Details of the emerging variants analysis can be found in “BV-BRC SARS-CoV-2 Emerging Variant Report – 20220920.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 09/17/22 estimates that **BA.5** proportions are now dominating in the United States at 84.8% (95% PI: 83.2-86.3%). Significant regional differences exist: [https://covid.cdc.gov/covid-data-tracker/#variant-proportions](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 1.8% (95% PI: 1.6-1.9%); estimates for **BA.4.6** proportions are now at 10.3% (95% PI: 9.1-11.7%).
  - The US CDC Nowcast estimates that **BA.2.12.1** proportions are now at 0.0% (95% PI: 0.0-0.0%).
  - **BF.7 has been added to the tracker and is currently estimated at 1.7% (95% PI: 1.2-2.4%)**
  - **BA.2.75 has been added to the tracker and is currently estimated at 1.3% (95% PI: 0.8-2.2%)**

- Lineages with sequence prevalence >0.5% or growth rate > 3 fold in September so far are (ranked in order of sequence prevalence):
  - **BA.5.2.1** - 30%, 0.98 fold growth
  - **BA.5.2** - 18%, 1.21 fold growth
  - **BA.5.1** - 13%, 0.96 fold growth
  - **BA.4.6** – 8.8%, 1.4 fold growth
  - **BA.5** – 6.4%, 1.4 fold growth
  - **BA.5.6** – 4.9%, 0.86 fold growth
  - **BA.5.5** – 4.3%, 0.61 fold growth
  - **BF.5** – 1.8%, 1.2 fold growth
- BA.4.1 – 1.7%, 0.52 fold growth
- BE.1.1 – 1.6%, 1.3 fold growth
- BE.1 – 1.5%, 0.85 fold growth
- BE.3 – 1.4%, 1.1 fold growth
- BA.4 – 1.1%, 0.62 fold growth
- BA.5.1.1 – 1.0%, 0.59 fold growth
- BA.2.75 - 0.7%, 1.8 fold growth
- BA.3 – 1.4%, 1.1 fold growth
- BA.5.1.3 - 0.62%, 1.3 fold growth
- BA.5.1.2 – 0.51%, 1.2 fold growth


- Notable substitutions present within the top ten BA.5.x sub-lineages in the US in September so far:
  - One BA.5 sub-lineage carries the T76I substitution (BA.5.5)
  - One BA.5 sub-lineage carries the R346T substitution (BA.5.2.1)
  - One BA.5 sub-lineage carries the L84I substitution (BA.5.2)(first time reported)

- Notable substitutions present within the top five BA.4.x sub-lineages in the US in September so far:
  - 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 R346T, N658S, and S494P substitutions (first time reported)

- 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)

- Two 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; none in September so far
- XM – none in August; none in September so far
- XY – 1 sequence in the US in August; none in September so far
- XAA – none in August; none in September so far
- XAC – none in August; none in September so far
- XAF - none in August; none in September so far
- 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 September so far:
  - BA.5.2.1 - 26%, 1.1 fold growth
  - BA.5.2 - 23%, 1.2 fold growth
  - BA.5.1 - 19%, 1.1 fold growth
  - BA.4.6 - 4.8%, 1.3 fold growth
  - BA.5 - 4.7%, 1.2 fold growth
  - BE.1.1 - 4.0%, 1.2 fold growth
  - BF.5 - 3.2%, 1.0 fold growth
  - BA.5.6 - 2.0%, 0.70 fold growth
  - BA.2.75 – 1.8%, **1.8 fold growth**
  - BA.5.5 – 1.6%, 0.50 fold growth
  - BE.1 – 1.6%, 0.89 fold growth
  - BA.4.1 – 1.2%, 0.55 fold growth
  - BA.5.2.3 - 0.93%, **1.8 fold growth**
  - BA.4 - 0.79%, 0.53 fold growth
  - BA.5.1.3 - 0.74%, 1.3 fold growth
  - BA.5.1.2 - 0.62%, 1.3 fold growth
  - BA.5.3.1 - 0.58%, 0.95 fold growth
  - BE.3 - 0.51%, 0.89 fold growth
  - BA.5.1.1 - 0.50%, 0.55 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. The reporting for September is still quite low (n=236 sequences globally) but the trend toward increasing growth appears to be continuing.

- **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. Therefore the assignment to BA.3 could be erroneous.

- 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 September so far:
  - One BA.5 sub-lineage carries the R346T substitution
  - One BA.5 sub-lineage carries the T76I substitution
  - One BA.5 sub-lineage carries the N450D substitution (first time reported)
• Notable substitutions present within the top five BA.4 sub-lineages globally in September so far:
  o Two BA.4 sub-lineage (including the most prevalent) carry the R346T and N658S substitutions (BA.4.6)
  o One BA.4 sub-lineage carries the V3G substitution only
  o One BA.4 sub-lineage carries the N658S substitution only
  o One BA.4 sub-lineage carries the R346T, N658S, and W152L substitutions (first time reported) (BA.4.6)

• Substitutions in spike that we are monitoring (>3 fold growth from August to September with counts >10) include the following (but note that the numbers are still relatively small for most of these):
  o A260V - 0.14%, 14 fold growth
  o K1073N - 0.2%, 10 fold growth
  o D1163H - 0.09%, 9 fold growth
  o V445P - 0.08%, 8 fold growth
  o L1224F - 0.21%, 7 fold growth
  o M153T - 0.14%, 7 fold growth
  o E224Q - 0.13%, 6.5 fold growth
  o H245N - 0.13%, 6.5 fold growth
  o F490S - 0.23%, 5.8 fold growth
  o P272L - 0.17%, 5.7 fold growth
  o Q183E - 0.1%, 5 fold growth
  o Q14H - 0.17%, 4.3 fold growth
  o G257D - 0.14%, 3.5 fold growth
  o E654K - 0.1%, 3.3 fold growth
  o W152L - 0.33%, 3.3 fold growth
  o A647S - 0.13%, 3.3 fold growth
  o H146Q - 0.16%, 3.2 fold growth
  o V83A - 0.09%, 3 fold growth

Note on convergent mutations: Over the past two months we have noted an increase in convergent mutations at several antigenically important sites: R346*, K356*, K444*, V445*, and N460*. These mutations, as well as several others previously reported in Omicron and other lineages are discussed in a new preprint below, although V445* is relatively new.

“Imprinted SARS-CoV-2 humoral immunity induces convergent Omicron RBD evolution (on convergent mutations at sites: R346, R356, K444, L452, N460K and F486)”

DELTA (B.1.617.2 and AY sub-lineages)
  • 14 Delta isolates globally in August; 6 in September so far

World (other VOIs)
  • No Alpha genome in August or September

World – Recombinants
  • XAJ – 45 in July; 3 in August; none in September so far
  • XAG – 17 in July; none in August; none in September so far
- **XAN** – 14 in July; 6 in August; none in September so far
- **XAF** – 13 in July; one in August; none in September so far
- **XE** – 8 sequences in July; none in August; none in September so far
- **XM** – 2 in July; none in August; none in September so far
- **XAC** – 2 in July; none in August; none in September so far
- **XJ** – 1 in July; none in August; none in September so far
- **XAA** – 1 in July; none in August; none in September so far
- **XAD** – 1 in July; none in August; none in September so far
- **XAE** – 1 in July; none in August; none in September so far
- **XY** – 1 in August; none in September 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:**

- Omicron sublineage BA.2.75.2 exhibits extensive escape from neutralising antibodies
- BA.2.75.2, the new subvariant of Omicron that worries scientists
- Bivalent SARS-CoV-2 mRNA vaccines increase breadth of neutralization and protect against the BA.5 Omicron variant
- A Bivalent Omicron-Containing Booster Vaccine against Covid-19
- Outcomes of Bebtelovimab Treatment is Comparable to Ritonavir-boosted Nirmatrelvir among High-Risk Patients with Coronavirus Disease-2019 during SARS-CoV-2 BA.2 Omicron Epoch
- Illinois reports 3,111 new cases, 19 new deaths
- ‘Very Harmful’ Lack of Data Blunts U.S. Response to Outbreaks
- Just in time for fall, there’s a brand new COVID variant making headway in the U.S. (BF.7)
- Imprinted SARS-CoV-2 humoral immunity induces convergent Omicron RBD evolution (on convergent mutations at sites: R346, R356, K444, L452, N460K and F486)

**Recombinant lineages:**

Two new recombinant lineages have been added this week: XBA and XBB. 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-XBB 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.

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**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/1mAgO2wRJvEyGtL-SBe3NgOjUk7a5nZTeKmSorVkaHSU/edit#gid=0](https://docs.google.com/spreadsheets/d/1mAgO2wRJvEyGtL-SBe3NgOjUk7a5nZTeKmSorVkaHSU/edit#gid=0)