CAPRISA

CENTRE FOR THE AIDS PROGRAMME OF RESEARCH IN SOUTH AFRICA

COVID-19 UPDATES

23 January 2023

science & innovation
Department:
Science and Innovation
REPUBLIC OF SOUTH AFRICA

NRF National Research Foundation

CAPRISA hosts a DSI-NRF Centre of Excellence in HIV Prevention

UNAIDS
CAPRISA is the UNAIDS Collaborating Centre for HIV Research and Policy

GVN
GLOBAL VIRUS NETWORK

german cooperation
DEUTSCHE ZUSAMMENARBEIT
CAPRISA has a GIZ-funded Epidemic Intelligence Unit

saMRC advancinglife
CAPRISA hosts a MRC HIV-TB Pathogenesis and Treatment Research Unit
CAPRISA hosts a DoH-MRC Special Initiative for HIV Prevention Technology

health
Department:
Health
REPUBLIC OF SOUTH AFRICA

COLUMBIA UNIVERSITY
MAILMAN SCHOOL of PUBLIC HEALTH

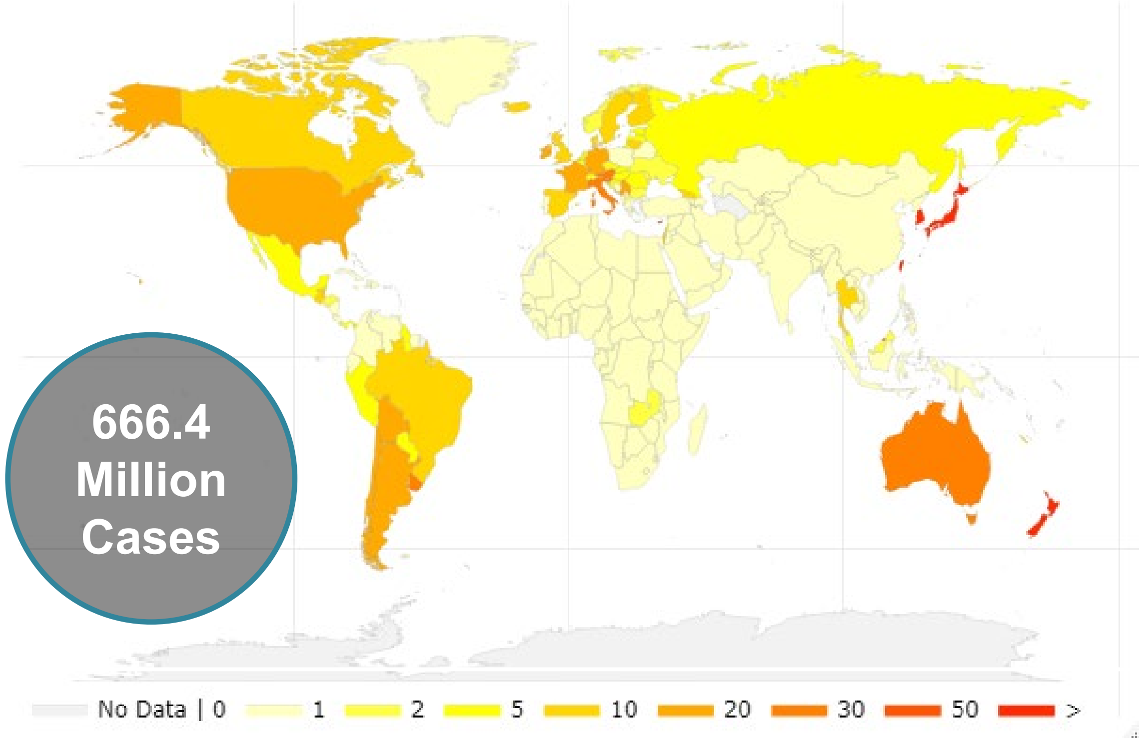
UNIVERSITY OF KWAZULU-NATAL
INYUVESI YAKWAZULU-NATALI

Global COVID-19 Pandemic

Data up to 13th January 2023

Confirmed cases per 100,000 people

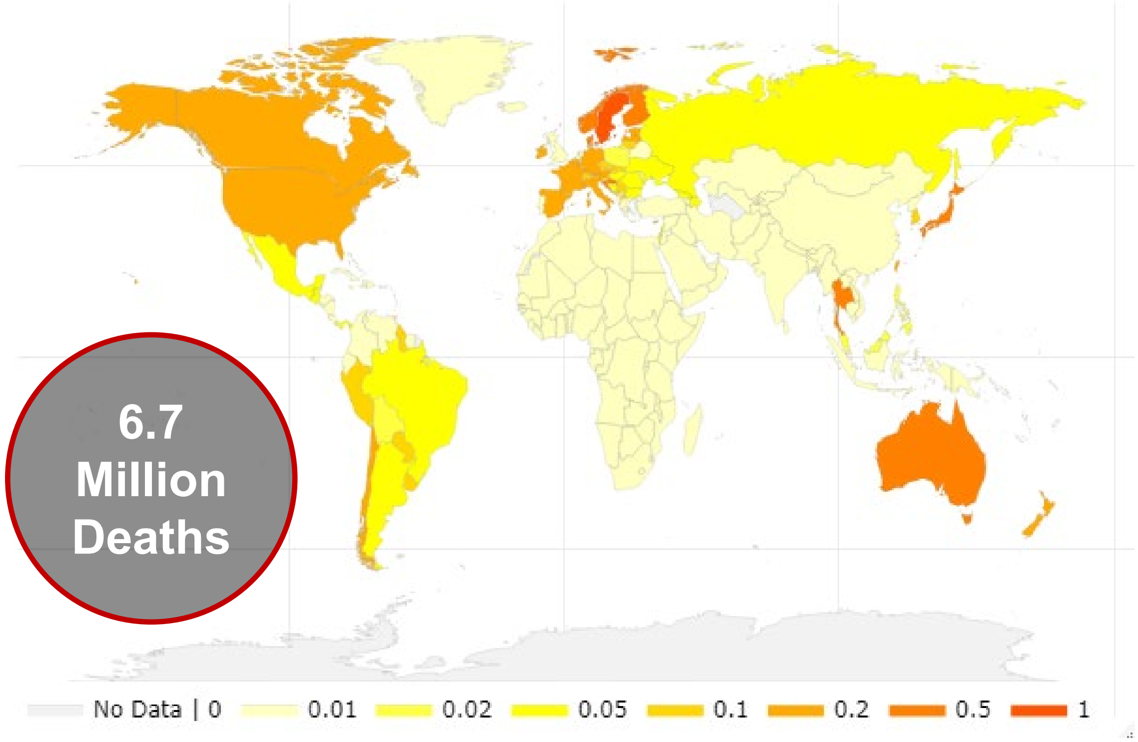
7-day rolling average



666.4 Million Cases

Confirmed deaths per 100,000 people

7-day rolling average



6.7 Million Deaths

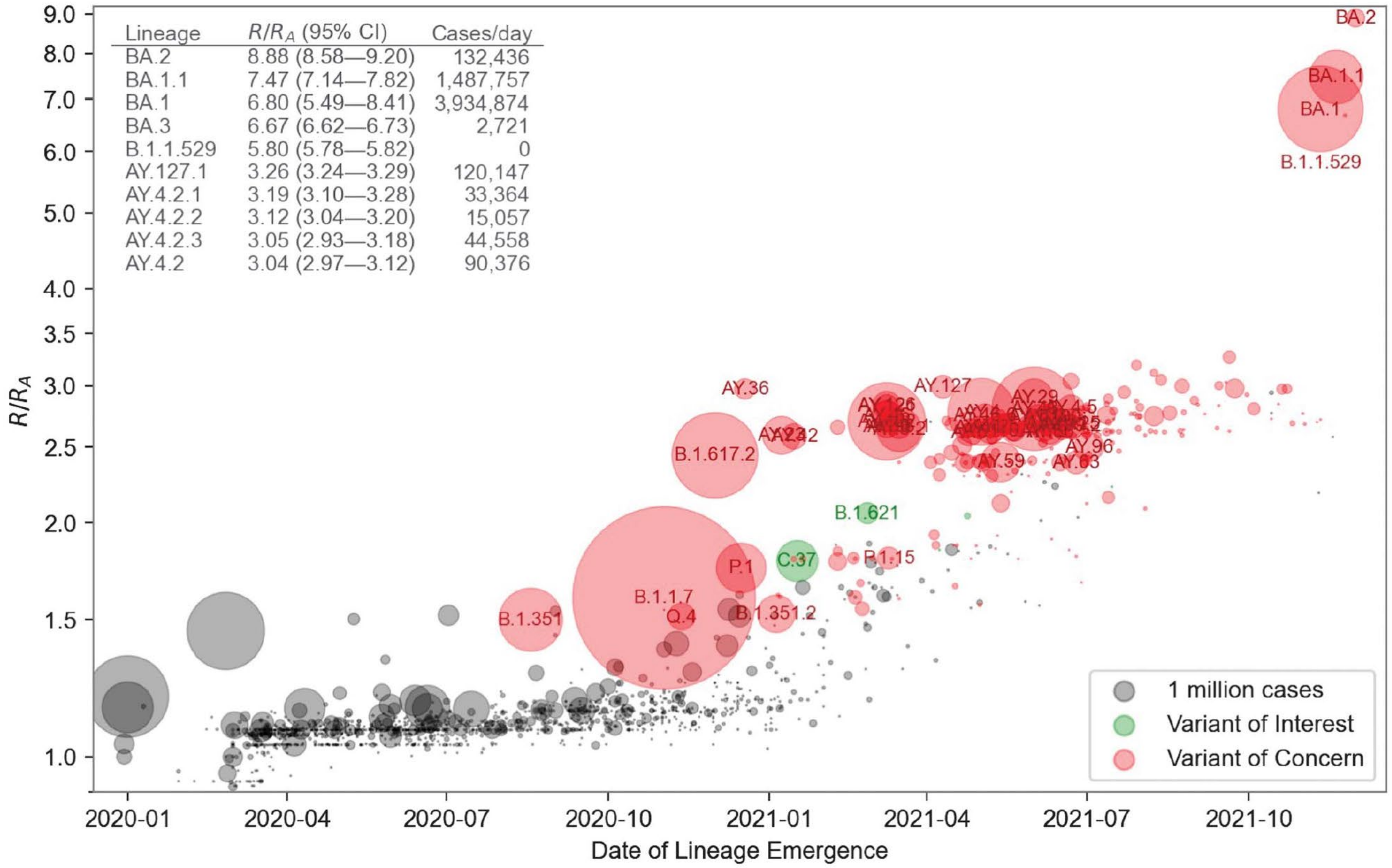
Source: Our World in Data; data explorer; Johns Hopkins University COVID-19 Dashboard

nature

CORONAVIRUS

Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness

Fritz Obermeyer[1,2]*†, Martin Jankowiak[1,2], Nikolaos Barkas[1], Stephen F. Schaffner[1,3,4],
Jesse D. Pyle[1]†, Leonid Yurkovetskiy[5], Matteo Rosso[5], Daniel J. Park[1], Mehrtash Babadi[1]



Lineage	R/R_A (95% CI)	Cases/day
BA.2	8.88 (8.58—9.20)	132,436
BA.1.1	7.47 (7.14—7.82)	1,487,757
BA.1	6.80 (5.49—8.41)	3,934,874
BA.3	6.67 (6.62—6.73)	2,721
B.1.1.529	5.80 (5.78—5.82)	0
AY.127.1	3.26 (3.24—3.29)	120,147
AY.4.2.1	3.19 (3.10—3.28)	33,364
AY.4.2.2	3.12 (3.04—3.20)	15,057
AY.4.2.3	3.05 (2.93—3.18)	44,558
AY.4.2	3.04 (2.97—3.12)	90,376

Fig. 1. Relative fitness versus date of lineage emergence. Circle size is proportional to cumulative case count inferred from lineage proportion estimates and confirmed case counts. The inset table lists the 10 fittest lineages inferred by the model. R/R_A is the fold increase in relative fitness over the Wuhan (A) lineage, assuming a fixed generation time of 5.5 days.

SARS-CoV-2 is evolving with enhanced fitness at a rapid rate- more transmissible than Wuhan strain

Alpha	**= 1.7 times faster**
Beta	**= 1.6 times faster**
Delta	**= 2.5 times faster**
Omicron	**= 5.8 times faster**
BA.2	**= 8.9 times faster**

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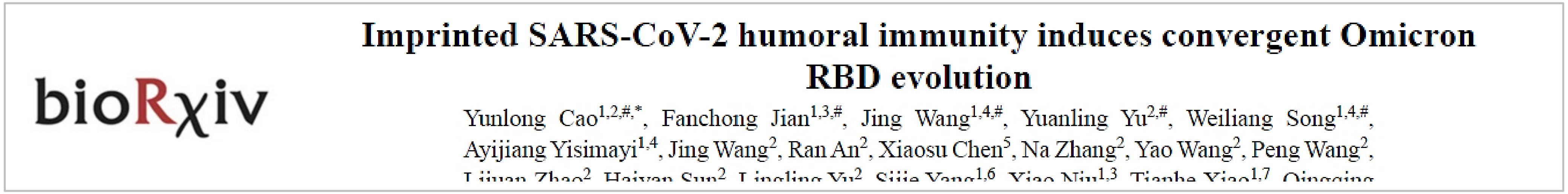
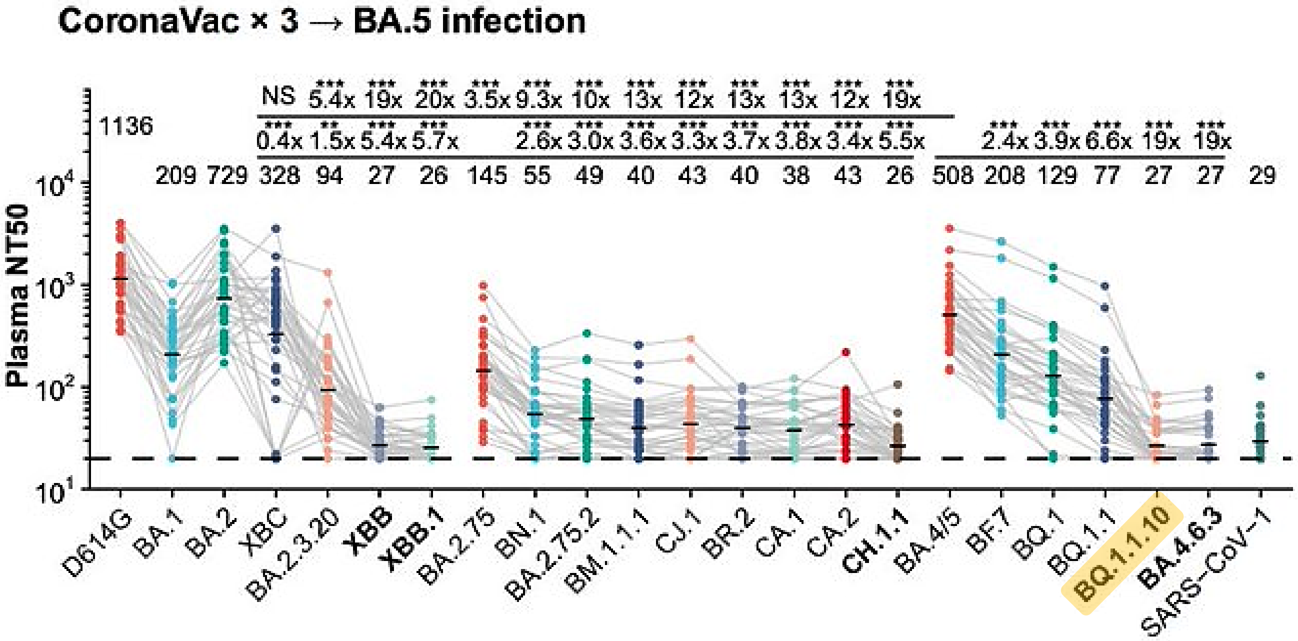


bioRxiv

Imprinted SARS-CoV-2 humoral immunity induces convergent Omicron RBD evolution

Yunlong Cao[1,2,#,*], Fanchong Jian[1,3,#], Jing Wang[1,4,#], Yuanling Yu[2,#], Weiliang Song[1,4,#], Ayijiang Yisimayi[1,4], Jing Wang[2], Ran An[2], Xiaosu Chen[5], Na Zhang[2], Yao Wang[2], Peng Wang[2], Lijuan Zhao[2], Haiyan Sun[2], Lingling Yu[2], Sijie Yang[1,6], Xiao Niu[1,3], Tianhe Xiao[1,7], Qingqing



- **BQ.1.1.10 more evasive than BQ.1.1 after 3 x CoronaVac plus a BA.5 breakthrough infection**
- **Current most immune-evasive strains to monitor**
    - **XBB, XBB.1, CH.1.1, BA.4.6.3, and BQ.1.1.10**
- **BQ.1+NTD mutations, such as Y144del – more immune evasive.**

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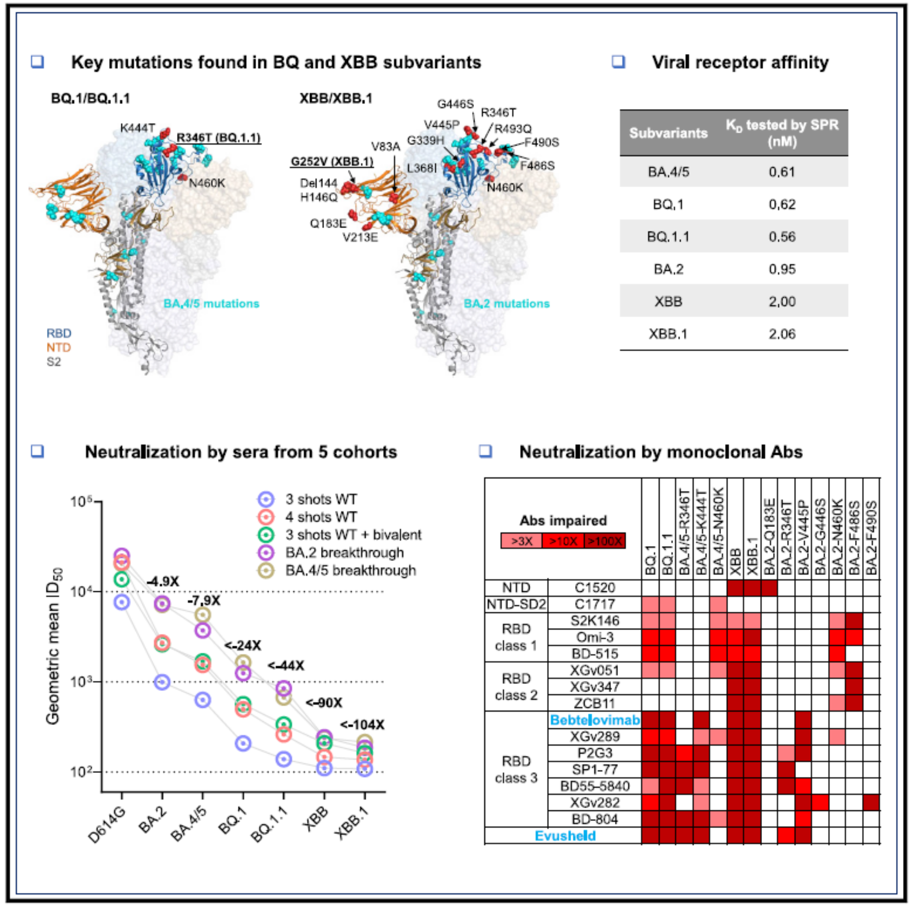
Cell

Article

Alarming antibody evasion properties of rising SARS-CoV-2 BQ and XBB subvariants

Graphical abstract



Viral receptor affinity

Subvariants	K_D tested by SPR (nM)
BA.4/5	0.61
BQ.1	0.62
BQ.1.1	0.56
BA.2	0.95
XBB	2.00
XBB.1	2.06

Abs impaired: >3X, >10X, >100X

		BQ.1	BQ.1.1	BA.4/5-R346T	BA.4/5-K444T	BA.4/5-N460K	XBB	XBB.1	BA.2-Q183E	BA.2-R346T	BA.2-V445P	BA.2-G446S	BA.2-N460K	BA.2-F486S	BA.2-F490S
NTD	C1520						>100X	>100X	>100X						
NTD-SD2	C1717	>3X	>3X			>3X									
RBD class 1	S2K146	>3X	>3X			>3X	>3X	>3X					>3X	>100X	
	Omi-3	>10X	>10X			>10X	>10X	>100X					>10X	>10X	
	BD-515	>10X	>10X			>10X	>10X	>10X					>10X		
RBD class 2	XGv051	>3X	>3X			>3X	>100X	>100X					>3X	>100X	
	XGv347						>100X	>100X						>100X	
	ZCB11						>100X	>100X					>3X	>100X	
RBD class 3	Bebtelovimab	>100X	>100X		>100X		>100X	>100X			>100X				
	XGv289	>10X	>10X		>3X	>3X	>100X	>100X			>100X		>3X		
	P2G3	>100X	>100X	>10X	>100X		>100X	>100X		>3X	>100X				
	SP1-77	>100X	>100X	>100X	>100X		>100X	>100X		>100X					
	BD55-5840	>3X	>100X	>100X	>3X		>100X	>100X		>100X	>10X				
	XGv282	>10X	>100X		>3X		>100X	>100X			>100X	>10X			>100X
	BD-804	>100X	>100X	>100X	>100X	>3X	>100X	>100X			>10X				
Evusheld		>100X	>100X	>100X	>100X		>100X	>100X		>10X	>100X				

Authors

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In brief

Recent BQ and XBB subvariants of SARS-CoV-2 demonstrate dramatically increased ability to evade neutralizing antibodies, even those from people who received the bivalent mRNA booster or who are immunized and had previous breakthrough Omicron infection. Additionally, both BQ and XBB are completely resistant to bebtelovimab, meaning there are now no clinically authorized therapeutic antibodies effective against these circulating variants.

Highlights

- BQ.1, BQ.1.1, XBB, and XBB.1 are the most resistant SARS-CoV-2 variants to date
- Serum neutralization was markedly reduced, including with the bivalent booster
- All clinical monoclonal antibodies were rendered inactive against these variants
- The ACE2 affinity of these variants were similar to their parental strains

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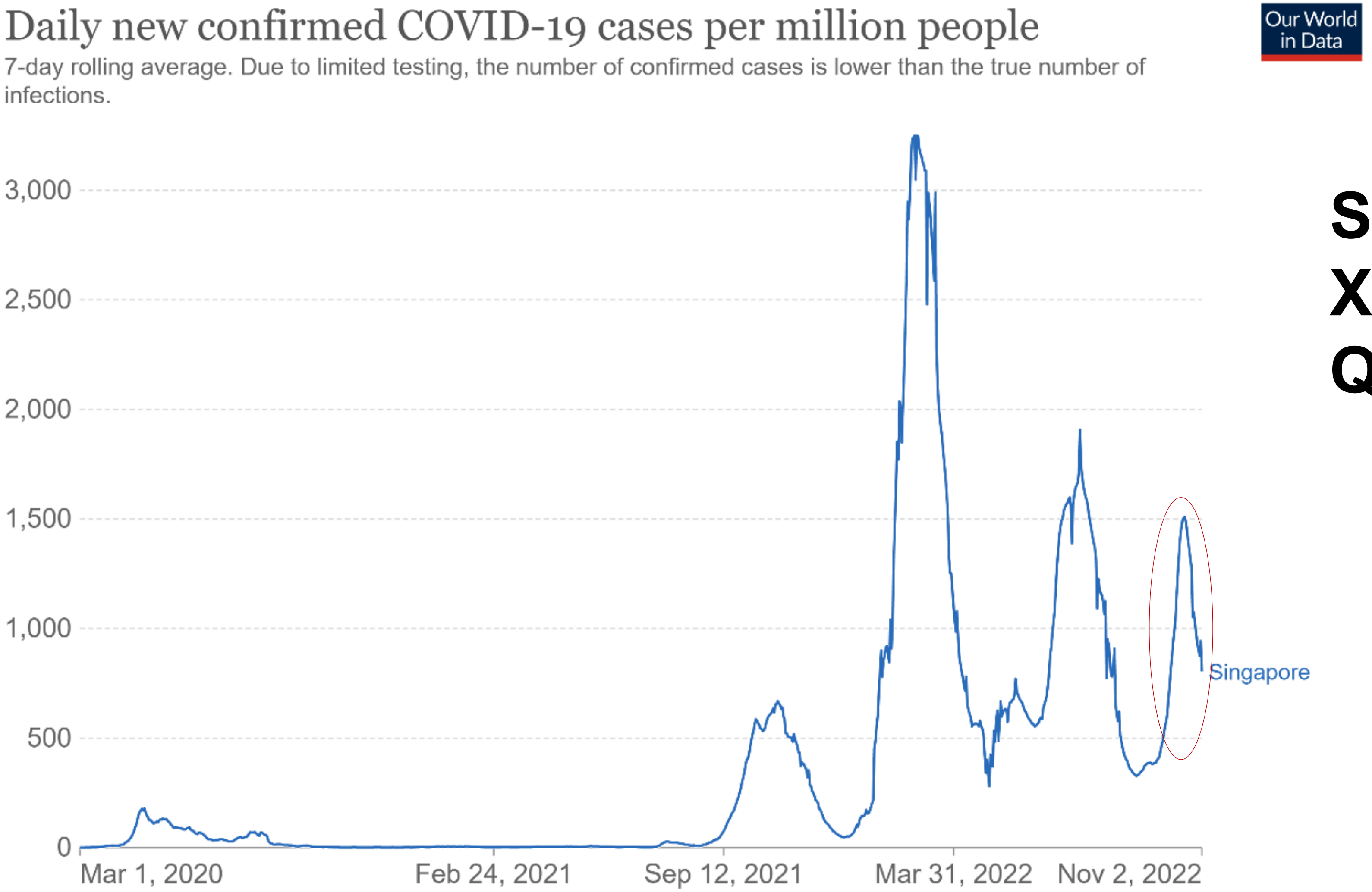
Waves of infection in Singapore



Singapore had an XBB.1.5 wave in Q4 2022

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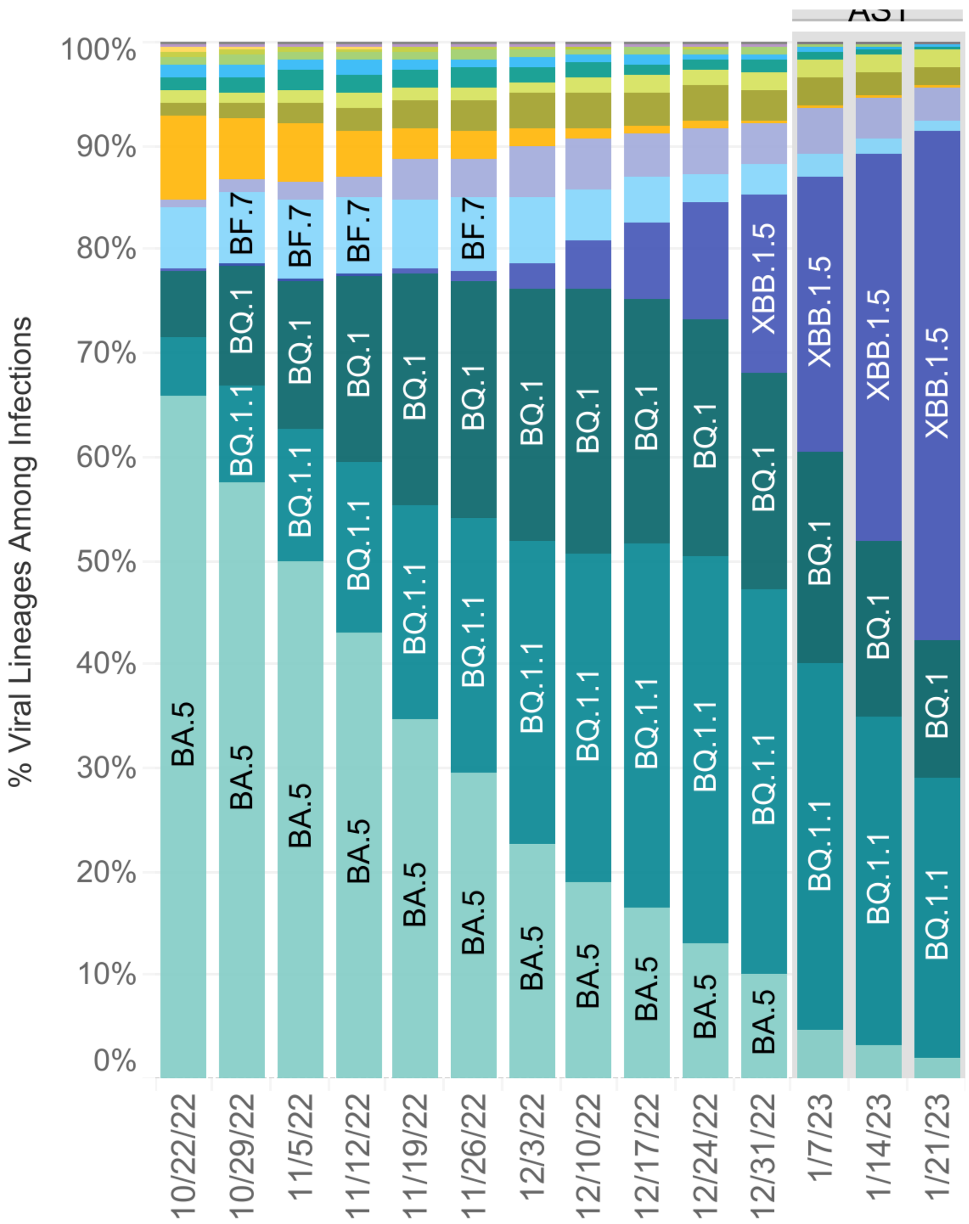

Frequency distribution of variants in the USA

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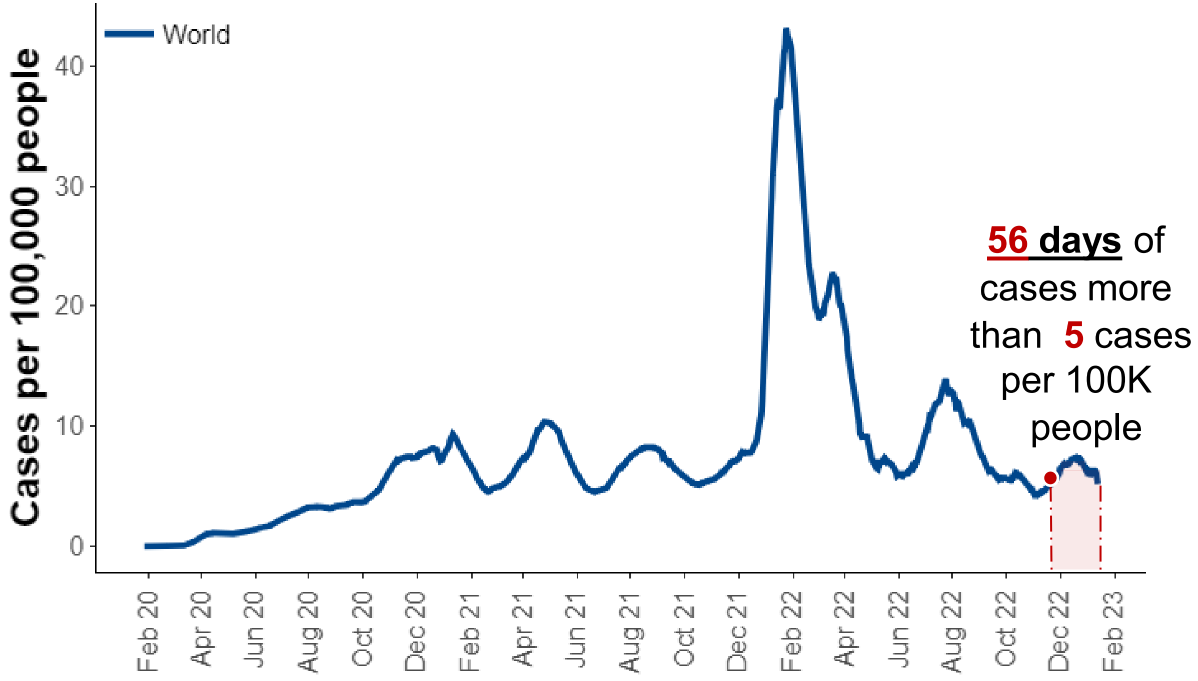
Trends in the Covid-19 pandemic

Data up to 13th January 2023

A world time series of confirmed cases

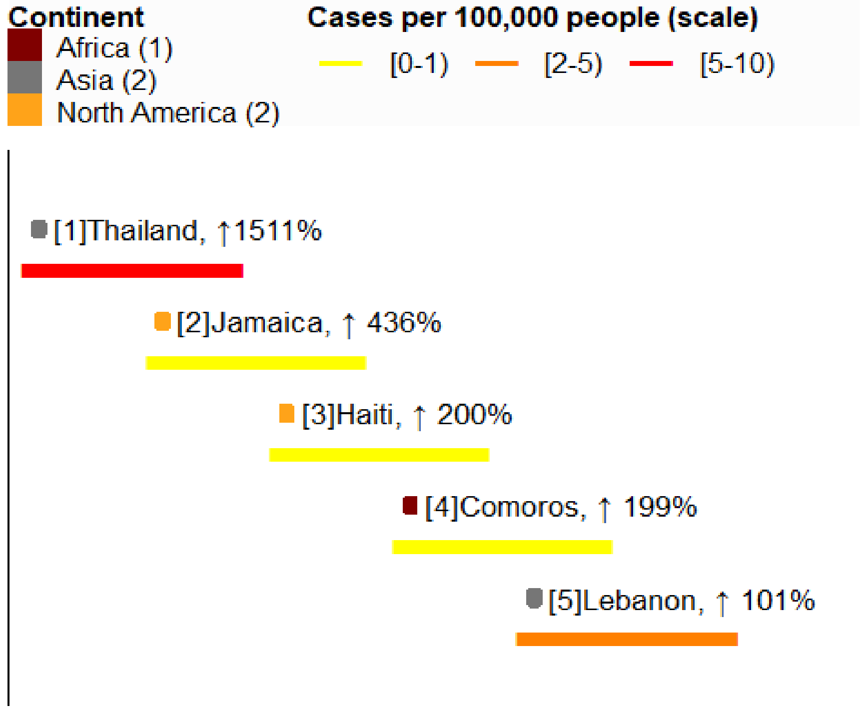
7-day rolling average cases per 100,000 people



56 days of cases more than **5** cases per 100K people

TOP 5 with increased % change | Worldwide

7-day rolling average cases per 100,000 people



Source: Our World in Data; data explorer; Johns Hopkins University [COVID-19 Dashboard]

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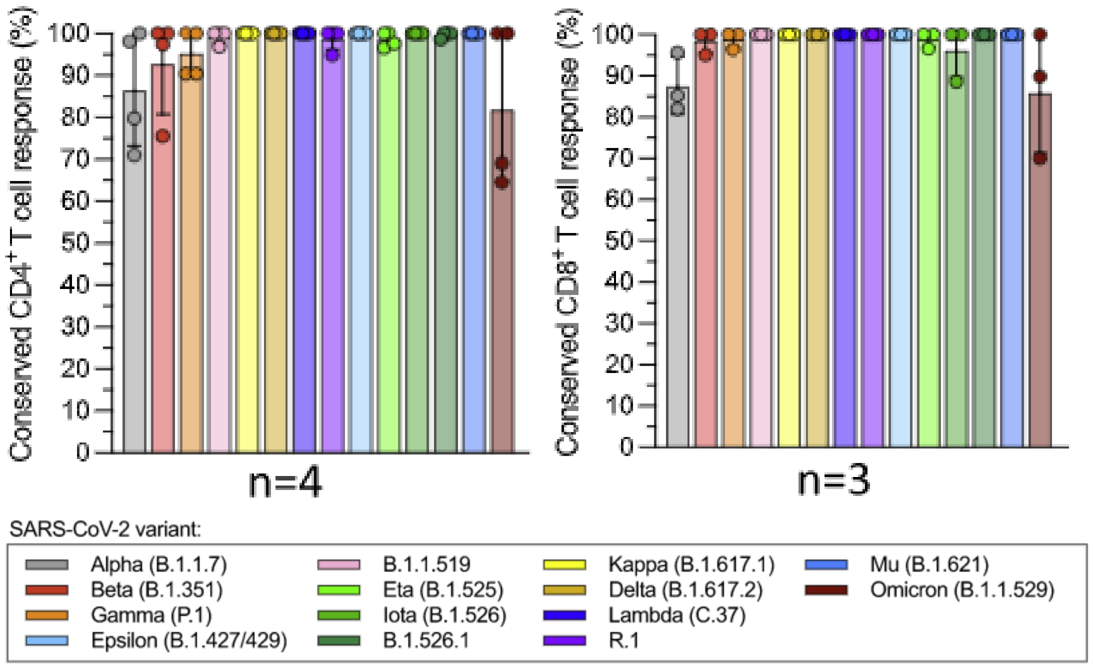
Variants rarely escape vaccine T-cell responses

Cell

SARS-CoV-2 vaccination induces immunological T cell memory able to cross-recognize variants from Alpha to Omicron

Alison Tarke,[1,2,6] Camila H. Coelho,[1,6] Zeli Zhang,[1,6] Jennifer M. Dan,[1,3,6] Esther Dawen Yu,[1] Nils Methot,[1]
Nathaniel I. Bloom,[1] Benjamin Goodwin,[1] Elizabeth Phillips,[4] Simon Mallal,[4] John Sidney,[1] Gilberto Filaci,
Daniela Weiskopf,[1] Ricardo da Silva Antunes,[1] Shane Crotty,[1,3,7,*] Alba Grifoni,[1,7,*] and Alessandro Sette[1]

- **96 adults with various vaccines:** Moderna (mRNA-1273), Pfizer (BNT162b2), J&J (Ad26.COV2.S) & Novovax (NVX-CoV2373)
- **$CD4^+$ & $CD8^+$ T cell responses conserved against α, β, δ, γ, B.1.1.519, κ, λ, and R.1 variants, ie. effective across variants & vaccine platform**
- **~6 months post-vaccination:**
  - 90% ($CD4^+$) & 87% ($CD8^+$) memory T cell responses preserved against the various variants
  - 84% ($CD4^+$) & 85% ($CD8^+$) preserved against Omicron



Two boosters better against XBB than single booster

The NEW ENGLAND JOURNAL of MEDICINE

Neutralization against BA.2.75.2, BQ.1.1, and XBB from mRNA Bivalent Booster

Meredith E. Davis-Gardner, Lilin Lai, Bushra Wali, Hady Samaha

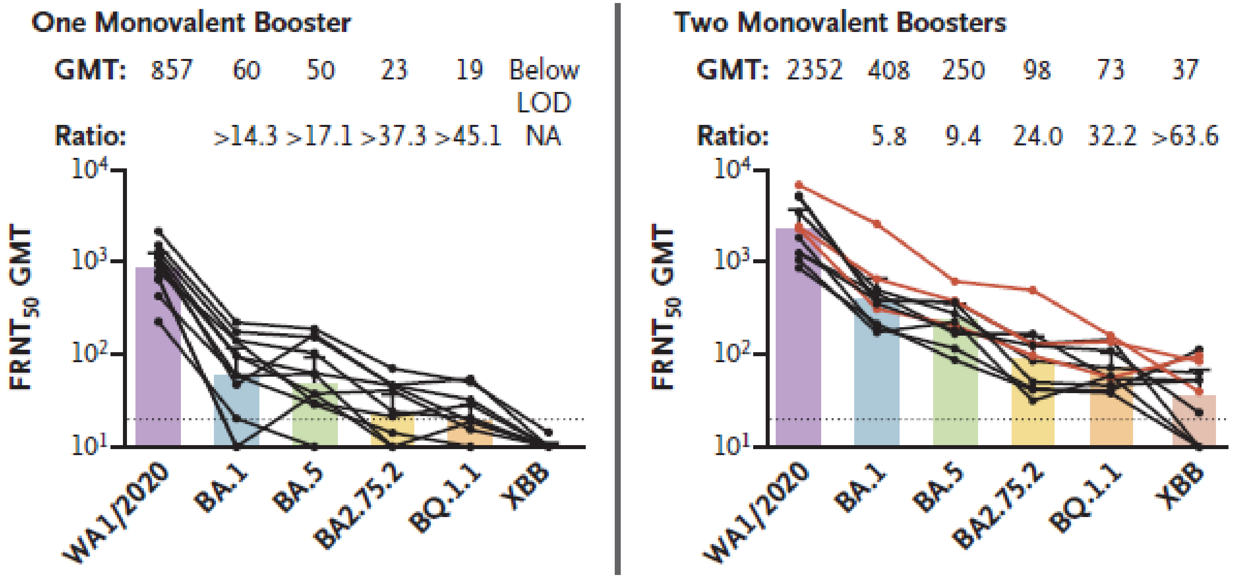


Figure. Neutralizing Responses against the WA1/2020 Strain and Omicron Subvariants

- **Three cohorts**
  1. 12 participants 7-28 days after 1st monovalent booster
  2. 11 participants 6-57 days after 2nd monovalent booster
  3. 12 participants 16-42 days after a bivalent booster
- **↑ neutralization against SARS-CoV-2 strains after 2 monovalent boosters**

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