

BV-BRC SARS-CoV-2 Emerging Variant Report July 19, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20220719.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 July 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 to date in June and July are **Omicron**. In the last month, the predominant BA.2 sublineage in the United States, BA.2.12.1, is being displaced by BA.5 and BA.4 lineages.
 - The CDC Nowcast for the week ending 7/16/22 estimates that **BA.5** proportions are now dominating in the United States at 77.9% (95% PI: 75.8-79.9%). Significant regional differences exist: <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>.
 - The CDC Nowcast estimates that **BA.4** proportions are now at 12.8% (95% PI: 11.3-14.4%)
 - The US CDC Nowcast estimates that **BA.2.12.1** proportions are 8.6% (95% PI: 7.9-9.5.0%)
- BA sub-lineages with sequence prevalence > 0.5% in July so far are (ranked in order of sequence prevalence)(note that a major re-organization of PANGO lineage nomenclature has occurred which has impacted some of these data):
 - **BA.2.12.1** - 17%, 0.35 fold growth
 - **BA.5.2.1** - 16%, 2.1 fold growth
 - **BA.5.5** - 10%, 1.4 fold growth
 - **BA.5.1** – 7.6%, **2.5 fold growth**
 - **BA.4.1** – 7.3%, 1.2 fold growth
 - **BA.5.2** – 5.4%, **2.8 fold growth**
 - **BA.5** – 5.2%, **4.0 fold growth**
 - **BA.5.6** – 4.3%, 1.8 fold growth
 - **BA.4** – 4.0%, 1.3 fold growth
 - **BA.2** – 2.6%, 0.36 fold growth
 - **BA.5.1.1** – 2.1%, 2.1 fold growth
 - **BA.4.6** – 1.8%, **2.7 fold growth**

- **BE.3** – 1.6%, 1.9 fold growth
 - **BE.1** – 1.5%, 2.2 fold growth
 - **BF.5** - 0.64%, 2.2 fold growth
 - **BE.1.1** - 0.5%, 2.3 fold growth
- ***In aggregate, BA.5.x sequences constitute 17% of sequences in June and 52% in July so far in the US***
 - ***In aggregate, BA.4.x sequences constitute 5.8% of sequences in June and 14% in July so far in the US***
 - Many sub-lineage variants appear to carry ancestral reversion in comparison to the original Omicron consensus, including inconsistent occurrence of A67V, H69-, V70-, G142D, V143-, Y144-, Y145-, N211-, L212I, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, N764K. However, these changes are likely due to sequencing artifacts caused by inefficient amplification by certain PCR primers affected by Omicron substitutions.
 - Notable substitutions present within the top ten BA.5 sub-lineages in July so far in the US:
 - One **BA.5** sub-lineage (second most prevalent) carries the T76I substitution only
 - One **BA.5** sub-lineage carries the L5F substitution
 - ***One BA.5 sub-lineage carries the Q183L substitution (new)***
 - One **BA.5** sub-lineage carries the T76I and K1073T substitutions
 - Notable substitutions present within the top ten BA.4 sub-lineages in July so far in the US:
 - Two **BA.4** sub-lineages (including the most prevalent) carry the V3G substitution only
 - Two **BA.4** sub-lineages carry the N658S substitution only
 - One **BA.4** sub-lineage carries the N658S and R346T substitutions
 - One **BA.4** sub-lineage carries the V3G and I670V substitutions
 - ***One BA.4 sub-lineage carries the T259A substitution only (new)***
 - One **BA.4** sub-lineage carries the N658S and A701V substitutions
 - Clusters of BA.2.13 and BA.2 genomes from June and July carry the L452M substitution at the same position as L452Q and show growth rates > 1 fold from May and June

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

- No Delta sequences in the US in July so far.

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

- **One B.1.429 (Epsilon) sequence detected in CA in June; notably, Epsilon variants have not been detected in the US since 2021.**

USA – Recombinants

- XE – 2 sequences in the US in July so far
- No other recombinant viruses detected in US
- 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 July so far (note the high relative growth of BA.4, BA.5, BA.5.1 globally):
 - **BA.5.1** - 19%, 1.6 fold growth
 - **BA.5.2.1** - 14%, **2.0 fold growth**
 - **BA.5.2** – 8.8%, **2.0 fold growth**
 - **BA.2.12.1** – 6.4%, 0.27 fold growth
 - **BA.4.1** – 5.6%, 1.1 fold growth
 - **BA.4** – 4.8%, 1.2 fold growth
 - **BA.5** – 3.7%, **2.0 fold growth**
 - **BA.5.5** – 3.4%, 1.0 fold growth
 - **BF.5** – 3.4%, **3.3 fold growth**
 - **BE.1.1** – 3.0%, 1.6 fold growth
 - **BA.2** – 2.9%, 0.25 fold growth
 - **BE.1** – 2.2%, 1.8 fold growth
 - **BA.5.6** – 1.8%, 1.5 fold growth
 - **BA.4.6** – 1.0%, **2.1 fold growth**
 - **BF.1** - 0.75%, 0.99 fold growth
 - **BA.5.1.1** - 0.7%, 1.3 fold growth
 - **BA.5.3.1** - 0.65%, 1.5 fold growth
 - **BA.5.2.3** - 0.59%, **2.5 fold growth**
 - **BE.3** - 0.57%, 1.3 fold growth
- **BA.2.75**: *this sublineage shows a high growth rate in India (98.34 fold), although it is present in 14 other countries, including the United States (CA, IL, NY, NC, WA, WI)..*
- **BA.2.76**: *this sublineage shows a high growth rate globally (9.2 fold) and in several countries (particularly India-4.6 fold). Notable spike substitutions in this variant include Y248N and R346T, both of which occur in antigenically important sites.*
- **BA.2.12.1** and **BA.2.12** *global expansion has slowed in June and July compared to May, giving way to BA.5 and BA.4 lineages and sub-lineages.*
- **BA.5** *has been divided into a number of sub-lineages that show high growth in sequence prevalence*
- **BA.4** *sub-lineages also shows high growth in sequence prevalence*
- Similar issues with variable ancestral reversion that are likely due to sequencing artifacts, as described above for US sequences
- Notable substitutions present within the top ten **BA.5** sub-lineages globally in July so far:
 - One **BA.5** sub-lineage carries the T76I substitution
 - One **BA.5** sub-lineage carries the P1162L substitution
- Notable substitutions present within the top ten **BA.4** sub-lineages globally in July so far (note that any substitutions that appear to revert to ancestral could be due to technical artifacts):
 - Two **BA.4** sub-lineages (including the most prevalent) carry the V3G substitution only
 - One **BA.4** sub-lineage carries the N658S substitution only
 - One **BA.4** sub-lineage carries the N658S and R346T substitutions
 - One **BA.4** sub-lineage carries the V3G and lacks the R408S substitution
 - One **BA.4** sub-lineage carries the V3G and I670V substitutions
 - One **BA.4** sub-lineage lacks the G142G and N440K substitutions

- One **BA.4** sub-lineage carries the V3G and lacks several substitutions around N440K
- One **BA.4** sub-lineage carries the V3G and C1235F substitutions
- Substitutions in spike that we are monitoring (> 5 fold growth May to June) include:
 - **Q183L** - 0.12%, 12 fold growth
 - **N460K** - 0.1%, 10 fold growth
 - **A1020S** – 1.2%, 9.8 fold growth
 - **P1263Q** - 0.09%, 9 fold growth
 - **A829T** - 0.09%, 9 fold growth
 - **W152R** - 0.09%, 9 fold growth
 - **G339H** - 0.09%, 9 fold growth
 - **T259A** - 0.17%, 8.5 fold growth
 - **V289I** - 0.41%, 8.2 fold growth
 - **G181A** - 0.08%, 8 fold growth
 - **Y248N** - 0.46%, 7.7 fold growth
 - **F486V** - 50%, 7.3549 fold growth (found in BA.4 and BA.5 lineages)
 - **L452R** - 49%, 7.0838 fold growth (found in BA.4 and BA.5 lineages)
 - **T76I** – 3.4%, 6.4 fold growth
 - **V70-** - 50%, 6.1 fold growth (found in BA.4 and BA.5 lineages)
 - **H69-** - 50%, 6.1 fold growth (found in BA.4 and BA.5 lineages)
 - **R346S** - 0.06%, 6 fold growth (**putative immune escape mutation**)
 - **T547I** - 0.18%, 6 fold growth
 - **A701S** - 0.12%, 6 fold growth
 - **S247N** - 0.06%, 6 fold growth
 - **R346I** - 0.11%, 5.5 fold growth (**putative immune escape mutation**)
 - **N658S** – 3.1%, 5.1 fold growth

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

- No Delta isolates globally in July so far

World (other VOIs)

- None in July so far

World – Recombinants

- **XE** – 4 sequences in July so far
- One **XAF** in July so far
- See a summary of recombinant lineages at the end of this report.

World – Novel variants

- **BG.2** (Omicron) – 19 in July so far
- **BG.4** (Omicron) – 4 in July so far

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

- [Protection of SARS-CoV-2 natural infection against reinfection with the BA.4 or BA.5 Omicron subvariants](#)
- [Enhanced innate immune suppression by SARS-CoV-2 Omicron subvariants BA.4 and BA.5](#)

- [Neutralization sensitivity of Omicron BA.2.75 to therapeutic monoclonal antibodies](#)
- [Preliminary data from Yunlong Cao on twitter for BA.2.75.](#)
- [Novavax NVX-COV2373 triggers potent neutralization of Omicron sub-lineages](#)
- [The SARS-CoV-2 Delta variant induces an antibody response largely focused on class 1 and 2 antibody epitopes](#)
- [Effectiveness of Naturally Acquired and Vaccine-Induced Immune Responses to SARS-CoV-2 Mu Variant](#)
- [Covid Rises Across U.S. Amid Muted Warnings and Murky Data](#)
- [Germany's COVID-19 summer spike pushes nurses beyond their limits](#)
- [Europe Can't Shake Off Covid as Variant Fuels Summer Spike](#)
- [India hits 2 billion Covid-19 vaccinations as infections hit four-month high](#)
- [North Korea says nearing end of COVID crisis](#)
- <https://www.theguardian.com/world/2022/jul/17/unexpected-changing-waves-covid-seasonal>
- UK faces up to changing waves of Covid. The pandemic has not settled into a seasonal pattern. New variants have driven a rapid succession of recent waves.

Recombinant lineages:

No new recombinant lineages have been designated this week. A summary table of previously identified recombinant lineages can be found below. 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-XAH are 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 week. The XE 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	3429	#189	B.1.634	B.1.631	N. America
XC	25	#263	Delta (AY.29)	B.1.1.7	Japan
XD	28	#444	Delta (AY.4)	BA.1	France
XE	2763	#454	BA.1	BA.2	UK
XF	34	#445	Delta	BA.1	UK
XG	477	#447	BA.1	BA.2	Denmark
XH	173	#448	BA.1	BA.2	Denmark
XJ	251	#449	BA.1	BA.2	Finland
XK	18	#460	BA.1	BA.2	Belgium

XL	119	#464	BA.1	BA.2	UK
XM	497	#472	BA.1.1	BA.2	Multiple EU
XN	158	#480	BA.1	BA.2	UK
XP	57	#481	BA.1.1	BA.2	UK
XQ	141	#468	BA.1.1	BA.2	UK
XR	181	#469	BA.1.1	BA.2	UK
XS	59	#471	Delta	BA.1.1	USA
XT	13	#478	BA.2	BA.1*	S. Africa
XU	16	#522	BA.1*	BA.2	India
XV	42	#463	BA.1*	BA.2*	Denmark
XW	96	#591	BA.1*	BA.2*	JP, DE, SI, CA, UK, US
XY	116	#606	BA.1*	BA.2*	FR, IL, UK, US
XZ	100	#636	BA.2*	BA.1*	Multiple
XAA	93	#664	BA.1*	BA.2*	US, IL
XAB	110	#665	BA.1*	BA.2*	IT, FR, DE, CH, DK
XAC	201	#590	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
XAD	50	#607	BA.2*	BA.1*	CZ,DE,UK
XAE	124	#637	BA.2*	BA.1*	CA,US,NL,CH
XAF	240	#676	BA.1*	BA.2*	CR
XAG	259	#709	BA.1.1	BA.2.23	BR
XAH	81	#755	BA.2*	BA.1*	SI

Newly designated Pango lineages:

BF.7: Sublineage of BA.5.2.1 with S:R346T and N:S33F; [designation issue #827](#)

BA.2.3.19: BA.2.3 sublineage with additional spike K417T; designation issue #824

BF.6: BA.5.2.1 sublineage with S:G181A mainly in the UK; [designation issue #821](#)

Variants being monitored by various public health agencies:

The ECDC has specifically designated **BA.2.75** as a variant under monitoring. **BA.2.75** contains the following concerning spike mutations: K147E, W152R, F157L, I210V, G257S, D339H, G446S, N460K, R493Q.

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

<https://docs.google.com/spreadsheets/d/1mAgO2wRJyEyGtL-SBe3NgOjUk7a5nZTeKmSorVkaHSU/edit#gid=0>