

BV-BRC SARS-CoV-2 Emerging Variant Report December 6, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20221206.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

- Based on CDC Nowcast estimates (<https://covid.cdc.gov/covid-data-tracker/#variant-proportions>) for the week ending 12/03/22 in the US: virtually all sequences reported since July are **Omicron**.
 - **BA.5** proportions are no longer dominating in the United States at 13.8% (down from 29.7% on 11/12/22)
 - **BA.4.6** proportions continue to decrease, now at 2.3%
 - **BQ.1.1 and BQ.1 continue to grow dramatically. BQ.1 is currently estimated at 30.9%, up from last week. BQ.1.1 has overtaken BQ.1 and is currently estimated at 31.9%, up from last week.**
 - **BF.7 has been added to the Nowcast tracker and is currently estimated at 6.3%, slightly down from last week**
 - **BA.5.2.6** is steady at 1.8%
 - **XBB has been added to the tracker and has increased from last week to 5.5%**
 - **BN.1 has been added to the tracker and has increased from last week to 4.6%**
 - **BF.11 has been added to the tracker and has slightly decreased from last week to 0.9%**
- Listed below are lineages with sequence prevalence >1.0% or a growth rate >3 fold and count >50 in November (ranked in order of sequence prevalence) in comprehensive data collected from GISAID. Lineages with fold growth >4 from October to November so far are highlighted in **bold italic**:
 - BQ.1.1 - 10%, 2.6 fold growth
 - BQ.1 – 8.8%, 2.3 fold growth
 - BA.5.2.1 – 7.1%, 0.48 fold growth
 - BA.5.2 – 6.1%, 0.56 fold growth
 - BA.4.6 – 3.9%, 0.51 fold growth
 - BA.2.75 – 3.3%, 1.3 fold growth
 - BA.5.1 – 3.1%, 0.54 fold growth

- BF.7 – 3.1%, 0.93 fold growth
- **BQ.1.12 – 1.7%, 4.0 fold growth**
- **XBB – 1.6%, 5.0 fold growth**
- BQ.1.3 – 1.5%, 2.7 fold growth
- BA.5.2.6 – 1.5%, 1.3 fold growth
- BQ.1.2 – 1.3%, 1.9 fold growth
- **BQ.1.1.4 – 1.3%, 5.4 fold growth**
- BQ.1.11 – 1.3%, 3.5 fold growth
- BF.10 – 1.3%, 0.58 fold growth
- BQ.1.14 – 1.2%, 2.5 fold growth
- **BQ.1.1.3 – 1.2%, 4.5 fold growth**
- BQ.1.1.5 – 1.2%, 3.5 fold growth
- BF.26 – 1.1%, 0.75 fold growth
- BA.5 – 1.1%, 0.59 fold growth
- BE.1.1 – 1.1%, 0.97 fold growth
- XBB.1 - 0.91%, 3.8 fold growth
- BQ.1.13 - 0.77%, 3.7 fold growth
- **BQ.1.18 - 0.75%, 8.3 fold growth**
- BQ.1.1.18 - 0.74%, 3.9 fold growth
- **BQ.1.1.15 - 0.53%, 53 fold growth**
- **CQ.2 - 0.5%, 10 fold growth**
- **BQ.1.1.7 - 0.4%, 4.4 fold growth**
- **CR.1.1 - 0.34%, 11 fold growth**
- BQ.1.8 - 0.33%, 3.3 fold growth
- CK.1 - 0.31%, 3.1 fold growth
- **BQ.1.1.1 - 0.24%, 4 fold growth**

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

- One Delta sequences in the US in November so far; three in October

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

- None

USA – Recombinants

- **XBB** - 383 sequences in November so far; 200 sequences in October
- **XBB.1** - 221 sequences in November so far; 153 sequences in October
- **XBB.2** - 24 sequences in November so far; 15 sequences in October
- **XBD** - 6 sequences in November so far; 8 sequences in October
- **XBB.3** - 4 sequences in November so far; 19 sequences in October
- **XAZ** - 4 sequences in November so far; 39 sequences in October
- **XBE** - 3 sequences in November so far; 15 sequences in October
- **XAV** - 1 sequences in November so far; 2 sequences in October
- **XBB.4** - 1 sequences in November so far; 1 sequences in October
- **XAS** - no sequences in November so far; 6 sequences in October
- **XBB.1.1** - no sequences in November so far; 6 sequences in October
- **XBB.1.3** - no sequences in November so far; 1 sequences 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 and count >50 in November. Lineages with fold growth >4 from October to November are highlighted in **bold italic**:
 - BQ.1.1 – 9.4%, 2.2 fold growth
 - BA.5.2 – 7.5%, 0.53 fold growth
 - BA.2.75 – 6.2%, 1.9 fold growth
 - BA.5.2.1 – 6.0%, 0.51 fold growth
 - BQ.1 – 5.1%, 2.1 fold growth
 - BF.7 – 5.0%, 0.84 fold growth
 - BA.5.1 – 3.3%, 0.51 fold growth
 - ***XBB – 2.8%, 5.3 fold growth***
 - BF.5 – 2.5%, 0.66 fold growth
 - BA.4.6 – 2.2%, 0.60 fold growth
 - BA.5.2.6 – 1.4%, 1.0 fold growth
 - ***BQ.1.18 – 1.2%, 5.2 fold growth***
 - BA.2 - 0.89%, 3.9 fold growth
 - BQ.1.12 - 0.57%, 3.6 fold growth
 - BQ.1.11 - 0.56%, 3.1 fold growth
 - BQ.1.1.15 - 0.5%, 3.3 fold growth
 - BQ.1.1.3 - 0.49%, 3.3 fold growth
 - BQ.1.1.10 - 0.45%, 3.8 fold growth
 - BQ.1.1.3 - 0.36%, 3.3 fold growth
 - CK.1 - 0.18%, 3 fold growth
 - ***BN.1.3.1 - 0.16%, 5.3 fold growth***
 - ***CQ.2 - 0.16%, 8 fold growth***
 - ***BQ.1.1.13 - 0.15%, 5 fold growth***
 - BQ.1.10.1 - 0.11%, 3.7 fold growth
 - ***BN.1.4 - 0.1%, 5 fold growth***
 - ***CR.1.1 - 0.1%, 10 fold growth***
 - BN.1.2 - 0.09%, 3 fold growth
 - ***XBC.1 - 0.08%, 4 fold growth***
- Substitutions in spike that we are monitoring (>3 fold growth from October to November with counts >50) include those listed below (but note that the numbers are still relatively small for some of these). Only one of substitutions (G252V) has a sequence prevalence >1% in November:
 - N148Q - 0.24%, 12 fold growth
 - Y144L - 0.24%, 12 fold growth
 - Y145P - 0.24%, 12 fold growth
 - S673G - 0.11%, 11 fold growth
 - N149Q - 0.24%, 8 fold growth
 - F486P - 0.74%, 7.4 fold growth

- H146K - 0.26%, 6.5 fold growth
- Q613H - 0.19%, 4.8 fold growth
- V62I - 0.14%, 4.7 fold growth
- F486I - 0.63%, 4.2 fold growth
- M177T - 0.12%, 4 fold growth
- K182I - 0.08%, 4 fold growth
- K147Q - 0.11%, 3.7 fold growth
- T859S - 0.11%, 3.7 fold growth
- G485D - 0.07%, 3.5 fold growth
- K147- - 0.19%, 3.2 fold growth
- N148- - 0.19%, 3.2 fold growth
- **G252V – 2.6%, 3.1 fold growth**
- D253G - 0.7%, 3.0 fold growth
- L18F - 0.06%, 3 fold growth
- T19R - 0.06%, 3 fold growth
- T208M - 0.06%, 3 fold growth
- E156G - 0.15%, 3 fold growth
- R158- - 0.15%, 3 fold growth

***Note on convergent mutations:** In addition to previously noted convergent mutations in the receptor binding domain (RBD) (L452*: R346*(T/I/S/K), K356*(T/R), K444*(M/T/R/N), V445*(A/P), G446*(D/S/V), N450*, N460*(K/S), 478*, 485*, & F486*), we have begin to notice convergent mutations in the N-terminal domain (NTD). More details are provided below:*

Positions between 144>152

144: in addition to **Y144-** (which has grown from ~2% to ~19% prevalence in the past 3 months) a bump in November of genomes with **Y144L** (only 207 genomes, ~0.2%) has also been noticed. **Y144L** has increased by 12 fold in the past month.

145: Commonly seen mutations at this position include **Y145P** (~0.2%), **Y145H**(~0.4%), & **Y145-** (~0.4%). **Y145P** has increased by 12 fold in the past month.

146: Commonly seen mutations at this position include **H146K** (~0.3%), **H146L** (~0.2%), **H146Q** (~0.4%), & **H146-** (~0.1%). Frequency of multiple mutations at this position have increased in the past month: H146K (6.5 fold increase) H146L (~3 fold increase), H146Q (~2.5 fold increase).

147: Commonly seen mutations at this position include **K147Q-** (~0.1%), **K147-** (~0.2%), **K147E** (~9% mainly from BA.2.75 lineages), **K147I** (~0.2%), **K147N** (~0.4%), & **K147T** (~0.1%).

Mutations at both **K147Q** & **K147-** have increase by more than 3 fold in the past month.

148: Commonly seen mutations at this position include **N148Q** (~0.2%) & **N148-** (~0.2%). These have increased by 12 fold and ~3.2 fold respectively in the past month.

149: One main mutation at this position: **N149Q** (~0.2%), but has increased by 8 fold in the past month.

150: One main mutation at this position **K150E** (~0.4%), but has increased by 3 fold in the past month.

Small sporadic increases in mutations at position 150, 151, 152 (BA.2.75 lineages).

Positions between 156-158

There has been an increase in mutations at this position, including E156G, E156-, F157-, F157L, and R158-. Some of these are Delta like mutations and are attributable to recent increases in Delta/Omicron recombinant lineages such as **XBC** and **XAY** (and a few XBA). However there are also some BA.2.75

sublineages with E156-, F157- (mainly from Turkey), and of course most BA.2.75 already have **F157L**.

Positions between 208-215

Moderate increases in proportions of variants carrying mutations at these positions. These numbers are generally low, but appear to all occur in similar regions. This is a similar pattern to what was observed in Delta.

208: **T208M** (<0.1%, 3 fold increase in November)

209: **P209L** (0.5%, 2 fold increase in November)

210: **I210V** (7%, 1.9 fold increase in November, mainly due to BA.2.75 background)

211: **N211-** (0.15%, 2 fold increase in November, mainly occurs in BA.2.75 lineages)

212: **L212I** and **L212S** (both at ~0.15%, ~2 fold increase in November)

213: **V213E** and **V213G** (found in more than 95% genomes, both of these mutations are found in currently circulating XBB and BA.2/BA.4/5 lineages)

215: **D215G** (~0.1%, 2.6 fold increase) & **D215H** (~0.2% and 2 fold increase)

Positions between 243-253

While mutations at these particular positions do not appear to be particularly convergent (different mutations at same site), the general area between these coordinates seems to be experiencing evolutionary pressure.

243 & 244: Deletions (**A243-**,**L244-**) occur simultaneously at both these positions in XBC* lineages (~0.1%, 2.2 fold increase)

245: **H245N**, **H245Y** (0.9% and 0.1% respectively, no fold increase)

247: **S247N** (0.2%, 2.2 fold increase, BF*)

248: **Y248-** (0.15%, 2 fold increase)

251: **P251H** (0.18%, 2.2 fold increase)

252: **G252V** (0.26%, 3 fold increase)

253: **G253G** (0.7%, 3 fold increase)

DELTA (B.1.617.2 and AY sub-lineages)

- 12 Delta genomes in November

World (other VOIs)

- 2 Alpha genome in November so far

World – Recombinants

- **XBB** - 2394 sequences in November so far; 1371 sequences in October
- **XBB.1** - 630 sequences in November so far; 1646 sequences in October
- **XBB.2** - 81 sequences in November so far; 206 sequences in October
- **XAZ** - 32 sequences in November so far; 245 sequences in October
- **XBB.3** - 30 sequences in November so far; 244 sequences in October
- **XBD** - 27 sequences in November so far; 82 sequences in October
- **XBB.1.1** - 19 sequences in November so far; 143 sequences in October
- **XBB.4** - 12 sequences in November so far; 22 sequences in October
- **XBE** - 3 sequences in November so far; 52 sequences in October
- **XBB.5** - 2 sequences in November so far; 11 sequences in October

- **XBC** - 2 sequences in November so far; 15 sequences in October
- **XAV** - 1 sequences in November so far; 3 sequences in October
- **XBB.1.3** - 1 sequence in November so far; 7 sequences in October
- **XAH** - no sequences in November so far; 1 sequence in October
- **XAK** - no sequences in November so far; 1 sequence in October
- **XAY** - no sequences in November so far; 10 sequences in October
- **XBB.1.2** - no sequences in November so far; 5 sequences in October
- **XBB.3.1** - no sequences in November so far; 20 sequences in October
- **XE** - no sequences in November so far; 1 sequence in October
- **XAN** - no sequences in November so far; 3 sequences in October
- **XAS** - no sequences in November so far; 7 sequences in October

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

- [Boston-area COVID Wastewater Data Spikes 88%](#)
- [Covid hospitalizations rising post-Thanksgiving after an autumn lull](#)
- [COVID-19 cases spike all across Florida after Thanksgiving holiday](#)
- [Covid evolution wipes out another antibody treatment, threatening the country's medicine cabinet](#)
- [SARS-CoV-2 BW.1, a fast-growing Omicron variant from southeast Mexico bearing relevant escape mutations](#)
- [Gradual emergence followed by exponential spread of the SARS-CoV-2 Omicron variant in Africa](#)
- [Convergent evolution of the SARS-CoV-2 Omicron subvariants leading to the emergence of BQ.1.1 variant](#)

Recombinant lineages:

One new recombinant lineage has 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-XBJ 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	2836	#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	546	#759	BA.1.1	BA.2.9	Panama
XAN	213	#771	BA.2*	BA.5.1	Multiple

XAP	359	#789	BA.2*	BA.1*	US
XAQ	81	#798	BA.1*	BA.2*	Canada
XAR	21	#860	BA.1*	BA.2*	Reunion/France
XAS	192	#882	BA.5*	BA.2*	N. America
XAT	32	#885	BA.2.3.13	BA.1*	Japan
XAU	44	#894	BA.1.1*	BA.2.9*	Multiple
XAV	82	#911	BA.2*	BA.5*	France
XAW	45	#895	BA.2*	AY.122	Russia
XAY*	71	#844	BA.2	AY.45	S. Africa
XAZ	2348	#797	BA.2.5, BA.5	BA.2.5	Multiple
XBA	4603	#844	AY.45	BA.2	S. Africa
XBB*	9868	#1058	BJ.1	BM.1.1.1	Singapore/US
XBC*	297	#1100	Delta	BA.2	Philippines
XBD	388	#1137	BA.2.75.2	BF.5	Multiple
XBE*	5397	#1246	BA.5.2	BE.4	USA
XBF	618	#1259	BA.5.2.3	CJ.1	Australia
XBG	50	#896	BA.2.76	BA.5.2	UK
XBH	~100	#1229	BA.2.3.17	BA.2.75.2	Multiple
XBJ	~25	#1268	BA.2.3.20	BA.5.2	Multiple

Newly designated Pango lineages:

New lineages designated this week:

- BA.5.2.45: Sublineage of BA.5.2 (ORF1b:T1050N) with S:K444Q & ORF7a:A55V (92 seq)
- CH.3: BM.4.1.1 sublineage with S:F486P recently emerged in Indonesia and already exported to New Zealand, Denmark and Australia - 14 sequences
- CV.2: New BM.1.1.3 sublineage with S:F486P + ORF1a:G514E , ORF1b:Y1147C circulating in Chile and Usa (28 sequences)
- BQ.1.26.1: Potential BQ.1.26 sublineage with ORF1a:S248N (136 good seqs as of 2022-12-03; Denmark, USA, Germany)