

## BV-BRC SARS-CoV-2 Emerging Variant Report July 26, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20220726.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 7/23/22 estimates that **BA.5** proportions are now dominating in the United States at 81.9% (95% PI: 79.9-83.8%). Significant regional differences exist: <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>.
  - The CDC Nowcast estimates that **BA.4** proportions are now at 12.9% (95% PI: 11.2-14.7%)
  - The US CDC Nowcast estimates that **BA.2.12.1** proportions are 5.0% (95% PI: 4.5-5.4%)
- A major re-organization of PANGO lineage nomenclature in mid-July impacted some of the earlier sequence prevalence data.
- 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.5.2.1** - 19%, 2.3 fold growth
  - **BA.2.12.1** - 15%, 0.33 fold growth
  - **BA.5.5** – 9.7%, 1.3 fold growth
  - **BA.5.1** – 8.1%, 2.6 fold growth
  - **BA.4.1** – 7.1%, 1.1 fold growth
  - **BA.5.2** – 6.0%, 2.9 fold growth
  - **BA.5.6** – 4.7%, 1.9 fold growth
  - **BA.5** – 4.1%, **3.2 fold growth**
  - **BA.4** – 4.1%, 1.3 fold growth
  - **BA.4.6** – 2.2%, **3.3 fold growth**

- **BA.5.1.1** – 1.9%, 1.9 fold growth
  - **BA.2** – 1.9%, 0.28 fold growth
  - **BE.3** – 1.7%, 1.9 fold growth
  - **BE.1** – 1.5%, 2.1 fold growth
  - **BE.1.1** - 0.76%, **3.3 fold growth**
  - **BF.5** - 0.64%, 2.1 fold growth
- ***In aggregate, BA.5.x sequences constitute 17% of sequences in June and 54% 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 only
    - One **BA.5** sub-lineage carries the A701S substitution only
    - One **BA.5** sub-lineage carries the P1162L substitution only
  - 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
    - One **BA.4** sub-lineage carries the N658S and R346T substitutions
    - One **BA.4** sub-lineage carries the N658S substitution only
    - One **BA.4** sub-lineage carries the V3G and I670V substitutions
    - One **BA.4** sub-lineage carries the N658S and A701V substitutions
    - One **BA.4** sub-lineage carries the V3G and R346T substitutions
    - One **BA.4** sub-lineage carries the V3G substitution and lacks the N440K substitution
    - One **BA.4** sub-lineage carries the R346T and D936N substitutions
  - Several Omicron sub-lineages appear to carry a recurring mutation at position 346 in the S proteins (S:R346T in BA.2.76, BA.4.6, BA.2.12.1, BA.2 or S:R346I in BA.2.12.1, BA.4, BA.4.1). and show growth rates > 1 fold from May and June
  - Clusters of BA.2 sub-lineage (BA.2.13, BA.2 56, BA.2.81) 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. None in July so far.**

**USA – Recombinants**

- **XE – 5 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:
  - **BA.5.1** - 17%, 1.4 fold growth
  - **BA.5.2.1** - 14%, 1.9 fold growth
  - **BA.5.2** – 8.8%, 2.0 fold growth
  - **BA.2.12.1** – 6.7%, 0.31 fold growth
  - **BA.4.1** – 5.3%, 1.0 fold growth
  - **BA.4** – 4.4%, 1.1 fold growth
  - **BE.1.1** – 3.9%, 1.5 fold growth
  - **BA.5.5** – 3.6%, 1.2 fold growth
  - **BA.2** – 3.4%, 0.30 fold growth
  - **BA.5** – 3.4%, 1.7 fold growth
  - **BF.5** – 3.0%, **3.1 fold growth**
  - **BA.5.6** – 2.1%, 1.7 fold growth
  - **BE.1** – 1.8%, 1.5 fold growth
  - **BA.4.6** – 1.2%, 2.6 fold growth
  - **BA.5.1.1** - 0.78%, 1.5 fold growth
  - **BF.1** - 0.65%, 0.84 fold growth
  - **BE.3** - 0.61%, 1.5 fold growth
  - **BA.5.1.3** - 0.56%, 1.2 fold growth
  - **BA.5.3.1** - 0.54%, 1.2 fold growth
- **BA.2.75**: sometimes nicknamed “Centaurus”, this sublineage shows a high growth rate in India (111 fold in June and 2.7 fold in July), and is present in 14 other countries, including the United States (CA, IL, NY, NC, WA, WI, AZ, IA, VA). Preliminary signs of increasing growth rates for July in Australia, Japan and Nepal.
- **BA.2.76**: this sublineage shows a high growth rate globally (9.6 fold in June) and in several countries (Australia-18 Several Omicron sub-lineages appear to carry a recurring mutation at position 346 in the S proteins (S:R346T in BA.2.76, BA.4.6, BA.2.12.1, BA.2 or S:R346I in BA.2.12.1, BA.4, BA.4.1). and show growth rates > 1 fold from May and June
- .5 fold, Japan-13.8 fold, Singapore and Denmark-11 fold, Canada-8.7 fold, USA-6 fold, 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
- **Some BA.4 sub-lineages also show 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 S373P substitution
  - One **BA.5** sub-lineage lacks the R408S 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:
  - One **BA.4** sub-lineage carries the R346T and N658S substitutions (BA.4.6)
  - One **BA.4** sub-lineage carries the N658S substitution and lacks the N440K substitution
  - One **BA.4** sub-lineage carries the N658S and A701V substitutions
  - One **BA.4** sub-lineage carries the V3G and lacks the N440K substitution
  - One **BA.4** sub-lineage carries the N658S substitution only
  - One **BA.4** sub-lineage carries the V3G and lacks the R408S substitution
  - One **BA.4** sub-lineage carries the V3G only
  - One **BA.4** sub-lineage carries the N658S and D936N substitutions
  - One **BA.4** sub-lineage carries the V3G and lacks the T19I substitution
- Substitutions in spike that we are monitoring (> 3 fold growth June to July) include the following (but note that the numbers are still relatively small for most of these):
  - **A879S** - 0.04%, 4 fold growth
  - **D1163Y** - 0.04%, 4 fold growth
  - **G1099D** - 0.04%, 4 fold growth
  - **S221L** - 0.04%, 4 fold growth
  - **K444T** - 0.07%, 3.5 fold growth
  - **A1020S** – **3.8%**, 3.3333 fold growth
  - **E180V** - 0.03%, 3 fold growth
  - **E583D** - 0.03%, 3 fold growth
  - **F486I** - 0.06%, 3 fold growth
  - **G1099S** - 0.03%, 3 fold growth
  - **K444M** - 0.03%, 3 fold growth
  - **P251L** - 0.03%, 3 fold growth
  - **Q218E** - 0.03%, 3 fold growth
  - **V193L** - 0.03%, 3 fold growth
  - **G261V** - 0.06%, 3 fold growth
  - **G252D** - 0.03%, 3 fold growth

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

- One Delta isolate globally in July so far
- The AY.57 sub-lineage of the Delta variant appears to have spiked in Viet Nam in June, showing a prevalence of 23.44% (n=15) and a growth rate of 21.5 fold.
- Five (5) AY.45 like genomes have been detected in the Gauteng province of South Africa in June. These are part of a larger group of viruses (n=8) that appear to have features of both Delta and Omicron (BA.5). More information can be found on slide 19 of the [NGS-SA](#) report and on this github designation issue [here](#).

### World (other VOIs)

- None in July so far

### World – Recombinants

- **XE** – 6 sequences in July so far
- **XAF** – 2 in July so far
- See a summary of recombinant lineages at the end of this report.

### World – Other Omicron variants

- **BG.2** – 67 in July so far
- **BG.4** – 14 in July so far
- **BG.1** – 7 in July so far
- **BG.3** – 2 in July so far

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

- [UKHSA: SARS-CoV-2 variants of concern and variants under investigation in England Technical briefing 44](#)
- [Coronavirus: Japan struggles with record-setting seventh wave](#)
- [The risk from the coronavirus is rising in much of the United States.](#)
- [China approves Genuine Biotech's HIV drug for COVID patients \(Azvudine\)](#)
- [Risk of Reinfection, Vaccine Protection, and Severity of Infection with the BA.5 Omicron Subvariant: A Danish Nation-Wide Population-Based Study](#)
- [Durability of the Neutralizing Antibody Response to mRNA Booster Vaccination Against SARS-CoV-2 BA.2.12.1 and BA.4/5 Variants](#)
- [Omicron spike function and neutralizing activity elicited by a comprehensive panel of vaccines](#)
- [Evasion of neutralizing antibodies by Omicron sublineage BA.2.75](#)

### Recombinant lineages:

Two new recombinant lineages have been designated this week (XAJ and XAK). 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 weeks. The XE lineage appears to have the largest number of genomes.

Name	number	Github#	Lineage 1	Lineage 2	Location first detected
<a href="#">XA</a>	45	NA	B.1.1.7	B.1.177	UK
<a href="#">XB</a>	3429	<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>	28	<a href="#">#444</a>	Delta (AY.4)	BA.1	France
<a href="#">XE</a>	2763	<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>	477	<a href="#">#447</a>	BA.1	BA.2	Denmark
<a href="#">XH</a>	173	<a href="#">#448</a>	BA.1	BA.2	Denmark
<a href="#">XJ</a>	251	<a href="#">#449</a>	BA.1	BA.2	Finland
<a href="#">XK</a>	18	<a href="#">#460</a>	BA.1	BA.2	Belgium
<a href="#">XL</a>	119	<a href="#">#464</a>	BA.1	BA.2	UK
<a href="#">XM</a>	497	<a href="#">#472</a>	BA.1.1	BA.2	Multiple EU
<a href="#">XN</a>	158	<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>	141	<a href="#">#468</a>	BA.1.1	BA.2	UK
<a href="#">XR</a>	181	<a href="#">#469</a>	BA.1.1	BA.2	UK
<a href="#">XS</a>	59	<a href="#">#471</a>	Delta	BA.1.1	USA
<a href="#">XT</a>	13	<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>	96	<a href="#">#591</a>	BA.1*	BA.2*	JP, DE, SI, CA, UK, US
<a href="#">XY</a>	116	<a href="#">#606</a>	BA.1*	BA.2*	FR, IL, UK, US
<a href="#">XZ</a>	100	<a href="#">#636</a>	BA.2*	BA.1*	Multiple
XAA	93	<a href="#">#664</a>	BA.1*	BA.2*	US, IL
XAB	110	<a href="#">#665</a>	BA.1*	BA.2*	IT, FR, DE, CH, DK
XAC	201	<a href="#">#590</a>	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
XAD	50	<a href="#">#607</a>	BA.2*	BA.1*	CZ,DE,UK
XAE	124	<a href="#">#637</a>	BA.2*	BA.1*	CA,US,NL,CH
XAF	240	<a href="#">#676</a>	BA.1*	BA.2*	CR
XAG	259	<a href="#">#709</a>	BA.1.1	BA.2.23	BR
XAH	81	<a href="#">#755</a>	BA.2*	BA.1*	SI
XAJ	35	<a href="#">#709</a>	BA.2.12.1	BA.4	UK
XAK	55	<a href="#">#755</a>	BA.1*	BA.2*	DE

### **Newly designated Pango lineages:**

*BA.2.36.1: Fast and internationally widespread BA.2.36 sublineage with S:R346T circulating in Australia #874*

*BF.11: BA.5.2.1 +26151T+28271C+C140T sublineage with S:346T (65 sequences Uk, Israel, Spain) designated #837*

*BA.5.1.5: Sublineage of BA.5.1 with S:P1263Q, 250+ Sequences, 18 Countries designated #835*

*BA.2.38 sublineage defined by S:K444N, Orf1a:T1543I, Orf1a:N3725S, Orf1a:T4355I and S:F157S circulating in India (142 sequences) #828*

*BF.7: Proposal for a Sublineage of BA.5.2.1 with S:R346T and N:S33F #827*

*XAJ: Potential BA.2.12.1 and BA.4 recombinant with multiple breakpoints (mainly UK) #826*

*XAK: German BA.2/BA.1/BA.2 recombinant with S:K147E, S:R346K, S:460K, S:493 reversion, S:H1101Y [55 seq as of 2022-07-22] #823*

### **Variants being monitored by various public health agencies:**

The UKHSA has designated BA.2.75 as a monitored variant: V-22JUL-01 (BA.2.75)

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>