQ	4	0	4
XW	7	0	7
XZ	1	0	1
Non-VOC/VOI	**6,131**	**0**	**6,131**
Total sequenced	**211,766**	**11,698**	**223,464**

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 February 15, 2023 at approximately 2:00 a.m.
- Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on February 15, 2023 at approximately 9:30 a.m.

The Hospital for Sick Children (HSC)

- Data were received by PHO on February 14, 2023 at approximately 11:00 a.m.

Kingston Health Sciences Centre (KHSC)

- Data were received by PHO on February 14, 2023 at approximately 1:00 p.m.

Shared Hospital Laboratory (SHL)

- Data were received by PHO on February 14, 2023 at approximately 3:00 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were received by PHO on February 15, 2023 at approximately 11:00 a.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on February 14, 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 (2.8%), then public health unit was assigned using OCGN patient postal code or ordering provider postal code if patient postal code was missing.

- For representative surveillance, results may not be representative of Ontario overall. Samples selected include a proportion of eligible samples received by OCGN laboratories according to the whole genome sequencing strategy. Individual VOC PCR laboratories may have implemented the strategy and/or increased the proportion of samples selected on different dates. Cumulative data included do not reflect all whole genome sequencing conducted in Ontario.
    - Data from the OCGN laboratories cover different time periods: PHO since January 1, 2021, HSC since April 21, 2021, KHSC since January 1, 2021, SHL since March 26, 2021, and HRLMP since April 11, 2021.
    - Past testing algorithms have led to preferential sequencing of samples with N501Y and/or E484K mutations detected by VOC PCR. This has created a sampling bias reflected in the distribution of lineage results prior to May 2, 2021.

Methods: Nowcast Estimates, Projections and Weekly Relative Growth Rate

- Nowcast estimates and projections are generated using a multinomial logistic regression model. The Nowcast model uses twelve weeks of daily representative surveillance data up to the most recent date, with date as the univariate model predictor. Lineages that had at least one day with an estimated or projected prevalence of 5% or greater were included in the table and figure. Lineages with at least fourteen days of non-zero case counts were included in the model.
- Projected Nowcast estimates are future predictions of prevalence after the most recent date of observed data.
- Relative growth rate is a measure of a lineage's growth relative to a reference lineage.[6] Relative growth rates greater than 1 suggest an increased growth rate compared to the reference; relative growth rates less than 1 suggest a decreased growth rate compared to the reference.
- These relativized growth rates can be calculated by exponentiating the selection rate coefficient from the Nowcast model.
    - The selection rate coefficient is the difference in growth rate between two lineages ($\Delta r = r_{lineage} - r_{reference}$), and can be derived from a logistic regression model where the outcome is the relative frequency of a lineage and the predictor is time.[6,7]
- The weekly relative growth rate and projections may be overestimated for emerging lineages.

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

- CCM is a dynamic disease reporting system, which allows ongoing updates to data previously entered. As a result, data extracted from CCM represent a snapshot at the time of extraction and may differ from previous or subsequent reports.
- Methods for processing the CCM case data are described in the Technical Notes of the COVID-19 Data Tool.

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

- Dates associated with COVID-19 cases in Ontario were assigned using a hierarchy to best align with the sample date used for representative surveillance: sample collection date > test reported date > case reported date. As a result, the number of cases may differ from other reports which use different dates.

- Cases were linked to CCM if they had the same health card number or if they had the same first name, last name, and date of birth. Cases may not have linked to CCM due to discrepancies in patient identifiers or if they were not residents of Ontario (diagnosing health unit was reported as MOH).

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

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

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

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

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

- For surveillance purposes, a COVID-19 death is defined as a death resulting from a clinically compatible illness unless there is a clear alternative cause of death that cannot be related to COVID-19 (e.g., trauma, medically assisted death). There should be no period of complete recovery from COVID-19 between illness and reported death.

- Deaths are determined by using the outcome and Type of Death fields in CCM. COVID-19 deaths are counted where the Outcome value is 'Fatal' and the Type of Death value is not 'DOPHS was unrelated to cause of death' or 'Under PHU Review'.

Data Caveats and Methods: COVaxON

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

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

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

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

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

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

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

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