

NIH SAVE update 2023-08-23

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BA.2.86

See: Jesse Bloom: https://slides.com/jbloom/new_2nd_gen_ba2_variant

And: <https://github.com/cov-lineages/pango-designation/issues/2183>

Highlights:, emphasis

- i. BA.2.86: A novel SARS-CoV-2 variant with a very distinctive spike was discovered in Israel and Denmark last week. It is still very rarely sampled but found in 5 countries. It has been designated a WHO variant under monitoring.
- ii. EG.5.1 is still the most rapidly expanding variant
- iii. XBC.1.6 still has a presence in Australia but is not expanding.

Sequences and Metadata



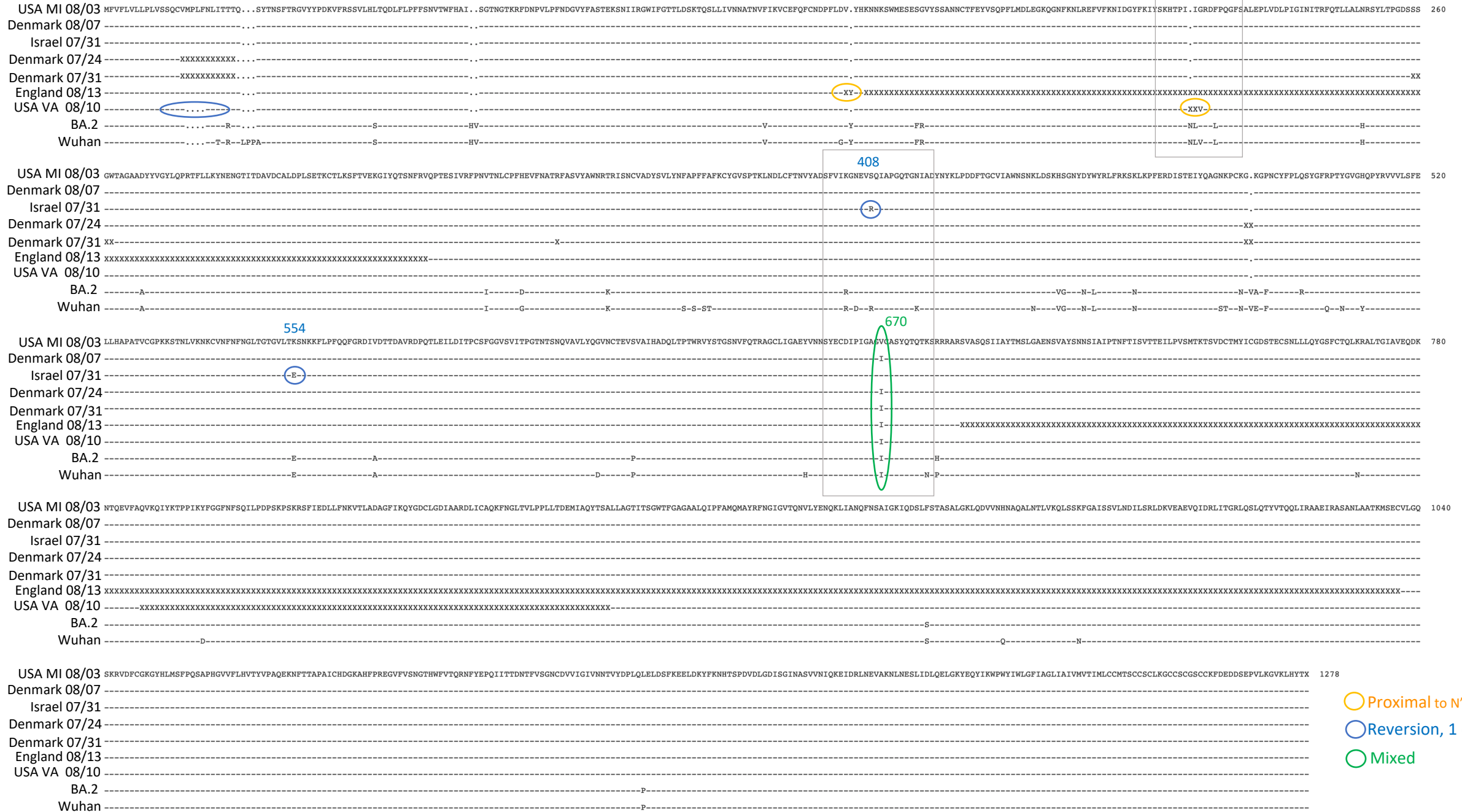
Figures are made from tools available at: cov.lanl.gov
We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID on which this research is based. The original data are available from <https://www.gisaid.org>



Considerations for Spike reagents and choice of natural isolates:

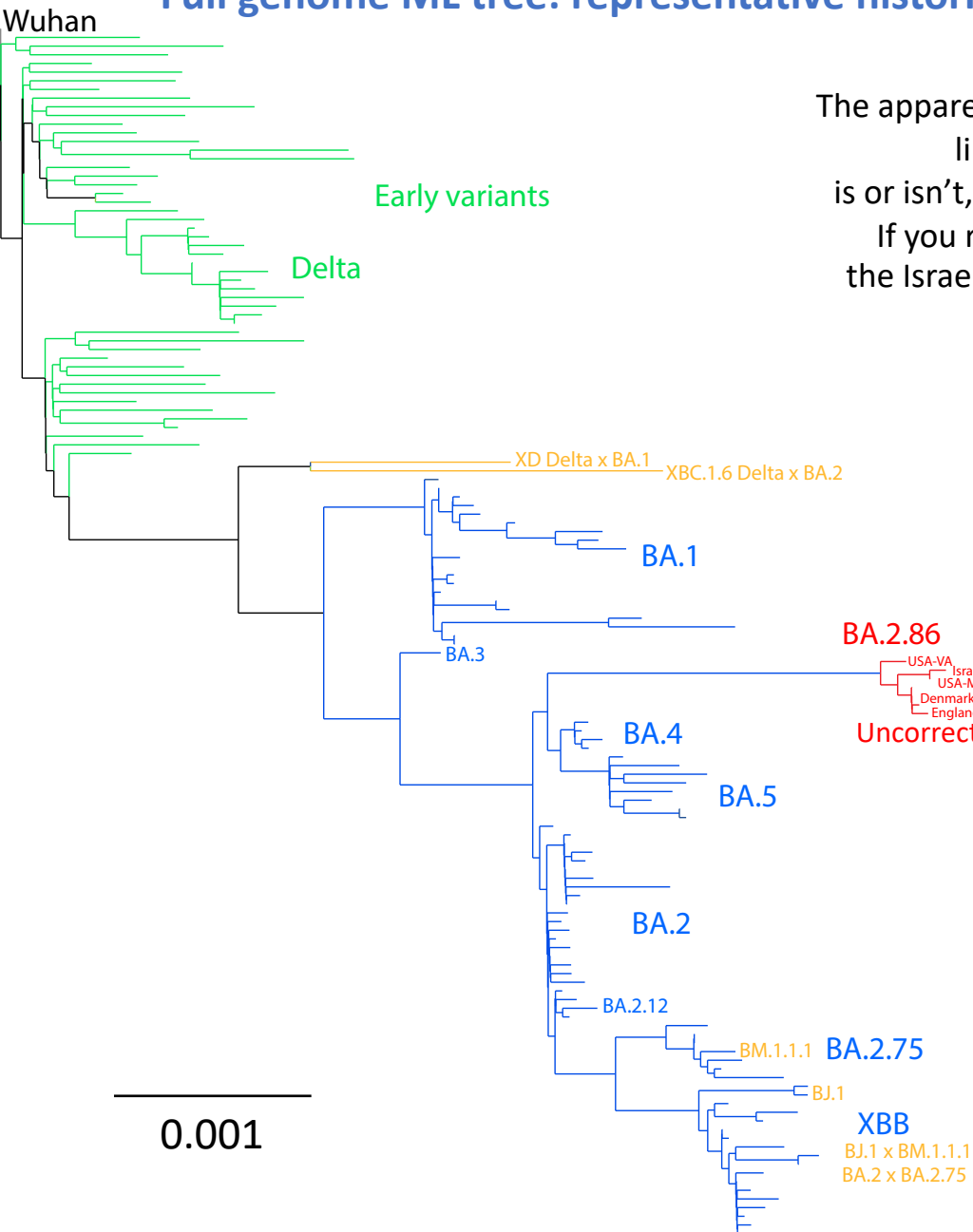
- Representative of the most common expanding form of an emerging lineage – it may not be the ancestral form, and not many variants can be tested so which do you choose?
- I emphasize variants that are both natural and most representative, as co-variation may impact phenotype.
- Often historically with newly divergent forms there have been issues with amplicon drop out, assembly... that needs some time to resolve.
- People want to order Spikes very quickly in a case like BA.2.86, so uncertainty has to be weighed against a best guess...

Comparing BA.2.86 Spikes to the Michigan sequence, X's are codons with ambiguous base calls

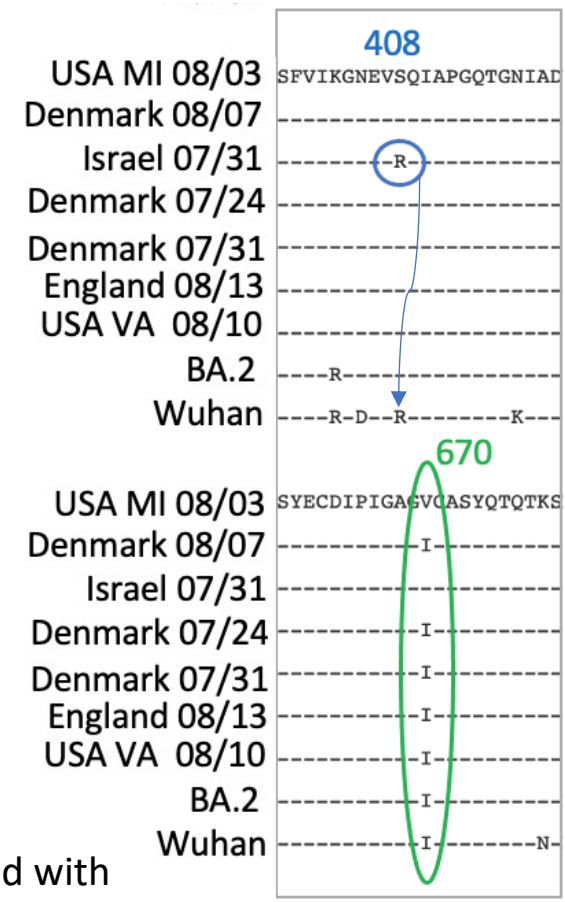


- Proximal to N's
- Reversion, 1 example
- Mixed

Full genome ML tree: representative historic SAVE VOIs



The apparent R408S reversion to R in Israel 07/31 likely sequencing artifact, but whether it is or isn't, one-offs are good to avoid in reagents. If you remove these two cases (408 and 554), the Israeli and Michigan sequences are identical



I670V is found 2x's and associated with the Israel/US clade and tracks with 4 mutations that define the clade

We will need more intact sequences to be sure we have a good call of the most common version of the spreading forms, but right now, I think the Michigan sequence or the August 7th Denmark Spike would be good choices for reagent design. They are intact in Spike only vary at I670V, so represent the Spike forms of the two clades.

Corrected:

hCoV-19/USA/MI-UM-10052670540/2023|EPI_ISL_18110065|2023-08-03

ins16MPLF, T19I, R21T, L24-, P25-, P26-, A27S, S50L, H69-, V70-, V127F, G142D, Y144-, F157S, R158G, N211-, L212I, V213G, L216F, H245N, A264D, I332V, G339H, K356T, S371F, S373P, S375F, T376A, R403K, R408S, D405N, K417N, N440K, V445H, G446S, N450D, L452W, N460K, S477N, T478K, N481K, V483-, E484K, F486P, Q498R, N501Y, Y505H, E554K, A570V, D614G, P621S, H655Y, I670V, N679K, P681R, N764K, D796Y, S939F, Q954H, N969K, P1143L

hCoV-19/Denmark/DCGC-647694/2023|EPI_ISL_18114953|2023-08-07

ins16MPLF, T19I, R21T, L24-, P25-, P26-, A27S, S50L, H69-, V70-, V127F, G142D, Y144-, F157S, R158G, N211-, L212I, V213G, L216F, H245N, A264D, I332V, G339H, K356T, S371F, S373P, S375F, T376A, R403K, R408S, D405N, K417N, N440K, V445H, G446S, N450D, L452W, N460K, S477N, T478K, N481K, V483-, E484K, F486P, Q498R, N501Y, Y505H, E554K, A570V, D614G, P621S, H655Y, N679K, P681R, N764K, D796Y, S939F, Q954H, N969K, P1143L

Phenotypic assessment of spike mutations in BA.2.86 (new highly mutated BA.2 variant: Jesse Bloom)

https://slides.com/jbloom/new_2nd_gen_ba2_variant

Likely effects of mutations relative to BA.2

These are **only estimates** of mutation effects from deep mutational scanning experiments.

- **ins16MPFL**: antibody escape (NTD supersite)
- R21T
- S50L
- del69-70
- V127F
- **delY144**: antibody escape (NTD supersite)
- **F157S**: antibody escape (NTD supersite)
- **R158G**: antibody escape (NTD supersite)
- delN211
- L212I
- L216F
- **H245N**: antibody escape (NTD supersite)
- **A264D**: antibody escape (NTD supersite)
- I332V
- D339H
- **K356T**: antibody escape, adds N-glycosylation site
- **R403K**: improves ACE2 affinity, antibody escape
- **V445H**: antibody escape
- **G446S**: antibody escape
- **N450D**: antibody escape
- **L452W**: antibody escape
- **N460K**: improves ACE2 affinity, antibody escape
- N481K
- **delV483**: reduces ACE2 affinity, antibody escape
- **A484K**: antibody escape
- **F486P**: reduces ACE2 affinity, antibody escape
- **R493Q**: improves ACE2 affinity
- E554K
- A570V
- P621S
- I670V*
- H681R
- S939F
- **P1143L**: increases spike-mediated entry in cell culture

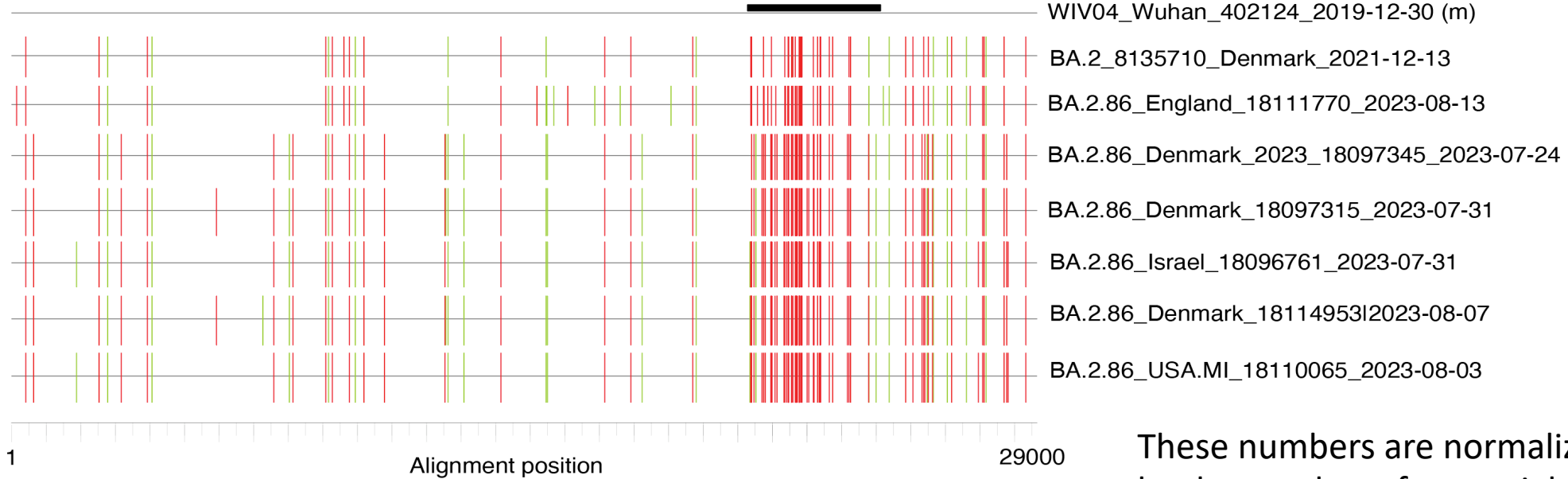
Estimates of effects of mutations from [RBD deep mutational scanning](#) by Tyler Starr, [full-spike deep mutational scanning of BA.2](#) and [XBB.1.5](#) by Bernadeta Dadonaite (Bloom lab), the Bloom lab [RBD escape calculator](#) informed by data from Yunlong Cao, and definition of the [NTD supersite](#) by Matthew McCallum & David Veessler. Experiments were performed in various genetic backgrounds and so there could be unmodeled epistasis. The * indicates mutations only in some sequences of the new variant.

Mutations are focused in Spike, and under positive selection in Spike

Syn mutation vs reference
Nonsyn mutations vs reference

I didn't mark the N's into this figure

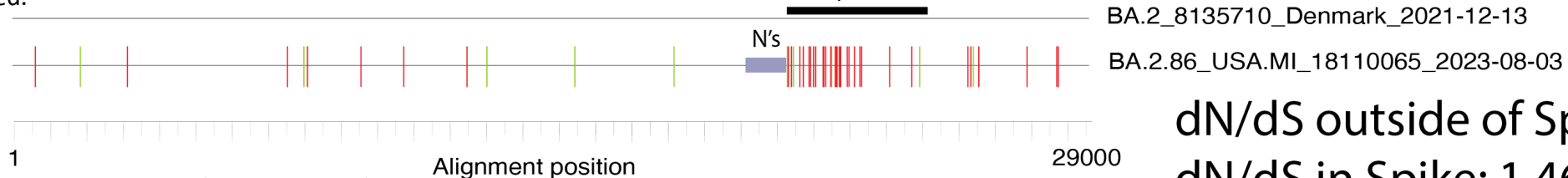
Silent and Non-silent Mutations compared to ancestral Wuhan spike



These numbers are normalized by the number of potential mutations, nonsyn mutation are ~

In this comparison the N's are marked.

Silent and Non-silent Mutations comparing BA.2.86 to BA.2



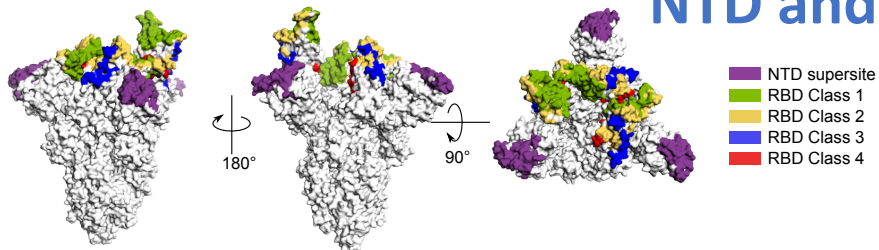
dN/dS outside of Spike: 0.61
dN/dS in Spike: 1.46



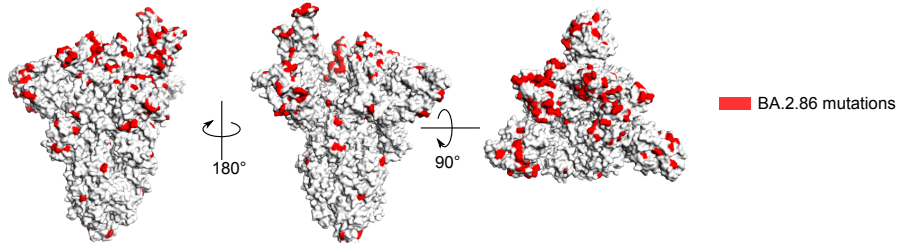
Syn	Nonsyn	Potential syn	Potential nonsyn	non-Spike	Spike
6	13	5365	19124		
6.5	33.5	838	2960		

NTD and RBD mutations in BA.2.86

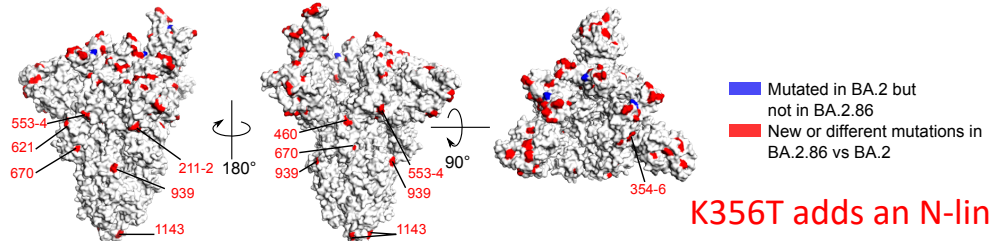
A Immudominant epitopes of CoV-2 Spike



B BA.2.86 mutations from Wuhan-1

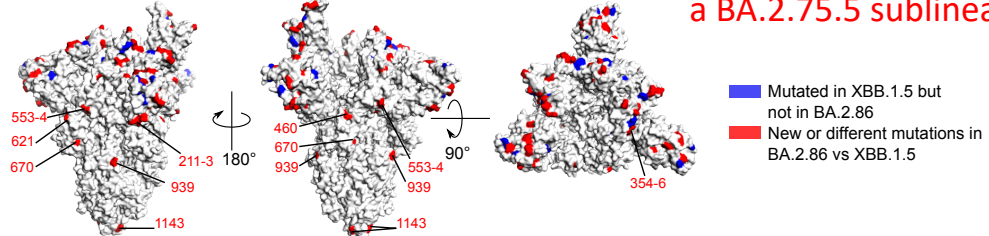


C BA.2.86 differences from BA.2

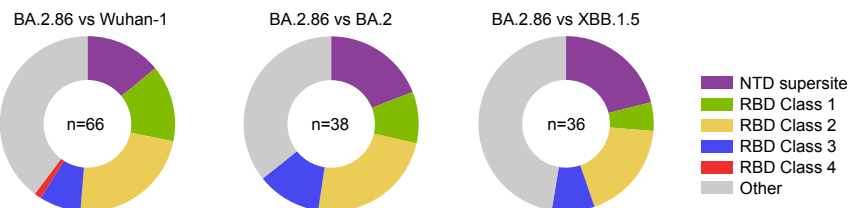


K356T adds an N-linked glycosylation site: NRT
 Rare, but occasional, for example BN.1 carries it a BA.2.75.5 sublineage

D BA.2.86 differences from XBB.1.5



E Epitope distribution of BA.2.86 mutations



An enrichment for BA.2.86 mutations in the NTD and RBD class 2

Row	Mutation	Epitope	Shared with BA.2	Shared with XBB.1.5
1	-16M	NTD	No	No
2	-16P	NTD	No	No
3	-16L	NTD	No	No
4	-16F	NTD	No	No
7	R21T	-	No	No
12	S50L	-	No	No
13	H69-	-	No	No
14	V70-	-	No	No
15	V127F	-	No	No
17	Y144-	NTD	No	No
18	F157S	NTD	No	No
19	R158G	NTD	No	No
20	N211-	-	No	No
21	L212I	-	No	No
23	L216F	-	No	No
24	H245O	NTD	No	No
25	A264D	-	No	No
26	I332V	-	No	No
28	N354O	Class3	No	No
29	K356T	Class3	No	No
34	R403K	Class2, Class1	No	No
39	V445H	Class2, Class3	No	No
41	N450D	Class2	No	No
42	L452W	Class2	No	No
46	N481K	Class2	No	No
47	V483-	Class2	No	No
48	E484K	Class2, Class1	No	No
53	E554K	-	No	No
54	A570V	-	No	No
56	P621S	-	No	No
58	I670V	-	No	No
60	P681R	-	No	No
63	S939F	-	No	No
66	P1143L	-	No	No
22	V213G	-	Yes	No
27	G339H	Class2, Class3	No	Yes
40	G446S	Class2, Class3	No	Yes
43	N460K	Class1	No	Yes
49	F486P	Class2, Class1	No	Yes
5	O17N	NTD	Yes	Yes
6	T19I	NTD	Yes	Yes
8	L24-	-	Yes	Yes
9	P25-	-	Yes	Yes
10	P26-	-	Yes	Yes
11	A27S	-	Yes	Yes
16	G142D	NTD	Yes	Yes
30	S371F	Class4, Class2	Yes	Yes
31	S373P	Class2	Yes	Yes
32	S375F	-	Yes	Yes
33	T376A	-	Yes	Yes
35	D405N	Class2, Class1	Yes	Yes
36	R408S	Class1	Yes	Yes
37	K417N	Class2, Class1	Yes	Yes
38	N440K	Class3	Yes	Yes
44	S477N	Class1	Yes	Yes
45	T478K	Class2	Yes	Yes
50	Q498R	Class2, Class1	Yes	Yes
51	N501Y	Class2, Class1	Yes	Yes
52	Y505H	Class2, Class1	Yes	Yes

BA.2.86: loss of the proline P1143L may impact conserved S2 stem helix antibody epitope

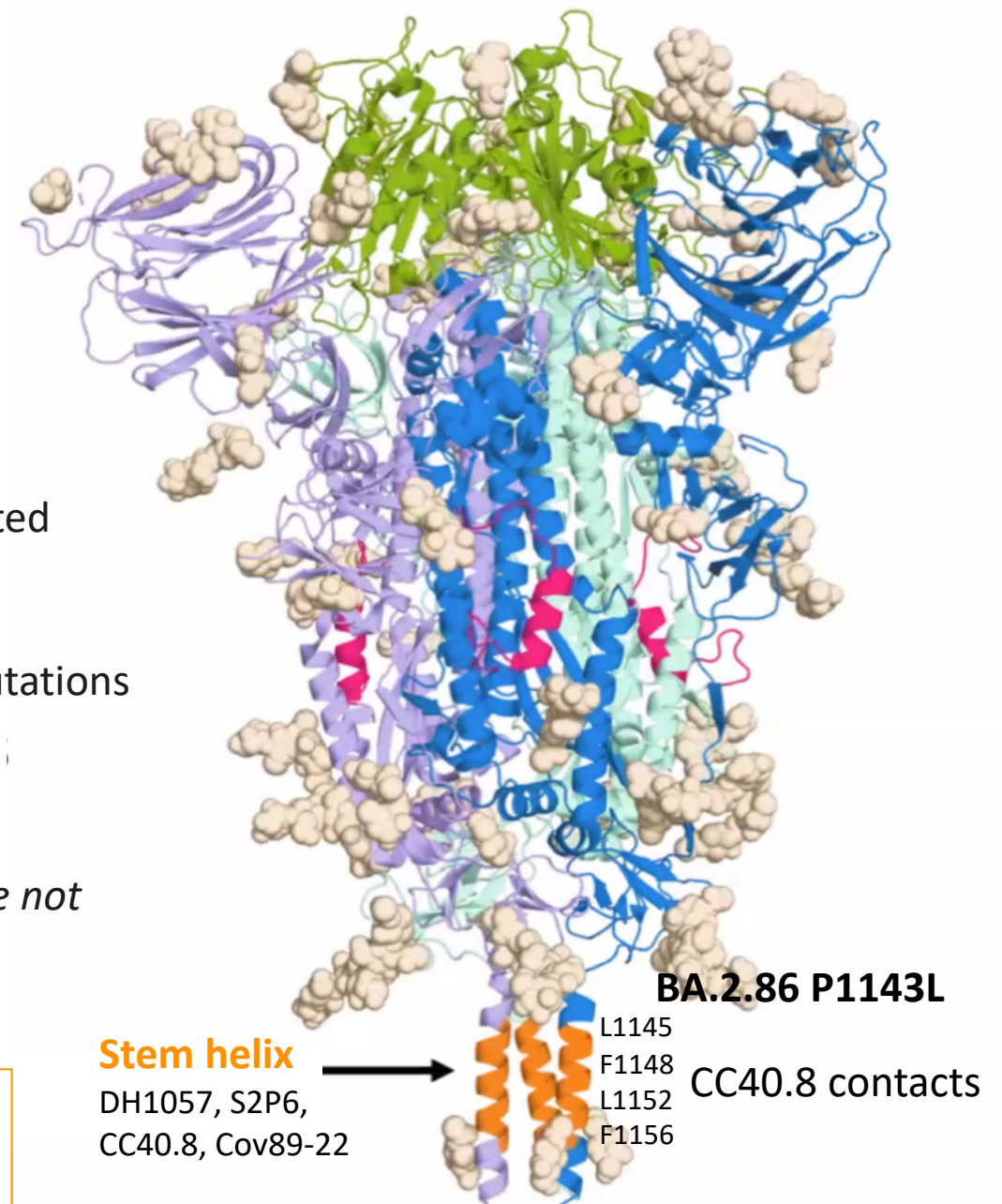
Stem helix antibodies

- rarely induced in natural infection, requires ACE2 binding for epitope exposure
- very broadly neutralizing across sarbecovirus clades and across SARS-CoV-2 VOCs
- Can protect against challenge in animals by inhibiting S-mediated membrane fusion

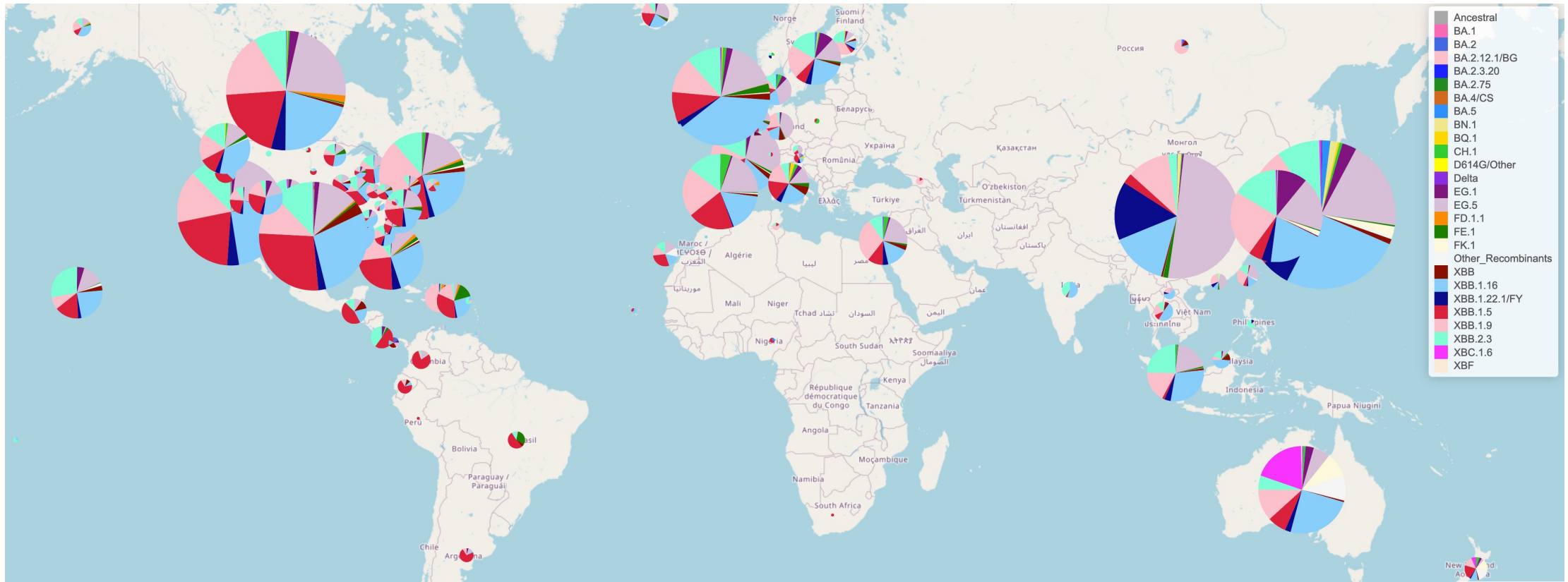
Also: Jesse Bloom points out deep mutational scanning shows mutations in P1143 and P1140 improve viral entry

(During the call Jesse noted he tested the stem helix antibodies CC67.105 and CC9.104 with Dennis Burton, and happily, they were not compromised by a mutation at 1143.)

Kapingidza... Mihai Azoitei bioRxiv
Engineered Immunogens to Expose Conserved Epitopes Targeted by Broad Coronavirus Antibodies
doi: <https://doi.org/10.1101/2023.02.27.530277>



GISAID sampling: Jul 13 – August 13



In the last month, (Jul 21 – Aug 21), this is the number of sequences deposited in GISAID by continent:

- 24 African sequences
- 55 from South America
- 6557 from North America
- 4787 Asia
- 3531 from Europe
- 551 from Oceania

The Southern Hemisphere is currently only marginally sampled. It would be important to find ways so facilitate outreach to collaborate and improve this situation.

Jul13 – Aug 13

USA Michigan

BA.2: 1
 EG.5: 13
 FE.1: 1
 FK.1: 1
 XBB.1.16: 27
 XBB.1.22.1/FY: 1
 XBB.1.5: 23
 XBB.1.9: 9
 XBB.2.3: 13
 total: 89

United Kingdom

BA.2: 1
 BA.2.3.20: 1
 BA.5: 1
 BQ.1: 4
 CH.1: 13
 EG.1: 22
 EG.5: 181
 FD.1.1: 1
 FE.1: 30
 FK.1: 5
 XBB: 23
 XBB.1.16: 413
 XBB.1.22.1/FY: 22
 XBB.1.5: 108
 XBB.1.9: 128
 XBB.2.3: 123
 XBC.1.6: 3
 total: 1079

Denmark

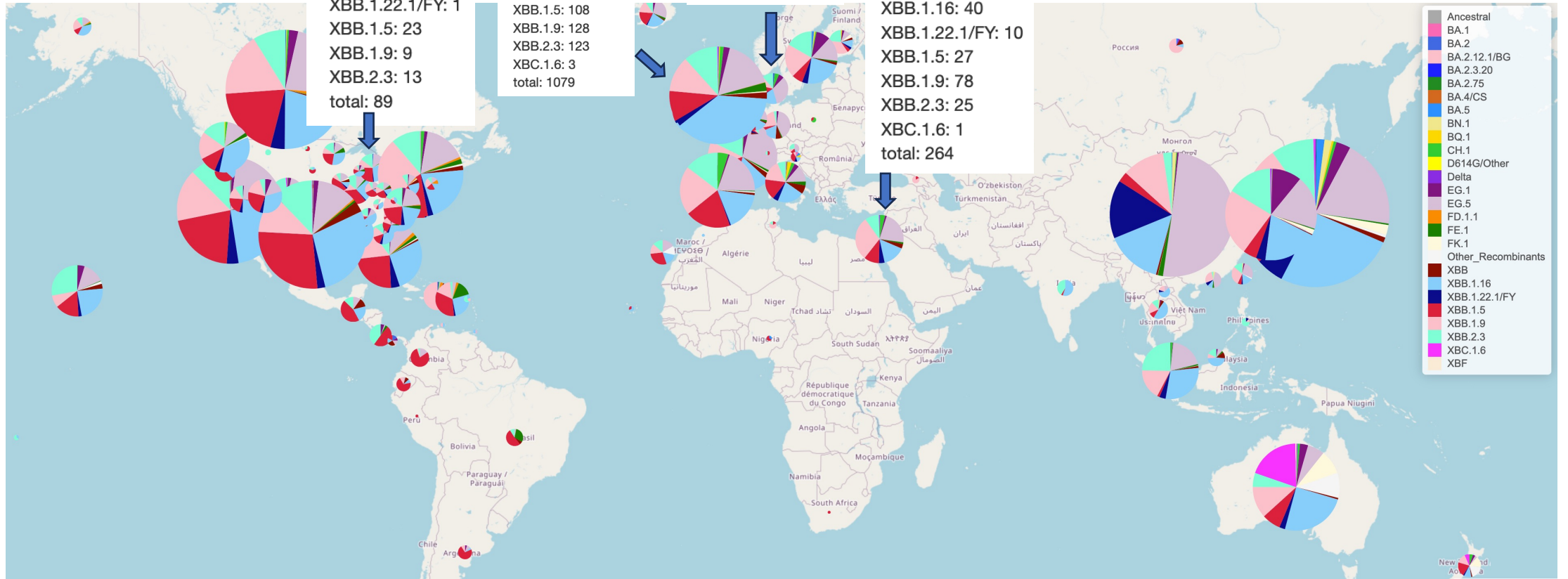
BA.2: 2
 CH.1: 5
 EG.1: 6
 EG.5: 36
 XBB.1.16: 21
 XBB.1.22.1/FY: 1
 XBB.1.5: 13
 XBB.1.9: 11
 XBB.2.3: 12
 total: 107

Israel

BA.2: 1
 CH.1: 9
 EG.1: 3
 EG.5: 59
 FE.1: 3
 XBB: 8
 XBB.1.16: 40
 XBB.1.22.1/FY: 10
 XBB.1.5: 27
 XBB.1.9: 78
 XBB.2.3: 25
 XBC.1.6: 1
 total: 264

Sources of BA.2.86;

In this slide the BA.2's
 Data were not yet updated to be called
 BA.2.86, the "BA.2's" are actually
 the BA.2.86.



BA.2.86 metadata in GISAID and discovery

Virus name	Accession ID	Collection date	Location	Additional host information	Sampling strategy
hCoV-19/Israel/ICH-741198454/2023	EPI_ISL_18096761	7/31/23	Asia / Israel		
hCoV-19/Denmark/DCGC-647646/2023	EPI_ISL_18097315	7/31/23	Europe / Denmark	n_infections=2,last_infection_date=2022-01-31	
hCoV-19/Denmark/DCGC-647676/2023	EPI_ISL_18097345	7/24/23	Europe / Denmark	n_infections=2,last_infection_date=2022-01-10	
* hCoV-19/Denmark/DCGC-647694/2023	EPI_ISL_18114953	8/7/23	Europe / Denmark	n_infections=2,last_infection_date=2022-03-21	
* hCoV-19/USA/MI-UM-10052670540/2023	EPI_ISL_18110065	8/3/23	North America / USA / Michigan		Baseline surveillance
hCoV-19/England/GSTT-YYBYBN4/2023	EPI_ISL_18111770	8/13/23	Europe / United Kingdom / England / London		
hCoV-19/USA/VA-GBW-H20-330-6734/2023	EPI_ISL_18121060	8/10/23	North America / USA / Virginia / Loudoun County	Traveler from Japan	
hCoV-19/South Africa/NICD-N55999/2023	EPI_ISL_18125249	7/28/23	Africa / South Africa / Mpumalanga		Baseline Surveillance
hCoV-19/South Africa/NICD-N55967/2023	EPI_ISL_18125259	7/24/23	Africa / South Africa / Gauteng		Baseline Surveillance

*Currently proposed reference Spikes based on available data

SUPPLEMENTAL TABLE

Data Availability

GISAID Identifier: EPI_SET_230823eb

doi: [10.55876/gis8.230823eb](https://doi.org/10.55876/gis8.230823eb)

All genome sequences and associated metadata in this dataset are published in GISAID's EpiCoV database. To view the contributors of each individual sequence with details such as accession number, Virus name, Collection date, Originating Lab and Submitting Lab and the list of Authors, visit [10.55876/gis8.230823eb](https://gisaid.org/epicov/230823eb)

Data Snapshot

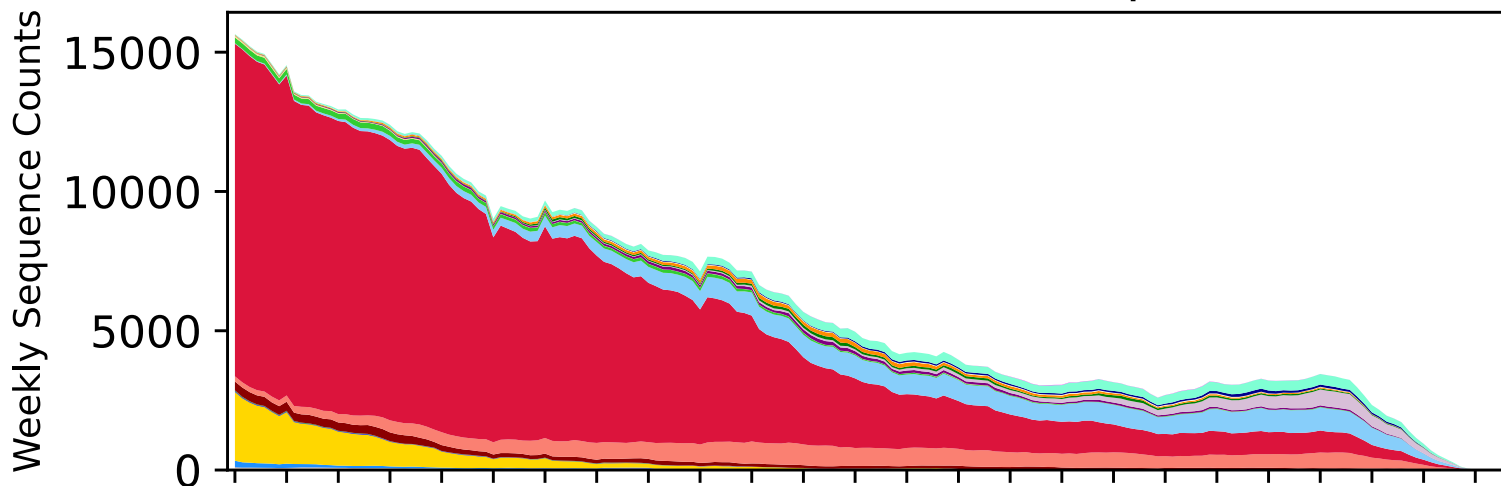
- EPI_SET_230823eb is composed of 7 individual genome sequences.
- The collection dates range from 2023-07-24 to 2023-08-13;
- Data were collected in 4 countries and territories;
- All sequences in this dataset are compared relative to hCoV-19/Wuhan/WIV04/2019 (WIV04), the official reference sequence employed by GISAID (EPI_ISL_402124). Learn more at <https://gisaid.org/WIV04>.

https://epicov.org/epi3/epi_set/230823eb?main=true

Thank you!

New

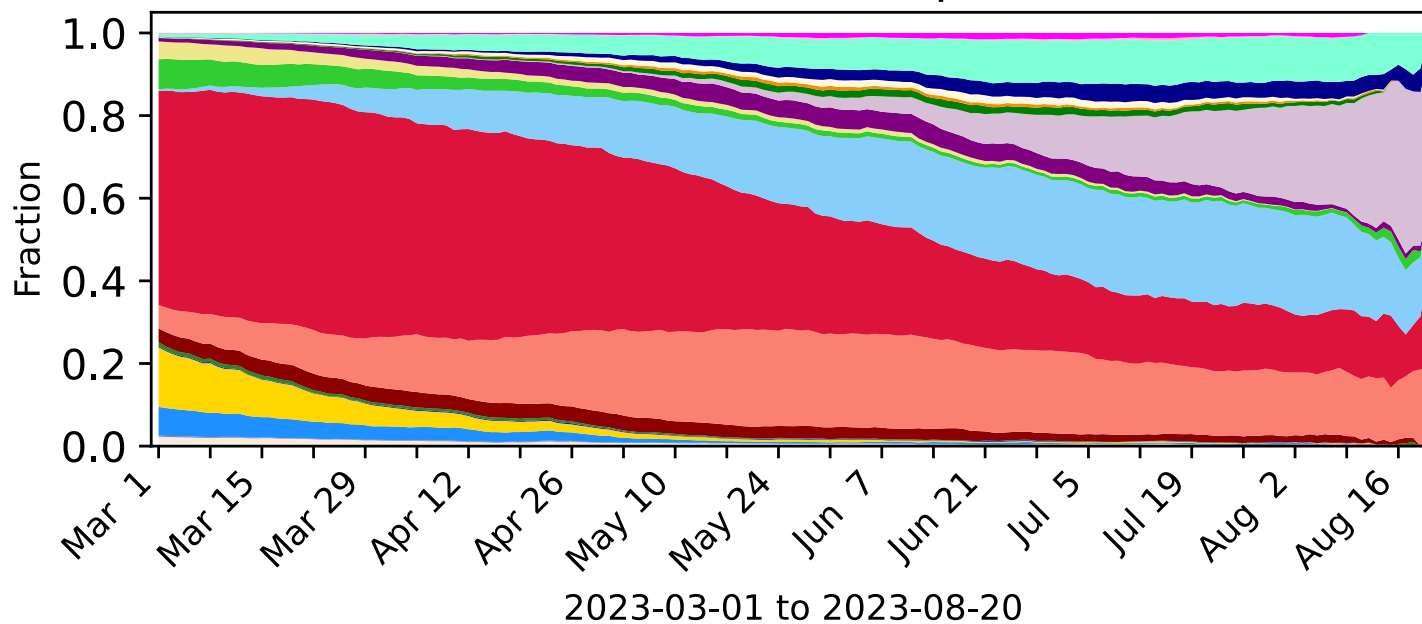
North-America: 160561 sequences



Grouped Lineages

- XBC.1.6
- XBC
- XBB.2.3
- XBB.1.22.1/FY
- FK.1
- FD.1.1
- FE.1
- EG.5
- EG.1
- BN.1
- CH.1
- XBB.1.16
- XBB.1.5
- XBB.1.9
- XBB
- BA.2.75
- BA.2.3.20
- BQ.1
- BA.5
- BA.4/CS
- BA.2.12.1/BG
- BA.2
- BA.1
- Delta
- Iota
- Epsilon
- Mu
- Gamma
- Beta
- Alpha
- D614G/Other
- Ancestral
- XBF
- Other_Recombinants

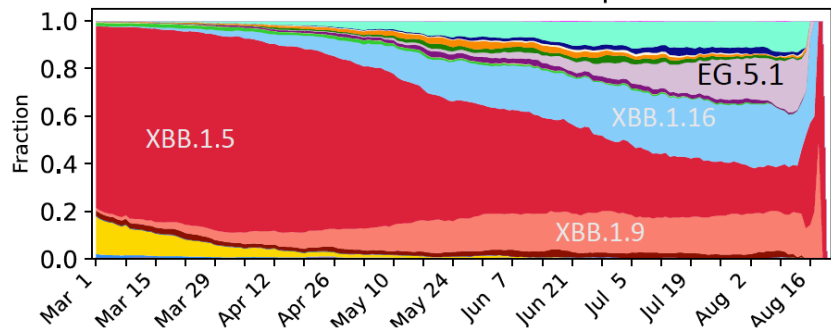
Global: 484779 sequences



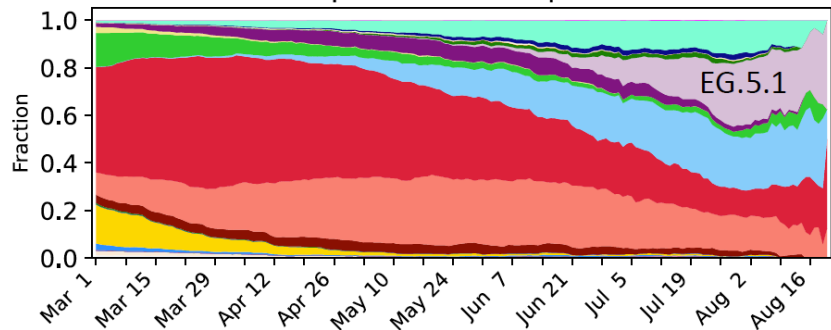
EG.5.1
lineage

Frequency

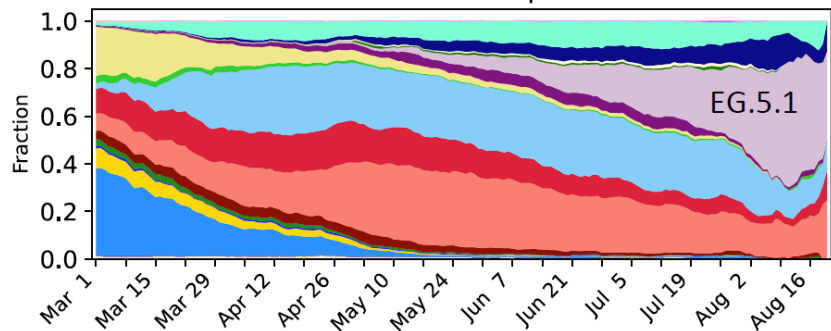
North-America: 160561 sequences



Europe: 156956 sequences



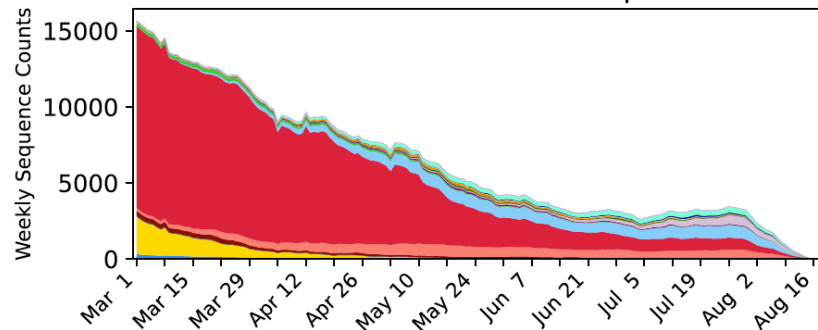
Asia: 124696 sequences



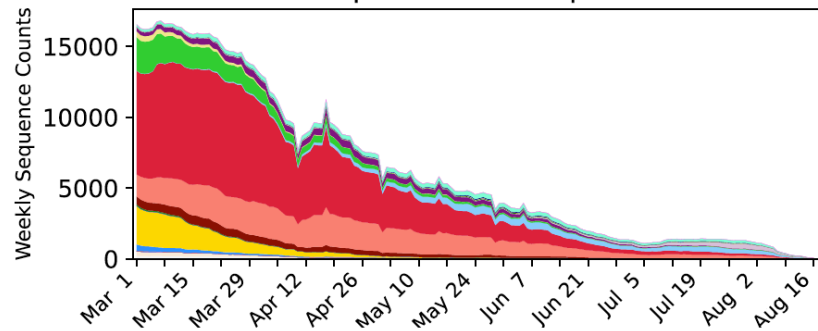
2023-03-01 to 2023-08-20

Counts

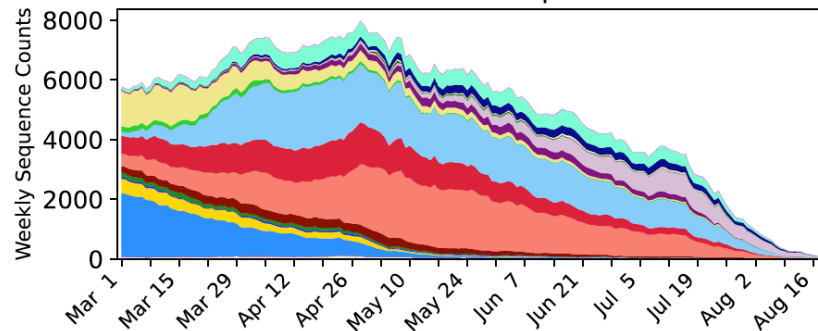
North-America: 160561 sequences



Europe: 156956 sequences

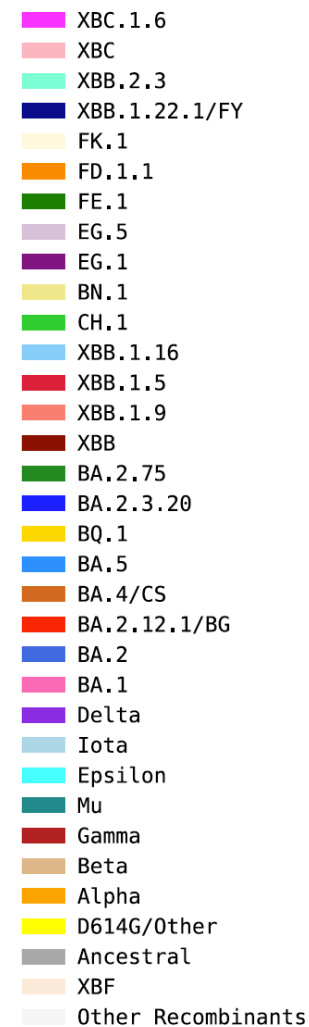


Asia: 124696 sequences



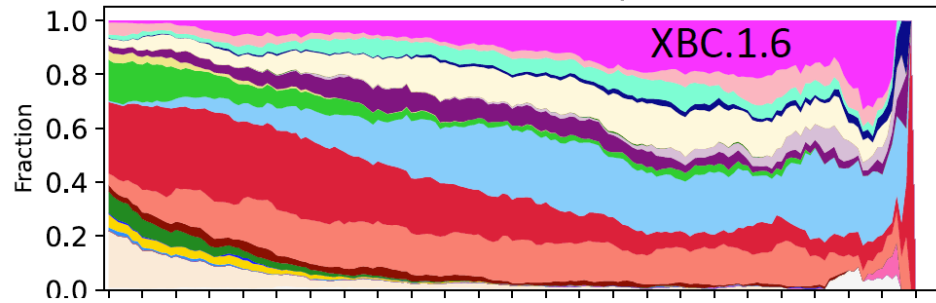
2023-03-01 to 2023-08-20

Grouped Lineages



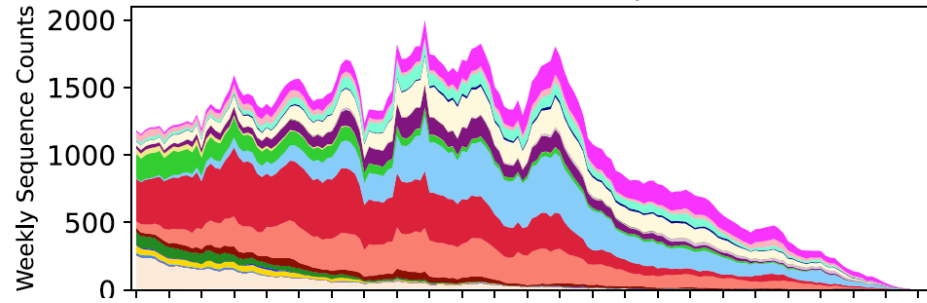
Frequency

Oceania: 25936 sequences



Counts

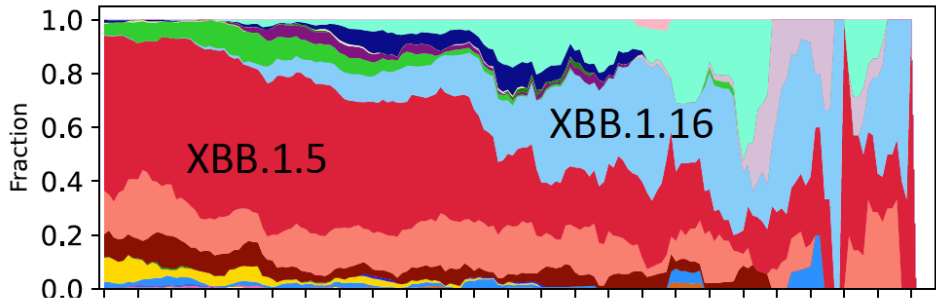
Oceania: 25936 sequences



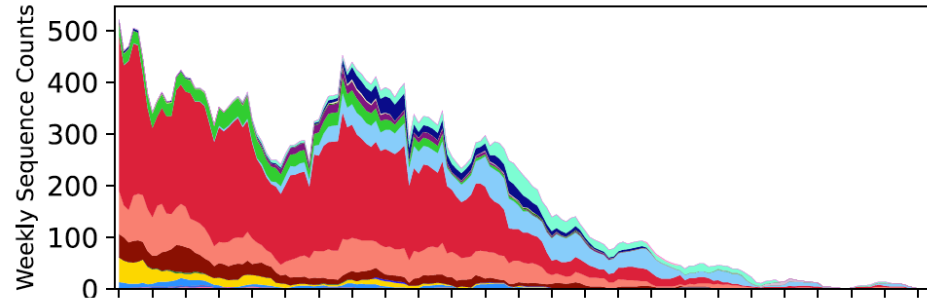
Grouped Lineages

- XBC.1.6
- XBC
- XBB.2.3
- XBB.1.22.1/FY
- FK.1
- FD.1.1
- FE.1
- EG.5
- EG.1
- BN.1
- CH.1
- XBB.1.16
- XBB.1.5
- XBB.1.9
- XBB
- BA.2.75
- BA.2.3.20
- BQ.1
- BA.5
- BA.4/CS
- BA.2.12.1/BG
- BA.2
- BA.1
- Delta
- Iota
- Epsilon
- Mu
- Gamma
- Beta
- Alpha
- D614G/Other
- Ancestral
- XBF
- Other_Recombinants

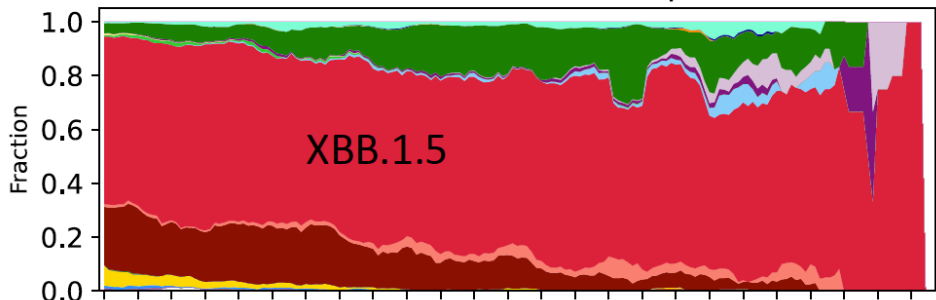
Africa: 5047 sequences



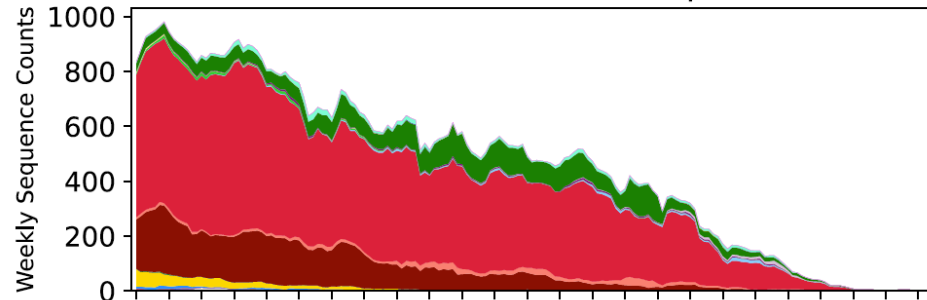
Africa: 5047 sequences



South-America: 11583 sequences



South-America: 11583 sequences



2023-03-01 to 2023-08-20

2023-03-01 to 2023-08-20

Pango lineage designation in GISAID

Test lineage(s): EG.5, EG.5.1

Background lineage(s): All

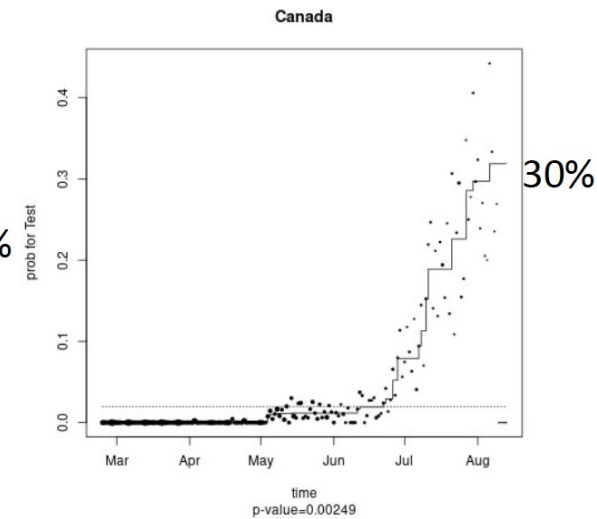
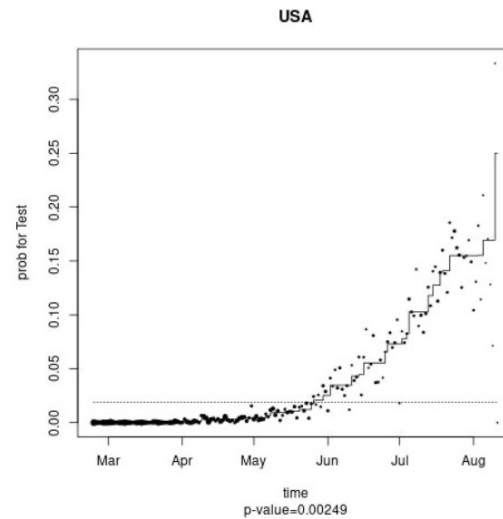
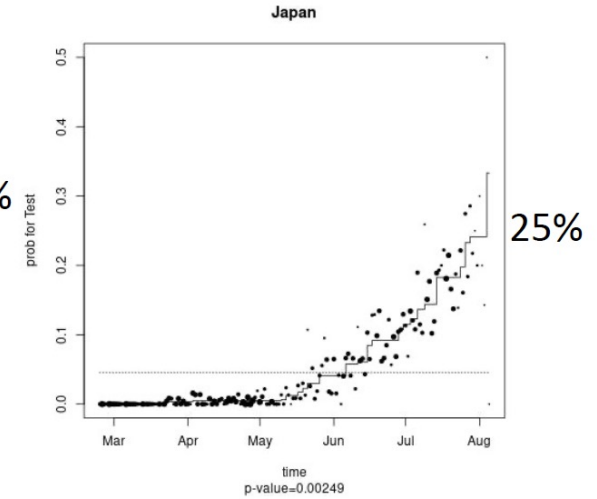
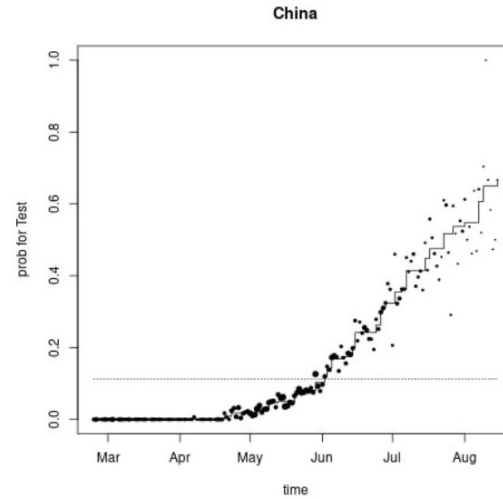
Assumption: Test lineages are increasing over time

Range of dates: 2023-02-23 - 2023-08-20

EG.5 Isotonic Regression Results

There were 10,978 sequences that matched your search term, It was significantly increasing in all 35 countries where it was found more than 10 times:

	# Test	# Others	Total	Test/Total (%)	# days	Time window	p-val
Australia	206	21748	21954	0.94	168	167	0.00249
Austria	85	16977	17062	0.50	146	165	0.00249
Belgium	17	3699	3716	0.46	146	165	0.00249
Canada	694	34587	35281	1.97	172	171	0.00249
Canary-Islands	14	461	475	2.95	156	166	0.00249
China	3402	27027	30429	11.18	174	173	0.00249
Colombia	29	1483	1512	1.92	146	148	0.00249
Costa-Rica	19	1273	1292	1.47	153	154	0.00249
Denmark	66	4742	4808	1.37	116	165	0.00249
Finland	13	2631	2644	0.49	150	160	0.00249
France	260	18277	18537	1.40	163	165	0.00249
Germany	136	17760	17896	0.76	156	160	0.00249
Guatemala	15	633	648	2.31	115	154	0.00249
Hong-Kong	74	632	706	10.48	149	163	0.00249
Iceland	28	460	488	5.74	137	166	0.00249
Indonesia	39	3738	3777	1.03	123	134	0.02239
Ireland	103	3209	3312	3.11	173	172	0.00249
Israel	106	3480	3586	2.96	149	172	0.00249
Italy	52	7039	7091	0.73	165	165	0.00249
Japan	1188	24803	25991	4.57	164	163	0.00249
Laos	23	146	169	13.61	69	103	0.10697
Luxembourg	60	2652	2712	2.21	144	150	0.00249
Malaysia	22	3310	3332	0.66	151	155	0.00249
Netherlands	35	4717	4752	0.74	165	173	0.00249
New-Zealand	20	3971	3991	0.50	144	145	0.00249
Portugal	102	1955	2057	4.96	136	146	0.00249
Puerto-Rico	16	2427	2443	0.65	146	154	0.00249
Singapore	197	7534	7731	2.55	156	160	0.00249
South-Korea	890	32292	33182	2.68	154	153	0.00249
Spain	246	15024	15270	1.61	174	173	0.00249
Sweden	91	7942	8033	1.13	168	167	0.00249
Taiwan	34	721	755	4.50	126	151	0.00249
Thailand	15	2524	2539	0.59	162	166	0.00249
USA	2263	118083	120346	1.88	170	169	0.00249
United-Kingdom	347	36006	36353	0.95	164	163	0.00249



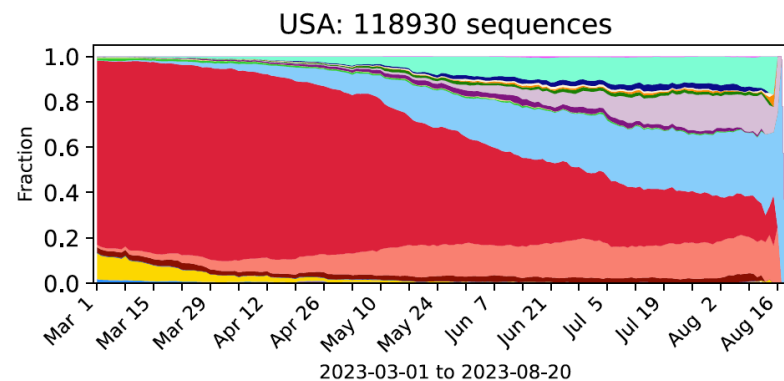
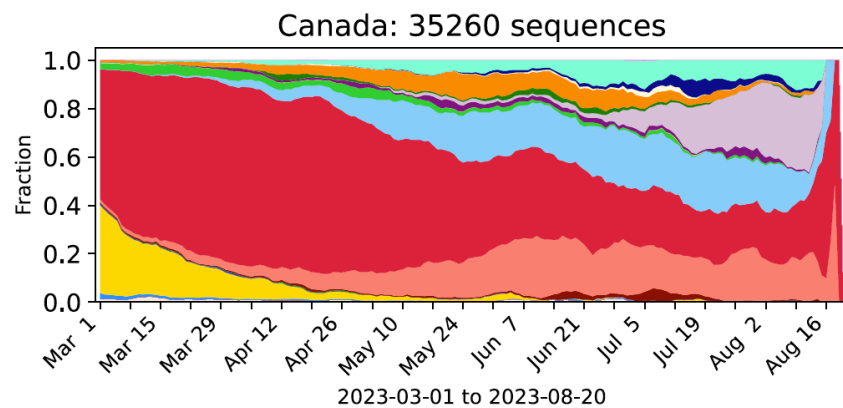
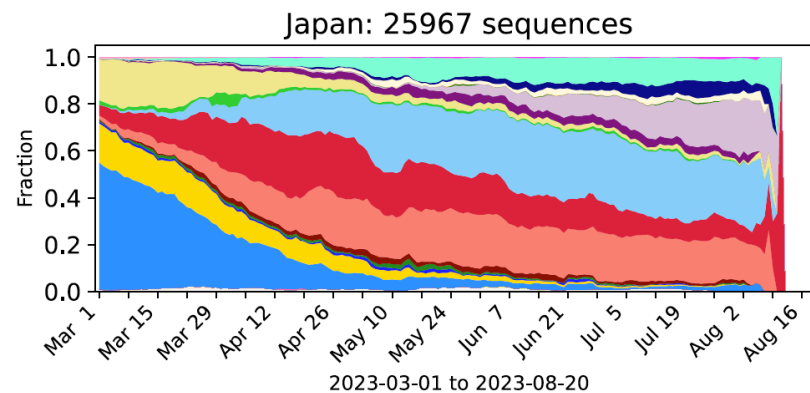
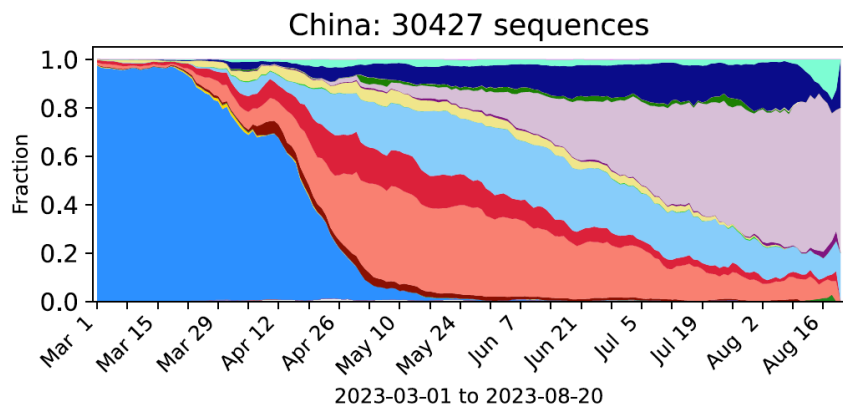
EG.5 and EG.5.1 in GISAID: the five or six most common forms

EG.5 Alias of XBB.1.9.2.5, S:F456L
 EG.5.1 Alias of XBB.1.9.2.5.1, S:Q52H

Pango lineage
 designations not
 yet is GISAID

Lineage	Count	Count	Pct	HD	[Form as mutation string]	
EG.5.1	6068	4310	71.0%	0	+ [Q52H, F456L] (consensus)	
EG.5.1	6068	139	2.3%	1	+ [Q52H, H146K, F456L] - [H146Q]	
EG.5.1	6068	87	1.4%	1	+ [Q52H, L455F, F456L]	HK.3
EG.5.1	6068	75	1.2%	1	+ [Q52H, F157L, F456L]	EG.5.1.6
EG.5.1	6068	61	1.0%	1	+ [Q52H, G257V, F456L]	HK.1
EG.5.1	6068	37	0.6%	2	+ [Q52H, F157L, L452R, F456L]	HV.1
EG.5	550	268	48.7%	0	+ [F456L] (consensus)	
EG.5	550	49	8.9%	2	+ [F456L, S704L, N1178D]	EG.5.2.3
EG.5	550	42	7.6%	1	+ [F456L, S704L]	EG.5.2.1
EG.5	550	23	4.2%	2	+ [H69-, V70-, F456L]	
EG.5	550	17	3.1%	2	+ [L5F, F456L, S704L]	

Grouped Lineages



- XBC.1.6
- XBC
- XBB.2.3
- XBB.1.22.1/FY
- FK.1
- FD.1.1
- FE.1
- EG.5
- EG.1
- BN.1
- CH.1
- XBB.1.16
- XBB.1.5
- XBB.1.9
- XBB
- BA.2.75
- BA.2.3.20
- BQ.1
- BA.5
- BA.4/CS
- BA.2.12.1/BG
- BA.2
- BA.1
- Delta
- Iota
- Epsilon
- Mu
- Gamma
- Beta
- Alpha
- D614G/Other
- Ancestral
- XBF
- Other_Recombinants

Fastest increasing forms of Spike sampled >60 times in the last 60 days globally, and a representative Pango lineage carrying that form

↓ Most interesting column is Relative differences, but Absolute (Abs) and counts are also of interest

Pango Lineage	Global Count	Form Count	Form Pct	Counts Early/Later	Fractions Early/Later	Differences Abs	Differences Relative	pval	HD	[Form as mutation string relative to XBB.1.5]
v means variant										
FE.1	31444	1402	4.5%	662/740	0.04319/0.04591	+0.27%	+5.9%	3e-1	1	+ [F456L] Brazil. XBB.1.18.1, XBB.1.5, XBB.1.16, XBB.1.9
EG.5.1	31444	3047	9.7%	1155/1892	0.07536/0.11738	+4.20%	+35.8%	<1e-9	2	+ [Q52H, F456L] XBB.1.9.2
EG.5.1v	31444	111	0.4%	43/68	0.00281/0.00422	+0.14%	+33.5%	4e-2	3	+ [Q52H, H146K, F456L] - [H146Q]
XBB.1.16.6	31444	471	1.5%	176/295	0.01148/0.01830	+0.68%	+37.3%	6e-7	3	+ [E180V, F456L, T478R] - [T478K] XBB.1.16
FL.1	31444	330	1.0%	53/277	0.00346/0.01719	+1.37%	+79.9%	<1e-9	3	+ [F456L, T478R, A701V] - [T478K] XBB.1.9.1
XBB.2.3.3	31444	496	1.6%	229/267	0.01494/0.01657	+0.16%	+9.8%	3e-1	6	+ [K182N, D253G, P521S] - [G252V]
GE.1	31444	165	0.5%	56/109	0.00365/0.00676	+0.31%	+46.0%	2e-4	8	+ [N185I, F186-, D253G, T478R, P521S] - [G252V, T478K]
FY.3v	31444	94	0.3%	39/55	0.00254/0.00341	+0.09%	+25.4%	2e-1	4	+ [Y200C, I210T] XBB.1.22.1 sublineage
XBB.1.19.1v	31444	266	0.8%	97/169	0.00633/0.01049	+0.42%	+39.6%	6e-5	3	+ [E554K] FL.10.1, FL.25
XBB.1.16v	31444	207	0.7%	96/111	0.00626/0.00689	+0.06%	+9.0%	5e-1	5	+ [E180V, K304N, T478R] - [T478K]
XBB.1.16v	31444	187	0.6%	47/140	0.00307/0.00869	+0.56%	+64.7%	<1e-9	5	+ [E180V, T478R, P521T] - [T478K]
FU.2v	31444	127	0.4%	45/82	0.00294/0.00509	+0.22%	+42.3%	3e-3	6	+ [E180V, T478R, T547I, E619Q] - [T478K]

F456L
 P521S

Forms listed are both increasing and sampled >100 times in the last 60 days

Data: Take all non-ambiguous Spike sequences in the last 60 days. Divide that the number in half, and find the day where the split occurs. Count the number of every variant of Spike before and after the split, and see if the fraction is increasing. The Pango lineage is just the most common designation with that form of Spike.

XBC.1.6

Pango lineage designation in GISAID

Test lineage(s): XBC.1.6, XBC.1.6.1, XBC.1.6.2, XBC.1.6.3

Background lineage(s): All

Assumption: Test lineages are increasing over time

Range of dates: 2023-02-23 - 2023-08-21

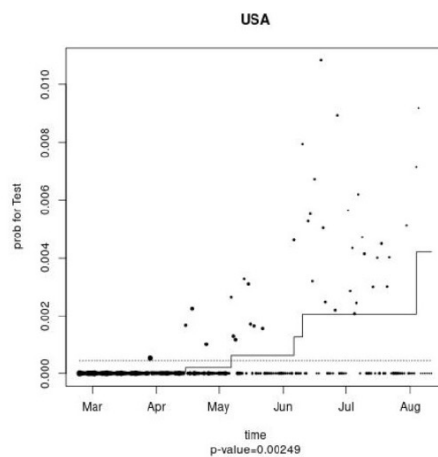
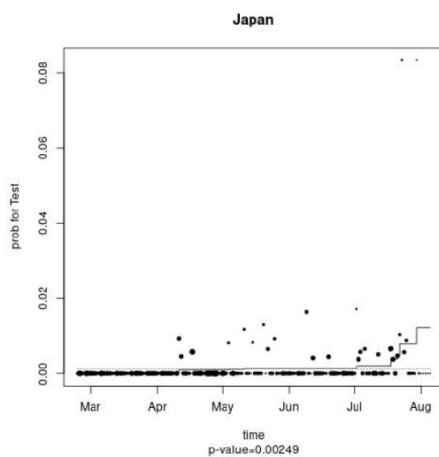
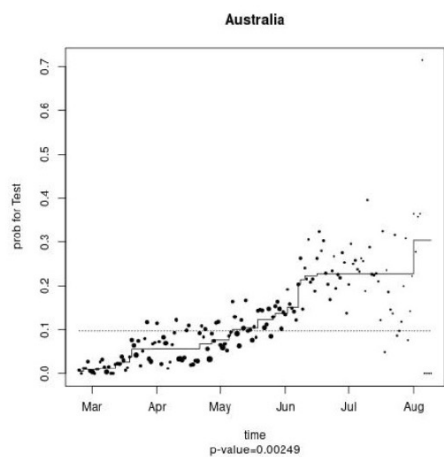
Hosts: include all

[Download plots and data](#)

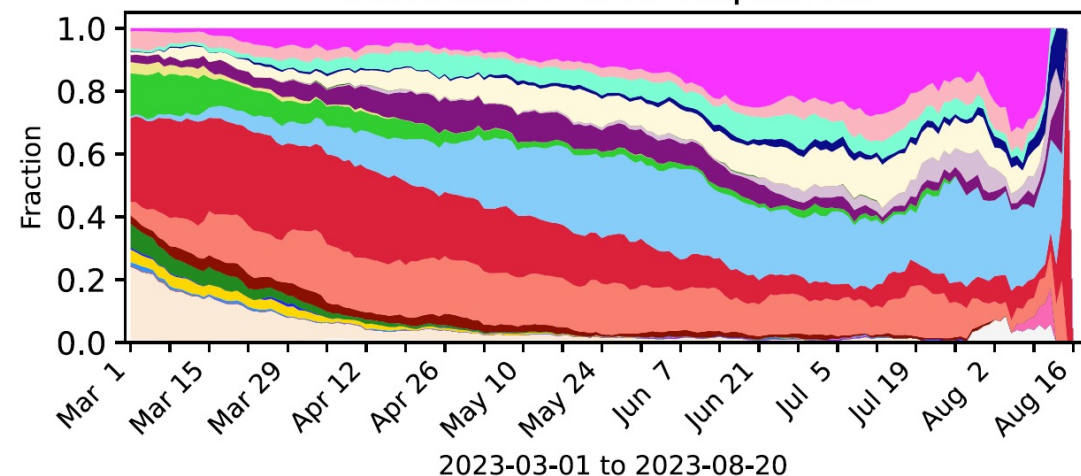
Country level

There were 2,278 sequences that matched your search term, the following summarizes the form in locations where it was found more than 10 times.

	# Test	# Others	Total	Test/Total (%)	# days	Time window	p-val
Australia	2138	19816	21954	9.74	168	167	0.00249
Japan	32	25959	25991	0.12	164	163	0.00249
USA	55	120346	0.05	170	169	0.00249	



Australia: 21907 sequences



California is state in the US in which XBC.1.6 was been sampled most, scattered samples: not increasing

