

BV-BRC SARS-CoV-2 Emerging Variant Report July 6, 2022

Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20220706.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 June 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 May and June are **Omicron**. While **BA.1** and its sub-lineages predominated in February and March, **BA.2** and its sub-lineages are predominant since April. However, in the last month the predominant BA.2 sublineage in the united states, BA.2.12.1, may soon be displaced by BA.5 and BA.4 lineages.
 - The CDC Nowcast estimates that **BA.5** proportions are now dominating in the united states at 53.6% (95% PI: 49.5-57.6%), with BA.5 overtaking BA.2.12.1 during the week of 7/2/2022. 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 27.2% (95% PI: 24.2-30.3%)
 - The CDC Nowcast estimates that **BA.4** proportions are now at 16.5% (95% PI: 13.9-19.4%)
- BA sub-lineages with sequence prevalence > 0.5% in June so far are (ranked in order of sequence prevalence):
 - **BA.2.12.1** – 53.12%, 0.99 fold growth
 - **BA.5** - 15%, **7.13 fold growth**
 - **BA.2** - 10.6%, 0.4 fold growth
 - **BA.4** – 8.4%, **4.3 fold growth**
 - **BA.5.1** – 2.6%, 10.7 fold growth
 - **BA.2.3** – 1.6%, 0.35 fold growth
 - **BA.2.9** – 1.5%, 0.39 fold growth
 - **BA.2.18** - 0.72%, 1 fold growth
 - **BA.2.13** - 0.66%, 1.29 fold growth
- ***BA.2.12.1 continues to predominate in the US***

- **11022 BA.5 sequences (14.84%) in the US in June so far; this is a 7.13 fold growth in sequence prevalence from May**
- **6217 BA.4 sequences (8.4%) in the US in June so far; this is a 4.3 fold growth in sequence prevalence from May**
- 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 some of the top ten BA.2.x sub-lineages in June in the US so far:
 - One **BA.2.x** sub-lineage carries the L452Q and S704L substitution
 - One of the **BA.2.x** sub-lineages carries the L452Q, S704L, and N164K substitutions
 - One of the **BA.2.x** sub-lineages carries the L452Q, S704L, and L5F substitutions
 - One of the **BA.2.x** sub-lineages carries the L452Q, S704L, and A879V substitutions
 - One of the **BA.2.x** sub-lineages carries the K417T substitution instead of the K417N substitution
 - One of the **BA.2.x** sub-lineages carries the L452M substitution
 - One of the **BA.2.x** sub-lineages carries the Y248S substitution
- Notable substitutions present within the top five BA.4 sub-lineages in June in the US so far:
 - One **BA.4** sub-lineage carries the V3G substitution
 - One **BA.4** sub-lineage carries the V3G and I670V substitutions
 - One **BA.4** sub-lineage carries the N658S substitution
 - One **BA.4** sub-lineage carries the N658S and R346T substitutions
- Notable substitutions present within the top five BA.5 sub-lineages in June in the US so far:
 - Two **BA.5** sub-lineages carry the T76I substitution
 - One **BA.5** sub-lineage carries the T76I and K1073T substitutions
 - One **BA.5** sub-lineage carries the A1020S substitution
 - One **BA.5** sub-lineage carries the P1162L substitution
 - Other substitutions present in a number of BA.5 sub-lineages include: L5F, A701S.
- 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 so far

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

- Last week one B.1.429 sequence detected in CA in June; notably, this variant has not been detected in the US since 2021. However an excessive number of ambiguous bases in the genome indicate that it may be a result of contamination or coinfection. This variant has since been withdrawn from GISAID.

USA – Recombinants

- **XE** – 26 sequences in the US in June so far, in 22 states
- **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 (>2.5 fold) in June so far (note the high relative growth of BA.4, BA.5, BA.5.1 globally):
 - **BA.2.12.1** - 27%, 1 fold growth
 - **BA.2** - 19%, 0.5 fold growth
 - **BA.5** - 18%, **8 fold growth**
 - **BA.5.1** - 9%, **5.9 fold growth**
 - **BA.4** – 8.8%, **4.2 fold growth**
 - **BA.2.9** – 2.8%, 0.38 fold growth
 - **BA.2.3** – 2.1%, 0.37 fold growth
 - **BA.2.18** – 0.74%, 1 fold growth
 - **BA.2.38** - 0.7%, 1.7 fold growth
 - **BA.2.36** - 0.06%, 0.7 fold growth
- *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 BA.5 and BA.5.1 lineages; both show high growth in sequence prevalence –BA.5: 13.1 fold in May and 8.1 fold in June globally; BA.5.1: 38 fold in May and 5.9 fold in June globally. BA.5 and BA.5.1 sequences have been reported in 139 countries.*
- *BA.4 shows high growth in sequence prevalence – 5.7 fold in May and 4.2 fold in June globally; BA.4 sequences have been reported in 71 countries*
- Similar issues with variable ancestral reversion that are likely due to sequencing artifacts, as described above for US sequences
- Notable substitutions present within some of the top 10 Omicron BA.2.x sub-lineages in June globally:
 - One **BA.2.x** sub-lineage carries the **L452Q** and **S704L** substitutions (**BA.2.12.1**)
 - One **BA.2.x** sub-lineage carries the novel **N164K** substitution in addition to the **L542Q** and **S704L** substitutions (**BA.2.12.1**)
 - One **BA.2.x** sub-lineage carries the novel **I68T** substitution (**BA.2.36**)
 - One **BA.2.x** sub-lineage carries the **H69-** and **V70-** deletions and the **L452R** substitution instead of the **L452Q** substitution (likely misassigned **BA.4** or **BA.5**)
 - Another **BA.2.x** sub-lineage carries the **H69-** and **V70-** deletions without the **L452R** substitution, but the absence of **L452R** is likely due to a sequencing artifact since other neighboring substitutions are also missing
 - One **BA.2** sub-lineage carries the novel **L452M** substitution
- Notable substitutions present within the top five BA.4 sub-lineages globally in June so far:
 - One **BA.4** sub-lineage carries the **V3G** substitution
 - One **BA.4** sub-lineage carries the **V3G** and **I670V** substitutions
 - One **BA.4** sub-lineage carries the **N658S** substitution
 - One **BA.4** sub-lineage carries the **N658S** and **R346T** substitutions
- Notable substitutions present within the top five BA.5 sub-lineages globally in June so far:
 - One **BA.5** sub-lineage carries the **T76I** substitution

- One **BA.5** sub-lineage carries the **A1020S** substitution
- One **BA.5** sub-lineage carries the **V289I** substitution
- One **BA.5** sub-lineage carries the **P1162L** substitution
- One **BA.5** sub-lineage lacks the **N440K** substitution (may be a reversion)
- Substitutions in Omicron spike that we are monitoring (> 5 fold growth May to June) include:
 - **A829T** - 0.13%, 13 fold growth
 - **Q183L** - 0.11%, 11 fold growth
 - **A1020S** – **1.16%**, **9.67 fold growth**
 - P1263Q – 0.09%, 9 fold growth
 - **V289I** - 0.44%, 8.8 fold growth
 - **T259A** - 0.14%, 7 fold growth
 - **R346I** - 0.13%, 6.5 fold growth (**immune escape mutation**)
 - **F486V** – **42.07%**, 6.3 fold growth (found in BA.4 and BA.5 lineages)
 - **Y248N** – 0.31%, 6.2 fold growth
 - **L452R** – **41.44%**, 6.1 fold growth (found in BA.4 and BA.5 lineages)
 - **C1235** – 0.18%, 6 fold growth
 - **Q1201L** – 0.06%, 6 fold growth
 - W152R – 0.06%, 6 fold growth
 - **H69del** – 42.7%, 5.2 fold growth (found in BA.4 and BA.5 lineages)
 - **V70del** – 42.7%, 5.2 fold growth (found in BA.4 and BA.5 lineages)
 - T76I – 2.8%, 5.1 fold growth
- **BA.1** lineage and sub-lineages: few BA.1/BA.1.* lineages in in June (0.01% of all global sequences)

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

- 18 Delta isolates globally in June so far

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

- 1 Alpha (B.1.1.7) variant reported in Sweden in June

World – Recombinants

- **XE** – 65 sequences in June so far, from Israel, UK, and US
- No other recombinants detected in June so far
- See a summary of recombinant lineages at the end of this report.

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

- [Scientists keeping an eye on new COVID variant BA.2.75](#)
- [New ultra-contagious Omicron subvariants BA.4, BA.5 fueling California coronavirus wave](#)
- [Connecticut Patient Infected for 471 Days, Evolved 3 New Lineages](#)
- [New York City's COVID test positivity rate surpasses 10% for the first time since January](#)
- [The Omicron subvariants BA.4 and BA.5 have together become dominant in the U.S., the C.D.C. estimates](#)
- [China records first cases of new Omicron variant BA5](#)
- [SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 43](#)

- [Risk assessment for SARS-CoV-2 variants VOC-22APR-03 \(Omicron BA.4\) and VOC-22APR-04 \(Omicron BA.5\)](#)
- [Coronavirus \(COVID-19\) Update: FDA Recommends Inclusion of Omicron BA.4/5 Component for COVID-19 Vaccine Booster Doses](#)
- [Fast detection of SARS-CoV-2 variants including Omicron using one-step RT-PCR and Sanger sequencing](#)
- [Clinical severity of SARS-CoV-2 Omicron BA.4 and BA.5 lineages in South Africa](#)

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.

More details on recombinants can be found in the BV-BRC's research summary here:

The [BV-BRC Research Summary on Recombination in SARS-CoV-2](#)

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.5.1.4** from #801: Fast growing sublineage of BA.5.1 with ORF1b:R1078L, ORF1a:V1117I, ORF1a:S1510C circulating in Europe
- **BA2.76** from #787: Sublineage of BA.2 with Spike Y248N and R346T, primarily in India

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.

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

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