

BV-BRC SARS-CoV-2 Emerging Variant Report January 10, 2023

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20230110.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 1/7/2023 in the US in order of prevalence (note that the Nowcast estimates are sensitive to sampling bias and updates to the PANGO annotations):
 - *XBB.1.5 has rapidly emerged and become one of the predominant variants over the last month and is currently estimated at 27.6% in the U.S., a significant rise from previous weeks*
 - **BQ.1.1** is currently estimated at 34.4%, essentially flat from previous weeks
 - **BQ.1** is currently estimated at 21.4%, down from 24.1% in December
 - **BA.5** is currently estimated at 3.7%, down from 6.5% in December
 - The original **XBB** is currently estimated at 4.9%, essentially flat from previous weeks
 - **BN.1** is currently estimated at 3.0%, essentially flat from previous weeks
 - **BF.7** is currently estimated at 2.2%, essentially flat from previous weeks
 - **BA.2.75** is currently estimated at 1.3%, essentially flat from previous weeks
 - **BA.5.2.6** is currently estimated at 0.7%, down from 1.0% in December
 - **BA.4.6** is currently estimated at 0.2%, down from 0.6% in December
- **XBB.1.5**
 - *Appears to have emerged in the northeastern U.S. (NY & CT) in October 2022*
 - *Recombinant between two different BA.2 subvariants - BJ.1 and BA.2.75*
 - *Has an F486P substitution in S instead of the F486S found in the S of XBB*
 - *Likely founder differs from ancestral Wuhan 1 by the following substitutions in S:*
 - *T19I,L24-,P25-,P26-,A27S,V83A,G142D,Y144-,H146Q,Q183E,V213E,G339H,R346T,L368I,S371F,S373P,S375F,T376A,D405N,R408S,K417N,N440K,V445P,G446S,N460K,S477N,T478K,E484A,F486P,F490S,Q498R,N501Y,Y505H,D614G,H655Y,N679K,P681H,N764K,D796Y,Q954H,N969K*
 - Note that the*

- *The XBB.1.5 sub-lineage predominant in December has also acquired the G252V substitution*
- *Note that the Y144-, H146Q annotation from GISAID is equivalent to Y145Q, H146- at the amino acid level; the latter is probably the correct translation from the nucleotide sequence*
- *The F486P substitution likely increases affinity for ACE2 receptor*
- *Neutralization of XBB and XBB.1 (and likely XBB.1.5) by sera from vaccinees and infected persons was markedly impaired - <https://www.biorxiv.org/content/10.1101/2022.11.23.517532v1.full.pdf>*
- *Monoclonal antibodies capable of neutralizing the original Omicron variant, including those with Emergency Use Authorization, were largely inactive against the XBB and XBB.1 subvariants (and likely XBB.1.5) - <https://www.biorxiv.org/content/10.1101/2022.11.23.517532v1.full.pdf>*
- **XBB**
 - *Likely founder differs from ancestral Wuhan 1 by the following substitutions in S: T19I,L24-,P25-,P26-,A27S,V83A,G142D, Y144-,H146Q,Q183E,V213E,G339H,R346T,L368I,S371F,S373P,S375F,T376A,D405N,R408S,K417N,N440K,V445P,G446S,N460K,S477N,T478K,E484A,F486S,F490S,Q498R,N501Y,Y505H,D614G,H655Y,N679K,P681H,N764K,D796Y,Q954H,N969K*
 - *The XBB sub-lineage predominant in December has acquired the additional G252V substitution*
 - *Note that the Y144-, H146Q annotation from GISAID is equivalent to Y145Q, H146- at the amino acid level; the latter is probably the correct translation from the nucleotide sequence*
- Based on BV-BRC analysis of comprehensive data from GISAID, listed below are lineages with sequence prevalence >2.0% or a growth rate >3 fold and count >30 in December so far (ranked in order of sequence prevalence). Lineages with fold growth >3 from November to December so far are highlighted in ***bold italic***:
 - ***BQ.1.1*** - 17%, 1.5 fold growth
 - ***BQ.1*** – 8.8%, 1.1 fold growth
 - ***XBB.1.5*** – 6.3%, 9.4 fold growth
 - ***BA.2.75*** – 4.0%, 1.1 fold growth
 - ***XBB.1*** – 2.7%, 1.5 fold growth
 - ***BQ.1.1.22*** – 2.5%, 2.6 fold growth
 - ***BQ.1.1.4*** – 2.4%, 1.5 fold growth
 - ***BQ.1.1.5*** – 2.0%, 1.4 fold growth
 - ***BQ.1.3*** – 2.0%, 1.2 fold growth
 - ***XBB*** - 0.93%, 3.4 fold growth
 - ***BA.2*** - 0.29%, 3.2 fold growth (*Note, the majority of these are misclassified by GISAID as XBB* genomes by GISAID*)
 - ***BE.9*** - 0.1%, 3.3 fold growth

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

- ~~One?~~ Delta sequence in the US in December; six in November

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

- None

USA – Recombinants

- **XBB.1.5** - 2989 sequences in December; 541 sequences in November
- **XBB.1** - 1267 sequences in December; 1442 sequences in November
- **XBB** - 442 sequences in December; 221 sequences in November
- **XBB.2** - 278 sequences in December; 470 sequences in November
- **XBB.3** - 53 sequences in December; 101 sequences in November
- **XBB.4** - 23 sequences in December; 13 sequences in November
- **XBB.1.1** - 16 sequences in December; 66 sequences in November
- **XBD** - 9 sequences in December; 42 sequences in November
- **XBB.1.3** - 3 sequences in December; 6 sequences in November
- **XBB.1.4** - 7 sequences in December; 6 sequences in November
- **XBF** - 3 sequences in December; 2 sequences in November
- **XBC.1** - 6 sequences in December; 20 sequences in November
- **XBJ** - 3 sequences in December; 13 sequences in November
- **XBB.3.1** - 2 sequences in December; 2 sequences in November
- **XBG** - 1 sequence in December; 3 sequences in November
- **XAY.1** - 1 sequence in December; 5 sequences in November
- **XBE** - 1 sequence in December; 19 sequences in November

World – VOC

OMICRON

- Omicron remains dominant globally. Listed below are lineages showing the highest sequence prevalence (> 2.0%) or a fold growth > 3 fold and count >50 in December so far. Lineages with fold growth >3 from November to December are highlighted in ***bold italic***:
 - **BQ.1.1** - 15%, 1.5 fold growth
 - **BA.2.75** – 7.4%, 1.3 fold growth
 - **BQ.1** – 4.7%, 1.2 fold growth
 - **BF.7** – 3.7%, 0.80 fold growth
 - **BQ.1.1.22** – 3.1%, 2.6 fold growth
 - **BA.5.2** – 2.9%, 0.40 fold growth
 - **XBB.1** – 2.8%, 1.1 fold growth
 - ***XBB.1.5 – 2.4%, 11 fold growth***
 - **BA.5.2.1** – 2.3%, 0.39 fold growth
 - **CH.1.1** – 2.1%, 2.8 fold growth
 - **BQ.1.1.18** – 2.1%, 1.4 fold growth
 - ***BQ.1.1.20 – 1.4%, 3.6 fold growth***
 - ***BQ.1.1.10 - 0.38%, 3.2 fold growth***
 - ***XAY.2 - 0.16%, 5.3 fold growth***
 - ***BQ.1.21 - 0.1%, 3.3 fold growth***
 - ***CJ.1 - 0.04%, 4 fold growth***
- Substitutions in spike that we are monitoring (>3 fold growth from November to December with counts >50) include those listed below (but note that the numbers are still relatively

small for some of these). Substitutions with sequence prevalence >1.0% in December so far are highlighted in ***bold italic***:

- F456L - 0.05%, 5 fold growth
- Q52H - 0.05%, 5 fold growth
- Y248D - 0.05%, 5 fold growth
- R21G - 0.18%, 4.5 fold growth
- ***F486P – 3.8%, 4.3218 fold growth***
- K1149R - 0.04%, 4 fold growth
- L18F - 0.19%, 3.8 fold growth
- T19R - 0.19%, 3.8 fold growth
- V1133A - 0.07%, 3.5 fold growth
- F186L - 0.22%, 3.1429 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 two months (November and December 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
- ***Details about these NTD substitutions can be found in previous reports***

DELTA (B.1.617.2, AY sub-lineages and some X recombinants)

- 255 Delta genomes in December (mostly XAY.2 in Denmark)

World (other VOIs)

- none in December

World – Recombinants (count >5 in December)

- **XBB.1** - 3942 sequences in December; 6871 sequences in November
- **XBB.1.5** - 3357 sequences in December; 577 sequences in November
- **XBB** - 1157 sequences in December; 1089 sequences in November
- **XBB.2** - 898 sequences in December; 2467 sequences in November
- **XBB.1.4.1** - 304 sequences in December; 301 sequences in November
- **XAY.2** - 231 sequences in December; 92 sequences in November
- **XBC.1** - 182 sequences in December; 260 sequences in November
- **XBB.1.1** - 144 sequences in December; 367 sequences in November
- **XBB.3** - 117 sequences in December; 401 sequences in November
- **XBB.1.4** - 86 sequences in December; 110 sequences in November
- **XBF** - 36 sequences in December; 29 sequences in November
- **XBB.4** - 32 sequences in December; 102 sequences in November
- **XBD** - 25 sequences in December; 98 sequences in November
- **XBJ** - 21 sequences in December; 40 sequences in November
- **XBG** - 15 sequences in December; 51 sequences in November

- **XAY.1** - 11 sequences in December; 14 sequences in November
- **XAZ** - 11 sequences in December; 71 sequences in November
- **XBB.3.1** - 10 sequences in December; 8 sequences in November
- **XAY.1.1** - 7 sequences in December; 2 sequences in November
- **XBB.1.3** - 5 sequences in December; 15 sequences in November

China

- Data from China is somewhat limited; only 590 sequences reported in December
- The proportion of the currently circulating lineages in China are quite different from the rest of the world:
 - **BA.5.2** - 33%, 1.3 fold growth
 - **BF.7** - 31%, 1.2 fold growth
 - **BQ.1.1** – 5.3%, 0.58 fold growth
 - **BA.2.75** – 3.4%, 0.67 fold growth
 - **BA.5.2.1** – 2.7%, 0.80 fold growth
 - **XBB.1** – 2.0%, 0.60 fold growth
 - **BQ.1** – 1.9%, 0.66 fold growth
 - **BA.2** – 1.7%, 1 fold growth

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

- [Coronavirus variant XBB.1.5 rises in the United States — is it a global threat?](#)
- [Child Mortality in England During the First 2 Years of the COVID-19 Pandemic](#)
- [Full protection from SARS-CoV-2 brain infection and damage in susceptible transgenic mice conferred by MVA-CoV2-S vaccine candidate](#)
- [Bivalent mRNA vaccine improves antibody-mediated neutralization of many SARS-CoV-2 Omicron lineage variants](#)
- [Antibodies to Severe Acute Respiratory Syndrome Coronavirus 2 \(SARS-CoV-2\) in All of Us Research Program Participants, 2 January to 18 March 2020](#)
- [COVID-19 vaccine induced myocarditis in young males: A systematic review](#)
- [Association between COVID-19 and consistent mask wearing during contact with others outside the household—A nested case-control analysis, November 2020–October 2021](#)
- Enhanced transmissibility of XBB.1.5 is contributed by both strong ACE2 binding and antibody evasion

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-XBK 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	33	#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	256	#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	17	#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	49	#636	BA.2*	BA.1*	Multiple
XAA	965	#664	BA.1*	BA.2*	US, IL
XAB	131	#665	BA.1*	BA.2*	IT, FR, DE, CH, DK
XAC	16	#590	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US

XAD	51	#607	BA.2*	BA.1*	CZ,DE,UK
XAE	6	#637	BA.2*	BA.1*	CA,US,NL,CH
XAF	39	#676	BA.1*	BA.2*	CR
XAG	35	#709	BA.1.1	BA.2.23	BR
XAH	88	#755	BA.2*	BA.1*	SI
XAJ	273	#826	BA.2.12.1	BA.4	UK
XAK	96	#823	BA.1*	BA.2*	DE
XAL	2	#757	BA.1.1	BA.2*	DE
XAM	51	#759	BA.1.1	BA.2.9	Panama
XAN	167	#771	BA.2*	BA.5.1	Multiple
XAP	173	#789	BA.2*	BA.1*	US
XAQ	3	#798	BA.1*	BA.2*	Canada
XAR	70	#860	BA.1*	BA.2*	Reunion/France
XAS	633	#882	BA.5*	BA.2*	N. America
XAT	20	#885	BA.2.3.13	BA.1*	Japan
XAU	21	#894	BA.1.1*	BA.2.9*	Multiple
XAV	131	#911	BA.2*	BA.5*	France
XAW	48	#895	BA.2*	AY.122	Russia
XAY*	395	#844	BA.2	AY.45	S. Africa
XAZ	2166	#797	BA.2.5, BA.5	BA.2.5	Multiple
XBA	1	#844	AY.45	BA.2	S. Africa
XBB*	22673	#1058	BJ.1	BM.1.1.1	Singapore/US
XBC*	650	#1100	Delta	BA.2	Philippines
XBD	502	#1137	BA.2.75.2	BF.5	Multiple
XBE*	6725	#1246	BA.5.2	BE.4	USA
XBF	1854	#1259	BA.5.2.3	CJ.1	Australia
XBG	125	#896	BA.2.76	BA.5.2	UK
XBH	~128	#1229	BA.2.3.17	BA.2.75.2	Multiple
XBJ	~247	#1268	BA.2.3.20	BA.5.2	Multiple
XBK	~50	#1381	CJ.1	BA.5.2	Denmark

Newly designated Pango lineages last week (<https://github.com/cov-lineages/pango-designation/milestones>):

- [BA.5.2.49](#)

- [XBB.1.5](#)
- [BM.1.1.4](#)
- [BN.1.4.1](#)
- [XBM](#)
- [BA.2.3.22](#)
- [CK.1.2](#)
- [CM.12](#)
- [BQ.1.1.34](#)
- [DT.1](#)
- [CM.11](#)
- [XBL](#)
- [BF.7.15](#)
- [CH.1.1.4](#)
- [BL.6](#)
- [XBB.1.8](#)
- [BA.5.2.48](#)
- [BF.7.14](#)