WEEKLY EPIDEMIOLOGICAL SUMMARY

SARS-CoV-2 Whole Genome Sequencing in Ontario, July 28, 2021

This report summarizes the results of SARS-CoV-2 whole genome sequencing completed by Public Health Ontario as of July 22, 2021 and partner laboratories in the Ontario COVID-19 Genomics Network as of July 21, 2021.

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). Current VOCs include B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma) and B.1.617.2 (Delta). 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[1], the World Health Organization[2], and the European Centre for Disease Prevention and Control.[3]

The Ontario COVID-19 Genomics Network 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

- From June 13 to July 10, 2021, there were 3,911 cases sequenced by the Ontario COVID-19 Genomics Network for representative surveillance. The majority were Pango lineage B.1.617.2 (Delta; 63.6%), followed by B.1.1.7 (Alpha; 30.0%), P.1 (Gamma; 2.3%), and B.1.1.318 (2.3%).
- The proportion that were B.1.617.2 (Delta) remained stable between June 27 to July 3 (78.6%) and July 4 to July 10 (78.0%).
- The public health units with the highest proportion of B.1.617.2 (Delta) from July 4 to July 10, 2021 were: Grey Bruce Health Unit (100%), Region of Waterloo Public Health and Emergency Services (94.2%), and Wellington-Dufferin-Guelph Public Health (91.7%); excluding public health units with fewer than 20 cases sequenced.
- From January 1, 2021 to July 10, 2021, a total of 18 cases have been identified as B.1.621 and seven cases have been identified as C.37 (Lambda).

> The OCGN has implemented a representative surveillance strategy and moved to sequencing 100% of eligible samples on June 14. This will allow for provincial estimates of the prevalence of VOC, VOI, and other lineages.
>
> For cumulative whole genome sequencing results, the selection of samples has historically been influenced by laboratory testing algorithms. This has created a sampling bias prior to the implementation of representative surveillance that prevents the interpretation of relative proportions of circulating lineages during that time.

Representative Surveillance

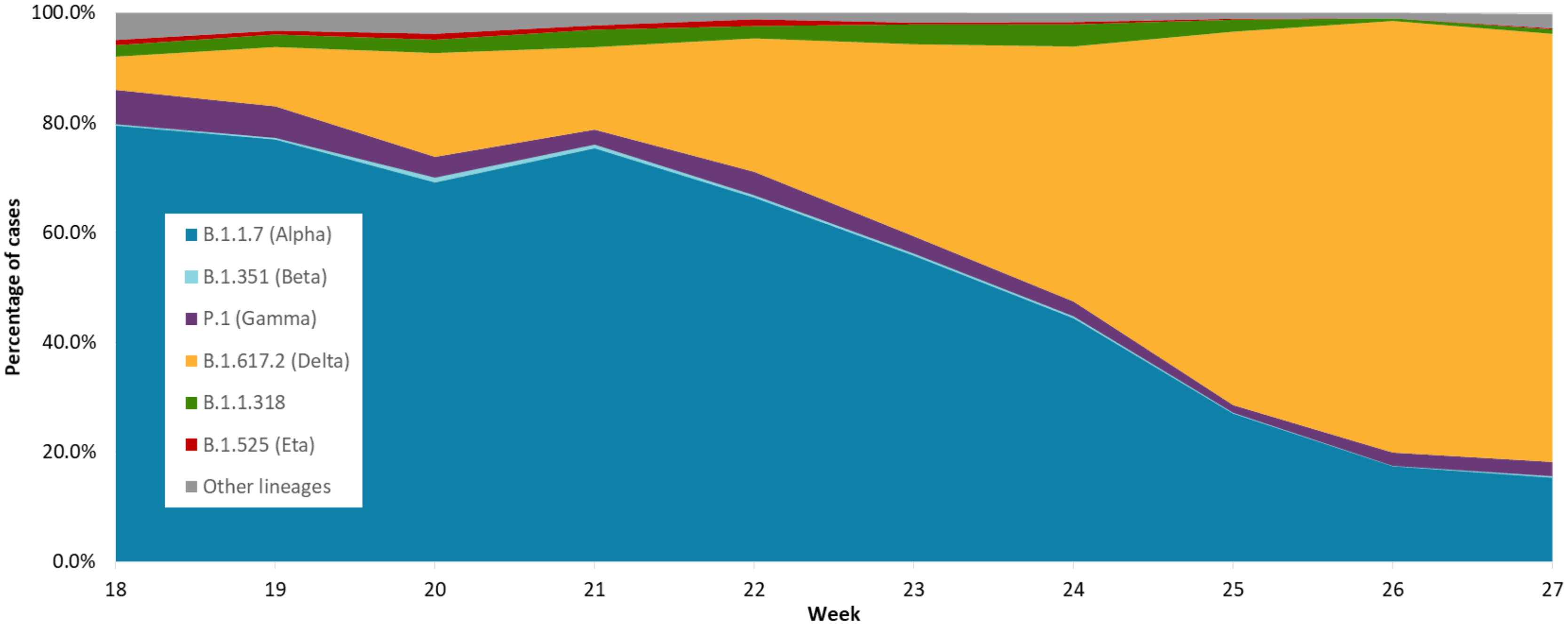
Table 1. Number of COVID-19 cases, number and percentage of cases sequenced for representative surveillance by week, Ontario, June 13 to July 10, 2021

Week	Number of cases	Number sequenced	Percentage sequenced
Week 24 (June 13 to 19)	2,348	1,442	61.4%
Week 25 (June 20 to 26)	1,810	1,145	63.3%
Week 26 (June 27 to July 3)	1,399	824	58.9%
Week 27 (July 4 to July 10)	1,229	500	40.7%
Total	**6,786**	**3,911**	**57.6%**

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. For representative surveillance: The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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 source: CCM, PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Figure 1. Percentage of COVID-19 cases by top 6 most prevalent VOC/VOI lineages and week, representative surveillance, Ontario, May 2 to July 10, 2021



Note: Results may not be representative of Ontario overall, particularly in earlier weeks. PHO began sequencing 10% of eligible samples on May 2 (week 18), 50% on May 30 (week 22), and 100% on June 14 (week 24). Other VOC PCR testing laboratories were asked to submit 10% of eligible samples to the Ontario COVID-19 Genomics Network (OCGN) on May 26, 50% on June 2, and 100% on June 14. 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 source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 2. Number and percentage of cases by VOC/VOI Pango lineage and week, representative surveillance, Ontario, June 13 to July 10, 2021

Pango lineage (WHO label)	Week 24 (June 13-19)	Week 25 (June 20-26)	Week 26 (June 27-July 3)	Week 27 (July 4-July 10)	Total (June 13-July 10)
Variant of concern (VOC)					
B.1.1.7 (Alpha)	641 (44.5%)	310 (27.1%)	144 (17.5%)	77 (15.4%)	1,172 (30.0%)
B.1.351 (Beta)	4 (0.3%)	1 (0.1%)	0 (0.0%)	1 (0.2%)	6 (0.2%)
P.1 (Gamma)	39 (2.7%)	16 (1.4%)	20 (2.4%)	13 (2.6%)	88 (2.3%)
B.1.617.2 (Delta)	670 (46.5%)	779 (68.0%)	648 (78.6%)	390 (78.0%)	2,487 (63.6%)
Variant of interest (VOI)					
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	58 (4.0%)	25 (2.2%)	4 (0.5%)	4 (0.8%)	91 (2.3%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	6 (0.4%)	2 (0.2%)	0 (0.0%)	1 (0.2%)	9 (0.2%)
B.1.526 (Iota)	2 (0.1%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (0.1%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	3 (0.2%)	3 (0.3%)	4 (0.5%)	4 (0.8%)	14 (0.4%)
C.37 (Lambda)	1 (0.1%)	0 (0.0%)	0 (0.0%)	1 (0.2%)	2 (0.1%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	18 (1.2%)	9 (0.8%)	4 (0.5%)	9 (1.8%)	40 (1.0%)
Total sequenced	**1,442 (100%)**	**1,145 (100%)**	**824 (100%)**	**500 (100%)**	**3,911 (100%)**

Note: Results may not be representative of Ontario overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. Week was assigned based on the earliest date available for the sample. If more than one sample was sequenced for a case, the most recent sample was included. 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 source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Table 3. Percentage of B.1.617.2 (Delta) cases identified (number identified/total sequenced) by public health unit (PHU), region, and week, representative surveillance, Ontario, June 13 to July 10, 2021

Public Health Unit	Week 24 (June 13-19)	Week 25 (June 20-26)	Week 26 (June 27-July 3)	Week 27 (July 4-July 10)	Total (June 13-July 10)
Northwestern Health Unit	100% (1/1)	66.7% (2/3)	100% (1/1)	0.0% (0/0)	80.0% (4/5)
Thunder Bay District Health Unit	0.0% (0/2)	0.0% (0/2)	0.0% (0/0)	0.0% (0/0)	0.0% (0/4)
TOTAL NORTH WEST	**33.3% (1/3)**	**40.0% (2/5)**	**100% (1/1)**	**0.0% (0/0)**	**44.4% (4/9)**
Algoma Public Health	0.0% (0/1)	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)	0.0% (0/1)
North Bay Parry Sound District Health Unit	0.0% (0/30)	2.4% (1/42)	0.0% (0/6)	100% (3/3)	4.9% (4/81)
Porcupine Health Unit	2.1% (1/47)	0.0% (0/20)	0.0% (0/7)	33.3% (1/3)	2.6% (2/77)
Public Health Sudbury & Districts	0.0% (0/19)	0.0% (0/10)	60.0% (3/5)	100% (1/1)	11.4% (4/35)
Timiskaming Health Unit	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)	0.0% (0/0)
TOTAL NORTH EAST	**1.0% (1/97)**	**1.4% (1/72)**	**16.7% (3/18)**	**71.4% (5/7)**	**5.2% (10/194)**
Ottawa Public Health	7.3% (7/96)	17.6% (9/51)	35.7% (5/14)	85.7% (6/7)	16.1% (27/168)
Eastern Ontario Health Unit	0.0% (0/4)	0.0% (0/2)	0.0% (0/0)	33.3% (1/3)	11.1% (1/9)
Hastings Prince Edward Public Health	0.0% (0/1)	100% (1/1)	100% (3/3)	100% (2/2)	85.7% (6/7)
Kingston, Frontenac and Lennox & Addington Public Health	0.0% (0/5)	60.0% (3/5)	50.0% (1/2)	28.6% (2/7)	31.6% (6/19)
Leeds, Grenville & Lanark District Health Unit	0.0% (0/3)	0.0% (0/2)	0.0% (0/0)	100% (1/1)	16.7% (1/6)
Renfrew County and District Health Unit	0.0% (0/5)	0.0% (0/0)	0.0% (0/2)	0.0% (0/1)	0.0% (0/8)
TOTAL EASTERN	**6.1% (7/114)**	**21.3% (13/61)**	**42.9% (9/21)**	**57.1% (12/21)**	**18.9% (41/217)**
Durham Region Health Department	38.9% (21/54)	51.4% (18/35)	60.0% (9/15)	63.6% (7/11)	47.8% (55/115)
Haliburton, Kawartha, Pine Ridge District Health Unit	81.8% (9/11)	100% (4/4)	90.0% (9/10)	85.7% (6/7)	87.5% (28/32)
Peel Public Health	44.9% (84/187)	67.7% (65/96)	67.2% (43/64)	63.9% (53/83)	57.0% (245/430)
Peterborough Public Health	0.0% (0/10)	60.0% (3/5)	20.0% (3/15)	36.4% (4/11)	24.4% (10/41)
Simcoe Muskoka District Health Unit	65.0% (26/40)	82.4% (14/17)	71.4% (15/21)	88.9% (8/9)	72.4% (63/87)
York Region Public Health	32.7% (18/55)	63.3% (19/30)	78.3% (18/23)	90.9% (10/11)	54.6% (65/119)
TOTAL CENTRAL EAST	**44.3% (158/357)**	**65.8% (123/187)**	**65.5% (97/148)**	**66.7% (88/132)**	**56.6% (466/824)**
Toronto Public Health	41.3% (100/242)	59.1% (104/176)	77.2% (61/79)	66.0% (33/50)	54.5% (298/547)
TOTAL TORONTO	**41.3% (100/242)**	**59.1% (104/176)**	**77.2% (61/79)**	**66.0% (33/50)**	**54.5% (298/547)**
Chatham-Kent Public Health	0.0% (0/3)	100% (1/1)	100% (3/3)	60.0% (3/5)	58.3% (7/12)
Grey Bruce Health Unit	100% (24/24)	96.2% (102/106)	97.0% (96/99)	100% (37/37)	97.4% (259/266)

Public Health Unit	Week 24 (June 13-19)	Week 25 (June 20-26)	Week 26 (June 27-July 3)	Week 27 (July 4-July 10)	Total (June 13-July 10)
Huron Perth Public Health	87.5% (7/8)	83.3% (5/6)	100% (17/17)	100% (3/3)	94.1% (32/34)
Lambton Public Health	37.5% (6/16)	66.7% (18/27)	85.7% (6/7)	100% (2/2)	61.5% (32/52)
Middlesex-London Health Unit	15.7% (8/51)	68.0% (17/25)	69.4% (25/36)	43.5% (10/23)	44.4% (60/135)
Southwestern Public Health	41.2% (7/17)	16.7% (2/12)	62.5% (5/8)	77.8% (7/9)	45.7% (21/46)
Windsor-Essex County Health Unit	0.0% (0/22)	33.3% (2/6)	0.0% (0/14)	33.3% (1/3)	6.7% (3/45)
TOTAL SOUTH WEST	**36.9% (52/141)**	**80.3% (147/183)**	**82.6% (152/184)**	**76.8% (63/82)**	**70.2% (414/590)**
Brant County Health Unit	35.7% (5/14)	66.7% (6/9)	75.0% (3/4)	50.0% (3/6)	51.5% (17/33)
City of Hamilton Public Health Services	32.4% (23/71)	54.7% (35/64)	73.2% (30/41)	100% (6/6)	51.6% (94/182)
Haldimand-Norfolk Health Unit	33.3% (2/6)	16.7% (1/6)	100% (2/2)	100% (1/1)	40.0% (6/15)
Halton Region Public Health	56.0% (28/50)	67.7% (21/31)	95.1% (39/41)	88.2% (15/17)	74.1% (103/139)
Niagara Region Public Health	26.0% (13/50)	57.9% (22/38)	50.0% (14/28)	75.0% (12/16)	46.2% (61/132)
Region of Waterloo Public Health and Emergency Services	94.5% (258/273)	97.5% (274/281)	92.0% (208/226)	94.2% (130/138)	94.8% (870/918)
Wellington-Dufferin-Guelph Public Health	91.3% (21/23)	96.8% (30/31)	96.7% (29/30)	91.7% (22/24)	94.4% (102/108)
TOTAL CENTRAL WEST	**71.9% (350/487)**	**84.6% (389/460)**	**87.4% (325/372)**	**90.9% (189/208)**	**82.1% (1,253/1,527)**
UNKNOWN	100% (1/1)	0.0% (0/1)	0.0% (0/1)	0.0% (0/0)	33.3% (1/3)
TOTAL ONTARIO	**46.5% (670/1,442)**	**68.0% (779/1,145)**	**78.6% (648/824)**	**78.0% (390/500)**	**63.6% (2,487/3,911)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. Week was assigned based on the earliest date available for the sample. If more than one sample was sequenced for a case, the most recent sample was included. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used if patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 4a. Number and percentage of cases by VOC/VOI Pango lineage and public health unit (PHU), representative surveillance, North West Region, June 13 to July 10, 2021

Pango lineage (WHO label)	Northwestern Health Unit	Thunder Bay District Health Unit	Total
Variant of concern			
B.1.1.7 (Alpha)	1 (20.0%)	2 (50.0%)	3 (33.3%)
B.1.351 (Beta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.1 (Gamma)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.2 (Delta)	4 (80.0%)	0 (0.0%)	4 (44.4%)
Variant of interest			
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	0 (0.0%)	2 (50.0%)	2 (22.2%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.526 (Iota)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	0 (0.0%)	0 (0.0%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	0 (0.0%)	0 (0.0%)	0 (0.0%)
Total sequenced	**5 (100%)**	**4 (100%)**	**9 (100%)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used if patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 4b. Number and percentage of cases by VOC/VOI Pango lineage and public health unit (PHU), representative surveillance, North East Region, June 13 to July 10, 2021

Pango lineage (WHO label)	Algoma Public Health	North Bay Parry Sound District Health Unit	Porcupine Health Unit	Public Health Sudbury & Districts	Timiskaming Health Unit	Total
Variant of concern						
B.1.1.7 (Alpha)	1 (100%)	76 (93.8%)	74 (96.1%)	30 (85.7%)	0 (0.0%)	181 (93.3%)
B.1.351 (Beta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.1 (Gamma)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.2 (Delta)	0 (0.0%)	4 (4.9%)	2 (2.6%)	4 (11.4%)	0 (0.0%)	10 (5.2%)
Variant of interest						
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.526 (Iota)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (2.9%)	0 (0.0%)	1 (0.5%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	0 (0.0%)	1 (1.2%)	1 (1.3%)	0 (0.0%)	0 (0.0%)	2 (1.0%)
Total sequenced	**1 (100%)**	**81 (100%)**	**77 (100%)**	**35 (100%)**	**0 (100%)**	**194 (100%)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used it patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 4c. Number and percentage of cases by VOC/VOI Pango lineage and public health unit (PHU), representative surveillance, Eastern Region, June 13 to July 10, 2021

Pango lineage (WHO label)	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
Variant of concern							
B.1.1.7 (Alpha)	6 (66.7%)	0 (0.0%)	13 (68.4%)	5 (83.3%)	140 (83.3%)	8 (100%)	172 (79.3%)
B.1.351 (Beta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.6%)	0 (0.0%)	1 (0.5%)
P.1 (Gamma)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.2 (Delta)	1 (11.1%)	6 (85.7%)	6 (31.6%)	1 (16.7%)	27 (16.1%)	0 (0.0%)	41 (18.9%)
Variant of interest							
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.526 (Iota)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	2 (22.2%)	1 (14.3%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (1.4%)
Total sequenced	**9 (100%)**	**7 (100%)**	**19 (100%)**	**6 (100%)**	**168 (100%)**	**8 (100%)**	**217 (100%)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used if patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 4d. Number and percentage of cases by VOC/VOI Pango lineage and public health unit (PHU), representative surveillance, Central East Region, June 13 to July 10, 2021

Pango lineage (WHO label)	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
Variant of concern							
B.1.1.7 (Alpha)	49 (42.6%)	4 (12.5%)	140 (32.6%)	31 (75.6%)	20 (23.0%)	37 (31.1%)	281 (34.1%)
B.1.351 (Beta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.1 (Gamma)	0 (0.0%)	0 (0.0%)	14 (3.3%)	0 (0.0%)	1 (1.1%)	5 (4.2%)	20 (2.4%)
B.1.617.2 (Delta)	55 (47.8%)	28 (87.5%)	245 (57.0%)	10 (24.4%)	63 (72.4%)	65 (54.6%)	466 (56.6%)
Variant of interest							
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	9 (7.8%)	0 (0.0%)	16 (3.7%)	0 (0.0%)	0 (0.0%)	6 (5.0%)	31 (3.8%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	2 (1.7%)	0 (0.0%)	5 (1.2%)	0 (0.0%)	0 (0.0%)	1 (0.8%)	8 (1.0%)
B.1.526 (Iota)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	0 (0.0%)	2 (0.5%)	0 (0.0%)	3 (3.4%)	0 (0.0%)	5 (0.6%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	0 (0.0%)	0 (0.0%)	8 (1.9%)	0 (0.0%)	0 (0.0%)	5 (4.2%)	13 (1.6%)
Total sequenced	**115 (100%)**	**32 (100%)**	**430 (100%)**	**41 (100%)**	**87 (100%)**	**119 (100%)**	**824 (100%)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used if patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 4e. Number and percentage of cases by VOC/VOI Pango lineage and public health unit (PHU), representative surveillance, Toronto Region, June 13 to July 10, 2021

Pango lineage (WHO label)	Toronto Public Health	Total
Variant of concern		
B.1.1.7 (Alpha)	190 (34.7%)	190 (34.7%)
B.1.351 (Beta)	1 (0.2%)	1 (0.2%)
P.1 (Gamma)	24 (4.4%)	24 (4.4%)
B.1.617.2 (Delta)	298 (54.5%)	298 (54.5%)
Variant of interest		
A.23.1	0 (0.0%)	0 (0.0%)
B.1.1.318	23 (4.2%)	23 (4.2%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	1 (0.2%)	1 (0.2%)
B.1.526 (Iota)	0 (0.0%)	0 (0.0%)
B.1.616	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)
B.1.621	5 (0.9%)	5 (0.9%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	5 (0.9%)	5 (0.9%)
Total sequenced	**547 (100%)**	**547 (100%)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used if patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 4f. Number and percentage of cases by VOC/VOI Pango lineage and public health unit (PHU), representative surveillance, South West Region, June 13 to July 10, 2021

Pango lineage (WHO label)	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
Variant of concern								
B.1.1.7 (Alpha)	5 (41.7%)	7 (2.6%)	1 (2.9%)	19 (36.5%)	52 (38.5%)	19 (41.3%)	26 (57.8%)	129 (21.9%)
B.1.351 (Beta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.1 (Gamma)	0 (0.0%)	0 (0.0%)	1 (2.9%)	1 (1.9%)	19 (14.1%)	6 (13.0%)	1 (2.2%)	28 (4.7%)
B.1.617.2 (Delta)	7 (58.3%)	259 (97.4%)	32 (94.1%)	32 (61.5%)	60 (44.4%)	21 (45.7%)	3 (6.7%)	414 (70.2%)
Variant of interest								
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	12 (26.7%)	12 (2.0%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.526 (Iota)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (4.4%)	2 (0.3%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (0.7%)	0 (0.0%)	0 (0.0%)	1 (0.2%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (2.2%)	0 (0.0%)	1 (2.2%)	4 (0.7%)
Total sequenced	**12 (100%)**	**266 (100%)**	**34 (100%)**	**52 (100%)**	**135 (100%)**	**46 (100%)**	**45 (100%)**	**590 (100%)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used if patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 4g. Number and percentage of cases by VOC/VOI Pango lineage and public health unit (PHU), representative surveillance, Central West Region, June 13 to July 10, 2021

Pango lineage (WHO label)	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
Variant of concern								
B.1.1.7 (Alpha)	5 (15.2%)	78 (42.9%)	3 (20.0%)	25 (18.0%)	56 (42.4%)	43 (4.7%)	4 (3.7%)	214 (14.0%)
B.1.351 (Beta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	4 (0.4%)	0 (0.0%)	4 (0.3%)
P.1 (Gamma)	2 (6.1%)	2 (1.1%)	0 (0.0%)	1 (0.7%)	11 (8.3%)	0 (0.0%)	0 (0.0%)	16 (1.0%)
B.1.617.2 (Delta)	17 (51.5%)	94 (51.6%)	6 (40.0%)	103 (74.1%)	61 (46.2%)	870 (94.8%)	102 (94.4%)	1,253 (82.1%)
Variant of interest								
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	8 (24.2%)	3 (1.6%)	6 (40.0%)	6 (4.3%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	23 (1.5%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525 (Eta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.526 (Iota)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	0 (0.0%)	0 (0.0%)	2 (1.4%)	0 (0.0%)	0 (0.0%)	2 (1.9%)	4 (0.3%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	1 (3.0%)	5 (2.7%)	0 (0.0%)	2 (1.4%)	4 (3.0%)	1 (0.1%)	0 (0.0%)	13 (0.9%)
Total sequenced	**33 (100%)**	**182 (100%)**	**15 (100%)**	**139 (100%)**	**132 (100%)**	**918 (100%)**	**108 (100%)**	**1,527 (100%)**

Note: Results may not be representative of public health units overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. 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. Public health unit was assigned based on diagnosing health unit in CCM. If a case did not link to CCM (4.0%), OCGN patient postal code was used or ordering provider postal code was used if patient postal code was missing.

Data source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program, CCM

Table 5. Number and percentage (row %) of outbreak-associated and non outbreak-associated cases by VOC/VOI Pango lineage, representative surveillance, Ontario, June 13 to July 10, 2021

Pango lineage (WHO label)	Outbreak-associated	Non outbreak-associated	Total cases
Variant of concern			
B.1.1.7 (Alpha)	136 (12.3%)	972 (87.7%)	1,108 (100%)
B.1.351 (Beta)	0 (0.0%)	6 (100%)	6 (100%)
P.1 (Gamma)	20 (23.5%)	65 (76.5%)	85 (100%)
B.1.617.2 (Delta)	347 (14.4%)	2,057 (85.6%)	2,404 (100%)
Variant of interest			
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	12 (13.3%)	78 (86.7%)	90 (100%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525	2 (22.2%)	7 (77.8%)	9 (100%)
B.1.526 (Iota)	0 (0.0%)	2 (100%)	2 (100%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	10 (100%)	10 (100%)
C.37 (Lambda)	0 (0.0%)	2 (100%)	2 (100%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	2 (5.9%)	32 (94.1%)	34 (100%)
Total sequenced	**519 (13.8%)**	**3,231 (86.2%)**	**3,750 (100%)**

Note: Cases include only those that linked to CCM (96.0%). 'Outbreak-associated cases' include cases linked to a confirmed outbreak as declared by the local medical officer of health or their designate. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction.
Data Sources: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Hamilton Regional Laboratory Medicine Program, The Shared Hospital Laboratory, CCM (outbreak Indicator)

Table 6. Number and percentage (row %) of ever hospitalized and deceased cases by VOC/VOI Pango lineage, representative surveillance, Ontario, June 13 to July 10, 2021

Pango lineage (WHO label)	Ever hospitalized	Deceased	Total cases
Variant of concern			
B.1.1.7 (Alpha)	84 (7.6%)	11 (1.0%)	1,108 (100%)
B.1.351 (Beta)	1 (16.7%)	0 (0.0%)	6 (100%)
P.1 (Gamma)	7 (8.2%)	3 (3.5%)	85 (100%)
B.1.617.2 (Delta)	204 (8.5%)	39 (1.6%)	2,404 (100%)
Variant of interest			
A.23.1	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.1.318	2 (2.2%)	1 (1.1%)	90 (100%)
B.1.427/B.1.429 (Epsilon)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.525	1 (11.1%)	0 (0.0%)	9 (100%)
B.1.526 (Iota)	1 (50.0%)	0 (0.0%)	2 (100%)
B.1.616	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.1 (Kappa)	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.617.3	0 (0.0%)	0 (0.0%)	0 (0.0%)
B.1.621	0 (0.0%)	0 (0.0%)	10 (100%)
C.37 (Lambda)	0 (0.0%)	0 (0.0%)	2 (100%)
P.2 (Zeta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
P.3 (Theta)	0 (0.0%)	0 (0.0%)	0 (0.0%)
Non-VOC/VOI	4 (11.8%)	1 (2.9%)	34 (100%)
Total sequenced	**304 (8.1%)**	**55 (1.5%)**	**3,750 (100%)**

Note: Cases include only those that linked to CCM (96.0%). Hospitalized cases include cases that reported hospitalization at time of data extraction. Deceased cases include cases that reported a “Fatal” outcome at the time of data extraction. Hospitalized cases and deceased cases are not mutually exclusive. Results may not be representative of Ontario overall. The Ontario COVID-19 Genomics Network (OCGN) began sequencing 100% of eligible samples on June 14. 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. Not all sequencing and bioinformatics analyses for recent weeks were complete at the time of data extraction.
Data Sources: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Hamilton Regional Laboratory Medicine Program, The Shared Hospital Laboratory, CCM (hospitalization and death indicators)

Cumulative Whole Genome Sequencing Results

Table 7. Number of cases by VOC/VOI Pango lineage, cumulative counts, Ontario, January 1, 2021 to July 10, 2021

Pango lineage (WHO label)	January 1 - June 12	June 13 - July 10	Total
Variant of concern (VOC)			
B.1.1.7 (Alpha)	10,319	1,202	11,521
B.1.351 (Beta)	1,210	6	1,216
P.1 (Gamma)	3,777	88	3,865
B.1.617.2 (Delta)	1,620	2,506	4,126
Variant of interest (VOI)			
A.23.1	96	0	96
B.1.1.318	1,628	91	1,719
B.1.427/B.1.429 (Epsilon)	21	0	21
B.1.525 (Eta)	377	9	386
B.1.526 (Iota)	132	3	135
B.1.616	0	0	0
B.1.617.1 (Kappa)	87	0	87
B.1.617.3	3	0	3
B.1.621	4	14	18
C.37 (Lambda)	5	2	7
P.2 (Zeta)	46	0	46
P.3 (Theta)	1	0	1
Non-VOC/VOI	3,647	41	3,688
Total sequenced	**22,973**	**3,962**	**26,935**

Note: Results do not represent all Ontario cases. Includes results from PHO since January 1, 2021, The Hospital for Sick Children since April 21, 2021, Kingston Health Sciences Centre since January 1, 2021, Shared Hospital Laboratory since March 26, 2021, and Hamilton Regional Laboratory Medicine Program since April 11, 2021. 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 source: PHO, The Hospital for Sick Children, Kingston Health Sciences Centre, Shared Hospital Laboratory, Hamilton Regional Laboratory Medicine Program

Technical Notes

Data Sources

- Public Health Ontario (PHO)
    - Data were extracted from the PHO Laboratory Information Management System on July 22 at approximately 5:00 a.m.
    - Data were extracted from the PHO SARS-CoV-2 Whole Genome Sequencing Database on July 22 at approximately 9:00 a.m.
- The Hospital for Sick Children (HSC)
    - Data were received by PHO on July 21, 2021 at approximately 12:00 p.m.
- Kingston Health Sciences Centre (KHSC)
    - Data were received by PHO on July 21, 2021 at approximately 3:00 p.m.
- Shared Hospital Laboratory (SHL)
    - Data were received by PHO on July 21, 2021 at approximately 6:00 p.m.
- Hamilton Regional Laboratory Medicine Program (HRLMP)
    - Data were received by PHO on July 21, 2021 at approximately 6:30 p.m.
- Public Health Case and Contact Management Solution (CCM)
    - Data were extracted from the Public Health Case and Contact Management Solution on July 21 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).

- Ontario’s strategy has recently shifted to representative surveillance with VOC PCR testing laboratories being asked to send 10% 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; 50% on May 30; and 100% on June 14. 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; 50% on June 2; and 100% on June 14. The proportion of samples sequenced may change over time with changes in provincial case trends.

Data Caveats and Methods

- 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.

- 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.

- 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.

Data Caveats and Methods: 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.

- PHO is unable to confirm whether VOC PCR testing laboratories have submitted eligible samples.

- 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 (4.0%), then public health unit was assigned using OCGN patient postal code or ordering provider postal code if patient postal code was missing.

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 COVID-19 Daily Epidemiological Summary

- 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.

- Tables for outbreak, hospitalized, and deceased indicators include only cases that linked to CCM (96.0% of cases). 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).

- 'Outbreak-associated cases' include cases linked to a confirmed outbreak as declared by the local medical officer of health or their designate in accordance to the Health Protection and Promotion Act and criteria outlined in Ministry guidance documents.

- Outbreaks in settings outside of Ontario are excluded from all outbreak counts.

- 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.

- Hospitalization includes all cases for which a hospital admission date was reported or hospitalization/ICU admission was reported as 'Yes' at the time of data extraction. It includes cases that have been discharged from hospital as well as cases that are currently hospitalized. Emergency room visits are not included in the number of reported hospitalizations.

- Deaths are determined by using the outcome field in CCM. Any case marked 'Fatal' is included in the deaths data. The CCM field Type of Death is not used to further categorize the data.

Data Caveats and Methods: Cumulative Whole Genome Sequencing Results

- The 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. Data submitted to PHO from other laboratories in the OCGN have not been independently verified.

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 2021 May 14; cited 2021 May 29]. 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 2021 July 6; cited 2021 July 9]. 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 8 July 2021 [Internet]. Stockholm, Sweden; 2021 [modified 2021 July 9; cited 2021 July 9]. 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

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