

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

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20220913.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 September 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 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 09/10/22 estimates that **BA.5** proportions are now dominating in the United States at 87.5% (95% PI: 86.2-88.7%). 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 2.2% (95% PI: 2.1-2.4%); estimates for **BA.4.6** proportions are now at 9.2% (95% PI: 8.1-10.4%)
  - The US CDC Nowcast estimates that **BA.2.12.1** proportions are now at 0.1% (95% PI: 0.1-0.1%)
- Lineages with sequence prevalence >0.5% or growth rate > 3 fold in August (sequence numbers in September are still too low to be reliable) are (ranked in order of sequence prevalence):
  - **BA.5.2.1** - 30%, 1.2 fold growth
  - **BA.5.2** - 14%, 1.6 fold growth
  - **BA.5.1** - 13%, 1.2 fold growth
  - **BA.5.5** – 7.2%, 0.71 fold growth
  - **BA.4.6** – 6.0%, **2.1 fold growth**
  - **BA.5.6** – 5.7%, 0.94 fold growth
  - **BA.5** – 4.6%, 1.3 fold growth
  - **BA.4.1** – 3.3%, 0.53 fold growth
  - **BA.4** – 1.9%, 0.53 fold growth
  - **BE.1** – 1.8%, 1.1 fold growth
  - **BA.5.1.1** – 1.8%, 0.94 fold growth
  - **BF.5** – 1.6%, 1.5 fold growth

- **BE.3** – 1.4%, 0.83 fold growth
  - **BA.2.12.1** – 1.2%, 0.14 fold growth
  - **BE.1.1** – 1.2%, 1.1 fold growth
  - **BA.2** - 0.66%, 0.52 fold growth
  - **BA.2.75** - 0.38%, **4.8 fold growth**
- 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.x sub-lineages in August in the US:
    - One **BA.5** sub-lineage carries the T76I substitution (BA.5.5)
    - One **BA.5** sub-lineage carries the R346T substitutions (BA.5.2.1)
    - One **BA.5** sub-lineage lacks the N440K substitution (BA.5.2.1)
  - Notable substitutions present within the top five BA.4.x sub-lineages in August in the US:
    - One **BA.4** sub-lineage carries the R346T and N658S substitutions
    - One **BA.4** sub-lineages carries the V3G substitution only
    - One **BA.4** sub-lineage carries the N658S substitution only
    - One **BA.4** sub-lineage carries the V3G and R346T substitutions
  - **Several Omicron sub-lineages appear to carry a recurring mutation at position 346 in the S protein (S:R346T in BA.2.74, BA.2.76, BA.4, BA.4.1, BA.4.6, BA.4.7, BA.5, BA.5.1, BA.2.12.1, BA.2, S:R346S in BA.5.2.1 or S:R346I in BA.4.1)**
  - **Several Omicron sub-lineages appear to carry a recurring mutation at position 444 in the S protein (K444R in BA.5.2.1 with 2.2 fold growth rate and K444T in BA.5.6 with 1.7 fold growth rate in August)**

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

- No Delta sequences in the US in August or September so far.

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

- None in August or September.

**USA – Recombinants**

- **XE** –none in August
- **XM** –none in August
- **XY** – 1 sequence in the US in August
- **XAA** –none in August
- **XAC** –none in August
- **XAF** - none in August
- 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%) in August (sequence numbers in September are still too low to be reliable):
  - **BA.5.2.1** - 23%, 1.2 fold growth
  - **BA.5.2** - 20%, 1.4 fold growth
  - **BA.5.1** - 17%, 0.94 fold growth
  - **BA.5** – 3.8%, 1.1 fold growth
  - **BA.4.6** – 3.5%, **2.2 fold growth**
  - **BA.5.5** – 3.3%, 0.81 fold growth
  - **BE.1.1** – 3.2%, 0.88 fold growth
  - **BF.5** – 3.1%, 0.99 fold growth
  - **BA.5.6** – 2.9%, 1.0 fold growth
  - **BA.4.1** – 2.3%, 0.52 fold growth
  - **BE.1** – 1.8%, 0.91 fold growth
  - **BA.4** – 1.5%, 0.46 fold growth
  - **BA.2** – 1.2%, 0.48 fold growth
  - **BA.5.1.1** - 0.91%, 1.0 fold growth
  - **BA.2.75** - 0.9%, 1.5 fold growth
  - **BA.2.12.1** - 0.7%, 0.16 fold growth
  - **BA.5.3.1** - 0.61%, 0.94 fold growth
  - **BE.3** - 0.59%, 0.91 fold growth
  - **BA.5.1.3** - 0.58%, 0.94 fold growth
  - **BA.5.2.3** - 0.53%, 1.1 fold growth
- ***BA.2.75: shows a high growth rate in India (71 fold in June, 4.6 fold in July, and 1.7 fold in August) and comprises 39% of sequences in India in August. It is also present in 37 other countries, including the United States (22 states). Signs of very high growth rates for August (> 5 fold) in Netherlands, Belgium, Israel, Austria, UK, France, Germany, and Spain***
- ***BF.3: shows a high growth rate in the UK (6.8 fold in August and 4 fold in July) but the numbers are small (n=44 in August)***
- BA.3 shows a slight increase in August (2.3 fold growth rate), with the majority of genomes originating in India. However upon closer inspection, these genomes are of poor quality, and are missing large sections of the spike protein coding region, and are therefore likely to be misassigned as BA.3.
- 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 August:
  - One **BA.5** sub-lineage carries the T76I substitution
  - One **BA.5** sub-lineage carries the R346T substitution
  - Two **BA.5** sub-lineage lack the N440K substitution

- Notable substitutions present within the top five **BA.4** sub-lineages globally in August:
  - One **BA.4** sub-lineage (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 N658S substitution only
  - One **BA.4** sub-lineage carries the V3G and the R346T substitutions
- Substitutions in spike that we are monitoring (>3 fold growth from July to August with counts >10) include the following (but note that the numbers are still relatively small for most of these):
  - **F486S** - 0.23%, 23 fold growth
  - **G261D** - 0.09%, 9 fold growth
  - **D1199N** - 0.15%, 7.5 fold growth
  - **K356T** - 0.12%, 6 fold growth
  - **A264T** - 0.04%, 4 fold growth
  - **F490S** - 0.04%, 4 fold growth
  - **P9L** - 0.04%, 4 fold growth
  - **Q14H** - 0.04%, 4 fold growth
  - **Y200C** - 0.04%, 4 fold growth
  - **G142** - 0.03%, 3 fold growth
  - **G339Y** - 0.03%, 3 fold growth
  - **G72R** - 0.03%, 3 fold growth
  - **I1216T** - 0.03%, 3 fold growth
  - **K147T** - 0.03%, 3 fold growth
  - **L1224F** - 0.03%, 3 fold growth
  - **L141** - 0.03%, 3 fold growth
  - **Q954Y** - 0.03%, 3 fold growth
  - **S1003I** - 0.03%, 3 fold growth
  - **T1116N** - 0.09%, 3 fold growth
  - **V445A** - 0.27%, 3 fold growth

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

- Twelve Delta isolates globally in August; 36 in July.
- Countries where Delta lineages have been detected in July and August 2022: Austria, Belgium, France, India, Indonesia, Italy, Luxembourg, Philippines, Russia, South Africa, Spain, Switzerland, Ukraine, United Kingdom, USA

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

- 1 Alpha genome (B.1.1.7) detected in July in the USA; none in August.

#### **World – Recombinants**

- **XAJ** – 45 in July, 3 in August
- **XAG** – 17 in July; none in August
- **XAN** – 14 in July; 6 in August
- **XAF** – 13 in July; one in August
- **XE** – 8 sequences in July; none in August
- **XM** – 2 in July; none in August

- **XAC** – 2 in July; none in August
- **XJ** – 1 in July; none in August
- **XAA** – 1 in July; none in August
- **XAD** – 1 in July; none in August
- **XAE** – 1 in July; none in August
- **XY** – 1 in August
- See a summary of recombinant lineages at the end of this report.

**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 45](#)
- [Bivalent SARS-CoV-2 mRNA vaccines increase breadth of neutralization and protect against the BA.5 Omicron variant](#)
- [Mucosal vaccination for SARS-CoV-2 elicits superior systemic T central memory function and cross-neutralizing antibodies against variants of concern](#)
- [Neutralization of SARS-CoV-2 Omicron BA.2.75 after mRNA-1273 Vaccination](#)
- [Effects of Vaccination and Previous Infection on Omicron Infections in Children](#)
- [Application of Statistical Learning to Identify Omicron Mutations in SARS-CoV-2 Viral Genome Sequence Data From Populations in Africa and the United States](#)
- [Plaque-neutralizing antibody to BA.2.12.1, BA.4 and BA.5 in individuals with three doses of BioNTech or CoronaVac vaccines, natural infection and breakthrough infection](#)
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**Recombinant lineages:**

No new recombinant lineages have 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-XAZ 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 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>	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>	34	<a href="#">#444</a>	Delta (AY.4)	BA.1	France
<a href="#">XE</a>	2815	<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>	254	<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>	539	<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>	143	<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>	60	<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>	17	<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>	102	<a href="#">#591</a>	BA.1*	BA.2*	JP, DE, SI, CA, UK, US
<a href="#">XY</a>	121	<a href="#">#606</a>	BA.1*	BA.2*	FR, IL, UK, US
<a href="#">XZ</a>	112	<a href="#">#636</a>	BA.2*	BA.1*	Multiple
XAA	96	<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	206	<a href="#">#590</a>	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
XAD	56	<a href="#">#607</a>	BA.2*	BA.1*	CZ,DE,UK
XAE	130	<a href="#">#637</a>	BA.2*	BA.1*	CA,US,NL,CH
XAF	287	<a href="#">#676</a>	BA.1*	BA.2*	CR
XAG	360	<a href="#">#709</a>	BA.1.1	BA.2.23	BR
XAH	82	<a href="#">#755</a>	BA.2*	BA.1*	SI
XAJ	79	<a href="#">#826</a>	BA.2.12.1	BA.4	UK
XAK	55	<a href="#">#823</a>	BA.1*	BA.2*	DE
XAL	95	<a href="#">#757</a>	BA.1.1	BA.2*	DE
XAM	341	<a href="#">#759</a>	BA.1.1	BA.2.9	Panama
XAN	30	<a href="#">#771</a>	BA.2*	BA.5.1	Multiple
XAP	69	<a href="#">#789</a>	BA.2*	BA.1*	US

XAQ	74	<u>#798</u>	BA.1*	BA.2*	Canada
XAR	49	<u>#860</u>	BA.1*	BA.2*	Reunion/France
XAS	48	<u>#882</u>	BA.5*	BA.2*	N. America
XAT	74	<u>#885</u>	BA.2.3.13	BA.1*	Japan
XAU	77	<u>#894</u>	BA.1.1*	BA.2.9*	Multiple
XAV	60	<u>#911</u>	BA.2*	BA.5*	France
XAW	5	<u>#895</u>	BA.2*	AY.122	Russia
XAY	8	<u>#844</u>	BA.2	AY.45	S. Africa
XAZ	974	<u>#797</u>	BA.2.5, BA.5	BA.2.5	Multiple

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

Few new lineages designated this week:

- [BU.1](#): Sublineage of BA.5.2.16 with S:K444M, S:N460K
- [BA.5.2.15](#): BA.5.2 + Orf1b:T1050N sublineage with Spike: K97T circulating in NYC
- [BS.1](#): BA.2.3.2 with 7 extra S1 mutations detected in 4 travellers in Japan coming from Vietnam
- [BF.23](#): BA.5.2.1 with S:1020S with growth in Czechia
- [BA.5.2.14](#): BA.5.2 sublineage with Orf1a:T2152I, S:W64L, S:K444M (29 sequences Denmark, Pakistan, Canada, New Zealand, Germany, Netherlands, Uk, Portugal, Switzerland) BA.5.1.20:
- [BA.5.1.20](#): BA.5.1+C29614T sublineage with Orf1a:K1407M and S:346T (55 sequences)
- [BA.5.1.21](#): BA.5.1 sublineage with Orf1b:D1903N and Orf1b:G662S (1120 Seqs) Dominant in Gambia

### **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>