

BV-BRC SARS-CoV-2 Emerging Variant Report July 12, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20220712.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 estimates that **BA.5** proportions are now dominating in the United States at 65% (95% PI: 62.2-67.7%). Significant regional differences exist: <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>.
 - The US CDC Nowcast estimates that **BA.2.12.1** proportions are 17.3% (95% PI: 15.7-19.0%)
 - The CDC Nowcast estimates that **BA.4** proportions are now at 16.3% (95% PI: 14.5-18.3%)
- BA sub-lineages with sequence prevalence > 0.5% in June so 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** - 49 %, 0.91 fold growth
 - **BA.2** – 8.4 %, 0.34 fold growth
 - **BA.5.5** – 6.1 %, **5.9 fold growth**
 - **BA.4.1** – 5.6 %, 4.8 fold growth
 - **BA.5.2.1** – 5.3 %, **12 fold growth**
 - **BA.5** – 3.6 %, **12 fold growth**
 - **BA.4** – 3.4 %, 4.6 fold growth
 - **BA.5.1** – 2.8 %, **13 fold growth**
 - **BA.5.2** – 1.4 %, **15 fold growth**
 - **BA.2.3** – 1.3 %, 0.30 fold growth
 - **BA.2.9** – 1.3 %, 0.33 fold growth
 - **BA.5.3.1** - 0.09 %, **13 fold growth**
 - **BA.2.18** - 0.07 %, 0.95 fold growth

- **BE.1** - 0.07 %, *13 fold growth*
- *In aggregate, BA.5.x sequences constitute 17% of sequences in June and 55% in July so far in the US*
- *In aggregate, BA.4.x sequences constitute 5.8% of sequences in June and 8.1% 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.x sub-lineages in June in the US:
 - One **BA.5** sub-lineage (the most prevalent) carries the T76I substitution only
 - One **BA.5** sub-lineage carries the T76I and K1073T substitutions
 - One **BA.5** sub-lineage carries the T76I and T883I substitutions
 - One **BA.5** sub-lineage carries the A1020S substitution
 - One **BA.5** sub-lineage carries the A701S substitution
 - Other substitutions present in a number of BA.5 sub-lineages include L5F.
- Notable substitutions present within the top ten BA.4 sub-lineages in June in the US:
 - One **BA.4** sub-lineage (the most prevalent) carries 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 I670V substitutions
 - One **BA.4** sub-lineage carries the N658S and A701V substitutions
 - One **BA.4** sub-lineage carries the N658S and D936N substitutions
- Clusters of BA.2.13 and BA.2 genomes from June carry the L452M substitution at the same position as L452Q and show growth rates > 1 fold from May

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

- Only 4 Delta sequences (AY.116.1, AY.117, AY.44 and AY.25.1) in the US in June.

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** – 39 sequences in the US in June; none 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 June so far (note the high relative growth of BA.4, BA.5, BA.5.1 globally):
 - **BA.2.12.1** - 25%, 0.95 fold growth
 - **BA.2** - 15%, 0.39 fold growth
 - **BA.5.1** – 9.5%, **6.7 fold growth**
 - **BA.5.2.1** – 6.3%, **12 fold growth**
 - **BA.4** – 4.5%, **4.6 fold growth**
 - **BA.4.1** – 4.4%, **4.3 fold growth**
 - **BA.5** – 3.6%, **8.2 fold growth**
 - **BA.5.2** – 3.6%, **17 fold growth**
 - **BA.5.5** – 2.7%, **5.8 fold growth**
 - **BE.1** – 2.6%, **13 fold growth**
 - **BA.2.9** – 2.3%, 0.32 fold growth
 - **BA.2.3** – 1.7%, 0.33 fold growth
 - **BF.1** - 0.71%, **4.7 fold growth**
 - **BA.2.38** - 0.71%, 1.6 fold growth
 - **BA.2.18** - 0.7%, 0.89 fold growth
 - **BA.5.3.1** - 0.63%, **7.9 fold growth**
 - **BA.2.36** - 0.53%, 0.60 fold growth
 - **BA.4.1.1** - 0.24%, **3.4 fold growth**
 - **BG.2** - 0.16%, **3.2 fold growth**
- **BA.2.73**: *this sublineage shows a high growth rate in India (53.67 fold), although it is present in 13 other countries, including the United States. Closer inspection of genomes with this designation indicate that the majority of these genomes may in fact be incorrectly designated BA.2.75, a lineage with several concerning new mutations in Spike. We expect data next week to clarify this.*
- **BA.2.12.1** and **BA.2.12** global expansion has slowed in June 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 ten five **BA.5** sub-lineages globally in June:
 - One **BA.5** sub-lineage carries the T76I substitution
 - One **BA.5** sub-lineage carries the A1020S substitution
 - One **BA.5** sub-lineage lacks the N440K substitution (may be a reversion)
 - One **BA.5** sub-lineage carries the V289I substitution
 - One **BA.5** sub-lineage carries the P1162L substitution
- Notable substitutions present within the top ten **BA.4** sub-lineages globally in June:
 - Two **BA.4** sub-lineages 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 I670V substitutions
 - One **BA.4** sub-lineage carries the V3G and lacks the R408S substitution

- One **BA.4** sub-lineage carries the N658S and lacks the N440K substitution
- One **BA.4** sub-lineage carries the V3G and lacks the N440K substitution
- One **BA.4** sub-lineage carries the V3G and C1235F substitutions
- Substitutions in Omicron spike that we are monitoring (> 5 fold growth May to June) include:
 - **G181A** - 0.07%, 7 fold growth
 - **F486V** - 46%, 6.9566 fold growth (found in BA.4 and BA.5 lineages)
 - **L452R** - 46%, 6.7426 fold growth (found in BA.4 and BA.5 lineages)
 - **T547I** - 0.18%, 6 fold growth
 - **R346I** - 0.12%, 6 fold growth (**immune escape mutation**)
 - **E1258Q** - 0.06%, 6 fold growth
 - **T76I** - 3.1%, 5.9057 fold growth
 - **V70** - 47%, 5.7576 fold growth (found in BA.4 and BA.5 lineages)
 - **H69** - 47%, 5.7549 fold growth (found in BA.4 and BA.5 lineages)
 - **A701S** - 0.11%, 5.5 fold growth
 - **R346S** - 0.05%, 5 fold growth
 - **S247N** - 0.05%, 5 fold growth

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

- 33 Delta isolates globally in June

World (other VOIs) *(no significant change since previous report)*

- 1 Alpha (**B.1.1.7**) variant reported in Sweden in June
- 1 Epsilon (**B.1.429**) variants reported in US in June

World – Recombinants

- XE – 81 sequences in June so far, from Israel, UK, and US
- One XAA, two XAG and 1 XZ recombinants detected in June
- See a summary of recombinant lineages at the end of this report.

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

- [SARS-CoV-2 Omicron BA.5: Evolving tropism and evasion of potent humoral responses and resistance to clinical immunotherapeutics relative to viral variants of concern.](#)
- [Post-vaccination Omicron infections induce broader immunity across antigenic space than prototype mRNA COVID-19 booster vaccination or primary infection](#)
- [Protection of SARS-CoV-2 natural infection against reinfection with the BA.4 or BA.5 Omicron subvariants](#)
- [BA.5, now dominant U.S. variant, may pose the biggest threat to immune protection yet](#)
- [Undercounted Covid-19 cases leave US with a blind spot as BA.5 variant becomes dominant](#)
- [Texas Medical Center's COVID data is back, and it's not looking good for Houston](#)
- [Alabama COVID hospitalizations rise, fueled by BA.4 and BA.5 variants](#)
- [Shanghai identifies new COVID Omicron subvariant \(clarification: BA.5.2.1\)](#)
- [COVID variants found in sewage weeks before showing up in tests](#)
- [WHO warns covid 'nowhere near over' as variants spike in U.S., Europe](#)

- [New omicron variant worries experts as it spreads in India, and Moderna says new booster offers better protection against BA.4 and BA.5](#)
- [South Korea's PM warns of COVID surge as cases hit two-month high](#)

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 recombinant 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	3406	#189	B.1.634	B.1.631	N. America
XC	28	#263	Delta (AY.29)	B.1.1.7	Japan
XD	26	#444	Delta (AY.4)	BA.1	France
XE	2389	#454	BA.1	BA.2	UK
XF	33	#445	Delta	BA.1	UK
XG	209	#447	BA.1	BA.2	Denmark
XH	54	#448	BA.1	BA.2	Denmark
XJ	69	#449	BA.1	BA.2	Finland
XK	15	#460	BA.1	BA.2	Belgium
XL	61	#464	BA.1	BA.2	UK
XM	41	#472	BA.1.1	BA.2	Multiple EU
XN	107	#480	BA.1	BA.2	UK
XP	57	#481	BA.1.1	BA.2	UK
XQ	65	#468	BA.1.1	BA.2	UK
XR	78	#469	BA.1.1	BA.2	UK
XS	37	#471	Delta	BA.1.1	USA
XT	12	#478	BA.2	BA.1*	S. Africa
XU	7	#522	BA.1*	BA.2	India

XV	28	#463	BA.1*	BA.2*	Denmark
XW	53	#591	BA.1*	BA.2*	JP, DE, SI, CA, UK, US
XY	62	#606	BA.1*	BA.2*	FR, IL, UK, US
XZ	61	#636	BA.2*	BA.1*	Multiple
XAA	49	#664	BA.1*	BA.2*	US, IL
XAB	81	#665	BA.1*	BA.2*	IT, FR, DE, CH, DK
XAC	129	#590	BA.1*	BA.2*	IL, DE, CA, IR, NL, JP, UK, US
XAD	39	#607	BA.2*	BA.1*	CZ,DE,UK
XAE	59	#637	BA.2*	BA.1*	CA,US,NL,CH
XAF	71	#676	BA.1*	BA.2*	CR
XAG	47	#709	BA.1.1	BA.2.23	BR
XAH	56	#755	BA.2*	BA.1*	SI

Newly designated Pango lineages:

BA.2.38.1: designation issue#809 with 33 new sequence designations
BA.2.74: designation issue#775 with 28 new sequence designations
BA.2.75: designation issue#773 with 4 new sequence designations
BA.2.76: designation issue#787 with 170 new sequence designations
BA.2.77: designation issue#732 with 13 new sequence designations
BA.2.78: designation issue#814 with 104 new sequence designations
BA.2.79: designation issue#812 with 113 new sequence designations
BA.2.79.1: designation issue#814 with 14 sequence designations
BA.2.80: designation issue#733 with 19 new sequence designations,
BA.4.1.3 with 31 new sequence designations
BA.4.1.4 with 51 new sequence designations
BA.4.2 with 230 new sequence designations
BA.4.3 with 44 new sequence designations
BA.4.4 with 473 new sequence designations
BA.4.5 with 29 new sequence designations
BA.4.6: designation issue#741 with 113 new sequence designations
BA.5.1.1 with 192 new sequence designations
BA.5.1.2: designation issue#790 with 89 new sequence designations
BA.5.1.3: designation issue#765 with 243 new sequence designations
BA.5.1.4: designation issue#801 with 92 new sequence designations
BA.5.2.2 with 82 new sequence designations
BA.5.2.3 with 94 new sequence designations
BA.5.2.4 with 9 new designations
BA.5.3.3 with 147 new sequence designations

BA.5.3.4 with 143 new sequence designations
BA.5.6 with 393 new sequence designations
BE.1.1 with 956 new sequence designations
BE.2 with 37 new sequence designations
BE.3 with 220 new designations
BF.1.1 with 114 new sequence designations
BF.2 with 133 new sequence designations
BF.3 with 38 new sequence designations
BF.4: designation issue#788 with 80 new sequence designations,
BF.5 with 986 new designations
BG.3: designation issue#784 with 28 new sequence designations
BG.4 with 102 new sequence designations

Variants being monitored by various public health agencies:

No recent official additions, however social media tweets indicate that the WHO and several scientists are monitoring **BA.2.75** which contains the following concerning spike mutations: K147E, W152R, F157L, I210V, G257S, D339H, G446S, N460K, R493Q. *note: most genomes with these mutations are currently mis-labeled in GISAID as BA.2.73.*

The latest summary table for all agencies can be found here:
<https://docs.google.com/spreadsheets/d/1mAgO2wRjyEyGtL-SBe3NgOjUk7a5nZTeKmSorVkaHSU/edit#gid=0>

Commented [SR1]: These sections need updating