

BV-BRC SARS-CoV-2 Emerging Variant Report November 15, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20221115.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.

This report includes preliminary/incomplete stats for the month of November in order to identify early signs of novel variants emerging.

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 11/12/22 estimates that **BA.5** proportions are still dominating in the United States at 29.7%, but this is a significant decrease from last week. Significant regional differences exist: <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>.
 - The CDC Nowcast estimates for **BA.4.6** proportions are slowly decreasing, now at 5.5%
 - **BQ.1.1 and BQ.1 have been added to the Nowcast tracker. BQ.1 is currently estimated at 20.1%, an increase since last week. BQ.1.1 has overtaken BQ.1 this week and is currently estimated at 24.1%, an increase since last week.**
 - **BF.7 has been added to the Nowcast tracker and is currently estimated at 7.8%, slightly down from last week**
 - **BA.5.2.6 has been added to the Nowcast tracker and is steady at 2.9%**
 - **BN.1 has been added to the tracker and is at 4.3%**
- Listed below are lineages with sequence prevalence >1.0% or a growth rate >3 fold and count >5 in November so far (ranked in order of sequence prevalence). Lineages with fold growth >3 from October to November so far are highlighted in **bold italic**:
 - BA.5.2.1 - 12%, 0.76 fold growth
 - BQ.1 - 11%, 1.9 fold growth
 - BQ.1.1 - 10%, 2.2 fold growth
 - BA.5.2 - 10%, 0.93 fold growth
 - BF.7 – 5.1%, 1.2 fold growth
 - BA.4.6 – 5.1%, 0.63 fold growth
 - BA.5.1 – 5.1%, 0.82 fold growth
 - **BQ.1.3 – 2.3%, 4.1 fold growth**

- **BA.5.2.24 – 1.3%, 3.4 fold growth**
- **BE.1.1.1 – 1.3%, 6.1 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*)

- No Delta sequences in the US in November so far; one in October

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

- None

USA – Recombinants

- **XBB** – 3 sequences in November so far; 194 in October
- **XAV** – 1 sequences in November so far; 2 in October
- **XBB.1** – No sequences in November so far; 46 in October
- **XAZ** – No sequences in November so far; 34 in October

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 November so far. Lineages with fold growth >3 from October to November are highlighted in **bold italic**:
 - BQ.1.1 - 10%, 2.1 fold growth
 - BF.7 – 8.2%, 1.1 fold growth
 - BA.5.2 – 8.0%, 0.61 fold growth
 - BQ.1 – 7.8%, 2.0 fold growth
 - BA.2.75 – 7.1%, 2.3 fold growth
 - BA.5.2.1 – 4.9%, 0.43 fold growth
 - BA.5.1 – 4.3%, 0.65 fold growth
 - **XBB – 3.6%, 4.0 fold growth**
 - BA.2 – 2.3%, 2.3 fold growth
 - BF.5 – 1.9%, 0.62 fold growth
 - BA.5.2.6 – 1.9%, 0.90 fold growth
 - BA.4.6 – 1.7%, 0.44 fold growth

- BA.5 – 1.1%, 0.82 fold growth
 - ***BN.1 – 1.1%, 3.9 fold growth***
 - BF.14 – 1.1%, 2.2 fold growth
- Substitutions in spike that we are monitoring (>3 fold growth from October to November so far with counts >10) include those listed below (but note that the numbers are still relatively small for some of these). Substitutions with sequence prevalence >1% are highlighted in ***bold italic***:
 - V83F - 0.48%, 16 fold growth
 - E156- - 0.31%, 10 fold growth
 - T208M - 0.19%, 9.5 fold growth
 - F486P - 0.89%, 8.9 fold growth
 - L368J - 0.29%, 7.3 fold growth
 - ***F486I – 1.1%, 6.6 fold growth***
 - F157- - 0.52%, 6.5 fold growth
 - K147- - 0.45%, 6.4 fold growth
 - N148- - 0.45%, 6.4 fold growth
 - Q183R - 0.28%, 5.6 fold growth
 - P25S - 0.16%, 5.3 fold growth
 - N703I - 0.16%, 5.3 fold growth
 - E156G - 0.22%, 4.4 fold growth
 - R158- - 0.22%, 4.4 fold growth
 - ***G252V – 3.4%, 4.2 fold growth***
 - A243- - 0.16%, 4 fold growth
 - L244- - 0.16%, 4 fold growth
 - P812L - 0.2%, 4 fold growth
 - H146K - 0.16%, 4 fold growth
 - K150E - 0.39%, 3.9 fold growth
 - A222V - 0.19%, 3.8 fold growth
 - ***F490S – 9.5%, 3.4 fold growth***
 - ***V445P – 4.5%, 3.4 fold growth***
 - ***Q183E – 4.6%, 3.3 fold growth***
 - ***V83A – 4.6%, 3.3 fold growth***
 - ***H146Q – 4.5%, 3.2 fold growth***
 - ***L368I – 4.1%, 3.2 fold growth***
 - ***V213E – 4.7%, 3.2 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 recent preprint below.*

“[Imprinted SARS-CoV-2 humoral immunity induces convergent Omicron RBD evolution](#) (on convergent mutations at sites: R346, R356, K444, L452, N460K and F486)”

DELTA (B.1.617.2 and AY sub-lineages)

- No Delta genomes in November so far; 6 in October

World (other VOIs)

- No Alpha genome in November so far; 16 in October

World – Recombinants

- **XBB** – 247 in November so far; 1808 in October
- **XBB.1** – 39 in November so far; 669 in October
- **XAZ** – 3 in November so far; 189 in October
- **XAV** – 1 in November so far; 2 in October
- **XBC** – None in November so far; 19 in October
- **XAY** – None in November so far; 15 in October

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

- U.S. Coronavirus Cases Start to Increase as Omicron Subvariants BQ.1.1, BQ.1 Spread
- CDC now tracking BN.1, the latest new COVID variant on the rise
- Variant-specific symptoms of COVID-19 in a study of 1,542,510 adults in England
- Omicron BA.2 tied to more symptoms and, rarely, brain swelling in kids
- Divergent SARS-CoV-2 variant emerges in white-tailed deer with deer-to-human transmission
- Florida COVID cases rising again as BQ subvariants of omicron spread

Recombinant lineages:

No new recombinant lineages have been added this week. 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-XBF are Omicron/Omicron or Omicron/Delta recombinants. With the exception of XBB, the majority of these recombinant lineages do not appear to have taken off and several have not been detected in recent weeks. The XBB 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
XB	3435	#189	B.1.634	B.1.631	N. America
XC	25	#263	Delta (AY.29)	B.1.1.7	Japan
XD	34	#444	Delta (AY.4)	BA.1	France
XE	2832	#454	BA.1	BA.2	UK
XF	34	#445	Delta	BA.1	UK
XG	479	#447	BA.1	BA.2	Denmark
XH	174	#448	BA.1	BA.2	Denmark

XJ	253	#449	BA.1	BA.2	Finland
XK	25	#460	BA.1	BA.2	Belgium
XL	120	#464	BA.1	BA.2	UK
XM	526	#472	BA.1.1	BA.2	Multiple EU
XN	288	#480	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	#469	BA.1.1	BA.2	UK
XS	60	#471	Delta	BA.1.1	USA
XT	14	#478	BA.2	BA.1*	S. Africa
XU	16	#522	BA.1*	BA.2	India
XV	42	#463	BA.1*	BA.2*	Denmark
XW	195	#591	BA.1*	BA.2*	JP, DE, SI, CA, UK, US
XY	126	#606	BA.1*	BA.2*	FR, IL, UK, US
XZ	216	#636	BA.2*	BA.1*	Multiple
XAA	104	#664	BA.1*	BA.2*	US, IL
XAB	114	#665	BA.1*	BA.2*	IT, FR, DE, CH, DK
XAC	207	#590	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
XAD	99	#607	BA.2*	BA.1*	CZ,DE,UK
XAE	133	#637	BA.2*	BA.1*	CA,US,NL,CH
XAF	300	#676	BA.1*	BA.2*	CR
XAG	412	#709	BA.1.1	BA.2.23	BR
XAH	169	#755	BA.2*	BA.1*	SI
XAJ	106	#826	BA.2.12.1	BA.4	UK
XAK	149	#823	BA.1*	BA.2*	DE
XAL	122	#757	BA.1.1	BA.2*	DE
XAM	544	#759	BA.1.1	BA.2.9	Panama
XAN	209	#771	BA.2*	BA.5.1	Multiple
XAP	81	#789	BA.2*	BA.1*	US
XAQ	81	#798	BA.1*	BA.2*	Canada
XAR	54	#860	BA.1*	BA.2*	Reunion/France
XAS	202	#882	BA.5*	BA.2*	N. America

XAT	100	#885	BA.2.3.13	BA.1*	Japan
XAU	108	#894	BA.1.1*	BA.2.9*	Multiple
XAV	83	#911	BA.2*	BA.5*	France
XAW	45	#895	BA.2*	AY.122	Russia
XAY*	62	#844	BA.2	AY.45	S. Africa
XAZ	2314	#797	BA.2.5, BA.5	BA.2.5	Multiple
XBA	4603	#844	AY.45	BA.2	S. Africa
XBB*	1771	#1058	BJ.1	BM.1.1.1	Singapore/US
XBC*	123	#1100	Delta	BA.2	Philippines
XBD	133	#1137	BA.2.75.2	BF.5	Multiple
XBE*	132	#1246	BA.5.2	BE.4	USA
XBF	9	#1259	BA.5.2.3	CJ.1	Australia

Newly designated Pango lineages:

New lineages designated this week:

- BA.5.2.41: BA.5.2 + orf1b:1050N + C29762T sublineage with S:444R and Orf1a:S2797F
- BF.7.5.1: Potential BF.7.5 sublineage with ORF1a:H712N
- BQ.1.26: Potential BQ.1 sublineage with E:R61L and ORF3a:I169V
- BN.1.7: BN.1 Sublineage with S:I210del, S:M177T, & S:H1101Y
- BE.9: Increasing prevalence of BA.5.3.1 sublineage in Amazonas, Brazil, with S:K444T, S:N460K and S:Y144del