

EVIDENCE BRIEF

COVID-19 Omicron Variant Sub-lineage BA.2: Available Evidence and Risk Assessment

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Key Messages

- The Omicron variant (B.1.1.529) consists of four sub-lineages (BA.1, B.1.1, BA.2, and BA.3). The BA.2 sub-lineage, was designated a variant under investigation (VUI) by the United Kingdom (UK) on January 21, 2022. BA.2 sub-lineage is new and evolving with very limited information available.
- As of January 25, 2022, 51 cases of the BA.2 sub-lineage have been reported in Canada with the earliest case reported in December 2021.
- As of January 27, 2022, more than 18,000 BA.2 sub-lineage sequences have been reported globally from 54 countries. Initial reports were made on November 17, 2021 from the Philippines, but the origin of the sub-lineage is unknown.
- Denmark has reported the majority of cases globally, followed by India, the UK, Norway, Sweden and Singapore.
- There are early indications of sharp increases in the number of BA.2 sub-lineage cases reported in Denmark, Norway and the UK. It is important to note that growth rates may be overestimated early in the emergence of a variant.
- The current risk of BA.2 sub-lineage transmission in Ontario is unknown. The risk of severe disease, reinfection and breakthrough infection in Ontario is unknown at this time, with a high degree of uncertainty. The impact of the BA.2 sub-lineage on testing is considered low with a moderate degree of uncertainty and the impact on surveillance is considered low with a low degree of uncertainty.

Issue and Research Question

The BA.2 sub-lineage, has been identified in 54 countries with highest case counts reported in Denmark, United Kingdom (UK), India, Sweden and Singapore.¹ Considering evidence of increased transmissibility of the Omicron variant seen with BA.1 sub-lineage, it is important to closely monitor the potential impact that the BA.2 sub-lineage might have in Ontario. Our two main research questions were:

- What are the key characteristics of the BA.2 variant?
- What are the risks the BA.2 variant pose to Ontarians?

Methods

PHO Library Services conducted daily searches of primary and preprint literature using the MEDLINE database from January 1 to 24, 2022. A search was also conducted in PubMed on January 26, 2022 including keywords BA.2 and Omicron. The details of this search strategy are available upon request. In addition, an international jurisdictional search of disease surveillance and monitoring websites was conducted on January 28, 2022 in select jurisdictions (e.g., Denmark, Norway, UK, United States [US], India).

Genomic Features

The Omicron variant lineage (B.1.1.529) consists of four sub-lineages: BA.1, BA.1.1, BA.2, BA.3.² The BA.1 and BA.2 sub-lineages share 38 genetic mutations, with 21 of these occurring in the Spike protein. Aside from these shared mutations, BA.1 and BA.2 sub-lineages house an additional 20 and 27 mutations that are unique from one another.³

From a diagnostic perspective, the most notable difference in the BA.2 sub-lineage Spike is the lack of deletion at 69/70 that causes S-gene-target-failure (SGTF) in some PCR tests. SGTF is used as a proxy for the BA.1 sub-lineage.⁴ However, some VOC screening assays could be used to detect single nucleotide polymorphisms (SNPs) that are present in the BA.2 sub-lineage.

Epidemiology

Global

Data accessed on January 27, 2022 reports that 54 countries have uploaded 18,751 BA.2 sub-lineage sequences to GISAID,¹ with the first sequences reported to GISAID on November 17, 2021.⁴ Most cases have been reported by Denmark, followed by India, UK, Norway, Sweden and Singapore.¹ The Philippines was the first country to submit BA.2 sub-lineage sequences to GISAID; however, its origin is unknown.⁴

Canada

As of January 26, 2022 the National Genomics Database had 51 sample sequences uploaded that were identified as the BA.2 sub-lineage.⁵ Between January 2 and January 8, 2022, five cases were identified as BA.2 sub-lineage through representative surveillance in Ontario. A total of 15 BA.2 cases have been identified since January 1, 2021 in Ontario.⁶

Denmark

The Staten Serum Institut (SSI) reported an increase in the proportion of confirmed cases attributable to the BA.2 sub-lineage. During week 52 (last week of December 2021), the BA.2 sub-lineage accounted for 20% of all sequenced confirmed cases and increased to 45% in week 2 (second week of January, 2022).⁷ According to the GISAID initiative database, as of January 27, 2022, a cumulative total of 14,371 BA.2 sub-lineage sequences have been reported in Denmark.¹

United Kingdom

As of January 24, 2022, 1,072 sequences confirmed as BA.2 have been identified in England.⁸ This represents an increase from a recent UK Health Security Agency (UKHSA) report which confirmed a cumulative total of 426 cases of BA.2 sub-lineage that occurred between December 6, 2021 and January 21, 2022.⁴ This increase over a short time period led to the designation of the BA.2 sub-lineage as a variant under investigation (VUI) by the UK.⁴

Norway

The Norwegian Institute of Public Health (NIPH) has reported that cases of the BA.2 sub-lineage are increasing rapidly. As of January 26, 2022, BA.2 sub-lineage accounts for 9.8% of all genome-sequenced samples during the month of January.⁹ The total number of BA.2 sub-lineage cases increased from seven on January 4, 2022 to 611 on January 19, 2022.¹⁰

India

Omicron BA.2 sub-lineage has been reported in India. According to the GISAID initiative database, as of January 27, 2022, the BA.2 sub-lineage was found in 1,249 sequenced cases (1% of sequenced samples).¹

Singapore

Omicron BA.2 sub-lineage has been reported in Singapore. According to the GISAID initiative database, as of January 27, 2022, the BA.2 sub-lineage was found in 233 sequenced cases (16% of sequenced samples).¹

Sweden

Omicron BA.2 sub-lineage has been reported in Sweden. According to the GISAID initiative database, as of January 27, 2022, the BA.2 sub-lineage was found in 247 sequenced cases (4% of sequenced samples).¹

United States

Omicron BA.2 sub-lineage has been detected in seven states, with a total of 127 sequenced samples positive as of January 27, 2022 (<0.5% of sequenced samples).¹

Transmissibility

Several countries are reporting a rapid increase in the number of confirmed cases sequenced as the BA.2 sub-lineage.^{7,9} England has reported an increased growth rate for BA.2 sub-lineage compared to BA.1, however growth rates may be overestimated early in the emergence of a variant.⁸ The UKHSA has also reported higher secondary attack rates amongst BA.2 cases in households, however, the secondary attack rates are not adjusted for vaccination status and reflect overall growth advantage rather than transmissibility.⁸

Given the rise of BA.2 sub-lineage cases at a time when many countries are relaxing public health measures, it will be prudent to monitor scientific evidence on the degree of BA.2 sub-lineage transmission and any differences compared to the BA.1 sub-lineage.

Disease Severity

An initial analysis from Denmark reports no differences in hospitalizations between BA.1 and BA.2 sub-lineages. Early observations from India and Denmark suggest there is no difference in severity of disease caused by the BA.2 sub-lineage compared to BA.1.¹¹

Vaccine Effectiveness

Initial reports from the SSI (Denmark) and UKHSA indicate minimal difference in vaccine effectiveness between BA.1 and BA.2 sub-lineages to prevent severe illness and symptomatic disease.^{7,8,12} This analysis is ongoing.

Re-infection

No data was found discussing BA.2 sub-lineage re-infection cases.

Diagnostics

Given the BA.2 sub-lineage does not contain the deletion at S:69-70 it is S-gene target positive (SGTP) on PCR diagnostic tests.⁸ Given it is SGTP, SGTF screening method previously used to differentiate the Omicron BA.1 sub-lineage from other SARS-CoV-2 strains, cannot be used to rapidly identify the Omicron BA.2 sub-lineage, such as Delta variant. Variant surveillance supported by whole genome sequencing can be used to distinguish the BA.2 sub-lineage from other variants. Use of rapid antigen tests for BA.2 sub-lineage diagnostic purposes requires a better understanding of the test characteristics of this modality.¹³⁻¹⁵

Ontario Risk Assessment

The current risk of BA.2 sub-lineage transmission in Ontario is unknown, with a high degree of uncertainty. The risk of severe disease, reinfection and breakthrough infection in Ontario is unknown at this time but assumed to be the same the BA.1 sub-lineage, with a high degree of uncertainty. The impact of the BA.2 sub-lineage on testing considered low with a moderate degree of uncertainty and the impact on surveillance is considered low with a low degree of uncertainty.

The overall risk assessment may change as new evidence emerges (see Table 1).

Table 1. Risk Assessment for Omicron variant sub-lineage BA.2

Issues	Risk Level	Degree of Uncertainty
Increased Transmissibility	Unknown	High
Disease Severity	Unknown	High
COVID-19 Re-infection	Unknown	High
Lowered Vaccine Effectiveness/Breakthrough Infections	Unknown	High
Impact on Testing	Low	Moderate
Impact on Surveillance	Low	Low

Implications for Practice

A cautious approach should be used when assessing the risk of BA.2 sub-lineage in Ontario. Given its recent emergence, many unknowns for the BA.2 sub-lineage remain including evidence of its transmissibility, disease severity, vaccine effectiveness, and diagnostics. Despite unique mutations between BA.1 and BA.2 sub-lineages, early data appears to show no significant difference in disease severity or vaccine effectiveness. With rapid increases in the proportion of cases attributable to BA.2 compared to BA.1 sub-lineages in some countries, close monitoring of its transmissibility is required. Similar to BA.1 sub-lineage, existing public health measures (e.g., masking, physical distancing, gathering limits) and accelerated booster vaccinations are likely to remain the most important measures to mitigate impacts to the health system.

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