



Date: 24 January 2023

SARS-CoV-2 Variants of Concern Update

Executive Summary

Note: New information in this report is shown in *red text*.

Section updated: 20 January 2023

Since the second half of 2022, many new Omicron subvariants have been reported. These variants demonstrate convergent evolution whereby variants from different lineages accumulate similar mutations. Mutations in the spike protein appear to be responsible for the enhanced characteristics of these variants.

New information in this report includes:

- The variant landscape in New Zealand continues to evolve with no single variant accounting for more than 50% of genomically sequenced samples. Globally, there are differences in dominant mutations and highlights the difficulty in predicting the range of mutations likely to establish within New Zealand. However, two variants, XBB.1.5 and BF.7 are currently being watched carefully.
- XBB.1.5 is a sublineage of XBB that is rapidly increasing in frequency in some regions of the USA. It has been present in New Zealand since December 2022. XBB.1.5 has a growth advantage over XBB, with mutations associated with both immune evasion and enhanced ACE-2 binding. XBB.1.5 represents an increase in overall risk (compared to New Zealand's variant landscape in late December 2022) and may contribute to an increase in cases in New Zealand. However, differences in immune landscape between New Zealand and USA populations (for example, higher vaccine coverage in New Zealand and differences in prior infections in terms of timing and variant type) mean the effects seen in the USA might not translate to the New Zealand setting.
- BF.7 is a sublineage of BA.5.2.1 and, based on limited reporting, may account for a substantial proportion of cases in the current large wave in China. BF.7 has been observed to outcompete BA.5 in the UK, but comparison of growth estimates suggest it is unlikely to outcompete more recent Omicron subvariants that are common globally and in New Zealand (e.g. BQ.1 and its sublineages). There is currently no suggestion that BF.7 possesses concerning properties such as enhanced severity.
- China is reporting a large increase in COVID-19 cases and deaths. The number of sequences from China uploaded into GISAID has also increased substantially. Results from genomic testing in China and from passengers arriving from China are concordant and have not detected concerning mutations. The most common lineages reported are BA5.2.48 and BA.5.2.49, BA.5.1.32 and BF.7.14 (a BA.5.2.1 sublineage). There is no evidence to date that the wave of infections in China has produced a novel variant with concerning mutations.



Section 1 Key Omicron information

Circulating variants across Aotearoa New Zealand

Section updated: 19 January 2023

The Institute of Environmental Science and Research (ESR) COVID-19 Genomics Insights (CGI) report was last produced on 19 January 2023, with data from the period of 10 December – 13 January 2023.(1)

The percentage of sequenced cases (community, including hospital, and “border” cases combined) of each variant in this period are shown in figure 1 (noting that ~1.2% of all cases were sequenced in this reporting period, and only variants with a frequency above 1% are shown).(1)

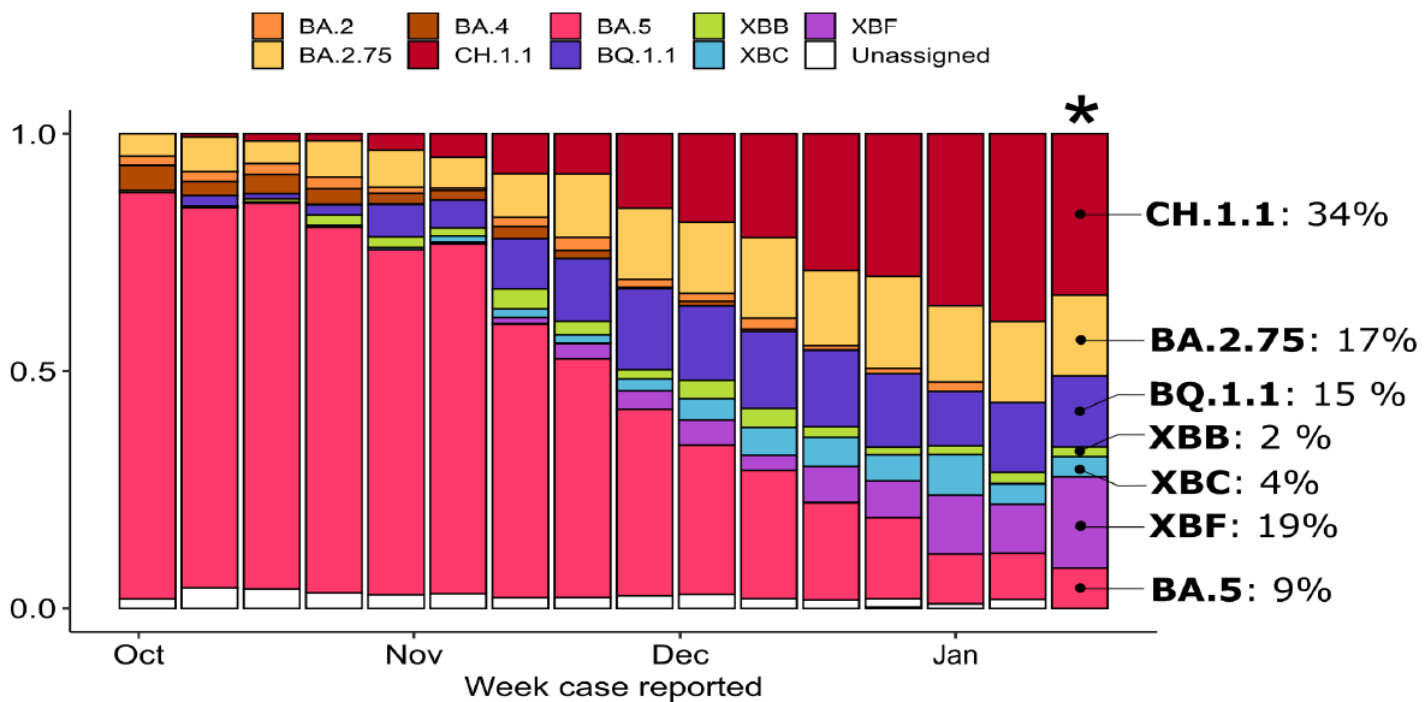


Figure 4. Frequency of variants/lineages in the past 16 weeks. Frequencies >1% are annotated in the last week. Note, data for the most recent fortnight is preliminary, as it will be updated as additional cases reported within these weeks are converted into genomes. Frequencies from the most recent reporting week are based on 47 samples. Cases classified as ‘Unassigned’ are typically partial genomes where it is difficult to be definitive regarding variant/lineage. Source: [ESR link](#)

A publicly accessible version of the genomic report produced by ESR is available [here](#).

Wastewater sampling is less prone to selection bias than samples from cases (which, for example, overrepresents hospitalised cases and under-represent some regions in New Zealand). Wastewater surveillance in early January 2023 has seen similar patterns in variants to that seen in cases.



CH.1.1 was the most widespread and common variant in wastewater in the second week of January 2023, being detected at 84% of sites and comprising 55% of sequencing reads nationally.

Other sublineages in the BA.2.75 group (including BM.4, BR.2, XBF and BA.2.75) accounted for another 22% of sequencing reads nationally, being detected at 61% of sites. Thus, as a whole, the BA.2.75 group (including CH.1.1) represented 78% of sequencing reads nationally. (1)

The publicly accessible ESR Wastewater surveillance dashboard can be accessed [here](#).

Current overall variant risk status

Section updated: 19 January 2023

Despite the development of a large range of Omicron variants demonstrating convergent evolution, there has been relatively little change in the overall variant landscape. The large outbreak of cases in China and the development of XBB.1.5 in the United States could change the current situation. The potential development of concerning new variants from China has been identified as an ongoing risk and the growth advantage of XBB.1.5 has the potential to cause an increase in cases in New Zealand.

There is no strong evidence of an increase in disease severity associated with these variants.

Features of Omicron

Growth advantage/transmissibility

Section updated: 19 January 2023

Growth advantage has become challenging to estimate with the backdrop of numerous circulating variants. In particular, estimates will vary with each country's specific prior variant mix and are specific to a point in time. Consequently, applying international estimates to New Zealand is unlikely to be informative. Additionally, fewer data are now available as whole genome sequencing surveillance is being less thoroughly conducted worldwide. For data about estimates of growth advantage, see previously published versions of this report. [This report provides information on XBB.1.5 which appears to have a significant growth advantage.](#) Details are presented in the Risk assessment table.

Vaccine effectiveness, immune evasion

Section updated: 19 January 2023

Formal estimates of vaccine effectiveness (VE) require cases to accumulate (usually requiring some time) before estimates can be calculated. VE estimates are therefore currently not available for most variants that emerged after BA.2 and BA.5. Where VE estimates are not available, laboratory testing can provide some information by, for example, measuring how well antibodies in the serum from vaccinated people neutralise each variant. However, results from such laboratory tests need to be confirmed by epidemiological data. [The development of bivalent vaccines has added further difficulties to reporting the VE of circulating variants.](#)



Vaccine effectiveness

Section Updated: 19 January 2023

Vaccine effectiveness reported here is only for periods including BA.4/5 waves, as variants prior to BA.4/5 are now not often seen. VE for previous variants such as BA.1 are included in previous Variants of Concern Updates and so are not repeated here. VE is also only reported here for mRNA vaccines.

VE against infection

Monovalent (Wild Type) original formulation vaccines

Three doses: Moderna vaccine shows VE (against BA.2, BA.2.12.1, BA.4 and BA.5) was 61.0% - 90.6% at 14 – 30 days post-third dose. (2) However, this diminished to levels below 20% against all subvariants after 5 months.(2)

Four doses: Moderna vaccine shows VE ranged between 64.3%-75.7% for BA.2, BA.2.12.1, and BA.4 and was 30.8%) against BA.5 at 14-30 days post-fourth dose. VE was low beyond 90 days for all subvariants. (2)

Bivalent (BA.4/5, Wild type) mRNA vaccines

Absolute VE (compared to those who have received no doses of any COVID-19 vaccine) against symptomatic SARS-CoV-2 infection ranged from 22% (95% CI: 15-29) in those aged 65 and older, to 43% (95% CI: 39-46) in those aged 18-49 years at a maximum of 2.5 months after the bivalent vaccine dose. (3) Relative VE (that is, compared to those who have received the same number of previous monovalent doses but not the bivalent booster) increased in all age group with the time since the most recent previous dose. (3) Due to lack of a comparison group these data do not show whether the effect of the BA.4/5 dose is superior to the original formulation.

VE against severe disease

Monovalent (Wild Type) original formulation vaccines

Two doses: mRNA vaccines during a BA.4/5 dominant period show VE against hospitalisation or urgent care visit was 25% (95% CI: 17 - 32) at > 150 days post-vaccination. (4) Two doses also provide high VE against death for adolescents and children, but data about duration of this effect in young people are limited. (5)

Three doses: Moderna vaccine shows VE against hospitalisation (time since vaccination unclear) was 97.5%, 82.0%, and 72.4% for BA.1, BA.2 and BA.4/5 respectively. (2) During a BA.4/5 dominant period, mRNA vaccines show VE against hospitalisation or urgent care visit was 68% (95% CI: 50 - 80) at 7-119 days post-vaccination, and 36% (95% CI: 29 – 42 at > 120 days post-vaccination.(4)

Four doses: Moderna vaccine shows VE against hospitalisation (time since vaccination unclear) for BA.4/BA.5 was 88.5%. (2) During a BA.4/5 dominant period, a second mRNA booster dose yielded a VE against hospitalisation to 66% (95% CI: 53-75%) at 7-59 days post-vaccination in those aged 65 years or older, and 57% (95%CI 44-66%) at more than 60 days post-vaccination.(4)

Bivalent (BA.4/5, Wild type) mRNA vaccines

There are currently no studies directly comparing the clinical efficacy of a recent bivalent vaccine booster to the clinical efficacy of a recent WT vaccine booster.

However, two CDC-led VE studies found that receiving bivalent mRNA vaccine boosters are effective against severe COVID-19 related outcomes in immunocompetent adults when compared to those with no previous vaccination, and provided additional protection when compared with previous monovalent mRNA vaccine doses only. (6) VE of a bivalent booster dose (after 2, 3, or 4 monovalent doses) against hospitalisation for COVID-19-associated illness was estimated at 57% (95% CI = 41%–69%) compared with no vaccination, and 45% (95% CI = 25%–60%) compared with receipt of most recent monovalent dose ≥11 months earlier. (6)



Among people aged 65 years and older, VE is estimated at 81% for COVID-19 related hospitalisations and 86% for COVID-19 related death for those who received a bivalent Pfizer booster compared to those who did not receive a bivalent booster. (7)

Protection from vaccination plus prior Omicron infection

Previous Omicron infection in triple-vaccinated individuals provides a high level of protection against BA.5 and BA.2 infections (92.7 - 97.1%) and hospitalisation (91.2 -96.4%). (8)

Hybrid immunity following infections from BA.1 or BA.5 when compared with vaccine-only immunity leads to substantially increased protection against BA.5 reinfection for up to 8 months. (9)

Immunological data

Section Updated: 19 January 2023

Monovalent (Wild Type) original formulation vaccines

Evidence continues to accumulate that neutralising antibody levels against Omicron decline after a primary course of Pfizer vaccine (original monovalent, wild type (WT) vaccine), and are higher after a booster (third) dose, than after the primary course. (10-13) Similar results from a phase II clinical suggest that antibody titres increased following a booster (third or fourth) dose of Novavax (NVX-CoV2373) without increasing reactogenicity. (14)

Immunological data suggest hybrid immunity after monovalent vaccine and (Delta or Omicron) infection is likely to be robust. (15)

Data show that the memory T cell response generated by monovalent WT (original formulation) remains robust and is mostly unaffected by the mutations in Omicron (B.1.1.529). (16)

Bivalent (BA.4/5, Wild type) mRNA vaccines

Immunogenicity data for BA.4/5 bivalent vaccines generally suggest BA.4/5 bivalent vaccines elicit greater neutralisation titres against Omicron variants than the monovalent WT vaccines. (17-20) However, a few studies have found boosting with BA.4/5 bivalent mRNA vaccines did not elicit a superior neutralising antibody response but instead was comparable to that of the original WT monovalent vaccines. (21-23)

For example, the geometric mean titres (GMTs), used to quantify neutralisation activity, suggest that bivalent mRNA boosters are immunological superior to monovalent mRNA boosters, however, neutralisation titres against BA.2.75.2, BQ.1.1. and XBB are 12 to 26 times lower than against the WT strain (compared to 23 to 64 times in those who received a monovalent booster. (20)

Additionally, a pre-print study found that a fourth dose-bivalent boosters enhance neutralisation antibody titres against Omicron lineage viruses including BA.2.75, BA.2.75.2, BN.1, BQ.1, BQ.1.1, XBB, and XBB.1. compared to third dose monovalent boosters. (24) Particularly of note was a 10-fold increase in neutralization of BQ.1 and BQ.1.1 induced by bivalent vaccination, compared to monovalent vaccination. (24) The data from this study supports that the BA.4/5 mRNA bivalent vaccine booster strengthens protection against Omicron subvariants that evolved from BA.5 and BA.2. (24)

Of note when interpreting these data, studies using live virus support a superior NAb response conferred by BA.4/5 bivalent boosters, whilst those using pseudovirus show mixed results of BA.4/5 bivalent boosters compared to that of WT monovalent boosters.

Immunological data for bivalent vaccines will be superseded by clinical data (see section Vaccine Effectiveness, above) as clinical data becomes available.



Bivalent vaccines for children

Preliminary safety findings from the first 11 weeks of bivalent booster vaccination in children aged 5–11 years are reassuring and similar to those described for monovalent booster vaccination. (25)

Emergency use authorisations (USA) or recommendation for marketing authorisation (EU) have been made on data including safety, immunogenicity, efficacy, and observational effectiveness data for the monovalent WT (original formulation) vaccine, and immunogenicity data from other Pfizer bivalent vaccines. (26, 27)

Immunological response from vaccination plus prior Omicron infection

There is some evidence to suggest that an individual's first exposure to a variant (either through infection or vaccination) shapes the immune response to future infections (how well the antibody produced neutralises a variant not previously encountered). (28, 29)

A US Study assessing the extent of antibody response against the original WT strain as well as Omicron sublineages BA.2.75 and BA.2.75.2 found that GMTs were highest in the group of people who had a breakthrough infection after receiving three or four monovalent doses. (23)

Safety of second booster

Section Updated: 19 January 2023

A pre-print of a study (including 250,000 people in Israel) about the safety of a second booster of Pfizer's BNT162b2 vaccine, found no significant differences in frequency of self-reported adverse events after the second booster compared with the first booster dose. (30) Similarly to a primary course, a booster of Pfizer vaccine is associated with an increased risk rate of myocarditis in 12- to 39-year-old males (Relative Risk of 2.28 (95% CI, 0.77 to 6.80), however, compared to a primary course the risk appears to be lower. (31)

Bivalent vaccines

Data generally continue to support the safety profile of BA.4/5 mRNA bivalent vaccines being similar to that of the original formulation monovalent mRNA vaccines. (32, 33) However, a signal has been detected in a single database in the US (CDC's Vaccine Safety Datalink (VSD) for ischemic stroke after the Pfizer bivalent vaccine in people ages 65 and older. This signal is being investigated but has not yet been observed in any other US study/database (including VAERS) or in other countries. (34) This signal will continue to be monitored. The CDC states that no change is recommended in COVID-19 vaccination practice. (34)

Disease course and clinical features (symptoms and severity)

Section Updated: 5 December 2022

Various studies continue to indicate a reduction in severity and lower mortality for the Omicron variant (and subvariants) as compared with the Delta variant. (35-37) However, Omicron infections still contribute to excess total mortality. A study from Italy found that excess total mortality persisted during the circulation of the Omicron variant in Italy (although data only available to 31 January 2022), contributing to a reversal in the long-term trend towards increasing life expectancy. (38)

Analysis from a large study in England from 1 May 2020 to 31 March 2022 showed some changes in symptom profiles associated with the different variants over that period, such as lower reporting of loss of sense of smell or taste for Omicron compared to previous variants. (39)

Laboratory studies have also been conducted to investigate pathogenicity of variants on cells. Such studies have supported Omicron severity being lower than previous variants (with one researcher suggesting that



descendants of BA.5 and BA.2 (including BQ.1 and BQ.1.1) could cause slightly more severe disease than BA.1 or the original Omicron). However, these findings require validation from clinical data. (36, 40)

A study published in November 2022 reported an increased risk of death, hospitalisation, and sequelae with reinfection compared to no reinfection. (41) These results have been widely reported; however, the results should be interpreted very carefully as the follow-up time after symptom onset is not the same in the comparison groups, introducing bias.

Therapeutics effectiveness

Section Updated: 19 January 2023

Monoclonal antibody treatments: laboratory-based studies suggest that monoclonal antibody treatments (such as Evusheld) are ineffective against some emerging variants. (42-45) The proportion of variants that Evusheld cannot neutralise is greater than 50%. (46) Clinical effectiveness data for Evusheld (Aotearoa New Zealand's most used monoclonal antibody treatment) are available for a period of BA.1 predominance, (47) but not for later variants.

Real-world evidence suggests that Paxlovid, New Zealand's most prescribed antiviral, remains effective against Omicron variants (including BA.4 and BA.5) in vaccinated populations. (48-51). **Initial clinical data (February 2022) reported that molnupiravir caused a 30% reduction in hospitalisations and deaths in unvaccinated adults with mild-to-moderate COVID-19 symptoms and at least one risk factor. (52) In contrast, recent clinical data (December 2022) suggests that that molnupiravir treatment may not be associated with any meaningful clinical benefit in vaccinated adults. (53) However it remains unclear if changes in efficacy are due to methodological differences between the studies or changes in the SARS-CoV-2 virus.**

Detection/testing

Section Updated: 5 December 2022

There is some evidence to suggest changes in the performance of RATs to detect Omicron variants. However, data are limited, and changes appear to be dependent on both the individual device and subvariant. Use of techniques such as serial testing may maximise sensitivity.

Growing international evidence suggests that clinically relevant changes in RAT performance for detection of Omicron variants differ on an individual device basis. (54-58) Comparability between studies is limited by difference in study design and objectives. The results are also dependent on which Omicron variant was assessed, making it difficult to determine whether evidence of reduced sensitivity is indicative of real-world device performance. Studies indicate that despite reports of reduced sensitivity, data support the continued use of RATs for self-testing. (54-58) Emerging evidence also highlights the need for techniques such as serial testing to maximise sensitivity against new Omicron variants of concern. (56, 58)

Associated documentation

The following documents or ongoing work programmes draw upon the evidence in this document:

- New Variants of Concern Monitoring and preparedness
- Outlook Strategy Group
- New Variant Public Health Risk Assessments



Key recent international documents

Section updated: 23 January 2023

In addition to selected recent pre-prints and published studies, key reports used in this update include the following risk assessments for XBB.1.5 from key peak bodies.

World Health Organization update

The WHO's Technical Advisory Group on Virus Evolution (TAG-VE) met on 05 January 2023 to discuss the Omicron XBB.1.5 variant, which has been reported in 38 countries with most of the sequences coming from the United States (82.2%), the United Kingdom (8.1%), and Denmark (2.2%). Based on its genetic characteristics and early growth rate estimates, XBB.1.5 may contribute to increases in case incidence. However, the overall confidence in the assessment is currently low as growth advantage estimates are only from one country, the United States.

The WHO and the TAG-VE recommend Member States to prioritize studies to better address uncertainties relating to the growth advantage, antibody escape, and severity of XBB.1.5, with suggested timelines varying based on national capacities. The rapid risk assessment will be revised regularly as more evidence and data from additional countries become available. (59)

UK Health Security Agency update

The UK currently has high incidence of the BQ.1 variant and its sublineages. Two other variants, CH.1.1 and XBB.1.5, are showing positive growth compared to BQ.1. CH.1.1 is at moderate prevalence and XBB.1.5 is at low prevalence. The growth advantage of XBB.1.5 is biologically plausible due to its immune escape properties and ACE-2 affinity. CH.1.1 and XBB.1.5 are currently the most likely variants to predominate in the UK following BQ.1. However, there is high uncertainty in the growth estimates for XBB.1.5 due to the small number of sequenced samples.

There is no increase in risk of hospitalization for people with BQ.1 compared to BA.5, but further analysis is ongoing. A preliminary analysis of vaccine effectiveness against hospitalization for BQ.1 compared to BA.5 has been undertaken, but the numbers of sequences in the available data are too small to make a confident assessment. (60)



Section 2: Summary of Variants

Public Health Risk Assessments for the Omicron subvariants BA.5 and BA.4.6, can be found in the previous SARS-CoV-2 Variant of Concern Update [here](#).

Public Health Risk Assessment for XBB.1.5

Updated: 19 January 2023

XBB.1.5 is a sublineage of XBB, with additional spike protein mutations 252V, S486P (61)

	Overall risk assessment*	Confidence level **	Assessment and rationale
Overall growth advantage	Increased risk	Low	<p>Evidence of a growth advantage compared to Omicron subvariants including BA.5 and BQ.1.1 (59, 62)</p> <p>Informal analyses suggest XBB.1.5 has a growth advantage over BQ.1 and associated sublineages, (63) of approximately 10% per day in early January 2023.(64) Additional informal analyses suggest it has a high effective reproduction number compared to other variants at a similar point in their outbreak.(65) However, growth advantage is context specific (e.g. to the immune landscape) and it is not yet clear how this will translate to the New Zealand setting.</p> <p>It is currently present in New Zealand, with only small numbers of sequences reported (six identified to 5th January 2023, from cases in mid-December 2022).(1) In the week ending 13 January 2023, XBB.1.5 made up 3% of wastewater samples. (1)</p>
Transmissibility	Increased risk	Low	<p>Evidence of increased transmissibility</p> <p>There is laboratory evidence that ACE2 binding is increased for XBB.1.5 compared to prior Omicron variants, which is likely to affect transmissibility/infectivity by increasing the ability of the variant to attach and enter cells. (61, 63, 66)</p>



Immune evasion	Insufficient data	Insufficient data	<p>Limited data available about immune evasion.</p> <p>Early laboratory studies suggest there is an ability to evade antibody that is similar to XBB (that is, more resistant to neutralisation by antibody than all other variants to date).(59, 61, 63) There are currently no data on real world vaccine effectiveness against severe disease or death.(59)</p>
Severity	Insufficient data	Insufficient data	<p>No evidence of a change in severity compared to previous Omicron subvariants</p> <p>XBB.1.5 does not carry any mutation known to be associated with potential change in severity. Severity assessments are ongoing. No early signals from informal sources of marked increase in severity.</p>
Therapeutics	Increased risk	Low	<p>Currently no evidence of resistance to Paxlovid or Molnupiravir.</p> <p><i>In vitro</i> studies showed loss of efficacy of all currently approved clinical monoclonal antibody therapies including Evusheld and Bebtelovimab. (61)</p>
Testing	Insufficient data	Insufficient data	<p>There is some evidence that suggests a clinically relevant decrease in the performance of RATs for detection of the Omicron variant (varies by device),(54-58) but it is uncertain how this will affect sensitivity specifically for XBB.1.5.</p>
Overall Assessment	<p>Based on its genetic characteristics and early growth rate estimates there is an increase in overall risk compared to the New Zealand variant landscape of late December 2022. XBB.1.5 may contribute to increases in cases in New Zealand. Differences in immune landscape between New Zealand and USA populations mean effects seen in parts of the USA might not directly translate to the New Zealand setting.</p>		

*The 'Overall risk assessment' is presented in comparison to the prior variant landscape in Aotearoa New Zealand. 'Increased risk' indicates the assessed variant as worse than the previous variant landscape with regards to that characteristic; 'no change' means that the assessed variant poses equivalent risk; and 'decreased risk' means that the assessed variant is better than the previous variant landscape.

**'Confidence level' indicates the overall quality of data that are available to make the risk assessment: 'High' (high quality, robust data); 'Moderate' (good data with limitations); 'Low' (very little data available). 'Insufficient data' indicates that there are no data of reasonable quality on which to base an assessment at this time.



Public Health Risk assessment for XBB

Updated: 19 January 2023

XBB is a recombinant virus (related to BA.2 and BJ.1) with additional spike protein mutations 364T, 445P, 446S and 490V. (67)

	Overall risk assessment*	Confidence level **	Assessment and rationale
Overall growth advantage	Increased risk	Low	<p>Evidence of a growth advantage compared to BA.5</p> <p>XBB has an estimated growth advantage of 56.9% per week (95% Credible Interval: 46.9 to 67.2%) compared to BA.5.2 in the UK (at 9 November 2022).(68)</p> <p>Currently present in New Zealand and is continuing to fluctuate between 1-4% of sequenced cases. In the week ending 13 January 2023, it made up 2% of all sequenced cases and 2% of isolates from hospital cases. (1)</p>
Transmissibility	Insufficient data	Insufficient data	<p>No direct data on intrinsic transmissibility and there is no current ability to measure from surveillance data. There is some laboratory evidence that ACE2 binding is increased for XBB compared to prior Omicron variants which may affect transmissibility/infectivity. (42)</p>
Immune evasion	Increased risk	Moderate	<p>Evidence of increased immune evasion.</p> <p>More resistant to neutralisation from sera of vaccinated and breakthrough infected individuals. (42, 69)</p>
Severity	Insufficient data	Insufficient data	<p>In late October 2022 the World Health Organization Technical Advisory Group on SARS-CoV-2 Virus Evolution noted that current (limited) information does not indicate an increase in severity for XBB. (70)</p>
Therapeutics	Increased risk	Low	<p><i>In vitro</i> studies showed loss of efficacy of all currently approved clinical monoclonal antibody therapies including Evusheld and Bebtelovimab. (42, 69)</p>



Testing	Insufficient data	Insufficient data	Evidence that suggests a clinically relevant decrease in the performance of RATs for detection of the Omicron variant (varies by device), (54-58) but it is uncertain how this will affect sensitivity specifically for XBB.
Overall Assessment	No change in risk		

**The 'Overall risk assessment' is presented in comparison to the prior variant landscape in Aotearoa New Zealand. 'Increased risk' indicates the assessed variant as worse than the previous variant landscape with regards to that characteristic; 'no change' means that the assessed variant poses equivalent risk; and 'decreased risk' means that the assessed variant is better than the previous variant landscape.*

***Confidence level' indicates the overall quality of data that are available to make the risk assessment: 'High' (high quality, robust data); 'Moderate' (good data with limitations); 'Low' (very little data available). 'Insufficient data' indicates that there are no data of reasonable quality on which to base an assessment at this time.*



Public Health Risk Assessment for BF.7

Updated: 12 January 2023

BF.7 is a sublineage of BA.5.2.1 but with spike protein mutations R346T

	Overall risk assessment*	Confidence level **	Assessment and rationale
Overall growth advantage	Insufficient data	Insufficient data	<p>Insufficient data to assess growth advantage</p> <p>Sequences uploaded by China to GISAID between 01 December 2022 to 03 January 2023, show 33% of all sequences were BF.7.(71) BF.7 has been observed to have a growth advantage compared to BA.5 in the UK,(72) but comparison of growth estimates suggest it is unlikely to outcompete other circulating variants such as BQ.1 and associated sublineages.</p> <p>BF.7 has been present in New Zealand at low levels since October 2022.(73)</p>
Transmissibility	Insufficient data	Insufficient data	<p>No evidence of increased intrinsic transmissibility compared to prior Omicron subvariants</p>
Immune evasion	Increased risk	Low	<p>Evidence of increased immune evasion.</p> <p>Some laboratory data suggests a higher resistance to neutralisation from sera of vaccinated and infected individuals,(74, 75) whilst one study found a similar resistance to neutralisation as BA.4/5. (76)</p>
Severity	Insufficient data	Insufficient data	<p>No evidence of a change in severity compared to previous Omicron subvariants</p>
Therapeutics	Increased risk	Moderate	<p>Currently there is no evidence of resistance to antivirals Paxlovid or Molnupiravir. <i>In vitro</i> studies showed loss of efficacy of Evusheld.(76)</p>



Testing	Insufficient data	Insufficient data	There is some evidence that suggests a clinically relevant decrease in the performance of RATs for detection of the Omicron variant (varies by device), (54-58) but it is uncertain how this will affect sensitivity specifically for BF.7.
Overall Assessment	No change in risk compared to the New Zealand variant landscape of late December 2022.		

**The 'Overall risk assessment' is presented in comparison to the prior variant landscape in Aotearoa New Zealand. 'Increased risk' indicates the assessed variant as worse than the previous variant landscape with regards to that characteristic; 'no change' means that the assessed variant poses equivalent risk; and 'decreased risk' means that the assessed variant is better than the previous variant landscape.*

***'Confidence level' indicates the overall quality of data that are available to make the risk assessment: 'High' (high quality, robust data); 'Moderate' (good data with limitations); 'Low' (very little data available). 'Insufficient data' indicates that there are no data of reasonable quality on which to base an assessment at this time.*



Public Health Risk assessment for BA.2.75

Updated: 19 January 2023

BA.2.75 has 8 key mutations from BA.2: 147E, 152R, 157L, 210V, 257S, 339H, 446S, 460K. (67)

Sublineages of BA.2.75 include BA.2.75.2, BN.1, BR.2.1 and CH.1.1 all of which have been discussed in previous [variant updates](#)

	Overall risk assessment*	Confidence level **	Assessment and rationale
Overall growth advantage	Increased Risk	Moderate	<p>Evidence of a growth advantage compared to BA.5. Prevalence in New Zealand is increasing gradually.</p> <p>There is evidence that BA.2.75 has a growth advantage against BA.4/5 in some countries (India, Austria, Singapore). BA.2.75 and sublineages (excluding BN.1) have an estimated growth advantage of 22.5% per week (95% Credible Interval: 19.1 to 26.0%) compared to BA.5.2 in the UK (at 9 November 2022). (68)</p> <p>In the fortnight ending 13 January 2023, BA.2.75 made up 17% and CH.1.1 made up 34% of all sequenced cases in New Zealand. (1)</p> <p>BA.2.75 made up of 17% and CH.1.1 made up 32% of all sequenced hospitalised cases. (1)</p>
Transmissibility	Insufficient data	Insufficient data	There are no direct data on intrinsic transmissibility and there is no current ability to measure this directly from surveillance data.
Immune evasion	No change in risk	Low	<p>There is evidence of increased immune evasion by BA.2.75 lineages in the form of increased representation in reinfection cases.</p> <p>Mutations suggest that BA.2.75 may have immune evasion potential. However, there are very limited data to evaluate immune evasion against vaccination, prior infection with BA.5, or a combination of the two (hybrid immunity). There are no estimates of vaccine effectiveness against BA.2.75.</p>



			<p>Laboratory data: Neutralisation studies found that BA.2.75 was similar or slightly less able to be neutralised by antibodies produced after vaccination and BA.2 infection, compared to BA.4 or BA.5. (77-81) Potentially higher receptor binding compared to other Omicron lineages. There are no data on the ability of antibodies produced after BA.5 infection to neutralise BA.2.75.</p> <p>A pre-print study found CH.1.1 to have a higher resistance to neutralisation from sera of vaccinated and infected individuals. (66)</p> <p>During the fortnight ending 13 January 2023, CH.1.1 was strongly over-represented in reinfection cases, accounting for 41% of reinfection cases and also represented 19% of first-time sequenced infections. (1)</p>
Severity	Insufficient data	Insufficient data	<p>No evidence of a change in severity compared to BA.5</p> <p>Few formal evaluations of BA.2.75 severity are available. An early assessment of the severity of BA.2 sublineages in India indicates that BA.2.74, BA.2.75, and BA.2.76 are causing 'mild' disease with no evidence of an increased risk of hospital admission or severe disease. (82) Lab and animal studies suggest mixed results for binding compared to BA.5, (81) but overall pathogenicity similar to BA.5. (83) Some <i>in vitro</i> evidence suggest an increase in cell-cell fusion and ability to infect lower airways compared to BA.2 which could alter pathogenicity. (84)</p>
Therapeutics	Insufficient data	Insufficient data	Currently there is no evidence of resistance to antivirals Paxlovid or Molnupiravir.
Testing	Insufficient data	Insufficient data	There is some evidence that suggests a clinically relevant decrease in the performance of RATs for detection of the Omicron variant (varies by device), (54-58) but it is uncertain how this will affect sensitivity specifically for CH.1.1.
Overall Assessment	<p>There is an increase in overall risk from the previous predominant variant, BA.5. (Moderate confidence)</p> <p>BA.2.75 and associated sublineages, particularly CH.1.1, are increasing in frequency in New Zealand and appear to be more transmissible and immune evasive. BA.2.75 and CH.1.1 combined currently account for 50% of sequenced genomes in New Zealand.</p>		

*The 'Overall risk assessment' is presented in comparison to the prior variant landscape in Aotearoa New Zealand. 'Increased risk' indicates the assessed variant as worse than the previous variant landscape with regards to that characteristic; 'no change' means that the assessed variant poses equivalent risk; and 'decreased risk' means that the assessed variant is better than the previous variant landscape.

**'Confidence level' indicates the overall quality of data that are available to make the risk assessment: 'High' (high quality, robust data); 'Moderate' (good data with limitations); 'Low' (very little data available). 'Insufficient data' indicates that there are no data of reasonable quality on which to base an assessment at this time.



Public Health Risk assessment for BQ.1.1

Updated: 19 January 2023

BQ.1.1 is related to BA.5.3 but with Spike protein mutations 444T, 460K, 346T (67)

	Overall risk assessment*	Confidence level **	Assessment and rationale
Overall growth advantage	Increased risk	Moderate	<p>Evidence of a growth advantage compared to BA.5. (72, 85, 86)</p> <p>BQ.1.1 variant has an estimated growth advantage of 48.5% per week (95% Credible Interval: 43.3 to 54.1%) compared to BA.5.2 in the UK (at 9 November 2022).(68)</p> <p>Currently present in New Zealand. In the week ending 13 January 2023, BQ.1.1 made up 15% of all sequenced cases. In the fortnight ending 13 January 2023 it made up 16% of sequenced isolates from hospital cases. (1)</p>
Transmissibility	Insufficient data	Insufficient data	<p>No direct data on intrinsic transmissibility and there is no current ability to measure from surveillance data. There is some laboratory evidence that ACE2 binding is increased for BQ.1.1 compared to prior Omicron variants which may affect transmissibility/infectivity. (42)</p>
Immune evasion	Increased risk	Moderate	<p>Evidence of increased immune evasion.</p> <p>More resistant to neutralisation from sera of vaccinated and infected individuals. (42, 69) At least two small studies show that mRNA bivalent BA.4/5 vaccine produces robust neutralising activity against BQ.1.1 compared to monovalent wild type vaccine. (18, 69, 87)</p>
Severity	Insufficient data	Insufficient data	<p>No evidence of a change in severity compared to BA.5</p> <p>Evidence from a surge of cases of this variant in France suggests it is not causing increased rates of hospitalisations and deaths. (88)</p>



Therapeutics	Increased risk	Low	<i>In vitro</i> studies showed loss of efficacy of all currently approved clinical monoclonal antibody therapies including Evusheld and Bebtelovimab. (42, 69)
Testing	Insufficient data	Insufficient data	Evidence that suggests a clinically relevant decrease in the performance of RATs for detection of the Omicron variant (varies by device), (54-58) but it is uncertain how this will affect sensitivity specifically for BQ.1.1
Overall Assessment	<p>There is an increase in overall risk from the previous predominant variant, BA.5. (Moderate confidence)</p> <p>BQ.1.1 is increasing in frequency overseas and appears to be more transmissible and immune evasive. The frequency in NZ has remained relatively stable at approximately 15%</p>		

*The 'Overall risk assessment' is presented in comparison to the prior variant landscape in Aotearoa New Zealand. 'Increased risk' indicates the assessed variant as worse than the previous variant landscape with regards to that characteristic; 'no change' means that the assessed variant poses equivalent risk; and 'decreased risk' means that the assessed variant is better than the previous variant landscape.

**'Confidence level' indicates the overall quality of data that are available to make the risk assessment: 'High' (high quality, robust data); 'Moderate' (good data with limitations); 'Low' (very little data available). 'Insufficient data' indicates that there are no data of reasonable quality on which to base an assessment at this time.



New signals

Section updated: 19 January 2023

With the rapid development of new variants with convergent mutations, future variant updates will focus on the mutations present in the variant landscape rather than specific variants. Any variants with markedly different clinical features will be monitored and reported.

In the second half of 2022, many new Omicron subvariants have been reported. These variants demonstrate convergent evolution which is a process whereby variants from different lineages accumulate similar mutations. For example, the European Centre for Disease Prevention and Control (ECDC) has designated Omicron lineages with mutations at N460X and at either F490X or K444X (these include BQ.1, BQ.1.1, XBB, BN.1 and BN.2) as a variant under monitoring (VUM). The location of these mutations might produce a significant effect on neutralising activity. (89, 90)

For many BA.2.75 sublineages, mutations on N-terminal domain (NTD) can cause reduction in neutralisation titres. (42)

In Australia and New Zealand, there is currently no single variant driving case numbers. (91)

Details of BA.5, BA.2.75, BQ.1.1, BA.4.6, and XBB can be found above in the risk assessment section. Short summaries are provided here of newer variants which are not covered in the risk assessment section but are of heightened concern because of their growth rate in New Zealand or internationally, or because there are other features of concern (e.g., if increased severity was suspected). Because these variants have only been recently detected, the growth advantage, immune escape potential, and characteristics of disease they cause (e.g., severity) is often not yet well understood.

Details of the Omicron subvariants BR.2.1, BN.1 and BA.2.75.2, can be found in the previous SARS-CoV-2 Variant of Concern Update [here](#).

XBC

- XBC is a recombinant lineage that combines sequences from the Delta and Omicron variants. (92) Some studies suggest that chronic infections may be contributing to the emergence of such recombinant variant lineages. (93)
- **In the week ending 13 January 2023, XBC made up 4% of all sequenced cases, and 7% of wastewater samples. (1) In the fortnight ending 13 January 2023 it made up 6% of sequenced isolates from hospital cases. (1)**
- XBC appears to be most common in the Philippines and Brunei, circulating at a prevalence of around 5%. Sublineage XBC.1 (S:L452M) has been rising in Australia.(94)
- The XBC lineage has been present in Australia and Southeast Asia for some time, with no indication of increased disease severity (albeit this is based on small case numbers). (92)

XBF

- Sublineage from a BA.5.2.3 and CJ.1 (a BA.2.75 sublineage) recombinant. Spike identical to CJ.1, additional mutations (from BA.2.75) S:486P, S:R346T, S:F490S. (94)
- Growing in Australia and Denmark. (94) Appears to be growing less rapidly in South Asia than CH.1.1 (another BA.2.75 sublineage),(94) but epidemiology could be different in New Zealand.
- **In the week ending 13 January 2023, XBC made up 19% of all sequenced cases. (1) In the fortnight ending 13 January 2023 it made up 7% of sequenced isolates from hospital cases. (1)**
- No data have yet emerged about the severity of XBF disease.



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