Evidence table

SARS-CoV-2 variants

4 April 2023

This is the final version of the living evidence table on SARS-CoV-2 variants. This evidence table was last updated in March 2023. This table is no longer a 'living' document and the information within it is not updated on a regular basis.

Background

Viruses constantly change through mutation and over time, new variants of a virus are expected to occur. Some variants have characteristics that have a significant impact on transmissibility, severity of disease and effectiveness of vaccines.

The World Health Organization (WHO) announced the variant naming system on 1 June 2021.

This table includes information on Omicron subvariants that are currently causing concern in the scientific community and are under monitoring by the World Health Organization. Details are tabulated when variants meet the World Health Organization (WHO) definition of Variant of Concern (VOC).

- Previously circulating VOC listed by WHO: Alpha (B.1.1.7), Beta (B.1.351), Gamma (P.1) and Delta (B.1.617.2)
- Variant of Concern lineages under monitoring (VOC-LUM) by WHO: BF.7, BQ.1, BA.2.75, CH.1.1, XBB, XBB.1.5 and XBF.
- Previously circulating Variants of Interest by WHO: Epsilon, Zeta, Eta, Theta, Iota, Kappa, Lambda, Mu
- Recombinant lineages: XD and XF (combination of Delta AY.4 and BA.1, XD has the Omicron S gene incorporated into a Delta genome), XE (combination of BA.1 and BA.2, with the majority of the genome including the S gene belonging to BA.2), and XBB (combination of BA.2.10.1 and BA.2.75 sublineages, i.e. BJ1 and BM.1.1.1, with a breakpoint in S1). The XD recombinant is now classified as a formally monitored variant (FMV) by WHO and XE is being tracked as part of the Omicron variant.

Topic	BF.7	BQ.1	BA.2.75	CH.1.1	XBB	XBB.1.5	XBF
Mutations	BA.5 + S:R346T It is a BA.5 sublineage.	One or several of the five mutations: S:R346X, S:K444X, S:V445X, S:N450D, and S:N460X It is a BA.5 sublineage. BQ.1 and BQ.1.1 have additional spike mutations S:K444T, S:N460K, and S:R346T	S:D339H, S:G446S, S:N460K, and S:Q493R reversion It is a BA.2 sublineage. BA.2.75.2 has additional spike mutations S:R346T, S:F486S, and S:D1199N.	BA.2.75 + S:L452R, S:F486S It is a BA.2.75 sublineage.	S:G339H, S:R346T, S:L368I, S:V445P, S:G446S, S:N460K, S:F486S, and S:F490S It is a recombinant of BA.2.10.1 and BA.2.75. XBB.1.5 has an additional spike mutation S:F486P.	XBB + S:F486P	BA.5 + S:K147E, S:W152R, S:F157L, S:I210V, S:G257S, S:G339H, S:R346T, S:G446S, S:N460K, S:F486P, S:F490S It is a recombinant of BA.5.2.3 and CJ.1
Transmissibility	Has a growth advantage over BA.5. ACE2-binding affinity: similar to BA.4/5.	Has a growth advantage over BA.5.2. ACE2-binding affinity: • BQ.1 and BQ.1.1: similar to BA.4 and BA.5	Has a growth advantage over BA.5.2. ACE2-binding affinity: higher than BA.4, BA.5 and BA.2	Has a growth advantage over BQ.1.1.	Has a growth advantage over BA.5.2. Has a growth advantage over BA.5.2. ACE2-binding affinity: XBB/XBB.1: weaker than BA.2*^	Has a growth advantage over other circulating Omicron sublineages, including BQ.1.1. ACE2-binding affinity: substantially higher than BQ.1.1 and XBB/XBB.1 XBB.1.5 has more than 1.2-fold greater relative effective reproduction number than XBB.1.	Insufficient data

Topic	BF.7	BQ.1	BA.2.75	CH.1.1	XBB	XBB.1.5	XBF
Virulence and severity	Insufficient data	Preliminary analysis of the risk of hospital admission following presentation to emergency care shows no increase in risk for BQ.1 compared to BA.5.	Insufficient data	Preliminary analysis of the risk of hospital admission following presentation to emergency care shows no increase in risk for CH.1.1 compared to BA.5.	Insufficient data	Preliminary analysis suggests that no change in disease severity.	Insufficient data
Impact on immunity	More resistant to the neutralisation antibodies induced by prior vaccination and infection than BA.4/5. Less resistant to the neutralisation antibodies induced by prior vaccination and infection than BQ.1 and BQ.1.1.	In-vitro studies show that BQ.1 and BQ.1.1 are more resistant to the neutralisation antibodies induced by prior infection and vaccination (including booster) than BA.5. BA.5-adapted bivalent booster vaccine elicited better neutralising response against BQ.1.1 than the original monovalent booster vaccine. Previous infection enhanced the magnitude and breadth of BA.5-bivalent-booster-	More neutralisation resistant to sera from vaccinated/boosted individuals than BA.2. Less neutralisation resistant to sera from vaccinated/boosted individuals than BA.4/5. Less neutralisation resistant to sera from unvaccinated individuals who had recovered from BA.1 or BA.2 infections than BA.5.	More resistant to the neutralisation antibodies induced by prior infection and vaccination than BA.2, BA.4/5 and XBB.	XBB.1 and XBB.3 variants were more resistant to the neutralisation antibodies induced by prior vaccination (either primary or booster) and prior infection than BA.2, BA.4/5, BQ.1.1 and BA.2.75.2. BA.4/5-adapted bivalent booster vaccines elicited better neutralising response against XBB.1 than original monovalent booster vaccine. The neutralising response elicited by the bivalent vaccine against XBB.1 was further enhanced	XBB.1.5 is equally immune evasive as XBB.1 but slightly less resistant to neutralising antibodies induced by BA.1, BA.5, and BF.7 breakthrough infections.^ XBB.1.5 is highly resistant to monovalent vaccine elicited antibody neutralisation. Bivalent vaccine restores the antibody response.	Insufficient data

Topic	BF.7	BQ.1	BA.2.75	CH.1.1	XBB	XBB.1.5	XBF
		elicited neutralisation.	BA.1-adapted and BA.4/5-adapted bivalent booster vaccines elicited better neutralising titres against BA.2.75 than the original monovalent booster vaccine. elicited higher neutralising titres against BA.2.75 than against BA.4 and BA.5. A real-life study suggested that previous infection with BA.5 or BA.4 provided better protection against BA.2.75 than previous infection with BA.1 or BA.2 (~80% versus 50%).		in individuals with a prior infection history. A real-life study suggested that the bivalent mRNA booster vaccine effectiveness against symptomatic XBB/XBB.1.5 infection in persons who had previously received 2–4 monovalent vaccine doses ranged from 38% to 48% at 2-3 months after vaccination.		
Treatment	Not sensitive to neutralisation by tixagevimab + cligavimab.	BQ.1.1 not sensitive to neutralisation by imdevimab + casirivimab and tixagevimab + cligavimab.	More sensitive to neutralisation by sotrovimab than BA.2, but less sensitive than BA.5.	Insufficient data	Not sensitive to neutralisation by imdevimab + casirivimab and tixagevimab + cligavimab.	Not sensitive to neutralisation by Evusheld (tixagevimab + cligavimab), but weakly sensitive to sotrovimab.	Insufficient data

Topic	BF.7	BQ.1	BA.2.75	CH.1.1	XBB	XBB.1.5	XBF
		Mixed findings for BQ.1.1 sensitivity to sotrovimab. One study reported no sensitivity; while the other reported reduced sensitivity compared to BA.5 and increased sensitivity compared to BA.2.^ BQ.1.1 had similar susceptibility to remdesivir, molnupiravir and nirmatrelvir compared to the ancestral strain.	Less sensitive to neutralisation by cilgavimab than BA.2 and BA.5 More sensitive to neutralisation by tixagevimab than BA.2 and BA.5 Not sensitive to neutralisation by imdevimab More sensitive to neutralisation by casirivimab than BA.2 and BA.6 Remdesivir, molnupiravir, and nirmatrelvir retained neutralising activities against BA.2.75.		Mixed findings for sotrovimab; In one study, XBB.1 was sensitive to neutralisation by sotrovimab,^ while in the other it was not sensitive. Similar susceptibility to remdesivir, molnupiravir and nirmatrelvir compared to the ancestral strain.	Susceptible to neutralisation by remdesivir, molnupiravir, nirmatrelvir.	
Countries reporting detection	100	123	112		101	67	39

Notes

*Preliminary data, not fully established, in some cases small numbers or short follow up; interpret with caution

^ Commentary grey literature, pre-peer review or news

The "last updated" date refers to the date when the evidence was last reviewed.

Background evidence checks

Evidence check - Emerging variants (PDF)

Evidence check - Omicron (BA.2 sub-lineage) (PDF)

Evidence check - Omicron (B.1.1.529) variant (PDF)

Evidence check - SARS-CoV-2 variants (PDF)

Living evidence tables include some links to low quality sources and an assessment of the original source has not been undertaken. Sources are monitored regularly but due to rapidly emerging information, tables may not always reflect the most current evidence. The tables are not peer reviewed, and inclusion does not imply official recommendation nor endorsement of NSW Health.

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