

ENHANCED EPIDEMIOLOGICAL SUMMARY

Early Dynamics of Omicron in Ontario, November 1 to December 23, 2021

Published: January 1, 2022

Purpose

We used data from Public Health Ontario (PHO) Laboratory SARS-CoV-2 testing, specifically the presence of S-gene target failure (SGTF), to estimate the prevalence of Omicron (B.1.1.529) in Ontario, and examine the growth rate of Omicron relative to Delta.

For more information on variants confirmed by whole genome sequencing, refer to the PHO's [SARS-CoV-2 Whole Genome Sequencing](#) weekly report.

Highlights

- SGTF – a genetic marker seen in the Omicron variant, can be used as a sensitive variant screening method for identifying the Omicron SARS-CoV-2 lineage.
- The modeled proportion of samples screening positive for SGTF increased from <1% in November to 90% for specimens collected on December 23, 2021.
- It is estimated that each Omicron case is infecting 3.5 times more individuals than Delta in Ontario during the November 28 to December 23 period.

Background

The SARS-CoV-2 Omicron variant is rapidly spreading in countries globally. Among other mutations, the Omicron variant has the 69/70 deletion, which is known to trigger SGTF in the TaqPath COVID-19 PCR test. Given that Delta was the dominant variant in early November 2021 and lacks the 69/70 deletion, SGTF can be used as a real-time, and comprehensive variant screening method for suspected SARS-CoV-2 infection with the Omicron variant.

Trends in SGTF prevalence among SARS-CoV-2 cases can be used as an indicator of whether a region is experiencing strain replacement from Delta to Omicron, and to estimate the relative growth rate advantage of the Omicron variant. Such methods were used to identify strain replacement of wild-type virus with Alpha in Canada and the United Kingdom in the early 2021.¹

We used data from SGTF screening conducted by PHO Laboratory to estimate the prevalence of Omicron in Ontario, and examine the growth rate of Omicron relative to Delta.

Methods

All SARS-CoV-2 clinical samples that were tested using TaqPath COVID-19 PCR at PHO, and with results available since November 1, 2021 were included. Samples were primarily collected with nasopharyngeal swabs. In response to the emergence of Omicron, Ontario implemented universal SGTF screening on December 6. Several laboratories began submitting SARS-CoV-2 positive specimens to PHO for SGTF screening on this day.

SGTF was defined as non-detection of the S-gene target among samples that had a medium to high viral load (cycle threshold ≤ 30 for both the N gene or the orf 1ab gene targets, representing approximately 90% of positive samples). This approach is estimated to yield a false positive rate of 0.1%.²

We modeled the proportion of SGTF positive samples using a binomial regression with a term capturing the daily change in the log-odds of SGTF. The date refers to the specimen collection date, or if missing, the login date. SGTF counts before November 28 (the date of the first Omicron-confirmed SGTF case in PHO data) were excluded. We then used the proportion model to estimate the current counts of SGTF cases and non-SGTF cases, province-wide.

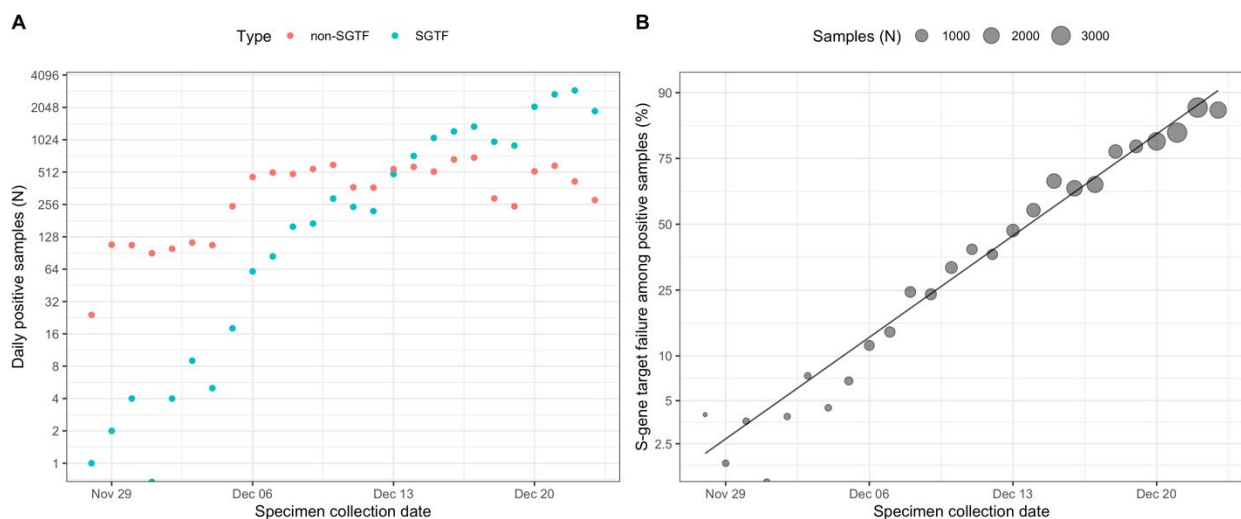
The daily relative growth rate of Omicron compared to Delta was estimated, as well as the relative R_t (real-time reproduction number – an estimate of the number of secondary cases per index case) assuming a generation interval of 5.2 days.³ Statistical analyses used the `mgcv` package within R (version 4.0.2). We conducted a nowcast to estimate the likely SGTF prevalence among persons at risk of being infected on December 23, based on a median incubation period of 5 days,⁴ and a median collection delay of 2 days (based on Ontario surveillance data from November 2021). Confirmatory whole genome sequencing was applied to all SGTF cases in the province, including those of other laboratories.

Results

Of 27,210 SARS-CoV-2 samples screened in the study period, 17,630 (64.8%) had SGTF (Figure 1, Panel A). The estimated proportion of samples with SGTF increased from $<1\%$ prior to November 28th to 90% on December 23 (Figure 1, Panel B). From province-wide whole genome sequencing, the first Omicron case was identified in a traveller on November 22. All SGTF cases identified by PHO Laboratory since November 22 with conclusive whole genome sequencing results have been confirmed as Omicron.

We estimated a daily relative growth rate for SGTF cases that was 48% faster than non-SGTF cases (Figure 1, panel B, selection coefficient = 0.24, 95%CI: 0.23 to 0.26). We estimated that each case of Omicron is infecting 3.5 times more individuals than Delta (95%CI: 3.3 to 3.8). Using nowcasting to account for delays due to the incubation period of SARS-CoV-2 and delays in presentation, testing, and reporting, the projected SGTF prevalence among persons infected with SARS-CoV-2 on December 31 was estimated to be greater than 95%.

Figure 1. Province-wide daily SGTF positive and SGTF negative counts tested by PHOL (panel A), and estimated SGTF prevalence on logistic scale (panel B).



Source: PHO Laboratory (PHOL)

Note: Samples are restricted to those with a cycle threshold of 30 or less; these cases with medium to high viral load with cycle threshold ≤ 30 represent the majority of SARS-CoV-2 cases in Ontario. The specificity of SGTF for detecting 69/70 deletion for samples with cycle threshold ≤ 30 in other targets is estimated to be approximately 99.9%. Panel A shows case counts with SGTF overtaking Delta around December 13. Panel B shows the increase in the proportion of samples with SGTF which is linear on a logit scale.

Discussion

We observed rapid growth of SGTF prevalence, beginning in late November in Ontario, Canada. A selection coefficient of 0.24 suggests that each Omicron case is infecting 3.5 times more individuals than Delta in Ontario, and is leading to rapid increases in SARS-CoV-2 in the province. Data from this study confirm that Omicron is highly transmissible and that the Omicron variant is already be the dominant variant circulating in Ontario.

Limitations

Note that current estimates of the selection coefficient are based on SGTF data from a short time period, and as such may be somewhat unstable. But our estimates are consistent with those based on data from UK (selection coefficient = 0.32)⁵ and Denmark (selection coefficient = 0.41).⁶ Note that SGTF cannot detect the BA.2 Omicron sublineage, though this sublineage only accounts for 3.3% (47/1439) of globally sequenced Omicron samples on GISAID as of December 12, 2021.

The data for this report were extracted from the PHO Laboratory Information Management System on December 30 at 5:00AM. As a result, data extracted represent a snapshot at the time of extraction and may differ from previous or subsequent reports.

References

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Citation

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Early dynamics of omicron in Ontario, November 1 to December 23, 2021. Toronto, ON: Queen's Printer for Ontario; 2022.

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