Public Health Ontario | Santé publique Ontario

SURVEILLANCE REPORT

Respiratory Syncytial Virus Genomic Surveillance in Ontario: 2025–26

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Introduction

This report summarizes the results of respiratory syncytial virus (RSV) whole genome sequencing (WGS) completed by Public Health Ontario (PHO) for the 2025–26 season. The 2024–25 report can be found on PHO's website.

Highlights

- A total of 2,770 RSV positive specimens were detected at PHO between August 24, 2025, and April 25, 2026. A random sample of 236 (8.5%) were sequenced.
- Among the 236 specimens sequenced, 58 (24.6%) were RSV-A and 178 (75.4%) were RSV-B.
- The most common RSV-A clade was A.D.3 (9.3% of all RSV specimens).
- The most common RSV-B clade was B.D.E.1 (66.1% of all RSV specimens).

Background

RSV is a major cause of lower respiratory illness, particularly among premature infants or infants under six months of age, children with underlying health conditions, and adults over 65 years of age.[1] RSV is classified into two antigenic subgroups (RSV-A and RSV-B) based on variation in the G protein, a component of the viral envelope.[2]

As RSV spreads through populations, it accumulates genetic changes (mutations), which allow further classification into subgroups and clades.[3] While many of these genetic differences do not affect the virus's ability to cause disease, some mutations may influence characteristics such as virulence.[4]

Genomic surveillance uses WGS to monitor these changes as the virus evolves over time. This allows us to provide context to the current season, understand which clades are circulating and how this may impact the population.[5] While formal national surveillance programs similar to those in place for influenza may not yet exist, it is important to monitor circulating clades to establish baseline values for future comparison as Health Canada has authorized three vaccines: ABRYSVO®, AREXVY, and mRESVIA® for adults, as well as ABRYSVO® for pregnant women to prevent lower respiratory tract disease in infants.[6,7] Ontario has also introduced a publicly funded RSV prevention program targeting high-risk individuals and settings.[8]

PHO conducts approximately 17% of all RSV testing in Ontario, based on data from the Ontario Laboratories Information System. The remainder of testing is performed outside of PHO, primarily by hospitals and community laboratories.

PHO performs routine testing for seasonal respiratory viruses in select population groups, including individuals with respiratory symptoms who are in congregate living settings, part of an outbreak, or hospitalized.[9]

To understand the diversity of the RSV viruses circulating in Ontario, PHO sequenced a random sample of eligible specimens positive for RSV in the 2025–26 season. Specimens were eligible if they had a PCR cycle threshold (Ct) value ≤ 27, sufficient volume remaining, and no co-infection. For outbreak-associated samples, only the first specimen was eligible. Sequences were processed and analyzed using bioinformatics tools and were assigned to an RSV subgroup and clade.

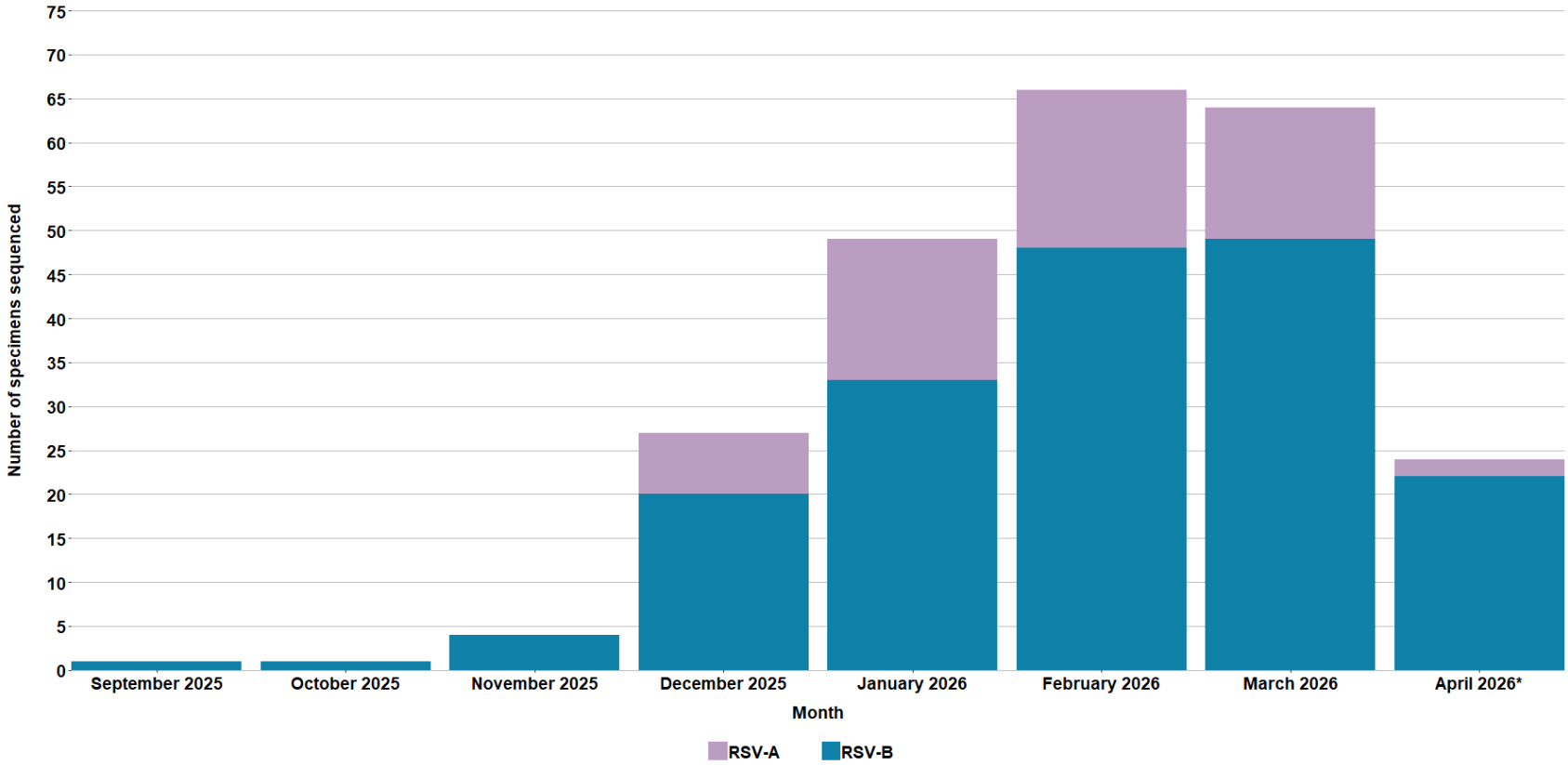
Results

Table 1: Number of Positive RSV Specimens, Number and Percentage Sequenced, Public Health Ontario, August 24, 2025 to April 25, 2026

Month	Number of Positive Specimens	Number Sequenced	Percentage Sequenced
August 2025*	1	0	0.0%
September 2025	5	1	20.0%
October 2025	28	1	3.6%
November 2025	105	4	3.8%
December 2025	331	27	8.2%
January 2026	717	49	6.8%
February 2026	701	66	9.4%
March 2026	647	64	9.9%
April 2026*	235	24	10.2%
Total	**2,770**	**236**	**8.5%**

Note: *August 2025 and April 2026 are partial months. Of the 236 specimens sequenced, 16.9% (40/236) were outbreak-associated.

Figure 1: Number of Positive RSV Specimens Sequenced by Subgroup and Month, Public Health Ontario, August 24, 2025 to April 25, 2026



Note: *April 2026 is a partial month. There were no specimens successfully sequenced for August 2025.

Table 2: Number and Percentage of Positive RSV Specimens Sequenced by Genetic Characterization and Month, Public Health Ontario, August 24, 2025 to April 25, 2026

Genetic Characterization	September 2025	October 2025	November 2025	December 2025	January 2026	February 2026	March 2026	April 2026*	Total
RSV-A clades	**0 (0.0%)**	**0 (0.0%)**	**0 (0.0%)**	**7 (25.9%)**	**16 (32.7%)**	**18 (27.3%)**	**15 (23.4%)**	**2 (8.3%)**	**58 (24.6%)**
A.D.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (7.4%)	1 (2.0%)	4 (6.1%)	1 (1.6%)	0 (0.0%)	8 (3.4%)
A.D.1.4	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (3.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.4%)
A.D.1.5	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (3.7%)	1 (2.0%)	2 (3.0%)	0 (0.0%)	0 (0.0%)	4 (1.7%)
A.D.1.6	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.0%)	2 (3.0%)	1 (1.6%)	0 (0.0%)	4 (1.7%)
A.D.2.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (1.5%)	0 (0.0%)	0 (0.0%)	1 (0.4%)
A.D.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (3.7%)	9 (18.4%)	4 (6.1%)	7 (10.9%)	1 (4.2%)	22 (9.3%)
A.D.3.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (3.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.4%)
A.D.3.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.0%)	0 (0.0%)	2 (3.1%)	0 (0.0%)	3 (1.3%)
A.D.3.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.0%)	2 (3.0%)	3 (4.7%)	0 (0.0%)	6 (2.5%)
A.D.5.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.0%)	1 (1.5%)	1 (1.6%)	1 (4.2%)	4 (1.7%)
A.D.5.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (3.7%)	1 (2.0%)	2 (3.0%)	0 (0.0%)	0 (0.0%)	4 (1.7%)
RSV-B clades	**1 (100%)**	**1 (100%)**	**4 (100%)**	**20 (74.1%)**	**33 (67.3%)**	**48 (72.7%)**	**49 (76.6%)**	**22 (91.7%)**	**178 (75.4%)**
B.D.4.1.1	0 (0.0%)	1 (100%)	1 (25.0%)	2 (7.4%)	5 (10.2%)	9 (13.6%)	2 (3.1%)	2 (8.3%)	22 (9.3%)
B.D.E.1	1 (100%)	0 (0.0%)	3 (75.0%)	18 (66.7%)	28 (57.1%)	39 (59.1%)	47 (73.4%)	20 (83.3%)	156 (66.1%)
Total sequenced	**1 (100%)**	**1 (100%)**	**4 (100%)**	**27 (100%)**	**49 (100%)**	**66 (100%)**	**64 (100%)**	**24 (100%)**	**236 (100%)**

Note: *April 2026 is a partial month. There were no specimens successfully sequenced for August 2025.

Table 3: Number and Percentage of Positive RSV Specimens Sequenced by Genetic Characterization and Age Group, Public Health Ontario, August 24, 2025 to April 25, 2026

Genetic Characterization	Less than 1 Year	1–4 Years	5–19 Years	20–64 Years	65 Years and Over	Total
RSV-A clades	**1 (20.0%)**	**5 (55.6%)**	**1 (25.0%)**	**7 (28.0%)**	**44 (22.8%)**	**58 (24.6%)**
A.D.1	0 (0.0%)	1 (11.1%)	1 (25.0%)	0 (0.0%)	6 (3.1%)	8 (3.4%)
A.D.1.4	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	1 (0.4%)
A.D.1.5	0 (0.0%)	1 (11.1%)	0 (0.0%)	1 (4.0%)	2 (1.0%)	4 (1.7%)
A.D.1.6	0 (0.0%)	1 (11.1%)	0 (0.0%)	0 (0.0%)	3 (1.6%)	4 (1.7%)
A.D.2.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	1 (0.4%)
A.D.3	1 (20.0%)	1 (11.1%)	0 (0.0%)	3 (12.0%)	17 (8.8%)	22 (9.3%)
A.D.3.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.5%)	1 (0.4%)
A.D.3.2	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (1.6%)	3 (1.3%)
A.D.3.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (4.0%)	5 (2.6%)	6 (2.5%)
A.D.5.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (8.0%)	2 (1.0%)	4 (1.7%)
A.D.5.2	0 (0.0%)	1 (11.1%)	0 (0.0%)	0 (0.0%)	3 (1.6%)	4 (1.7%)
RSV-B clades	**4 (80.0%)**	**4 (44.4%)**	**3 (75.0%)**	**18 (72.0%)**	**149 (77.2%)**	**178 (75.4%)**
B.D.4.1.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	5 (20.0%)	17 (8.8%)	22 (9.3%)
B.D.E.1	4 (80.0%)	4 (44.4%)	3 (75.0%)	13 (52.0%)	132 (68.4%)	156 (66.1%)
Total sequenced	**5 (100%)**	**9 (100%)**	**4 (100%)**	**25 (100%)**	**193 (100%)**	**236 (100%)**

Note: Age was assigned based on the birth date provided on the test requisition.

Table 4: Number and Percentage of Positive RSV Specimens Sequenced by Genetic Characterization and Setting, Public Health Ontario, August 24, 2025 to April 25, 2026

Genetic Characterization	Intensive Care Unit	Hospital/Emergency Department	Congregate Living	Other/No Setting Reported	Total
RSV-A clades	**1 (100%)**	**13 (32.5%)**	**43 (23.6%)**	**1 (7.7%)**	**58 (24.6%)**
A.D.1	0 (0.0%)	2 (5.0%)	6 (3.3%)	0 (0.0%)	8 (3.4%)
A.D.1.4	0 (0.0%)	0 (0.0%)	1 (0.5%)	0 (0.0%)	1 (0.4%)
A.D.1.5	0 (0.0%)	2 (5.0%)	2 (1.1%)	0 (0.0%)	4 (1.7%)
A.D.1.6	1 (100%)	2 (5.0%)	1 (0.5%)	0 (0.0%)	4 (1.7%)
A.D.2.1	0 (0.0%)	1 (2.5%)	0 (0.0%)	0 (0.0%)	1 (0.4%)
A.D.3	0 (0.0%)	2 (5.0%)	20 (11.0%)	0 (0.0%)	22 (9.3%)
A.D.3.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (7.7%)	1 (0.4%)
A.D.3.2	0 (0.0%)	0 (0.0%)	3 (1.6%)	0 (0.0%)	3 (1.3%)
A.D.3.3	0 (0.0%)	3 (7.5%)	3 (1.6%)	0 (0.0%)	6 (2.5%)
A.D.5.1	0 (0.0%)	0 (0.0%)	4 (2.2%)	0 (0.0%)	4 (1.7%)
A.D.5.2	0 (0.0%)	1 (2.5%)	3 (1.6%)	0 (0.0%)	4 (1.7%)
RSV-B clades	**0 (0.0%)**	**27 (67.5%)**	**139 (76.4%)**	**12 (92.3%)**	**178 (75.4%)**
B.D.4.1.1	0 (0.0%)	3 (7.5%)	17 (9.3%)	2 (15.4%)	22 (9.3%)
B.D.E.1	0 (0.0%)	24 (60.0%)	122 (67.0%)	10 (76.9%)	156 (66.1%)
Total sequenced	**1 (100%)**	**40 (100%)**	**182 (100%)**	**13 (100%)**	**236 (100%)**

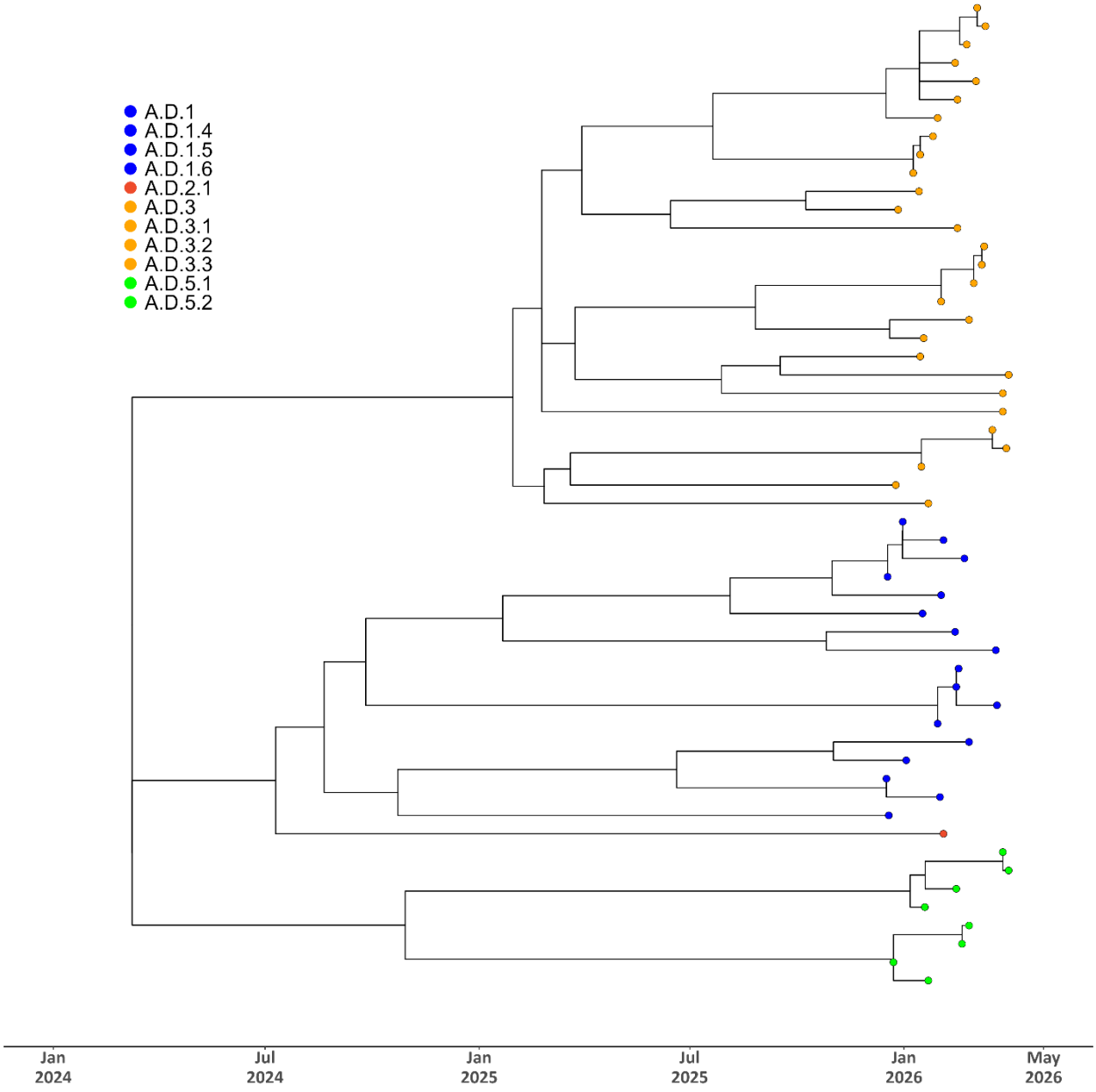
Note: Setting represents the health care facility at which an individual received care. “Congregate Living” includes long-term care homes, retirement homes, correctional facilities, and undefined institutions (excluding hospitals).

Table 5: Number and Percentage of Positive RSV Specimens Sequenced by Genetic Characterization and Region, Public Health Ontario, August 24, 2025 to April 25, 2026

Genetic Characterization	Northern	Eastern	Central East	Toronto	South West	Central West	Total
RSV-A clades	**1 (16.7%)**	**16 (50.0%)**	**14 (23.3%)**	**4 (9.5%)**	**14 (28.0%)**	**9 (19.6%)**	**58 (24.6%)**
A.D.1	0 (0.0%)	0 (0.0%)	2 (3.3%)	1 (2.4%)	1 (2.0%)	4 (8.7%)	8 (3.4%)
A.D.1.4	0 (0.0%)	0 (0.0%)	1 (1.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.4%)
A.D.1.5	1 (16.7%)	0 (0.0%)	0 (0.0%)	1 (2.4%)	2 (4.0%)	0 (0.0%)	4 (1.7%)
A.D.1.6	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (6.0%)	1 (2.2%)	4 (1.7%)
A.D.2.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.0%)	0 (0.0%)	1 (0.4%)
A.D.3	0 (0.0%)	6 (18.8%)	7 (11.7%)	0 (0.0%)	5 (10.0%)	4 (8.7%)	22 (9.3%)
A.D.3.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.4%)	0 (0.0%)	0 (0.0%)	1 (0.4%)
A.D.3.2	0 (0.0%)	2 (6.2%)	1 (1.7%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (1.3%)
A.D.3.3	0 (0.0%)	4 (12.5%)	0 (0.0%)	0 (0.0%)	2 (4.0%)	0 (0.0%)	6 (2.5%)
A.D.5.1	0 (0.0%)	4 (12.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (1.7%)
A.D.5.2	0 (0.0%)	0 (0.0%)	3 (5.0%)	1 (2.4%)	0 (0.0%)	0 (0.0%)	4 (1.7%)
RSV-B clades	**5 (83.3%)**	**16 (50.0%)**	**46 (76.7%)**	**38 (90.5%)**	**36 (72.0%)**	**37 (80.4%)**	**178 (75.4%)**
B.D.4.1.1	1 (16.7%)	0 (0.0%)	1 (1.7%)	9 (21.4%)	1 (2.0%)	10 (21.7%)	22 (9.3%)
B.D.E.1	4 (66.7%)	16 (50.0%)	45 (75.0%)	29 (69.0%)	35 (70.0%)	27 (58.7%)	156 (66.1%)
Total sequenced	**6 (100%)**	**32 (100%)**	**60 (100%)**	**42 (100%)**	**50 (100%)**	**46 (100%)**	**236 (100%)**

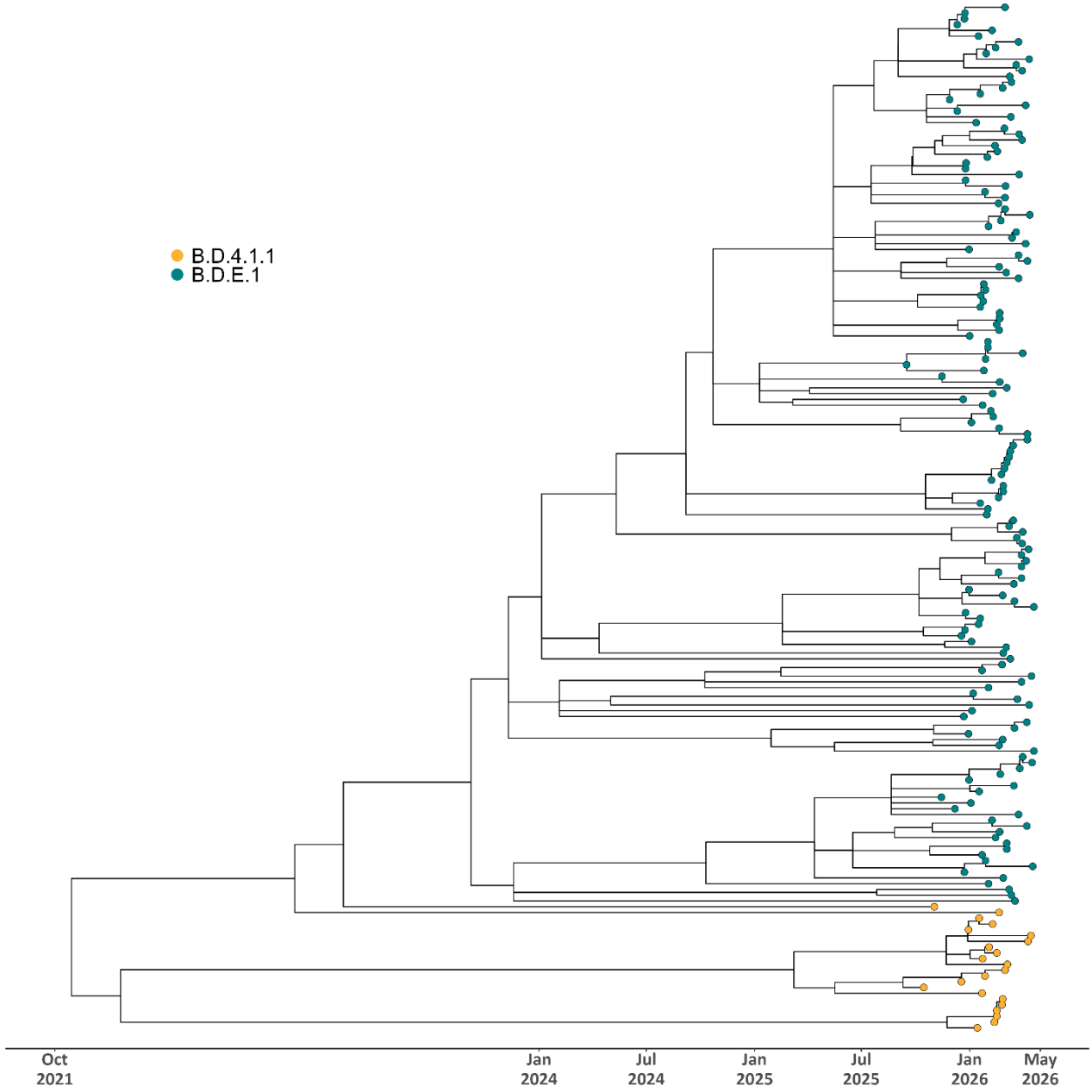
Note: Region was assigned using patient address when available. If missing, region was assigned using submitter address. For additional information on which public health units are included in each region, see Technical Notes.

Figure 2a: Time-Scaled Phylogenetic Tree of RSV-A Specimens Sequenced, Public Health Ontario, August 24, 2025 to April 25, 2026



Note: Sequences of the RSV G gene (which encodes the virus' surface attachment protein) were analyzed for 54 RSV-A specimens and are shown in the phylogenetic tree. The G gene is commonly used for RSV genotyping and molecular epidemiology due to variability within its sequence. Each circle (tip) represents one specimen, and the colour indicates its RSV-A clade. The branches (horizontal lines) show the estimated time to a common ancestor, with the tips representing individual specimens (descendants). The x-axis represents time and can be used to infer the specimen date.

Figure 2b: Time-Scaled Phylogenetic Tree of RSV-B Specimens Sequenced, Public Health Ontario, August 24, 2025 to April 25, 2026



Note: Sequences of the RSV G gene (which encodes the virus' surface attachment protein) were analyzed for 178 RSV-B specimens and are shown in the phylogenetic tree. The G gene is commonly used for RSV genotyping and molecular epidemiology due to variability within its sequence. Each circle (tip) represents one specimen, and the colour indicates its RSV-B clade. The branches (horizontal lines) show the estimated time to a common ancestor, with the tips representing individual specimens (descendants). The x-axis represents time and can be used to infer the specimen date.

Technical Notes

Data Sources

Public Health Ontario

- Data were extracted from the PHO Laboratory Information Management System on April 28, 2026 at approximately 10:00am.
- Bioinformatics processing of data by the Biocomputing Centre were completed on May 21, 2026 at approximately 10:00am.

RSV Whole Genome Sequencing Strategy

- Public Health Ontario used random sampling to select 300 eligible RSV PCR positive specimens for whole genome sequencing. Of the 300 specimens, 236 had sufficient volume and were successfully sequenced.
- Specimens were eligible for WGS if they had Ct value ≤ 27 for RSV, sufficient volume remaining, and were PCR positive only for RSV (no co-infection). Additionally, only the first specimen from an outbreak was eligible for WGS and specimens that were submitted on behalf of the Sentinel Practitioner Surveillance Network (SPSN) were excluded.
- Only upper respiratory specimens (e.g. nasopharyngeal or throat swabs) were included.
- Genetic characterization of specimens was completed using WGS and analyzed by a bioinformatics pipeline using ivar (1.3.1), bwa-mem (0.7.17), bcftools (1.12), and vcftools (0.1.16).[10-13] Clade was assigned with Nextclade (3.20.0) analysis.[14] Time-scaled phylogenetic tree was created using IQ-TREE 3 and TreeTime.[15,16] The maximum likelihood phylogenetic tree was generated based on RSV G-gene sequences using IQ-TREE 3 with a TIM2+F+G4 model (for RSV-A), TN+F+R2 model (for RSV-B), and 1000 bootstrap replicates.

Respiratory Testing Methods

- RSV testing at PHO is performed using:
  - A laboratory-developed multiplex respiratory virus PCR panel assay (MRVP). The assay detects 11 viral targets including RSV.
  - A FLUVID PCR assay which detects RSV, influenza A and B, and SARS-CoV-2 (COVID-19).

Respiratory Testing Algorithm

- PHO's laboratory respiratory testing algorithm is based on patient setting.
- MRVP testing is offered to individuals exhibiting respiratory symptoms that meet at least one of the following eligibility criteria:
  - Hospitalized patients requiring intensive care
  - Hospitalized admitted patients that are
    - Children < 18 years who are at risk of complications, in the presence of community-acquired pneumonia, or

        - immunocompromised or immunosuppressed, or
        - pregnant
    - Patients/residents who are part of a hospital or PHU-declared respiratory outbreak. Only the first four symptomatic patients in a respiratory outbreak are eligible, subsequent patients will be tested by FLUVID.
- FLUVID testing is offered to individuals exhibiting respiratory symptoms that meet at least one of the following eligibility criteria:
    - Residents in congregate living setting (long-term care, retirement home, and correctional facilities) that are not in an outbreak
    - Residents of a congregate living setting that is in an outbreak beyond the first four specimens tested by MRVP
    - Adults admitted to the hospital
    - Staff from congregate living settings that are part of an outbreak.
- Individuals attending physician offices that are part of the Sentinel Practitioner Surveillance Network (SPSN)[17] are tested by MRVP and are exempt from laboratory testing restrictions.

Data Caveats

- PHO conducts approximately 17% of RSV testing in Ontario. Further, only 8.5% of positive specimens were sequenced during the current season. Biases may be introduced due to eligibility criteria for diagnostic testing, catchment area of PHO testing, the volume of specimen available, WGS specimen selection criteria, and whether a specimen can be successfully sequenced. As a result, the results may not be representative of Ontario overall.
- Numbers and proportions may not align with the Ontario Respiratory Virus Tool as only specimens tested at PHO and eligible for WGS (Ct value ≤ 27 for RSV, sufficient volume remaining, and first specimen from an outbreak) were included in the report.
- The report includes specimens tested from the start of the respiratory season (August 24, 2025) to when a stable decrease in the percent positivity was observed. Thus, the time period covered may not represent the entire season. Counts based on specimens do not represent unique individuals, as some individuals may have more than one specimen tested.
- The specimen date was assigned using the sample collection date when available, or the date of entry into PHO's laboratory information system if the collection date was missing.
- Sequences from four RSV-A specimens were not included in the phylogenetic tree due to low G-gene coverage.
- Age was assigned based on the birth date provided and the specimen date (sample collection date when available, or the date of entry into PHO's laboratory information system if the collection date was missing).
- Region was assigned based on patient address when available or submitter address when missing. As such, individuals with missing patient address on the requisition may be misclassified.
    - Northern region includes Algoma Public Health, Northeastern Public Health (formerly Porcupine Health Unit and Timiskaming Health Unit), Northwestern Health Unit, North Bay Parry Sound District Health Unit, Public Health Sudbury & Districts, and Thunder Bay District Health Unit;

- Eastern includes Eastern Ontario Health Unit, Ottawa Public Health, Renfrew County and District Health Unit, and Southeast Public Health (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 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 includes Toronto Public Health;
- South West 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 includes City of Hamilton Public Health Services, Grand Erie Public Health (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.

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