

## BV-BRC SARS-CoV-2 Emerging Variant Report December 13, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20221213.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 12/10/22 in the US in order of prevalence:
  - ***BQ.1.1 has overtaken BQ.1 and is currently estimated at 36.8%, up from last week's 31.9.***
  - ***BQ.1 is currently estimated at 31.1%, up slightly from last week's 30.9%.***
  - **BA.5** proportions continue to drop in the United States, down from 13.8% last week to 11.5% this week
  - ***BF.7 has been added to the Nowcast tracker and is currently estimated at 5.7%, slightly down from last week***
  - ***XBB has been added to the tracker and is relatively steady from last week at 4.7%***
  - ***BN.1 has been added to the tracker and is relatively steady from last week at 4.3%***
  - **BA.5.2.6** is steady at 1.8%
  - **BA.4.6** continue to decrease in proportions, now at 1.6%
- Based on BV-BRC analysis of comprehensive data from GISAID, 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). Lineages with fold growth >4 from October to November so far are highlighted in ***bold italic***:
  - BQ.1.1 - 12%, 2.9 fold growth
  - BQ.1 – 9.0%, 2.4 fold growth
  - BA.5.2.1 – 6.8%, 0.46 fold growth
  - BA.5.2 – 5.9%, 0.55 fold growth
  - BA.4.6 – 3.7%, 0.49 fold growth
  - BA.2.75 – 3.4%, 1.4 fold growth
  - BF.7 – 3.3%, 1.0 fold growth
  - BA.5.1 – 3.0%, 0.51 fold growth
  - ***BQ.1.12 – 1.8%, 4.0 fold growth***
  - ***XBB – 1.7%, 5.0 fold growth***

- BQ.1.3 – 1.7%, 2.8 fold growth
- BQ.1.2 – 1.5%, 2.1 fold growth
- BA.5.2.6 – 1.4%, 1.3 fold growth
- **BQ.1.1.4 – 1.4%, 5.9 fold growth**
- BF.10 – 1.3%, 0.59 fold growth
- BQ.1.11 – 1.3%, 3.4 fold growth
- BQ.1.14 – 1.3%, 2.6 fold growth
- **BQ.1.1.3 – 1.2%, 4.7 fold growth**
- BQ.1.1.5 – 1.2%, 3.3 fold growth
- BF.26 – 1.2%, 0.79 fold growth
- BA.5 – 1.2%, 0.65 fold growth
- BE.1.1 – 1.1%, 0.98 fold growth
- **XBB.1 – 1.0%, 4.3 fold growth**
- **BQ.1.18 - 0.93%, 9.3 fold growth**
- **BQ.1.1.18 - 0.79%, 4.2 fold growth**
- BQ.1.13 - 0.78%, 3.6 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**
- BQ.1.8 - 0.38%, 3.8 fold growth
- **CR.1.1 - 0.31%, 10 fold growth**
- **BQ.1.1.1 - 0.25%, 4.2 fold growth**
- BQ.1.1.6 - 0.19%, 3.8 fold growth
- BE.4.2 - 0.18%, 3.6 fold growth
- BA.5.10.1 - 0.18%, 3.6 fold growth
- **BW.1 - 0.15%, 5 fold growth**

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

- Two 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** - 630 sequences in November so far; 221 sequences in October
- **XBB.1** - 378 sequences in November so far; 155 sequences in October
- **XBB.2** - 40 sequences in November so far; 15 sequences in October
- **XBD** - 8 sequences in November so far; 8 sequences in October
- **XAZ** - 7 sequences in November so far; 39 sequences in October
- **XBB.3** - 6 sequences in November so far; 19 sequences in October
- **XBE** - 3 sequences in November so far; 15 sequences in October
- **XBB.1.3** - 2 sequences in November so far; 1 sequence in October
- **XAV** - 1 sequence in November so far; 2 sequences in October
- **XBB.4** - 1 sequence in November so far; 1 sequence 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

## 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 – 9.9%, 2.3 fold growth
  - BA.5.2 – 7.5%, 0.53 fold growth
  - BA.2.75 – 6.3%, 1.9 fold growth
  - BA.5.2.1 – 5.9%, 0.51 fold growth
  - BQ.1 – 4.9%, 2.1 fold growth
  - BF.7 – 4.9%, 0.84 fold growth
  - BA.5.1 – 3.2%, 0.50 fold growth
  - ***XBB – 2.7%, 4.0 fold growth***
  - BF.5 – 2.5%, 0.68 fold growth
  - BA.4.6 – 2.0%, 0.55 fold growth
  - ***BQ.1.18 – 1.5%, 6.3 fold growth***
  - BA.5.2.6 – 1.3%, 0.96 fold growth
  - ***BA.2 – 1.2%, 4.8 fold growth***
  - BQ.1.1.18 – 1.1%, 2.9 fold growth
  - BQ.1.1.4 - 0.77%, 3.2 fold growth
  - ***BQ.1.1.15 - 0.62%, 4.1 fold growth***
  - BQ.1.12 - 0.61%, 3.6 fold growth
  - BQ.1.1.5 - 0.59%, 3.1 fold growth
  - BQ.1.11 - 0.57%, 3.2 fold growth
  - ***BQ.1.1.10 - 0.52%, 4.3 fold growth***
  - BQ.1.1.3 - 0.52%, 3.5 fold growth
  - BQ.1.1.1 - 0.37%, 3.1 fold growth
  - BQ.1.13 - 0.37%, 3.4 fold growth
  - CL.1 - 0.35%, 3.9 fold growth
  - ***BQ.1.1.13 - 0.19%, 6.3 fold growth***
  - ***BN.1.3.1 - 0.18%, 6 fold growth***
  - ***CQ.2 - 0.15%, 7.5 fold growth***
  - ***BQ.1.10.1 - 0.14%, 4.7 fold growth***
  - ***BN.1.4 - 0.12%, 6 fold growth***
  - ***CR.1.1 - 0.09%, 9 fold growth***
  - ***BE.4.2 - 0.06%, 6 fold growth***
  - ***BQ.1.21 - 0.06%, 6 fold growth***
  - ***BQ.1.22 - 0.04%, 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 these substitutions (G252V) has a sequence prevalence >1% in November:
  - N148Q - 0.23%, 12 fold growth

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- Y144L - 0.23%, 12 fold growth
- Y145P - 0.23%, 12 fold growth
- S673G - 0.11%, 11 fold growth
- F486P - 0.83%, 6.9 fold growth
- R21G - 0.06%, 6 fold growth
- N764R - 0.05%, 5 fold growth
- Q613H - 0.19%, 4.8 fold growth
- H146K - 0.23%, 4.6 fold growth
- K182I - 0.09%, 4.5 fold growth
- N148- - 0.22%, 4.4 fold growth
- M177T - 0.13%, 4.3 fold growth
- V62I - 0.13%, 4.3 fold growth
- F486I - 0.6%, 4 fold growth
- A475V - 0.04%, 4 fold growth
- T208M - 0.04%, 4 fold growth
- K147- - 0.23%, 3.8 fold growth
- K150E - 0.48%, 3.7 fold growth
- T859S - 0.11%, 3.7 fold growth
- L18F - 0.07%, 3.5 fold growth
- G485D - 0.07%, 3.5 fold growth
- T19R - 0.07%, 3.5 fold growth
- D215G - 0.1%, 3.3 fold growth
- K147Q - 0.1%, 3.3 fold growth
- H146L - 0.19%, 3.2 fold growth
- **G252V – 2.6%, 3.1 fold growth**

Convergent mutations in the N-Terminal Domain (NTD) of the Spike protein: (more information here)

- We noticed a sharp increase in mutations located in the NTD in the past month (November 2022)
- The majority of these mutations occur in structural loops know as N1-N5 loops, especially the N3 loop
- Evidence exists that these NTD mutations are highly convergent
- Evidence suggest that these mutations result in antigenic escape
- These NTD mutations also occur in other VOCs and long-term infections
- NTD mutations may occur sequentially after RBD escape mutations occur

Positions in N1 Loop (14 to 26)

- L18F (~0.01%), 3.5-fold increase
- T19R (~0.07%), 3.5-fold increase
- T19V(~0.02%), 2-fold increase
- T19I (occurs in 96% genomes – signature Omicron mutation)
- R21G (~0.06%), 6-fold increase
- L24-, P25-, P26-, A27S are signature Omicron mutations that occur in > 97% circulating November genomes.

Positions in N2 Loop (67-79)

- No significant increase in mutations in this region although H69- and Y70- are predominant in BA.4/5\* derived sublineages (>83% November genomes).

#### Positions between 144 – 157 (N3 loop: 141 to 156)

- Y144L (only 207 genomes, ~0.2%); increased by 12-fold in past month
- Y144- (from ~2% to ~19% prevalence in the past 3 months) 2-fold increase
- Y145P (~0.2%), Y145P has increased by 12-fold in the past month
- Y145H (~0.5%)
- Y145- (~0.4%)
- H146K (~0.3%), (4.6-fold increase)
- H146L (~0.2%), (~3-fold increase)
- H146Q (~0.4%), (~2.3-fold increase)
- H146- (~0.1%)
- K147- (~0.1%), (4-fold increase)
- K147Q (~0.2%), (~3-fold increase)
- K147E (~9% mainly from BA.2.75 lineages),
- K147I (~0.2%)
- K147N (~0.4%)
- K147T (~0.07%)
- N148Q (~0.2%), 12-fold increase
- N148- (~0.2%), ~4.4-fold increase
- N148T (~0.05%), ~2-fold increase
- N149Q (0.2%), 12-fold increase; removes the N149 glycan.
- K150E (~0.4%), 4-fold increase
- S151G (~0.03%), 3-fold increase
- W152R (BA.2.75 lineages); steady
- M153V/T sporadic increases in October and November.
- moderate increase (2-3-fold in November) in mutations at these positions, including E156G, E156-, F157-, F157L, and R158-
- Delta like mutations attributable to recent increases in Delta/Omicron recombinant lineages such as XBC and XAY (and a few XBA)
- Some BA.2.75 sub-lineages with E156-, F157- (mainly from Turkey), and of course most BA.2.75 already have F157L. But it's an interesting pattern

#### Positions in N4 Loop (177 to 186)

- M177T (~0.13%), 4-fold increase
- M177L (~0.02%), 2-fold increase
- G181V (~0.4%), no increase
- K182I (~0.1%), 4.5-fold increase
- Q183E (~4%), 2.4-fold increase
- Q183P (~0.02%), 2-fold increase
- F186L (~0.08%), 2-fold increase

#### Positions between 243-253 (N5 loop: 246 to 260)

- 243 & 244: deletions (A243-,L244-) occur simultaneously at both these positions in XBC\* lineages (~0.1%, 1.8-fold increase)
- 245: H245N, H245Y (0.9% and 0.1% respectively, no increase)
- 247: S247N (0.2%, 1.7-fold increase, BF\*)

- 248: Y248- (0.1%, 1.6-fold increase)
- 251: P251S/L/H (0.03%, 0.2%, 0.1% ; 3-, 2.4, 1.5-fold increase)
- 252: G252V (2.6%, 3-fold increase)
- 253: G253G (0.7%, 3-fold increase)
- 255: S255P, S255F (0.05% and 0.8%, 2.5-fold and 1-fold respectively)
- 257: G257S and G257D found in BA.2.75 and BA.2.3.20\*

#### **DELTA (B.1.617.2 and AY sub-lineages)**

- 16 Delta genomes in November

#### **World (other VOIs)**

- 1 Alpha genome in November (in Canada)
- 1 Beta genome in November (in South Africa)

#### **World – Recombinants**

- **XBB** - 3703 sequences in November so far; 1789 sequences in October
- **XBB.1** - 1081 sequences in November so far; 1674 sequences in October
- **XBB.2** - 141 sequences in November so far; 212 sequences in October
- **XBB.3** - 60 sequences in November so far; 261 sequences in October
- **XAZ** - 44 sequences in November so far; 247 sequences in October
- **XBD** - 32 sequences in November so far; 83 sequences in October
- **XBB.1.1** - 28 sequences in November so far; 145 sequences in October
- **XBB.4** - 17 sequences in November so far; 22 sequences in October
- **XBB.1.3** - 4 sequence in November so far; 7 sequences in October
- **XBE** - 3 sequences in November so far; 52 sequences in October
- **XBC** - 3 sequences in November so far; 15 sequences in October
- **XBB.5** - 2 sequences in November so far; 13 sequences in October
- **XAV** - 1 sequence in November so far; 3 sequences in October

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

- [Japan Logs 847,371 New COVID-19 Cases in Past Week](#)
- ['A huge burden': L.A. hospitals strained by COVID surge, very bad flu season](#)
- [Omicron subvariants that more easily dodge immunity are causing more than 70% of U.S. infections](#)
- [US flu surge continues amid jump in COVID activity](#)
- [China medical expert says COVID has mutated, should be renamed - state media](#)
- [Meta-analysis estimates 29% vaccine effectiveness against long COVID](#)
- [Duration of viral shedding of the Omicron variant in asymptomatic and mild COVID-19 cases from Shanghai, China](#)
- [Alpha to Omicron: Disease Severity and Clinical Outcomes of Major SARS-CoV-2 Variants](#)
- [BA.2 and BA.5 omicron differ immunologically from both BA.1 omicron and pre-omicron variants](#)
- Neutralising antibody potency against SARS-CoV-2 wild-type and omicron BA.1 and BA.4/5 variants in patients with inflammatory bowel disease treated with infliximab and vedolizumab after three doses of COVID-19 vaccine (CLARITY IBD)

- [Efficacy of Antiviral Agents against Omicron Subvariants BQ.1.1 and XBB](#)

### **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.

<b>Name</b>	<b>number</b>	<b>Github#</b>	<b>Lineage 1</b>	<b>Lineage 2</b>	<b>Location first detected</b>
<a href="#">XA</a>	45	NA	B.1.1.7	B.1.177	UK
<a href="#">XB</a>	3435	<a href="#">#189</a>	B.1.634	B.1.631	N. America
<a href="#">XC</a>	25	<a href="#">#263</a>	Delta (AY.29)	B.1.1.7	Japan
<a href="#">XD</a>	33	<a href="#">#444</a>	Delta (AY.4)	BA.1	France
<a href="#">XE</a>	2836	<a href="#">#454</a>	BA.1	BA.2	UK
<a href="#">XF</a>	34	<a href="#">#445</a>	Delta	BA.1	UK
<a href="#">XG</a>	479	<a href="#">#447</a>	BA.1	BA.2	Denmark
<a href="#">XH</a>	174	<a href="#">#448</a>	BA.1	BA.2	Denmark
<a href="#">XJ</a>	256	<a href="#">#449</a>	BA.1	BA.2	Finland
<a href="#">XK</a>	25	<a href="#">#460</a>	BA.1	BA.2	Belgium
<a href="#">XL</a>	120	<a href="#">#464</a>	BA.1	BA.2	UK
<a href="#">XM</a>	526	<a href="#">#472</a>	BA.1.1	BA.2	Multiple EU
<a href="#">XN</a>	288	<a href="#">#480</a>	BA.1	BA.2	UK
<a href="#">XP</a>	57	<a href="#">#481</a>	BA.1.1	BA.2	UK
<a href="#">XQ</a>	145	<a href="#">#468</a>	BA.1.1	BA.2	UK
<a href="#">XR</a>	183	<a href="#">#469</a>	BA.1.1	BA.2	UK
<a href="#">XS</a>	60	<a href="#">#471</a>	Delta	BA.1.1	USA
<a href="#">XT</a>	17	<a href="#">#478</a>	BA.2	BA.1*	S. Africa
<a href="#">XU</a>	16	<a href="#">#522</a>	BA.1*	BA.2	India
<a href="#">XV</a>	42	<a href="#">#463</a>	BA.1*	BA.2*	Denmark
<a href="#">XW</a>	195	<a href="#">#591</a>	BA.1*	BA.2*	JP, DE, SI, CA, UK, US

<a href="#">XY</a>	126	<a href="#">#606</a>	BA.1*	BA.2*	FR, IL, UK, US
<a href="#">XZ</a>	217	<a href="#">#636</a>	BA.2*	BA.1*	Multiple
XAA	104	<a href="#">#664</a>	BA.1*	BA.2*	US, IL
XAB	114	<a href="#">#665</a>	BA.1*	BA.2*	IT, FR, DE, CH, DK
XAC	207	<a href="#">#590</a>	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
XAD	99	<a href="#">#607</a>	BA.2*	BA.1*	CZ,DE,UK
XAE	133	<a href="#">#637</a>	BA.2*	BA.1*	CA,US,NL,CH
XAF	301	<a href="#">#676</a>	BA.1*	BA.2*	CR
XAG	423	<a href="#">#709</a>	BA.1.1	BA.2.23	BR
XAH	169	<a href="#">#755</a>	BA.2*	BA.1*	SI
XAJ	106	<a href="#">#826</a>	BA.2.12.1	BA.4	UK
XAK	149	<a href="#">#823</a>	BA.1*	BA.2*	DE
XAL	122	<a href="#">#757</a>	BA.1.1	BA.2*	DE
XAM	547	<a href="#">#759</a>	BA.1.1	BA.2.9	Panama
XAN	213	<a href="#">#771</a>	BA.2*	BA.5.1	Multiple
XAP	81	<a href="#">#789</a>	BA.2*	BA.1*	US
XAQ	4	<a href="#">#798</a>	BA.1*	BA.2*	Canada
XAR	10	<a href="#">#860</a>	BA.1*	BA.2*	Reunion/France
XAS	190	<a href="#">#882</a>	BA.5*	BA.2*	N. America
XAT	27	<a href="#">#885</a>	BA.2.3.13	BA.1*	Japan
XAU	43	<a href="#">#894</a>	BA.1.1*	BA.2.9*	Multiple
XAV	80	<a href="#">#911</a>	BA.2*	BA.5*	France
XAW	45	<a href="#">#895</a>	BA.2*	AY.122	Russia
XAY*	72	<a href="#">#844</a>	BA.2	AY.45	S. Africa
XAZ	2308	<a href="#">#797</a>	BA.2.5, BA.5	BA.2.5	Multiple
XBA	3	<a href="#">#844</a>	AY.45	BA.2	S. Africa
XBB*	12582	<a href="#">#1058</a>	BJ.1	BM.1.1.1	Singapore/US
XBC*	398	<a href="#">#1100</a>	Delta	BA.2	Philippines
XBD	411	<a href="#">#1137</a>	BA.2.75.2	BF.5	Multiple
XBE*	5429	<a href="#">#1246</a>	BA.5.2	BE.4	USA
XBF	843	<a href="#">#1259</a>	BA.5.2.3	CJ.1	Australia
XBG	50	<a href="#">#896</a>	BA.2.76	BA.5.2	UK



XBH	~100	<a href="#">#1229</a>	BA.2.3.17	BA.2.75.2	Multiple
XBJ	~25	#1268	BA.2.3.20	BA.5.2	Multiple

**Newly designated Pango lineages:**

Few new lineages designated this week:

- [DJ.1.2: DJ.1 sublineage with S:N460K \(and multiple AA substitutions\) emerged in Peru](#)
- [BQ.1.1.25: BQ.1.18 with S:Y144-, S:F490S and N:G30- in New York](#)