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SURVEILLANCE REPORT

SARS-CoV-2 Genomic Surveillance in Ontario: June 29, 2026

Updated: July 2026

Background

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by the Ontario COVID-19 Genomics Network as of June 24, 2026.

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 four weeks (May 17 to June 13), a total of 61 cases were sequenced. The most prevalent lineage was PQ.2.8.1 (34.4%), followed by PQ.17 (8.2%), XFG.1.1 (8.2%), and XFG.17.3 (8.2%).
- The proportion of PQ.2.8.1 decreased from 51.6% (April 19 to May 16) to 34.4% (May 17 to June 13).
- The proportion of PQ.17 increased from 0.0% (April 19 to May 16) to 8.2% (May 17 to June 13).
- The proportion of XFG.1.1 remained stable at 9.1% (April 19 to May 16) and 8.2% (May 17 to June 13).
- The proportion of XFG.17.3 increased from 0.4% (April 19 to May 16) to 8.2% (May 17 to June 13).

Due to low case counts, tables 1 and 2 have been updated to present four-week periods instead of one-week periods. The Nowcast model has also been removed. As a result, counts and proportions may differ 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).

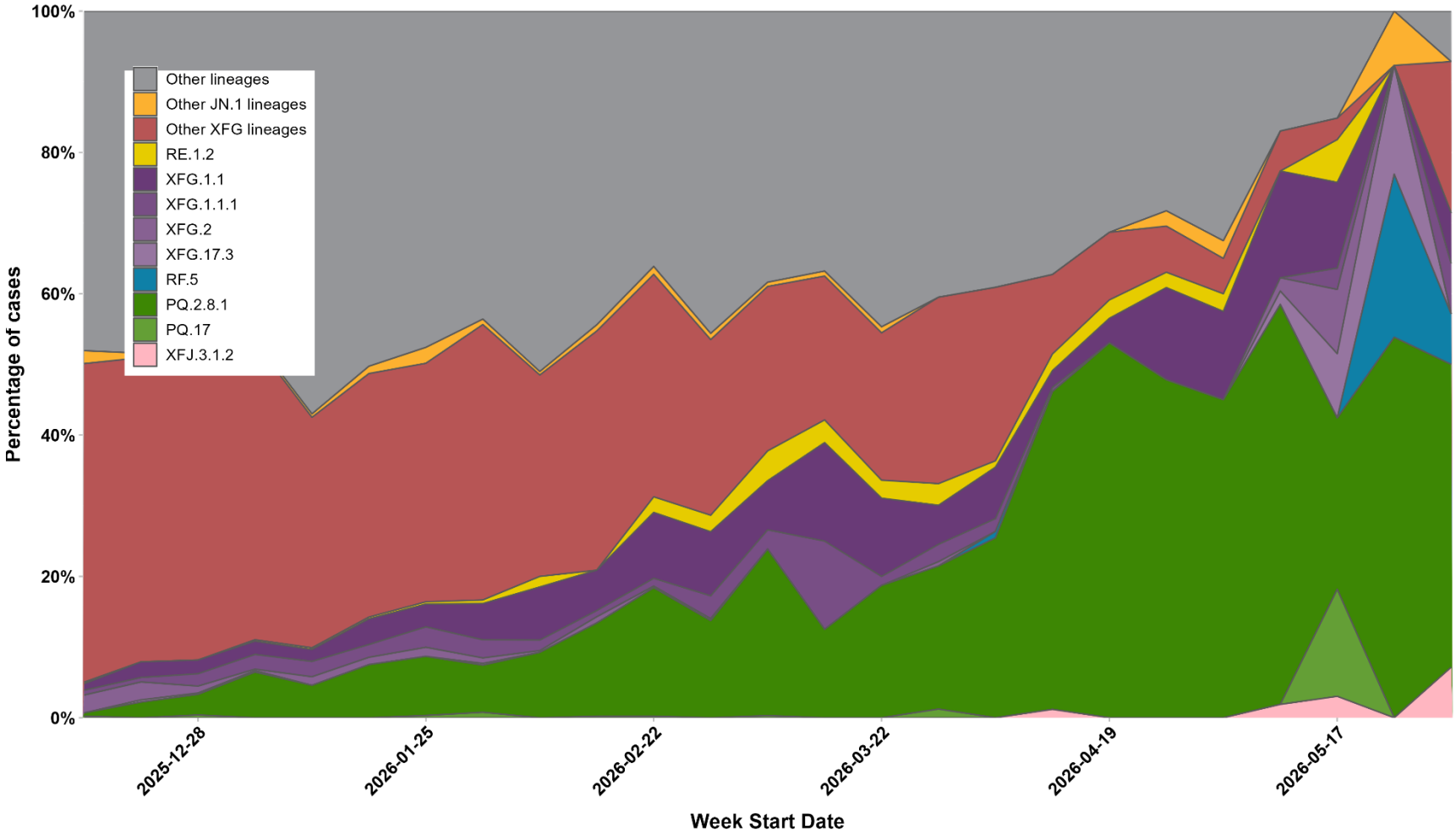
Representative Surveillance

Table 1: Number of SARS-CoV-2 Positive Specimens, Number and Percentage of Specimens Sequenced for Representative Surveillance by Four-Week Period, Ontario, February 22 to June 13, 2026

Four-Week Period	Number of Positive Specimens	Number of Specimens Sequenced	Percentage of Specimens Sequenced
February 22 - March 21	2,604	1,470	56.5%
March 22 - April 18	1,436	704	49.0%
April 19 - May 16	494	259	52.4%
May 17 - June 13	201	61	30.3%
Total	**4,735**	**2,494**	**52.7%**

Note: The 2,494 specimens sequenced were associated with 2,396 unique cases; in the most recent week, 61 specimens sequenced were associated with 61 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, December 14, 2025, to June 6, 2026



Note: The most recent week (June 7 - June 13) was excluded due to low counts (n=1). 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 Four-Week Period, Representative Surveillance, Ontario, February 22 to June 13, 2026

Pango Lineage	February 22 - March 21	March 22 - April 18	April 19 - May 16	May 17 - June 13	Total (February 22 - June 13)
PQ.2.8.1	242 (17.2%)	181 (26.7%)	131 (51.6%)	21 (34.4%)	575 (24.0%)
PQ.17	2 (0.1%)	2 (0.3%)	0 (0.0%)	5 (8.2%)	9 (0.4%)
XFG.1.1	135 (9.6%)	47 (6.9%)	23 (9.1%)	5 (8.2%)	210 (8.8%)
XFG.17.3	0 (0.0%)	0 (0.0%)	1 (0.4%)	5 (8.2%)	6 (0.3%)
RF.5	0 (0.0%)	1 (0.1%)	0 (0.0%)	4 (6.6%)	5 (0.2%)
XFG.1.1.1	60 (4.3%)	10 (1.5%)	0 (0.0%)	3 (4.9%)	73 (3.0%)
XFG.2	2 (0.1%)	1 (0.1%)	1 (0.4%)	3 (4.9%)	7 (0.3%)
RE.1.2	41 (2.9%)	16 (2.4%)	5 (2.0%)	2 (3.3%)	64 (2.7%)
XFJ.3.1.2	0 (0.0%)	2 (0.3%)	1 (0.4%)	2 (3.3%)	5 (0.2%)
Other lineages	922 (65.7%)	417 (61.6%)	92 (36.2%)	11 (18.0%)	1,442 (60.2%)
Total sequenced	**1,404 (100%)**	**677 (100%)**	**254 (100%)**	**61 (100%)**	**2,396 (100%)**

Note: Includes the most prevalent lineages detected in the past four-week period. 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)

Table 3: Number and Percentage of SARS-CoV-2 Cases by Pango Lineage and Age Group, Representative Surveillance, Ontario, May 17 to June 13, 2026

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
PQ.2.8.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (50.0%)	1 (33.3%)	4 (26.7%)	15 (44.1%)	21 (34.4%)
PQ.17	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (6.7%)	4 (11.8%)	5 (8.2%)
XFG.1.1	1 (16.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (26.7%)	0 (0.0%)	5 (8.2%)
XFG.17.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (14.7%)	5 (8.2%)
RF.5	2 (33.3%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (33.3%)	0 (0.0%)	1 (2.9%)	4 (6.6%)
XFG.1.1.1	1 (16.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (13.3%)	0 (0.0%)	3 (4.9%)
XFG.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (6.7%)	2 (5.9%)	3 (4.9%)
RE.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (5.9%)	2 (3.3%)
XFJ.3.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (33.3%)	0 (0.0%)	1 (2.9%)	2 (3.3%)
Other lineages	2 (33.3%)	1 (100%)	0 (0.0%)	1 (50.0%)	0 (0.0%)	3 (20.0%)	4 (11.8%)	11 (18.0%)
Total Sequenced	**6 (100%)**	**1 (100%)**	**0 (0.0%)**	**2 (100%)**	**3 (100%)**	**15 (100%)**	**34 (100%)**	**61 (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 4: Number and Percentage of SARS-CoV-2 Cases by Pango Lineage and Geographic Region, Representative Surveillance, Ontario, May 17 to June 13, 2026

Pango Lineage	North West	North East	Eastern	Central East	Toronto	South West	Central West	Unknown	Total
PQ.2.8.1	0 (0.0%)	2 (100%)	1 (100%)	0 (0.0%)	0 (0.0%)	10 (76.9%)	3 (25.0%)	5 (35.7%)	21 (34.4%)
PQ.17	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (10.0%)	4 (44.4%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (8.2%)
XFG.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (20.0%)	1 (11.1%)	0 (0.0%)	0 (0.0%)	2 (14.3%)	5 (8.2%)
XFG.17.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (41.7%)	0 (0.0%)	5 (8.2%)
RF.5	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (16.7%)	2 (14.3%)	4 (6.6%)
XFG.1.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (8.3%)	2 (14.3%)	3 (4.9%)
XFG.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (30.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (4.9%)
RE.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (15.4%)	0 (0.0%)	0 (0.0%)	2 (3.3%)
XFJ.3.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (11.1%)	0 (0.0%)	1 (8.3%)	0 (0.0%)	2 (3.3%)
Other lineages	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (40.0%)	3 (33.3%)	1 (7.7%)	0 (0.0%)	3 (21.4%)	11 (18.0%)
Total Sequenced	**0 (0.0%)**	**2 (100%)**	**1 (100%)**	**10 (100%)**	**9 (100%)**	**13 (100%)**	**12 (100%)**	**14 (100%)**	**61 (100%)**

Note: Cases with missing/unassigned patient postal code (23.0%) or out of province postal codes (0.0%) 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 5: Number of SARS-CoV-2 Cases by Pango Lineage, Cumulative Counts, Ontario, May 17 to June 13, 2026

WHO Label / Pango Lineage	May 17 - June 13, 2026
MC.10.1.7	1
PQ.17	5
PQ.2.1.7	1
PQ.2.5.3	1
PQ.2.8.1	21
RE.1.2	2
RE.2.1.1	1
RE.2.2.3	1
RE.2.2.4	1
RF.5	4
RV.1	1
XFG.1.1	5
XFG.1.1.1	3
XFG.1.1.2	1
XFG.14.1.1	1
XFG.17.3	5
XFG.2	3
XFG.3.24	1
XFG.6	1
XFJ.3.1.2	2
Total Sequenced	61

Note: Results do not represent all Ontario cases. Includes results from the OHDP-PHAE from the past four-week period. 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 June 25, 2026 at approximately 9:00 a.m.

Public Health Ontario (PHO)

- Data were submitted to the OHDP-PHAE on June 16, 2026 at approximately 12:00 p.m.

The Hospital for Sick Children (HSC)

- Data were submitted to the OHDP-PHAE on June 23, 2026 at approximately 10:30 a.m.

Kingston Health Sciences Centre (KHSC)

- Data were submitted to the OHDP-PHAE on June 24, 2026 at approximately 11:15 a.m.

Shared Hospital Laboratory (SHL)

- Data were submitted to the OHDP-PHAE on May 26, 2026 at approximately 12:45 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were submitted to the OHDP-PHAE on June 18, 2026 at approximately 3:00 p.m.

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

- OLIS data were extracted from Public Health Ontario's ORVT on June 26, 2026 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 4.3.4, pangolin data version 1.38, pangolin assignment version 1.38, 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. 23.0% of cases had missing/unassigned patient postal code, and 0.0% 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 (formerly Porcupine Health Unit and Timiskaming 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 (formerly Hastings and Prince Edward Counties Health Unit, Kingston, Frontenac and Lennox and Addington Health Unit, and Leeds, Grenville and Lanark District Health Unit).
    - Central East region includes Durham Region Health Department, Lakelands Public Health (formerly Haliburton, Kawartha, Pine Ridge District Health Unit and Peterborough County-City 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 (formerly Brant County Health Unit and Haldimand-Norfolk 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.

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.

References

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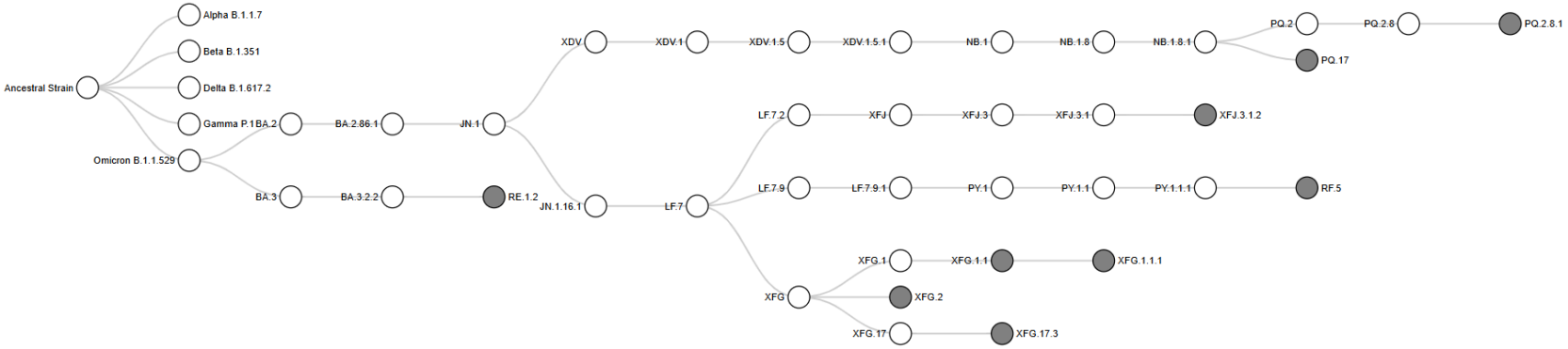
Appendix A: Pango Lineages

Figure 1: Relationship of the most prevalent SARS-CoV-2 Pango lineages in Ontario, May 17 to June 13, 2026



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. XDV is a recombinant of XDE and JN.1; XFJ is a recombinant of LF.7.2 and LS.2.1.1; and XFG is a recombinant of LF.7 and LP.8.1.2.
Data source: cov-lineages.org

Citation

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