Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Whole Genome Sequencing in Ontario, April 5, 2022

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of March 31, 2022 and partner laboratories in the Ontario COVID-19 Genomics Network as of March 30, 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 Delta to include descendant AY lineages (e.g., AY.4.2). 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. At this time there is no definitive evidence that descendant lineages have different biological characteristics (e.g., immune escape) from the parent lineage. 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 7,367 cases sequenced by the OCGN for representative surveillance from February 20 to March 19, 2022.
- In the most recent week (March 13 to March 19, 2022), BA.2 was the most prevalent lineage (54.0%), followed by BA.1.1 (41.2%), and BA.1 (4.9%).
- The proportion of cases identified as BA.2 through representative surveillance increased between March 6 to 12 (36.8%), and March 13 to 19 (54.0%).
    - Over the past twelve weeks, the weekly growth rate of BA.2 was 1.57 times that of BA.1.1.
    - In the most recent week, Halton Region Public Health reported the highest proportion of BA.2 cases (68.3%) followed by Peel Public Health (67.7%); excluding public health units with fewer than 50 cases sequenced.
    - A total of 3,699 BA.2 cases have been identified since January 1, 2021.

> As of December 31, 2021, diagnostic PCR testing was restricted to high-risk populations. As such, representative surveillance only pertains to tested populations.
>
> The OCGN moved from sequencing 20% of eligible samples to 50% on March 9, 2022.

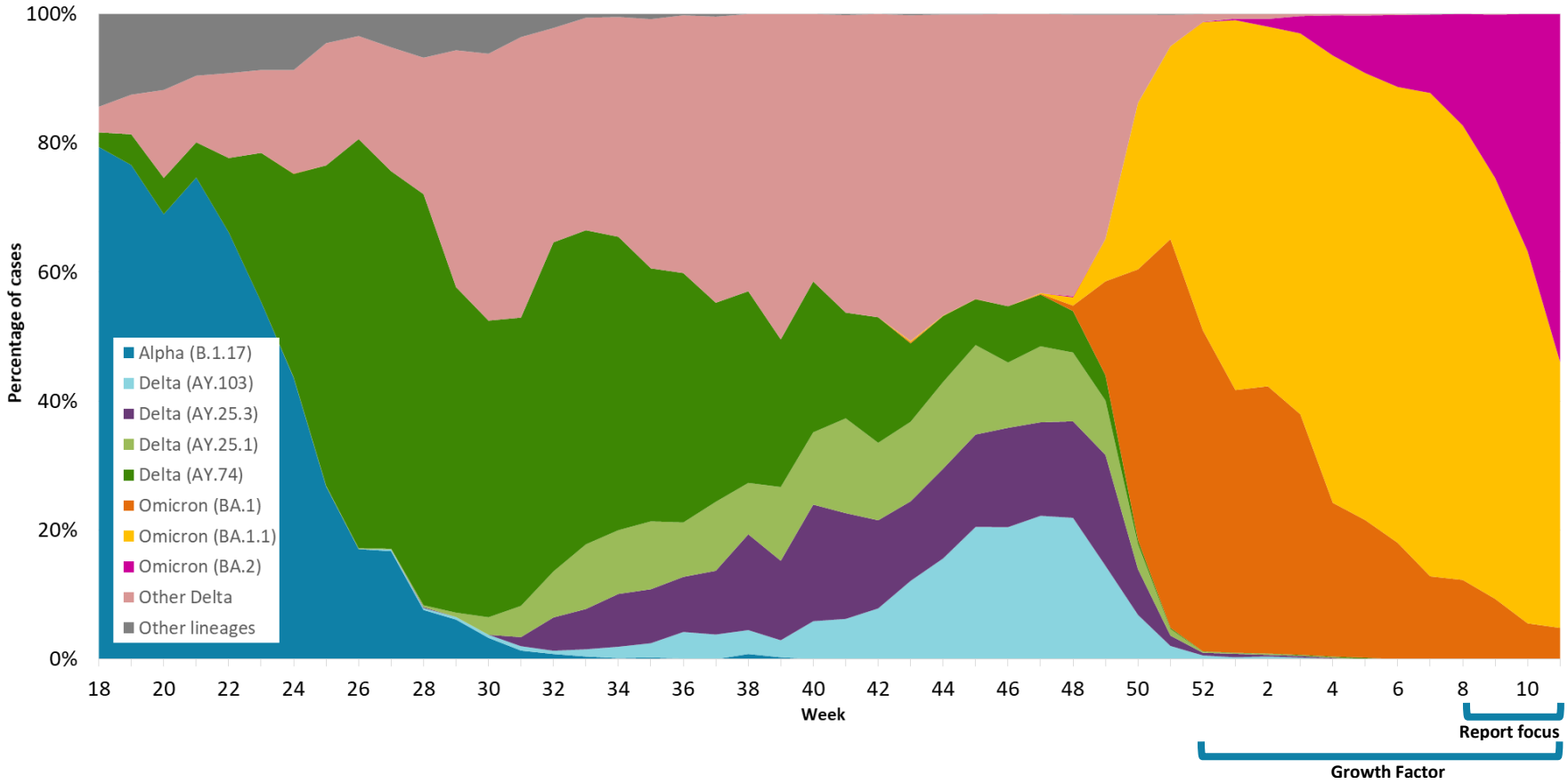
Representative Surveillance

Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, February 20 to March 19, 2022

Week	Number of cases	Number sequenced	Percentage sequenced
Week 8 (February 20 to February 26)	12,406	1,286	10.4%
Week 9 (February 27 to March 5)	11,411	1,251	11.0%
Week 10 (March 6 to March 12)	11,396	2,109	18.5%
Week 11 (March 13 to March 19)	11,311	2,721	24.1%
Total	**46,524**	**7,367**	**15.8%**

Note: 'Number of cases' is the number of confirmed positive cases of COVID-19 in Ontario. Date was assigned to best align with sample collection date, which may differ from other PHO products. 'Number sequenced' is the number of cases sequenced for representative surveillance. Results may not be representative of Ontario overall, and do not include all samples tested for other reasons including travel, outbreak investigation, coroner's cases, reinfection or possible vaccine escape. 'Percentage sequenced' may be lower than the sampling proportion because not all cases are eligible to be sequenced (i.e. excludes samples with cycle threshold >30 or insufficient volume). For representative surveillance: details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction and will be included in subsequent reports.
Data 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 March 19, 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. Weekly relative growth rate by Pango lineage, representative surveillance, Ontario, December 26, 2021 to March 19, 2022

WHO label/Pango lineage	Number (% of total cases)	Weekly relative growth rate (95% Confidence Interval)
Delta	**219 (1.0%)**	**0.63 (0.58 - 0.69)**
Omicron		
BA.1	6,112 (27.4%)	0.80 (0.79 - 0.81)
BA.1.1	12,760 (57.2%)	1.00 (reference)
BA.2	3,231 (14.5%)	1.57 (1.54 - 1.60)
Total cases	**22,322 (100%)**	

Note: Includes Delta and all Omicron lineages detected in the past month. 'Number (% of total cases)' presents the number and percentage of cases for a given lineage out of all cases sequenced with lineages presented in the table. The weekly relative growth rate is a measure of a lineage's growth rate relative to the reference lineage. Details on the methodology used to calculate 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 3. Number and percentage of cases by Pango lineage and week, representative surveillance, Ontario, February 20 to March 19, 2022

WHO label/Pango lineage	Week 8 (February 20 to February 26)	Week 9 (February 27 to March 5)	Week 10 (March 6 to March 12)	Week 11 (March 13 to March 19)	Total (February 20 to March 19)
Delta	**1 (0.1%)**	**1 (0.1%)**	**0 (0.0%)**	**0 (0.0%)**	**2 (<0.1%)**
Omicron	**1,285 (99.9%)**	**1,250 (99.9%)**	**2,109 (100%)**	**2,721 (100%)**	**7,365 (>99.9%)**
BA.1	157 (12.2%)	117 (9.4%)	117 (5.5%)	132 (4.9%)	523 (7.1%)
BA.1.1	906 (70.5%)	816 (65.3%)	1,216 (57.7%)	1,121 (41.2%)	4,059 (55.1%)
BA.2	222 (17.3%)	317 (25.4%)	776 (36.8%)	1,468 (54.0%)	2,783 (37.8%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**1,286 (100%)**	**1,251 (100%)**	**2,109 (100%)**	**2,721 (100%)**	**7,367 (100%)**

Note: Includes Delta and all Omicron 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

Table 4. Number and percentage of cases by Pango lineage and age group, representative surveillance, Ontario, February 20 to March 19, 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
Delta	**1 (0.5%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**1 (<0.1%)**	**0 (0.0%)**	**0 (0.0%)**	**2 (<0.1%)**
Omicron	**218 (99.5%)**	**425 (100%)**	**638 (100%)**	**2,680 (100%)**	**2,212 (>99.9%)**	**788 (100%)**	**400 (100%)**	**7,361 (>99.9%)**
BA.1	18 (8.3%)	23 (5.4%)	29 (4.5%)	210 (7.8%)	163 (7.4%)	56 (7.1%)	23 (5.8%)	522 (7.1%)
BA.1.1	117 (53.7%)	220 (51.8%)	365 (57.2%)	1,417 (52.9%)	1,203 (54.4%)	476 (60.4%)	258 (64.5%)	4,056 (55.1%)
BA.2	83 (38.1%)	182 (42.8%)	244 (38.2%)	1,053 (39.3%)	846 (38.2%)	256 (32.5%)	119 (29.8%)	2,783 (37.8%)
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	**219 (100%)**	**425 (100%)**	**638 (100%)**	**2,680 (100%)**	**2,213 (100%)**	**788 (100%)**	**400 (100%)**	**7,363 (100%)**

Note: Includes Delta and all Omicron 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.2 (Omicron) cases identified (number identified/total sequenced) by public health unit (PHU), region, and week, representative surveillance, Ontario, February 20 to March 19, 2022

Public Health Unit	Week 8 (February 20 to February 26)	Week 9 (February 27 to March 5)	Week 10 (March 6 to March 12)	Week 11 (March 13 to March 19)	Total (February 20 to March 19)
Northwestern Health Unit	20.8% (5/24)	14.3% (3/21)	21.4% (6/28)	25.0% (5/20)	20.4% (19/93)
Thunder Bay District Health Unit	13.3% (4/30)	13.0% (3/23)	6.7% (3/45)	7.0% (3/43)	9.2% (13/141)
TOTAL NORTH WEST	**16.7% (9/54)**	**13.6% (6/44)**	**12.3% (9/73)**	**12.7% (8/63)**	**13.7% (32/234)**
Algoma Public Health	16.7% (1/6)	0.0% (0/1)	50.0% (2/4)	60.0% (3/5)	37.5% (6/16)
North Bay Parry Sound District Health Unit	2.9% (1/34)	2.4% (1/42)	4.1% (2/49)	40.0% (4/10)	5.9% (8/135)
Porcupine Health Unit	0.0% (0/29)	10.0% (1/10)	5.0% (1/20)	12.5% (4/32)	6.6% (6/91)
Public Health Sudbury & Districts	0.0% (0/3)	0.0% (0/2)	0.0% (0/5)	28.6% (6/21)	19.4% (6/31)
Timiskaming Health Unit	0.0% (0/1)	0.0% (0/4)	28.6% (2/7)	14.3% (1/7)	15.8% (3/19)
TOTAL NORTH EAST	**2.7% (2/73)**	**3.4% (2/59)**	**8.2% (7/85)**	**24.0% (18/75)**	**9.9% (29/292)**
Ottawa Public Health	12.4% (12/97)	14.0% (14/100)	23.4% (25/107)	39.2% (49/125)	23.3% (100/429)
Eastern Ontario Health Unit	0.0% (0/16)	8.3% (2/24)	0.0% (0/27)	37.9% (11/29)	13.5% (13/96)
Hastings Prince Edward Public Health	12.5% (3/24)	0.0% (0/19)	17.6% (6/34)	36.5% (23/63)	22.9% (32/140)
Kingston, Frontenac and Lennox & Addington Public Health	6.6% (4/61)	10.0% (6/60)	22.9% (36/157)	39.3% (77/196)	25.9% (123/474)
Leeds, Grenville & Lanark District Health Unit	6.1% (2/33)	8.3% (2/24)	22.2% (6/27)	29.0% (9/31)	16.5% (19/115)
Renfrew County and District Health Unit	0.0% (0/25)	12.5% (3/24)	8.7% (2/23)	50.0% (16/32)	20.2% (21/104)
TOTAL EASTERN	**8.2% (21/256)**	**10.8% (27/251)**	**20.0% (75/375)**	**38.9% (185/476)**	**22.7% (308/1,358)**
Durham Region Health Department	13.5% (10/74)	19.2% (14/73)	44.1% (49/111)	57.1% (80/140)	38.4% (153/398)
Haliburton, Kawartha, Pine Ridge District Health Unit	0.0% (0/13)	0.0% (0/15)	8.0% (2/25)	56.7% (17/30)	22.9% (19/83)
Peel Public Health	39.2% (29/74)	54.1% (40/74)	52.4% (55/105)	67.7% (84/124)	55.2% (208/377)
Peterborough Public Health	23.1% (3/13)	14.3% (1/7)	42.1% (8/19)	43.5% (10/23)	35.5% (22/62)
Simcoe Muskoka District Health Unit	15.2% (7/46)	18.3% (11/60)	33.7% (33/98)	48.8% (79/162)	35.5% (130/366)
York Region Public Health	30.0% (18/60)	24.2% (16/66)	49.5% (49/99)	64.5% (80/124)	46.7% (163/349)
TOTAL CENTRAL EAST	**23.9% (67/280)**	**27.8% (82/295)**	**42.9% (196/457)**	**58.0% (350/603)**	**42.5% (695/1,635)**
Toronto Public Health	25.1% (47/187)	36.7% (80/218)	48.4% (184/380)	65.7% (353/537)	50.2% (664/1322)
TOTAL TORONTO	**25.1% (47/187)**	**36.7% (80/218)**	**48.4% (184/380)**	**65.7% (353/537)**	**50.2% (664/1,322)**

Public Health Unit	Week 8 (February 20 to February 26)	Week 9 (February 27 to March 5)	Week 10 (March 6 to March 12)	Week 11 (March 13 to March 19)	Total (February 20 to March 19)
Chatham-Kent Public Health	4.5% (1/22)	11.8% (2/17)	9.1% (1/11)	29.4% (5/17)	13.4% (9/67)
Grey Bruce Health Unit	5.6% (1/18)	12.5% (2/16)	18.5% (5/27)	28.1% (9/32)	18.3% (17/93)
Huron Perth Public Health	21.4% (3/14)	25.0% (2/8)	9.1% (1/11)	73.3% (22/30)	44.4% (28/63)
Lambton Public Health	0.0% (0/13)	16.7% (2/12)	26.3% (5/19)	61.5% (16/26)	32.9% (23/70)
Middlesex-London Health Unit	21.1% (12/57)	17.1% (7/41)	39.5% (32/81)	52.5% (53/101)	37.1% (104/280)
Southwestern Public Health	0.0% (0/18)	13.3% (2/15)	41.7% (10/24)	45.7% (16/35)	30.4% (28/92)
Windsor-Essex County Health Unit	20.9% (9/43)	39.5% (15/38)	37.9% (25/66)	61.5% (75/122)	46.1% (124/269)
TOTAL SOUTH WEST	**14.1% (26/185)**	**21.8% (32/147)**	**33.1% (79/239)**	**54.0% (196/363)**	**35.7% (333/934)**
Brant County Health Unit	22.2% (2/9)	57.1% (4/7)	31.0% (9/29)	52.9% (9/17)	38.7% (24/62)
City of Hamilton Public Health Services	15.6% (12/77)	34.7% (25/72)	42.9% (79/184)	54.9% (112/204)	42.5% (228/537)
Haldimand-Norfolk Health Unit	33.3% (4/12)	40.0% (6/15)	39.1% (9/23)	67.9% (19/28)	48.7% (38/78)
Halton Region Public Health	35.7% (15/42)	50.0% (19/38)	59.0% (36/61)	68.3% (69/101)	57.4% (139/242)
Niagara Region Public Health	7.1% (2/28)	30.6% (11/36)	40.4% (21/52)	67.4% (31/46)	40.1% (65/162)
Region of Waterloo Public Health and Emergency Services	20.0% (11/55)	32.6% (14/43)	52.6% (50/95)	53.7% (73/136)	45.0% (148/329)
Wellington-Dufferin-Guelph Public Health	14.8% (4/27)	34.6% (9/26)	39.3% (22/56)	63.4% (45/71)	44.4% (80/180)
TOTAL CENTRAL WEST	**20.0% (50/250)**	**37.1% (88/237)**	**45.2% (226/500)**	**59.4% (358/603)**	**45.4% (722/1,590)**
UNKNOWN	0.0% (0/1)	0.0% (0/0)	0.0% (0/0)	0.0% (0/1)	0.0% (0/2)
TOTAL ONTARIO	**17.3% (222/1,286)**	**25.3% (317/1,251)**	**36.8% (776/2,109)**	**54.0% (1,468/2,721)**	**37.8% (2,783/7,367)**

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, February 20 to March 19, 2022

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two booster doses	Total cases
Delta	**2 (100%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**2 (100%)**
Omicron	**995 (14.0%)**	**156 (2.2%)**	**2,079 (29.3%)**	**3,750 (52.8%)**	**124 (1.7%)**	**7,104 (100%)**
BA.1	82 (16.3%)	11 (2.2%)	132 (26.2%)	266 (52.9%)	12 (2.4%)	503 (100%)
BA.1.1	556 (14.2%)	90 (2.3%)	1,179 (30.2%)	2,009 (51.4%)	76 (1.9%)	3,910 (100%)
BA.2	357 (13.3%)	55 (2.0%)	768 (28.5%)	1,475 (54.8%)	36 (1.3%)	2,691 (100%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**997 (14.0%)**	**156 (2.2%)**	**2,079 (29.3%)**	**3,750 (52.8%)**	**124 (1.7%)**	**7,106 (100%)**

Note: Includes Delta and all Omicron 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 in post-series completion 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 ever hospitalized cases by vaccination status and Pango lineage, representative surveillance, Ontario, February 20 to March 19, 2022

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two booster doses
Delta	**0.0% (0/2)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**
Omicron	**8.1% (81/994)**	**3.8% (6/156)**	**2.4% (50/2,079)**	**2.6% (96/3,750)**	**8.1% (10/124)**
BA.1	6.1% (5/82)	9.1% (1/11)	3.8% (5/132)	5.3% (14/266)	8.3% (1/12)
BA.1.1	11.7% (65/556)	3.3% (3/90)	3.1% (37/1,179)	3.0% (61/2,009)	10.5% (8/76)
BA.2	3.1% (11/357)	3.6% (2/55)	1.0% (8/768)	1.4% (21/1475)	2.8% (1/36)
Other lineages	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**
Total sequenced	**8.1% (81/996)**	**3.8% (6/156)**	**2.4% (50/2,079)**	**2.6% (96/3,750)**	**8.1% (10/124)**

Note: Includes Delta and all Omicron lineages detected in the past month. Percentage is the number of hospitalized 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. Hospitalized cases include cases that reported hospitalization at 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 (hospitalization indicator), COVaxON

Table 7b. Percentage of deceased cases by Pango lineage and vaccination status, representative surveillance, Ontario, February 20 to March 19, 2022

WHO label / Pango lineage	Unvaccinated	Post-series initiation	Post-series completion	Post-booster dose	Post-two booster doses
Delta	**0.0% (0/2)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**
Omicron	**1.6% (16/994)**	**0.6% (1/156)**	**0.2% (5/2,079)**	**0.3% (12/3,750)**	**0.0% (0/124)**
BA.1	0.0% (0/82)	0.0% (0/11)	0.0% (0/132)	0.8% (2/266)	0.0% (0/12)
BA.1.1	2.5% (14/556)	1.1% (1/90)	0.4% (5/1,179)	0.4% (9/2,009)	0.0% (0/76)
BA.2	0.6% (2/357)	0.0% (0/55)	0.0% (0/768)	0.1% (1/1,475)	0.0% (0/36)
Other lineages	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**	**0.0% (0/0)**
Total sequenced	**1.6% (16/996)**	**0.6% (1/156)**	**0.2% (5/2,079)**	**0.3% (12/3,750)**	**0.0% (0/124)**

Note: Includes Delta and all Omicron 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' 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, February 20 to March 19, 2022

WHO label / Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
Delta	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Omicron	**93 (100%)**	**141 (100%)**	**234 (100%)**
BA.1	21 (22.6%)	30 (21.3%)	51 (21.8%)
BA.1.1	53 (57.0%)	98 (69.5%)	151 (64.5%)
BA.2	19 (20.4%)	13 (9.2%)	32 (13.7%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**93 (100%)**	**141 (100%)**	**234 (100%)**

Note: Includes Delta and all Omicron 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, February 20 to March 19, 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
Delta	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Omicron	**16 (100%)**	**135 (100%)**	**91 (100%)**	**31 (100%)**	**19 (100%)**	**292 (100%)**
BA.1	2 (12.5%)	5 (3.7%)	7 (7.7%)	2 (6.5%)	0 (0.0%)	16 (5.5%)
BA.1.1	8 (50.0%)	122 (90.4%)	78 (85.7%)	23 (74.2%)	16 (84.2%)	247 (84.6%)
BA.2	6 (37.5%)	8 (5.9%)	6 (6.6%)	6 (19.4%)	3 (15.8%)	29 (9.9%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**16 (100%)**	**135 (100%)**	**91 (100%)**	**31 (100%)**	**19 (100%)**	**292 (100%)**

Note: Includes Delta and all Omicron 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, February 20 to March 19, 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
Delta	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Omicron	**96 (100%)**	**140 (100%)**	**474 (100%)**	**115 (100%)**	**429 (100%)**	**104 (100%)**	**1,358 (100%)**
BA.1	8 (8.3%)	12 (8.6%)	42 (8.9%)	12 (10.4%)	50 (11.7%)	9 (8.7%)	133 (9.8%)
BA.1.1	75 (78.1%)	96 (68.6%)	309 (65.2%)	84 (73.0%)	279 (65.0%)	74 (71.2%)	917 (67.5%)
BA.2	13 (13.5%)	32 (22.9%)	123 (25.9%)	19 (16.5%)	100 (23.3%)	21 (20.2%)	308 (22.7%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**96 (100%)**	**140 (100%)**	**474 (100%)**	**115 (100%)**	**429 (100%)**	**104 (100%)**	**1,358 (100%)**

Note: Includes Delta and all Omicron 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, February 20 to March 19, 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
Delta	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Omicron	**398 (100%)**	**83 (100%)**	**377 (100%)**	**62 (100%)**	**366 (100%)**	**349 (100%)**	**1,635 (100%)**
BA.1	30 (7.5%)	5 (6.0%)	22 (5.8%)	1 (1.6%)	16 (4.4%)	23 (6.6%)	97 (5.9%)
BA.1.1	215 (54.0%)	59 (71.1%)	147 (39.0%)	39 (62.9%)	220 (60.1%)	163 (46.7%)	843 (51.6%)
BA.2	153 (38.4%)	19 (22.9%)	208 (55.2%)	22 (35.5%)	130 (35.5%)	163 (46.7%)	695 (42.5%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**398 (100%)**	**83 (100%)**	**377 (100%)**	**62 (100%)**	**366 (100%)**	**349 (100%)**	**1,635 (100%)**

Note: Includes Delta and all Omicron 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, February 20 to March 19, 2022

WHO label / Pango lineage	Toronto Public Health	Total
Delta	**1 (0.1%)**	**1 (0.1%)**
Omicron	**1,321 (99.9%)**	**1,321 (99.9%)**
BA.1	71 (5.4%)	71 (5.4%)
BA.1.1	586 (44.3%)	586 (44.3%)
BA.2	664 (50.3%)	664 (50.3%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**1,322 (100%)**	**1,322 (100%)**

Note: Includes Delta and all Omicron 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, February 20 to March 19, 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
Delta	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Omicron	**67 (100%)**	**93 (100%)**	**63 (100%)**	**70 (100%)**	**280 (100%)**	**92 (100%)**	**269 (100%)**	**934 (100%)**
BA.1	6 (9.0%)	4 (4.3%)	4 (6.3%)	3 (4.3%)	17 (6.1%)	4 (4.3%)	10 (3.7%)	48 (5.1%)
BA.1.1	52 (77.6%)	72 (77.4%)	31 (49.2%)	44 (62.9%)	159 (56.8%)	60 (65.2%)	135 (50.2%)	553 (59.2%)
BA.2	9 (13.4%)	17 (18.3%)	28 (44.4%)	23 (32.9%)	104 (37.1%)	28 (30.4%)	124 (46.1%)	333 (35.7%)
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	**67 (100%)**	**93 (100%)**	**63 (100%)**	**70 (100%)**	**280 (100%)**	**92 (100%)**	**269 (100%)**	**934 (100%)**

Note: Includes Delta and all Omicron 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, February 20 to March 19, 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
Delta	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**1 (0.3%)**	**0 (0.0%)**	**1 (0.1%)**
Omicron	**62 (100%)**	**537 (100%)**	**78 (100%)**	**242 (100%)**	**162 (100%)**	**328 (99.7%)**	**180 (100%)**	**1,589 (99.9%)**
BA.1	2 (3.2%)	37 (6.9%)	5 (6.4%)	12 (5.0%)	7 (4.3%)	31 (9.5%)	13 (7.2%)	107 (6.7%)
BA.1.1	36 (58.1%)	272 (50.7%)	35 (44.9%)	91 (37.6%)	90 (55.6%)	149 (45.4%)	87 (48.3%)	760 (47.8%)
BA.2	24 (38.7%)	228 (42.5%)	38 (48.7%)	139 (57.4%)	65 (40.1%)	148 (45.1%)	80 (44.4%)	722 (45.4%)
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	**62 (100%)**	**537 (100%)**	**78 (100%)**	**242 (100%)**	**162 (100%)**	**329 (100%)**	**180 (100%)**	**1,590 (100%)**

Note: Includes Delta and all Omicron 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, February 20 to March 19, 2022

WHO label / Pango lineage	Outbreak-associated	Non outbreak-associated	Total cases
Delta	**0 (0.0%)**	**2 (100%)**	**2 (100%)**
Omicron	**560 (7.9%)**	**6,545 (92.1%)**	**7,105 (100%)**
BA.1	42 (8.3%)	461 (91.7%)	503 (100%)
BA.1.1	353 (9.0%)	3,557 (91.0%)	3,910 (100%)
BA.2	165 (6.1%)	2,527 (93.9%)	2,692 (100%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**560 (7.9%)**	**6,547 (92.1%)**	**7,107 (100%)**

Note: Includes Delta and all Omicron 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 March 19, 2022

WHO label / Pango lineage	January 1, 2021 – February 19, 2022	February 20 – March 19, 2022	Total
Variant of concern (VOC)			
Alpha	**11,879**	**0**	**11,879**
B.1.1.7	11,856	0	11,856
Q.1	23	0	23
Beta	**1,236**	**0**	**1,236**
B.1.351	1,217	0	1,217
B.1.351.2	3	0	3
B.1.351.3	16	0	16
Gamma	**3,928**	**0**	**3,928**
P.1	221	0	221
P.1.10	2	0	2
P.1.12	2	0	2
P.1.12.1	1	0	1
P.1.13	1	0	1
P.1.14	3,664	0	3,664
P.1.17	33	0	33
P.1.7	4	0	4
Delta	**46,107**	**3**	**46,110**
B.1.617.2	1,463	0	1,463
AY.1	2	0	2
AY.10	23	0	23
AY.100	748	0	748
AY.101	1	0	1
AY.102	135	0	135
AY.103	5,122	0	5,122
AY.103.2	4	0	4
AY.104	8	0	8
AY.105	43	0	43
AY.106	37	0	37
AY.107	66	0	66
AY.108	53	0	53
AY.109	26	0	26
AY.110	24	0	24
AY.111	6	0	6
AY.112	56	0	56
AY.113	36	0	36
AY.114	3	0	3
AY.116	72	0	72

WHO label / Pango lineage	January 1, 2021 – February 19, 2022	February 20 – March 19, 2022	Total
AY.116.1	10	0	10
AY.117	116	0	116
AY.118	37	0	37
AY.119	323	0	323
AY.119.1	3	0	3
AY.119.2	227	0	227
AY.120	50	0	50
AY.120.1	5	0	5
AY.120.2	1	0	1
AY.121	105	0	105
AY.121.1	3	0	3
AY.122	1,336	0	1,336
AY.122.1	10	0	10
AY.122.4	8	0	8
AY.123	1	0	1
AY.124	11	0	11
AY.124.1	3	0	3
AY.124.1.1	5	0	5
AY.125	63	0	63
AY.126	142	0	142
AY.127	396	0	396
AY.127.1	21	0	21
AY.128	15	0	15
AY.129	30	0	30
AY.13	48	0	48
AY.131	8	0	8
AY.133	7	0	7
AY.14	39	0	39
AY.15	155	0	155
AY.16	122	0	122
AY.16.1	2	0	2
AY.18	10	0	10
AY.19	106	0	106
AY.2	2	0	2
AY.20	195	0	195
AY.22	5	0	5
AY.23	13	0	13
AY.23.1	4	0	4
AY.24	157	0	157
AY.25	1,369	0	1,369
AY.25.1	4,313	1	4,314
AY.25.1.2	11	0	11
AY.25.2	38	0	38

WHO label / Pango lineage	January 1, 2021 – February 19, 2022	February 20 – March 19, 2022	Total
AY.25.3	5,266	0	5,266
AY.26	96	0	96
AY.27	3,131	1	3,132
AY.28	32	0	32
AY.29	7	0	7
AY.3	1,014	0	1,014
AY.3.1	7	0	7
AY.3.2	5	0	5
AY.3.3	4	0	4
AY.30	3	0	3
AY.32	6	0	6
AY.33	87	0	87
AY.33.1	5	0	5
AY.34	33	0	33
AY.34.1	30	0	30
AY.35	1	0	1
AY.36	383	0	383
AY.37	30	0	30
AY.38	3	0	3
AY.39	269	0	269
AY.39.1	32	0	32
AY.39.1.2	1	0	1
AY.4	699	0	699
AY.4.12	2	0	2
AY.4.15	1	0	1
AY.4.2	47	0	47
AY.4.2.1	208	0	208
AY.4.2.2	15	0	15
AY.4.2.3	4	0	4
AY.4.3	1	0	1
AY.4.4	14	0	14
AY.4.5	7	0	7
AY.4.6	4	0	4
AY.4.7	5	0	5
AY.4.9	2	0	2
AY.40	33	0	33
AY.41	7	0	7
AY.42	40	0	40
AY.43	613	0	613
AY.43.3	1	0	1
AY.43.4	9	0	9
AY.43.8	5	0	5
AY.44	1,168	0	1,168

WHO label / Pango lineage	January 1, 2021 – February 19, 2022	February 20 – March 19, 2022	Total
AY.45	128	0	128
AY.46	63	0	63
AY.46.1	8	0	8
AY.46.2	16	0	16
AY.46.4	6	0	6
AY.46.5	4	0	4
AY.46.6	31	0	31
AY.47	119	0	119
AY.48	8	0	8
AY.49	1	0	1
AY.5	31	0	31
AY.5.2	1	0	1
AY.5.3	9	0	9
AY.5.4	2	0	2
AY.5.6	1	0	1
AY.51	5	0	5
AY.53	4	0	4
AY.54	41	0	41
AY.55	7	0	7
AY.57	18	0	18
AY.58	2	0	2
AY.59	5	0	5
AY.6	11	0	11
AY.60	4	0	4
AY.61	475	0	475
AY.62	6	0	6
AY.64	5	0	5
AY.65	19	0	19
AY.66	2	0	2
AY.67	3	0	3
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	11	0	11
AY.71	51	0	51
AY.72	3	0	3
AY.73	4	0	4
AY.74	12,319	1	12,320
AY.75	485	0	485
AY.75.2	2	0	2
AY.76	2	0	2

WHO label / Pango lineage	January 1, 2021 – February 19, 2022	February 20 – March 19, 2022	Total
AY.77	8	0	8
AY.78	5	0	5
AY.79	8	0	8
AY.82	1	0	1
AY.83	6	0	6
AY.84	3	0	3
AY.85	3	0	3
AY.86	204	0	204
AY.87	8	0	8
AY.88	11	0	11
AY.9	14	0	14
AY.9.2	254	0	254
AY.9.2.1	686	0	686
AY.92	18	0	18
AY.93	105	0	105
AY.94	3	0	3
AY.95	2	0	2
AY.98	25	0	25
AY.98.1	21	0	21
AY.99	1	0	1
AY.99.2	19	0	19
Omicron	**23,983**	**8,737**	**32,720**
BA.1	10,514	712	11,226
BA.1.1	12,921	4,874	17,795
BA.2	548	3,151	3,699
Variant of interest (VOI)			
Mu	**240**	**0**	**240**
B.1.621	230	0	230
B.1.621.1	9	0	9
B.1.621.2	1	0	1
Lambda	**8**	**0**	**8**
C.37	8	0	8
Non-VOC/VOI	**6,212**	**0**	**6,212**
Total sequenced	**93,593**	**8,740**	**102,333**

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 March 31, 2022 at approximately 2:00 a.m.
- Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on March 31, 2022 at approximately 3:00 p.m.

The Hospital for Sick Children (HSC)

- Data were received by PHO on March 30, 2022 at approximately 4:30 p.m.

Kingston Health Sciences Centre (KHSC)

- Data were received by PHO on March 30, 2022 at approximately 3:30 p.m.

Shared Hospital Laboratory (SHL)

- Data were received by PHO on March 30, 2022 at approximately 4:00 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were received by PHO on March 30, 2022 at approximately 10:40 p.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on March 28, 2022 at approximately 1:00 p.m.

Ontario Ministry of Health's COVaxON application (COVaxON)

- COVID-19 vaccination data were extracted from the Ontario Ministry of Health's COVaxON application on March 28, 2022 at approximately 7:00 a.m. for vaccination records created on or after Jun 1, 2021. Data were extracted on March 24, 2022 at approximately 7:00 a.m. for vaccination records created up to May 31, 2021.
- 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; 50% on May 30; 100% 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; and 50% on March 9, 2022. 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; 50% on June 2; 100% 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; and 50% on March 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.

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: Weekly Relative Growth Rate

- 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.

    - 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]

- Twelve weeks of representative surveillance data up to the most recent week were used. After selecting only the lineages presented in the representative surveillance portion of this report, a multinomial logistic regression was employed with surveillance week as the predictor.

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 Daily Epidemiological Summary.

- 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.

- Hospitalization includes all cases hospitalized (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. Hospitalizations 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'.

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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