

BV-BRC SARS-CoV-2 Emerging Variant Report October 4, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20221004.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**, with **BA.2.12.1** displaced by **BA.5** and **BA.4** and their sub-lineages.
 - The CDC Nowcast for the week ending 10/01/22 estimates that **BA.5** proportions are now dominating in the United States at 81.3% (95% PI: 79.6-83.0%). Significant regional differences exist: <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>.
 - The CDC Nowcast has split BA.4 and BA.4.6; estimates for **BA.4** proportions are now at 1.1% (95% PI: 1.0-1.2%); estimates for **BA.4.6** proportions are now at 12.8% (95% PI: 11.5-14.1%)
 - **BF.7 has been added to the Nowcast tracker and is currently estimated at 3.4% (95% PI: 2.6-4.4%)**
 - **BA.2.75 has been added to the Nowcast tracker and is currently estimated at 1.4% (95% PI: 1.1-1.9%)**
- Lineages with sequence prevalence >0.5% or a growth rate >3 fold in September are (ranked in order of sequence prevalence):
 - **BA.5.2.1** - 24%, 0.91 fold growth
 - **BA.5.2** - 18%, 1.2 fold growth
 - **BA.5.1** - 12%, 0.96 fold growth
 - **BA.4.6** – 9.9%, 1.6 fold growth
 - **BA.5.6** – 4.0%, 0.73 fold growth
 - **BA.5.5** – 3.8%, 0.57 fold growth
 - **BF.10** – 3.0%, 0.98 fold growth
 - **BA.5** – 2.2%, 0.99 fold growth
 - **BE.1.1** – 1.8%, 1.5 fold growth
 - **BF.5** – 1.8%, 1.1 fold growth
 - **BE.1** – 1.6%, 0.81 fold growth
 - **BA.4.1** – 1.4%, 0.47 fold growth

- **BA.5.1.1** – 1.3%, 0.76 fold growth
 - **BF.7** – 1.1%, 2.7 fold growth
 - **BE.3** - 0.96%, 0.74 fold growth
 - **BA.5.1.10** - 0.91%, 0.95 fold growth
 - **BA.2.75** - 0.58%, 2.6 fold growth
 - **BF.8** - 0.54%, 0.68 fold growth
 - **BA.5.2.6** - 0.45%, **4.1 fold growth**
 - **BA.5.2.7** - 0.1%, **3.3 fold growth**
 - **BF.14** - 0.06%, **6 fold growth**
- Notable substitutions present within the top ten BA.5.x sub-lineages in the US in September:
 - One **BA.5** sub-lineage carries the T76I substitution (BA.5.5)
 - Two **BA.5** sub-lineages carry the R346T substitution (BA.5.1.10)
 - Notable substitutions present within the top five BA.4.x sub-lineages in the US in September so far:
 - One **BA.4** sub-lineage carries the R346T and N658S substitutions (most prevalent)
 - One **BA.4** sub-lineage carries the V3G substitution only
 - One **BA.4** sub-lineage carries the V3G and R346T substitutions
 - One **BA.4** sub-lineage carries the N658S substitution only
 - One **BA.4** sub-lineage carries the R346T and N658S and lacks the N440K substitution
 - Several Omicron sub-lineages appear to carry a recurring mutation at position 346 in the S protein (S:R346T in **BA.4.6**, **BF.7**, **BA.5.1**, **BA.5.2.6**, **BF.11**, **BA.5.2.1**; S:R346S in **BF.13**, **BA.5.2**, **BA.5.2.1**; or S:R346I in **BA.5.9**, **BA.5.2**)
 - Two Omicron sub-lineages appear to carry a recurring mutation at position 444 in the S protein (K444T in **BE.1.1** with a 15 fold growth rate and K444R in **BA.5.2.1** with a 1.6 fold growth rate in September)
 - At least 4 Omicron sublineages carry a recurring mutation at position 445, V445A (**BA.5.2.1** – 2.5 fold growth, **BA.5.2** – 9 fold growth, **BA.5.1.12** – 4 fold growth in September)
 - At least 4 Omicron sublineages carry a recurring mutation at position 446, G446S (**BA.2.75** – 5 fold growth, **BA.5.2** – 4 fold growth, **BA.5.1** – 2 fold growth in September). G446D also occurs in BA.5.2 and BA.5.2.1 (2 fold growth in September).
 - At least 4 Omicron sublineages carry a recurring mutation at position 460, N460K (**BE.1**– 14.5 fold growth, **BA.5.2.7** – 4 fold growth in September). N460KS also occurs in small numbers in BA.5 and BA.4.6.

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

- Four Delta sequences in the US in September

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

- One Alpha sequence in the US in September. This genome appears to 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).

USA – Recombinants

- **XAJ** – 5 sequences in the US in August; 1 in September
- **XAS** – 5 sequences in the US in August; none in September

- **XAN** –three in August; none in September so far
- **XY** – one in August; none in September so far
- See a summary of recombinant lineages at the end of this report.

World – VOC

OMICRON

- Omicron remains dominant globally, with the following lineages showing the highest sequence prevalence (> 0.5%) or growth rate >3 fold in September:
 - **BA.5.2** - 22%, 1.0 fold growth
 - **BA.5.2.1** - 18%, 0.91 fold growth
 - **BA.5.1** - 14%, 0.87 fold growth
 - **BA.4.6** – 5.6%, 1.6 fold growth
 - **BE.1.1** – 3.4%, 1.1 fold growth
 - **BF.5** – 3.1%, 0.96 fold growth
 - **BF.7** – 3.0%, 2.9 fold growth
 - **BA.5.6** – 2.0%, 0.73 fold growth
 - **BA.5** – 1.7%, 0.99 fold growth
 - **BA.5.5** – 1.7%, 0.58 fold growth
 - **BE.1** – 1.5%, 0.78 fold growth
 - **BF.10** – 1.5%, 0.95 fold growth
 - **BA.2.75** – 1.1%, 1.7 fold growth
 - **BA.4.1** - 0.94%, 0.47 fold growth
 - **BA.5.1.10** - 0.76%, 1.0 fold growth
 - **BA.5.1.1** - 0.62%, 0.70 fold growth
 - **BA.5.2.3** - 0.58%, 1.2 fold growth
 - **BA.5.3.1** - 0.57%, 0.89 fold growth
 - **BA.5.9** - 0.53%, 1.77 fold growth
 - **BA.5.1.5** - 0.53%, 1.4 fold growth
 - **BA.5.2.6** - 0.52%, **4.3 fold growth**
 - **BA.5.1.2** - 0.5%, 0.98 fold growth
 - **BF.14** - 0.33%, **3 fold growth**
 - **BA.2.75.5** - 0.04%, **4 fold growth**
- A **BA.2.3** sublineage (designated **BA.2.3.20**, not yet updated in GISAID) has several additional spike mutations (BA.2.3 + M153T, N164K, H245N, G257D, K444R, N450D, L452M, N460K, E484R, and a R493Q reversion) and has increased in September (n=80) compared to August (n=12) in several countries. Singapore: an increase from n=3/1566 (0.2%) to 24/617 (4%) ~19 fold. Denmark: from 0/13550 to 19/8583 genomes in September. USA: from n=6/123781 (0.005%) to n=8/26214 (0.03%) 6-fold increase. Austria: from n=0/13861 (0%) to n=10/4920 (0.2%). Canada: 0/14793 (0%) to 9/3274 (0.27%). Australia 3/7439 (0.04%) to 6/1161 (0.5%) 13-fold increase.
- Notable substitutions present within the top ten **BA.5** sub-lineages globally in September so far:
 - One **BA.5** sub-lineage carries the T76I substitution only

- One **BA.5** sub-lineage carries the R346T substitution only
- Notable substitutions present within the top five **BA.4** sub-lineages globally in September so far:
 - One **BA.4** sub-lineage (the most prevalent) carries the R346T and N658S substitutions (**BA.4.6**)
 - One **BA.4** sub-lineage carries the V3G substitution only
 - One **BA.4** sub-lineage carries the R346T and N658S substitutions and lacks the N440K substitution
 - One **BA.4** sub-lineage carries the V3G and R346T substitutions
 - One **BA.4** sub-lineage carries the N658S substitution only
- Substitutions in spike that we are monitoring (>3 fold growth from August to September with counts >10) include the following (but note that the numbers are still relatively small for most of these):
 - **M153T** - 0.16%, 8 fold growth
 - **H245N** - 0.16%, 8 fold growth
 - **V445P** - 0.07%, 7 fold growth
 - **G257D** - 0.16%, 5.3 fold growth
 - **D1163H** - 0.04%, 4 fold growth
 - **D80G** - 0.04%, 4 fold growth
 - **G252V** - 0.04%, 4 fold growth
 - **K1073N** - 0.08%, 4 fold growth
 - **K444T** - **1.1%**, 3.9 fold growth
 - **F490S** - 0.21%, 3.5 fold growth
 - **L368I** - 0.07%, 3.5 fold growth
 - **P272L** - 0.07%, 3.5 fold growth
 - **P209L** - 0.06%, 3 fold growth
 - **A1174V** - 0.03%, 3 fold growth
 - **A260V** - 0.03%, 3 fold growth
 - **A684S** - 0.03%, 3 fold growth
 - **D568N** - 0.03%, 3 fold growth
 - **G257V** - 0.03%, 3 fold growth
 - **G75A** - 0.06%, 3 fold growth
 - **I666V** - 0.03%, 3 fold growth
 - **K97T** - 0.0003%, 3 fold growth
 - **M740I** - 0.03%, 3 fold growth
 - **N148** - 0.03%, 3 fold growth
 - **N460Y** - 0.03%, 3 fold growth
 - **R237K** - 0.03%, 3 fold growth
 - **A522P** - 0.03%, 3 fold growth
 - **P681R** - 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.

“[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)

- 22 Delta isolates globally in September

World (other VOIs)

- One Alpha genome in September (in US)
- One Beta genome in September (in Germany)

World – Recombinants

- XAN – 4 in September
- XAK – 2 in September
- XAJ – 1 in September

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

- Updated data from Yunlong Cao on multiple variants’ immune and antiviral escape: BU.1, BR.2, BM.1.1.1, CA.1, XBB, BA.2.3.20, BN.1, BA.2.10.4, BN.2.1, BA.4.6.1, BQ.1, BQ.1.1
https://twitter.com/yunlong_cao/status/1577343549120872448
<https://www.biorxiv.org/content/10.1101/2022.09.15.507787>
- [The level of coronavirus in Eastern Mass. waste water just shot up](#)
- [Big COVID-19 waves may be coming, new Omicron strains suggest](#)
- [Latest Covid surge a ‘heavy straw on camel’s back’ for every hospital in UK](#)
- [Covid infections rise by 14% in a week in UK](#)
- [Germany warns of rise in COVID-19 cases going into fall](#)
- [Effectiveness of mRNA-1273 against infection and COVID-19 hospitalization with SARS-CoV-2 Omicron subvariants: BA.1, BA.2, BA.2.12.1, BA.4, and BA.5](#)
- [LA County reports 2,600 new COVID infections for three-day period](#)
- [Dutch Covid hospital total and coronavirus infections both doubled in about 2 weeks](#)
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Recombinant lineages:

Two new recombinant lineages have been added this week: XBA and XBB. 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-XBB 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.

		Github#	Lineage 1	Lineage 2	
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Name	number				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	2828	#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	18	#460	BA.1	BA.2	Belgium
XL	119	#464	BA.1	BA.2	UK
XM	558	#472	BA.1.1	BA.2	Multiple EU
XN	214	#480	BA.1	BA.2	UK
XP	57	#481	BA.1.1	BA.2	UK
XQ	143	#468	BA.1.1	BA.2	UK
XR	181	#469	BA.1.1	BA.2	UK
XS	60	#471	Delta	BA.1.1	USA
XT	13	#478	BA.2	BA.1*	S. Africa
XU	17	#522	BA.1*	BA.2	India
XV	42	#463	BA.1*	BA.2*	Denmark
XW	190	#591	BA.1*	BA.2*	JP, DE, SI, CA, UK, US
XY	126	#606	BA.1*	BA.2*	FR, IL, UK, US
XZ	212	#636	BA.2*	BA.1*	Multiple
XAA	100	#664	BA.1*	BA.2*	US, IL
XAB	114	#665	BA.1*	BA.2*	IT, FR, DE, CH, DK
XAC	206	#590	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
XAD	93	#607	BA.2*	BA.1*	CZ,DE,UK
XAE	132	#637	BA.2*	BA.1*	CA,US,NL,CH
XAF	291	#676	BA.1*	BA.2*	CR

XAG	373	#709	BA.1.1	BA.2.23	BR
XAH	166	#755	BA.2*	BA.1*	SI
XAJ	102	#826	BA.2.12.1	BA.4	UK
XAK	140	#823	BA.1*	BA.2*	DE
XAL	124	#757	BA.1.1	BA.2*	DE
XAM	519	#759	BA.1.1	BA.2.9	Panama
XAN	91	#771	BA.2*	BA.5.1	Multiple
XAP	81	#789	BA.2*	BA.1*	US
XAQ	81	#798	BA.1*	BA.2*	Canada
XAR	53	#860	BA.1*	BA.2*	Reunion/France
XAS	76	#882	BA.5*	BA.2*	N. America
XAT	76	#885	BA.2.3.13	BA.1*	Japan
XAU	77	#894	BA.1.1*	BA.2.9*	Multiple
XAV	60	#911	BA.2*	BA.5*	France
XAW	5	#895	BA.2*	AY.122	Russia
XAY	8	#844	BA.2	AY.45	S. Africa
XAZ	974	#797	BA.2.5, BA.5	BA.2.5	Multiple
XBA	4	#844	AY.45	BA.2	S. Africa
XBB	8	#1058	BJ.1	BM.1.1.1	Singapore/US
XBC	7	#1100	Delta	BA.2	Philippines

Newly designated Pango lineages:

New lineages designated this week:

- [BE.4, BE.4.1, BE.4.1.1](#): BA.5.3.1 with S:346T and S:209L [50 seqs], sublineage with S:444R
- [BF.26](#): BA.5.2.1 + ORF1b:G376S, mostly Sweden and US
- [BF.27](#): BA.5.2.1 + ORF1a:A2784V: mostly Singapore
- [BF.28](#): BA.5.2.1 + ORF1a:Q44L: mostly Europe
- [BA.2.75.9 & CB.1](#): BA.2.75 branch with nuc:17679T that acquired first S:346T, then S:486V
- [BS.1.1](#): BS.1 lineage with S:K356T
- [BA.5.1.22-BA.5.1.25](#): Collection of undesignated BA.5.1 diversity
- [BA.5.2.26-BA.5.2.28](#): Collection of large BA.5.2 diversity
- [BA.5.2.25](#): Big sublineage of BA.5.2 Orf1b:1050N with S:K444T (71 sequences) with high prevalence in Guinea
- [CG.1](#); New BA.5.2 + Orf1b:T1050N sublineage with S:K444M and Orf1a:S1520F (81 sequences)
- [XBC.1](#): XBC with S:L452M, ORF1a:S391F (6 seq. Philippines, USA, South Korea)

Variants being monitored by various public health agencies:

No new variants added to lists monitored by public health agencies.

The latest summary table for all agencies can be found here:

<https://docs.google.com/spreadsheets/d/1mAgO2wRjyEyGtL-SBe3NgOjUk7a5nZTeKmSorVkaHSU/edit#gid=0>