BV-BRC SARS-CoV-2 Emerging Variant Report November 01, 2022

Details of the emerging variants analysis can be found in "BV-BRC SARS-CoV-2 Emerging Variant Report – 20221101.xlsx" based on sequence data from GISAID.

Keep in mind that the information provided reflects sequence counts and sequence proportions and, as such, is impacted by sampling bias in the sequence databases and should not be interpreted as the prevalence of disease caused by these variants.

In addition, due to sequence anomalies (e.g., ambiguous nucleotides in many sequence records) and other issues, the absolute counts of Variants of Concern sequences are likely to be underestimates of the true sequence prevalence.

The key findings are summarized below.

USA – VOC

OMICRON

- In the US, virtually all sequences reported since July are **Omicron**.
 - The CDC Nowcast for the week ending 10/29/22 estimates that BA.5 proportions are still dominating in the United States at 49.6% (95% PI: 45.3-53.9%). Significant regional differences exist: <u>https://covid.cdc.gov/covid-data-tracker/#variantproportions</u>.
 - The CDC Nowcast estimates for **BA.4.6** proportions are slowly decreasing, now at 9.6% (95% PI: 8.6-10.7%)
 - BQ.1.1 and BQ.1 have been added to the Nowcast tracker. BQ.1 is currently estimated at 14.0% (95% PI: 11.2-17.5%); this increased by 50% since last week! BQ.1.1 is currently estimated at 13.1% (95% PI: 9.8-17.3%); this nearly doubled since last week.
 - *BF.7 has been added to the Nowcast tracker and is currently estimated at 7.5%* (95% PI: 6.6-8.5%)
 - BA.5.2.6 has been added to the Nowcast tracker and is currently estimated at 2.8% (95% PI: 2.3-3.5%)
 - BA.2.75 has been split into BA.2.75 and BA.2.75.2. BA.2.75 is currently estimated at 1.8% (95% PI: 1.5-1.2%). BA.2.75.2 is currently estimated at 1.2% (95% PI: 0.9-1.6%).
- Listed below are lineages with sequence prevalence >1.0% or a growth rate >3 fold and count >10 in October (ranked in order of sequence prevalence). Lineages with fold growth >3 from September to October are highlighted in *bold italic*:
 - BA.5.2.1 17%, 0.81 fold growth
 - BA.5.2 12%, 0.99 fold growth
 - BA.4.6 9.0%, 0.91 fold growth
 - \circ BA.5.1 6.8%, 0.80 fold growth
 - \circ BQ.1 4.1%, 5.5 fold growth
 - $\circ \quad BF.7-4.0\%, 2.5 \ fold \ growth$

- \circ BQ.1.1 3.0%, 8.9 fold growth
- BF.10 2.6%, 0.86 fold growth
- BA.2.75 2.1%, 5.6 fold growth
- BA.5 2.1%, 0.88 fold growth
- BA.5.2.9 1.9%, 0.80 fold growth
- BA.5.5 1.9%, 0.56 fold growth
- BF.5 1.8%, 0.99 fold growth
- BA.5.6 1.8%, 0.51 fold growth
- BA.5.2.6 1.7%, 3.2 fold growth
- BF.26 1.6%, 1.1 fold growth
- BA.5.2.21 1.1%, 0.93 fold growth
- BE.1 1.1%, 0.69 fold growth
- o BQ.1.2 0.61%, 10 fold growth
- o BA.2.3.20 0.48%, 3.4 fold growth
- BQ.1.3 0.45%, 11 fold growth
- BA.5.2.23 0.39%, 3 fold growth
- BA.5.2.24 0.34%, 3.1 fold growth
- o BF.14 0.24%, 4 fold growth
- XBB 0.23%, 12 fold growth
- BE.4.1.1 0.09%, 9 fold growth
- XBB.1 0.09%, 9 fold growth
- BE.1.2.1 0.09%, 4.5 fold growth
- BA.5.2.14 0.09%, 4.5 fold growth
- Several Omicron sub-lineages carry a recurring mutation at position *346* in the S protein (S:*R346T* in BA.4.6, BF.7, BF.11, BA.5.1.18, BA.5.2.6, BQ.1.1, BA.4.1.8, BA.5.2.1; S:*R346S* in BF.13, BA.5.2, BF.26, BA.5.2.1; or S:*R346I* in BA.5.9, BE.1.1, BA.5.2, BA.4.1)
- Several Omicron sub-lineages carry a recurring mutation at position 444 in the S protein (S:*K444T* in BQ.1, BQ.1.1, BA.5.6.2, BE.1.1.1, BE.1.1 and S:*K444R* in BA.5.2.1, BF.16, BA.2.3.20)
- Several Omicron sub-lineages carry a recurring mutation at position 445 (S:V445A in BF.25, BA.5.2.23, BA.4.6, BA.5.1.12, BA.5.2)
- Several Omicron sub-lineages carry a recurring mutation at position *446* (S:*G446S* in BA.2.75.2, BA.2.75.5, CA.1, BM.1.1, BY.1, BL.1). (S:*G446D* also occurs in BA.5.2, BA.5.2.1, CD.1).
- Several Omicron sub-lineages carry a recurring mutation at position *460* (S:*N460K* in BQ.1, BQ.1.1, BA.2.75.2, BA.2.3.20, BA.2.75.5, CA.1, BM.1.1, BE.1)

DELTA (B.1.617.2 and AY sub-lineages) (no significant change since previous report)

• Three Delta sequences in the US in September; one in October so far

USA – (other VOCs and VOIs) (no significant change since previous report)

• One Alpha sequence in the US in September. This genome appears to be have accumulated several other mutations in addition to those normally associated with B.1.1.7 genomes (P9L,D80G,G232V,S247N,Y248-,D253Y,Y449H,E484K,F490S,T547K,T572I,K1191N).

<u>USA – Recombinants</u>

• XBB – 21 sequences in the US in September; 52 in October so far

- XBB.1 8 in September; 20 in October so far
- XAZ 51 sequences in the US in September; 15 in October so far
- XAS 4 in September; 2 in October so far
- See a summary of recombinant lineages at the end of this report.

World – VOC

OMICRON

- Omicron remains dominant globally. Listed below are lineages showing the highest sequence prevalence (> 1.0%) or a fold growth > 3 fold in October so far. Lineages with fold growth >3 from September to October are highlighted in *bold italic*:
 - BA.5.2 13%, 0.76 fold growth
 - BA.5.2.1 12%, 0.71 fold growth
 - \circ BF.7 7.6%, 2.1 fold growth
 - BA.5.1 7.1%, 0.70 fold growth
 - BA.4.6 3.9%, 0.75 fold growth
 - \circ BQ.1.1 3.7%, 7.0 fold growth
 - \circ BQ.1 3.0%, 4.9 fold growth
 - BA.2.75 2.7%, 3.2 fold growth
 - BF.5 2.7%, 0.72 fold growth
 - BA.5.2.6 1.8%, 2.2 fold growth
 - BE.1.1 1.6%, 0.76 fold growth
 - \circ BA.2 1.5%, 6.4 fold growth
 - \circ BA.5 1.5%, 0.89 fold growth
 - \circ BA.5.2.20 1.3%, 0.91 fold growth
 - XBB 0.65%, 7.2 fold growth
 - XBB.1 0.44%, 4 fold growth
 - BQ.1.2 0.3%, 5 fold growth
 - BQ.1.3 0.17%, 8.5 fold growth
 - BE.4.1.1 0.08%, 8 fold growth
 - o BA.2.3 0.08%, 4 fold growth
 - o BA.5.10.1 0.08%, 4 fold growth
 - o BA.2.10.1 0.04%, 4 fold growth
- Substitutions in spike that we are monitoring (>3 fold growth from September to October with counts >10) include the following (but note that the numbers are still relatively small for some of these) (substitutions with sequence prevalence >1.0% are highlighted in *bold italic*:
 - G252V 0.76%, 6.3 fold growth
 - o I666V 0.37%, 5.3 fold growth
 - L368I 1.2%, 5.0 fold growth
 - E619Q 0.25%, 5 fold growth
 - I834M 0.05%, 5 fold growth
 - Y248- 0.05%, 5 fold growth
 - \circ Q183E 1.2%, 5.0 fold growth
 - \circ V445P 1.2%, 4.9 fold growth

- K444T 8.8%, 4.9 fold growth
- V83A 1.2%, 4.9 fold growth
- H146Q 1.2%, 4.3 fold growth
- F490S 2.2%, 4.2 fold growth
- I931V 0.04%, 4 fold growth
- K147- 0.08%, 4 fold growth
- o L368J 0.04%, 4 fold growth
- o R346E 0.04%, 4 fold growth
- o R78M 0.04%, 4 fold growth
- o T470I 0.04%, 4 fold growth
- V213E 1.3%, 3.9 fold growth
- o N148- 0.07%, 3.5 fold growth
- N460K 14%, 3.1 fold growth
- D614S 0.03%, 3 fold growth
- G75D 0.03%, 3 fold growth
- N703I 0.03%, 3 fold growth
- Q183K 0.03%, 3 fold growth

Note on convergent mutations: Over the past two months we have noted an increase in convergent mutations at several antigenically important sites in addition to $L452^*$: R346*(T/I/S/K), K356*(T/R), K444*(M/T/R/N), V445*(A/P), G446*(D/S/V), N450* and N460*(K/S). Most of these mutations, as well as several others previously reported in Omicron and other lineages, are discussed in a new preprint below.

"<u>Imprinted SARS-CoV-2 humoral immunity induces convergent Omicron RBD evolution</u> (on convergent mutations at sites: R346, R356, K444, L452, N460K and F486)"

DELTA (B.1.617.2 and AY sub-lineages)

• 24 Delta isolates globally in September; 3 in October so far

World (other VOIs)

- One Alpha genome in September (in US) ; none in October so far
- One Beta genome in September (in Germany); none in October so far

World – Recombinants

- **XBB** 693 in October so far
- XBB.1 475 in October so far
- XAZ 110 in October so far
- **XBC** 12 in October so far
- XAY 7 in October so far
- XAS 3 in October so far

Variants that have been mentioned in the media and/or social media:

- <u>Scientists have their eyes on several 'Deltacrons'—new COVID variants with the potential to</u> <u>attack the lungs like Delta and spread as easily as Omicron (XBC, XAY, and XAW)</u>
- <u>A soup of omicron subvariants could drive the next covid-19 wave</u> (XBB & BQ*)

- <u>'Scrabble variants' now cause the majority of new Covid-19 infections in the US</u> (XBB & BQ*))
- <u>New Omicron subvariants BQ.1 and BQ.1.1 make gains as BA.5 fades</u>
- Covid, Flu, RSV: Hospitalizations Rise as Wave of Viruses Hits New York
- China locks down part of Wuhan, nearly three years after first Covid case emerged
- <u>COVID in metro wastewater jumps to highest level since January</u>
- mRNA bivalent booster enhances neutralization against BA.2.75.2 and BQ.1.1
- <u>TAG-VE statement on Omicron sublineages BQ.1 and XBB</u>
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Recombinant lineages:

One new recombinant lineages have been added this week: XBE. A summary table of recombinant lineages can be found below with more details. We have added the number of recombinants genomes for each lineage. XA, XB, and XC have not been detected in the past 6 months. XD-XBD are Omicron/Omicron or Omicron/Delta recombinants. The majority of these recombinant lineages do not appear to have taken off and several have not been detected in recent weeks. The XB lineage appears to have the largest number of genomes.

Name	number	Github#	Lineage 1	Lineage 2	Location first detected
XA	45	NA	B.1.1.7	B.1.177	UK
<u>XB</u>	3435	<u>#189</u>	B.1.634	B.1.631	N. America
XC	25	<u>#263</u>	Delta (AY.29)	B.1.1.7	Japan
<u>XD</u>	34	<u>#444</u>	Delta (AY.4)	BA.1	France
<u>XE</u>	2829	<u>#454</u>	BA.1	BA.2	UK
<u>XF</u>	34	<u>#445</u>	Delta	BA.1	UK
XG	479	<u>#447</u>	BA.1	BA.2	Denmark
<u>XH</u>	174	<u>#448</u>	BA.1	BA.2	Denmark
<u>XJ</u>	253	<u>#449</u>	BA.1	BA.2	Finland
<u>XK</u>	25	<u>#460</u>	BA.1	BA.2	Belgium
<u>XL</u>	120	<u>#464</u>	BA.1	BA.2	UK
<u>XM</u>	554	<u>#472</u>	BA.1.1	BA.2	Multiple EU
XN	290	<u>#480</u>	BA.1	BA.2	UK
XP	57	#481	BA.1.1	BA.2	UK
XQ	145	#468	BA.1.1	BA.2	UK
XR	183	<u>#469</u>	BA.1.1	BA.2	UK

	XS	60	<u>#471</u>	Delta	BA.1.1	USA
ľ	<u>XT</u>	14	<u>#478</u>	BA.2	BA.1*	S. Africa
	<u>XU</u>	16	<u>#522</u>	BA.1*	BA.2	India
	XV	42	<u>#463</u>	BA.1*	BA.2*	Denmark
	XW	195	<u>#591</u>	BA.1*	BA.2*	JP, DE, SI, CA, UK, US
	<u>XY</u>	126	<u>#606</u>	BA.1*	BA.2*	FR, IL, UK, US
	<u>XZ</u>	218	<u>#636</u>	BA.2*	BA.1*	Multiple
	XAA	100	<u>#664</u>	BA.1*	BA.2*	US, IL
	XAB	114	# <u>665</u>	BA.1*	BA.2*	IT, FR, DE, CH, DK
	XAC	207	# <u>590</u>	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
	XAD	104	<u>#607</u>	BA.2*	BA.1*	CZ,DE,UK
	XAE	132	<u>#637</u>	BA.2*	BA.1*	CA,US,NL,CH
	XAF	300	<u>#676</u>	BA.1*	BA.2*	CR
	XAG	404	<u>#709</u>	BA.1.1	BA.2.23	BR
	XAH	168	<u>#755</u>	BA.2*	BA.1*	SI
	XAJ	103	<u>#826</u>	BA.2.12.1	BA.4	UK
	XAK	148	<u>#823</u>	BA.1*	BA.2*	DE
	XAL	124	<u>#757</u>	BA.1.1	BA.2*	DE
	XAM	543	<u>#759</u>	BA.1.1	BA.2.9	Panama
	XAN	206	<u>#771</u>	BA.2*	BA.5.1	Multiple
	XAP	81	<u>#789</u>	BA.2*	BA.1*	US
	XAQ	81	<u>#798</u>	BA.1*	BA.2*	Canada
	XAR	54	#860	BA.1*	BA.2*	Reunion/France
	XAS	195	<u>#882</u>	BA.5*	BA.2*	N. America
	XAT	99	<u>#885</u>	BA.2.3.13	BA.1*	Japan
	XAU	108	<u>#894</u>	BA.1.1*	BA.2.9*	Multiple
	XAV	80	<u>#911</u>	BA.2*	BA.5*	France
ľ	XAW	45	<u>#895</u>	BA.2*	AY.122	Russia
	XAY	40	<u>#844</u>	BA.2	AY.45	S. Africa
	XAZ	2165	<u>#797</u>	BA.2.5, BA.5	BA.2.5	Multiple
	XBA	4	#844	AY.45	BA.2	S. Africa

XBB*	2130	# <u>1058</u>	BJ.1	BM.1.1.1	Singapore/US
XBC*	49	#1100	Delta	BA.2	Philippines
XBD	27	<u>#1137</u>	BA.2.75.2	BF.5	Multiple
XBE	122	<u>#1246</u>	BA.5.2	BE.4	USA

Newly designated Pango lineages:

New lineages designated this week:

- **BN.1.3.1**: Potential BN.1.3 sublineage with T4435C, C3787T, and ORF1a:F3486L
- **BF.7.4.1**: Potential BF.7.4 sublineage with C9365T, T21180C, and ORF1b:P1427S
- **BF.32**: Sublineage of BA.5.2.1 with S:N450D, ORF1a:T1552N, & ORF1b:G662S
- <u>CY.1</u>: BA.5.2.7(S:K444M) sublineage with S:N460K (T22942G)