WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Whole Genome Sequencing in Ontario, January 18, 2022

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of January 13, 2022 and partner laboratories in the Ontario COVID-19 Genomics Network as of January 12, 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 11,427 cases sequenced by the OCGN for representative surveillance from December 5, 2021 to January 1, 2022.
- The proportion of cases identified as Omicron through representative surveillance increased from 89.8% (December 19-25, 2021) to 97.5% (December 26, 2021 to January 1, 2022).
- From December 5, 2021 to January 1, 2022, the lineage with the highest percentage of cases with vaccine breakthrough was Omicron (76.4%).

> As of December 31, 2021, diagnostic PCR testing was restricted to high-risk populations. As such, representative surveillance only pertains to tested populations.
>
> Due to the rapid increase in the number of cases and complex sample logistics, the OCGN was not able to sequence all representative surveillance samples between December 12, 2021 and January 1, 2022. Results should be interpreted with caution.
>
> The OCGN moved from sequencing 50% of eligible samples to 10% on December 20, 2021, and to 5% on December 30, 2021.

Representative Surveillance

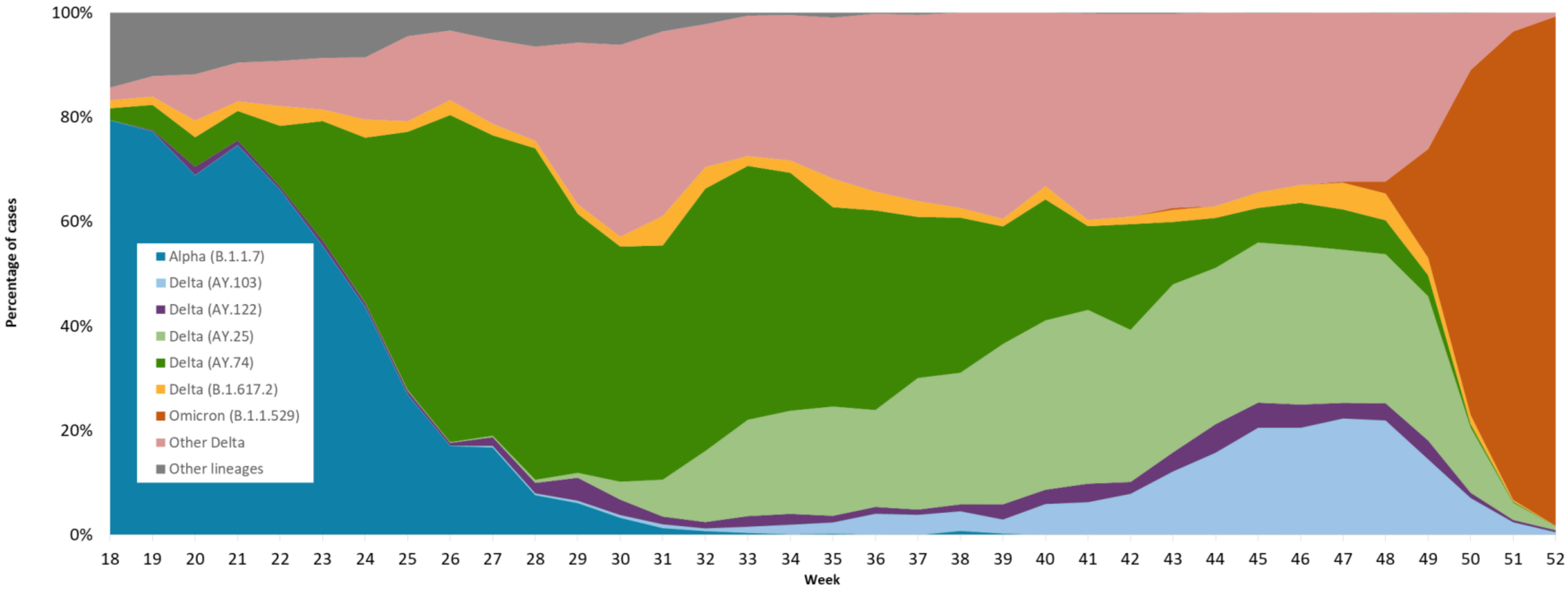
Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, December 5, 2021 to January 1, 2022

Week	Number of cases	Number sequenced	Percentage sequenced
Week 49 (December 5 to December 11)	10,118	4,190	41.4%
Week 50 (December 12 to December 18)	24,807	3,916	15.8%
Week 51 (December 19 to December 25)	65,830	1,328	2.0%
Week 52 (December 26, 2021 to January 1, 2022)	113,045	1,993	1.8%
Total	**213,800**	**11,427**	**5.3%**

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. 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 January 1, 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, December 5, 2021 to January 1, 2022

WHO label/Pango lineage	Week 49 (December 05 to December 11)	Week 50 (December 12 to December 18)	Week 51 (December 19 to December 25)	Week 52 (December 26 to January 01)	Total (December 5 to January 1)
Delta	**3,312 (79.0%)**	**1,326 (33.9%)**	**136 (10.2%)**	**49 (2.5%)**	**4,823 (42.2%)**
AY.25	1,157 (27.6%)	489 (12.5%)	44 (3.3%)	14 (0.7%)	1,704 (14.9%)
AY.103	606 (14.5%)	276 (7.0%)	31 (2.3%)	10 (0.5%)	923 (8.1%)
B.1.617.2	140 (3.3%)	68 (1.7%)	4 (0.3%)	1 (0.1%)	213 (1.9%)
AY.122	151 (3.6%)	40 (1.0%)	6 (0.5%)	8 (0.4%)	205 (1.8%)
AY.74	169 (4.0%)	25 (0.6%)	3 (0.2%)	1 (0.1%)	198 (1.7%)
AY.3	109 (2.6%)	48 (1.2%)	8 (0.6%)	2 (0.1%)	167 (1.5%)
AY.44	103 (2.5%)	52 (1.3%)	8 (0.6%)	0 (0.0%)	163 (1.4%)
AY.4	117 (2.8%)	33 (0.8%)	1 (0.1%)	1 (0.1%)	152 (1.3%)
AY.27	96 (2.3%)	50 (1.3%)	1 (0.1%)	1 (0.1%)	148 (1.3%)
AY.4.2	0 (0.0%)	2 (0.1%)	0 (0.0%)	0 (0.0%)	2 (<0.1%)
Other Delta	664 (15.8%)	243 (6.2%)	30 (2.3%)	11 (0.6%)	948 (8.3%)
Omicron	**873 (20.8%)**	**2,588 (66.1%)**	**1,192 (89.8%)**	**1,944 (97.5%)**	**6,597 (57.7%)**
B.1.1.529	873 (20.8%)	2,588 (66.1%)	1,192 (89.8%)	1,944 (97.5%)	6,597 (57.7%)
Other lineages	**5 (0.1%)**	**2 (0.1%)**	**0 (0.0%)**	**0 (0.0%)**	**7 (0.1%)**
Total sequenced	**4,190 (100%)**	**3,916 (100%)**	**1,328 (100%)**	**1,993 (100%)**	**11,427 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 3. Percentage of B.1.1.529 (Omicron) cases identified (number identified/total sequenced) by public health unit (PHU), region, and week, representative surveillance, Ontario, December 5, 2021 to January 1, 2022

WHO label/Pango lineage	Week 49 (December 05 to December 11)	Week 50 (December 12 to December 18)	Week 51 (December 19 to December 25)	Week 52 (December 26 to January 01)	Total (December 5 to January 1)
Northwestern Health Unit	0.0% (0/4)	0.0% (0/5)	0.0% (0/0)	0.0% (0/0)	0.0% (0/9)
Thunder Bay District Health Unit	3.7% (1/27)	16.7% (1/6)	0.0% (0/0)	0.0% (0/0)	6.1% (2/33)
TOTAL NORTH WEST	**3.2% (1/31)**	**9.1% (1/11)**	**0.0% (0/0)**	**0.0% (0/0)**	**4.8% (2/42)**
Algoma Public Health	2.4% (1/42)	0.0% (0/23)	100% (1/1)	0.0% (0/0)	3.0% (2/66)
North Bay Parry Sound District Health Unit	9.1% (1/11)	16.7% (1/6)	100% (1/1)	0.0% (0/0)	16.7% (3/18)
Porcupine Health Unit	0.0% (0/11)	25.0% (1/4)	0.0% (0/0)	0.0% (0/0)	6.7% (1/15)
Public Health Sudbury & Districts	0.0% (0/68)	0.0% (0/3)	0.0% (0/0)	0.0% (0/0)	0.0% (0/71)
Timiskaming Health Unit	0.0% (0/2)	33.3% (1/3)	0.0% (0/0)	0.0% (0/0)	20.0% (1/5)
TOTAL NORTH EAST	**1.5% (2/134)**	**7.7% (3/39)**	**100% (2/2)**	**0.0% (0/0)**	**4.0% (7/175)**
Ottawa Public Health	28.9% (79/273)	73.4% (168/229)	93.2% (110/118)	96.7% (296/306)	70.5% (653/926)
Eastern Ontario Health Unit	7.0% (3/43)	42.9% (12/28)	94.4% (34/36)	97.1% (34/35)	58.5% (83/142)
Hastings Prince Edward Public Health	5.2% (5/96)	31.8% (14/44)	80.8% (21/26)	100% (41/41)	39.1% (81/207)
Kingston, Frontenac and Lennox & Addington Public Health	64.5% (229/355)	84.8% (162/191)	95.7% (22/23)	96.9% (31/32)	73.9% (444/601)
Leeds, Grenville & Lanark District Health Unit	10.5% (10/95)	36.7% (22/60)	100% (9/9)	92.7% (51/55)	42.0% (92/219)
Renfrew County and District Health Unit	28.6% (4/14)	33.3% (2/6)	83.3% (5/6)	80.0% (4/5)	48.4% (15/31)
TOTAL EASTERN	**37.7% (330/876)**	**68.1% (380/558)**	**92.2% (201/218)**	**96.4% (457/474)**	**64.3% (1,368/2,126)**
Durham Region Health Department	14% (34/243)	75.2% (155/206)	92.9% (39/42)	96.9% (62/64)	52.3% (290/555)
Haliburton, Kawartha, Pine Ridge District Health Unit	8.3% (3/36)	50% (7/14)	87.5% (7/8)	100% (12/12)	41.4% (29/70)
Peel Public Health	25.4% (73/287)	69.9% (228/326)	94.8% (109/115)	98% (145/148)	63.4% (555/876)
Peterborough Public Health	4.5% (1/22)	55.6% (5/9)	100% (6/6)	100% (6/6)	41.9% (18/43)
Simcoe Muskoka District Health Unit	2.9% (9/307)	50% (118/236)	79.8% (75/94)	100% (19/19)	33.7% (221/656)
York Region Public Health	18.8% (71/378)	74.9% (308/411)	91.1% (82/90)	98.9% (91/92)	56.8% (552/971)
TOTAL CENTRAL EAST	**15% (191/1,273)**	**68.3% (821/1202)**	**89.6% (318/355)**	**98.2% (335/341)**	**52.5% (1,665/3,171)**

WHO label/Pango lineage	Week 49 (December 05 to December 11)	Week 50 (December 12 to December 18)	Week 51 (December 19 to December 25)	Week 52 (December 26 to January 01)	Total (December 5 to January 1)
Toronto Public Health	22.5% (149/661)	78.5% (812/1,035)	94.4% (386/409)	99.0% (675/682)	72.6% (2,022/2,787)
TOTAL TORONTO	**22.5% (149/661)**	**78.5% (812/1,035)**	**94.4% (386/409)**	**99.0% (675/682)**	**72.6% (2,022/2,787)**
Chatham-Kent Public Health	0.0% (0/35)	10.0% (1/10)	100% (2/2)	0.0% (0/0)	6.4% (3/47)
Grey Bruce Health Unit	28.6% (4/14)	84.6% (11/13)	100% (1/1)	100% (9/9)	67.6% (25/37)
Huron Perth Public Health	4.8% (1/21)	25.0% (4/16)	33.3% (1/3)	100% (4/4)	22.7% (10/44)
Lambton Public Health	0.0% (0/10)	0.0% (0/7)	0.0% (0/1)	87.5% (7/8)	26.9% (7/26)
Middlesex-London Health Unit	27.4% (23/84)	63.2% (43/68)	100% (25/25)	100% (28/28)	58.0% (119/205)
Southwestern Public Health	2.4% (1/41)	20.8% (5/24)	66.7% (2/3)	100% (2/2)	14.3% (10/70)
Windsor-Essex County Health Unit	0.0% (0/120)	11.3% (9/80)	0.0% (0/1)	100% (2/2)	5.4% (11/203)
TOTAL SOUTH WEST	**8.9% (29/325)**	**33.5% (73/218)**	**86.1% (31/36)**	**98.1% (52/53)**	**29.3% (185/632)**
Brant County Health Unit	8.9% (5/56)	48.4% (15/31)	50.0% (2/4)	100% (13/13)	33.7% (35/104)
City of Hamilton Public Health Services	13.7% (32/233)	58.5% (186/318)	77.5% (100/129)	96.5% (164/170)	56.7% (482/850)
Haldimand-Norfolk Health Unit	0.0% (0/35)	28.0% (7/25)	66.7% (6/9)	100% (10/10)	29.1% (23/79)
Halton Region Public Health	34.5% (71/206)	76.6% (151/197)	94.2% (49/52)	100% (58/58)	64.1% (329/513)
Niagara Region Public Health	5.0% (5/100)	27.7% (23/83)	100% (15/15)	93.3% (28/30)	31.1% (71/228)
Region of Waterloo Public Health and Emergency Services	23.4% (43/184)	59.0% (82/139)	78.1% (57/73)	91.1% (82/90)	54.3% (264/486)
Wellington-Dufferin-Guelph Public Health	19.7% (15/76)	54.7% (29/53)	88.9% (8/9)	94.4% (17/18)	44.2% (69/156)
TOTAL CENTRAL WEST	**19.2% (171/890)**	**58.3% (493/846)**	**81.4% (237/291)**	**95.6% (372/389)**	**52.7% (1,273/2,416)**
UNKNOWN	0.0% (0/0)	71.4% (5/7)	100% (17/17)	98.1% (53/54)	96.2% (75/78)
TOTAL ONTARIO	**20.8% (873/4,190)**	**66.1% (2,588/3,916)**	**89.8% (1,192/1,328)**	**97.5% (1,944/1,993)**	**57.7% (6,597/1,1427)**

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 (4.5%), 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 4. Number and percentage (row %) of cases by vaccine category and Pango lineage, representative surveillance, Ontario, December 5, 2021 to January 1, 2022

WHO label / Pango lineage	Unvaccinated	Partially vaccinated	Breakthrough (i.e., fully vaccinated)	Post-dose 3	Total cases
Delta	**2,190 (47.1%)**	**133 (2.9%)**	**2,298 (49.4%)**	**32 (0.7%)**	**4,653 (100%)**
AY.25	812 (49.2%)	62 (3.8%)	767 (46.5%)	9 (0.5%)	1,650 (100%)
AY.103	437 (48.6%)	24 (2.7%)	434 (48.2%)	5 (0.6%)	900 (100%)
B.1.617.2	87 (43.7%)	4 (2.0%)	106 (53.3%)	2 (1.0%)	199 (100%)
AY.122	76 (38.8%)	1 (0.5%)	117 (59.7%)	2 (1.0%)	196 (100%)
AY.74	127 (65.5%)	8 (4.1%)	58 (29.9%)	1 (0.5%)	194 (100%)
AY.3	69 (42.3%)	2 (1.2%)	91 (55.8%)	1 (0.6%)	163 (100%)
AY.44	60 (38.7%)	3 (1.9%)	91 (58.7%)	1 (0.6%)	155 (100%)
AY.4	74 (49.7%)	5 (3.4%)	69 (46.3%)	1 (0.7%)	149 (100%)
AY.27	68 (48.9%)	6 (4.3%)	63 (45.3%)	2 (1.4%)	139 (100%)
AY.4.2	1 (50.0%)	0 (0.0%)	1 (50.0%)	0 (0.0%)	2 (100%)
Other Delta	379 (41.8%)	18 (2.0%)	501 (55.3%)	8 (0.9%)	906 (100%)
Omicron	**1,124 (18.0%)**	**171 (2.7%)**	**4,781 (76.4%)**	**183 (2.9%)**	**6,259 (100%)**
B.1.1.529	1,124 (18.0%)	171 (2.7%)	4,781 (76.4%)	183 (2.9%)	6,259 (100%)
Other lineages	**4 (66.7%)**	**0 (0.0%)**	**2 (33.3%)**	**0 (0.0%)**	**6 (100%)**
Total sequenced	**3,318 (30.4%)**	**304 (2.8%)**	**7,081 (64.9%)**	**215 (2.0%)**	**10,918 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). Cases include those that linked to CCM (95.5%). Individuals with a vaccine not approved by Health Canada were excluded. Vaccine category definitions are included in the technical notes. A higher proportion of cases reported in partially vaccinated and breakthrough 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 5a. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North West Region, December 5, 2021 to January 1, 2022

WHO label / Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
Delta	**9 (100%)**	**31 (93.9%)**	**40 (95.2%)**
AY.25	4 (44.4%)	2 (6.1%)	6 (14.3%)
AY.103	0 (0.0%)	6 (18.2%)	6 (14.3%)
B.1.617.2	0 (0.0%)	1 (3.0%)	1 (2.4%)
AY.122	0 (0.0%)	0 (0.0%)	0 (0.0%)
AY.74	0 (0.0%)	0 (0.0%)	0 (0.0%)
AY.3	0 (0.0%)	0 (0.0%)	0 (0.0%)
AY.44	0 (0.0%)	0 (0.0%)	0 (0.0%)
AY.4	0 (0.0%)	0 (0.0%)	0 (0.0%)
AY.27	0 (0.0%)	1 (3.0%)	1 (2.4%)
AY.4.2	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other Delta	5 (55.6%)	21 (63.6%)	26 (61.9%)
Omicron	**0 (0.0%)**	**2 (6.1%)**	**2 (4.8%)**
B.1.1.529	0 (0.0%)	2 (6.1%)	2 (4.8%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**9 (100%)**	**33 (100%)**	**42 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 (4.5%), 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 5b. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North East Region, December 5, 2021 to January 1, 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	**64 (97.0%)**	**15 (83.3%)**	**14 (93.3%)**	**71 (100%)**	**4 (80.0%)**	**168 (96.0%)**
AY.25	0 (0.0%)	6 (33.3%)	3 (20.0%)	0 (0.0%)	0 (0.0%)	9 (5.1%)
AY.103	15 (22.7%)	1 (5.6%)	11 (73.3%)	2 (2.8%)	4 (80.0%)	33 (18.9%)
B.1.617.2	40 (60.6%)	0 (0.0%)	0 (0.0%)	1 (1.4%)	0 (0.0%)	41 (23.4%)
AY.122	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (4.2%)	0 (0.0%)	3 (1.7%)
AY.74	0 (0.0%)	5 (27.8%)	0 (0.0%)	64 (90.1%)	0 (0.0%)	69 (39.4%)
AY.3	6 (9.1%)	1 (5.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	7 (4.0%)
AY.44	1 (1.5%)	1 (5.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.1%)
AY.4	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
AY.27	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
AY.4.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other Delta	2 (3.0%)	1 (5.6%)	0 (0.0%)	1 (1.4%)	0 (0.0%)	4 (2.3%)
Omicron	**2 (3.0%)**	**3 (16.7%)**	**1 (6.7%)**	**0 (0.0%)**	**1 (20.0%)**	**7 (4.0%)**
B.1.1.529	2 (3.0%)	3 (16.7%)	1 (6.7%)	0 (0.0%)	1 (20.0%)	7 (4.0%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**66 (100%)**	**18 (100%)**	**15 (100%)**	**71 (100%)**	**5 (100%)**	**175 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 (4.5%), 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 5c. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Eastern Region, December 5, 2021 to January 1, 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	**59 (41.5%)**	**126 (60.9%)**	**157 (26.1%)**	**127 (58.0%)**	**273 (29.5%)**	**16 (51.6%)**	**758 (35.7%)**
AY.25	5 (3.5%)	120 (58.0%)	143 (23.8%)	95 (43.4%)	42 (4.5%)	0 (0.0%)	405 (19.0%)
AY.103	3 (2.1%)	1 (0.5%)	1 (0.2%)	10 (4.6%)	23 (2.5%)	0 (0.0%)	38 (1.8%)
B.1.617.2	1 (0.7%)	0 (0.0%)	1 (0.2%)	0 (0.0%)	46 (5.0%)	1 (3.2%)	49 (2.3%)
AY.122	4 (2.8%)	1 (0.5%)	0 (0.0%)	0 (0.0%)	6 (0.6%)	0 (0.0%)	11 (0.5%)
AY.74	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (0.2%)	13 (41.9%)	15 (0.7%)
AY.3	16 (11.3%)	3 (1.4%)	0 (0.0%)	3 (1.4%)	30 (3.2%)	1 (3.2%)	53 (2.5%)
AY.44	0 (0.0%)	0 (0.0%)	1 (0.2%)	4 (1.8%)	16 (1.7%)	0 (0.0%)	21 (1.0%)
AY.4	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (0.3%)	0 (0.0%)	3 (0.1%)
AY.27	18 (12.7%)	0 (0.0%)	0 (0.0%)	2 (0.9%)	36 (3.9%)	0 (0.0%)	56 (2.6%)
AY.4.2	0 (0.0%)	0 (0.0%)	1 (0.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (<0.1%)
Other Delta	12 (8.5%)	1 (0.5%)	10 (1.7%)	13 (5.9%)	69 (7.5%)	1 (3.2%)	106 (5.0%)
Omicron	**83 (58.5%)**	**81 (39.1%)**	**444 (73.9%)**	**92 (42.0%)**	**653 (70.5%)**	**15 (48.4%)**	**1,368 (64.3%)**
B.1.1.529	83 (58.5%)	81 (39.1%)	444 (73.9%)	92 (42.0%)	653 (70.5%)	15 (48.4%)	1368 (64.3%)
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	**142 (100%)**	**207 (100%)**	**601 (100%)**	**219 (100%)**	**926 (100%)**	**31 (100%)**	**2,126 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 (4.5%), 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 5d. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central East Region, December 5, 2021 to January 1, 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	**265 (47.7%)**	**41 (58.6%)**	**316 (36.3%)**	**25 (58.1%)**	**435 (66.3%)**	**419 (43.2%)**	**1,501 (47.4%)**
AY.25	71 (12.8%)	14 (20.0%)	88 (10.0%)	6 (14.0%)	199 (30.3%)	173 (17.8%)	551 (17.4%)
AY.103	22 (4.0%)	16 (22.9%)	41 (4.7%)	12 (27.9%)	149 (22.7%)	51 (5.3%)	291 (9.2%)
B.1.617.2	23 (4.1%)	0 (0.0%)	12 (1.4%)	1 (2.3%)	8 (1.2%)	11 (1.1%)	55 (1.7%)
AY.122	19 (3.4%)	2 (2.9%)	32 (3.7%)	0 (0.0%)	4 (0.6%)	19 (2.0%)	76 (2.4%)
AY.74	7 (1.3%)	0 (0.0%)	12 (1.4%)	0 (0.0%)	32 (4.9%)	7 (0.7%)	58 (1.8%)
AY.3	14 (2.5%)	1 (1.4%)	10 (1.1%)	4 (9.3%)	8 (1.2%)	17 (1.8%)	54 (1.7%)
AY.44	2 (0.4%)	0 (0.0%)	8 (0.9%)	0 (0.0%)	2 (0.3%)	7 (0.7%)	19 (0.6%)
AY.4	25 (4.5%)	0 (0.0%)	9 (1.0%)	0 (0.0%)	0 (0.0%)	39 (4.0%)	73 (2.3%)
AY.27	2 (0.4%)	0 (0.0%)	13 (1.5%)	0 (0.0%)	8 (1.2%)	7 (0.7%)	30 (0.9%)
AY.4.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other Delta	80 (14.4%)	8 (11.4%)	91 (10.4%)	2 (4.7%)	25 (3.8%)	88 (9.1%)	294 (9.3%)
Omicron	**290 (52.3%)**	**29 (41.4%)**	**555 (63.7%)**	**18 (41.9%)**	**221 (33.7%)**	**552 (56.8%)**	**1,665 (52.6%)**
B.1.1.529	290 (52.3%)	29 (41.4%)	555 (63.4%)	18 (41.9%)	221 (33.7%)	552 (56.8%)	1,665 (52.5%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**5 (0.6%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**5 (0.2%)**
Total sequenced	**555 (100%)**	**70 (100%)**	**876 (100%)**	**43 (100%)**	**656 (100%)**	**971 (100%)**	**3,171 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 (4.5%), 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 5e. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Toronto Region, December 5, 2021 to January 1, 2022

WHO label / Pango lineage	Toronto Public Health	Total
Delta	**765 (27.4%)**	**765 (27.4%)**
AY.25	197 (7.1%)	197 (7.1%)
AY.103	115 (4.1%)	115 (4.1%)
B.1.617.2	27 (1.0%)	27 (1.0%)
AY.122	93 (3.3%)	93 (3.3%)
AY.74	15 (0.5%)	15 (0.5%)
AY.3	22 (0.8%)	22 (0.8%)
AY.44	18 (0.6%)	18 (0.6%)
AY.4	46 (1.7%)	46 (1.7%)
AY.27	30 (1.1%)	30 (1.1%)
AY.4.2	0 (0.0%)	0 (0.0%)
Other Delta	202 (7.2%)	202 (7.2%)
Omicron	**2,022 (72.6%)**	**2,022 (72.6%)**
B.1.1.529	2,022 (72.6%)	2,022 (72.6%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**
Total sequenced	**2,787 (100%)**	**2,787 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 (4.5%), 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 5f. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, South West Region, December 5, 2021 to January 1, 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	**44 (93.6%)**	**12 (32.4%)**	**34 (77.3%)**	**19 (73.1%)**	**86 (42.0%)**	**60 (85.7%)**	**192 (94.6%)**	**447 (70.7%)**
AY.25	2 (4.3%)	4 (10.8%)	15 (34.1%)	9 (34.6%)	23 (11.2%)	32 (45.7%)	27 (13.3%)	112 (17.7%)
AY.103	13 (27.7%)	0 (0.0%)	12 (27.3%)	4 (15.4%)	25 (12.2%)	20 (28.6%)	118 (58.1%)	192 (30.4%)
B.1.617.2	1 (2.1%)	2 (5.4%)	1 (2.3%)	0 (0.0%)	2 (1.0%)	1 (1.4%)	3 (1.5%)	10 (1.6%)
AY.122	0 (0.0%)	1 (2.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.2%)
AY.74	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	6 (2.9%)	0 (0.0%)	0 (0.0%)	6 (0.9%)
AY.3	0 (0.0%)	1 (2.7%)	2 (4.5%)	0 (0.0%)	1 (0.5%)	0 (0.0%)	8 (3.9%)	12 (1.9%)
AY.44	1 (2.1%)	0 (0.0%)	0 (0.0%)	2 (7.7%)	6 (2.9%)	2 (2.9%)	2 (1.0%)	13 (2.1%)
AY.4	1 (2.1%)	0 (0.0%)	0 (0.0%)	2 (7.7%)	0 (0.0%)	1 (1.4%)	9 (4.4%)	13 (2.1%)
AY.27	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	12 (5.9%)	1 (1.4%)	10 (4.9%)	23 (3.6%)
AY.4.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other Delta	26 (55.3%)	4 (10.8%)	4 (9.1%)	2 (7.7%)	11 (5.4%)	3 (4.3%)	15 (7.4%)	65 (10.3%)
Omicron	**3 (6.4%)**	**25 (67.6%)**	**10 (22.7%)**	**7 (26.9%)**	**119 (58.0%)**	**10 (14.3%)**	**11 (5.4%)**	**185 (29.3%)**
B.1.1.529	3 (6.4%)	25 (67.6%)	10 (22.7%)	7 (26.9%)	119 (58.0%)	10 (14.3%)	11 (5.4%)	185 (29.3%)
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	**47 (100%)**	**37 (100%)**	**44 (100%)**	**26 (100%)**	**205 (100%)**	**70 (100%)**	**203 (100%)**	**632 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 (4.5%), 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 5g. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central West Region, December 5, 2021 to January 1, 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	**69 (66.3%)**	**368 (43.3%)**	**56 (70.9%)**	**184 (35.9%)**	**157 (68.9%)**	**220 (45.5%)**	**87 (56.1%)**	**1,141 (47.3%)**
AY.25	16 (15.4%)	149 (17.5%)	17 (21.5%)	51 (10.0%)	54 (23.7%)	88 (18.1%)	48 (31.0%)	423 (17.5%)
AY.103	12 (11.5%)	52 (6.1%)	21 (26.6%)	54 (10.5%)	32 (14.0%)	55 (11.3%)	20 (12.9%)	246 (10.2%)
B.1.617.2	1 (1.0%)	7 (0.8%)	1 (1.3%)	11 (2.1%)	1 (0.4%)	8 (1.6%)	1 (0.6%)	30 (1.2%)
AY.122	0 (0.0%)	2 (0.2%)	0 (0.0%)	9 (1.8%)	2 (0.9%)	7 (1.4%)	1 (0.6%)	21 (0.9%)
AY.74	9 (8.7%)	13 (1.5%)	1 (1.3%)	5 (1.0%)	1 (0.4%)	6 (1.2%)	0 (0.0%)	35 (1.4%)
AY.3	1 (1.0%)	4 (0.5%)	2 (2.5%)	2 (0.4%)	3 (1.3%)	6 (1.2%)	1 (0.6%)	19 (0.8%)
AY.44	25 (24.0%)	23 (2.7%)	6 (7.6%)	14 (2.7%)	13 (5.7%)	6 (1.2%)	3 (1.9%)	90 (3.7%)
AY.4	0 (0.0%)	9 (1.1%)	0 (0.0%)	1 (0.2%)	4 (1.8%)	2 (0.4%)	1 (0.6%)	17 (0.7%)
AY.27	1 (1.0%)	1 (0.1%)	0 (0.0%)	4 (0.8%)	0 (0.0%)	0 (0.0%)	2 (1.3%)	8 (0.3%)
AY.4.2	0 (0.0%)	1 (0.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (<0.1%)
Other Delta	4 (3.8%)	107 (12.6%)	8 (10.1%)	33 (6.4%)	47 (20.6%)	42 (8.6%)	10 (6.5%)	251 (10.4%)
Omicron	**35 (33.7%)**	**482 (56.7%)**	**23 (29.1%)**	**329 (64.1%)**	**71 (31.1%)**	**264 (54.5%)**	**69 (44.2%)**	**1,273 (52.7%)**
B.1.1.529	35 (33.7%)	482 (56.7%)	23 (29.1%)	329 (64.1%)	71 (31.1%)	264 (54.3%)	69 (44.2%)	1,273 (52.7%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**2 (0.4%)**	**0 (0.0%)**	**2 (0.1%)**
Total sequenced	**104 (100%)**	**850 (100%)**	**79 (100%)**	**513 (100%)**	**228 (100%)**	**486 (100%)**	**156 (100%)**	**2,416 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). 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 (4.5%), 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 6. Number and percentage (row %) of outbreak-associated and non outbreak-associated cases by Pango lineage, representative surveillance, Ontario, December 5, 2021 to January 1, 2022

WHO label / Pango lineage	Outbreak-associated	Non outbreak-associated	Total cases
Delta	**765 (16.4%)**	**3,888 (83.6%)**	**4,653 (100%)**
AY.25	313 (19.0%)	1,337 (81.0%)	1,650 (100%)
AY.103	127 (14.1%)	773 (85.9%)	900 (100%)
B.1.617.2	44 (22.1%)	155 (77.9%)	199 (100%)
AY.122	28 (14.3%)	168 (85.7%)	196 (100%)
AY.74	18 (9.3%)	176 (90.7%)	194 (100%)
AY.3	19 (11.7%)	144 (88.3%)	163 (100%)
AY.44	25 (16.1%)	130 (83.9%)	155 (100%)
AY.4	38 (25.5%)	111 (74.5%)	149 (100%)
AY.27	22 (15.8%)	117 (84.2%)	139 (100%)
AY.4.2	0 (0.0%)	2 (100%)	2 (100%)
Other Delta	131 (14.5%)	775 (85.5%)	906 (100%)
Omicron	**645 (10.3%)**	**5,614 (89.7%)**	**6,259 (100%)**
B.1.1.529	645 (10.3%)	5,614 (89.7%)	6,259 (100%)
Other lineages	**3 (50.0%)**	**3 (50.0%)**	**6 (100%)**
Total sequenced	**1,413 (13.0%)**	**9,505 (87.0%)**	**10,918 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). Cases include only those that linked to CCM (95.5%). '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)

Table 7. Number and percentage (row %) of ever hospitalized and deceased cases by Pango lineage, representative surveillance, Ontario, December 5, 2021 to January 1, 2022

WHO label / Pango lineage	Ever hospitalized	Deceased	Total cases
Delta	**152 (3.3%)**	**32 (0.7%)**	**4,653 (100%)**
AY.25	62 (3.8%)	17 (1.0%)	1,650 (100%)
AY.103	24 (2.7%)	5 (0.6%)	900 (100%)
B.1.617.2	0 (0.0%)	0 (0.0%)	199 (100%)
AY.122	10 (5.1%)	3 (1.5%)	196 (100%)
AY.74	4 (2.1%)	1 (0.5%)	194 (100%)
AY.3	3 (1.8%)	1 (0.6%)	163 (100%)
AY.44	9 (5.8%)	1 (0.6%)	155 (100%)
AY.4	3 (2.0%)	0 (0.0%)	149 (100%)
AY.27	1 (0.7%)	0 (0.0%)	139 (100%)
AY.4.2	0 (0.0%)	0 (0.0%)	2 (100%)
Other Delta	36 (4.0%)	4 (0.4%)	906 (100%)
Omicron	**43 (0.7%)**	**3 (0.0%)**	**6,259 (100%)**
B.1.1.529	43 (0.7%)	3 (0.0%)	6,259 (100%)
Other lineages	**0 (0.0%)**	**0 (0.0%)**	**6 (100%)**
Total sequenced	**195 (1.8%)**	**35 (0.3%)**	**10,918 (100%)**

Note: Includes most prevalent Delta lineages detected in the past month, AY.4.2, and Omicron (B.1.1.529). Cases include only those that linked to CCM (95.5%). Hospitalized cases include cases that reported hospitalization at time of data extraction. Deceased cases include cases that reported a “Fatal” outcome at the time of data extraction. Hospitalized cases and deceased cases are not mutually exclusive. 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 and death indicators)

Cumulative Whole Genome Sequencing Results

Table 8. Number of cases by Pango lineage, cumulative counts, Ontario, January 1, 2021 to December 25, 2021

WHO label / Pango lineage	January 1, 2021 – December 4, 2021	December 5, 2021 – January 1, 2022	Total
Variant of concern (VOC)			
Alpha	**11,890**	**0**	**11,890**
B.1.1.7	11,885	0	11,885
Q.1	5	0	5
Beta	**1,236**	**0**	**1,236**
B.1.351	1,197	0	1,197
B.1.351.2	3	0	3
B.1.351.3	**17**	**0**	**17**
B.1.351.5	19	0	19
Gamma	**3,934**	**0**	**3,934**
P.1	225	0	225
P.1.10	2	0	2
P.1.12	3	0	3
P.1.14	3,666	0	3,666
P.1.16	1	0	1
P.1.17	33	0	33
P.1.7	4	0	4
Delta	**40,054**	**5,606**	**45,660**
B.1.617.2	1,667	266	1,933
AY.1	3	0	3
AY.10	24	0	24
AY.100	100	13	113
AY.101	**1**	**2**	**3**
AY.102	136	10	146
AY.103	3,938	1,083	5,021
AY.104	5	1	6
AY.105	2	0	2
AY.106	55	1	56
AY.107	61	4	65
AY.108	56	3	59
AY.109	22	0	22
AY.11	5	11	16
AY.110	35	4	39
AY.111	5	1	6
AY.113	27	8	35
AY.114	9	0	9
AY.116	68	0	68
AY.116.1	10	0	10

WHO label / Pango lineage	January 1, 2021 – December 4, 2021	December 5, 2021 – January 1, 2022	Total
AY.117	91	29	120
AY.118	32	4	36
AY.119	495	55	550
AY.119.1	5	1	6
AY.120	43	2	45
AY.120.1	2	3	5
AY.120.2	4	0	4
AY.121	101	18	119
AY.121.1	1	0	1
AY.122	1,134	224	1,358
AY.122.1	10	0	10
AY.123	1	0	1
AY.124	25	0	25
AY.125	50	10	60
AY.126	123	13	136
AY.127	310	102	412
AY.13	149	0	149
AY.14	69	4	73
AY.15	102	0	102
AY.16	123	0	123
AY.16.1	3	0	3
AY.17	12	0	12
AY.19	149	1	150
AY.2	2	0	2
AY.20	167	25	192
AY.21	38	0	38
AY.23	13	0	13
AY.24	100	35	135
AY.25	8,555	1,931	10,486
AY.26	115	6	121
AY.27	2,825	172	2,997
AY.28	34	0	34
AY.29	5	0	5
AY.29.1	1	0	1
AY.3	779	213	992
AY.3.1	9	2	11
AY.32	3	0	3
AY.33	66	20	86
AY.34	23	10	33
AY.34.1	30	0	30
AY.35	6	0	6
AY.36	364	21	385
AY.37	28	0	28
AY.38	6	0	6

WHO label / Pango lineage	January 1, 2021 – December 4, 2021	December 5, 2021 – January 1, 2022	Total
AY.39	234	89	323
AY.39.1	23	6	29
AY.39.1.1	1	0	1
AY.4	539	158	697
AY.4.1	3	0	3
AY.4.2	47	2	49
AY.4.2.1	121	80	201
AY.4.2.2	12	3	15
AY.4.2.3	3	1	4
AY.4.3	1	0	1
AY.4.4	13	0	13
AY.4.5	7	1	8
AY.4.6	5	0	5
AY.40	33	0	33
AY.41	3	0	3
AY.42	21	9	30
AY.43	524	94	618
AY.43.3	1	0	1
AY.43.4	5	0	5
AY.44	1,028	195	1,223
AY.45	133	0	133
AY.46	59	0	59
AY.46.1	8	0	8
AY.46.4	6	0	6
AY.46.5	3	2	5
AY.46.6	272	108	380
AY.47	103	21	124
AY.48	1	0	1
AY.49	3	0	3
AY.5	30	1	31
AY.5.2	1	0	1
AY.5.3	11	0	11
AY.5.4	7	0	7
AY.51	20	0	20
AY.53	5	0	5
AY.54	16	0	16
AY.55	17	0	17
AY.56	51	0	51
AY.57	11	2	13
AY.58	27	10	37
AY.59	8	4	12
AY.6	10	0	10
AY.61	469	3	472
AY.62	4	0	4

WHO label / Pango lineage	January 1, 2021 – December 4, 2021	December 5, 2021 – January 1, 2022	Total
AY.64	11	0	11
AY.65	19	2	21
AY.66	1	1	2
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	14	0	14
AY.71	1	0	1
AY.72	3	0	3
AY.73	3	0	3
AY.74	11,910	290	12,200
AY.75	392	66	458
AY.75.2	4	0	4
AY.76	55	0	55
AY.77	4	3	7
AY.78	4	1	5
AY.80	3	0	3
AY.82	0	1	1
AY.83	11	0	11
AY.84	3	3	6
AY.85	2	0	2
AY.86	147	36	183
AY.87	7	0	7
AY.88	53	26	79
AY.89	3	0	3
AY.9	47	0	47
AY.9.2	196	47	243
AY.9.2.1	630	16	646
AY.91	1	0	1
AY.92	15	0	15
AY.93	102	3	105
AY.94	10	0	10
AY.95	3	0	3
AY.96	1	0	1
AY.98	26	2	28
AY.98.1	20	3	23
AY.99	3	2	5
AY.99.2	12	7	19
Omicron	**125**	**7,723**	**7,848**
B.1.1.529	125	7,723	7,848
Variant of interest (VOI)			
Mu	**243**	**0**	**243**

WHO label / Pango lineage	January 1, 2021 – December 4, 2021	December 5, 2021 – January 1, 2022	Total
B.1.621	232	0	232
B.1.621.1	11	0	11
Lambda	**8**	**0**	**8**
C.37	8	0	8
Non-VOC/VOI	**6,195**	**8**	**6,203**
Total sequenced	**63,685**	**13,337**	**77,022**

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 January 13, 2022 at approximately 6:30 a.m.

- Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on January 13, 2022 at approximately 3:00 p.m.

The Hospital for Sick Children (HSC)

- Data were received by PHO on January 12, 2022 at approximately 4:30 p.m.

Kingston Health Sciences Centre (KHSC)

- Data were received by PHO on January 12, 2022 at approximately 11:00 a.m.

Shared Hospital Laboratory (SHL)

- Data were received by PHO on January 12, 2022 at approximately 4:00 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were received by PHO on January 13, 2022 at approximately 1:00 a.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on January 4, 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 January 11, 2022 at approximately 7:00 a.m. for vaccination records created on or after Jun 1, 2021. Data were extracted on January 6, 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; and 5% on December 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; 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; and 5% on December 30. 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 (4.5%), 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.

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 include only cases that linked to CCM (96.2% of cases).
- 'Outbreak-associated cases' include cases linked to a confirmed outbreak as declared by the local medical officer of health or their designate in accordance to the Health Protection and Promotion Act and criteria outlined in Ministry guidance documents.
- Outbreaks in settings outside of Ontario are excluded from all outbreak counts.

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

- 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.

- Deaths are determined by using the outcome field in CCM. Any case marked 'Fatal' is included in the deaths data. The CCM field Type of Death is not used to further categorize the data.

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 partially vaccinated and breakthrough cases 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.

- The definitions for partially vaccinated and breakthrough cases used in this report were modelled after proposed national definitions, and do not necessarily align with those used in other jurisdictions. Further, the definitions may be revised over time.

  - **Unvaccinated case:** Cases that have not received a dose of a COVID-19 vaccine, as well as cases that are not yet protected from vaccination (0 to 13 days following the first dose of a Health Canada authorized COVID-19 vaccine) as this time period from vaccination is not sufficient to develop immunity, therefore these cases are not considered protected from vaccination.

  - **Partially vaccinated case:** Cases with a symptom onset date that was 14 or more days following the first dose of a 2-dose series of a Health Canada authorized COVID-19 vaccine or 0 to <14 days after receiving the second dose of a 2-dose Health Canada authorized COVID-19 vaccine series. This time period from vaccination may be sufficient to develop some degree of immunity, but these cases are not considered fully protected as they have not yet received the second dose or have only recently received the second dose.

  - **Breakthrough (i.e., fully vaccinated) case**: Cases with a symptom onset date that was 14 or more days following receipt of the second dose of a 2-dose series of a Health Canada authorized COVID-19 vaccine, 14 or more days following the first dose of a Health Canada authorized COVID-19 vaccine product with a 1-dose schedule, or 0 to <14 days after receiving the third dose of a Health Canada authorized COVID-19 vaccine. These cases are considered fully protected from vaccination, however, as vaccine effectiveness is not 100%, it is expected that a small number of cases will occur among fully vaccinated individuals.

  - **Post-dose 3 case (i.e. cases following a third dose):** Cases with a symptom onset date that was 14 or more days following the receipt of a third dose of a Health Canada authorized COVID-19 vaccine, following two doses of Health Canada authorized COVID-19 vaccine products. The third dose is recommended to complete a primary series for select immunocompromised individuals and as a booster for waning immunity in select populations, including older adults.

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