Public Health Ontario | Santé publique Ontario

WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, October 16, 2023

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by the Ontario COVID-19 Genomics Network as of October 11, 2023.

Background

The continued monitoring of global SARS-CoV-2 genomic data has identified changes in the genome as it spreads through populations. These random changes or mutations arise as a virus evolves over time. The accumulation of these mutations can result in a new lineage of the virus, which is a common occurrence. These new lineages will differ slightly in genome sequence and are termed variants. Although many variants will have no difference in the ability to spread or cause disease, some variants have mutations which may enhance virulence, transmissibility, and/or allow the virus to escape natural or vaccine-induced immunity.

The identification of variants and mutations occurs through whole genome sequencing (WGS) of select samples. Through global surveillance of SARS-CoV-2 genomes, a number of variants have been identified with evidence of clinical and/or public health significance, termed variants of concern (VOC). Variants designated as VOCs include B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta), and B.1.1.529 (Omicron), some of which have been de-escalated due to their diminishing prevalence globally. WGS has also identified a number of variants of interest (VOI), which may share one or more mutations in common with a VOC, but do not have sufficient evidence at this time to be categorized as a VOC (i.e. evidence of increased transmissibility, disease severity, or immune escape). These variants are also characterized and monitored through genomic surveillance. A VOI may be re-classified as a VOC where there is sufficient scientific evidence to support this designation. The VOC/VOI categories used in this report were derived from the Public Health Agency of Canada (PHAC)[1], the World Health Organization (WHO)[2], and the European Centre for Disease Prevention and Control (ECDC).[3]

As SARS-CoV-2 continues to evolve, lineages will naturally divide into descendant sub-lineages - a genetically closely related group derived from a common ancestor. The descendant branches are given new lineage aliases, such as for B.1.1.529 (Omicron) lineages (e.g., BA.1 [alias for B.1.1.529.1], BA.5 [alias for B.1.1.529.5]), and BA.5 sublineages (e.g., BQ.1, BF.7). When a host is infected with two or more descendant lineages, lineages can recombine to form a new recombinant lineage (e.g., BA.2.10.1 and BA.2.75 recombine to form XBB). New designations represent refined genetic groups that can be tracked separately. As more research is conducted, there may be evidence of an important difference in terms of transmissibility, severity, or immune escape, at which time a new WHO Greek letter classification may be assigned to a lineage.

The Ontario COVID-19 Genomics Network (OCGN) performs WGS on samples received for SARS-CoV-2 diagnostic testing or VOC PCR testing. Sequences are processed using bioinformatics analyses and assigned a Pango lineage[4] using the pangolin tool[5], allowing for the identification of VOC, VOI and other lineages.

Highlights

- In the most recent week (September 24 to September 30), a total of 1,954 cases were sequenced. EG.5.1.1 was the most prevalent lineage (13.7%), followed by HV.1 (12.4%), XBB.1.16.6 (9.2%), and HK.3 (8.2%).
- The proportion of EG.5.1.1 remained stable at 14.5% (September 17 to September 23) and 13.7% (September 24 to September 30).
    - Based on the Nowcast model, EG.5.1.1 is projected to decrease to 7.3% (95% CI: 5.7% - 9.3%) by October 18, 2023.
- The proportion of HV.1 increased from 7.1% (September 17 to September 23) to 12.4% (September 24 to September 30).
    - Based on the Nowcast model, HV.1 is projected to increase to 22.4% (95% CI: 16.8% - 29.2%) by October 18, 2023. The weekly growth rate of HV.1 is 1.53 (95% CI: 1.42 - 1.66) times that of EG.5.1.1.

> Due to global interest, BA.2.86 has been added to the tables throughout the report. Lineage counts may change between reports as the Pango lineage assignment models are updated.

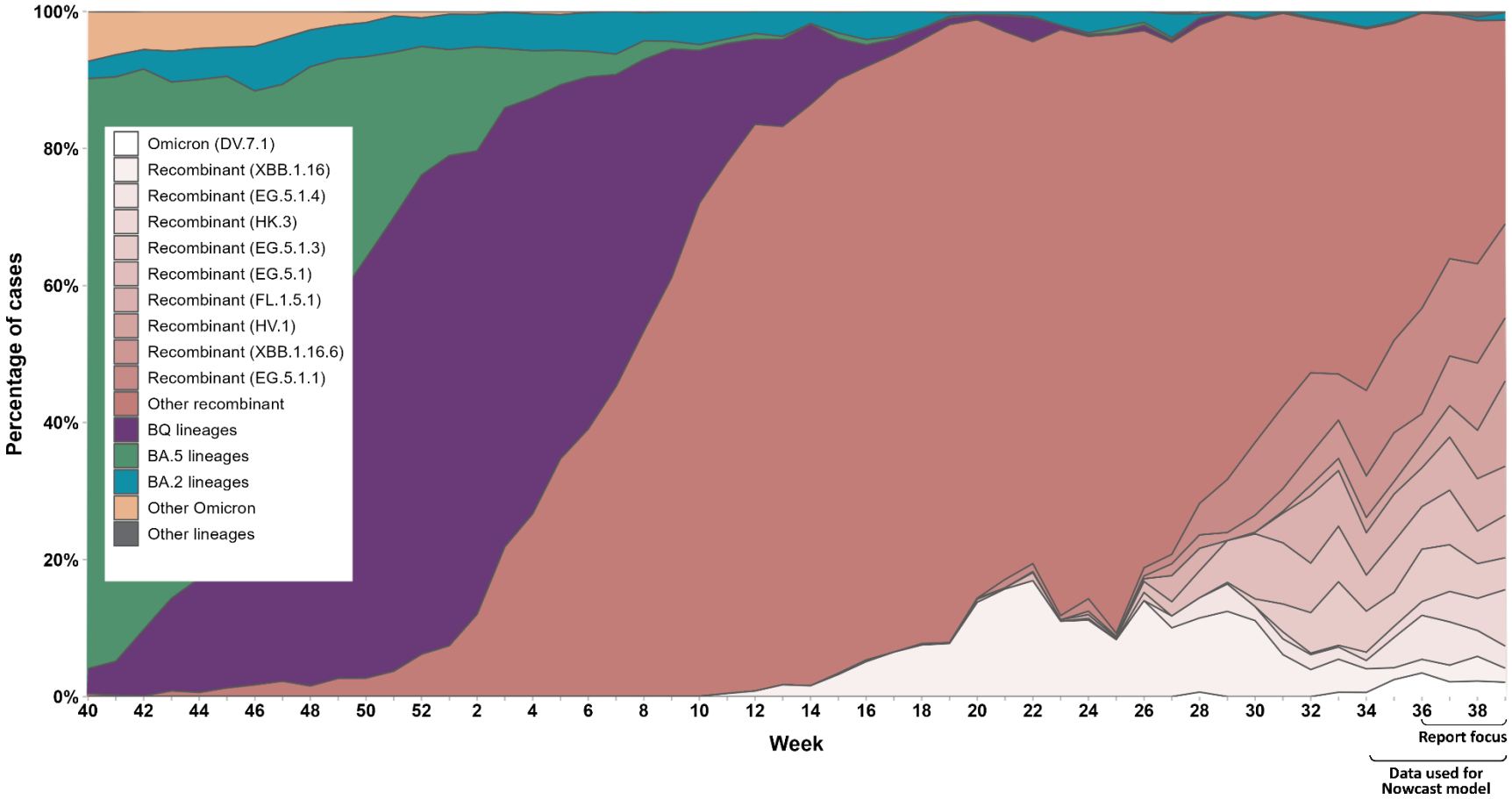
Representative Surveillance

Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, September 3 to September 30, 2023

Week	Number of cases	Number sequenced	Percentage sequenced
Week 36 (September 3 - September 9)	1,956	1,306	66.8%
Week 37 (September 10 - September 16)	2,229	1,394	62.5%
Week 38 (September 17 - September 23)	2,869	1,855	64.7%
Week 39 (September 24 - September 30)	3,298	1,954	59.2%
Total	10,352	6,509	62.9%

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

Figure 1. Percentage of COVID-19 cases by the most prevalent lineages and week, representative surveillance, Ontario, October 2, 2022 to September 30, 2023



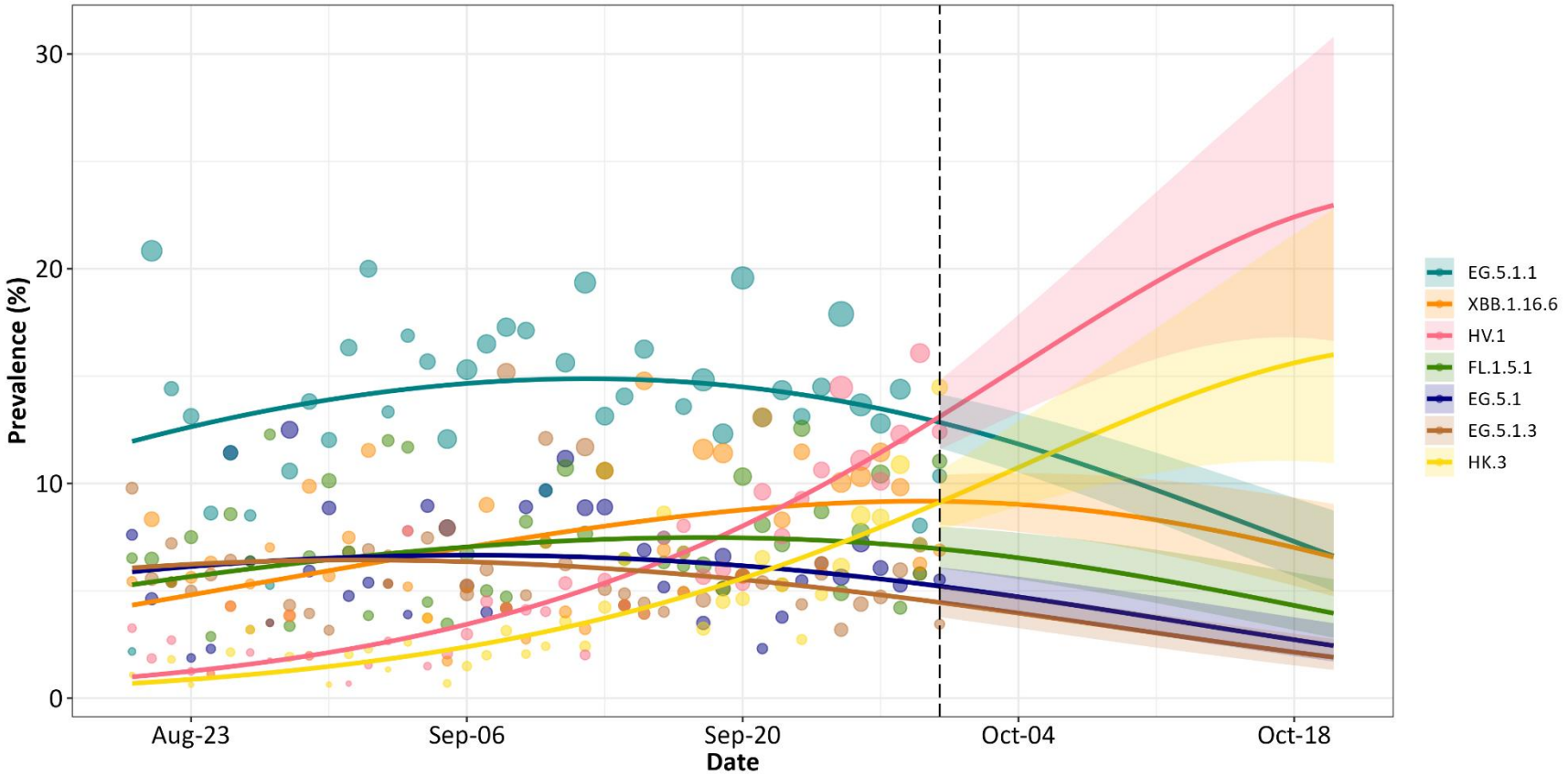
Note: Results may not be representative of Ontario overall, particularly in earlier weeks. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for a case, the most recent sample was included. Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction and will be included in subsequent reports.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 2. Number and percentage of cases by Pango lineage and week, representative surveillance, Ontario, September 3 to September 30, 2023

Pango lineage	Week 36 (September 3 - September 9)	Week 37 (September 10 - September 16)	Week 38 (September 17 - September 23)	Week 39 (September 24 - September 30)	Total (September 3 - September 30)
EG.5.1.1	201 (15.4%)	198 (14.2%)	269 (14.5%)	268 (13.7%)	936 (14.4%)
XBB.1.16.6	58 (4.4%)	101 (7.2%)	182 (9.8%)	180 (9.2%)	521 (8.0%)
HV.1	45 (3.4%)	64 (4.6%)	131 (7.1%)	243 (12.4%)	483 (7.4%)
FL.1.5.1	74 (5.7%)	108 (7.7%)	142 (7.7%)	140 (7.2%)	464 (7.1%)
EG.5.1	81 (6.2%)	111 (8.0%)	88 (4.7%)	121 (6.2%)	401 (6.2%)
EG.5.1.3	100 (7.7%)	95 (6.8%)	94 (5.1%)	91 (4.7%)	380 (5.8%)
HK.3	26 (2.0%)	62 (4.4%)	87 (4.7%)	161 (8.2%)	336 (5.2%)
EG.5.1.4	84 (6.4%)	88 (6.3%)	70 (3.8%)	63 (3.2%)	305 (4.7%)
XBB.1.16	26 (2.0%)	34 (2.4%)	67 (3.6%)	40 (2.0%)	167 (2.6%)
DV.7.1	45 (3.4%)	30 (2.2%)	42 (2.3%)	41 (2.1%)	158 (2.4%)
EG.6.1	26 (2.0%)	33 (2.4%)	39 (2.1%)	42 (2.1%)	140 (2.2%)
GK.1.1	19 (1.5%)	35 (2.5%)	46 (2.5%)	39 (2.0%)	139 (2.1%)
GJ.1.2	40 (3.1%)	12 (0.9%)	36 (1.9%)	32 (1.6%)	120 (1.8%)
XBB.1.16.11	35 (2.7%)	26 (1.9%)	34 (1.8%)	25 (1.3%)	120 (1.8%)
EG.5.1.6	35 (2.7%)	22 (1.6%)	29 (1.6%)	21 (1.1%)	107 (1.6%)
BA.2.86	1 (0.1%)	2 (0.1%)	6 (0.3%)	16 (0.8%)	25 (0.4%)
Other recombinant	408 (31.2%)	370 (26.5%)	488 (26.3%)	424 (21.7%)	1,690 (26.0%)
Other Omicron	2 (0.2%)	3 (0.2%)	5 (0.3%)	7 (0.4%)	17 (0.3%)
Total sequenced	**1,306 (100%)**	**1,394 (100%)**	**1,855 (100%)**	**1,954 (100%)**	**6,509 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Week was assigned based on the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Figure 2. Estimated daily prevalence (%) by Pango lineage, using Nowcast model, Ontario, August 20, 2023 to October 21, 2023



Note: Each curve represents the estimated prevalence of a given lineage from Nowcast modelling, which uses six weeks of daily representative surveillance data in a multinomial logistic regression. Each set of dots represents the observed daily prevalence of a given lineage, while their size represents the relative number of samples. The vertical dashed line indicates the most recent day of data, after which projected Nowcast prevalence estimates are presented with their 95% confidence intervals. The vertical grey lines indicate the mid-point of the week. Lineages with at least 21 days of non-zero case counts were included in the model and lineages that did not have at least 21 days of non-zero case counts were included but not shown. Figure includes all lineages with at least one day of an estimated prevalence of 5% or greater during the 12 week period (six observed and six projected). Only three weeks of projected data are shown. Prevalence projections may be overestimated for emerging lineages.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 3. Estimated prevalence (%), projected prevalence (%), and weekly relative growth rate (with 95% confidence intervals) by Pango lineage, using Nowcast model, Ontario, August 20, 2023 to October 21, 2023

Pango lineage	Week 38 (September 20): Estimated	Week 39 (September 27): Estimated	Week 40 (October 4): Projected	Week 41 (October 11): Projected	Week 42 (October 18): Projected	Weekly relative growth rate
EG.5.1.1	14.5 (13.6 - 15.4)	13.5 (12.4 - 14.7)	11.8 (10.5 - 13.3)	9.7 (8.2 - 11.4)	7.3 (5.7 - 9.3)	1.00 (reference)
XBB.1.16.6	8.8 (8.1 - 9.5)	9.2 (8.2 - 10.2)	9.0 (7.8 - 10.5)	8.3 (6.7 - 10.2)	7.0 (5.2 - 9.3)	1.12 (1.06 - 1.19)
HV.1	8.0 (7.4 - 8.7)	11.4 (10.3 - 12.7)	15.4 (13.3 - 17.9)	19.4 (15.8 - 23.6)	22.4 (16.8 - 29.2)	1.53 (1.42 - 1.66)
FL.1.5.1	7.5 (6.8 - 8.2)	7.2 (6.4 - 8.1)	6.5 (5.5 - 7.7)	5.5 (4.4 - 6.9)	4.3 (3.2 - 5.9)	1.04 (0.97 - 1.10)
EG.5.1	6.2 (5.6 - 6.8)	5.6 (4.8 - 6.4)	4.7 (3.9 - 5.7)	3.7 (2.9 - 4.8)	2.7 (2.0 - 3.8)	0.97 (0.91 - 1.03)
EG.5.1.3	5.5 (5.0 - 6.1)	4.8 (4.2 - 5.6)	4.0 (3.3 - 4.8)	3.0 (2.4 - 3.9)	2.1 (1.5 - 3.0)	0.94 (0.88 - 1.00)
HK.3	5.6 (5.0 - 6.2)	8.0 (7.0 - 9.1)	10.7 (8.9 - 12.9)	13.5 (10.5 - 17.2)	15.6 (11.1 - 21.6)	1.54 (1.41 - 1.68)
Other lineages	11.7 (10.9 - 12.6)	9.3 (8.4 - 10.2)	6.9 (6.0 - 7.9)	4.8 (4.0 - 5.8)	3.1 (2.4 - 4.0)	0.85 (0.81 - 0.89)

Note: The Nowcast model uses six weeks of daily representative surveillance data in a multinomial logistic regression that estimates and projects the prevalence of SARS-CoV-2 lineages. The weekly relative growth rate is a measure of a lineage's growth rate relative to the reference lineage and is estimated in the Nowcast model. The weekly relative growth rate and projections may be overestimated for emerging lineages. The prevalence estimates and projections presented are from the Wednesday (mid-point) of the specified week. Lineages with at least 21 days of non-zero case counts were included in the model separately. 'Other lineages' includes all lineages that did not have at least 21 days of non-zero case counts. Lineages that had at least one day with a prevalence of 5% or greater in the 12 week period (six observed and six projected) were included in the table. Only two weeks of observed and three weeks of projected data are shown. Prevalence estimates are based on the model and are not expected to be the same as the observed data (e.g. Table 2). Details on the methodology used to calculate Nowcast prevalence estimates, projections, and the weekly relative growth rates can be found in the technical notes.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 4. Number and percentage of cases by Pango lineage and age group, representative surveillance, Ontario, September 3 to September 30, 2023

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
EG.5.1.1	24 (13.5%)	3 (15.0%)	4 (9.8%)	96 (13.6%)	117 (14.3%)	233 (13.4%)	458 (15.3%)	935 (14.4%)
XBB.1.16.6	13 (7.3%)	3 (15.0%)	4 (9.8%)	43 (6.1%)	67 (8.2%)	128 (7.3%)	263 (8.8%)	521 (8.0%)
HV.1	25 (14.0%)	1 (5.0%)	11 (26.8%)	75 (10.6%)	69 (8.4%)	124 (7.1%)	178 (6.0%)	483 (7.4%)
FL.1.5.1	13 (7.3%)	2 (10.0%)	1 (2.4%)	56 (7.9%)	56 (6.8%)	135 (7.7%)	198 (6.6%)	461 (7.1%)
EG.5.1	5 (2.8%)	0 (0.0%)	0 (0.0%)	50 (7.1%)	56 (6.8%)	117 (6.7%)	173 (5.8%)	401 (6.2%)
EG.5.1.3	10 (5.6%)	2 (10.0%)	3 (7.3%)	48 (6.8%)	50 (6.1%)	83 (4.8%)	183 (6.1%)	379 (5.8%)
HK.3	12 (6.7%)	0 (0.0%)	1 (2.4%)	29 (4.1%)	32 (3.9%)	103 (5.9%)	159 (5.3%)	336 (5.2%)
EG.5.1.4	5 (2.8%)	0 (0.0%)	3 (7.3%)	19 (2.7%)	33 (4.0%)	93 (5.3%)	151 (5.1%)	304 (4.7%)
XBB.1.16	3 (1.7%)	0 (0.0%)	0 (0.0%)	14 (2.0%)	22 (2.7%)	43 (2.5%)	85 (2.8%)	167 (2.6%)
DV.7.1	0 (0.0%)	1 (5.0%)	1 (2.4%)	15 (2.1%)	17 (2.1%)	45 (2.6%)	79 (2.6%)	158 (2.4%)
EG.6.1	3 (1.7%)	1 (5.0%)	0 (0.0%)	12 (1.7%)	13 (1.6%)	35 (2.0%)	75 (2.5%)	139 (2.1%)
GK.1.1	3 (1.7%)	0 (0.0%)	2 (4.9%)	11 (1.6%)	12 (1.5%)	40 (2.3%)	71 (2.4%)	139 (2.1%)
GJ.1.2	5 (2.8%)	0 (0.0%)	1 (2.4%)	8 (1.1%)	12 (1.5%)	34 (1.9%)	60 (2.0%)	120 (1.8%)
XBB.1.16.11	2 (1.1%)	0 (0.0%)	0 (0.0%)	14 (2.0%)	18 (2.2%)	36 (2.1%)	50 (1.7%)	120 (1.8%)
EG.5.1.6	4 (2.2%)	0 (0.0%)	0 (0.0%)	18 (2.5%)	18 (2.2%)	27 (1.5%)	40 (1.3%)	107 (1.6%)
BA.2.86	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (0.4%)	1 (0.1%)	12 (0.7%)	9 (0.3%)	25 (0.4%)
Other recombinant	51 (28.7%)	7 (35.0%)	10 (24.4%)	194 (27.5%)	224 (27.3%)	449 (25.7%)	752 (25.2%)	1,687 (26.0%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.1%)	4 (0.5%)	7 (0.4%)	5 (0.2%)	17 (0.3%)
Total sequenced	**178 (100%)**	**20 (100%)**	**41 (100%)**	**706 (100%)**	**821 (100%)**	**1,744 (100%)**	**2,989 (100%)**	**6,499 (100%)**

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

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5a. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North West Region, September 3 to September 30, 2023

Pango lineage	Northwestern Health Unit	Thunder Bay District Health Unit	Total
EG.5.1.1	3 (30.0%)	46 (37.4%)	49 (36.8%)
XBB.1.16.6	0 (0.0%)	3 (2.4%)	3 (2.3%)
HV.1	0 (0.0%)	15 (12.2%)	15 (11.3%)
FL.1.5.1	2 (20.0%)	2 (1.6%)	4 (3.0%)
EG.5.1	0 (0.0%)	1 (0.8%)	1 (0.8%)
EG.5.1.3	0 (0.0%)	1 (0.8%)	1 (0.8%)
HK.3	0 (0.0%)	2 (1.6%)	2 (1.5%)
EG.5.1.4	0 (0.0%)	2 (1.6%)	2 (1.5%)
XBB.1.16	0 (0.0%)	1 (0.8%)	1 (0.8%)
DV.7.1	0 (0.0%)	1 (0.8%)	1 (0.8%)
EG.6.1	1 (10.0%)	2 (1.6%)	3 (2.3%)
GK.1.1	0 (0.0%)	1 (0.8%)	1 (0.8%)
GJ.1.2	1 (10.0%)	2 (1.6%)	3 (2.3%)
XBB.1.16.11	0 (0.0%)	0 (0.0%)	0 (0.0%)
EG.5.1.6	0 (0.0%)	5 (4.1%)	5 (3.8%)
BA.2.86	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other recombinant	3 (30.0%)	38 (30.9%)	41 (30.8%)
Other Omicron	0 (0.0%)	1 (0.8%)	1 (0.8%)
Total sequenced	**10 (100%)**	**123 (100%)**	**133 (100%)**

Note: Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.6%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5b. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, North East Region, September 3 to September 30, 2023

Pango lineage	Algoma Public Health	North Bay Parry Sound District Health Unit	Porcupine Health Unit	Public Health Sudbury & Districts	Timiskaming Health Unit	Total
EG.5.1.1	0 (0.0%)	0 (0.0%)	5 (21.7%)	2 (2.2%)	1 (6.2%)	8 (3.8%)
XBB.1.16.6	8 (14.8%)	3 (10.7%)	0 (0.0%)	42 (46.2%)	1 (6.2%)	54 (25.5%)
HV.1	1 (1.9%)	1 (3.6%)	2 (8.7%)	12 (13.2%)	0 (0.0%)	16 (7.5%)
FL.1.5.1	0 (0.0%)	0 (0.0%)	1 (4.3%)	2 (2.2%)	0 (0.0%)	3 (1.4%)
EG.5.1	0 (0.0%)	1 (3.6%)	1 (4.3%)	3 (3.3%)	0 (0.0%)	5 (2.4%)
EG.5.1.3	0 (0.0%)	2 (7.1%)	0 (0.0%)	3 (3.3%)	0 (0.0%)	5 (2.4%)
HK.3	1 (1.9%)	1 (3.6%)	0 (0.0%)	1 (1.1%)	0 (0.0%)	3 (1.4%)
EG.5.1.4	0 (0.0%)	4 (14.3%)	0 (0.0%)	7 (7.7%)	0 (0.0%)	11 (5.2%)
XBB.1.16	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (6.2%)	1 (0.5%)
DV.7.1	0 (0.0%)	2 (7.1%)	0 (0.0%)	2 (2.2%)	0 (0.0%)	4 (1.9%)
EG.6.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	11 (68.8%)	11 (5.2%)
GK.1.1	27 (50.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	27 (12.7%)
GJ.1.2	0 (0.0%)	5 (17.9%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (2.4%)
XBB.1.16.11	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (4.4%)	0 (0.0%)	4 (1.9%)
EG.5.1.6	7 (13.0%)	0 (0.0%)	1 (4.3%)	1 (1.1%)	0 (0.0%)	9 (4.2%)
BA.2.86	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other recombinant	10 (18.5%)	9 (32.1%)	10 (43.5%)	11 (12.1%)	2 (12.5%)	42 (19.8%)
Other Omicron	0 (0.0%)	0 (0.0%)	3 (13.0%)	1 (1.1%)	0 (0.0%)	4 (1.9%)
Total sequenced	**54 (100%)**	**28 (100%)**	**23 (100%)**	**91 (100%)**	**16 (100%)**	**212 (100%)**

Note: Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.6%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5c. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Eastern Region, September 3 to September 30, 2023

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
EG.5.1.1	5 (4.7%)	7 (7.3%)	76 (27.4%)	18 (25.7%)	99 (13.7%)	6 (10.5%)	211 (15.9%)
XBB.1.16.6	5 (4.7%)	2 (2.1%)	6 (2.2%)	0 (0.0%)	32 (4.4%)	1 (1.8%)	46 (3.5%)
HV.1	14 (13.2%)	4 (4.2%)	13 (4.7%)	3 (4.3%)	12 (1.7%)	6 (10.5%)	52 (3.9%)
FL.1.5.1	10 (9.4%)	3 (3.1%)	16 (5.8%)	3 (4.3%)	37 (5.1%)	9 (15.8%)	78 (5.9%)
EG.5.1	13 (12.3%)	6 (6.2%)	31 (11.2%)	8 (11.4%)	52 (7.2%)	1 (1.8%)	111 (8.4%)
EG.5.1.3	5 (4.7%)	2 (2.1%)	9 (3.2%)	5 (7.1%)	38 (5.3%)	14 (24.6%)	73 (5.5%)
HK.3	5 (4.7%)	16 (16.7%)	7 (2.5%)	4 (5.7%)	33 (4.6%)	1 (1.8%)	66 (5.0%)
EG.5.1.4	5 (4.7%)	2 (2.1%)	8 (2.9%)	3 (4.3%)	115 (16.0%)	7 (12.3%)	140 (10.6%)
XBB.1.16	1 (0.9%)	2 (2.1%)	2 (0.7%)	3 (4.3%)	26 (3.6%)	0 (0.0%)	34 (2.6%)
DV.7.1	0 (0.0%)	0 (0.0%)	1 (0.4%)	0 (0.0%)	6 (0.8%)	0 (0.0%)	7 (0.5%)
EG.6.1	2 (1.9%)	1 (1.0%)	8 (2.9%)	3 (4.3%)	46 (6.4%)	1 (1.8%)	61 (4.6%)
GK.1.1	0 (0.0%)	1 (1.0%)	2 (0.7%)	0 (0.0%)	6 (0.8%)	0 (0.0%)	9 (0.7%)
GJ.1.2	1 (0.9%)	37 (38.5%)	2 (0.7%)	0 (0.0%)	6 (0.8%)	1 (1.8%)	47 (3.5%)
XBB.1.16.11	3 (2.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	11 (1.5%)	0 (0.0%)	14 (1.1%)
EG.5.1.6	12 (11.3%)	0 (0.0%)	1 (0.4%)	0 (0.0%)	10 (1.4%)	0 (0.0%)	23 (1.7%)
BA.2.86	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Other recombinant	25 (23.6%)	12 (12.5%)	95 (34.3%)	20 (28.6%)	192 (26.6%)	10 (17.5%)	354 (26.7%)
Other Omicron	0 (0.0%)	1 (1.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.1%)
Total sequenced	**106 (100%)**	**96 (100%)**	**277 (100%)**	**70 (100%)**	**721 (100%)**	**57 (100%)**	**1,327 (100%)**

Note: Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.6%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5d. Number and percentage of cases by Pango lineage health unit and public (PHU), representative surveillance, Central East Region, September 3 to September 30, 2023

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
EG.5.1.1	17 (6.9%)	2 (4.2%)	48 (9.5%)	16 (12.5%)	23 (14.4%)	109 (29.4%)	215 (14.8%)
XBB.1.16.6	31 (12.7%)	0 (0.0%)	78 (15.5%)	2 (1.6%)	24 (15.0%)	30 (8.1%)	165 (11.3%)
HV.1	19 (7.8%)	4 (8.3%)	53 (10.5%)	4 (3.1%)	5 (3.1%)	24 (6.5%)	109 (7.5%)
FL.1.5.1	13 (5.3%)	7 (14.6%)	28 (5.6%)	4 (3.1%)	24 (15.0%)	15 (4.0%)	91 (6.3%)
EG.5.1	10 (4.1%)	6 (12.5%)	16 (3.2%)	3 (2.3%)	2 (1.2%)	25 (6.7%)	62 (4.3%)
EG.5.1.3	6 (2.4%)	3 (6.2%)	18 (3.6%)	20 (15.6%)	14 (8.8%)	27 (7.3%)	88 (6.0%)
HK.3	44 (18.0%)	2 (4.2%)	18 (3.6%)	0 (0.0%)	4 (2.5%)	19 (5.1%)	87 (6.0%)
EG.5.1.4	10 (4.1%)	1 (2.1%)	9 (1.8%)	2 (1.6%)	6 (3.8%)	29 (7.8%)	57 (3.9%)
XBB.1.16	2 (0.8%)	3 (6.2%)	14 (2.8%)	45 (35.2%)	5 (3.1%)	8 (2.2%)	77 (5.3%)
DV.7.1	15 (6.1%)	5 (10.4%)	5 (1.0%)	2 (1.6%)	12 (7.5%)	4 (1.1%)	43 (3.0%)
EG.6.1	1 (0.4%)	1 (2.1%)	8 (1.6%)	1 (0.8%)	3 (1.9%)	0 (0.0%)	14 (1.0%)
GK.1.1	6 (2.4%)	0 (0.0%)	27 (5.4%)	1 (0.8%)	0 (0.0%)	3 (0.8%)	37 (2.5%)
GJ.1.2	1 (0.4%)	0 (0.0%)	3 (0.6%)	2 (1.6%)	1 (0.6%)	2 (0.5%)	9 (0.6%)
XBB.1.16.11	11 (4.5%)	2 (4.2%)	9 (1.8%)	13 (10.2%)	0 (0.0%)	5 (1.3%)	40 (2.7%)
EG.5.1.6	1 (0.4%)	0 (0.0%)	9 (1.8%)	0 (0.0%)	2 (1.2%)	6 (1.6%)	18 (1.2%)
BA.2.86	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.8%)	0 (0.0%)	0 (0.0%)	1 (0.1%)
Other recombinant	56 (22.9%)	11 (22.9%)	160 (31.8%)	12 (9.4%)	33 (20.6%)	64 (17.3%)	336 (23.1%)
Other Omicron	2 (0.8%)	1 (2.1%)	0 (0.0%)	0 (0.0%)	2 (1.2%)	1 (0.3%)	6 (0.4%)
Total sequenced	**245 (100%)**	**48 (100%)**	**503 (100%)**	**128 (100%)**	**160 (100%)**	**371 (100%)**	**1,455 (100%)**

Note: Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.6%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5e. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Toronto Region, September 3 to September 30, 2023

Pango lineage	Toronto Public Health	Total
EG.5.1.1	128 (9.8%)	128 (9.8%)
XBB.1.16.6	132 (10.2%)	132 (10.2%)
HV.1	89 (6.8%)	89 (6.8%)
FL.1.5.1	109 (8.4%)	109 (8.4%)
EG.5.1	101 (7.8%)	101 (7.8%)
EG.5.1.3	121 (9.3%)	121 (9.3%)
HK.3	125 (9.6%)	125 (9.6%)
EG.5.1.4	24 (1.8%)	24 (1.8%)
XBB.1.16	18 (1.4%)	18 (1.4%)
DV.7.1	31 (2.4%)	31 (2.4%)
EG.6.1	16 (1.2%)	16 (1.2%)
GK.1.1	11 (0.8%)	11 (0.8%)
GJ.1.2	10 (0.8%)	10 (0.8%)
XBB.1.16.11	16 (1.2%)	16 (1.2%)
EG.5.1.6	19 (1.5%)	19 (1.5%)
BA.2.86	1 (0.1%)	1 (0.1%)
Other recombinant	348 (26.8%)	348 (26.8%)
Other Omicron	1 (0.1%)	1 (0.1%)
Total sequenced	**1,300 (100%)**	**1,300 (100%)**

Note: Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.6%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5f. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, South West Region, September 3 to September 30, 2023

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
EG.5.1.1	6 (16.2%)	70 (29.2%)	4 (7.7%)	3 (6.7%)	71 (20.9%)	13 (21.7%)	14 (8.4%)	181 (19.2%)
XBB.1.16.6	0 (0.0%)	5 (2.1%)	2 (3.8%)	1 (2.2%)	6 (1.8%)	2 (3.3%)	23 (13.8%)	39 (4.1%)
HV.1	3 (8.1%)	5 (2.1%)	9 (17.3%)	6 (13.3%)	43 (12.6%)	7 (11.7%)	11 (6.6%)	84 (8.9%)
FL.1.5.1	2 (5.4%)	3 (1.2%)	9 (17.3%)	1 (2.2%)	49 (14.4%)	3 (5.0%)	14 (8.4%)	81 (8.6%)
EG.5.1	4 (10.8%)	3 (1.2%)	0 (0.0%)	1 (2.2%)	9 (2.6%)	1 (1.7%)	26 (15.6%)	44 (4.7%)
EG.5.1.3	0 (0.0%)	6 (2.5%)	1 (1.9%)	0 (0.0%)	5 (1.5%)	1 (1.7%)	11 (6.6%)	24 (2.6%)
HK.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (8.9%)	2 (0.6%)	0 (0.0%)	13 (7.8%)	19 (2.0%)
EG.5.1.4	1 (2.7%)	3 (1.2%)	4 (7.7%)	0 (0.0%)	23 (6.8%)	1 (1.7%)	1 (0.6%)	33 (3.5%)
XBB.1.16	0 (0.0%)	1 (0.4%)	0 (0.0%)	1 (2.2%)	8 (2.4%)	0 (0.0%)	8 (4.8%)	18 (1.9%)
DV.7.1	0 (0.0%)	34 (14.2%)	1 (1.9%)	1 (2.2%)	18 (5.3%)	1 (1.7%)	0 (0.0%)	55 (5.8%)
EG.6.1	12 (32.4%)	3 (1.2%)	0 (0.0%)	1 (2.2%)	2 (0.6%)	1 (1.7%)	2 (1.2%)	21 (2.2%)
GK.1.1	0 (0.0%)	42 (17.5%)	0 (0.0%)	2 (4.4%)	1 (0.3%)	0 (0.0%)	0 (0.0%)	45 (4.8%)
GJ.1.2	0 (0.0%)	21 (8.8%)	0 (0.0%)	1 (2.2%)	0 (0.0%)	7 (11.7%)	0 (0.0%)	29 (3.1%)
XBB.1.16.11	0 (0.0%)	10 (4.2%)	2 (3.8%)	0 (0.0%)	8 (2.4%)	0 (0.0%)	1 (0.6%)	21 (2.2%)
EG.5.1.6	0 (0.0%)	1 (0.4%)	6 (11.5%)	2 (4.4%)	16 (4.7%)	0 (0.0%)	0 (0.0%)	25 (2.7%)
BA.2.86	0 (0.0%)	0 (0.0%)	4 (7.7%)	0 (0.0%)	10 (2.9%)	0 (0.0%)	0 (0.0%)	14 (1.5%)
Other recombinant	9 (24.3%)	32 (13.3%)	10 (19.2%)	21 (46.7%)	69 (20.3%)	23 (38.3%)	43 (25.7%)	207 (22.0%)
Other Omicron	0 (0.0%)	1 (0.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.1%)
Total sequenced	**37 (100%)**	**240 (100%)**	**52 (100%)**	**45 (100%)**	**340 (100%)**	**60 (100%)**	**167 (100%)**	**941 (100%)**

Note: Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.6%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 5g. Number and percentage of cases by Pango lineage and public health unit (PHU), representative surveillance, Central West Region, September 3 to September 30, 2023

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
EG.5.1.1	1 (1.6%)	57 (18.5%)	3 (5.6%)	17 (10.8%)	19 (7.3%)	10 (5.5%)	37 (32.7%)	144 (12.7%)
XBB.1.16.6	2 (3.1%)	27 (8.8%)	1 (1.9%)	18 (11.4%)	9 (3.5%)	14 (7.7%)	11 (9.7%)	82 (7.2%)
HV.1	12 (18.8%)	23 (7.5%)	3 (5.6%)	12 (7.6%)	11 (4.2%)	31 (17.0%)	26 (23.0%)	118 (10.4%)
FL.1.5.1	6 (9.4%)	11 (3.6%)	7 (13.0%)	10 (6.3%)	41 (15.8%)	19 (10.4%)	3 (2.7%)	97 (8.5%)
EG.5.1	4 (6.2%)	31 (10.1%)	8 (14.8%)	15 (9.5%)	10 (3.9%)	6 (3.3%)	3 (2.7%)	77 (6.8%)
EG.5.1.3	3 (4.7%)	18 (5.8%)	0 (0.0%)	0 (0.0%)	17 (6.6%)	26 (14.3%)	4 (3.5%)	68 (6.0%)
HK.3	9 (14.1%)	2 (0.6%)	2 (3.7%)	2 (1.3%)	7 (2.7%)	7 (3.8%)	5 (4.4%)	34 (3.0%)
EG.5.1.4	1 (1.6%)	10 (3.2%)	0 (0.0%)	4 (2.5%)	21 (8.1%)	2 (1.1%)	0 (0.0%)	38 (3.3%)
XBB.1.16	0 (0.0%)	3 (1.0%)	1 (1.9%)	1 (0.6%)	9 (3.5%)	1 (0.5%)	2 (1.8%)	17 (1.5%)
DV.7.1	1 (1.6%)	6 (1.9%)	1 (1.9%)	1 (0.6%)	6 (2.3%)	0 (0.0%)	2 (1.8%)	17 (1.5%)
EG.6.1	1 (1.6%)	4 (1.3%)	5 (9.3%)	0 (0.0%)	1 (0.4%)	1 (0.5%)	2 (1.8%)	14 (1.2%)
GK.1.1	0 (0.0%)	3 (1.0%)	0 (0.0%)	0 (0.0%)	4 (1.5%)	1 (0.5%)	1 (0.9%)	9 (0.8%)
GJ.1.2	0 (0.0%)	2 (0.6%)	0 (0.0%)	1 (0.6%)	12 (4.6%)	1 (0.5%)	1 (0.9%)	17 (1.5%)
XBB.1.16.11	1 (1.6%)	2 (0.6%)	18 (33.3%)	1 (0.6%)	0 (0.0%)	2 (1.1%)	1 (0.9%)	25 (2.2%)
EG.5.1.6	0 (0.0%)	2 (0.6%)	0 (0.0%)	0 (0.0%)	1 (0.4%)	2 (1.1%)	3 (2.7%)	8 (0.7%)
BA.2.86	0 (0.0%)	8 (2.6%)	0 (0.0%)	1 (0.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	9 (0.8%)
Other recombinant	23 (35.9%)	99 (32.1%)	5 (9.3%)	74 (46.8%)	91 (35.1%)	58 (31.9%)	11 (9.7%)	361 (31.7%)
Other Omicron	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.6%)	0 (0.0%)	1 (0.5%)	1 (0.9%)	3 (0.3%)
Total sequenced	**64 (100%)**	**308 (100%)**	**54 (100%)**	**158 (100%)**	**259 (100%)**	**182 (100%)**	**113 (100%)**	**1,138 (100%)**

Note: Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (2.6%), OCGN patient postal code was used. Ordering provider postal code was used if patient postal code was missing.

Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM)

Table 6. Number and percentage (row %) of cases admitted to hospital and deceased cases by Pango lineage, representative surveillance, Ontario, July 9, 2023 to September 30, 2023

Pango lineage	Hospital admissions	Deceased	Total cases
EG.5.1.1	101 (7.3%)	16 (1.1%)	1,392 (100%)
XBB.1.16.6	57 (7.8%)	6 (0.8%)	735 (100%)
HV.1	62 (11.6%)	5 (0.9%)	534 (100%)
FL.1.5.1	69 (9.7%)	9 (1.3%)	709 (100%)
EG.5.1	74 (10.6%)	7 (1.0%)	701 (100%)
EG.5.1.3	48 (8.2%)	8 (1.4%)	586 (100%)
HK.3	20 (5.5%)	2 (0.5%)	365 (100%)
EG.5.1.4	31 (7.6%)	7 (1.7%)	410 (100%)
XBB.1.16	26 (6.3%)	5 (1.2%)	414 (100%)
DV.7.1	10 (5.2%)	2 (1.0%)	191 (100%)
EG.6.1	17 (7.4%)	3 (1.3%)	231 (100%)
GK.1.1	10 (6.8%)	1 (0.7%)	146 (100%)
GJ.1.2	7 (3.1%)	1 (0.4%)	229 (100%)
XBB.1.16.11	15 (8.7%)	1 (0.6%)	173 (100%)
EG.5.1.6	7 (4.8%)	2 (1.4%)	146 (100%)
BA.2.86*	5 (20.0%)	0 (0.0%)	25 (100%)
Other recombinant	339 (8.8%)	41 (1.1%)	3,840 (100%)
Other Omicron	9 (10.0%)	0 (0.0%)	90 (100%)
Total sequenced	**907 (8.3%)**	**116 (1.1%)**	**10,917 (100%)**

Note: *Nine of 25 BA.2.86 cases were associated with two hospital outbreaks. PHUs were specifically notified which may have led to more complete data collection. Includes the most prevalent lineages detected in the past month. Cases include only those that linked to CCM (97.2%). Hospital admissions include all cases admitted to hospital (or had their hospital stay extended) because of COVID-19 at time of data extraction. Deceased cases include cases that reported a "Fatal" outcome and the type of death value in CCM was not 'DOPHS was unrelated to cause of death' or 'Under PHU Review' at the time of data extraction. Factors, such as age, that may affect the risk of COVID-19 hospital admission and death are not accounted for in these analyses. Results may not be representative of Ontario overall. Details on the proportion of eligible samples sequenced by the OCGN can be found in the technical notes. Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction.

Data Sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE), Public Health Case and Contact Management Solution (CCM) - hospital admission and death indicators

Cumulative Whole Genome Sequencing Results

Table 7. Number of cases by Pango lineage, cumulative counts, Ontario, January 1, 2023 to September 30, 2023

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
Variant of Concern (VOC)			
Omicron	**18,487**	**200**	**18,687**
BA.1.1	7	0	7
BA.1.1.1	0	1	1
BA.2	10	1	11
BA.2.10.1	1	0	1
BA.2.12.1	3	0	3
BA.2.3	2	0	2
BA.2.3.10	1	0	1
BA.2.3.20	13	0	13
BA.2.38	1	0	1
BA.2.73	1	0	1
BA.2.75	2	0	2
BA.2.75.5	6	0	6
BA.2.86	0	25	25
BA.2.86.1	1	0	1
BA.4	2	0	2
BA.4.4	1	0	1
BA.4.6	32	0	32
BA.4.6.2	5	0	5
BA.4.6.3	13	0	13
BA.4.6.5	3	0	3
BA.5	10	0	10
BA.5.1	35	0	35
BA.5.1.1	1	0	1
BA.5.1.12	7	0	7
BA.5.1.18	19	0	19
BA.5.1.2	10	0	10
BA.5.1.20	2	0	2
BA.5.1.23	4	0	4
BA.5.1.25	1	0	1
BA.5.1.27	17	0	17
BA.5.1.28	5	0	5
BA.5.1.30	4	0	4
BA.5.1.33	3	0	3
BA.5.1.34	1	0	1

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
BA.5.1.36	1	0	1
BA.5.1.37	13	0	13
BA.5.1.5	4	0	4
BA.5.1.7	7	0	7
BA.5.11	13	0	13
BA.5.12	1	0	1
BA.5.2	59	0	59
BA.5.2.1	87	0	87
BA.5.2.12	1	0	1
BA.5.2.13	37	0	37
BA.5.2.14	6	0	6
BA.5.2.19	7	0	7
BA.5.2.20	2	0	2
BA.5.2.21	1	0	1
BA.5.2.22	1	0	1
BA.5.2.23	2	0	2
BA.5.2.24	2	0	2
BA.5.2.25	6	0	6
BA.5.2.26	4	0	4
BA.5.2.28	10	0	10
BA.5.2.31	1	0	1
BA.5.2.34	77	0	77
BA.5.2.35	19	0	19
BA.5.2.37	2	0	2
BA.5.2.47	2	0	2
BA.5.2.48	3	0	3
BA.5.2.52	1	0	1
BA.5.2.57	3	0	3
BA.5.2.58	1	0	1
BA.5.2.6	44	0	44
BA.5.2.63	68	0	68
BA.5.2.9	41	0	41
BA.5.3	1	0	1
BA.5.3.1	7	0	7
BA.5.3.5	3	0	3
BA.5.5	1	0	1
BA.5.5.1	1	0	1
BA.5.6	3	0	3
BA.5.9	36	0	36
BE.1.1	2	0	2
BE.1.1.1	3	0	3

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
BE.1.1.2	2	0	2
BE.1.2	2	0	2
BE.1.2.1	74	1	75
BE.1.4	1	0	1
BE.1.4.2	6	0	6
BE.10	13	0	13
BE.13	6	0	6
BE.4.1.1	2	0	2
BE.6	1	0	1
BE.7	3	0	3
BE.9	40	0	40
BF.10	47	0	47
BF.11	80	0	80
BF.11.1	17	0	17
BF.11.2	2	0	2
BF.11.3	42	0	42
BF.13	12	0	12
BF.14	4	0	4
BF.21	1	0	1
BF.25	4	0	4
BF.26	10	0	10
BF.27	2	0	2
BF.28	2	0	2
BF.31.1	2	0	2
BF.34	9	0	9
BF.39	1	0	1
BF.5	10	0	10
BF.7	278	1	279
BF.7.1	1	0	1
BF.7.14	1	0	1
BF.7.14.1	1	0	1
BF.7.14.2	1	0	1
BF.7.16.1	5	0	5
BF.7.20	16	0	16
BF.7.21	6	0	6
BF.7.22	21	0	21
BF.7.23	45	0	45
BF.7.24	4	0	4
BF.7.4	18	0	18
BF.7.4.1	19	0	19
BF.7.5	6	0	6

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
BF.7.6	4	0	4
BF.7.7	26	0	26
BF.7.8	1	0	1
BF.8	1	0	1
BK.1	3	0	3
BL.1	1	0	1
BL.6	1	0	1
BM.1.1	10	0	10
BM.1.1.3	1	0	1
BM.2	1	0	1
BN.1	66	0	66
BN.1.1	3	0	3
BN.1.1.1	1	0	1
BN.1.10	12	0	12
BN.1.2	14	0	14
BN.1.2.1	19	0	19
BN.1.2.2	2	0	2
BN.1.2.3	2	0	2
BN.1.2.4	3	0	3
BN.1.2.6	3	0	3
BN.1.2.7	1	0	1
BN.1.3	41	0	41
BN.1.3.1	20	0	20
BN.1.3.3	1	0	1
BN.1.3.5	15	0	15
BN.1.3.6	1	0	1
BN.1.3.7	2	0	2
BN.1.4	13	0	13
BN.1.4.2	2	0	2
BN.1.4.3	2	0	2
BN.1.5	18	0	18
BN.1.5.2	19	0	19
BN.1.7	3	0	3
BN.1.9	2	0	2
BN.3.1	23	0	23
BN.6	1	0	1
BQ.1	1,265	0	1,265
BQ.1.1	5,176	0	5,176
BQ.1.1.1	283	0	283
BQ.1.1.10	151	0	151
BQ.1.1.11	16	0	16

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
BQ.1.1.13	10	0	10
BQ.1.1.15	74	0	74
BQ.1.1.16	2	0	2
BQ.1.1.17	9	0	9
BQ.1.1.18	202	0	202
BQ.1.1.2	77	0	77
BQ.1.1.20	11	0	11
BQ.1.1.21	1	0	1
BQ.1.1.22	2	0	2
BQ.1.1.23	15	0	15
BQ.1.1.24	11	0	11
BQ.1.1.27	2	0	2
BQ.1.1.28	4	0	4
BQ.1.1.29	3	0	3
BQ.1.1.3	169	0	169
BQ.1.1.30	159	0	159
BQ.1.1.31	9	0	9
BQ.1.1.32	63	0	63
BQ.1.1.35	196	0	196
BQ.1.1.36	1	0	1
BQ.1.1.37	64	0	64
BQ.1.1.38	8	0	8
BQ.1.1.39	162	0	162
BQ.1.1.4	167	0	167
BQ.1.1.40	465	0	465
BQ.1.1.41	109	0	109
BQ.1.1.42	12	0	12
BQ.1.1.43	5	0	5
BQ.1.1.44	65	0	65
BQ.1.1.45	87	0	87
BQ.1.1.46	103	0	103
BQ.1.1.47	91	0	91
BQ.1.1.48	62	0	62
BQ.1.1.5	163	0	163
BQ.1.1.51	134	0	134
BQ.1.1.52	66	0	66
BQ.1.1.53	1	0	1
BQ.1.1.54	22	0	22
BQ.1.1.55	49	0	49
BQ.1.1.56	7	0	7
BQ.1.1.58	9	0	9

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
BQ.1.1.6	30	0	30
BQ.1.1.61	45	0	45
BQ.1.1.63	3	0	3
BQ.1.1.65	75	0	75
BQ.1.1.67	80	0	80
BQ.1.1.68	57	0	57
BQ.1.1.69	79	0	79
BQ.1.1.7	187	0	187
BQ.1.1.72	3	0	3
BQ.1.1.73	6	0	6
BQ.1.1.74	2	0	2
BQ.1.1.76	1	0	1
BQ.1.1.77	117	0	117
BQ.1.1.8	64	0	64
BQ.1.1.9	40	0	40
BQ.1.10	138	0	138
BQ.1.10.1	125	0	125
BQ.1.10.2	4	0	4
BQ.1.11	122	0	122
BQ.1.12	293	1	294
BQ.1.13	262	0	262
BQ.1.13.1	148	0	148
BQ.1.14	276	0	276
BQ.1.15	2	0	2
BQ.1.15.1	24	0	24
BQ.1.16	2	0	2
BQ.1.18	5	0	5
BQ.1.2	158	0	158
BQ.1.2.1	5	0	5
BQ.1.2.2	5	0	5
BQ.1.2.3	179	0	179
BQ.1.20	1	0	1
BQ.1.22	123	0	123
BQ.1.23	84	0	84
BQ.1.24	2	0	2
BQ.1.25	133	0	133
BQ.1.25.1	52	0	52
BQ.1.27	3	0	3
BQ.1.28	2	0	2
BQ.1.3	15	0	15
BQ.1.3.1	146	0	146

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
BQ.1.3.2	51	0	51
BQ.1.30	154	0	154
BQ.1.31	3	0	3
BQ.1.4	2	0	2
BQ.1.5	400	0	400
BQ.1.6	13	0	13
BQ.1.8	73	0	73
BQ.1.9	60	0	60
BR.1.2	1	0	1
BR.2.1	78	0	78
BS.1.1	4	0	4
BT.2	1	0	1
BU.1	17	0	17
BW.1	8	0	8
BW.1.1	23	0	23
BW.1.1.1	66	0	66
BW.1.1.2	50	0	50
BW.1.2	4	0	4
BY.1	1	0	1
CA.3.1	5	0	5
CA.5	5	0	5
CA.7	34	0	34
CE.1	1	0	1
CH.1.1	680	0	680
CH.1.1.1	51	0	51
CH.1.1.10	16	0	16
CH.1.1.11	44	0	44
CH.1.1.15	1	0	1
CH.1.1.16	8	0	8
CH.1.1.18	2	0	2
CH.1.1.19	1	0	1
CH.1.1.2	55	1	56
CH.1.1.24	4	0	4
CH.1.1.25	4	0	4
CH.1.1.27	1	0	1
CH.1.1.28	27	0	27
CJ.1.1	9	0	9
CJ.1.3	19	0	19
CJ.1.3.2	1	0	1
CK.1	18	0	18
CK.1.3	5	0	5

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
CK.1.4	36	0	36
CK.1.5	50	0	50
CK.2	5	0	5
CK.2.1	2	0	2
CK.2.1.1	13	0	13
CK.3	11	0	11
CL.1	6	0	6
CL.1.2	1	0	1
CL.1.3	2	0	2
CM.1	9	0	9
CM.10	1	0	1
CM.12	3	0	3
CM.2	6	0	6
CM.4.1	1	0	1
CM.8.1	103	0	103
CM.8.1.2	1	0	1
CM.8.1.4	1	0	1
CN.1	6	0	6
CN.2	8	0	8
CP.1	2	0	2
CQ.2	18	0	18
CR.1	2	0	2
CR.1.1	5	0	5
CR.1.2	1	0	1
CV.1	3	0	3
CZ.2	188	0	188
DB.3	1	0	1
DE.2	1	0	1
DF.1.1	10	0	10
DG.1	2	0	2
DJ.1.1	9	0	9
DJ.1.1.1	3	0	3
DK.1	1	0	1
DN.1	2	0	2
DN.1.1.4	1	0	1
DN.2	26	0	26
DQ.1	1	0	1
DR.1	3	0	3
DR.2	21	0	21
DS.1	8	0	8
DT.2	13	0	13

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
DU.1	70	0	70
DV.1.1	53	0	53
DV.2	1	0	1
DV.3	1	0	1
DV.5	1	0	1
DV.6	16	0	16
DV.6.1	1	0	1
DV.6.2	1	0	1
DV.7	18	0	18
DV.7.1	36	158	194
DV.7.2	1	0	1
DY.1	2	0	2
DY.2	3	0	3
DY.3	1	0	1
EA.1	1	0	1
EB.1	9	0	9
ED.2	98	0	98
EE.1	47	0	47
EE.2	27	0	27
EE.3	125	0	125
EE.4	8	0	8
EE.5	2	0	2
EF.1	23	0	23
EF.1.1	19	0	19
EF.1.1.1	77	0	77
EF.1.2	4	0	4
EH.1	2	0	2
EN.1	1	0	1
ES.1	318	0	318
EZ.1	2	0	2
FB.1	5	0	5
FC.1	1	0	1
FK.1.1	48	3	51
FK.1.1.2	7	4	11
FK.1.2	1	0	1
FK.1.2.2	6	0	6
FK.1.3.2	0	1	1
FK.1.4	1	0	1
FK.1.5	25	0	25
FR.1	8	0	8
FR.1.1	2	1	3

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
FR.1.3	3	0	3
FS.1	1	0	1
GP.1	2	2	4
GP.3	2	0	2
Variant of Interest (VOI)			
Recombinant	**25,791**	**6,309**	**32,100**
EG.1	91	4	95
EG.1.2	3	0	3
EG.1.3	38	0	38
EG.1.4	8	3	11
EG.1.5	23	0	23
EG.1.6	3	0	3
EG.1.8	9	3	12
EG.10	1	0	1
EG.10.1	14	16	30
EG.11	2	0	2
EG.2	34	5	39
EG.4	31	1	32
EG.4.3	0	3	3
EG.4.4	2	0	2
EG.5	7	7	14
EG.5.1	364	401	765
EG.5.1.1	533	936	1,469
EG.5.1.2	3	9	12
EG.5.1.3	231	380	611
EG.5.1.4	126	305	431
EG.5.1.5	2	29	31
EG.5.1.6	41	107	148
EG.5.2	114	59	173
EG.5.2.1	2	12	14
EG.5.2.2	0	3	3
EG.5.2.3	1	0	1
EG.6	5	0	5
EG.6.1	157	140	297
EG.7	23	17	40
EG.9.1	1	0	1
EK.2	2	0	2
EK.2.1	5	0	5
EK.3	2	0	2
EK.4	1	0	1
EL.1	8	0	8

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
EM.1	1	1	2
EU.1	1	0	1
EU.1.1	77	2	79
EU.1.1.1	5	1	6
EU.1.1.3	0	2	2
FD.1.1	177	30	207
FD.2	41	0	41
FD.3	5	0	5
FD.4	24	0	24
FE.1	7	1	8
FE.1.1	10	4	14
FE.1.1.1	38	0	38
FE.1.2	44	1	45
FG.2	12	0	12
FG.3	2	0	2
FH.1	4	4	8
FL.1	10	0	10
FL.1.1	1	0	1
FL.1.2	1	1	2
FL.1.3	20	0	20
FL.1.4	3	0	3
FL.1.5	3	49	52
FL.1.5.1	275	464	739
FL.10	60	2	62
FL.10.1	29	14	43
FL.11	13	0	13
FL.12	2	0	2
FL.13	108	0	108
FL.13.3	28	0	28
FL.13.3.1	7	0	7
FL.14	4	0	4
FL.15	96	63	159
FL.16	3	1	4
FL.17	1	0	1
FL.18	97	3	100
FL.19	1	0	1
FL.19.1	2	2	4
FL.2	70	11	81
FL.2.1	2	0	2
FL.2.2.1	1	13	14
FL.2.3	17	0	17

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
FL.2.4	5	0	5
FL.2.5	5	0	5
FL.20	107	51	158
FL.21	11	2	13
FL.21.2	1	0	1
FL.22	6	0	6
FL.24	18	24	42
FL.25	5	2	7
FL.26	4	0	4
FL.27	3	0	3
FL.3	51	0	51
FL.3.1	5	0	5
FL.3.2	1	0	1
FL.3.3	1	0	1
FL.3.4	1	0	1
FL.4	322	0	322
FL.4.3	1	0	1
FL.4.5	36	0	36
FL.4.6	4	0	4
FL.4.7	2	0	2
FL.5	106	0	106
FL.5.1	3	0	3
FL.6	13	0	13
FL.7	23	0	23
FL.8	7	0	7
FL.9	3	0	3
FP.4	15	0	15
FT.1	489	0	489
FT.3	3	0	3
FT.3.1	1	0	1
FT.3.1.1	2	6	8
FU.1	110	10	120
FU.2	13	14	27
FU.2.1	21	14	35
FU.3	28	0	28
FU.4	1	0	1
FW.1	4	3	7
FY.1	3	0	3
FY.1.1	0	1	1
FY.1.2	13	2	15
FY.2	22	3	25

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
FY.2.1	1	0	1
FY.3	8	6	14
FY.3.1	26	2	28
FY.4.1	3	3	6
FY.4.2	4	1	5
FY.5	64	11	75
FY.6	3	1	4
FZ.2	1	0	1
GA.1	4	0	4
GA.2	1	0	1
GA.3	1	0	1
GA.4	2	8	10
GA.6	2	7	9
GB.1	29	2	31
GB.2	1	0	1
GC.2	1	0	1
GD.1	4	0	4
GE.1	46	81	127
GF.1	8	1	9
GH.1	1	0	1
GJ.1.1	11	1	12
GJ.1.2	148	120	268
GJ.1.2.1	0	2	2
GJ.2	0	1	1
GJ.3	1	0	1
GJ.4	8	18	26
GK.1	10	12	22
GK.1.1	9	139	148
GK.1.2	3	1	4
GK.1.3	30	10	40
GK.2	43	63	106
GK.3	2	21	23
GK.3.1	2	80	82
GL.1	1	1	2
GM.1	3	0	3
GM.2	33	3	36
GN.1	13	6	19
GN.1.1	6	5	11
GN.2	40	0	40
GR.1	24	0	24
GS.1	8	2	10

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
GU.1	8	0	8
GV.1	11	4	15
GW.1	57	0	57
GW.2	2	0	2
GW.5	12	12	24
GY.2	3	0	3
GY.5	21	3	24
GY.7	1	0	1
GY.8	0	2	2
GZ.1	18	1	19
HA.1	33	2	35
HB.1	2	0	2
HE.1	45	0	45
HF.1	45	25	70
HH.1	12	0	12
HH.2	10	0	10
HJ.1	2	0	2
HK.1	2	23	25
HK.3	34	336	370
HL.1	18	0	18
HM.1	1	0	1
HN.1	16	32	48
HP.1.1	34	0	34
HR.1	18	50	68
HS.1	2	7	9
HT.1	17	2	19
HT.2	18	0	18
HU.1.1	1	0	1
HU.2	0	1	1
HV.1	61	483	544
HW.1.1	3	3	6
HY.1	4	7	11
HZ.1	3	2	5
HZ.2	8	2	10
HZ.3	11	0	11
JA.1	1	20	21
XBB	9	0	9
XBB.1	87	0	87
XBB.1.1	1	0	1
XBB.1.10	2	0	2
XBB.1.11.1	10	0	10

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
XBB.1.15	95	0	95
XBB.1.15.1	1	0	1
XBB.1.16	1,104	167	1,271
XBB.1.16.1	342	33	375
XBB.1.16.10	5	0	5
XBB.1.16.11	62	120	182
XBB.1.16.12	2	4	6
XBB.1.16.13	15	0	15
XBB.1.16.14	8	36	44
XBB.1.16.15	14	54	68
XBB.1.16.16	3	2	5
XBB.1.16.17	3	5	8
XBB.1.16.18	8	4	12
XBB.1.16.19	17	2	19
XBB.1.16.2	125	1	126
XBB.1.16.20	15	0	15
XBB.1.16.21	13	2	15
XBB.1.16.22	30	0	30
XBB.1.16.3	77	0	77
XBB.1.16.4	7	0	7
XBB.1.16.5	24	6	30
XBB.1.16.6	236	521	757
XBB.1.16.7	2	0	2
XBB.1.16.8	40	46	86
XBB.1.16.9	36	16	52
XBB.1.17	1	0	1
XBB.1.17.1	11	5	16
XBB.1.18.1	8	0	8
XBB.1.19	7	0	7
XBB.1.19.1	26	3	29
XBB.1.21	2	0	2
XBB.1.22	5	1	6
XBB.1.22.1	9	10	19
XBB.1.22.2	3	0	3
XBB.1.24.1	2	0	2
XBB.1.25	1	0	1
XBB.1.26	3	0	3
XBB.1.28	1	0	1
XBB.1.30	14	0	14
XBB.1.32	32	0	32
XBB.1.33	1	0	1

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
XBB.1.37	5	0	5
XBB.1.38	1	0	1
XBB.1.4	7	0	7
XBB.1.4.2	2	0	2
XBB.1.41	6	5	11
XBB.1.41.1	2	4	6
XBB.1.42	4	1	5
XBB.1.42.1	4	10	14
XBB.1.42.2	29	3	32
XBB.1.43.1	0	1	1
XBB.1.44	3	0	3
XBB.1.45.1	1	0	1
XBB.1.5	9,745	89	9,834
XBB.1.5.1	284	0	284
XBB.1.5.10	183	6	189
XBB.1.5.100	63	0	63
XBB.1.5.11	67	0	67
XBB.1.5.12	73	0	73
XBB.1.5.13	133	0	133
XBB.1.5.14	17	0	17
XBB.1.5.15	186	0	186
XBB.1.5.16	32	0	32
XBB.1.5.17	200	0	200
XBB.1.5.18	165	1	166
XBB.1.5.19	43	0	43
XBB.1.5.2	42	0	42
XBB.1.5.20	391	0	391
XBB.1.5.21	112	0	112
XBB.1.5.23	42	0	42
XBB.1.5.24	93	0	93
XBB.1.5.25	7	1	8
XBB.1.5.26	5	0	5
XBB.1.5.28	19	0	19
XBB.1.5.3	46	0	46
XBB.1.5.30	56	0	56
XBB.1.5.31	289	0	289
XBB.1.5.32	252	0	252
XBB.1.5.33	34	2	36
XBB.1.5.34	22	0	22
XBB.1.5.35	42	0	42
XBB.1.5.36	27	0	27

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
XBB.1.5.37	82	17	99
XBB.1.5.38	1	0	1
XBB.1.5.39	601	0	601
XBB.1.5.4	142	0	142
XBB.1.5.40	9	1	10
XBB.1.5.42	42	0	42
XBB.1.5.43	6	0	6
XBB.1.5.44	105	3	108
XBB.1.5.45	1	0	1
XBB.1.5.46	19	0	19
XBB.1.5.47	127	0	127
XBB.1.5.48	36	0	36
XBB.1.5.49	185	1	186
XBB.1.5.5	8	4	12
XBB.1.5.50	14	0	14
XBB.1.5.51	62	0	62
XBB.1.5.52	38	0	38
XBB.1.5.55	112	0	112
XBB.1.5.56	16	0	16
XBB.1.5.57	27	0	27
XBB.1.5.59	26	2	28
XBB.1.5.6	14	0	14
XBB.1.5.61	51	0	51
XBB.1.5.62	66	0	66
XBB.1.5.63	22	0	22
XBB.1.5.64	4	0	4
XBB.1.5.65	9	0	9
XBB.1.5.66	66	0	66
XBB.1.5.67	121	3	124
XBB.1.5.68	7	0	7
XBB.1.5.69	55	0	55
XBB.1.5.7	506	0	506
XBB.1.5.70	8	18	26
XBB.1.5.71	3	0	3
XBB.1.5.72	180	19	199
XBB.1.5.73	52	0	52
XBB.1.5.75	4	0	4
XBB.1.5.76	12	0	12
XBB.1.5.77	55	0	55
XBB.1.5.78	10	0	10
XBB.1.5.79	2	0	2

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
XBB.1.5.8	20	0	20
XBB.1.5.80	6	0	6
XBB.1.5.81	14	0	14
XBB.1.5.83	2	0	2
XBB.1.5.85	4	0	4
XBB.1.5.86	23	0	23
XBB.1.5.89	1	0	1
XBB.1.5.9	125	0	125
XBB.1.5.91	30	0	30
XBB.1.5.92	37	0	37
XBB.1.5.93	1	0	1
XBB.1.5.94	5	0	5
XBB.1.5.95	83	0	83
XBB.1.5.96	25	0	25
XBB.1.5.97	1	0	1
XBB.1.5.98	2	0	2
XBB.1.7	1	0	1
XBB.1.9	3	0	3
XBB.1.9.1	369	25	394
XBB.1.9.2	143	54	197
XBB.1.9.3	2	0	2
XBB.1.9.6	1	0	1
XBB.2	8	0	8
XBB.2.11	12	0	12
XBB.2.11.1	2	0	2
XBB.2.3	75	49	124
XBB.2.3.1	3	0	3
XBB.2.3.10	1	0	1
XBB.2.3.11	94	49	143
XBB.2.3.12	13	0	13
XBB.2.3.13	3	1	4
XBB.2.3.14	3	0	3
XBB.2.3.2	75	23	98
XBB.2.3.3	26	5	31
XBB.2.3.4	8	0	8
XBB.2.3.5	45	0	45
XBB.2.3.6	15	0	15
XBB.2.3.8	54	2	56
XBB.2.3.9	1	0	1
XBB.2.4	3	0	3
XBB.2.6	27	0	27

WHO label / Pango lineage	January 1, 2023 - September 2, 2023	September 3, 2023 - September 30, 2023	Total
XBB.3	1	0	1
XBB.3.4	3	0	3
XBB.6.1	1	0	1
XBB.8	1	0	1
XBB.8.2	1	0	1
XBB.9	1	0	1
XBC.1	10	0	10
XBC.1.1	1	0	1
XBC.1.3	3	0	3
XBC.1.4	1	0	1
XBC.1.6	1	0	1
XBC.1.6.1	1	0	1
XBF	168	0	168
XBF.1	2	0	2
XBF.2	2	0	2
XBF.3	13	0	13
XBF.5	1	0	1
XBF.7	1	0	1
XBF.7.1	1	0	1
XBF.9	1	0	1
XBJ.4	1	0	1
XBK	2	0	2
XBK.1	3	0	3
XBL	34	0	34
XBL.2	4	0	4
XBM	179	0	179
XBP	2	0	2
XBR	1	0	1
XBW	2	0	2
XCC	9	0	9
XCE	1	0	1
XCF	13	6	19
XCF.2	3	0	3
Non-VOC/VOI	**0**	**0**	**0**
Total sequenced	**44,278**	**6,509**	**50,787**

Note: Results do not represent all Ontario cases. Includes results from the OHDP-PHAE since January 1, 2023. Past testing algorithms have led to preferential sequencing of samples with N501Y and/or E484K mutations detected by PCR, which has biased the results toward lineages with these mutations. Pango lineage assignments may change over time, which may impact cumulative totals. Results should be interpreted with caution as frequencies do not reflect prevalence. Sample date represents the earliest date available for the sample. If more than one sample was sequenced for a case, the most recent sample was included.
Data sources: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Technical Notes

Data Sources

Ontario Health Data Platform – Public Health Analytic Environment (OHDP-PHAE)

- Ontario COVID-19 Genomics Network (OCGN) Data were extracted from the Ontario Health Data Platform – Public Health Analytic Environment on October 12, 2023 at approximately 9:00 a.m.

Public Health Ontario (PHO)

- Data were submitted to the OHDP-PHAE on October 10, 2023 at approximately 5:00 p.m.

The Hospital for Sick Children (HSC)

- Data were submitted to the OHDP-PHAE on October 10, 2023 at approximately 12:45 p.m.

Kingston Health Sciences Centre (KHSC)

- Data were submitted to the OHDP-PHAE on October 10, 2023 at approximately 10:45 a.m.

Shared Hospital Laboratory (SHL)

- Data were submitted to the OHDP-PHAE on October 11, 2023 at approximately 11:45 a.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were submitted to the OHDP-PHAE on October 10, 2023 at approximately 12:00 p.m.

Public Health Case and Contact Management Solution (CCM)

- Data were extracted from the Public Health Case and Contact Management Solution on October 10, 2023 at approximately 1:00 p.m.

Ontario SARS-CoV-2 Whole Genome Sequencing Strategy

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

- As of May 2, 2021, Ontario's strategy shifted to representative surveillance with VOC PCR testing laboratories being asked to send a proportion of eligible samples (Ct ≤ 30 and sufficient volume remaining) to Ontario COVID-19 Genomics Network (OCGN) sequencing laboratories. PHO began sequencing a 10% systematic sample of eligible samples on May 2 and 50% on May 30. Other VOC PCR testing laboratories were asked to begin submitting a 10% systematic or random sample of eligible samples to OCGN laboratories on May 26 and 50% on June 2. All VOC PCR/diagnostic testing laboratories shifted to submitting 100% of eligible samples to the OCGN on June 14; 50% on August 27; 10% on September 10; 25% on October 8; 100% on November 5; 50% on December 7; 10% on December 20; 5% on December 30; 20% on February 16; 50% on March 9; 25% on March 30; 10% on April 13; 25% on May 12; 100% on June 10; 50% on July 8; 20% on July 22; 50% on August 24; 75% on November 23; and 100% on December 9, 2022. The proportion of samples sequenced may change over time with changes in provincial case trends. Due to logistics, not all laboratories may have implemented sampling proportion changes at the same time.

- As of November 12, 2021, VOC PCR testing has been discontinued. The 73 diagnostic testing laboratories were asked to send all eligible samples (diagnostic PCR Ct≤ 30 and sufficient volume remaining) to one of the five OCGN laboratories for whole genome sequencing.

- As of December 6, 2021, VOC PCR testing for S gene target failure (SGTF) was implemented across Ontario to screen for Omicron. Diagnostic testing laboratories were asked to send all eligible samples (diagnostic PCR Ct≤35 and sufficient volume remaining) to one of eight SGTF testing laboratories. The SGTF testing laboratories will then submit a proportion of eligible samples (SGTF PCR Ct≤30 and sufficient volume remaining) for WGS according to the representative surveillance strategy.

    - Due to logistics, not all laboratories may have implemented SGTF testing at the same time.

- As of December 30, 2021, SGTF testing of all eligible samples was discontinued in Ontario. The 73 diagnostic testing laboratories were asked to send a proportion of eligible samples (diagnostic PCR Ct≤ 30 and sufficient volume remaining) to one of the five OCGN laboratories for whole genome sequencing, according to the representative surveillance strategy.

- As of December 31, 2021, diagnostic PCR testing was restricted to high-risk populations. Since then, the Ministry of Health continues to update its guidance on testing. As such, representative surveillance only pertains to tested populations.

Data Caveats and Methods: Ontario COVID-19 Genomics Network (OCGN)

- Lineage is assigned using the Phylogenetic Assignment of Named Global Outbreak Lineages (pangolin) tool, a software package for predicting SARS-CoV-2 lineages from genome sequences and global lineages. Lineages were reported using pangolin version 4.3.1, scorpio version 0.3.17, and constellations version 0.1.12.

- 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 the OHDP-PHAE from OCGN laboratories have not been independently verified.

- The dates associated with samples submitted by network laboratories vary due to sample logistics and different laboratory information systems. Dates associated with WGS samples were assigned based on a hierarchy: sample collection date > SARS-CoV-2 diagnostic received date > SARS-CoV-2 diagnostic reported date > VOC PCR received date > VOC PCR reported date > WGS received date > WGS reported date. Weeks were created to align with surveillance weeks used by the Public Health Agency of Canada for influenza reporting.

- Samples from the same case were linked if they had the same health card number or if they had the same first name, last name, and date of birth. If more than one sample was sequenced for a case, the most recent sample was used. This may shift a case to a more recent week if a subsequent sample was sequenced from the same case. A small proportion of cases may have samples that were not linked due to inconsistencies or data entry errors.

- Results for recent weeks are incomplete as not all sequencing and bioinformatics analyses were complete at the time of data extraction.

- Public health unit was assigned using diagnosing health unit in CCM. If the case did not link to CCM (2.6%), then public health unit was assigned using OCGN patient postal code or ordering provider postal code if patient postal code was missing.

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

Methods: Nowcast Estimates, Projections and Weekly Relative Growth Rate

- Nowcast estimates and projections are generated using a multinomial logistic regression model. The Nowcast model uses twelve weeks of daily representative surveillance data up to the most recent date, with date as the univariate model predictor. Lineages that had at least one day with an estimated or projected prevalence of 5% or greater were included in the table and figure. Lineages with at least 21 days of non-zero case counts were included in the model.
- Projected Nowcast estimates are future predictions of prevalence after the most recent date of observed data.
- Relative growth rate is a measure of a lineage's growth relative to a reference lineage.[6] Relative growth rates greater than 1 suggest an increased growth rate compared to the reference; relative growth rates less than 1 suggest a decreased growth rate compared to the reference.
- These relativized growth rates can be calculated by exponentiating the selection rate coefficient from the Nowcast model.
    - The selection rate coefficient is the difference in growth rate between two lineages ($\Delta r = r_{lineage} - r_{reference}$), and can be derived from a logistic regression model where the outcome is the relative frequency of a lineage and the predictor is time.[6,7]
- The weekly relative growth rate and projections may be overestimated for emerging lineages.

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

- CCM is a dynamic disease reporting system, which allows ongoing updates to data previously entered. As a result, data extracted from CCM represent a snapshot at the time of extraction and may differ from previous or subsequent reports.
- Methods for processing the CCM case data are described in the Technical Notes of the Ontario Respiratory Virus Tool.
- Data corrections or updates can result in case records being removed and/or updated from past reports.
- Dates associated with COVID-19 cases in Ontario were assigned using a hierarchy to best align with the sample date used for representative surveillance: sample collection date > test reported date > case reported date. As a result, the number of cases may differ from other reports which use different dates.
- Cases were linked to CCM if they had the same health card number or if they had the same first name, last name, and date of birth. Cases may not have linked to CCM due to discrepancies in patient identifiers or if they were not residents of Ontario (diagnosing health unit was reported as MOH).
- Tables for hospital admission, and deceased indicators only include cases that linked to CCM (97.2% of cases).
- Data on hospital admissions and deaths are likely under-reported as these events may occur after the completion of public health follow up of cases. Cases that were admitted to hospital or died after follow-up was completed may not be captured in CCM.
- Hospital admission includes all cases ever admitted to a hospital (or that had their hospital stay extended) because of COVID-19. It includes cases that have been discharged from hospital as well as cases that are currently hospitalized. Includes cases in an Intensive Care Unit (ICU) but not emergency room visits. Hospital admissions were identified by a reported hospital admission date or reported 'Yes' for hospitalization/ICU.
- For surveillance purposes, a COVID-19 death is defined as a death resulting from a clinically compatible illness unless there is a clear alternative cause of death that cannot be related to COVID-19 (e.g., trauma, medically assisted death). There should be no period of complete recovery from COVID-19 between illness and reported death.
- Deaths are determined by using the outcome and Type of Death fields in CCM. COVID-19 deaths are counted where the Outcome value is 'Fatal' and the Type of Death value is not 'DOPHS was unrelated to cause of death' or 'Under PHU Review'.

References

1. Public Health Agency of Canada. SARS-CoV-2 variants: national definitions, classifications and public health actions [Internet]. Ottawa, ON: Government of Canada; 2021 [modified 2023 August 28; cited 2021 August 27]. Available from: https://www.canada.ca/en/public-health/services/diseases/2019-novel-coronavirus-infection/health-professionals/testing-diagnosing-case-reporting/sars-cov-2-variants-national-definitions-classifications-public-health-actions.html

2. World Health Organization. Tracking SARS-CoV-2 variants [Internet]. Geneva, Switzerland; 2021 [modified 2023 August 17; cited 2021 November 1]. Available from: https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/

3. European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern as of 24 August 2023 [Internet]. Stockholm, Sweden; 2021 [modified 2023 August 24; cited 2021 November 1]. Available from: https://www.ecdc.europa.eu/en/covid-19/variants-concern

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

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

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

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

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