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SURVEILLANCE REPORT

SARS-CoV-2 Genomic Surveillance in Ontario: November 2, 2026

Published: November 2026

Background

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by the Ontario COVID-19 Genomics Network as of October 28, 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 (September 20 to October 17), a total of 523 cases were sequenced. The most prevalent lineage was PJ.2.1 (25.2%) followed by ST.1 (12.8%), and SW.2.1 (8.2%).
    - The proportion of PJ.2.1 increased from 16.9% (August 23 to September 19) to 25.2% (September 20 to October 17).
    - The proportion of ST.1 increased from 1.1% (August 23 to September 19) to 12.8% (September 20 to October 17).
    - The proportion of SW.2.1 increased from 3.3% (August 23 to September 19) to 8.2% (September 20 to October 17).

Lineage counts and designations may change between reports as components of the Pango lineage assignment models are updated (see Technical Notes for details).

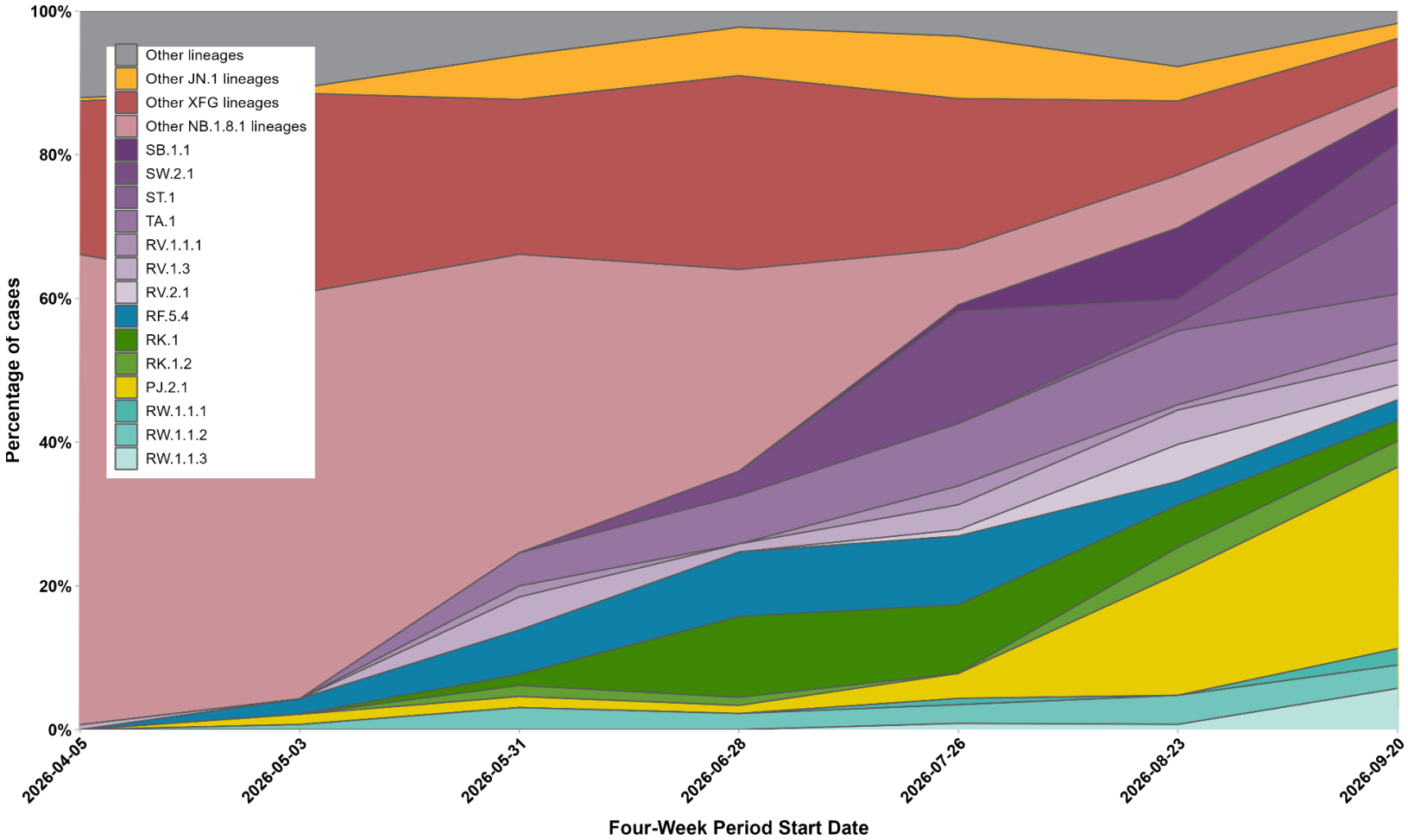
Representative Surveillance

Table 1: Number of SARS-CoV-2 Positive Specimens, Number and Percentage of Specimens Sequenced for Representative Surveillance by Four-Week Period, Ontario, June 28 to October 17, 2026

Four-Week Period	Number of Positive Specimens	Number of Specimens Sequenced	Percentage of Specimens Sequenced
June 28 - July 25	171	91	53.2%
July 26 - August 22	209	115	55.0%
August 23 - September 19	518	277	53.5%
September 20 - October 17	1,088	539	49.5%
Total	**1,986**	**1,022**	**51.5%**

Note: The 1,022 specimens sequenced were associated with 999 unique cases; in the most recent four-week period, 539 specimens sequenced were associated with 523 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, April 5 to October 17, 2026



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 Four-Week Period, Representative Surveillance, Ontario, June 28 to October 17, 2026

Pango Lineage	June 28 - July 25	July 26 - August 22	August 23 - September 19	September 20 - October 17	Total (June 28 - October 17)
PJ.2.1	1 (1.1%)	4 (3.5%)	46 (16.9%)	132 (25.2%)	183 (18.3%)
ST.1	0 (0.0%)	0 (0.0%)	3 (1.1%)	67 (12.8%)	70 (7.0%)
SW.2.1	3 (3.4%)	18 (15.7%)	9 (3.3%)	43 (8.2%)	73 (7.3%)
TA.1	6 (6.7%)	10 (8.7%)	28 (10.3%)	36 (6.9%)	80 (8.0%)
RW.1.1.3	0 (0.0%)	1 (0.9%)	2 (0.7%)	30 (5.7%)	33 (3.3%)
SB.1.1	0 (0.0%)	1 (0.9%)	27 (9.9%)	25 (4.8%)	53 (5.3%)
RK.1.2	1 (1.1%)	0 (0.0%)	10 (3.7%)	19 (3.6%)	30 (3.0%)
RV.1.3	1 (1.1%)	4 (3.5%)	13 (4.8%)	18 (3.4%)	36 (3.6%)
RW.1.1.2	2 (2.2%)	3 (2.6%)	11 (4.0%)	17 (3.3%)	33 (3.3%)
RF.5.4	8 (9.0%)	11 (9.6%)	9 (3.3%)	15 (2.9%)	43 (4.3%)
RK.1	10 (11.2%)	11 (9.6%)	16 (5.9%)	15 (2.9%)	52 (5.2%)
RV.1.1.1	0 (0.0%)	3 (2.6%)	2 (0.7%)	12 (2.3%)	17 (1.7%)
RW.1.1.1	0 (0.0%)	1 (0.9%)	0 (0.0%)	12 (2.3%)	13 (1.3%)
RV.2.1	0 (0.0%)	1 (0.9%)	14 (5.1%)	11 (2.1%)	26 (2.6%)
Other lineages	57 (64.0%)	47 (40.9%)	82 (30.1%)	71 (13.6%)	257 (25.7%)
Total sequenced	**89 (100%)**	**115 (100%)**	**272 (100%)**	**523 (100%)**	**999 (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, September 20 to October 17, 2026

Pango Lineage	Ages: 0-4	Ages: 5-11	Ages: 12-17	Ages: 18-39	Ages: 40-59	Ages: 60-79	Ages: 80 and over	Total
PJ.2.1	4 (19.0%)	0 (0.0%)	1 (33.3%)	10 (32.3%)	15 (41.7%)	41 (27.5%)	60 (21.4%)	131 (25.1%)
ST.1	1 (4.8%)	0 (0.0%)	0 (0.0%)	1 (3.2%)	2 (5.6%)	23 (15.4%)	40 (14.2%)	67 (12.8%)
SW.2.1	1 (4.8%)	0 (0.0%)	0 (0.0%)	3 (9.7%)	0 (0.0%)	10 (6.7%)	29 (10.3%)	43 (8.2%)
TA.1	4 (19.0%)	0 (0.0%)	0 (0.0%)	2 (6.5%)	3 (8.3%)	10 (6.7%)	17 (6.0%)	36 (6.9%)
RW.1.1.3	1 (4.8%)	0 (0.0%)	0 (0.0%)	1 (3.2%)	2 (5.6%)	9 (6.0%)	17 (6.0%)	30 (5.7%)
SB.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (3.2%)	4 (11.1%)	6 (4.0%)	14 (5.0%)	25 (4.8%)
RK.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	6 (4.0%)	13 (4.6%)	19 (3.6%)
RV.1.3	1 (4.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	7 (4.7%)	10 (3.6%)	18 (3.4%)
RW.1.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (3.4%)	12 (4.3%)	17 (3.3%)
RF.5.4	2 (9.5%)	0 (0.0%)	0 (0.0%)	3 (9.7%)	0 (0.0%)	3 (2.0%)	7 (2.5%)	15 (2.9%)
RK.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.8%)	5 (3.4%)	9 (3.2%)	15 (2.9%)
RV.1.1.1	1 (4.8%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (5.6%)	0 (0.0%)	9 (3.2%)	12 (2.3%)
RW.1.1.1	0 (0.0%)	0 (0.0%)	1 (33.3%)	1 (3.2%)	0 (0.0%)	2 (1.3%)	8 (2.8%)	12 (2.3%)
RV.2.1	1 (4.8%)	0 (0.0%)	0 (0.0%)	3 (9.7%)	0 (0.0%)	3 (2.0%)	4 (1.4%)	11 (2.1%)
Other lineages	5 (23.8%)	1 (100%)	1 (33.3%)	6 (19.4%)	7 (19.4%)	19 (12.8%)	32 (11.4%)	71 (13.6%)
Total Sequenced	**21 (100%)**	**1 (100%)**	**3 (100%)**	**31 (100%)**	**36 (100%)**	**149 (100%)**	**281 (100%)**	**522 (100%)**

Note: 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, September 20 to October 17, 2026

Pango Lineage	North West	North East	Eastern	Central East	Toronto	South West	Central West	Unknown	Total
PJ.2.1	0 (0.0%)	0 (0.0%)	9 (17.6%)	29 (20.4%)	58 (32.2%)	2 (11.8%)	22 (30.1%)	12 (21.1%)	132 (25.2%)
ST.1	0 (0.0%)	1 (33.3%)	0 (0.0%)	3 (2.1%)	38 (21.1%)	3 (17.6%)	19 (26.0%)	3 (5.3%)	67 (12.8%)
SW.2.1	0 (0.0%)	0 (0.0%)	1 (2.0%)	29 (20.4%)	7 (3.9%)	4 (23.5%)	0 (0.0%)	2 (3.5%)	43 (8.2%)
TA.1	0 (0.0%)	2 (66.7%)	0 (0.0%)	13 (9.2%)	4 (2.2%)	1 (5.9%)	10 (13.7%)	6 (10.5%)	36 (6.9%)
RW.1.1.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.4%)	28 (15.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	30 (5.7%)
SB.1.1	0 (0.0%)	0 (0.0%)	13 (25.5%)	3 (2.1%)	2 (1.1%)	0 (0.0%)	2 (2.7%)	5 (8.8%)	25 (4.8%)
RK.1.2	0 (0.0%)	0 (0.0%)	3 (5.9%)	7 (4.9%)	3 (1.7%)	1 (5.9%)	2 (2.7%)	3 (5.3%)	19 (3.6%)
RV.1.3	0 (0.0%)	0 (0.0%)	14 (27.5%)	3 (2.1%)	1 (0.6%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	18 (3.4%)
RW.1.1.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.7%)	14 (7.8%)	0 (0.0%)	0 (0.0%)	2 (3.5%)	17 (3.3%)
RF.5.4	0 (0.0%)	0 (0.0%)	2 (3.9%)	5 (3.5%)	3 (1.7%)	0 (0.0%)	2 (2.7%)	3 (5.3%)	15 (2.9%)
RK.1	0 (0.0%)	0 (0.0%)	1 (2.0%)	9 (6.3%)	3 (1.7%)	0 (0.0%)	1 (1.4%)	1 (1.8%)	15 (2.9%)
RV.1.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	10 (7.0%)	0 (0.0%)	0 (0.0%)	2 (2.7%)	0 (0.0%)	12 (2.3%)
RW.1.1.1	0 (0.0%)	0 (0.0%)	3 (5.9%)	4 (2.8%)	4 (2.2%)	1 (5.9%)	0 (0.0%)	0 (0.0%)	12 (2.3%)
RV.2.1	0 (0.0%)	0 (0.0%)	3 (5.9%)	2 (1.4%)	4 (2.2%)	0 (0.0%)	0 (0.0%)	2 (3.5%)	11 (2.1%)
Other lineages	0 (0.0%)	0 (0.0%)	2 (3.9%)	22 (15.5%)	11 (6.1%)	5 (29.4%)	13 (17.8%)	18 (31.6%)	71 (13.6%)
Total Sequenced	**0 (0.0%)**	**3 (100%)**	**51 (100%)**	**142 (100%)**	**180 (100%)**	**17 (100%)**	**73 (100%)**	**57 (100%)**	**523 (100%)**

Note: Cases with missing/unassigned patient postal code (10.9%) or out of province postal codes (0.0%) were included in the "Unknown" category. 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, September 20 to October 17, 2026

WHO Label / Pango Lineage	September 20 - October 17, 2026
PJ.2.1	132
RC.1	1
RF.5.2	3
RF.5.3.1	8
RF.5.4	15
RK.1	15
RK.1.2	19
RV.1	4
RV.1.1	6
RV.1.1.1	12
RV.1.3	18
RV.2.1	11
RW.1.1	1
RW.1.1.1	12
RW.1.1.2	17
RW.1.1.3	30
SB.1.1	25
ST.1	67
SV.1	2
SV.1.2	6
SV.2	7
SW.2	1
SW.2.1	43
TA.1	36
TD.1	1
XFG	1
XFG.1.1	7
XFG.1.1.1	1

WHO Label / Pango Lineage	September 20 - October 17, 2026
XFG.1.1.3	4
XFG.1.1.7	1
XFG.14.1.1	8
XFG.2.8	1
XFG.6.13	1
XFZ.4.1	1
XHA	6
Total Sequenced	**523**

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 October 29, 2026 at approximately 9:00 a.m.

Public Health Ontario (PHO)

- Data were submitted to the OHDP-PHAE on October 27, 2026 at approximately 2:15 p.m.

The Hospital for Sick Children (HSC)

- Data were submitted to the OHDP-PHAE on October 27, 2026 at approximately 11:30 a.m.

Kingston Health Sciences Centre (KHSC)

- Data were submitted to the OHDP-PHAE on October 27, 2026 at approximately 1:45 p.m.

Shared Hospital Laboratory (SHL)

- Data were submitted to the OHDP-PHAE on October 27, 2026 at approximately 12:30 p.m.

Hamilton Regional Laboratory Medicine Program (HRLMP)

- Data were submitted to the OHDP-PHAE on September 29, 2026 at approximately 12:15 p.m.

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

- OLIS data were extracted from Public Health Ontario's ORVT on October 30, 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 1.40, pangolin assignment version 1.40, 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. 10.9% 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

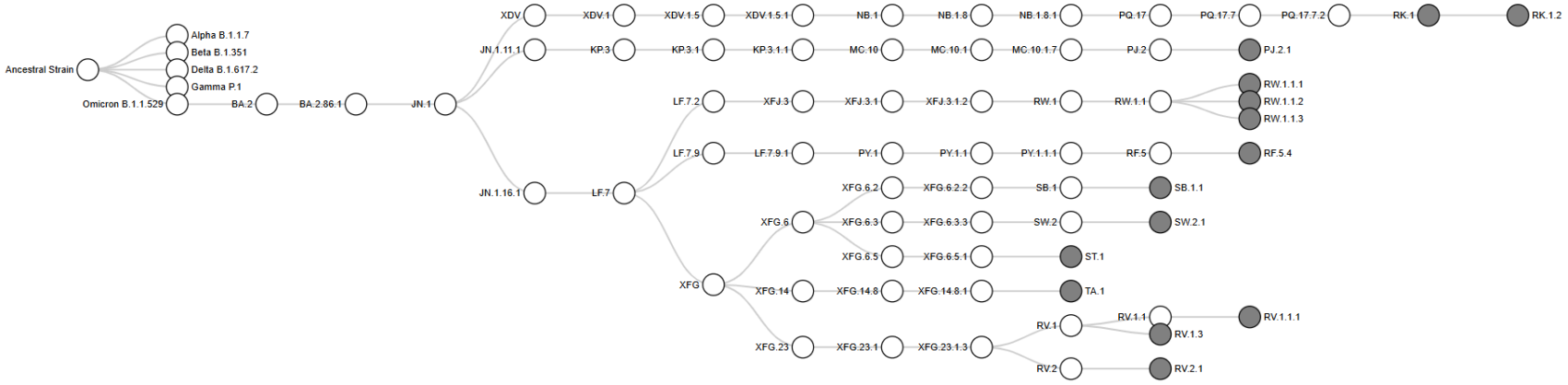
- Sample collection date is used to assign the date of the test.
- The number of tests performed does not reflect the number of specimens or persons tested. More than one test may be performed per specimen or per person. As such, the number of positive tests does not necessarily translate to the number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

References

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 2026 September 3; 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 2026 July 28; 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 26 September 2025 [Internet]. Stockholm, Sweden; 2021 [modified 2026 September 25; 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

Appendix A: Pango Lineages

Figure 1: Relationship of the most prevalent SARS-CoV-2 Pango lineages in Ontario, September 20 to October 17, 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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