

EVIDENCE BRIEF

COVID-19 Omicron Variant Sub-lineage BA.2: Evidence and Risk Assessment (up to date as of March 22, 2022)

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Key Messages

- The proportion of whole genome sequencing samples identified as BA.2 in Ontario have an increasing trend over the past several weeks: 12.3% the week of February 13 to 19, increasing to 24.9% February 27 to March 5, 2022.
- As of March 21, 2022, GISAID reported 409,959 sequences of the BA.2 sub-lineage, with reports from at least 102 countries.
- Studies and real world epidemiological data continue to show BA.2 is more transmissible than the Omicron sub-lineages that dominated recent and current Omicron epidemic waves (BA.1, BA.1.1). The relative contributions of increased transmissibility inherent in BA.2, immune evasion, and waning immunity, is unclear; but, limited, early evidence suggests immune evasion may not play a large role in BA.2's increased transmission relative to BA.1.
- It remains unclear if BA.2 causes more or less severe disease than previous SARS-CoV-2 variants; but, limited, early evidence suggests it may not be more severe than BA.1.
- S-gene target failure (SGTF) has been used as a proxy for the Omicron BA.1 and BA.1.1 variants, and S-gene target positivity (SGTP) has been used as a proxy for BA.2; however, the United Kingdom is reporting a small but potentially increasing proportion of BA.2 cases that are SGTF (0.13%).
- The current risk of BA.2 sub-lineage transmission in Ontario is high with a low degree of uncertainty. The risk of severe disease in Ontario is moderate, with a moderate degree of uncertainty. The risk of reinfection is high with a moderate degree of uncertainty. The risk of breakthrough infection in Ontario is high with a moderate degree of uncertainty. The risk of impact of the BA.2 sub-lineage on testing in Ontario is moderate, with a moderate degree of uncertainty. The risk of impact on surveillance in Ontario is moderate with a low degree of uncertainty.

Issue and Research Question

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Omicron (B.1.1.529) Variant of Concern (VOC) consists of sub-lineages, including BA.1, BA.1.1, BA.2, and BA.3.¹ The Omicron variant BA.2 sub-lineage has been identified in at least 102 countries.² Considering the increased transmissibility of the Omicron BA.1 sub-lineage compared to previously circulating VOCs, it is important to monitor the potential impact the BA.2 sub-lineage might have in Ontario. Since the last report published on March 11, 2022,³ more evidence has emerged regarding BA.2. This evidence brief updates the Public Health Ontario (PHO) report published March 11, 2022, and summarizes available information and evidence on the BA.2 sub-lineage relevant to the risk in Ontario up to March 22, 2022. Data from Ontario was available up to March 23, 2022. A section on animal transmission and reservoirs was added to this update. Since this is the first time zoonotic information is being included, the literature will include all SARS-CoV-2 lineages.

Methods

PHO Library Services conducted daily searches of primary and preprint literature using the MEDLINE database (search strategies available upon request). In addition, PHO performed grey literature searches daily using various news feeds and custom search engines. English-language peer-reviewed and non-peer-reviewed (preprint) records that described Coronavirus Disease 2019 (COVID-19) variants were included. In some of the literature, the term Omicron is used to refer to BA.1 and/or BA.1.1, which have been the dominant sub-lineages in most jurisdictions.

Genomic Features

The Omicron VOC (B.1.1.529) includes three commonly circulating sub-lineages: BA.1, BA.1.1, BA.2, and BA.3.¹ The Omicron sub-variants BA.1, BA.2 and BA.3 share 39 mutations (mostly in the spike protein); however, BA.2 has an additional 27 mutations, including 10 unique mutations.⁴ BA.1 differs from BA.2 by 28 mutations and 50 amino acids, which is approximately twice as many amino acid differences as the number of differences between four other VOC (Alpha, Beta, Gamma, Delta) and wild-type SARS-CoV-2.

S-gene target failure (SGTF) has been used as a proxy for the Omicron BA.1 and BA.1.1 variants due to the amino acid deletion at position 69 and 70 of the S protein, and S-gene target positivity (SGTP) has been used as a proxy for BA.2 because it is usually missing this deletion. Recently, however, a small number of BA.2 sequences containing the deletion at 69 and 70 have been identified.⁵ As of March 2, 2022, there were 123 BA.2 sequences in the United Kingdom (UK) genomic database with a deletion at 69 and 70, out of 93,937 confirmed or probable BA.2 sequences (0.13% of BA.2 cases),⁶ which is up from 20/27,179 (0.07%) in the previous report.

- Since the last PHO BA.2 Risk Assessment,³ a study reported that the emerging and circulating Omicron subvariants originate in part through recombination with other variants.⁷ Unlike BA.1, which shares nine amino acid spike mutations with most VOCs, BA.2 shares only six amino acid mutations in its spike protein with most VOCs, three of which are found in Alpha variants. The authors conclude that because BA.1 shares three additional amino acid mutations with Alpha, BA.1 and Alpha are phylogenetically closer. Based on their analysis of a large number of Omicron sequences, the authors conclude that recombination events between Omicron subvariants as well as with other variants is suggestive that co-infection and subsequent genome recombination plays an important role in the evolution of SARS-CoV-2.

- Fonager et al., analyzed the first BA.2 cases in Denmark and reported that BA.1 and BA.2 had different constellations of mutations, and structural mapping suggests different effects on receptor binding or changes in interaction with adjacent spike monomers.⁸ This study is described in greater detail later in this report.

SARS-CoV-2 Animal Reservoirs and Zoonotic Transmission

SARS-CoV-2 is known to infect non-human animal species.^{9,10} Although animals do not have a considerable role in spread to humans, SARS-CoV-2 transmission in animal species can impact the health of animals and can result in the emergence of new variants. The latter is of particular concern when considering future scenarios and the potential risk of ‘spillover’ of animal-adapted SARS-CoV-2 lineages back into humans. There are confirmed reports of humans infecting mink, and then mink spreading the infection back to humans, as well as growing evidence of North American deer as high risk for zoonotic transmission of SARS-CoV-2.¹¹⁻¹⁴ Early evidence suggests there is limited risk of zoonotic transmission from skunks, raccoons, rodents, sheep, and coyotes.¹⁵⁻¹⁷ The risk of zoonotic spillover or spillback infections could be higher for domestic pets than wild animals due to shared living space. Evidence for the risk of SARS-CoV-2 zoonotic transmission in common pets such as cats and dogs is varied.¹⁸⁻²³

There is evidence of distinct evolutionary SARS-CoV-2 trajectories in animals. For example, the Alpha and Delta VOCs were identified in white-tailed deer in the United States (US); but, when Delta displaced Alpha in the human population, Alpha persisted in the deer and continued to evolve along a trajectory unique from known human alpha lineages at the time.²⁴ This can present considerable risk to humans if the SARS-CoV-2 lineage evolves in animals to become more virulent and/or infectious and/or evades existing immunity. This is underscored by evidence of deer-to-human transmission,²⁵⁻²⁷ and hamster-to-human transmission.^{25,26,28}

Diagnostics

Since the last PHO BA.2 Risk Assessment, two additional publications about diagnostics were identified.

- Tsui et al., report validation of a novel RT-PCR assay capable of detecting most SARS-CoV-2 strains, as well as differentiating between Delta and Omicron variants.²⁹ The validation was done using 182 positive and 42 negative nasal samples (based on ThermoFisher TaqPath testing), with primers and probes designed using 169,454 Delta and 24,202 Omicron full or near-full genomes. The new assay produced the same results as the TaqPath assay. The differential test was designed based on the $\Delta 31-33$ amino acid deletion in the N-gene, which is present in BA.1, BA.2, and BA.3 and so the authors conclude the assay should detect these subtypes.
- Bloemen et al., report that Sanger sequencing of mutations in a 733 bp amplicon of the SARS-CoV-2 S gene receptor binding domain is sufficient for reliable identification of SARS-CoV-2 VOCs and rapid identification of newly emerging variants.³⁰ The authors conclude that Sanger is faster, cheaper and easier compared to whole genome sequencing (WGS). Validation was done with WGS on 147 selected samples with different variants, in parallel with Sanger sequencing. Although the methodology was not tested on BA.2, the authors state that because it contains extra mutations within the sequenced region, their assay should unambiguously distinguish BA.2 from the original Omicron (now redesignated as B.1.1.529.1 or BA.1).

Epidemiology

- Surveillance WGS across Canada indicated that of SARS-CoV-2 samples collected the week of February 27, 2022, 99.1% were Omicron (15.5% BA.1, 56.8% BA.1.1, 26.8% BA.2), but data were still accumulating.³¹ This is an increase in the proportion of BA.2 samples compared to the week of February 13, 2022 (99.9% Omicron: 25.1% BA.1, 59.3% BA.1.1, 15.5% BA.2). On March 23, 2022, Canada reported 5,360 new COVID-19 cases, 15 new deaths and 122,426 active cases. The daily percent positivity (over the previous 7 days) was 13.8%, and is a continuation of the increasing trend in test positivity observed since late February/early March. The Public Health Agency of Canada notes that due to changes in COVID-19 testing policies in many jurisdictions starting in late December 2021, case counts will underestimate the total burden of disease.
- PHO notes that as of December 31, 2021, diagnostic PCR testing was restricted to high-risk populations and therefore representative surveillance only pertains to tested populations, and Ontario case counts are an underestimate. The Ontario COVID-19 Genomics Network (OCGN) moved from sequencing 5% of eligible samples to 20% on February 16, 2022.
 - Based on WGS results completed by PHO as of March 17, 2022 and the OCGN as of March 16, 2022:^{32,33}
 - The proportion of cases identified as BA.2 have had an increasing trend over the past several weeks: 6.3% for week of January 23 to 29, 9.0% for week of January 30 to February 5, 11% for week of February 6 to 12, 12.3% for week of February 13 to 19, and 24.9% for February 27 to March 5, 2022.
 - From December 12, 2021 to March 5, 2022, the weekly growth rate of BA.2 was 1.53 (95% confidence interval [CI] 1.49 - 1.57) times that of BA.1.1.
 - A total of 1,144 BA.2 cases have been identified in Ontario since January 1, 2021.
 - Among BA.2 cases from February 6, 2022 to March 5, 2022 linked to Public Health Case and Contact Management Solution (n=681), the majority occurred in individuals who had completed their vaccination series, i.e. individuals who were post-booster dose (42.7%) or post-series completion (33.8%), followed by unvaccinated individuals (19.8%).

Notable epidemiological trends from select jurisdictions are:

- **Global:** As of March 21, 2022, GISAID reported 409,959 sequences of the BA.2 sub-lineage, with reports from at least 102 countries.² According to GISAID, the 7-day rolling average of BA.2-positive sequences globally on March 14, 2022 was 86% (95% CI 85-87) of submitted sequences. Of countries reporting to GISAID up to March 24, 2022, cumulative prevalence was highest in Hong Kong, at 75% for samples between December 27, 2021 and March 5, 2022.^{2,34} The WHO March 22, 2022 weekly epidemiological update (with data up to March 20, 2022) stated that although global COVID-19 cases were decreasing from the end of January 2022, cases have been increasing in the recent two weeks.¹ The WHO notes that due to surveillance limitations, their global VOC distribution data should be interpreted cautiously.

- Denmark:** The Danish Health Authority changed their COVID-19 test recommendations in week 10 to limit testing to primarily vulnerable groups and patients admitted to hospital, which is expected to impact trends in the coming weeks.³⁵ COVID-19 case numbers decreased from week nine to 10. In week 10, of 3,005 samples with WGS, the Statens Serum Institut reported that 69.5% were BA.2, 29.2% BA.2_H78Y, 0.8% BA.1.1, 0.3% BA.1, and 0.0% BA.3. The Danish Covid-19 Genome Consortium (DCGC) reported 98.8% of sequenced samples were BA.2 in week 11.³⁶ Fonager et al.'s study of the first BA.2 cases in Denmark reported that the prevalence of BA.2 increased from less than 0.1% to 89.2% of sequenced samples in a 10-week period.⁸
- Norway:** According to the Outbreak.Info website, using data from the GISAID initiative database, the BA.2 cumulative prevalence in Norway was 7% of sequenced samples between January 6 and March 10, 2022.²
- UK:**³⁷ For the week ending March 13, 2022, the Omicron BA.2 variant was the most common variant in England, Wales, Northern Ireland and Scotland, comprising 76.1% of all sequenced COVID-19 infections from the survey.³⁸ The BA.1 variant or its sub-variants comprised 23.9% of cases. The percentage of BA.2 cases is increasing in England, Scotland and Wales, and in parallel, the percentage of BA.1 variant cases is decreasing. The BA.2 trend is less clear in Ireland.
 - England:** The UK Health Security Agency's (UKHSA) most recent VOC and variants under investigation report for England reported that of all WGS cases between February 27 and March 6, 2022, 31.1% were BA.1, 68.6% were BA.2, and 0.3% were other variants.⁶ From January 27 to March 8, 2022, BA.2 accounted for over 95% of sequenced SGTP cases, making SGTP a reliable proxy for BA.2. The proportion of SGTP cases increased from 52.1% on February 20, 2022 to 83.3% on March 6, 2022. Based on data up to March 1, 2022, the growth rate is approximately 80% greater relative growth for BA.2 compared to BA.1.
- US:** According to sequences tested the week ending March 5, 2022 by the US Centers for Disease Control and Prevention (CDC), BA.2 makes up approximately 12.6% (95%CI 10.3, 15.2) of new infections.³⁹ According to NOWCAST modelling projections, the US CDC estimated that for the week ending March 19, 2022, 100% of SARS-CoV-2 cases were Omicron (57.3% BA.1.1 [95%CI 51.8, 62.6], 7.9% [95%CI 6.6, 9.3] B.1.1.529, 34.9% [95%CI 29.6, 40.4] BA.2). As of March 16, 2022, the 7-day moving average of daily new SARS-CoV-2 cases (30,040) decreased 16.6% compared to the previous week's 7-day moving average (36,010).⁴⁰

Transmissibility

Since the last PHO BA.2 Risk Assessment, additional studies suggest that BA.2 has a growth advantage over BA.1.^{41,42} It is unclear to what extent any increased transmission of BA.2 compared to BA.1 or BA.1.1 is due to inherent characteristics of this sub-lineage (i.e., enhanced ability to infect cells, tissue tropism) or due to immune evasion.

- Cheng et al., describe a single source outbreak (N=768) in a housing estate in Hong Kong.⁴³ The estimated doubling time based on the symptom onset date (or report date if asymptomatic), was 1.28 days (95% CI 0.560-1.935). Of the 438 specimens with WGS, 155 were identified as BA.2.
- An updated analysis of GISAID data reported by the WHO estimated a growth rate advantage of BA.2 over BA.1, with a pooled mean transmission advantage of 72% (95% CI: 55%-82%), assuming an unchanged generation time.¹ This is higher than the WHO's previous estimate of 56% (95% CI: 42%-72%) for BA.2 over BA.1.⁴⁴
- According to the most recent UKHSA variants of concern and variants under investigation report for England, secondary attack rates amongst contacts exposed in household and non-household settings (adjusted for factors including vaccination status) remain higher for BA.2 than other sequenced Omicron cases, but slightly reduced since the last briefing note.⁶ Based on case test dates January 1 to February 14, 2022 and contact tracing data up to March 8, 2022, the adjusted BA.2 secondary attack rate was 13.6% (13.2%-14.0%) for households and 5.3% (4.7%-5.8%) for non-households (adjusted for age and sex of the exposor and the contact, the week of positive test of the exposor and whether the contact completed contact tracing). For reference, the BA.1 SARs were 10.7% (10.6%-10.8%) and 4.2% (4.0%-4.3%), for households and non-households, respectively.
 - The UKHSA preliminary analyses of cycle threshold values suggest the median Ct values for BA.1 and BA.2 are very similar from day 0 to 2 since symptom onset; but, after day 3, there is evidence BA.2 may have a slightly higher Ct value, but there are too little data at this time to draw conclusions.

Disease Severity

Evidence of disease severity caused by BA.2 as compared to COVID-19 caused by ancestral SARS-CoV-2 and other variants is slowly emerging, but remains unclear.⁴¹ Evidence since the last PHO BA.2 Risk Assessment are described below.

- Fonager et al., described the first BA.2 cases in Denmark.⁸ No significant differences were observed between individuals infected with BA.1 and BA.2 for 30-day mortality or for the adjusted hospitalization risk ratio (RR) overall (p=0.19)(adjusting for sex, age, vaccination status, time period, geographic region, comorbidities and SARS-CoV-2 reinfection). When limiting hospitalized cases to those with a COVID-19 diagnosis, the RRs for hospitalization with BA.2 vs BA.1 remained non-significant (n=277 hospitalized cases; RR: 1.06 [95% CI: 0.77–1.47]).
- According to preliminary analyses in the most recent UKHSA variant technical report, the risk of hospitalization following a BA.2 infection appears similar to that of a BA.1 infection (hazard ratio 0.91, 95% CI: 85-98, up from the previous report estimate of 0.87, 95% CI: 0.75-1.00).^{5,6} The analyses used sequenced cases, and adjusted for age, reinfection status, sex, ethnicity, local area deprivation, vaccination status, and controlled for the effect of geography and specimen date.

- In week 8 in Denmark (68.8% of WGS samples were BA.2),³⁵ the number of new hospital admissions increased by 11% whereas admissions to the intensive care unit (ICU) and the proportion receiving COVID-specific treatment in the ICU were relatively stable. The number of COVID-related deaths increased in week 8 compared to week 7.

Vaccine Effectiveness (VE)

- Iketani et al., analyzed BA.2 neutralization compared to BA.1 sub-lineages and D614G ('wildtype') pseudovirus neutralization using polyclonal sera and monoclonal antibodies.⁴⁵ The authors observed significant loss of polyclonal serum neutralizing activity against BA.2 compared to D614G, with less prominent loss from the sera of boosted individuals. The mean serum neutralizing titer was slightly lower for BA.2, but the difference compared to BA.1 sub-lineages was not statistically significant ($p=0.242$). The study also used sera from individuals vaccinated with an mRNA vaccine and authentic virus, and again observed a significant decrease in titres against BA.2 virus compared to D614G virus. Using 19 neutralizing monoclonal antibodies to examine antigenic differences in the spike protein of Omicron sub-lineages, 17 out of 19 showed significantly impaired neutralization. The authors highlight that all class 4 antibodies tested lost more neutralizing potency against BA.2 compared to BA.1 sub-lineages, and two class 3 antibodies retained activity against BA.2 but had no activity against BA.1 viruses. Sotrovimab lost 27-fold neutralizing activity against BA.2, which the authors point out could be important for BA.2 treatment because Sotrovimab was found to retain activity against the original form of Omicron. The study also tested monoclonal antibody neutralizing activity using eight BA.2-specific spike mutations alone as pseudoviruses. From their observations, the authors suggest mutation S371F appears to be largely responsible for the loss in potency of Sotrovimab (S309), despite not having been previously identified as a marker for clinical resistance.
- In response to reports of broad neutralization escape for the individual mutations S371L and S371F in Omicron BA.1 and BA.2, Miller et al., studied existing computational and experimental escape measurements for S371 mutations, in an attempt to reconcile conflicting findings regarding receptor binding domain binding and impaired neutralization across all four antibody classes.⁴⁶ More specifically, they structurally examined the individual antibody-antigen interactions assayed by Liu et al. and Iketani et al. in the context of the spike trimer to help identify additional mechanistic details of S371L/F escape, which included computing the ratio of antibody epitope accessibility in the spike-closed conformation and comparing it to the spike-open conformation, and plotting this against the antibody escape for BA.1 and BA.2 mutations.^{45,47} The authors propose three mechanisms for how S371 mutations impact BA.1 and BA.2 binding and neutralization by antibody, with the greatest evidence to support a role for the N343 glycan. The authors hypothesize that interactions between L/F371 and the N343 glycan result in altered spike-closed versus spike-open conformational dynamics that result in broad escape from class 1 and 4 antibodies, whose epitopes are inaccessible in the spike-closed conformation.
- Bowen et al., compared the plasma neutralizing activity elicited by seven vaccines or SARS-CoV-2 infection in order to evaluate the immune evasion of the BA.1 and BA.2 Omicron sub-lineages using pseudotyped viruses.⁴⁸ Convalescent plasma was obtained from individuals infected with a Washington-1-like SARS-CoV-2 strain based on time of infection, and only 6/14 and 7/14 individuals had detectable, but mostly weak, neutralizing activity against BA.1 and BA.2, respectively. Individuals that received two doses of Moderna mRNA-1273 had G614, BA.1, and BA.2 neutralizing GMTs of 1155, 26, and 47, respectively. Individuals that received two doses of Pfizer BNT162b2 had G614, BA.1, and BA.2 neutralizing GMTs of 764, 23, and 34, respectively. 18/21 and 19/21 mRNA-vaccinated subjects retained neutralizing activity against BA.1 and BA.2,

respectively. Combining the mRNA vaccinated cohorts, there was an estimated ≥ 35 -fold reduction in GMT against BA.1 and a ≥ 24 -fold reduction against BA.2, compared to G614. Individuals who received two doses of Novavax had a ≥ 23 -fold drop in GMT against BA.1 and a ≥ 13 -fold drop in GMT against BA.2. Among individuals who received one dose of Janssen, 1/10 had detectable plasma neutralizing activity against either Omicron sub-lineage. Individuals who received two doses of AZD1222 had a ≥ 45 -fold drop in GMT for BA.1 and a ≥ 21 -fold drop for BA.2. Individuals with two doses of Sputnik vaccine had ≥ 12 -fold drop in GMT for BA.1 and ≥ 7 -fold drop for BA.2. Individuals vaccinated with two doses of Sinopharm had a ≥ 12 -fold drop in GMT for BA.1 and ≥ 6 -fold drop in GMT for BA.2. In terms of boosters, individuals that received three mRNA vaccine doses had neutralizing GMTs of 3324, 415 (8-fold drop), and 612 (5-fold drop) against G614, BA.1, and BA.2, respectively. Individuals who had two doses of Ad26.COV2.S or one dose followed by a Pfizer BNT162b2 booster had a 17-fold and 9-fold drop in GMT for BA.1 and BA.2, respectively, compared to G614. Individuals who had two doses AZD1222 followed by an mRNA booster had 9-fold and 6-fold drops in GMT against BA.1 and BA.2, respectively. Individuals vaccinated with two doses of Sputnik and boosted with AZD1222 or BNT162b2 had a 9-fold and 10-fold reduction against BA.1 and BA.2, respectively.

- The UKHSA COVID-19 vaccine surveillance report for week 11 reported results from their test-negative case control study of VE against symptomatic disease following BA.2 infection compared to BA.1 infection.⁴⁹ Based on symptomatic cases tested between December 27, 2021 and February 4, 2022, VE against symptomatic disease was similar for BA.1 and BA.2 sub-lineages. Two dose VE was 10% (9 to 11%) and 18% (5 to 29%), respectively, for BA.1 and BA.2, after 25+ weeks. The VE increased to 69% (68 to 69%) for BA.1 and 74% (69 to 77%) for BA.2 at 2 weeks after a booster vaccine, then decreased to 49% (48 to 50%) and 46% (37 to 53%) respectively after 10-plus weeks.

Re-infection

Since the last PHO BA.2 Risk Assessment, one additional publication on re-infections was identified. Fonager et al., described the first BA.2 cases in Denmark.⁸ No significant differences were observed between individuals infected with BA.1 (n=16,137) and BA.2 (n=2,623) in terms of reinfection.

Public Health Measures

Since the last risk assessment,³ the routinely monitored jurisdictions largely continued to ease public health measures and increased vaccine eligibility. The following changes were made since the last risk assessment:

- Some jurisdictions reported removing the general mandatory vaccination requirement by June 2022 (e.g., Italy)⁵⁰ or as a condition of employment (e.g., England),⁵¹ while other jurisdictions mandated vaccination for health care workers (e.g., Germany).⁵²
- Some jurisdictions extended the eligibility of booster doses (e.g., Finland, France, Ireland, Netherlands).⁵³⁻⁵⁶
- Some jurisdictions eased mask mandates (e.g., France, Italy, Netherlands)⁵⁷⁻⁵⁹ and lifted the use of the immunity pass system (e.g., France).⁶⁰
- Portugal reported that the lifting of the remaining public health measures cannot happen yet, as the threshold for lifting measures (i.e., 20 deaths per million) has not been reached.⁶¹

Ontario Risk Assessment

The current risk of BA.2 sub-lineage transmissibility in Ontario is high, with a low degree of uncertainty. The risk of severe disease in Ontario is moderate, with a moderate degree of uncertainty. The risk of reinfection is high with a moderate degree of uncertainty in Ontario. The risk of breakthrough infection is high with a moderate degree of uncertainty in Ontario. Early evidence suggests the risk of reinfection and degree of vaccine effectiveness is similar for BA.1 and BA.2. The risk of impact of the BA.2 sub-lineage on testing is moderate, with a moderate degree of uncertainty. The risk of impact on surveillance is moderate 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	High	Low
Disease Severity	Moderate	Moderate
COVID-19 Re-infection	High	Moderate
Lowered Vaccine Effectiveness/Breakthrough Infections	High	Moderate
Impact on Testing	Moderate	Moderate
Impact on Surveillance	Moderate	Low

Implications for Practice

- Given the prevalence of BA.2 globally and growing evidence of increased transmissibility relative to other dominant Omicron sub-lineages, a cautious approach to assessing its risk in Ontario is warranted.
- Epidemiological trends for SARS-CoV-2 in Ontario were decreasing, although the decreasing trends now have slowed and several public health units are reporting a higher case rate compared to the previous week, and percent positivity is slowly increasing in the province.⁶²⁻⁶⁴ Although case counts are an underestimate due to changes to PCR testing eligibility, case rates are higher than during much of the pandemic to date.⁶⁵
- Ontario lifted many existing public health measures on March 21, 2022 (e.g., removing mandatory masking requirements in most settings).⁶⁶⁻⁶⁸ With the growing evidence of increased transmissibility of BA.2, the steadily increasing proportion of BA.2 cases and the ongoing relaxation of public health measures, the rising case counts need to be closely monitored to determine if there is a corresponding impact on hospitalizations/ICU occupancy that may require increased public health measures. Close monitoring of epidemiologic trends in other jurisdictions with BA.2 pre-dominance or increasing prevalence will be useful, in particular the epidemiological trends following changes to public health measures.

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