

Epidemiology of America



The Rapid Response Podcasts



COVID-19 Updates: What We Know Now

Releases monthly

Newest Episodes:

- Monkeypox
- Long COVID



COVID-19 Allies in Infection Prevention





SAFE HEALTHCARE FOR ALL

SHEA COVID-19 Resources:





This program is designed to give US hospital epidemiologists who oversee infection control programs the skills, knowledge, and tools to provide effective leadership during facility-level outbreaks and large-scale public health emergencies.

- Simulations
- Tools Kits
- On-demand Webinars
- On-demand Workshop Sessions
- Expert Guidance on Incident Management and HICs, Crisis Strategies, Communication Guidance and Much More

www.ortp.shea-online.org



SAFE HEALTHCARE FOR ALL

COVID-19 Real-Time Learning Network



Specialty Society Collaborators:

- American Academy of Family Physicians
- American Academy of Pediatrics
- American College of Emergency Physicians
- American College of Physicians
- American Geriatrics Society
- American Thoracic Society
- Pediatric Infectious Diseases Society
- Society for Critical Care Medicine
- Society for Healthcare Epidemiology of America
- Society of Hospital Medicine
- Society of Infectious Diseases Pharmacists

With funding from the Centers for Disease Control and Prevention, IDSA has launched the COVID-19 Real Time Learning Network, an online community that brings together information and opportunities for discussion on latest research, guidelines, tools and resources from a variety of medical subspecialties around the world.

www.COVID19LearningNetwork.org @RealTimeCOVID19 | #RealTimeCOVID19

SHEA

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Prevention

The SHEA Prevention Course in HAI Knowledge and Control (Prevention CHKC) is online, interactive, and designed to give frontline personnel what they need to know to prevent healthcare-associated infections (HAIs).

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ICHE Journal – Fast Tracking COVID Article Submissions

Infection Control Hospital Epidemiology Artist: Lona Mody MBRIDGI

Infection Control & Hospital Epidemiology publishes scientifically authoritative, clinically applicable, peer-reviewed research on control and evaluation of the transmission of pathogens in healthcare institutions and on the use of epidemiological principles and methods to evaluate and improve the delivery of care. Major topics covered include infection control practices, surveillance, antimicrobial stewardship, cost-benefit analyses, resource use, occupational health, and regulatory issues.

www.cambridge.org/iche



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ASHE JOURNAL

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SEE YOU NEXTYEAR!

We hope to see you in Seattle, Washington for SHEA Spring 2023 April 12-14.



SHEA Webinar

COVID-19 Town Hall Round 81

In Case of Technical Difficulties:

• Audio:

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- For full participation, you will need to join by computer

• If you are having trouble joining:

- Use the emailed invitation to join via the URL, or call in with the provided phone numbers
- <u>https://support.zoom.us</u>



Webinar Recording Access:



This webinar will be recorded and uploaded to LearningCE's <u>Rapid Response Program</u>



Streaming Live on SHEA's Facebook page



Useful Features:



- **<u>Chat</u>**: Talk to each other or ask SHEA Staff questions if you are having technical difficulties
- **<u>Q&A</u>**: Type in your question to be read aloud by SHEA Staff and answered by the Panelists



SHEA Town Hall 81 Overview

SARS-CoV-2 VARIANTS, US, CDC

			Ur	nited	State	es: 7/	31/20	22 –	11/5/	2022					United States: 10/30/2022 – 11/5/2022 NOWCAST					
												N	OWC	AST				JSA		
100%		4															L L	JSA		
BA.4		BA.4		BA.4.6	BA.4.6	4.6	9	(0					5		WHO label	Lineage #	US Class	%Total	95%PI	
50 %				BA	BA.	BA.4.6	BA.4.6	BA.4.6	4.6		BF.7	Þ.	BQ.1.1	5	Omicron	BA.5	VOC	39.2%	36.2-42.3%	
000/									BA.4.6	4.6		BF.7		BQ.1.1		BQ.1.1	VOC	18.8%	15.7-22.4%	
80%										BA.4.6	9	BQ. 1	BF.7			BQ.1	VOC	16.5%	13.6-20.0%	
											BA.4.6			~		BA.4.6	VOC	9.5%	8.6-10.5%	
70%												BA.4.6	BQ.1	BF.7		BF.7	VOC	9.0%	7.9-10.1%	
												B				BA.5.2.6	VOC	3.1%	2.5-3.7%	
60%-													4.6	BQ.1		BA.2.75	VOC	2.3%	1.9-2.8%	
													BA.4.6	В		BA.2.75.2	VOC	1.3%	0.9-1.7%	
50%-																BA.4	VOC	0.2%	0.2-0.3%	
نى ب		BA.5	BA.5	BA.5	ŝ	с,	10							BA.4.6		BA.1.1	VOC	0.0%	0.0-0.0%	
40% – S'Y8		B	9	8	BA.5	BA.5	BA.5	BA.5	BA.5	ي ک				8		B.1.1.529	VOC	0.0%	0.0-0.0%	
										BA.5	BA.5					BA.2.12.1	VOC	0.0%	0.0-0.0%	
30%-												BA.5				BA.2	VOC	0.0%	0.0-0.0%	
													BA.5		Delta	B.1.617.2	VBM	0.0%	0.0-0.0%	
20%-													-	BA.5	Other	Other*		0.1%	0.0-0.1%	
10%-														8	nationally ir lineages wh ** These may differ f # BA.1,	n at least one w nich are circulat data include N rom weighted e BA.3 and their	eek period. " ting <1% nation owcast estim estimates gen sublineages (Other" rep onally duri ates, whic erated at except B/	A.1.1 and its sub	regation of played. projections that lineages) are
8/6/22	5	8/13/22	8/20/22	8/27/22	9/3/22	9/10/22	9/17/22	9/24/22	10/1/22	10/8/22	10/15/22	10/22/22	10/29/22	11/5/22	sublineages sublineages BQ.1.1, sub the above t respectively	s, BA.2 sublines s of BA.4 are as blineages of BA able, their subli y. Previously, B	ages are agg ggregated to .5 are aggreg neages are a A.5.2.6 were	regated w BA.4. Exc pated to B ggregated aggregated	A.2.75, BA.2.75.2 with BA.2. Except ept BF.7, BA.5.2 A.5. For all the list d to the listed pa ed with BA.5. Lir intain the spike s	BA.4.6, 2.6, BQ.1 and neages listed rental lineages leages

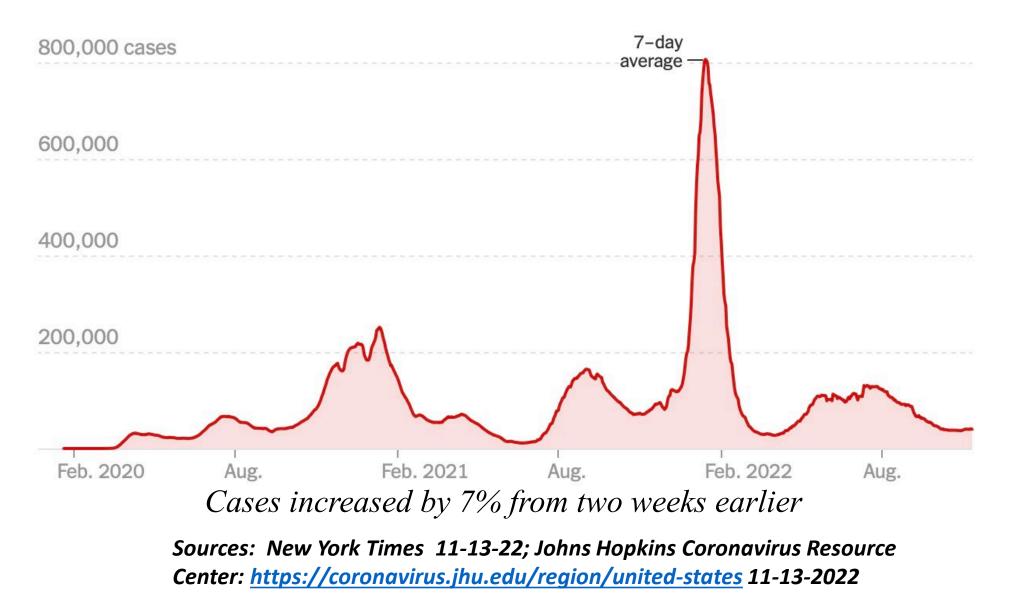
Collection date, week ending

https://covid.cdc.gov/covid-data-tracker/#variant-proportions

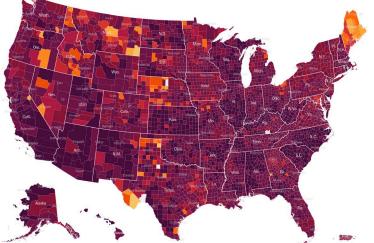
R346T.

REPORTED COVID-19 CASES IN THE UNITED STATES

Cumulative Cases – 97,995,355



US COVID-19 HOTSPOTS

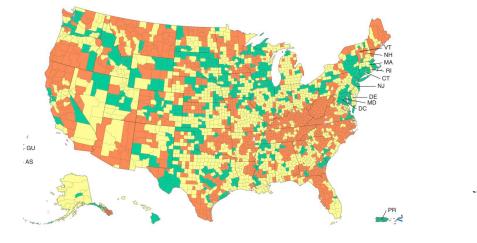


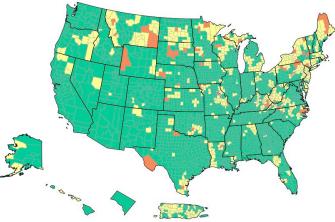
February 6, 2022





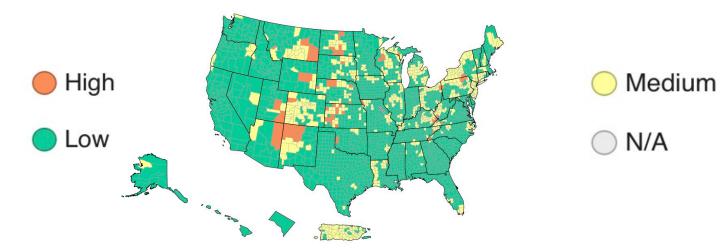
CDC COVID-19 COMMUNITY LEVELS





February 27, 2022

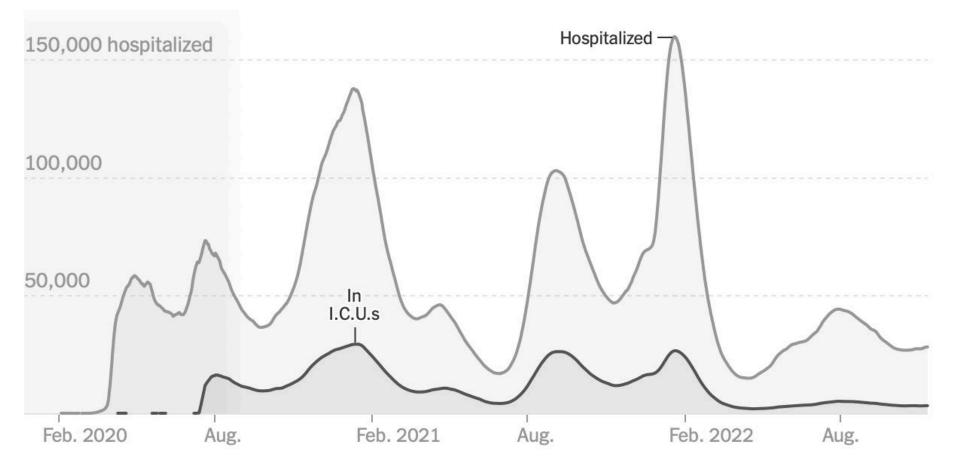
October 9, 2022



November 12, 2022

Source – https://covid.cdc.gov/covid-data-tracker/#countyview?list_select_state=all_states&list_select_county=all_counties&datatype=CommunityLevels&null=CommunityLevels

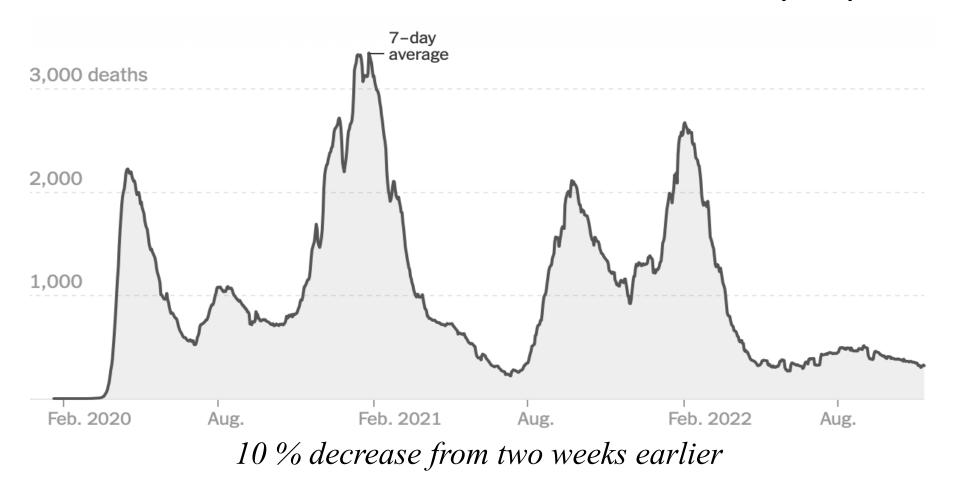
HOSPITALIZATIONS AND ICU ADMISSIONS FOR COVID-19 IN THE UNITED STATES



Hospitalizations increased 3 % from two weeks earlier ICU hospitalizations incfeased 1% from two weeks earlier

Source: New York Times 11-13-22

COVID-19 DEATHS IN THE UNITED STATES Cumulative Deaths – 1,074,484



Sources: New York Times 11-13-22,; Johns Hopkins Coronavirus Resource Center: <u>https://coronavirus.jhu.edu/region/united-states</u> 11-13-2022

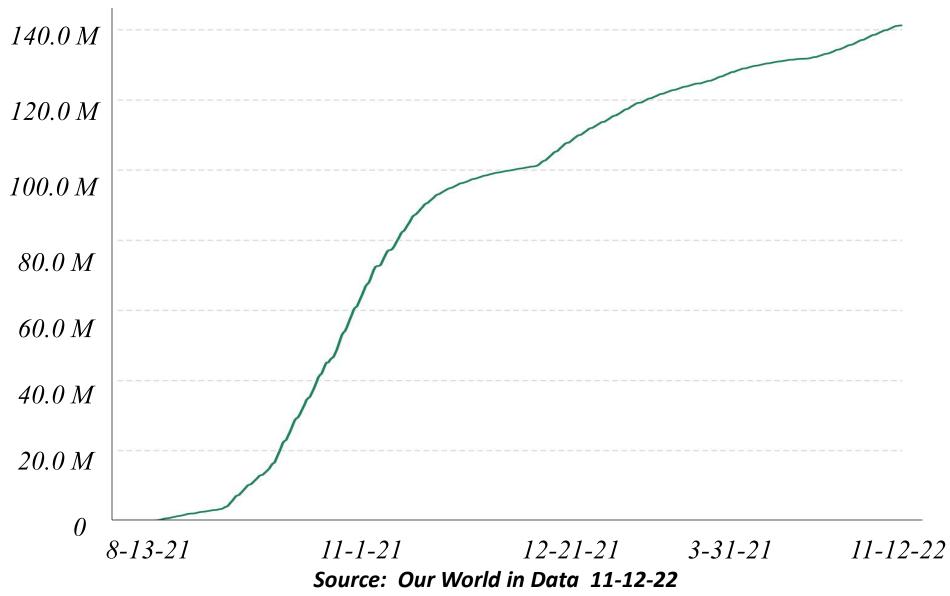
DAILY COVID-19 VACCINATIONS IN THE UNITED STATES



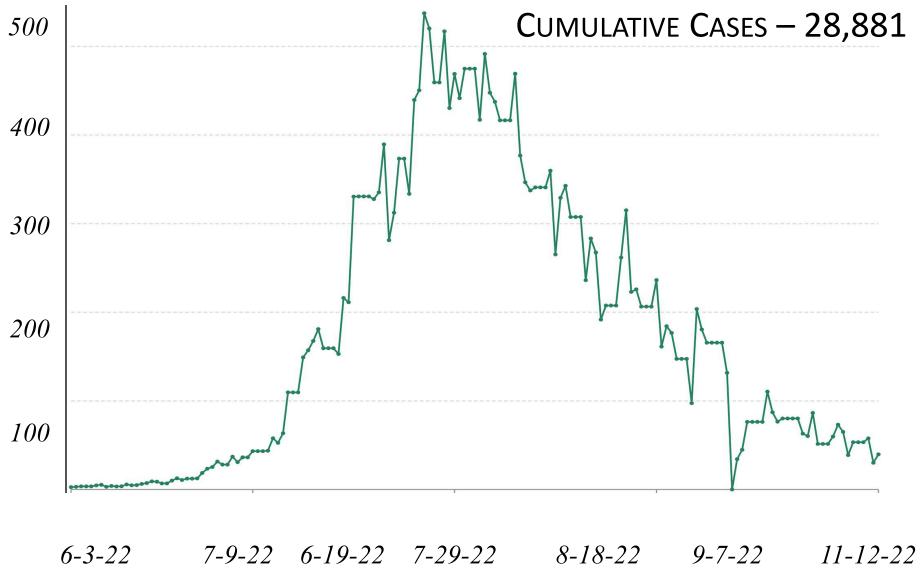
Source: Our World in Data 11-12-22

COVID-19 BOOSTER DOSES IN THE UNITED STATES

CUMULATIVE DOSES ADMINISTERED 141.3 M

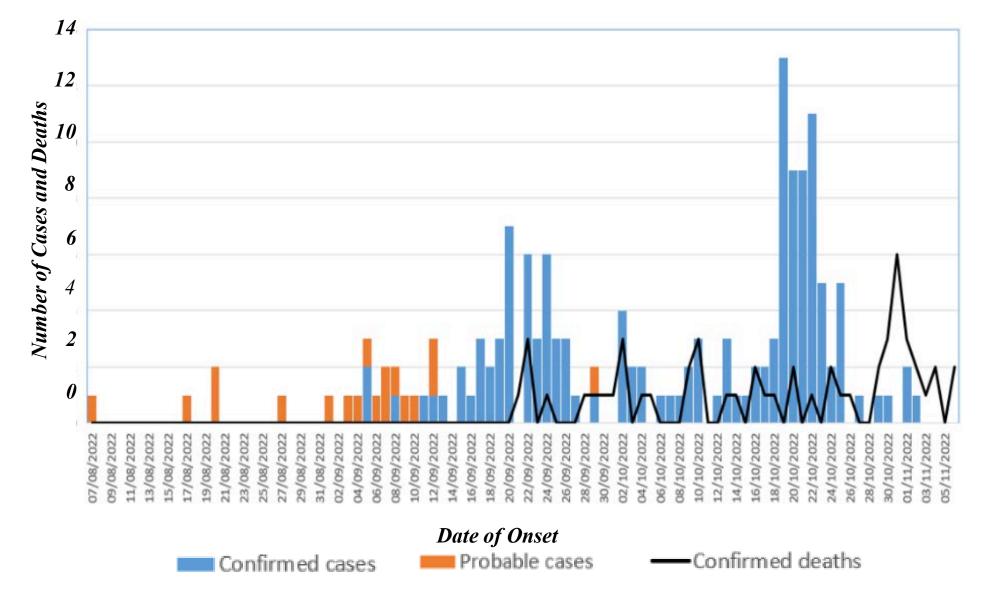


MONKEYPOX OUTBREAK CURVE: DAILY CASES, UNITED STATES



Source: CDC and Our World in Data 11-12-22

ONGOING EBOLA VIRUS DISEASE OUTBREAK, UGANDA



Source: WHO: https://www.who.int/emergencies/disease-outbreak-news/item/2022-DON423

This Week's Emerging Infectious Disease News

- 1. A **British Medical Journal** news feature comments on the so-called "triple epidemic" facing the US this fall and winter
- 2. A **JAMA** news article compares the pediatric epidemic of RSV to the COVID pandemic and relates what physicians need to know about the RSV surge.
- 3. A **New England Journal** paper demonstrated that lifting of masking requirements was associated with an additional 44.9 COVID-19 cases/1000 students and staff during the 15 weeks following lifting the masking requirement an editorial supports the conclusions.
- 4. Another **New England Journal** paper found that in two high-risk imprisoned populations that mRNA vaccination and previous infection were effective against omicron infection, with lower protection among those infected before the period of delta predominance.
- 5. Another **New England Journal** paper found that administration of two 25-μg doses of the Moderna vaccine to children 6 months to 5 years of age was safe and elicited immune responses that were noninferior to those found in young adults.
- 6. A **Cell** paper provided potential explanations for the pathophysiology of 'brain fog' following COVID.
- 7. A JAMA Network Open paper evaluated maternal and cord blood levels of antibody levels after COVID-19 vaccination or infection .
- 8. A Science Immunology paper describing a macaque model of COVID-19 vaccine-elicited CD8+ T cells, demonstrated that CD8+ T cells contribute substantially to vaccine protection against SARS-CoV-2.
- 9. Data from a *Clinical Infectious Disease* paper suggested that pre-booster antibody levels could be used to optimally time boosters.
- 10. The **WHO** website summarizes the status of the Ebola virus disease outbreak in Uganda..
- 11. An article in **The Atlantic** underscores the rationale for staying "up-to-date" with COVID boosters, emphasizing that it is a not a good time to be a "booster-slacker".. **References available in the chat**

Panelists:



Dr. David Henderson NIH Consultant



Dr. Sarah Haessler *Baystate Health*



Dr. Kristina Bryant University of Louisville



Dr. David Weber UNC School of Medicine



UPDATE: SARS-CoV-2 SUBLINEAGES: EPIDEMIOLOGY AND IMPACT

David J. Weber, MD, MPH, FIDSA, FSHEA, FRSM (London) Sanders Distinguished Professor of Medicine, Pediatrics and Epidemiology Associate Chief Medical Officer Medical Director, Hospital Epidemiology University of North Carolina, Chapel Hill, NC



Disclosures: Consultancy; Pfizer, Merck, Sanofi, PDI, BD, Germitec, Wellair All drugs/vaccines issues discussed consistent with FDA approvals or authorizations

SARS-CoV-2 Variants: Current Summary

- Epidemiology, US
 - Stable frequency of BA.4.6
 - Rapid increase of BQ.1, BQ.1.1, and BF.7
 - The sublineage BQ.1.1 carries an additional spike mutation in a key antigenic site (i.e. R346T); BQ.1 is showing a significant growth advantage over other circulating Omicron sublineages in many settings*
- XBB: Recombinant of BA.2.10.1 and BA.2.75 sublineages; early evidence pointing at a higher reinfection risk, as compared to other circulating Omicron sublineages *
- Escape from monoclonal prophylaxis and/or therapy (current frequency of sublineages, US, CDC)
 - Evusheld escape, ~53% (BQ.1, BQ1.1, BA.4.6, BA.5.2.6, BA.2.75.2)
 - Bebteluvimab escape, ~47% (BQ.1, BQ.1.1, BA5.6.2)
 - Alternative therapy = Remdesivir (IV x 3 days) {Remdesivir resistance report in 2 kidney transplant recipients}^
- Best evidence suggests that antivirals (e.g., Remdesivir, Paxlovid, Molnupivir) retain activity against all variants
- Bivalent COVID-19 vaccine likely exhibit modestly improved activity against BQ sublineages compared to the monovalent ancestral vaccine

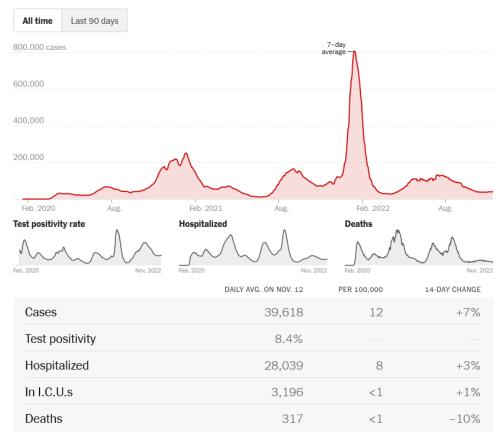
*https://www.who.int/news/item/27-10-2022-tag-ve-statement-on-omicron-sublineages-bq.1-and-xbb *Hogan JI, et al. Clin Infect Dis 2022;Sept 26,ciac769



COVID-19: UPDATE, 11/13

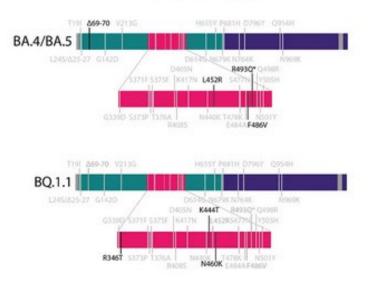
- Cases and hospitalizations continue to rise nationwide, driven in part by a growing outbreak in the Southwest.
- The nation's most rapid growth in hospitalizations with the virus is clustered in that region, with <u>Arizona</u>, <u>Colorado</u>, <u>Nevada</u> and <u>New Mexico</u> all seeing hospitalization counts increase by more than 30 percent in the past two weeks. Cases in those states are on a similar upward climb, particularly in New Mexico.
- By contrast, daily deaths from the coronavirus are decreasing. Death counts have fallen by 9 percent nationally in recent weeks, to about 325 per day.

New reported cases

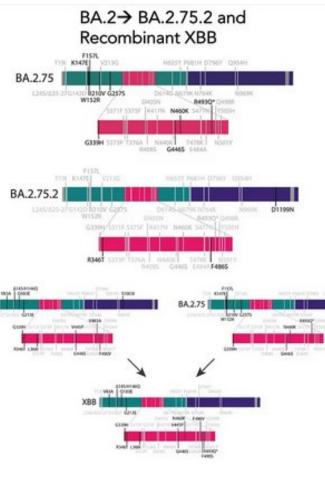


https://www.nytimes.com/interactive/2021/us/covid-cases.html

EVOLUTION OF NEW SARS-CoV-2 VARIANTS

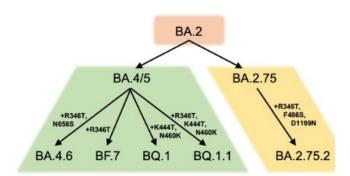


BA.5 → BQ.1.1



https://erictopol.substack.com/p/a-booster-is-your-best-shot-now Qu P, et al. https://www.biorxiv.org/content/10.1101/2022.10.19.512891v1.full.pdf

XBB is a recombinant of BA.2.10.1 and BA.2.75





COVID-19 VARIANTS, WORLDWIDE

SARS-CoV-2 sequences by variant, Nov 7, 2022

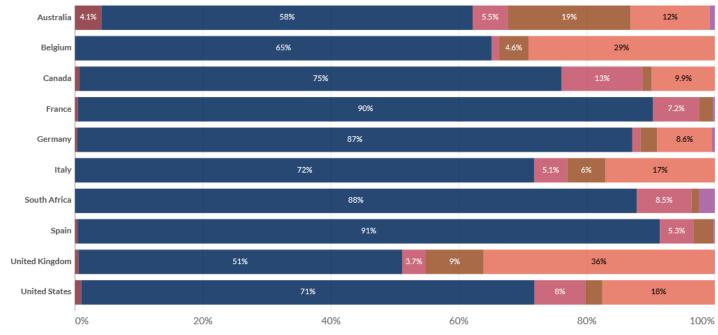
The share of analyzed sequences in the preceding two weeks that correspond to each variant group. This share may not reflect the complete breakdown of cases since only a fraction of all cases are sequenced.



Add country 🛛 🛛 Relative

📕 Alpha 📕 Beta 📕 Gamma 📕 Delta 📕 Omicron (BA.2) 📕 Omicron (BA.1) 📕 Omicron (BA.5) 📕 Omicron (BA.4) 📕 Omicron (BA.2.12.1) 📕 Omicron (BA.2.75)

Omicron (BQ.1) Recombinant Other



https://ourworldindata.org/coronavirus

Source: GISAID, via CoVariants.org - Last updated 9 November 2022

OurWorldInData.org/coronavirus • CC BY Note: Recently-discovered or actively-monitored variants may be overrepresented, as suspected cases of these variants are likely to be sequenced preferentially or faster than other cases.

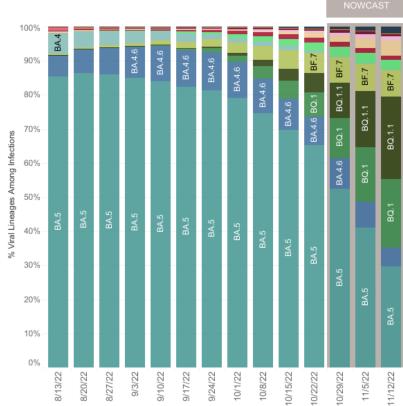


COVID-19 VARIANTS, US

United States: 8/7/2022 – 11/12/2022

United States: 11/6/2022 - 11/12/2022 NOWCAST

USA



WHO label	Lineage #	US Class	%Total	95%PI	
Omicron	BA.5	VOC	29.7%	27.2-32.3%	
	BQ.1.1	VOC	24.1%	21.3-27.3%	
	BQ.1	VOC	20.1%	17.2-23.4%	
	BF.7	VOC	7.8%	6.8-9.0%	
	BA.4.6	VOC	5.5%	5.0-6.2%	
	BN.1	VOC	4.3%	3.0-6.2%	
	BA.5.2.6	VOC	2.9%	2.5-3.4%	
	BA.2	VOC	1.3%	0.8-1.9%	
	BA.2.75	VOC	1.2%	1.0-1.5%	
	BA.2.75.2	VOC	0.9%	0.6-1.2%	
	BA.4	VOC	0.1%	0.1-0.1%	
	BA.1.1	VOC	0.0%	0.0-0.0%	
	B.1.1.529	VOC	0.0%	0.0-0.0%	
	BA.2.12.1	VOC	0.0%	0.0-0.0%	
Delta	B.1.617.2	VBM	0.0%	0.0-0.0%	
Other	Other*		2.0%	1.1-3.3%	

* Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all weeks displayed.

** These data include Nowcast estimates, which are modeled projections that may differ from weighted estimates generated at later dates

BA.1, BA.3 and their sublineages (except BA.1.1 and tis sublineages) are aggregated with B.1.1.529. Except BA.2.12.1, BA.2.75, BA.2.75.2, BN.1 and their sublineages, BA.2 sublineages are aggregated with BA.2. Except BA.4.6, sublineages of BA.4 are aggregated to BA.4. Except BF.7, BA.5.2.6, BQ.1 and BQ.1.1, sublineages of BA.5 are aggregated to BA.5. For all the lineages listed in the above table, their sublineages are aggregated to the listed parental lineages respectively. Previously, BN.1 was aggregated with BA.2.75. Lineages BA.2.75.2, BN.1, BA.4.6, BF.7, BA.5.2.6 and BQ.1.1 contain the spike substitution R346T. Evusheld escape, ~53% (BQ.1, BQ1.1, BA.4.6, BA.5.2.6, BA.2.75.2)

Bebteluvimab escape, ~47% (BQ.1, BQ.1.1, BA5.6.2)

https://covid.cdc.gov/covid-datatracker/#variant-proportions



Spread of the SARS-CoV-2 Omicron variant sub-lineage BQ.1 in the EU/EEA, 21 October 2022

- BQ.1, including its sub-lineages, has been designated as Variant of Interest (VOI) by ECDC as of 20 October 2022. Based on modelling estimates, it is expected that by mid-November to beginning of December 2022, more than 50% of SARS-CoV-2 infections will be due to BQ.1/BQ.1.1. By the beginning of 2023, more than 80% of SARS-CoV-2 cases are expected to be due to BQ.1/BQ.1.1.
- The observed increase in the growth rate of BQ.1 is probably driven mainly by immune escape. This variant and its sub-lineages will
 probably contribute to a further increase in cases of COVID-19 in the EU/EEA in the coming weeks and months. The extent of the
 increase in COVID-19 cases will depend on various factors, including immune protection against infection influenced by the timing and
 coverage of COVID-19 vaccination regimes, and the extent, timing and variant landscape of previous SARS-CoV-2 pandemic waves.
 Based on limited available data, there is no evidence of BQ.1 being associated with a greater infection severity than the circulating
 variants BA.4/BA.5.
- Countries should remain vigilant for signals of BQ.1 emergence and spread; maintain sensitive and representative testing and genomic surveillance with timely sequence reporting and strengthen sentinel surveillance systems (primary care ILI/ARI and SARI).
- Countries should continue to monitor COVID-19 case rates especially in people aged 65 years and older and severity indicators such as hospitalizations, ICU admissions, ICU occupancy and death.
- Improving COVID-19 vaccine uptake of the primary course and first booster dose remains a priority for all eligible individuals that are not up-to-date with the recommended schedule. For the time being, for current autumn/winter vaccination campaigns, an additional booster dose should also be offered, prioritizing individuals who are at risk of progression to severe disease, such as older adults (e.g. above 60 years of age), immunocompromised individuals and those with underlying medical conditions, and pregnant women. Residents and staff in long-term care facilities, as well as healthcare workers should also be considered among priority groups.

https://www.ecdc.europa.eu/en/publications-data/spread-sars-cov-2-omicron-variant-sub-lineage-bq1-eueea



IMPACT OF NEW VARIANTS ON MONOCLONAL THERAPIES

a —																		b		
	ango	REGN	REGN	REGN10933	COV2-	COV2-	COV2-	BRIF	BRII-	BRII-	S309	DXP-	LY-CoV	DAER	SA55	SA55+	Additional RBD		IC50 of hACE2 (µg/r	nL)
lin	eages	10933	10987	+10987	2196	2130	2196+2130	196	198	196+198	2208	604	1404	5430	9400	SA58	mutations	D614G	4	•• •0.24***
	BA.2	*	590	821	4312	6.3	8.2	8530	8990	8610	852	219	0.9	5.1	7.2	7.8		BA.2	• • • •	0.14
BA	.2.3.20	121		199	15	•	26	14	•	24	897	181	9.7	20	4.6	7.8	K444R+N450D+L452M +N460K+R493Q	BA.2.3.20	o o	0.11**
BA	.2.10.4	•	•	•	•	289	501	2109	7990	3984	706	6348	1.3	4.3	4.9	5.0	G446S+F486P+R493Q +S494P	BA.2.10.4	⊕- + - •	0.11**
1	BJ.1	•	•	•	3076	•	5985	7609	•	•	709	166	•	8163	3.7	8.6	D339H+R346T+L368I+ V445P+G446S+V483A +F490V	BJ.1	and ite	0.16
	ХВВ	·	·	•	•	•	•	•	•	•	963	•	•	8805	5.3	9.8	D339H+R346T+L368I+ V445P+G446S+N460K +F486S+F490S+R4930	XBB	₽ 4 •	0.15
B	A.2.75	278	*	410	119	352	121	1730	6622	3861	672	5920	2.2	246	4.3	9.6		BA.2.75	4	0.07***
	BL.1	260	*	511	93	*	174	1251	*	3075	508	7193	2.8	7975		10	R346T	BL1	0.000	0.09***
_	BR.1	319	*	679	117	*	170	1992	*	3160	564	6689	*	1616		9.7	L452R+K444M	BR.1	4	0.10***
	N.2.1	390	*	701	59	303	109	4101	*	8444	6979	8901	1.7	4960		9.4	K356T+F490S	BN.1	+=== + = =	0.09***
_	BN.1	344	*	599	70	*	166	3683	*	7791	*	6012	3.3	8295		9.0	R346T+K356T+F490S	BN.2.1	0 0 0 0 0	0.08***
	2.75.2	*	*	*	*	*	*	*	*	*	852	*	3.0	6922		9.7	R346T+F486S	BA.2.75.2	01-000-00	0.15
	M.1.1	*	*						*		879		2.3	8823		8.9	R346T+F486S	BM.1.1	o t e e e	0.16
B	4.1.1.1	*	*	*	*	*	*	*	*	*	956	*	1.9	8082	4.8	10.5	R346T+F486S+F490S	BM.1.1.1	0 0 40 0	0.15
	BR.2	*	*		*	*			*	*	921	*	2.6	7263	4.7	10.5	R346T+L452R+F486I	BR.2	ee ∳ 0	0.14
(CA.1	*	*	*	*	*	*	*	*	*	897	*	3.2	6927	6.0	11.5	R346T+L452R+F486S	CA.1	• • •• •	0.14
В	A.4/5	*	520	709		23	40	7124	*		1055	6264	0.8	3.9	5.0	4.5		BA.4/5	o t o l	0.12*
_	4.4.6.1	*	2338	5402	*	*	*	4763	*	7809	4456	4634	1.2	50	4.8	9.9	R346T	BA.4.6.1	** •• •	0.15
	.5.6.2	*	*	*	*	*		4636	*	7883	1408	5892	1662	58	5.1	8.9	K444T	BA.5.6.2	****	0.14
_	3Q.1	*	*				•		*	*	1709	*	1905	44	6.6	9.2	K444T+N460K	BQ.1	a ino a o	0.17
	BU.1	*	*		*	*		*	*	*	1082		26	56	5.3	10.5	K444M+N460K	BU.1	o o a ao	0.18**
В	Q.1.1	*	*	*	*	*	*	*	*		5581	*	*	900	5.9	10.3	R346T+K444T+N460K	BQ.1.1	• ⊢•• •́ •	0.16
											Ps	seudov	irus IC5	0 (ng/n	nL)	<100	100~1,000 >1,000		0.1 0.2	0.3

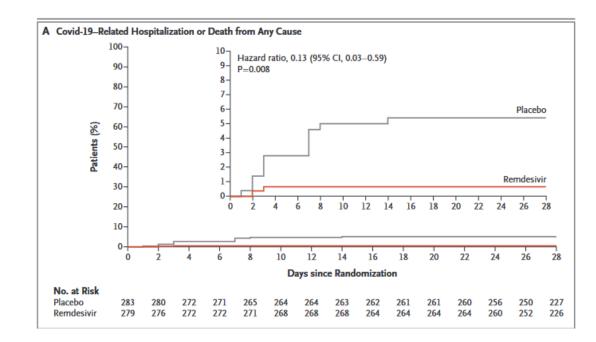
Bebtoluvimab = LY-CoV 1404; Evusheld = COV2-2196+COV2-2130 Cao Y, et al. https://www.biorxiv.org/content/10.1101/2022.09.15.507787v3



Early Remdesivir to Prevent Progression to Severe Covid-19 in Outpatients

- Methods: RCT of non-hospitalized patients with Covid-19 who had symptom onset within the previous 7 days and who had at least one risk factor for disease progression (age ≥60 years, obesity, or certain coexisting medical conditions). Patients were randomized to IV remdesivir (200 mg on day 1 and 100 mg on days 2 and 3) or placebo.
- Results: Covid-19–related hospitalization or death from any cause occurred in 2 patients (0.7%) in the remdesivir group and in 15 (5.3%) in the placebo group (hazard ratio, 0.13; 95% confidence interval [CI], 0.03 to 0.59; P = 0.008). A total of 4 of 246 patients (1.6%) in the remdesivir group and 21 of 252 (8.3%) in the placebo group had a Covid-19–related medically attended visit by day 28 (hazard ratio, 0.19; 95% CI, 0.07 to 0.56).
- Conclusion: 3 day course of remdesivir resulted in 87% lower risk of hospitalization or death

Gottlieb RL, et al. NEJM 2022;386:305 (Jan 27)



Subgroup	Remdesivir no./total no.	Placebo of patients (%)			Ha	zard R	atio (9	5% C	1)	
Residence in the United States	2/264 (0.8)	12/267 (4.5)				-			0.17	(0.04–0.76)
Age ≥60 yr	1/83 (1.2)	9/87 (10.3)	— —						0.11	(0.01-0.86)
Male sex	1/148 (0.7)	9/145 (6.2)	H						0.11	(0.01-0.84)
Diabetes mellitus	2/173 (1.2)	14/173 (8.1)	— —						0.14	(0.03-0.63)
Obesity	1/154 (0.6)	9/156 (5.8)	⊢•──						0.11	(0.01-0.88)
Hypertension	2/138 (1.4)	10/130 (7.7)	—			-			0.17	(0.04–0.76)
Ethnic group										
Not Hispanic or Latinx	2/146 (1.4)	8/158 (5.1)		•					0.26	(0.06-1.22)
Hispanic or Latinx	0/123	6/112 (5.4)								_
Chronic lung disease	0/67	4/68 (5.9)								_
Cardiovascular or cerebrovascular disease	0/20	2/24 (8.3)								_
Current cancer	0/12	2/18 (11.1)								_
			0.0 0.2	2 0.4	0.6	0.8	1.0	1.2	1.4	
			Re	emdesiv	/ir Bett	er	P	acebo	Better	r

Figure 2. Covid-19–Related Hospitalization or Death from Any Cause at Day 28 in More Than 5% of the Trial Population, According to Demographic and Clinical Characteristics at Baseline.

Efficacy of Antiviral Agents against the Omicron Subvariant BA.2.75

Table 1. Efficacy of Monoclonal Antibodies and Antiviral Drugs against Omicron Subvariants in Vitro*											
WHO Label (Pango Lineage): Virus Strain											
	REGN10987, Imdevimab	REGN10933, Casirivimab	COV2-2196, Tixagevimab	COV2-130, Cilgavimab	S309, Sotrovimab Precursor	LY-CoV1404, Bebtelovimab	REGN10987 plus REGN10933	plus COV2-	GS-441524, Remdesivir§	EIDD-1931, Molnupiravir¶	PF-07321332, Nirmatrelvir
				nanograms p	per milliliter					micromoles	
Ancestral strain (A): SARS-CoV-2/ UT-NC002-1T/ Human/2020/Tokyo	4.36 ±0.96	2.42 ±0.93	1.91 ±0.95	5.36 ±1.21	32.80 ±11.22	1.40 ±0.79	2.23 ±0.42	6.47 ±2.31	0.98 ±0.30	0.59 ±0.11	1.71 ±0.29
Omicron (BA.2): hCoV-19/Japan/UT- NCD1288-2N/2022	958.28 ±363.87	>50,000	4374.21 ±1483.72	21.59 ±8.57	>50,000	6.09 ±0.67	968.50 ±58.35	43.22 ±8.16	1.32 ±0.21	0.25 ±0.08	1.69 ±0.66
Omicron (BA.5): hCoV- 19/Japan/TY41- 702/2022	174.37 ±52.55	>50,000	>50,000	54.02 ±20.29	6240.39 ±1883.65	2.43 ±1.26	192.91 ±82.50	123.65 ±55.81	0.45 ±0.09	0.23 ±0.07	1.50 ±0.34
Omicron (BA.2.75): hCoV-19/Japan/ TY41-716/2022	>50,000	1153.19 ±104.61	122.31 ±67.08	101.71 ±53.24	28,536.48 ±6444.42	6.21 ±2.80	1811.78 ±600.23	34.19 ±7.60	1.52 ±0.42	0.90 ±0.18	1.78 ±0.35

* Plus-minus values are means ±SD. The antibodies used in this analysis were produced in the authors' laboratories and are not identical to the commercially available products. SARS-

CoV-2 denotes severe acute respiratory syndrome coronavirus 2, and WHO World Health Organization.

† The individual monoclonal antibodies were tested at a starting concentration of 50,000 ng per milliliter as a 50% focus reduction neutralization test titer. The monoclonal antibody combinations were tested at a starting concentration of 10,000 ng per milliliter for each antibody.

The values presented are the 50% inhibitory concentration of the mean micromole value of triplicate reactions.

GS-441524 is the main metabolite of remdesivir, an RNA-dependent RNA polymerase inhibitor.

EIDD-1931 is the active form of molnupiravir, an RNA-dependent RNA polymerase inhibitor.

PF-07321332, nirmatrelvir, is an inhibitor of the main protease, also called 3-chymotrypsin-like protease, of SARS-CoV-2.

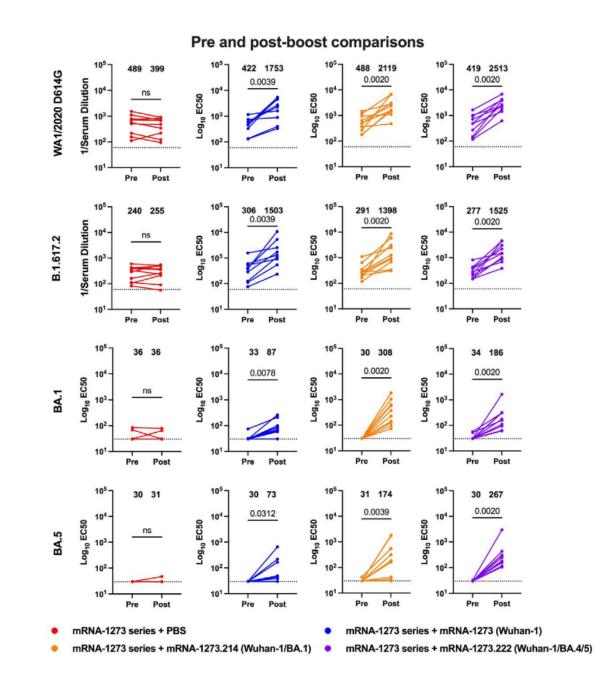
Takashita E, et al. NEDJM 2022;387:1236 (29 September)



Bivalent SARS-CoV-2 mRNA vaccines increase breadth of neutralization and protect against the BA.5 Omicron variant in mice

We evaluated the immunogenicity and protective efficacy of two, recently authorized, bivalent COVID-19 vaccines that contain two mRNAs encoding Wuhan-1 and either BA.1 (mRNA-1273.214) or BA.4/5 (mRNA-1273.222) spike protein. When administered to mice as a booster at 7 months after the primary vaccination series with mRNA-1273, the bivalent vaccines induced broadly neutralizing antibody responses. Whereas the majority of anti-Omicron receptor binding domain antibodies in serum induced by mRNA-1273, mRNA-1273.214, and mRNA-1273.222 boosters cross-reacted with the antecedent Wuhan-1 spike antigen, the mRNA-1273.214 and mRNA-1273.222 bivalent vaccine boosters also induced unique BA.1 and BA.4/5-specific responses, respectively. Although boosting with parental or bivalent mRNA vaccines substantially improved protection against BA.5 compared to mice receiving two vaccine doses, the levels of infection, inflammation, and pathology in the lung were lowest in animals administered the bivalent mRNA vaccines. Thus, boosting with bivalent Omicron-based mRNA-1273.214 or mRNA-1273.222 vaccines enhances immunogenicity and confers protection in mice against a currently circulating SARS-CoV-2 strain.

Scheaffer SM, et al. Nature Medicine;20 October 2022



5 Lab Studies Assessing the Bivalent BA.5 Booster vs the Original Booster

Lab	Assay	Bivalent vs. BA.5 Compared to Original	Bivalent vs. BQ.1.1 Compared to Original
Но	Pseudovirus	Minimal difference	Not assessed
Barouch	Pseudovirus	1.3-fold increase	Not assessed
Suthar	Live virus	4-fold improved	~10-fold increased (vs 1 booster)
Shi	Pseudovirus	3-fold improved	Low, but 3-fold GMT
Barouch	Pseudovirus	No difference	Modest ~1.2-fold increase

Wang Q, Ho DD. <u>https://www.biorxiv.org/content/10.1101/2022.10.22.513349v1.full.pdf</u> Davis-Gardner ME, Suthar MS. <u>https://www.biorxiv.org/content/10.1101/2022.10.31.514636v1</u> Kurhade C, p-Y Shi. <u>https://www.biorxiv.org/content/10.1101/2022.10.31.514580v1</u> Collier Ai-ris Y, Barouch DH. <u>https://www.biorxiv.org/search/bivalent%252Bcovid%252Bvaccine</u>

Eric Topol. Ground Truths

Antibody responses to Omicron BA.4/BA.5 bivalent mRNA vaccine booster shot

The SARS-CoV-2 Omicron variant and its numerous sub-lineages have exhibited a striking ability to evade humoral immune responses induced by prior vaccination or infection. The Food and Drug Administration (FDA) has recently granted Emergency Use Authorizations (EUAs) to new bivalent formulations of the original Moderna and Pfizer mRNA SARS-CoV-2 vaccines that target both the ancestral strain as well as the Omicron BA.4/BA.5 variant. Despite their widespread use as a vaccine boost, little is known about the antibody responses induced in humans. Here, we collected sera from several clinical cohorts: individuals after three or four doses of the original monovalent mRNA vaccines, individuals receiving the new bivalent vaccines as a fourth dose, and individuals with BA.4/BA.5 breakthrough infection following mRNA vaccination. Using pseudovirus neutralization assays, these sera were tested for neutralization against an ancestral SARS-CoV-2 strain, several Omicron sub-lineages, and several related sarbecoviruses. At ~3-5 weeks post booster shot, individuals who received a fourth vaccine dose with a bivalent mRNA vaccine targeting BA.4/BA.5 had similar neutralizing antibody titers as those receiving a fourth monovalent mRNA vaccine against all SARS-CoV-2 variants tested, including BA.4/BA.5. Those who received a fourth monovalent vaccine dose had a slightly higher neutralizing antibody titers than those who received the bivalent vaccine against three related sarbecoviruses: SARS-CoV, GD-Pangolin, and WIV1. When given as a fourth dose, a bivalent mRNA vaccine targeting Omicron BA.4/BA.5 and an ancestral SARS-CoV-2 strain did not induce superior neutralizing antibody responses in humans, at the time period tested, compared to the original monovalent vaccine formulation.

Wang Q, et al. https://doi.org/10.1101/2022.10.22.513349



Low neutralization of SARS-CoV-2 Omicron BA.2.75.2, BQ.1.1, and XBB.1 by 4 doses of parental mRNA vaccine or a BA.5-bivalent booster

Here we report neutralizing activities of three human serum panels collected from individuals 1-3 months after dose 4 of parental mRNA vaccine (post-dose-4), 1 month after a BA.5-bivalent-booster (BA.5ivalent-booster), or 1 month after a BA.5-bivalent-booster with previous SARS-CoV-2 infection (BA.5-bivalent-booster-infection). Post-dose-4 sera neutralized USA-WA1/2020, BA.5, BF.7, BA.4.6, BA.2.75.2, BQ.1.1, and XBB.1 SARS-CoV-2 with geometric mean titers (GMTs) of 1533, 95, 69, 62, 26, 22, and 15, respectively; BA.5bivalent-booster sera improved the GMTs to 3620, 298, 305, 183, 98, 73, and 35; BA.5-bivalent-booster-infection sera further increased the GMTs to 5776, 1558, 1223, 744, 367, 267, and 103. Thus, although BA.5-bivalent-booster elicits better neutralization than parental vaccine, it does not produce robust neutralization against the newly emerged Omicron BA.2.75.2, BQ.1.1, and XBB.1. Previous infection enhances the magnitude and breadth of BA.5bivalent-booster-elicited neutralization.

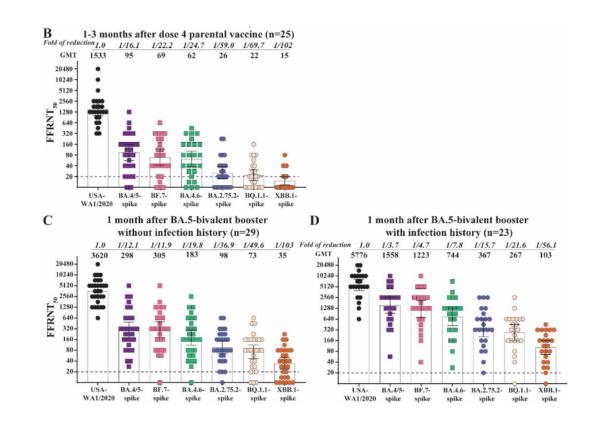
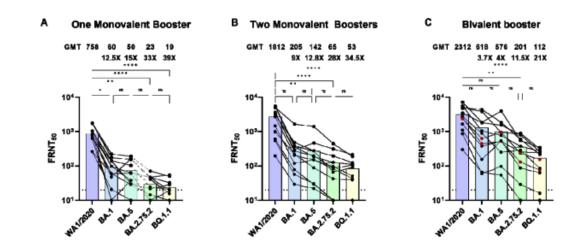


Figure 1. Neutralization of Omicron sublineages after 4 doses of parental mRNA vaccine or a BA.5-bivalent-booster

Karhade C, Shi Y-P, et al. https://www.biorxiv.org/content/10.1101/2022.10.31.514580v1.full.pdf

mRNA bivalent booster enhances neutralization against BA.2.75.2 and BQ.1.

Using a live virus neutralization assay, we evaluated serum samples from individuals who had received either one or two monovalent boosters or the bivalent booster to determine neutralizing activity against wild-type (WA1/2020) virus and Omicron subvariants BA.1, BA.5, BA.2.75.2, and BQ.1.1. In the one monovalent booster cohort, relative to WA1/2020, we observed a reduction in neutralization titers of 9-15-fold against BA.1 and BA.5 and 28-39-fold against BA.2.75.2 and BQ.1.1. In the BA.5-containing bivalent booster cohort, the neutralizing activity improved against all the Omicron subvariants. Relative to WA1/2020, we observed a reduction in neutralization titers of 3.7- and 4fold against BA.1 and BA.5, respectively, and 11.5- and 21fold against BA.2.75.2 and BQ.1.1, respectively. These data suggest that the bivalent mRNA booster vaccine broadens humoral immunity against the Omicron subvariants.



Neutralizing responses against WA1/2020, BA.1, BA.5, BA.2.75.2, and BQ.1.1

Davis-Gardner ME, et al. <u>https://doi.org/10.1101/2022.10.31.514636</u>