Lineage Summary

October 11th, 2022

- Outbreak.info lineage trends
- O CDC NOWCAST lineage trends
- O Pangolin update
- O BA.2.75 study
- O BQ.1.1, XBB, XBC trees

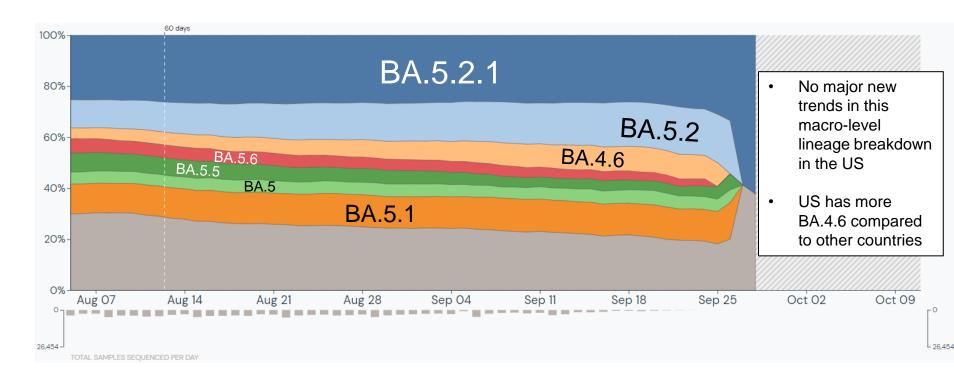


CDPH Gen Epi (reporting questions): genomicepi@cdph.ca.gov

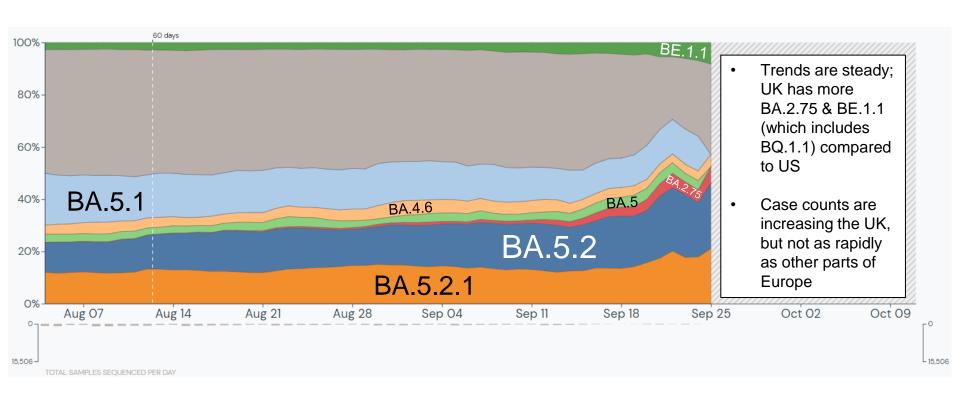
CDPH COVIDNet tech support: COVIDNet.TechSupport@cdph.ca.gov

My email: emily.smith@theiagen.com

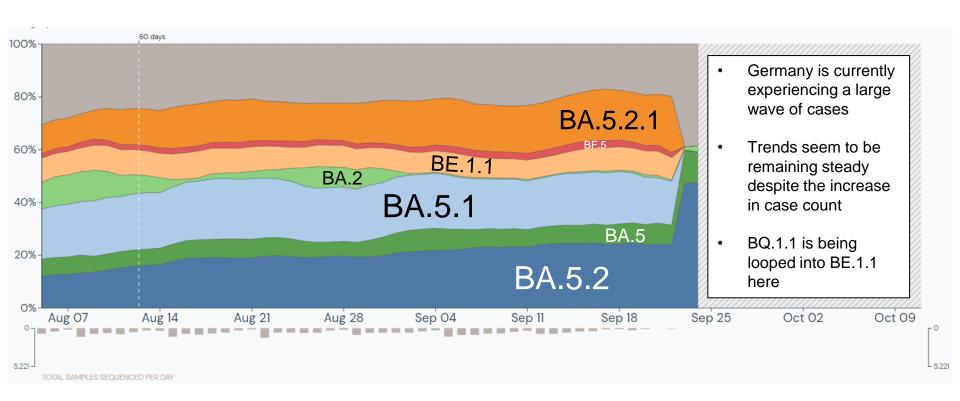
Outbreak.info – lineage prevalence in the US



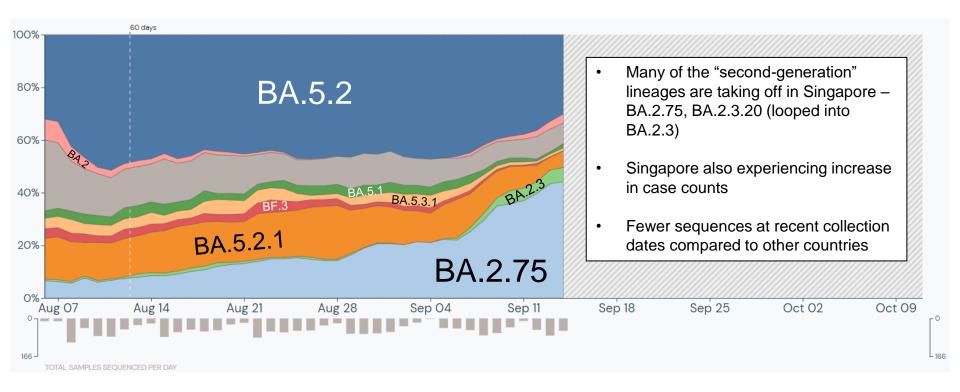
Outbreak.info – lineage prevalence in the UK



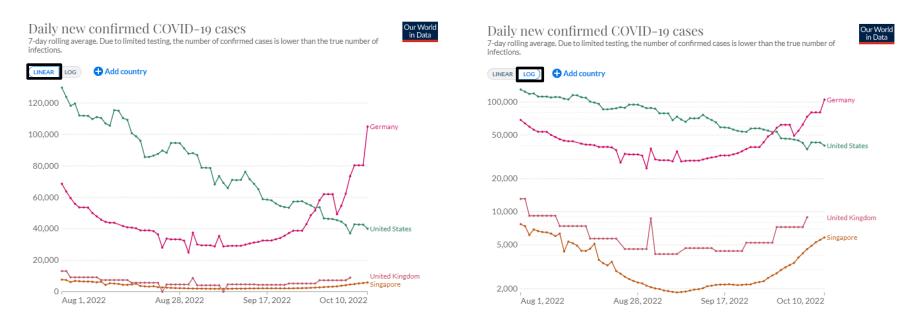
Outbreak.info – lineage prevalence in Germany



Outbreak.info – lineage prevalence in Singapore



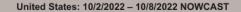
Case counts for comparison countries



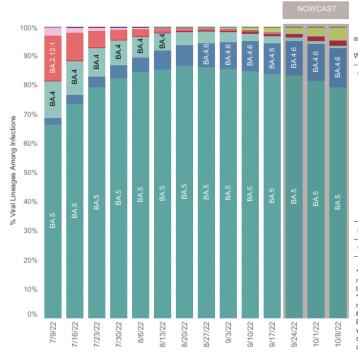
- Many countries are currently experiencing waves, but many of the newer lineages (e.g. BQ.1.1) aren't at high enough prevalence to be the only factor driving those waves
- Waning population immunity likely playing a role, and it will be interesting to see how differences in booster strains and booster uptakes impact lineage dynamics going forward

CDC NOWCAST – lineage prevalence in the US





USA



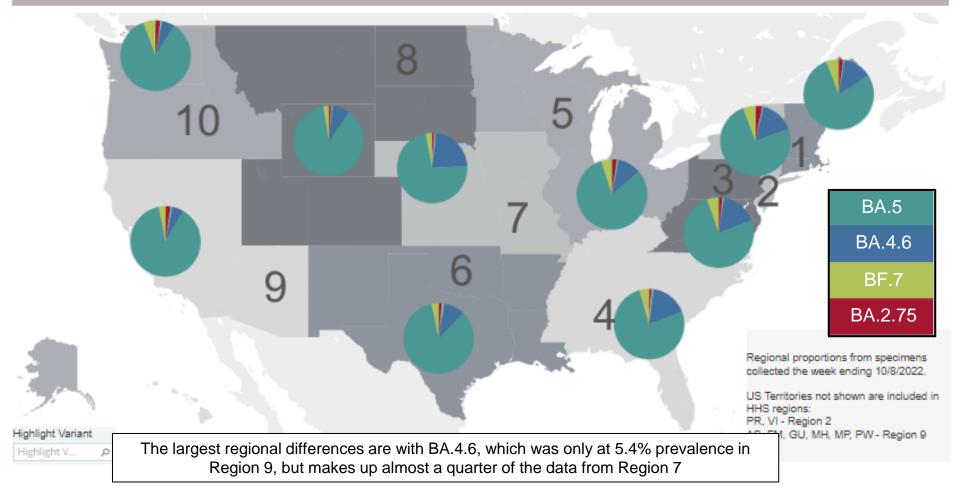
WHO label	Lineage #	US Class	%Total	95%PI	
Omicron	BA.5	VOC	79.2%	77.5-80.7%	-2.1%
	BA.4.6	VOC	13.6%	12.4-14.9%	+0.8%
	BF.7	VOC	4.6%	3.9-5.4%	+1.2%
	BA.2.75	VOC	1.8%	1.4-2.4%	+0.4%
	BA.4	VOC	0.8%	0.7-0.9%	-0.3%
	BA.2.12.1	VOC	0.0%	0.0-0.0%	
	BA.2	VOC	0.0%	0.0-0.0%	
	B.1.1.529	VOC	0.0%	0.0-0.0%	
	BA.1.1	VOC	0.0%	0.0-0.0%	
Delta	B.1.617.2	VBM	0.0%	0.0-0.0%	
Other	Other*		0.0%	0.0-0.0%	
					•

- * Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all weeks displayed.</p>
- ** These data include Nowcast estimates, which are modeled projections that may differ from weighted estimates generated at later dates
- # \(^{\text{ A}\times 1.4\times 1.617.2\). BA.1, BA.3 and their sublineages (accept BA.1.1\) and its sublineages) are aggregated with B.1.529. Except BA.2.12.1\, BA.2.75\) and their sublineages, BA.2 sublineages are aggregated with BA.2. Except BA.4.6\, sublineages of BA.4\) are aggregated with BA.2. Except BA.4.6\, sublineages of BA.4\) are aggregated to BA.5\) are aggregated to BA.5\) are aggregated to BA.5\). Sublineages of BA.1.1\) and BA.2.75\) are aggregated to the parental BA.1.1\) and BA.2.75\) respectively. Previously, BA.2.75\) was aggregated with BA.2\), and BF.7\) was aggregated with BA.5\). Lineages BA.4.6\, BF.7\, and many BA.2.75\) contain the spike substitution R346T.

- It appears that BA.5 is declining but remember that BF.7 is a BA.5 sublineage, which is increasing
- BA.4.6 continues a slow and steady increase
- BA.2.75 increasing for the first time in a few weeks

Collection date, week ending

United States: 10/2/2022 - 10/8/2022 NOWCAST



New pangolin update!

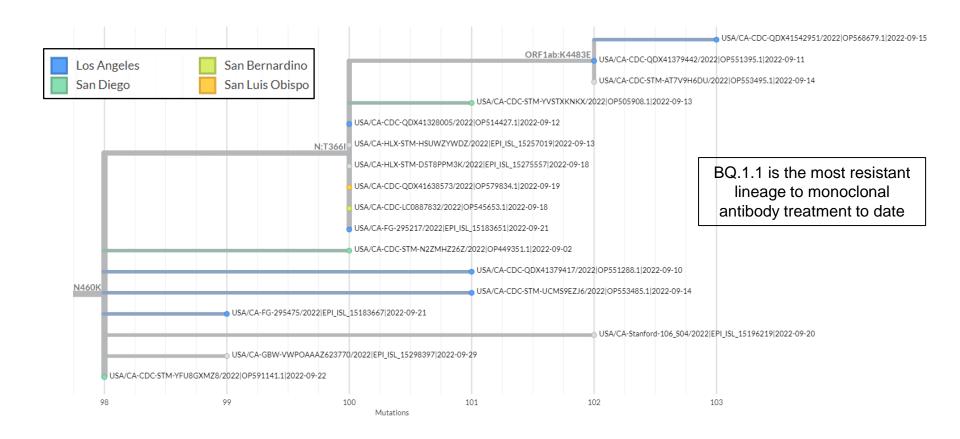
- The pangolin team has finally released an updated version, which will be available on Terra within a few days
- The newly designated lineages (BQ.1.1, BA.2.3.20, etc) and recombinants (XBB, XBC) will now be easier to track
- This week, lineages in the SARS-CoV-2 dashboard will be updated
- Hopefully GISAID will update their pangolin version as well (check the version next to the Pango Lineage field – Pango v. 4.1.3 is the new version)



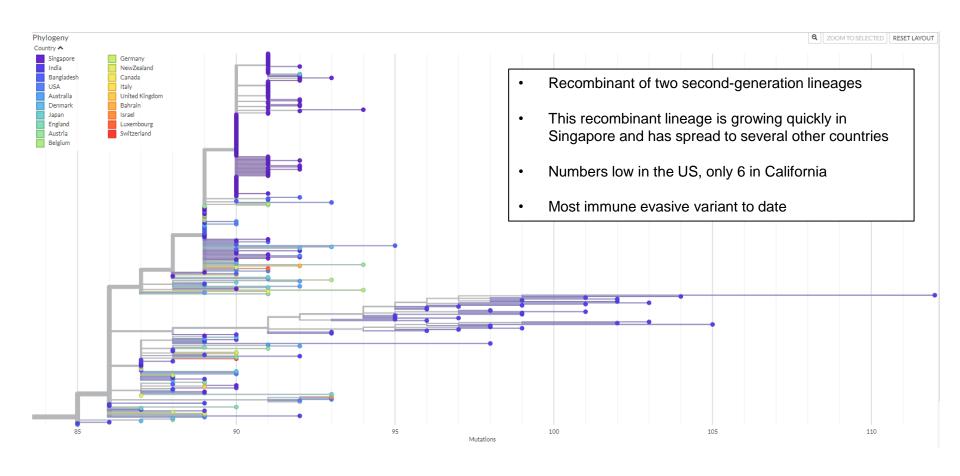
Virological characteristics of the SARS-CoV-2 Omicron BA.2.75 variant Akatsuki Saito 40 • Tomokazu Tamura 40 • Jiri Zahradnik 40 • ... Terumasa Ikeda 2 • • • Takasuke Fukuhara 2 • • Kei Sato 2 41, 42 • • Show all authors • Show footnotes Open Access • Published: October 09, 2022 • DOI: https://doi.org/10.1016/j.chom.2022.10.003

- Study published last week looking at immunogenicity, ACE2 affinity, fusogenicity, and pathogencity of BA.2.75 compared to Delta, BA.2, and BA.5
- Based on in vivo experiments in hamsters
- Major takeaway: BA.2.75 is more transmissible than BA.5, but pathogenicity not significantly different from BA.5
- While BA.2.75 prevalence is still low in the US, it has a greater prevalence in Asia and some European countries

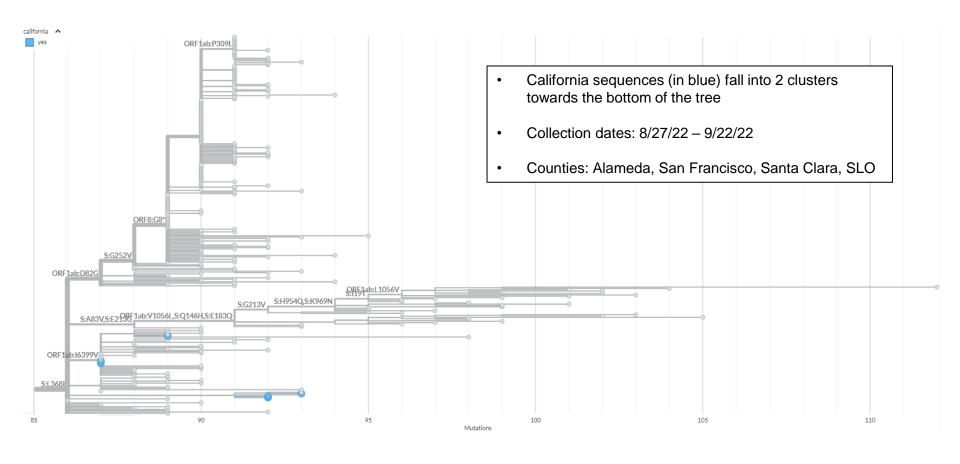
BQ.1.1s in California (GISAID data, n=17)



All XBBs in GISAID (plus 2 sequences not in GISAID yet)



All XBBs in GISAID (plus 2 sequences not in GISAID yet)



All XBCs in GISAID

