Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, July 29, 2022

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of July 27, 2022 and partner laboratories in the Ontario COVID-19 Genomics Network as of July 19 and July 26, 2022.

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). Current 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). 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 designations, such as the delineation of Omicron to include descendant BA lineages (e.g., BA.1, BA.2, BA.5). The designation of a descendant lineage does not 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

- There were 15,100 cases sequenced by the OCGN for representative surveillance from June 19 to July 16, 2022.
- The proportion of BA.5 cases (including all BA.5 sub-lineages) increased from 68.4% (July 3 to 9) to 78.2% (July 10 to 16) – see Table 5.
- In the most recent week (July 10 to 16), BA.5.2.1 was the most prevalent lineage (26.4%), followed by BA.5.1 (17.7%), and BA.5.2 (11.0%).
- The proportion of BA.5.2.1 cases increased from 20.9% (July 3 to 9) to 26.4% (July 10 to 16).
    - The weekly growth of BA.5.2.1 was 3.14 (95% CI: 3.03 - 3.25) times that of BA.2 over the past 12 weeks.
    - Based on Nowcast modelling, the proportion of BA.5.2.1 is projected to reach 37.3% (95% CI: 33.8% - 40.9%) by August 3, 2022.

As a result of updates to Pango lineage assignment models, this report includes additional sub-lineages of BA.2, BA.4, and BA.5. Some lengthy Omicron sub-lineage names have been abbreviated as lineages BC, BD, BE, BF, and BG (e.g., BC.1 is an alias for BA.1.1.529.1.1.1.1).

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.

The OCGN moved from sequencing 100% of eligible samples to 50% on July 8, 2022.

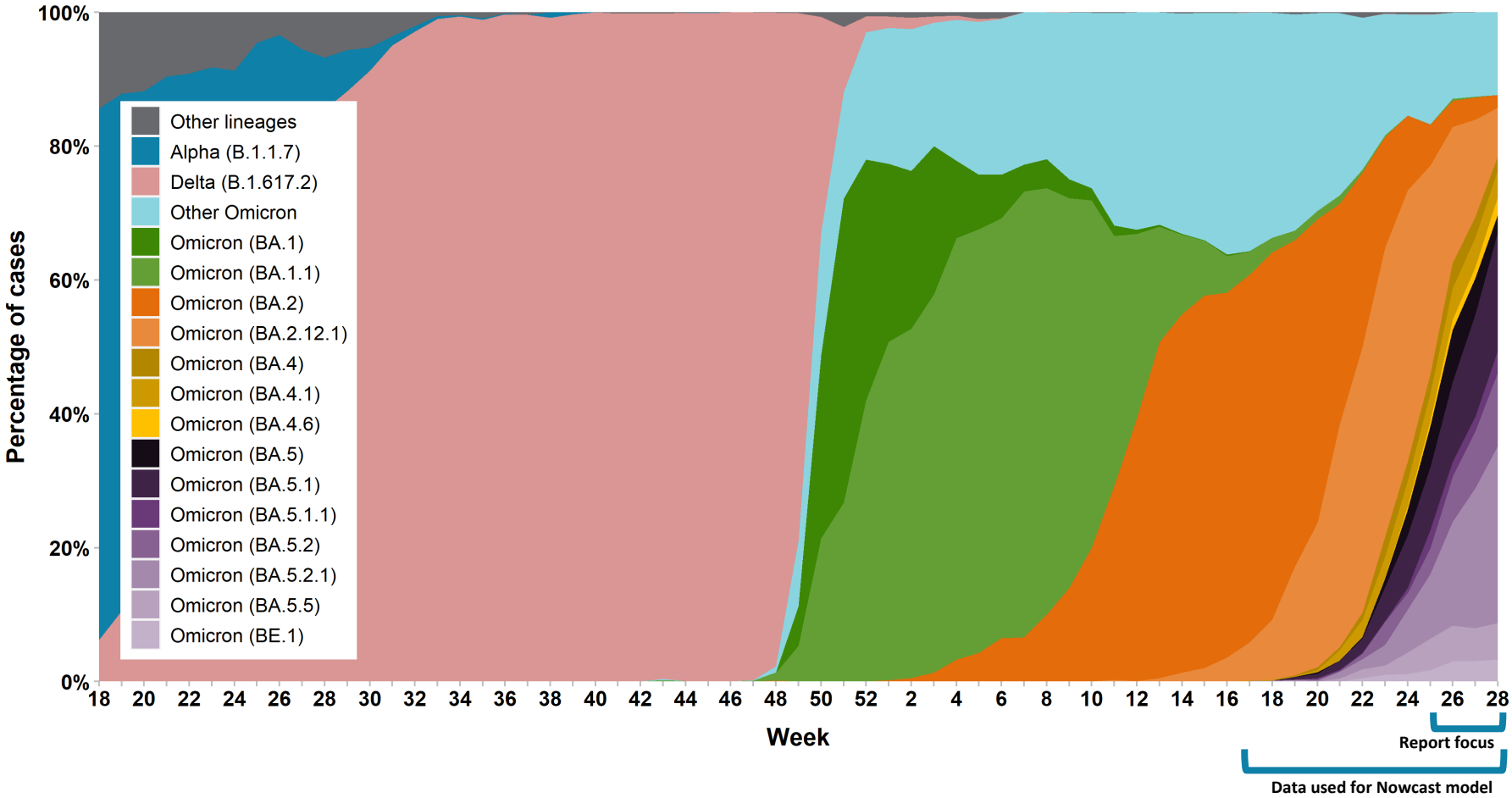
Representative Surveillance

Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, June 19 to July 16, 2022

Week	Number of cases	Number sequenced	Percentage sequenced
Week 25 (June 19 - June 25)	5,513	3,229	58.6%
Week 26 (June 26 - July 2)	6,801	4,063	59.7%
Week 27 (July 3 - July 9)	9,137	4,694	51.4%
Week 28 (July 10 - July 16)	11,192	3,114	27.8%
Total	**32,643**	**15,100**	**46.3%**

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 source: 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, May 2, 2021 to July 16, 2022



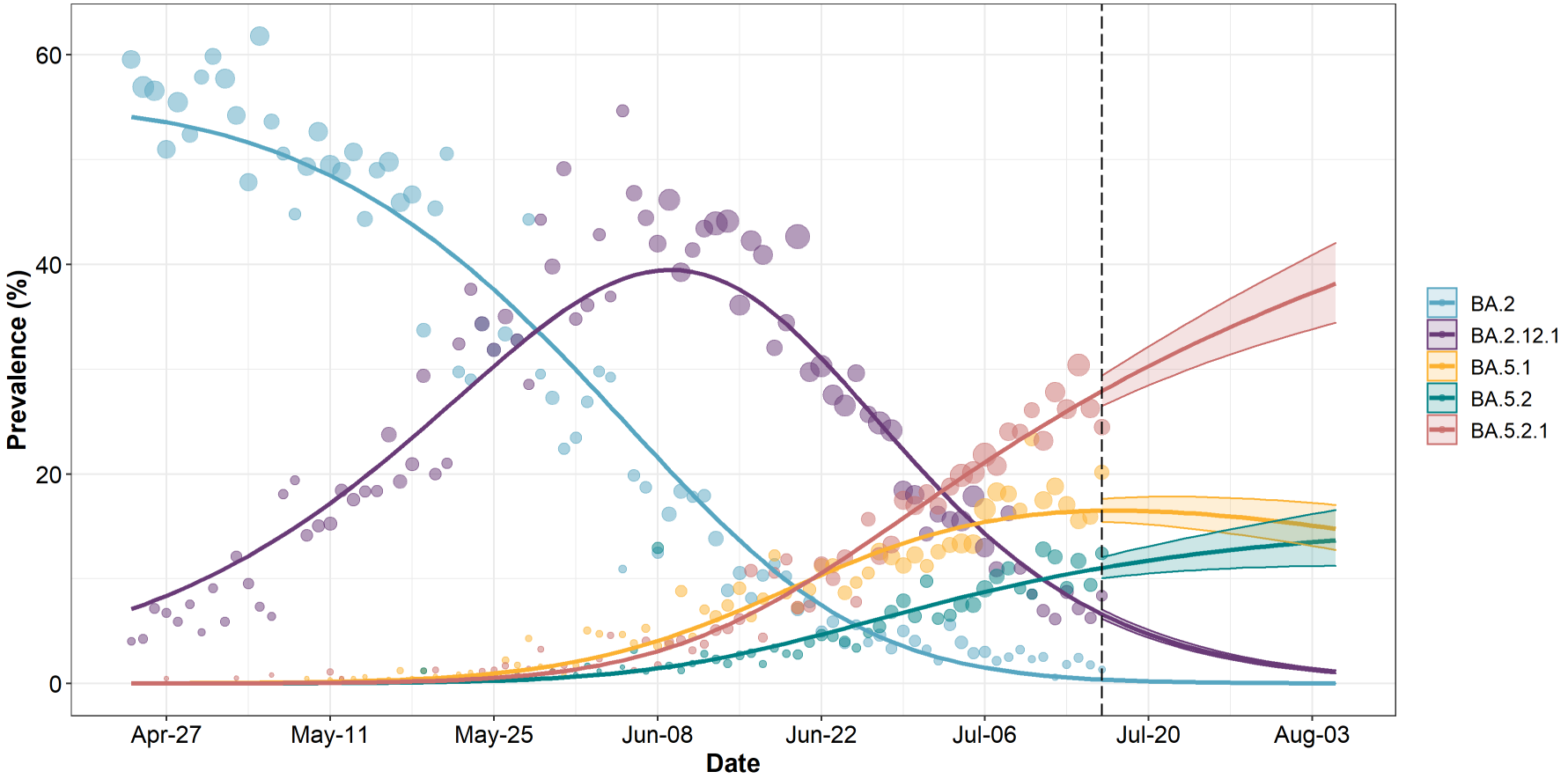
Note: Results may not be representative of Ontario overall, particularly in earlier weeks. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for a case, the most recent sample was included. Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction and will be included in subsequent reports.
Data source: 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, June 19 to July 16, 2022

WHO label/Pango lineage	Week 25 (June 19 to June 25)	Week 26 (June 26 to July 2)	Week 27 (July 3 to July 9)	Week 28 (July 10 to July 16)	Total (June 19 to July 16)
Omicron	**3,217 (99.6%)**	**4,061 (100%)**	**4,694 (100%)**	**3,114 (100%)**	**15,086 (99.9%)**
BA.2.12.1	1,006 (31.3%)	828 (20.4%)	684 (14.6%)	227 (7.3%)	2,745 (18.2%)
BA.5.2.1	312 (9.7%)	628 (15.5%)	980 (20.9%)	823 (26.4%)	2,743 (18.2%)
BA.5.1	302 (9.4%)	483 (11.9%)	715 (15.2%)	552 (17.7%)	2,052 (13.6%)
BA.5.2	123 (3.8%)	272 (6.7%)	397 (8.5%)	342 (11.0%)	1,134 (7.5%)
BA.5	199 (6.2%)	315 (7.8%)	257 (5.5%)	81 (2.6%)	852 (5.6%)
BA.5.5	151 (4.7%)	217 (5.3%)	229 (4.9%)	171 (5.5%)	768 (5.1%)
BA.4.1	132 (4.1%)	192 (4.7%)	207 (4.4%)	124 (4.0%)	655 (4.3%)
BA.2	196 (6.1%)	157 (3.9%)	156 (3.3%)	58 (1.9%)	567 (3.8%)
BA.4	94 (2.9%)	154 (3.8%)	145 (3.1%)	65 (2.1%)	458 (3.0%)
BE.1	56 (1.7%)	124 (3.1%)	146 (3.1%)	102 (3.3%)	428 (2.8%)
BA.5.1.1	90 (2.8%)	94 (2.3%)	103 (2.2%)	101 (3.2%)	388 (2.6%)
Other Omicron	556 (17.3%)	597 (14.7%)	675 (14.4%)	468 (15.0%)	2,296 (15.2%)
Other lineages	**12 (0.4%)**	**2 (<0.1%)**	**0 (0.0%)**	**0 (0.0%)**	**14 (0.1%)**
Total sequenced	**3,229 (100%)**	**4,063 (100%)**	**4,694 (100%)**	**3,114 (100%)**	**15,100 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data source: 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, April 24 to August 6, 2022



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. Includes all lineages with at least one day of an estimated prevalence of 10% or greater during the 15 week period (12 observed and 3 projected). Only lineages with at least seven days of non-zero case counts were included.
Data source: 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, April 24 to August 6, 2022

WHO label/Pango lineage	Week 27 (July 6): Estimated	Week 28 (July 13): Estimated	Week 29 (July 20): Projected	Week 30 (July 27): Projected	Week 31 (Aug 3): Projected	Weekly relative growth rate
BA.2	1.5 (1.4 - 1.7)	0.6 (0.5 - 0.7)	0.2 (0.2 - 0.3)	0.1 (0.1 - 0.1)	0.0 (0.0 - 0.0)	1.00 (reference)
BA.2.12.1	14.3 (13.7 - 14.9)	8.5 (8.0 - 9.0)	4.7 (4.4 - 5.1)	2.6 (2.3 - 2.8)	1.3 (1.2 - 1.5)	1.51 (1.48 - 1.53)
BA.5.2.1	21.1 (20.4 - 21.9)	26.0 (24.8 - 27.2)	30.3 (28.5 - 32.2)	34.0 (31.4 - 36.7)	37.3 (33.8 - 40.9)	3.14 (3.03 - 3.25)
BA.5.1	15.4 (14.8 - 16.1)	16.4 (15.5 - 17.3)	16.5 (15.2 - 17.8)	15.9 (14.3 - 17.7)	15.1 (13.1 - 17.2)	2.70 (2.61 - 2.80)
BA.5.2	8.8 (8.3 - 9.3)	10.4 (9.6 - 11.3)	11.7 (10.5 - 13.1)	12.8 (11.0 - 14.7)	13.5 (11.2 - 16.2)	3.03 (2.89 - 3.18)

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 prevalence estimates and projections presented are from the Wednesday (mid-point) of the specified week. Lineages that had at least one day with a prevalence of 10% or greater in the 15 week period (12 observed and 3 projected) were included. Lineages with at least seven days of non-zero case counts were included. Prevalence estimates are based on the model and are not expected to be the same as the observed data (e.g. Table 2). 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. 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 source: 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, June 19 to July 16, 2022

WHO label/Pango lineage	Ages: 0-4	Ages: 5-11	Ages: 12-19	Ages: 20-39	Ages: 40-59	Ages: 60-79	Ages: 80 and over	Total
Omicron	**381 (100%)**	**204 (100%)**	**421 (100%)**	**4,432 (100%)**	**4,217 (100%)**	**3,045 (99.9%)**	**2,377 (99.7%)**	**15,077 (99.9%)**
BA.2.12.1	64 (16.8%)	33 (16.2%)	88 (20.9%)	741 (16.7%)	776 (18.4%)	534 (17.5%)	508 (21.4%)	2,744 (18.2%)
BA.5.2.1	70 (18.4%)	32 (15.7%)	72 (17.1%)	786 (17.7%)	759 (18.0%)	558 (18.3%)	466 (19.6%)	2,743 (18.2%)
BA.5.1	44 (11.5%)	30 (14.7%)	58 (13.8%)	615 (13.9%)	548 (13.0%)	452 (14.8%)	304 (12.8%)	2,051 (13.6%)
BA.5.2	30 (7.9%)	17 (8.3%)	29 (6.9%)	371 (8.4%)	292 (6.9%)	242 (7.9%)	152 (6.4%)	1,133 (7.5%)
BA.5	50 (13.1%)	10 (4.9%)	18 (4.3%)	303 (6.8%)	262 (6.2%)	145 (4.8%)	64 (2.7%)	852 (5.7%)
BA.5.5	25 (6.6%)	9 (4.4%)	19 (4.5%)	211 (4.8%)	233 (5.5%)	162 (5.3%)	109 (4.6%)	768 (5.1%)
BA.4.1	13 (3.4%)	13 (6.4%)	27 (6.4%)	204 (4.6%)	189 (4.5%)	129 (4.2%)	80 (3.4%)	655 (4.3%)
BA.2	14 (3.7%)	5 (2.5%)	16 (3.8%)	152 (3.4%)	154 (3.7%)	98 (3.2%)	128 (5.4%)	567 (3.8%)
BA.4	10 (2.6%)	10 (4.9%)	17 (4.0%)	155 (3.5%)	115 (2.7%)	91 (3.0%)	60 (2.5%)	458 (3.0%)
BE.1	6 (1.6%)	4 (2.0%)	7 (1.7%)	109 (2.5%)	135 (3.2%)	80 (2.6%)	84 (3.5%)	425 (2.8%)
BA.5.1.1	4 (1.0%)	3 (1.5%)	8 (1.9%)	95 (2.1%)	91 (2.2%)	80 (2.6%)	107 (4.5%)	388 (2.6%)
Other Omicron	51 (13.4%)	38 (18.6%)	62 (14.7%)	690 (15.6%)	663 (15.7%)	474 (15.6%)	315 (13.3%)	2,293 (15.2%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**4 (0.1%)**	**8 (0.3%)**	**12 (0.1%)**
Total sequenced	**381 (100%)**	**204 (100%)**	**421 (100%)**	**4,432 (100%)**	**4,217 (100%)**	**3,049 (100%)**	**2,385 (100%)**	**15,089 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Age was assigned based on the birth date provided in OCGN, and if missing, based on the birth date from CCM; excludes cases with missing birth dates.

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

Table 5. Percentage of BA.5 cases (including all BA.5 sub-lineages), number identified, and total sequenced by public health unit (PHU), region, and week, representative surveillance, Ontario, June 19 to July 16, 2022

Public Health Unit	Week 25 (June 19 to June 25)	Week 26 (June 26 to July 2)	Week 27 (July 3 to July 9)	Week 28 (July 10 to July 16)	Total (June 19 to July 16)
Northwestern Health Unit	30.0% (3/10)	63.6% (7/11)	83.3% (5/6)	66.7% (6/9)	58.3% (21/36)
Thunder Bay District Health Unit	16.7% (7/42)	34.8% (16/46)	61.4% (27/44)	72.0% (18/25)	43.3% (68/157)
TOTAL NORTH WEST	**19.2% (10/52)**	**40.4% (23/57)**	**64.0% (32/50)**	**70.6% (24/34)**	**46.1% (89/193)**
Algoma Public Health	47.6% (10/21)	73.3% (22/30)	78.9% (15/19)	81.8% (9/11)	69.1% (56/81)
North Bay Parry Sound District Health Unit	50.0% (8/16)	52.4% (11/21)	66.7% (12/18)	54.5% (6/11)	56.1% (37/66)
Porcupine Health Unit	0.0% (0/7)	96.4% (27/28)	96.6% (28/29)	80.0% (12/15)	84.8% (67/79)
Public Health Sudbury & Districts	67.9% (19/28)	66.7% (30/45)	74.5% (35/47)	91.7% (33/36)	75% (117/156)
Timiskaming Health Unit	0.0% (0/0)	0.0% (0/0)	50.0% (1/2)	100% (1/1)	66.7% (2/3)
TOTAL NORTH EAST	**51.4% (37/72)**	**72.6% (90/124)**	**79.1% (91/115)**	**82.4% (61/74)**	**72.5% (279/385)**
Ottawa Public Health	40.0% (108/270)	54.8% (167/305)	69.3% (230/332)	79.5% (287/361)	62.5% (792/1,268)
Eastern Ontario Health Unit	58.1% (18/31)	45.0% (18/40)	48.7% (37/76)	75.8% (50/66)	57.7% (123/213)
Hastings Prince Edward Public Health	22.2% (4/18)	61.9% (13/21)	81.0% (34/42)	78.0% (39/50)	68.7% (90/131)
Kingston, Frontenac and Lennox & Addington Public Health	43.8% (28/64)	62.5% (45/72)	75.0% (99/132)	62.2% (51/82)	63.7% (223/350)
Leeds, Grenville & Lanark District Health Unit	44.7% (17/38)	40.5% (15/37)	63.3% (31/49)	64.2% (34/53)	54.8% (97/177)
Renfrew County and District Health Unit	75.0% (3/4)	80.0% (12/15)	85.7% (12/14)	81.8% (18/22)	81.8% (45/55)
TOTAL EASTERN	**41.9% (178/425)**	**55.1% (270/490)**	**68.7% (443/645)**	**75.6% (479/634)**	**62.4% (1,370/2,194)**
Durham Region Health Department	42.1% (59/140)	68.7% (123/179)	80.1% (153/191)	74.4% (87/117)	67.3% (422/627)
Haliburton, Kawartha, Pine Ridge District Health Unit	32.4% (11/34)	63.2% (24/38)	62.1% (18/29)	63.0% (17/27)	54.7% (70/128)
Peel Public Health	44.0% (117/266)	66.7% (222/333)	64.5% (276/428)	78.8% (246/312)	64.3% (861/1339)
Peterborough Public Health	61.3% (19/31)	66.7% (24/36)	59.0% (23/39)	93.8% (30/32)	69.6% (96/138)
Simcoe Muskoka District Health Unit	39.7% (52/131)	49.7% (79/159)	70.9% (122/172)	84.0% (79/94)	59.7% (332/556)
York Region Public Health	57.9% (175/302)	64.3% (272/423)	67.6% (303/448)	79.1% (238/301)	67.0% (988/1474)
TOTAL CENTRAL EAST	**47.9% (433/904)**	**63.7% (744/1,168)**	**68.5% (895/1,307)**	**78.9% (697/883)**	**65% (2,769/4,262)**

Public Health Unit	Week 25 (June 19 to June 25)	Week 26 (June 26 to July 2)	Week 27 (July 3 to July 9)	Week 28 (July 10 to July 16)	Total (June 19 to July 16)
Toronto Public Health	50.2% (413/822)	64.7% (706/1,091)	70.1% (914/1,304)	78.4% (728/928)	66.6% (2,761/4,145)
TOTAL TORONTO	**50.2% (413/822)**	**64.7% (706/1,091)**	**70.1% (914/1,304)**	**78.4% (728/928)**	**66.6% (2,761/4,145)**
Chatham-Kent Public Health	68.4% (26/38)	73.7% (14/19)	64.3% (9/14)	61.5% (8/13)	67.9% (57/84)
Grey Bruce Health Unit	28.6% (4/14)	28.6% (4/14)	72.2% (13/18)	64.3% (9/14)	50.0% (30/60)
Huron Perth Public Health	46.2% (6/13)	53.3% (8/15)	39.1% (9/23)	92.6% (25/27)	61.5% (48/78)
Lambton Public Health	21.1% (4/19)	61.5% (16/26)	80.0% (20/25)	84.2% (16/19)	62.9% (56/89)
Middlesex-London Health Unit	33.1% (42/127)	48.1% (51/106)	42.2% (54/128)	71.6% (53/74)	46.0% (200/435)
Southwestern Public Health	32.4% (11/34)	75.0% (27/36)	70.2% (40/57)	90.7% (39/43)	68.8% (117/170)
Windsor-Essex County Health Unit	46.1% (35/76)	41.3% (43/104)	57.9% (73/126)	78.9% (30/38)	52.6% (181/344)
TOTAL SOUTH WEST	**39.9% (128/321)**	**50.9% (163/320)**	**55.8% (218/391)**	**78.9% (180/228)**	**54.7% (689/1,260)**
Brant County Health Unit	51.5% (17/33)	42.6% (23/54)	72.4% (63/87)	78.6% (22/28)	61.9% (125/202)
City of Hamilton Public Health Services	42.9% (91/212)	49.7% (153/308)	65.5% (194/296)	70.1% (47/67)	54.9% (485/883)
Haldimand-Norfolk Health Unit	22.7% (5/22)	69.2% (18/26)	70.7% (29/41)	88.0% (22/25)	64.9% (74/114)
Halton Region Public Health	41.2% (49/119)	48.1% (50/104)	65.0% (76/117)	84.5% (49/58)	56.3% (224/398)
Niagara Region Public Health	37.8% (31/82)	66.7% (76/114)	68.8% (88/128)	74.5% (41/55)	62.3% (236/379)
Region of Waterloo Public Health and Emergency Services	51.7% (61/118)	68.1% (96/141)	78.2% (122/156)	85.5% (47/55)	69.4% (326/470)
Wellington-Dufferin-Guelph Public Health	54.5% (24/44)	63.9% (39/61)	78.2% (43/55)	78.9% (30/38)	68.7% (136/198)
TOTAL CENTRAL WEST	**44.1% (278/630)**	**56.3% (455/808)**	**69.9% (615/880)**	**79.1% (258/326)**	**60.7% (1,606/2,644)**
UNKNOWN	33.3% (1/3)	60.0% (3/5)	100% (2/2)	100% (7/7)	76.5% (13/17)
TOTAL ONTARIO	**45.8% (1,478/3,229)**	**60.4% (2,454/4,063)**	**68.4% (3,210/4,694)**	**78.2% (2,434/3,114)**	**63.4% (9,576/15,100)**

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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 6. Number and percentage (row %) of cases by vaccine category and Pango lineage, representative surveillance, Ontario, June 19 to July 16, 2022

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two booster doses	Total cases
Omicron	**2,338 (16.1%)**	**116 (0.8%)**	**1,859 (12.8%)**	**7,649 (52.6%)**	**2,582 (17.8%)**	**14,544 (100%)**
BA.2.12.1	371 (13.9%)	21 (0.8%)	360 (13.5%)	1,424 (53.5%)	484 (18.2%)	2,660 (100%)
BA.5.2.1	428 (16.2%)	25 (0.9%)	306 (11.6%)	1,343 (50.9%)	536 (20.3%)	2,638 (100%)
BA.5.1	320 (16.3%)	15 (0.8%)	257 (13.1%)	1,035 (52.6%)	339 (17.2%)	1,966 (100%)
BA.5.2	202 (18.5%)	10 (0.9%)	150 (13.7%)	549 (50.2%)	183 (16.7%)	1,094 (100%)
BA.5	156 (19.2%)	5 (0.6%)	124 (15.2%)	437 (53.7%)	92 (11.3%)	814 (100%)
BA.5.5	109 (14.7%)	8 (1.1%)	86 (11.6%)	389 (52.6%)	147 (19.9%)	739 (100%)
BA.4.1	107 (16.7%)	2 (0.3%)	86 (13.5%)	348 (54.5%)	96 (15.0%)	639 (100%)
BA.2	73 (13.2%)	3 (0.5%)	63 (11.4%)	309 (55.7%)	107 (19.3%)	555 (100%)
BA.4	67 (15.1%)	5 (1.1%)	51 (11.5%)	246 (55.4%)	75 (16.9%)	444 (100%)
BE.1	85 (20.6%)	4 (1.0%)	50 (12.1%)	210 (51.0%)	63 (15.3%)	412 (100%)
BA.5.1.1	51 (13.6%)	2 (0.5%)	47 (12.5%)	174 (46.4%)	101 (26.9%)	375 (100%)
Other Omicron	369 (16.7%)	16 (0.7%)	279 (12.6%)	1,185 (53.7%)	359 (16.3%)	2,208 (100%)
Other lineages	**1 (8.3%)**	**0 (0.0%)**	**2 (16.7%)**	**5 (41.7%)**	**4 (33.3%)**	**12 (100%)**
Total sequenced	**2,339 (16.1%)**	**116 (0.8%)**	**1,861 (12.8%)**	**7,654 (52.6%)**	**2,586 (17.8%)**	**14,556 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Cases include those that linked to CCM (96.5%). Individuals with a vaccine not approved by Health Canada were excluded. Vaccine category definitions can be found in the Confirmed Cases of COVID-19 Following Vaccination in Ontario report. A higher proportion of cases reported among more vaccinated cases is a reflection of both trends in vaccine administration (increasing number of doses administered over time) and trends in COVID-19 incidence. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction.

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

Table 7a. Percentage of cases ever admitted to hospital by vaccination status and Pango lineage, representative surveillance, Ontario, June 19 to July 16, 2022

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two booster doses
Omicron	**6.0% (141/2,338)**	**7.8% (9/116)**	**4.5% (84/1,859)**	**3.5% (267/7,649)**	**6.5% (169/2,582)**
BA.2.12.1	7.8% (29/371)	0.0% (0/21)	7.2% (26/360)	3.7% (52/1,424)	7.2% (35/484)
BA.5.2.1	6.1% (26/428)	12.0% (3/25)	2.6% (8/306)	3.0% (40/1,343)	4.7% (25/536)
BA.5.1	2.5% (8/320)	6.7% (1/15)	3.9% (10/257)	3.8% (39/1,035)	9.4% (32/339)
BA.5.2	7.4% (15/202)	20.0% (2/10)	2.7% (4/150)	3.1% (17/549)	8.2% (15/183)
BA.5	9.6% (15/156)	40.0% (2/5)	6.5% (8/124)	3.4% (15/437)	6.5% (6/92)
BA.5.5	5.5% (6/109)	0.0% (0/8)	1.2% (1/86)	2.8% (11/389)	3.4% (5/147)
BA.4.1	0.0% (0/107)	0.0% (0/2)	5.8% (5/86)	2.9% (10/348)	4.2% (4/96)
BA.2	6.8% (5/73)	0.0% (0/3)	6.3% (4/63)	5.5% (17/309)	5.6% (6/107)
BA.4	3.0% (2/67)	0.0% (0/5)	2.0% (1/51)	1.6% (4/246)	4.0% (3/75)
BE.1	7.1% (6/85)	25.0% (1/4)	2.0% (1/50)	3.8% (8/210)	4.8% (3/63)
BA.5.1.1	3.9% (2/51)	0.0% (0/2)	2.1% (1/47)	5.2% (9/174)	4.0% (4/101)
Other Omicron	7.3% (27/369)	0.0% (0/16)	5.4% (15/279)	3.8% (45/1,185)	8.6% (31/359)
Other lineages	**100% (1/1)**	**0.0% (0/0)**	**50.0% (1/2)**	**40.0% (2/5)**	**0.0% (0/4)**
Total sequenced	**6.1% (142/2,339)**	**7.8% (9/116)**	**4.6% (85/1,861)**	**3.5% (269/7,654)**	**6.5% (169/2,586)**

Note: Includes the most prevalent lineages detected in the past month. Percentage is the number of cases ever admitted to hospital (at the time of data extraction) divided by the total number of cases in that lineage and vaccine category. Cases include only those that linked to CCM (96.5%). Individuals with a vaccine not approved by Health Canada were excluded. Vaccine category definitions can be found in the Confirmed Cases of COVID-19 Following Vaccination in Ontario report. Factors, such as age, that may affect the risk of COVID-19 hospital admission 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. 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 indicator), COVaxON

Table 7b. Percentage of deceased cases by vaccination status and Pango lineage, representative surveillance, Ontario, June 19 to July 16, 2022

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two booster doses
Omicron	**0.3% (7/2,338)**	**0.0% (0/116)**	**0.3% (6/1,859)**	**0.2% (14/7,649)**	**0.8% (20/2,582)**
BA.2.12.1	0.8% (3/371)	0.0% (0/21)	1.1% (4/360)	0.3% (4/1,424)	1.0% (5/484)
BA.5.2.1	0.0% (0/428)	0.0% (0/25)	0.0% (0/306)	0.1% (2/1,343)	0.9% (5/536)
BA.5.1	0.0% (0/320)	0.0% (0/15)	0.0% (0/257)	0.1% (1/1,035)	1.2% (4/339)
BA.5.2	0.5% (1/202)	0.0% (0/10)	0.0% (0/150)	0.0% (0/549)	0.5% (1/183)
BA.5	0.0% (0/156)	0.0% (0/5)	0.8% (1/124)	0.2% (1/437)	0.0% (0/92)
BA.5.5	0.0% (0/109)	0.0% (0/8)	0.0% (0/86)	0.0% (0/389)	0.7% (1/147)
BA.4.1	0.0% (0/107)	0.0% (0/2)	0.0% (0/86)	0.3% (1/348)	1.0% (1/96)
BA.2	1.4% (1/73)	0.0% (0/3)	1.6% (1/63)	0.3% (1/309)	0.0% (0/107)
BA.4	0.0% (0/67)	0.0% (0/5)	0.0% (0/51)	0.0% (0/246)	0.0% (0/75)
BE.1	0.0% (0/85)	0.0% (0/4)	0.0% (0/50)	0.0% (0/210)	0.0% (0/63)
BA.5.1.1	2.0% (1/51)	0.0% (0/2)	0.0% (0/47)	0.6% (1/174)	0.0% (0/101)
Other Omicron	0.3% (1/369)	0.0% (0/16)	0.0% (0/279)	0.3% (3/1,185)	0.8% (3/359)
Other lineages	**0.0% (0/1)**	**0.0% (0/0)**	**0.0% (0/2)**	**20.0% (1/5)**	**0.0% (0/4)**
Total sequenced	**0.3% (7/2,339)**	**0.0% (0/116)**	**0.3% (6/1,861)**	**0.2% (15/7,654)**	**0.8% (20/2,586)**

Note: Includes the most prevalent lineages detected in the past month. Percentage is the number of deceased cases divided by the total number of cases in that lineage and vaccine category. Cases include only those that linked to CCM (96.5%). Individuals with a vaccine not approved by Health Canada were excluded. Vaccine category definitions can be found in the Confirmed Cases of COVID-19 Following Vaccination in Ontario report. 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 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. 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 (deceased indicator), COVaxON

Table 8a. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North West Region, June 19 to July 16, 2022

WHO label / Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
Omicron	**36 (100%)**	**157 (100%)**	**193 (100%)**
BA.2.12.1	1 (2.8%)	47 (29.9%)	48 (24.9%)
BA.5.2.1	5 (13.9%)	23 (14.6%)	28 (14.5%)
BA.5.1	2 (5.6%)	14 (8.9%)	16 (8.3%)
BA.5.2	0 (0.0%)	9 (5.7%)	9 (4.7%)
BA.5	0 (0.0%)	1 (0.6%)	1 (0.5%)
BA.5.5	14 (38.9%)	1 (0.6%)	15 (7.8%)
BA.4.1	2 (5.6%)	3 (1.9%)	5 (2.6%)
BA.2	2 (5.6%)	6 (3.8%)	8 (4.1%)
BA.4	1 (2.8%)	3 (1.9%)	4 (2.1%)
BE.1	0 (0.0%)	3 (1.9%)	3 (1.6%)
BA.5.1.1	0 (0.0%)	7 (4.5%)	7 (3.6%)
Other Omicron	9 (25.0%)	40 (25.5%)	49 (25.4%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**36 (100%)**	**157 (100%)**	**193 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. 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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 8b. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North East Region, June 19 to July 16, 2022

WHO label / Pango lineage	Algoma Public Health	North Bay Parry Sound District Health Unit	Porcupine Health Unit	Public Health Sudbury & Districts	Timiskaming Health Unit	Total
Omicron	**81 (100%)**	**66 (100%)**	**79 (100%)**	**156 (100%)**	**3 (100%)**	**385 (100%)**
BA.2.12.1	12 (14.8%)	11 (16.7%)	6 (7.6%)	24 (15.4%)	0 (0.0%)	53 (13.8%)
BA.5.2.1	13 (16.0%)	14 (21.2%)	52 (65.8%)	53 (34.0%)	0 (0.0%)	132 (34.3%)
BA.5.1	21 (25.9%)	5 (7.6%)	6 (7.6%)	35 (22.4%)	0 (0.0%)	67 (17.4%)
BA.5.2	6 (7.4%)	6 (9.1%)	7 (8.9%)	15 (9.6%)	2 (66.7%)	36 (9.4%)
BA.5	3 (3.7%)	0 (0.0%)	0 (0.0%)	3 (1.9%)	0 (0.0%)	6 (1.6%)
BA.5.5	3 (3.7%)	1 (1.5%)	0 (0.0%)	3 (1.9%)	0 (0.0%)	7 (1.8%)
BA.4.1	3 (3.7%)	4 (6.1%)	1 (1.3%)	4 (2.6%)	1 (33.3%)	13 (3.4%)
BA.2	4 (4.9%)	8 (12.1%)	4 (5.1%)	0 (0.0%)	0 (0.0%)	16 (4.2%)
BA.4	2 (2.5%)	1 (1.5%)	0 (0.0%)	1 (0.6%)	0 (0.0%)	4 (1.0%)
BE.1	0 (0.0%)	5 (7.6%)	1 (1.3%)	1 (0.6%)	0 (0.0%)	7 (1.8%)
BA.5.1.1	3 (3.7%)	1 (1.5%)	1 (1.3%)	0 (0.0%)	0 (0.0%)	5 (1.3%)
Other Omicron	11 (13.6%)	10 (15.2%)	1 (1.3%)	17 (10.9%)	0 (0.0%)	39 (10.1%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**81 (100%)**	**66 (100%)**	**79 (100%)**	**156 (100%)**	**3 (100%)**	**385 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. 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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 8c. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Eastern Region, June 19 to July 16, 2022

WHO label / Pango lineage	Eastern Ontario Health Unit	Hastings Prince Edward Public Health	Kingston, Frontenac and Lennox & Addington Public Health	Leeds, Grenville & Lanark District Health Unit	Ottawa Public Health	Renfrew County and District Health Unit	Total
Omicron	**211 (99.1%)**	**131 (100%)**	**350 (100%)**	**177 (100%)**	**1,268 (100%)**	**55 (100%)**	**2,192 (99.9%)**
BA.2.12.1	23 (10.9%)	16 (12.2%)	62 (17.7%)	47 (26.6%)	212 (16.7%)	3 (5.5%)	363 (16.6%)
BA.5.2.1	35 (16.6%)	21 (16.0%)	70 (20.0%)	43 (24.3%)	296 (23.3%)	5 (9.1%)	470 (21.4%)
BA.5.1	48 (22.7%)	22 (16.8%)	52 (14.9%)	16 (9.0%)	183 (14.4%)	29 (52.7%)	350 (16.0%)
BA.5.2	10 (4.7%)	16 (12.2%)	22 (6.3%)	9 (5.1%)	111 (8.8%)	1 (1.8%)	169 (7.7%)
BA.5	2 (0.9%)	4 (3.1%)	4 (1.1%)	6 (3.4%)	12 (0.9%)	1 (1.8%)	29 (1.3%)
BA.5.5	3 (1.4%)	7 (5.3%)	22 (6.3%)	4 (2.3%)	28 (2.2%)	0 (0.0%)	64 (2.9%)
BA.4.1	16 (7.6%)	18 (13.7%)	13 (3.7%)	15 (8.5%)	76 (6.0%)	1 (1.8%)	139 (6.3%)
BA.2	7 (3.3%)	1 (0.8%)	9 (2.6%)	1 (0.6%)	53 (4.2%)	0 (0.0%)	71 (3.2%)
BA.4	26 (12.3%)	1 (0.8%)	15 (4.3%)	3 (1.7%)	11 (0.9%)	1 (1.8%)	57 (2.6%)
BE.1	10 (4.7%)	3 (2.3%)	8 (2.3%)	1 (0.6%)	19 (1.5%)	3 (5.5%)	44 (2.0%)
BA.5.1.1	4 (1.9%)	4 (3.1%)	9 (2.6%)	8 (4.5%)	34 (2.7%)	6 (10.9%)	65 (3.0%)
Other Omicron	27 (12.8%)	18 (13.7%)	64 (18.3%)	24 (13.6%)	233 (18.4%)	5 (9.1%)	371 (16.9%)
Other lineages	**2 (0.9%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**2 (0.1%)**
Total sequenced	**213 (100%)**	**131 (100%)**	**350 (100%)**	**177 (100%)**	**1,268 (100%)**	**55 (100%)**	**2,194 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. 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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 8d. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central East Region, June 19 to July 16, 2022

WHO label / Pango lineage	Durham Region Health Department	Haliburton, Kawartha, Pine Ridge District Health Unit	Peel Public Health	Peterborough Public Health	Simcoe Muskoka District Health Unit	York Region Public Health	Total
Omicron	**627 (100%)**	**128 (100%)**	**1,338 (99.9%)**	**138 (100%)**	**556 (100%)**	**1,474 (100%)**	**4,261 (100%)**
BA.2.12.1	83 (13.2%)	22 (17.2%)	222 (16.6%)	22 (15.9%)	119 (21.4%)	295 (20.0%)	763 (17.9%)
BA.5.2.1	124 (19.8%)	25 (19.5%)	252 (18.8%)	40 (29.0%)	95 (17.1%)	255 (17.3%)	791 (18.6%)
BA.5.1	87 (13.9%)	28 (21.9%)	226 (16.9%)	31 (22.5%)	58 (10.4%)	184 (12.5%)	614 (14.4%)
BA.5.2	51 (8.1%)	6 (4.7%)	118 (8.8%)	6 (4.3%)	37 (6.7%)	106 (7.2%)	324 (7.6%)
BA.5	23 (3.7%)	1 (0.8%)	23 (1.7%)	4 (2.9%)	16 (2.9%)	75 (5.1%)	142 (3.3%)
BA.5.5	24 (3.8%)	3 (2.3%)	67 (5.0%)	2 (1.4%)	48 (8.6%)	75 (5.1%)	219 (5.1%)
BA.4.1	26 (4.1%)	13 (10.2%)	60 (4.5%)	3 (2.2%)	39 (7.0%)	51 (3.5%)	192 (4.5%)
BA.2	27 (4.3%)	7 (5.5%)	60 (4.5%)	7 (5.1%)	24 (4.3%)	28 (1.9%)	153 (3.6%)
BA.4	27 (4.3%)	5 (3.9%)	28 (2.1%)	0 (0.0%)	12 (2.2%)	25 (1.7%)	97 (2.3%)
BE.1	14 (2.2%)	2 (1.6%)	34 (2.5%)	2 (1.4%)	22 (4.0%)	36 (2.4%)	110 (2.6%)
BA.5.1.1	11 (1.8%)	0 (0.0%)	37 (2.8%)	0 (0.0%)	7 (1.3%)	86 (5.8%)	141 (3.3%)
Other Omicron	130 (20.7%)	16 (12.5%)	211 (15.8%)	21 (15.2%)	79 (14.2%)	258 (17.5%)	715 (16.8%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**1 (0.1%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**1 (<0.1%)**
Total sequenced	**627 (100%)**	**128 (100%)**	**1,339 (100%)**	**138 (100%)**	**556 (100%)**	**1,474 (100%)**	**4,262 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. 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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 8e. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Toronto Region, June 19 to July 16, 2022

WHO label / Pango lineage	Toronto Public Health	Total
Omicron	**4,134 (99.7%)**	**4,134 (99.7%)**
BA.2.12.1	678 (16.4%)	678 (16.4%)
BA.5.2.1	782 (18.9%)	782 (18.9%)
BA.5.1	570 (13.8%)	570 (13.8%)
BA.5.2	378 (9.1%)	378 (9.1%)
BA.5	121 (2.9%)	121 (2.9%)
BA.5.5	250 (6.0%)	250 (6.0%)
BA.4.1	165 (4.0%)	165 (4.0%)
BA.2	126 (3.0%)	126 (3.0%)
BA.4	119 (2.9%)	119 (2.9%)
BE.1	172 (4.1%)	172 (4.1%)
BA.5.1.1	144 (3.5%)	144 (3.5%)
Other Omicron	629 (15.2%)	629 (15.2%)
Other lineages	**11 (0.3%)**	**11 (0.3%)**
Total sequenced	**4,145 (100%)**	**4,145 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. 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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 8f. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, South West Region, June 19 to July 16, 2022

WHO label / Pango lineage	Chatham-Kent Public Health	Grey Bruce Health Unit	Huron Perth Public Health	Lambton Public Health	Middlesex-London Health Unit	Southwestern Public Health	Windsor-Essex County Health Unit	Total
Omicron	**84 (100%)**	**60 (100%)**	**78 (100%)**	**89 (100%)**	**435 (100%)**	**170 (100%)**	**344 (100%)**	**1,260 (100%)**
BA.2.12.1	14 (16.7%)	18 (30.0%)	18 (23.1%)	23 (25.8%)	138 (31.7%)	29 (17.1%)	66 (19.2%)	306 (24.3%)
BA.5.2.1	12 (14.3%)	6 (10.0%)	8 (10.3%)	21 (23.6%)	47 (10.8%)	35 (20.6%)	35 (10.2%)	164 (13.0%)
BA.5.1	6 (7.1%)	9 (15.0%)	8 (10.3%)	7 (7.9%)	34 (7.8%)	44 (25.9%)	48 (14.0%)	156 (12.4%)
BA.5.2	6 (7.1%)	3 (5.0%)	4 (5.1%)	10 (11.2%)	22 (5.1%)	7 (4.1%)	21 (6.1%)	73 (5.8%)
BA.5	1 (1.2%)	0 (0.0%)	3 (3.8%)	1 (1.1%)	5 (1.1%)	2 (1.2%)	4 (1.2%)	16 (1.3%)
BA.5.5	31 (36.9%)	5 (8.3%)	19 (24.4%)	4 (4.5%)	22 (5.1%)	6 (3.5%)	55 (16.0%)	142 (11.3%)
BA.4.1	0 (0.0%)	0 (0.0%)	4 (5.1%)	3 (3.4%)	19 (4.4%)	7 (4.1%)	24 (7.0%)	57 (4.5%)
BA.2	3 (3.6%)	2 (3.3%)	3 (3.8%)	4 (4.5%)	44 (10.1%)	7 (4.1%)	18 (5.2%)	81 (6.4%)
BA.4	6 (7.1%)	2 (3.3%)	0 (0.0%)	1 (1.1%)	5 (1.1%)	2 (1.2%)	6 (1.7%)	22 (1.7%)
BE.1	0 (0.0%)	1 (1.7%)	0 (0.0%)	0 (0.0%)	6 (1.4%)	4 (2.4%)	4 (1.2%)	15 (1.2%)
BA.5.1.1	0 (0.0%)	1 (1.7%)	1 (1.3%)	2 (2.2%)	3 (0.7%)	7 (4.1%)	0 (0.0%)	14 (1.1%)
Other Omicron	5 (6.0%)	13 (21.7%)	10 (12.8%)	13 (14.6%)	90 (20.7%)	20 (11.8%)	63 (18.3%)	214 (17.0%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**84 (100%)**	**60 (100%)**	**78 (100%)**	**89 (100%)**	**435 (100%)**	**170 (100%)**	**344 (100%)**	**1,260 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. 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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 8g. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central West Region, June 19 to July 16, 2022

WHO label / Pango lineage	Brant County Health Unit	City of Hamilton Public Health Services	Haldimand-Norfolk Health Unit	Halton Region Public Health	Niagara Region Public Health	Region of Waterloo Public Health and Emergency Services	Wellington-Dufferin-Guelph Public Health	Total
Omicron	**202 (100%)**	**883 (100%)**	**114 (100%)**	**398 (100%)**	**379 (100%)**	**470 (100%)**	**198 (100%)**	**2,644 (100%)**
BA.2.12.1	27 (13.4%)	202 (22.9%)	25 (21.9%)	104 (26.1%)	72 (19.0%)	77 (16.4%)	25 (12.6%)	532 (20.1%)
BA.5.2.1	18 (8.9%)	63 (7.1%)	26 (22.8%)	47 (11.8%)	72 (19.0%)	95 (20.2%)	53 (26.8%)	374 (14.1%)
BA.5.1	23 (11.4%)	35 (4.0%)	19 (16.7%)	61 (15.3%)	49 (12.9%)	51 (10.9%)	38 (19.2%)	276 (10.4%)
BA.5.2	32 (15.8%)	22 (2.5%)	4 (3.5%)	19 (4.8%)	30 (7.9%)	31 (6.6%)	6 (3.0%)	144 (5.4%)
BA.5	7 (3.5%)	300 (34.0%)	12 (10.5%)	54 (13.6%)	34 (9.0%)	117 (24.9%)	9 (4.5%)	533 (20.2%)
BA.5.5	5 (2.5%)	16 (1.8%)	3 (2.6%)	10 (2.5%)	16 (4.2%)	9 (1.9%)	10 (5.1%)	69 (2.6%)
BA.4.1	7 (3.5%)	23 (2.6%)	1 (0.9%)	9 (2.3%)	27 (7.1%)	13 (2.8%)	4 (2.0%)	84 (3.2%)
BA.2	2 (1.0%)	53 (6.0%)	6 (5.3%)	15 (3.8%)	12 (3.2%)	17 (3.6%)	7 (3.5%)	112 (4.2%)
BA.4	27 (13.4%)	77 (8.7%)	0 (0.0%)	17 (4.3%)	9 (2.4%)	17 (3.6%)	8 (4.0%)	155 (5.9%)
BE.1	8 (4.0%)	31 (3.5%)	5 (4.4%)	9 (2.3%)	9 (2.4%)	8 (1.7%)	7 (3.5%)	77 (2.9%)
BA.5.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (1.0%)	1 (0.3%)	5 (1.1%)	2 (1.0%)	12 (0.5%)
Other Omicron	46 (22.8%)	61 (6.9%)	13 (11.4%)	49 (12.3%)	48 (12.7%)	30 (6.4%)	29 (14.6%)	276 (10.4%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**202 (100%)**	**883 (100%)**	**114 (100%)**	**398 (100%)**	**379 (100%)**	**470 (100%)**	**198 (100%)**	**2,644 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. 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 (3.5%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data source: PHO, Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 9. Number and percentage (row %) of outbreak-associated and non outbreak-associated cases by Pango lineage, representative surveillance, Ontario, June 19 to July 16, 2022

WHO label / Pango lineage	Outbreak-associated	Non outbreak-associated	Total cases
Omicron	**2,609 (17.9%)**	**11,947 (82.1%)**	**14,556 (100%)**
BA.2.12.1	571 (21.4%)	2,093 (78.6%)	2,664 (100%)
BA.5.2.1	475 (18.0%)	2,164 (82.0%)	2,639 (100%)
BA.5.1	299 (15.2%)	1,670 (84.8%)	1,969 (100%)
BA.5.2	169 (15.4%)	927 (84.6%)	1,096 (100%)
BA.5	42 (5.2%)	772 (94.8%)	814 (100%)
BA.5.5	142 (19.2%)	597 (80.8%)	739 (100%)
BA.4.1	75 (11.7%)	564 (88.3%)	639 (100%)
BA.2	126 (22.7%)	429 (77.3%)	555 (100%)
BA.4	83 (18.7%)	361 (81.3%)	444 (100%)
BE.1	96 (23.2%)	317 (76.8%)	413 (100%)
BA.5.1.1	122 (32.4%)	254 (67.6%)	376 (100%)
Other Omicron	409 (18.5%)	1,799 (81.5%)	2,208 (100%)
Other lineages	**8 (66.7%)**	**4 (33.3%)**	**12 (100%)**
Total sequenced	**2,617 (18.0%)**	**11,951 (82.0%)**	**14,568 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Cases include only those that linked to CCM (96.5%). '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)

Cumulative Whole Genome Sequencing Results

Table 10. Number of cases by Pango lineage, cumulative counts, Ontario, January 1, 2021 to July 16, 2022

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
Variant of Concern (VOC)			
Alpha	**11,817**	**0**	**11,817**
B.1.1.7	11,747	0	11,747
Q.4	70	0	70
Beta	**1,232**	**0**	**1,232**
B.1.351	1,213	0	1,213
B.1.351.2	3	0	3
B.1.351.3	16	0	16
Gamma	**3,925**	**0**	**3,925**
P.1	223	0	223
P.1.10	2	0	2
P.1.12	1	0	1
P.1.12.1	1	0	1
P.1.14	3,661	0	3,661
P.1.17	33	0	33
P.1.7	4	0	4
Delta	**46,054**	**2**	**46,056**
B.1.617.2	2,180	0	2,180
AY.1	3	0	3
AY.10	19	0	19
AY.100	656	0	656
AY.101	1	0	1
AY.102	58	0	58
AY.103	5,122	0	5,122
AY.103.2	5	0	5
AY.104	8	0	8
AY.105	21	0	21
AY.106	36	0	36
AY.107	67	0	67
AY.108	57	0	57
AY.109	23	0	23
AY.110	23	0	23
AY.111	6	0	6
AY.112	31	0	31
AY.112.2	2	0	2

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
AY.113	32	0	32
AY.114	2	0	2
AY.116	70	0	70
AY.116.1	10	0	10
AY.117	119	0	119
AY.118	37	0	37
AY.119	306	0	306
AY.119.1	3	0	3
AY.119.2	224	0	224
AY.120	53	0	53
AY.120.1	5	0	5
AY.121	102	0	102
AY.121.1	4	0	4
AY.122	1,337	0	1,337
AY.122.1	8	0	8
AY.122.4	5	0	5
AY.122.6	1	0	1
AY.123	1	0	1
AY.124.1	3	0	3
AY.124.1.1	3	0	3
AY.125	18	0	18
AY.126	127	0	127
AY.127	397	0	397
AY.127.1	20	0	20
AY.128	5	0	5
AY.129	12	0	12
AY.13	43	0	43
AY.131	10	0	10
AY.133	6	0	6
AY.14	24	0	24
AY.15	156	0	156
AY.16	23	0	23
AY.18	109	0	109
AY.19	1	0	1
AY.2	2	0	2
AY.20	180	0	180
AY.23	14	0	14
AY.24	11	0	11
AY.25	1,458	0	1,458
AY.25.1	4,295	0	4,295

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
AY.25.1.2	12	0	12
AY.25.3	5,309	1	5,310
AY.26	89	0	89
AY.27	3,330	0	3,330
AY.28	37	0	37
AY.29	6	0	6
AY.3	1,074	0	1,074
AY.3.1	11	0	11
AY.3.3	4	0	4
AY.33	82	0	82
AY.34	31	0	31
AY.34.1	30	0	30
AY.35	4	0	4
AY.36	384	0	384
AY.37	30	0	30
AY.38	14	0	14
AY.39	315	0	315
AY.39.1	29	0	29
AY.4	660	0	660
AY.4.12	2	0	2
AY.4.2	48	0	48
AY.4.2.1	209	0	209
AY.4.2.2	15	0	15
AY.4.2.3	4	0	4
AY.4.3	2	0	2
AY.4.4	7	0	7
AY.4.5	7	0	7
AY.4.6	3	0	3
AY.4.7	1	0	1
AY.4.9	2	0	2
AY.40	2	0	2
AY.41	3	0	3
AY.42	21	0	21
AY.43	589	0	589
AY.43.3	1	0	1
AY.43.4	1	0	1
AY.43.8	5	0	5
AY.44	1,163	1	1,164
AY.45	5	0	5
AY.46	56	0	56

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
AY.46.1	9	0	9
AY.46.4	6	0	6
AY.46.5	5	0	5
AY.46.6	27	0	27
AY.47	117	0	117
AY.48	24	0	24
AY.49	1	0	1
AY.5	31	0	31
AY.5.2	1	0	1
AY.5.3	8	0	8
AY.5.4	2	0	2
AY.5.6	1	0	1
AY.51	4	0	4
AY.53	4	0	4
AY.54	16	0	16
AY.55	9	0	9
AY.57	12	0	12
AY.59	3	0	3
AY.6	11	0	11
AY.61	61	0	61
AY.62	4	0	4
AY.64	3	0	3
AY.65	20	0	20
AY.66	1	0	1
AY.68	1	0	1
AY.69	1	0	1
AY.7	1	0	1
AY.7.1	3	0	3
AY.7.2	1	0	1
AY.70	6	0	6
AY.72	4	0	4
AY.73	4	0	4
AY.74	12,585	0	12,585
AY.75	445	0	445
AY.75.2	2	0	2
AY.76	1	0	1
AY.77	7	0	7
AY.78	1	0	1
AY.83	6	0	6
AY.84	4	0	4

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
AY.85	1	0	1
AY.86	308	0	308
AY.88	10	0	10
AY.9	13	0	13
AY.9.2	233	0	233
AY.9.2.1	700	0	700
AY.92	8	0	8
AY.93	106	0	106
AY.94	3	0	3
AY.98	29	0	29
AY.98.1	21	0	21
AY.99	1	0	1
AY.99.2	18	0	18
Omicron	**61,820**	**15,614**	**77,434**
BA.1	6,346	1	6,347
BA.1.1	18,900	22	18,922
BA.1.1.1	44	0	44
BA.1.1.10	1,685	2	1,687
BA.1.1.12	1	0	1
BA.1.1.13	5	0	5
BA.1.1.14	521	2	523
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	139	0	139
BA.1.1.2	6	0	6
BA.1.1.6	3	0	3
BA.1.1.7	6	0	6
BA.1.1.8	3	0	3
BA.1.12	2	0	2
BA.1.13	35	0	35
BA.1.13.1	1	0	1
BA.1.14	68	0	68
BA.1.14.1	1	0	1
BA.1.14.2	1	0	1
BA.1.15	1,652	1	1,653
BA.1.15.1	22	0	22
BA.1.15.2	3	0	3
BA.1.16	2	0	2
BA.1.17	761	0	761

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
BA.1.17.2	1,484	0	1,484
BA.1.18	91	0	91
BA.1.19	24	0	24
BA.1.20	91	0	91
BA.1.21	5	0	5
BA.1.3	1	0	1
BA.1.4	1	0	1
BA.1.6	66	0	66
BA.1.7	2	0	2
BA.1.9	35	0	35
BA.2	14,900	570	15,470
BA.2.1	123	7	130
BA.2.10	389	0	389
BA.2.10.1	16	0	16
BA.2.10.3	1	0	1
BA.2.11	3	4	7
BA.2.12	47	8	55
BA.2.12.1	3,295	2,792	6,087
BA.2.12.2	2	0	2
BA.2.13	20	29	49
BA.2.15	1	0	1
BA.2.16	1	0	1
BA.2.17	6	0	6
BA.2.18	37	27	64
BA.2.2	0	3	3
BA.2.20	1,667	23	1,690
BA.2.21	237	84	321
BA.2.22	4	1	5
BA.2.23	53	2	55
BA.2.24	4	0	4
BA.2.26	8	0	8
BA.2.27	1	0	1
BA.2.3	2,232	111	2,343
BA.2.3.10	75	3	78
BA.2.3.12	5	2	7
BA.2.3.14	3	0	3
BA.2.3.15	1	0	1
BA.2.3.16	5	0	5
BA.2.3.17	3	0	3
BA.2.3.2	16	2	18

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
BA.2.3.4	949	8	957
BA.2.3.5	1	0	1
BA.2.3.6	82	5	87
BA.2.3.7	2	1	3
BA.2.3.8	2	0	2
BA.2.3.9	1	0	1
BA.2.31	12	7	19
BA.2.32	4	0	4
BA.2.34	1	2	3
BA.2.35	3	2	5
BA.2.36	17	2	19
BA.2.37	80	0	80
BA.2.38	608	56	664
BA.2.38.1	0	1	1
BA.2.40	0	2	2
BA.2.40.1	8	13	21
BA.2.41	3	1	4
BA.2.42	2	0	2
BA.2.43	1	0	1
BA.2.45	3	0	3
BA.2.47	2	0	2
BA.2.48	5	8	13
BA.2.49	4	0	4
BA.2.5	5	1	6
BA.2.50	10	1	11
BA.2.51	19	0	19
BA.2.52	3	4	7
BA.2.54	1	0	1
BA.2.55	1	0	1
BA.2.56	28	8	36
BA.2.57	2	0	2
BA.2.59	0	0	0
BA.2.6	4	2	6
BA.2.62	3	1	4
BA.2.64	13	1	14
BA.2.65	1,599	49	1,648
BA.2.66	22	1	23
BA.2.68	6	0	6
BA.2.69	1	0	1
BA.2.7	15	0	15

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
BA.2.72	7	1	8
BA.2.73	1	1	2
BA.2.74	5	23	28
BA.2.75	1	31	32
BA.2.76	11	41	52
BA.2.78	3	0	3
BA.2.79	0	4	4
BA.2.79.1	0	1	1
BA.2.8	9	0	9
BA.2.81	1	1	2
BA.2.9	1,511	48	1,559
BA.2.9.2	3	0	3
BA.2.9.3	6	8	14
BA.2.9.4	1	0	1
BA.2.9.5	2	0	2
BA.3.1	1	0	1
BA.4	135	469	604
BA.4.1	185	683	868
BA.4.1.1	4	9	13
BA.4.2	3	87	90
BA.4.3	1	8	9
BA.4.4	8	44	52
BA.4.6	15	267	282
BA.4.7	1	0	1
BA.5	118	861	979
BA.5.1	310	2,135	2,445
BA.5.1.1	28	397	425
BA.5.1.2	4	36	40
BA.5.1.3	2	7	9
BA.5.1.4	0	6	6
BA.5.2	120	1,206	1,326
BA.5.2.1	232	2,871	3,103
BA.5.2.2	0	20	20
BA.5.2.3	1	33	34
BA.5.3	1	15	16
BA.5.3.1	15	207	222
BA.5.3.2	4	4	8
BA.5.3.3	0	4	4
BA.5.3.4	2	2	4
BA.5.5	113	797	910

WHO label / Pango lineage	January 1, 2021 – June 18, 2022	June 19 – July 16, 2022	Total
BA.5.6	27	307	334
BC.2	1	0	1
BE.1	48	446	494
BE.1.1	25	213	238
BE.2	0	1	1
BE.3	8	78	86
BF.1	10	111	121
BF.1.1	3	5	8
BF.2	5	8	13
BF.3	0	5	5
BF.4	3	92	95
BF.5	6	102	108
BG.2	25	40	65
BG.4	7	7	14
Variant of Interest (VOI)			
Mu	**240**	**0**	**240**
B.1.621	231	0	231
B.1.621.1	9	0	9
Lambda	**0**	**0**	**0**
C.37	8	0	8
Recombinant	**43**	**12**	**55**
XAC	20	9	29
XAF	0	1	1
XB	1	0	1
XE	3	0	3
XM	1	0	1
XN	1	0	1
XQ	4	0	4
XW	12	2	14
XZ	1	0	1
Non-VOC/VOI	**6,351**	**0**	**6,351**
Total sequenced	**131,490**	**15,628**	**147,118**

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 source: 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 July 27, 2022 at approximately 2:00 a.m.
- Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on July 27, 2022 at approximately 12:00 p.m.

The Hospital for Sick Children (HSC)

- Data were received by PHO on July 26, 2022 at approximately 10:20 a.m.

Kingston Health Sciences Centre (KHSC)

- Data were received by PHO on July 26, 2022 at approximately 6:00 p.m.

Shared Hospital Laboratory (SHL)

- Data were received by PHO on July 26, 2022 at approximately 4:00 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were received by PHO on July 19, 2022 at approximately 10:00 p.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on July 18, 2022 at approximately 1:00 p.m.

Ontario Ministry of Health's COVaxON application (COVaxON)

- COVID-19 vaccination data were based on information successfully extracted from the Ontario Ministry of Health's COVaxON application as of July 18, 2022 at approximately 7:00 a.m.
- COVaxON data was linked to COVID-19 case data from CCM.

Ontario SARS-CoV-2 Whole Genome Sequencing Strategy

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

- As of May 2, 2021, Ontario's strategy shifted to representative surveillance with VOC PCR testing laboratories being asked to send a proportion of eligible samples (Ct ≤ 30 and sufficient volume remaining) to Ontario COVID-19 Genomics Network (OCGN) sequencing laboratories. PHO began sequencing a 10% systematic sample of eligible samples on May 2 and 50% on May 30. Other VOC PCR testing laboratories were asked to begin submitting a 10% systematic or random sample of eligible samples to OCGN laboratories on May 26 and 50% on June 2. All VOC PCR/diagnostic testing laboratories shifted to submitting 100% of eligible samples to the OCGN on June 14; 50% on August 27; 10% on September 10; 25% on October 8; 100% on November 5; 50% on December 7; 10% on December 20; 5% on December 30; 20% on February 16; 50% on March 9; 25% on March 30; 10% on April 13; 25% on May 12; 100% on June 10; and 50% on July 8, 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 (3.5%), 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 10% or greater were included in the table and figure. Lineages with at least seven days of non-zero case counts were included.

- 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]

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, hospitalized, and deceased indicators only include cases that linked to CCM (96.5% 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.

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, July 29, 2022. Toronto, ON: Queen's Printer for Ontario; 2022.

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