Whole genomic sequencing of the SARS-CoV-2 variants in Sri Lanka

14.01.2022

182 samples were sequenced from last week of December and 1st week of January from the community and arrival and departure samples from the airport.

Omicron: 160/182. These include a mix of the two main Omicron lineages BA.1 and BA.2.

Delta: 22/182 (please see details below)

Distribution of Omicron sub lineages and locations

BA.1: 139/182: BIA, Angoda, Colombo, Dehiwala, Galle, Kaduwela, Kandy, Matara, Minuwangoda, Negombo, Trincomalee

BA.2: 17/182 : BIA, Colombo

B.1.1.529: 4/182: BIA, Colombo

Note: 98 samples from BIA that were positive and were found to be infected with Omicron, are from departure passengers and not arrival passengers. While some of them were Sri Lankans some were foreign nationals.

Detection of different delta sub lineages and locations:

AY.28 (Sri Lanka delta sub-lineage): 4/182. BIA, Nugegoda

AY.104 (Sri Lanka delta sub-lineage): 10/182

AY.25: Colombo

AY.114: Colombo

AY.5.3: Angoda

B.1.617.2: Angoda, Colombo, Ratnapura

Timeline of the emergence and displacement of different variants in Sri Lanka

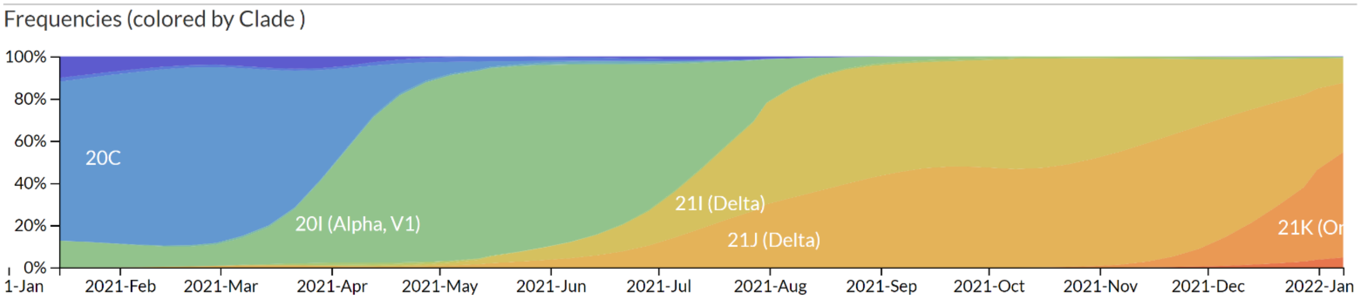


Figure 1: Change in the SARS-CoV-2 variants in Sri Lanka over time. The graph shows changes in the different variants

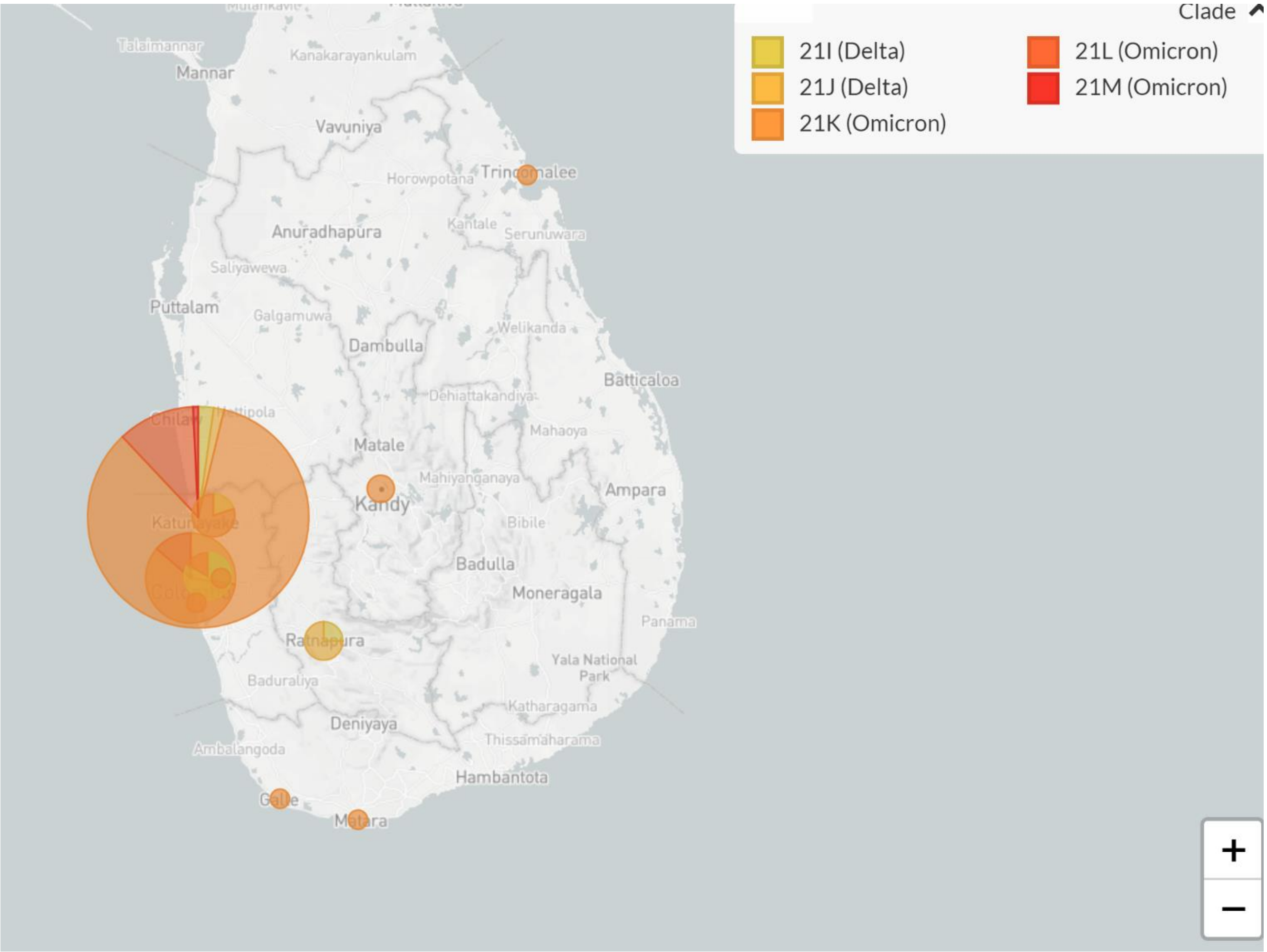
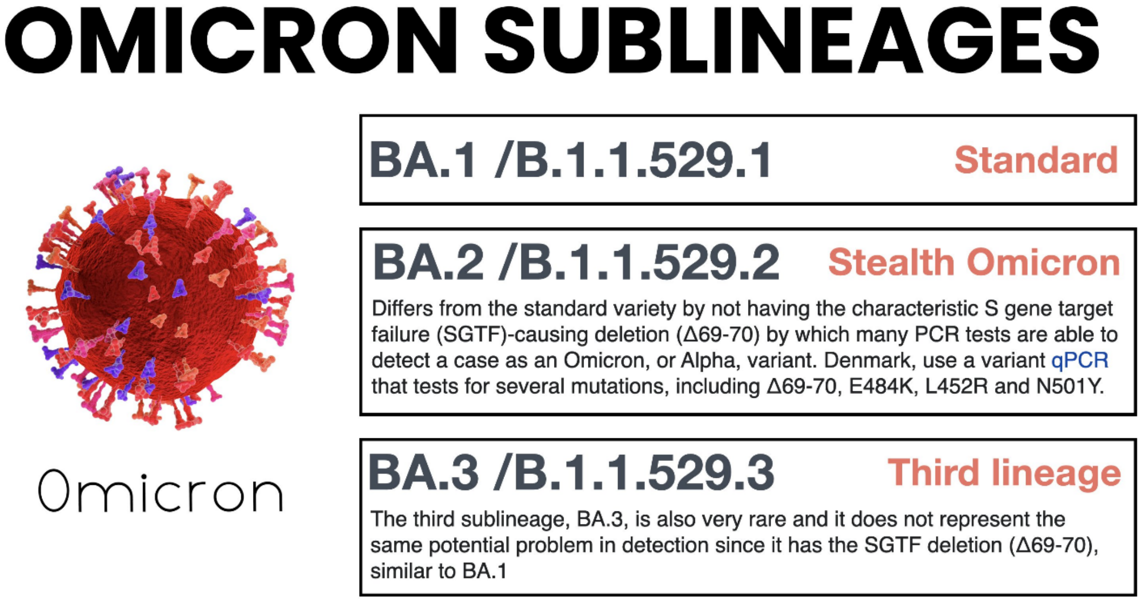


Figure 2: Locations of samples sequenced during the past week (4th week of December and 1st week of January)

Differences in Omicron BA.1 vs BA.2



OMICRON SUBLINEAGES

BA.1 /B.1.1.529.1 Standard

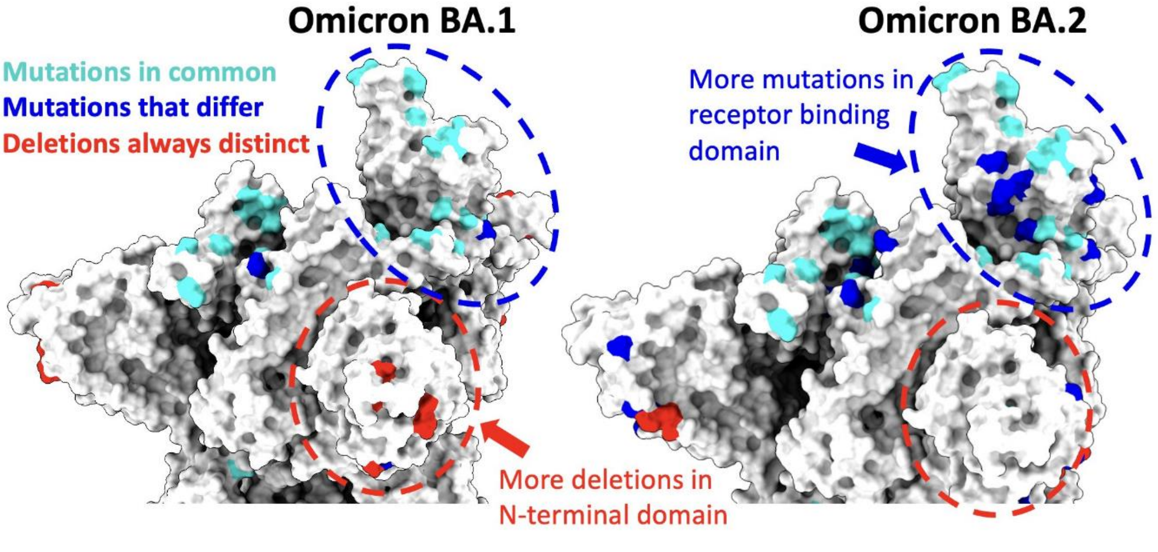
BA.2 /B.1.1.529.2 Stealth Omicron

Differs from the standard variety by not having the characteristic S gene target failure (SGTF)-causing deletion (Δ69-70) by which many PCR tests are able to detect a case as an Omicron, or Alpha, variant. Denmark, use a variant qPCR that tests for several mutations, including Δ69-70, E484K, L452R and N501Y.

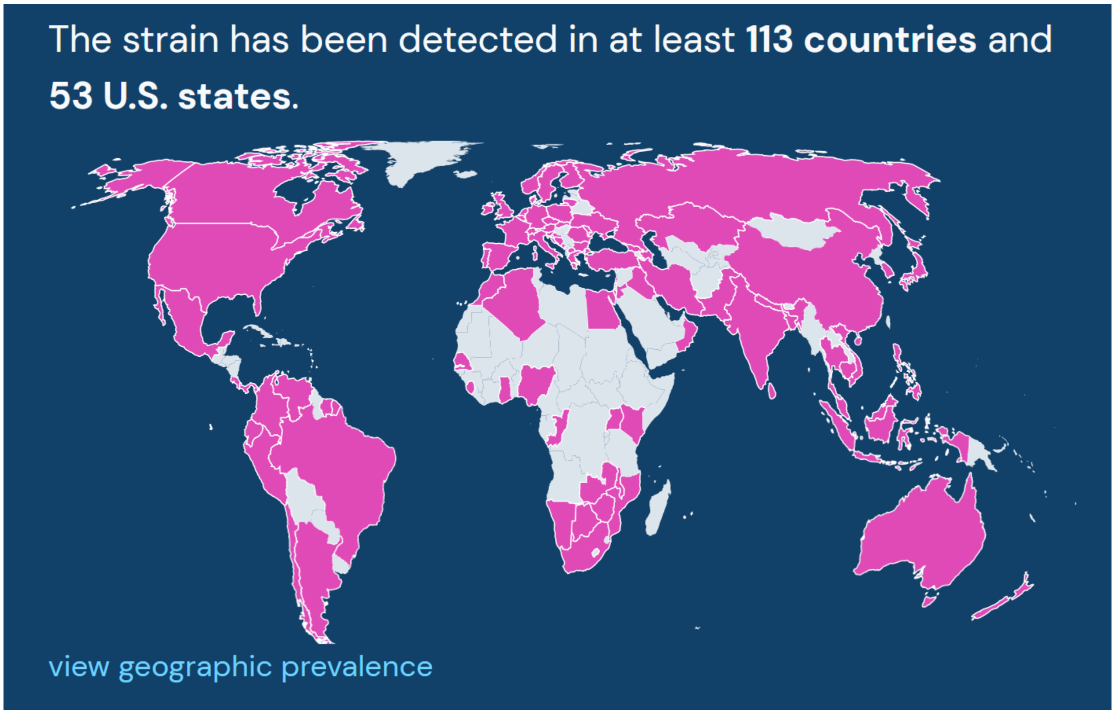
BA.3 /B.1.1.529.3 Third lineage

The third sublineage, BA.3, is also very rare and it does not represent the same potential problem in detection since it has the SGTF deletion (Δ69-70), similar to BA.1

BA.2: Does not have the 69/70 deletion and therefore, does not show the S gene target failure (SGTF) like other Omicron variants, by the Taqpath qRT-PCR kit. BA.2 shares 32 mutations with BA.1 but has an addition 28 unique mutations. As BA.2 has more mutations, it is possible that it might be more immune evasive, which is currently being investigated.



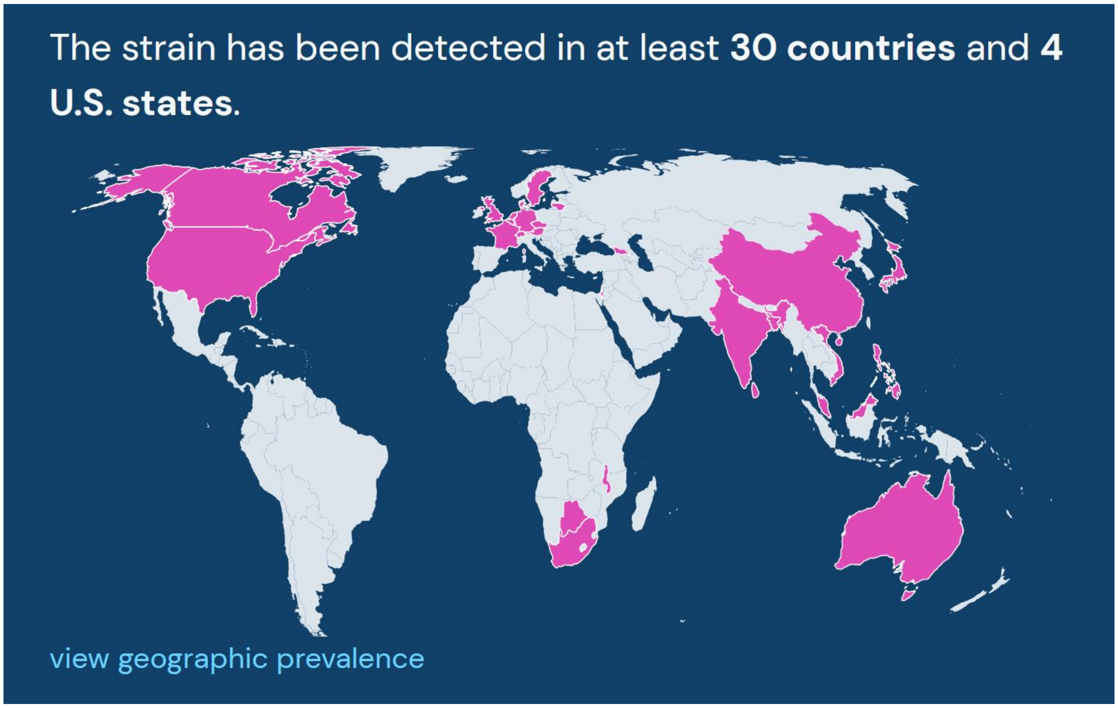
Countries reporting BA.1



The strain has been detected in at least **113 countries** and **53 U.S. states**.

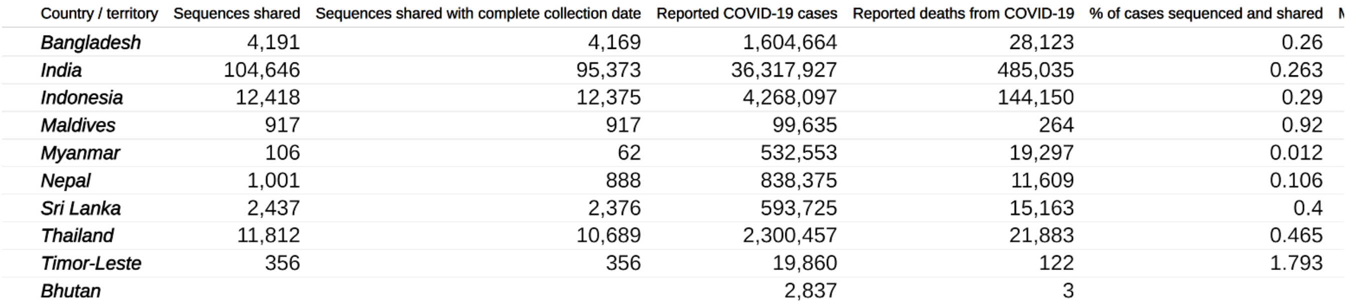
view geographic prevalence

Countries reporting BA.2



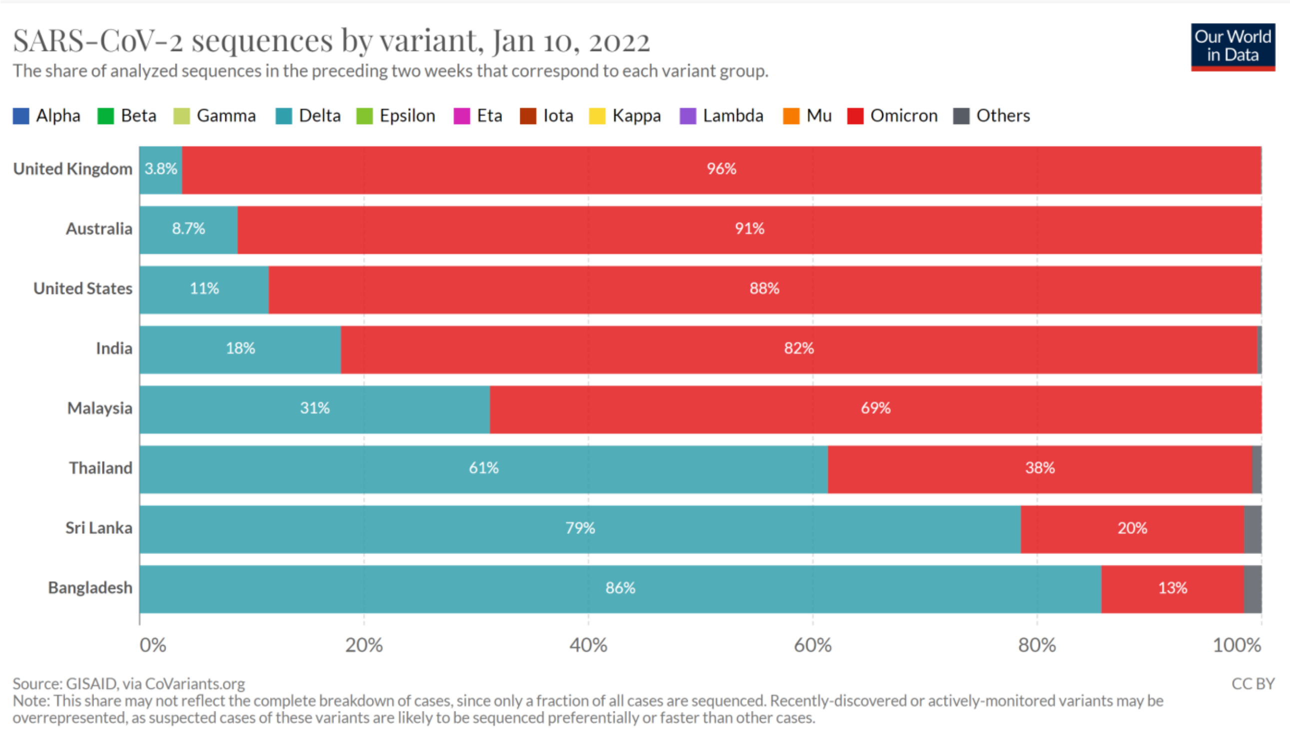
The strain has been detected in at least **30 countries** and **4 U.S. states**.

view geographic prevalence



Country / territory	Sequences shared	Sequences shared with complete collection date	Reported COVID-19 cases	Reported deaths from COVID-19	% of cases sequenced and shared
Bangladesh	4,191	4,169	1,604,664	28,123	0.26
India	104,646	95,373	36,317,927	485,035	0.263
Indonesia	12,418	12,375	4,268,097	144,150	0.29
Maldives	917	917	99,635	264	0.92
Myanmar	106	62	532,553	19,297	0.012
Nepal	1,001	888	838,375	11,609	0.106
Sri Lanka	2,437	2,376	593,725	15,163	0.4
Thailand	11,812	10,689	2,300,457	21,883	0.465
Timor-Leste	356	356	19,860	122	1.793
Bhutan			2,837	3	

Table 1: Number of sequences shared by each country in the SEARO region. (excluding samples sequenced in this round)



SARS-CoV-2 sequences by variant, Jan 10, 2022

The share of analyzed sequences in the preceding two weeks that correspond to each variant group.

Source: GISAID, via CoVariants.org

Note: This share may not reflect the complete breakdown of cases, since only a fraction of all cases are sequenced. Recently-discovered or actively-monitored variants may be overrepresented, as suspected cases of these variants are likely to be sequenced preferentially or faster than other cases.

Figure 4: Prevalence of Omicron in different countries in the world based on sequencing data (The current round of SL data does not appear yet in this website)

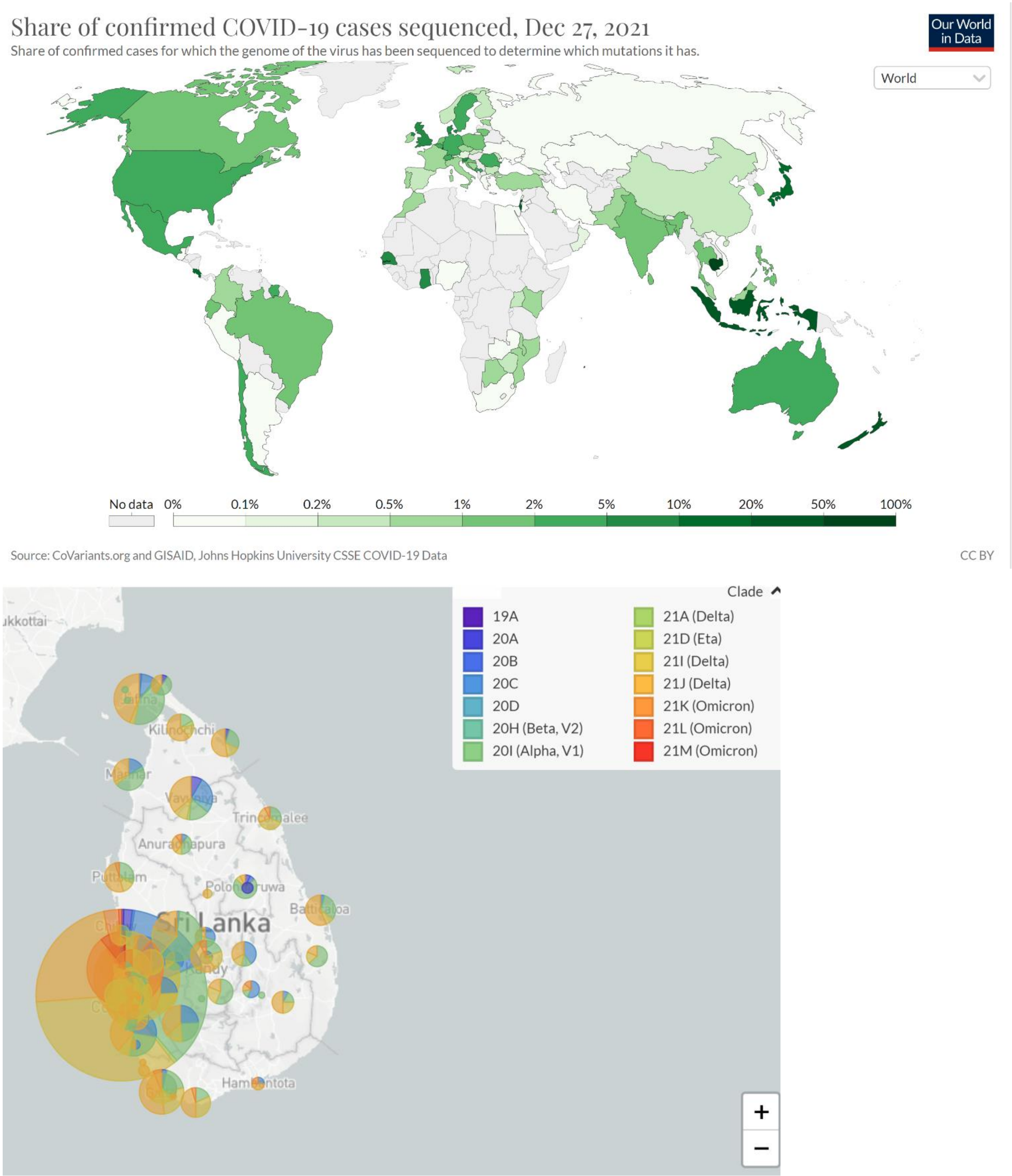


Figure 5: Sequencing of viruses carried out in Sri Lanka so far.

Other variants identified within Sri Lanka: B.1.411: Sri Lankan variant**,** B.1.1.25**,** B.1.258**,** B.1.428**,** B.4, B.4.7**,** B.1.1.365**,** B.1.525**,** B.1, B.1.1

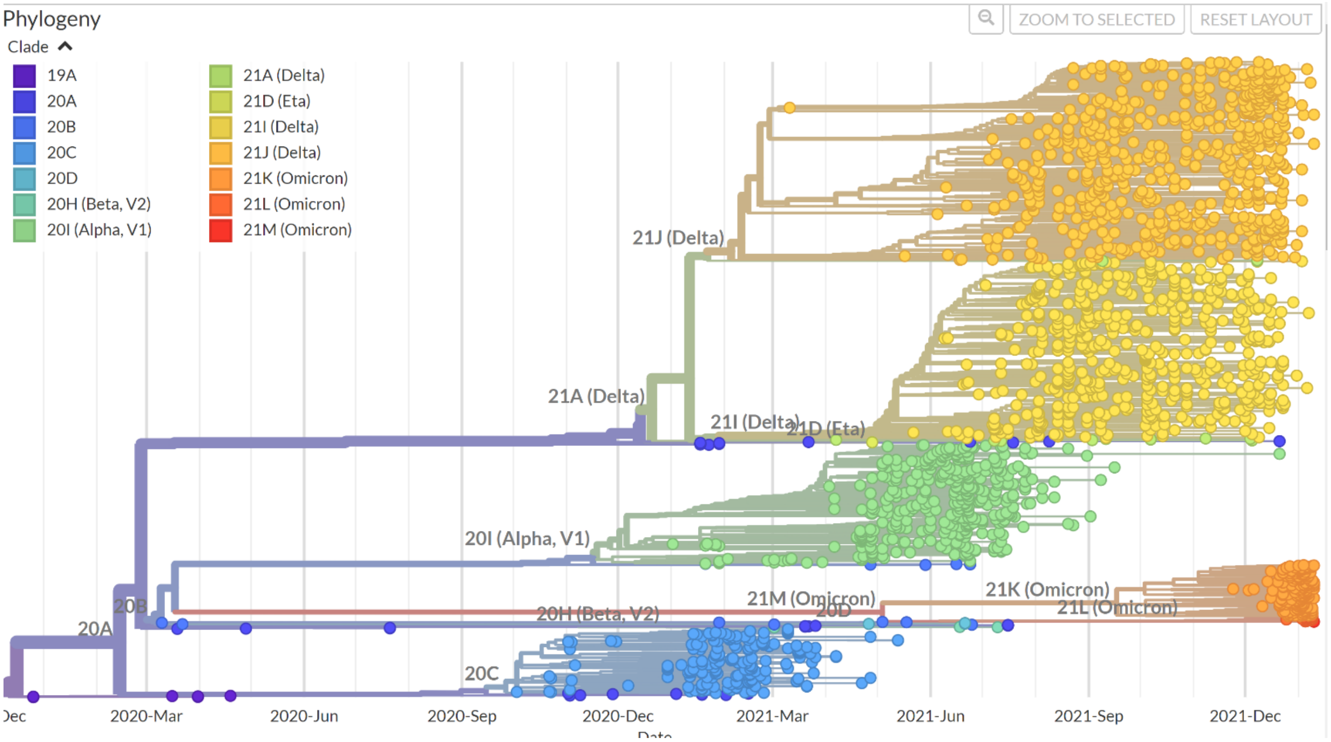


Figure 6: Phylogenetic tree of all SARS-CoV-2 sequences identified in Sri Lanka so far