Public Health Ontario | Santé publique Ontario

MONTHLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Genomic Surveillance in Ontario, September 29, 2025

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by the Ontario COVID-19 Genomics Network as of September 24, 2025.

Background

The continued monitoring of global SARS-CoV-2 genomic data has identified changes in the virus' 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.[1-3]

As SARS-CoV-2 continues to evolve, lineages will naturally divide into descendant sublineages - 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., JN.1 [alias for B.1.1.529.2.86.1.1]). When a host is infected with two or more descendant lineages, lineages can recombine to form a new recombinant lineage (e.g., LF.7 and LP.8.1.2 to form XFG). 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 WHO may assign a new Greek letter classification to a lineage.

The Ontario COVID-19 Genomics Network (OCGN) performs WGS on all eligible positive SARS-CoV-2 samples (see Technical Notes for details). Sequences are processed using bioinformatics analyses and assigned a Pango lineage[4] using the pangolin tool[5], allowing for the identification of lineages.

Highlights

- In the past month (August 17 to September 13), a total of 1,153 cases were sequenced. XFG.3 was the most prevalent lineage (33.5%), followed by XFG (29.3%), and XFG.2 (10.7%).
- The proportion of XFG.3 increased from 26.4% (August 17 to August 23) to 39.6% (September 7 to September 13).
  - Based on the Nowcast model, XFG.3 is projected to increase to 47.5% (95% CI: 38.1% - 57.0%) by October 1, 2025. The weekly relative growth rate of XFG.3 is 1.29 (95% CI: 1.19 - 1.40) times that of XFG.
- The proportion of XFG decreased from 38.6% (August 17 to August 23) to 26.2% (September 7 to September 13).
  - Based on the Nowcast model, XFG is projected to decrease to 14.3% (95% CI: 10.4% - 19.5%) by October 1, 2025.

> Due to logistical issues, data from Kingston Health Sciences Centre are incomplete for weeks 33 to 37 (August 17 to September 13). As a result, counts, proportions, and Nowcast projections may change compared to previous and subsequent reports.
>
> Lineage counts and designations may change between reports as components of the Pango lineage assignment models are updated (see Technical Notes for details).

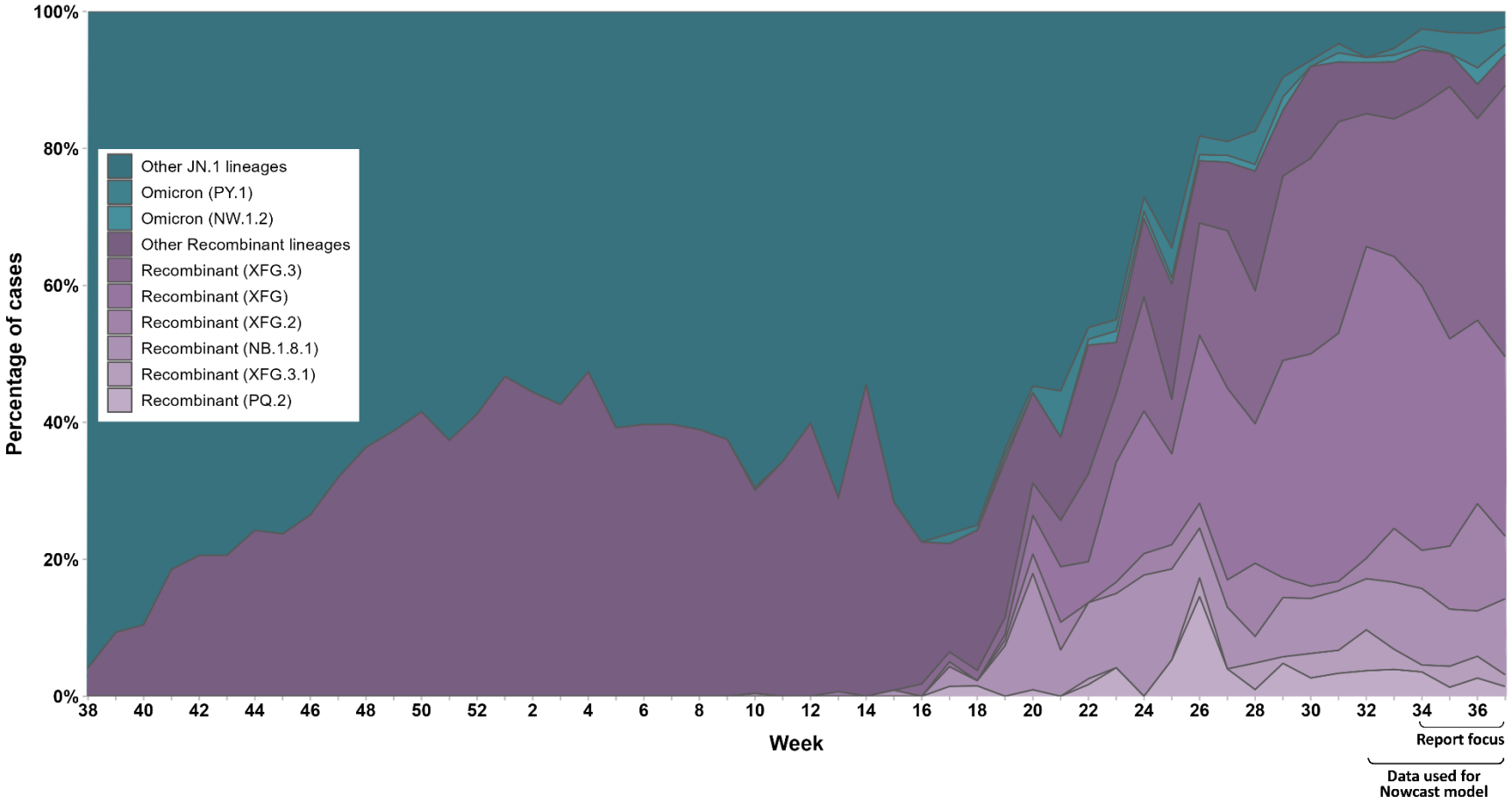
Representative Surveillance

Table 1: Number of SARS-CoV-2 positive specimens, number and percentage of specimens sequenced for representative surveillance by week, Ontario, August 17 to September 13, 2025

Week	Number of Positive Specimens	Number of Specimens Sequenced	Percentage of Specimens Sequenced
Week 34 (August 17 - August 23)	384	202	52.6%
Week 35 (August 24 - August 30)	405	233	57.5%
Week 36 (August 31 - September 6)	578	384	66.4%
Week 37 (September 7 - September 13)	727	355	48.8%
Total	**2,094**	**1,174**	**56.1%**

Note: The 1,174 specimens sequenced were associated with 1,153 unique cases; in the most recent week, 355 specimens sequenced were associated with 351 unique cases. Unique cases are the denominator for tables throughout the report. 'Number of positive specimens' is the number of tests positive for SARS-CoV-2 in Ontario. Date was assigned to best align with sample collection date, which may differ from other PHO products. 'Number of specimens sequenced' is the number of specimens sequenced for representative surveillance. 'Percentage sequenced' may be lower than the sampling proportion because not all specimens are eligible to be sequenced (i.e. excludes samples with cycle threshold >30 or insufficient volume). Results may not be representative of Ontario overall. 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. Not all sequencing and bioinformatics analyses for the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data sources: Ontario Laboratories Information System (OLIS) from the Ontario Respiratory Virus Tool (ORVT), Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Figure 1: Percentage of SARS-CoV-2 cases by the most prevalent lineages and week, representative surveillance, Ontario, September 15, 2024 to September 13, 2025



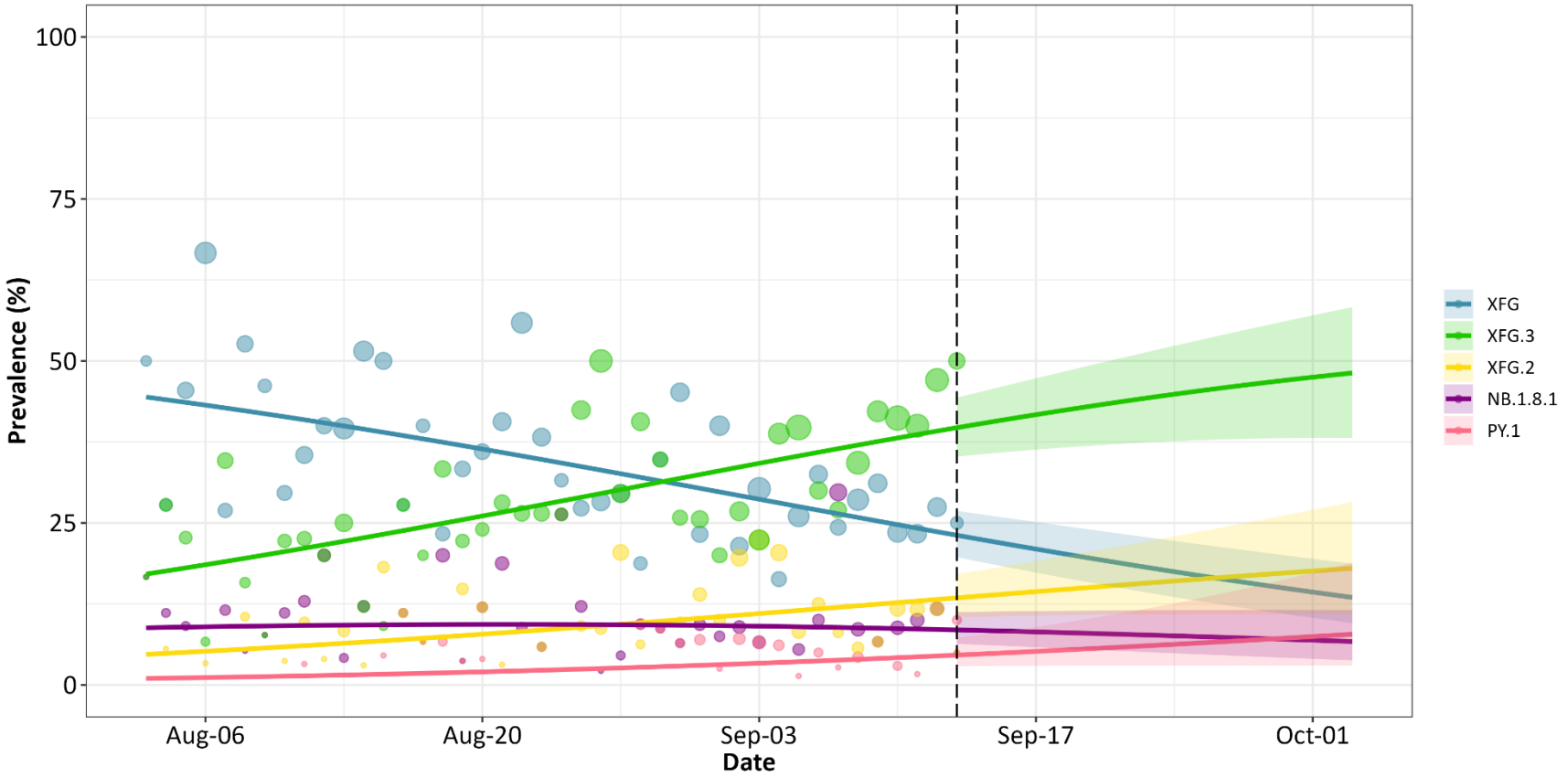
Note: Results may not be representative of Ontario overall. Details on the proportion of eligible samples sequenced by the OCGN can be found in the Technical Notes. Week was assigned based on earliest date available for a sample. If more than one sample was sequenced for a case, the most recent sample was included. Not all sequencing and bioinformatics analyses for the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data source: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 2: Number and percentage of SARS-CoV-2 cases by Pango lineage and week, representative surveillance, Ontario, August 17 to September 13, 2025

Pango Lineage	Week 34 (August 17 - August 23)	Week 35 (August 24 - August 30)	Week 36 (August 31 - September 6)	Week 37 (September 7 - September 13)	Total (August 17 - September 13)
XFG.3	52 (26.4%)	84 (36.8%)	111 (29.4%)	139 (39.6%)	386 (33.5%)
XFG	76 (38.6%)	69 (30.3%)	101 (26.8%)	92 (26.2%)	338 (29.3%)
XFG.2	11 (5.6%)	21 (9.2%)	59 (15.6%)	32 (9.1%)	123 (10.7%)
NB.1.8.1	22 (11.2%)	19 (8.3%)	25 (6.6%)	39 (11.1%)	105 (9.1%)
PY.1	5 (2.5%)	7 (3.1%)	19 (5.0%)	9 (2.6%)	40 (3.5%)
XFG.3.1	2 (1.0%)	7 (3.1%)	12 (3.2%)	6 (1.7%)	27 (2.3%)
PQ.2	7 (3.6%)	3 (1.3%)	10 (2.7%)	5 (1.4%)	25 (2.2%)
NW.1.2	1 (0.5%)	0 (0.0%)	9 (2.4%)	5 (1.4%)	15 (1.3%)
Other recombinant	16 (8.1%)	11 (4.8%)	19 (5.0%)	16 (4.6%)	62 (5.4%)
Other Omicron	5 (2.5%)	7 (3.1%)	12 (3.2%)	8 (2.3%)	32 (2.8%)
Total sequenced	**197 (100%)**	**228 (100%)**	**377 (100%)**	**351 (100%)**	**1,153 (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 the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports.
Data source: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Figure 2: Estimated daily SARS-CoV-2 prevalence (%) by Pango lineage, using Nowcast model, Ontario, August 3 to October 4, 2025



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. If daily prevalence is zero, a dot is not shown. 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 source: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 3: Estimated SARS-CoV-2 prevalence (%), projected prevalence (%), and weekly relative growth rate (with 95% confidence intervals) by Pango lineage, using Nowcast model, Ontario, August 3 to October 4, 2025

Pango Lineage	Week 36 (September 3): Estimated	Week 37 (September 10): Estimated	Week 38 (September 17): Projected	Week 39 (September 24): Projected	Week 40 (October 1): Projected	Weekly Relative Growth Rate
XFG	28.7 (26.0 - 31.4)	24.7 (21.6 - 28.2)	21.0 (17.3 - 25.1)	17.5 (13.6 - 22.2)	14.3 (10.4 - 19.5)	1.00 (reference)
XFG.3	34.2 (31.5 - 37.0)	38.1 (34.3 - 42.1)	41.7 (36.3 - 47.3)	44.9 (37.6 - 52.3)	47.5 (38.1 - 57.0)	1.29 (1.19 - 1.40)
XFG.2	11.0 (9.3 - 12.9)	12.7 (10.2 - 15.7)	14.4 (10.7 - 19.1)	16.0 (10.9 - 22.9)	17.6 (10.9 - 27.0)	1.34 (1.18 - 1.51)
NB.1.8.1	9.1 (7.5 - 10.9)	8.7 (6.7 - 11.1)	8.2 (5.8 - 11.4)	7.6 (4.9 - 11.5)	6.9 (4.0 - 11.6)	1.11 (0.99 - 1.25)
PY.1	3.3 (2.5 - 4.5)	4.2 (2.8 - 6.3)	5.2 (3.0 - 8.9)	6.3 (3.0 - 12.6)	7.5 (3.0 - 17.3)	1.45 (1.17 - 1.81)
Other lineages	9.4 (7.8 - 11.3)	8.0 (6.2 - 10.3)	6.7 (4.8 - 9.4)	5.5 (3.6 - 8.4)	4.5 (2.7 - 7.5)	0.99 (0.89 - 1.10)

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 other lineages combined that did not individually 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 source: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 4: Number and percentage of SARS-CoV-2 cases by Pango lineage and age group, representative surveillance, Ontario, August 17 to September 13, 2025

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
XFG.3	34 (37.0%)	2 (20.0%)	3 (33.3%)	33 (38.8%)	31 (33.0%)	93 (32.7%)	190 (32.8%)	386 (33.5%)
XFG	34 (37.0%)	4 (40.0%)	2 (22.2%)	20 (23.5%)	25 (26.6%)	88 (31.0%)	165 (28.5%)	338 (29.3%)
XFG.2	7 (7.6%)	1 (10.0%)	2 (22.2%)	12 (14.1%)	7 (7.4%)	25 (8.8%)	69 (11.9%)	123 (10.7%)
NB.1.8.1	9 (9.8%)	0 (0.0%)	1 (11.1%)	9 (10.6%)	8 (8.5%)	23 (8.1%)	55 (9.5%)	105 (9.1%)
PY.1	3 (3.3%)	1 (10.0%)	0 (0.0%)	1 (1.2%)	1 (1.1%)	10 (3.5%)	24 (4.1%)	40 (3.5%)
XFG.3.1	3 (3.3%)	0 (0.0%)	0 (0.0%)	2 (2.4%)	3 (3.2%)	9 (3.2%)	10 (1.7%)	27 (2.3%)
PQ.2	1 (1.1%)	0 (0.0%)	0 (0.0%)	2 (2.4%)	4 (4.3%)	4 (1.4%)	14 (2.4%)	25 (2.2%)
NW.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.1%)	3 (1.1%)	11 (1.9%)	15 (1.3%)
Other recombinant	0 (0.0%)	1 (10.0%)	1 (11.1%)	3 (3.5%)	9 (9.6%)	21 (7.4%)	27 (4.7%)	62 (5.4%)
Other Omicron	1 (1.1%)	1 (10.0%)	0 (0.0%)	3 (3.5%)	5 (5.3%)	8 (2.8%)	14 (2.4%)	32 (2.8%)
Total sequenced	**92 (100%)**	**10 (100%)**	**9 (100%)**	**85 (100%)**	**94 (100%)**	**284 (100%)**	**579 (100%)**	**1,153 (100%)**

Note: Includes the most prevalent lineages detected in the past month. Age was assigned based on the birth date provided in OCGN; excludes cases with missing birth dates.
Data source: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Table 5: Number and percentage of SARS-CoV-2 cases by Pango lineage and geographic region, representative surveillance, Ontario, August 17 to September 13, 2025

Pango Lineage	North West	North East	Eastern	Central East	Toronto	South West	Central West	Unknown	Total
XFG.3	1 (33.3%)	1 (20.0%)	11 (22.9%)	87 (23.1%)	137 (46.1%)	55 (39.9%)	46 (34.8%)	48 (31.4%)	386 (33.5%)
XFG	0 (0.0%)	2 (40.0%)	8 (16.7%)	128 (34.0%)	75 (25.3%)	23 (16.7%)	46 (34.8%)	56 (36.6%)	338 (29.3%)
XFG.2	1 (33.3%)	0 (0.0%)	5 (10.4%)	49 (13.0%)	33 (11.1%)	7 (5.1%)	18 (13.6%)	10 (6.5%)	123 (10.7%)
NB.1.8.1	1 (33.3%)	2 (40.0%)	14 (29.2%)	37 (9.8%)	18 (6.1%)	18 (13.0%)	4 (3.0%)	11 (7.2%)	105 (9.1%)
PY.1	0 (0.0%)	0 (0.0%)	3 (6.2%)	13 (3.4%)	5 (1.7%)	14 (10.1%)	2 (1.5%)	3 (2.0%)	40 (3.5%)
XFG.3.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	13 (3.4%)	4 (1.3%)	6 (4.3%)	2 (1.5%)	2 (1.3%)	27 (2.3%)
PQ.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	16 (4.2%)	4 (1.3%)	0 (0.0%)	2 (1.5%)	3 (2.0%)	25 (2.2%)
NW.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	8 (2.1%)	1 (0.3%)	0 (0.0%)	0 (0.0%)	6 (3.9%)	15 (1.3%)
Other recombinant	0 (0.0%)	0 (0.0%)	6 (12.5%)	16 (4.2%)	14 (4.7%)	4 (2.9%)	11 (8.3%)	11 (7.2%)	62 (5.4%)
Other Omicron	0 (0.0%)	0 (0.0%)	1 (2.1%)	10 (2.7%)	6 (2.0%)	11 (8.0%)	1 (0.8%)	3 (2.0%)	32 (2.8%)
Total sequenced	**3 (100%)**	**5 (100%)**	**48 (100%)**	**377 (100%)**	**297 (100%)**	**138 (100%)**	**132 (100%)**	**153 (100%)**	**1,153 (100%)**

Note: Cases with missing/unassigned patient postal code (13.1%) or out of province postal codes (0.2%) were included in the "Unknown" category. Sample date represents the earliest date available for the sample. Not all sequencing and bioinformatics analyses for the most recent weeks were complete at the time of data extraction. Case counts for these weeks may increase in subsequent reports. Geographic region was assigned based on OCGN patient postal code.
Data source: Ontario Health Data Platform - Public Health Analytic Environment (OHDP-PHAE)

Cumulative Whole Genome Sequencing Results

Table 6: Number of SARS-CoV-2 cases by Pango lineage, cumulative counts, Ontario, August 17 to September 13, 2025

WHO Label / Pango Lineage	August 17 - September 13, 2025
Omicron	**87**
JN.1.16.1	1
JN.1.16.5	1
LB.1.3.1	1
LF.7	5
LF.7.1.10	1
LF.7.9.1	1
LP.8.1.1	4
MC.31	1
NW.1.2	15
NY.16	1
NY.3	8
NY.7	1
NY.9	4
PF.2	1
PF.2.4	2
PY.1	40
Recombinant	**1,066**
NB.1.8.1	105
PQ.1	6
PQ.11	3
PQ.12	1
PQ.13	1
PQ.14	6
PQ.15	3
PQ.2	25
PQ.4	1
PQ.5	1
PQ.7	1
PQ.8	1
PQ.9	4
XBB.1.16.1	1

WHO Label / Pango Lineage	August 17 - September 13, 2025
XEC.27	4
XFC	1
XFC.1	8
XFG	338
XFG.1	10
XFG.2	123
XFG.3	386
XFG.3.1	27
XFJ	6
XFJ.3	3
XFN	1
Total Sequenced	**1,153**

Note: Results do not represent all Ontario cases. Includes results from the OHDP-PHAE from the past month. 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: 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 September 25, 2025 at approximately 9:00 a.m.

Public Health Ontario (PHO)

- Data were submitted to the OHDP-PHAE on September 23, 2025 at approximately 1:15 p.m.

The Hospital for Sick Children (HSC)

- Data were submitted to the OHDP-PHAE on September 23, 2025 at approximately 10:15 a.m.

Kingston Health Sciences Centre (KHSC)

- Data were submitted to the OHDP-PHAE on August 26, 2025 at approximately 11:45 a.m.

Shared Hospital Laboratory (SHL)

- Data were submitted to the OHDP-PHAE on September 23, 2025 at approximately 1:15 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were submitted to the OHDP-PHAE on September 18, 2025 at approximately 4:00 p.m.

Ontario Laboratories Information System (OLIS) data – Ontario Respiratory Virus Tool (ORVT)

- OLIS data were extracted from Public Health Ontario's ORVT on September 26, 2025 at approximately 11:30 a.m.

Ontario SARS-CoV-2 Whole Genome Sequencing Strategy

- Ontario's whole genome sequencing strategy began early 2021 to confirm the identification of VOCs from PCR testing. Since then, the strategy has shifted to representative surveillance as of May 2, 2021. Diagnostic testing laboratories currently send all eligible samples (diagnostic PCR Ct≤ 30 and sufficient volume remaining) to one of the five OCGN laboratories for whole genome sequencing.
- The Ministry of Health continues to update its guidance on testing and 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, pangolin data version 1.34, pangolin assignment version 1.34, scorpio version 0.3.19, 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.
- Whole genome sequencing sample logistics are complex and require samples to be transferred across a large network of laboratories. We are unable to verify all eligible samples are sent to the OCGN laboratories for sequencing.

- 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 > 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.
- Geographic region was assigned based on OCGN patient postal code. 13.1% of cases had missing/unassigned patient postal code, and 0.2% of cases had out of province postal codes.
    - North West region includes Northwestern Health Unit and Thunder Bay District Health Unit.
    - North East region includes Algoma Public Health, North Bay Parry Sound District Health Unit, Northeastern Health Unit, and Public Health Sudbury & Districts.
    - Eastern region includes Eastern Ontario Health Unit, Ottawa Public Health, Renfrew County and District Health Unit, and South East Health Unit.
    - Central East region includes Durham Region Health Department, Haliburton Kawartha Northumberland Peterborough Health Unit, Peel Public Health, Simcoe Muskoka District Health Unit, and York Region Public Health.
    - Toronto region includes Toronto Public Health.
    - South West region includes Chatham-Kent Public Health, Grey Bruce Health Unit, Huron Perth Public Health, Lambton Public Health, Middlesex-London Health Unit, Southwestern Public Health, and Windsor-Essex County Health Unit.
    - Central West region includes City of Hamilton Public Health Services, Grand Erie Health Unit, Halton Region Public Health, Niagara Region Public Health, Region of Waterloo Public Health and Emergency Services, and Wellington-Dufferin-Guelph Public Health.
- 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.
    - 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.

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 six 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.
- Weekly relative growth rate is a measure of a lineage's growth relative to a reference lineage, over a seven day period.[6] Relative growth rates greater than one suggest an increased growth rate compared to the reference; relative growth rates less than one suggest a decreased growth rate compared to the reference.
- These weekly relative growth rates can be calculated by exponentiating the weekly 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 the date, measured in weeks.[6,7]
- The weekly relative growth rate and projections may be overestimated for emerging lineages.

Data Caveats and Methods: Ontario Laboratories Information System Data – Ontario Respiratory Virus Tool

- Sample collection date is used to assign the date of the test.
- The number of tests performed does not reflect the number of specimens or persons tested. More than one test may be performed per specimen or per person. As such, the number of positive tests does not necessarily translate to the number of specimens or persons testing positive. For more information about this data source, see ORVT Technical Notes.

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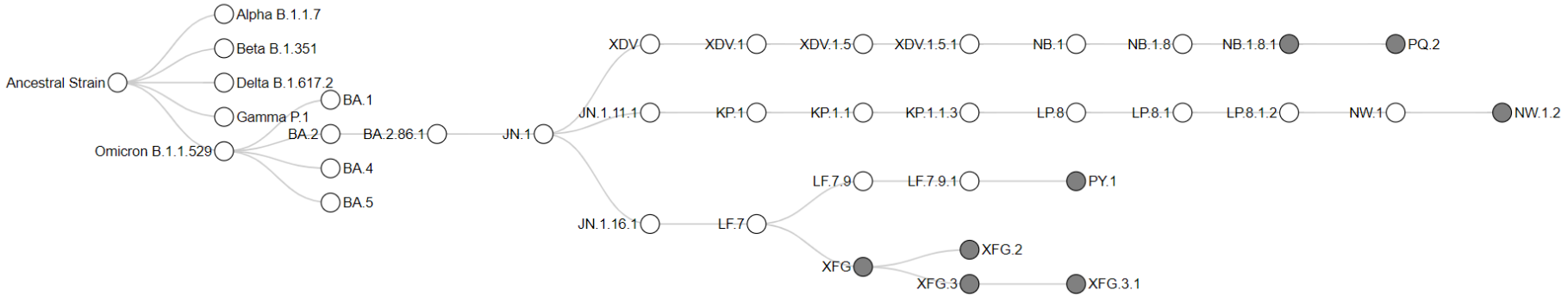
Appendix A: Pango Lineages

Figure 1: Relationship of the most prevalent SARS-CoV-2 Pango lineages in Ontario, August 17 to September 13, 2025



Note: The most prevalent lineages in the report are indicated in grey. Parent SARS-CoV-2 lineages and their respective descendant lineages branch from left to right. Lineages are aligned based on levels of the Pango designation and not on genetic relatedness. XFG is a recombinant of LF.7 and LP.8.1.2; and XDV is a recombinant of XDE and JN.1.
Data source: cov-lineages.org

Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Epidemiologic summary: SARS-CoV-2 whole genome sequencing in Ontario, September 29, 2025. Toronto, ON: King's Printer for Ontario; 2025.

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