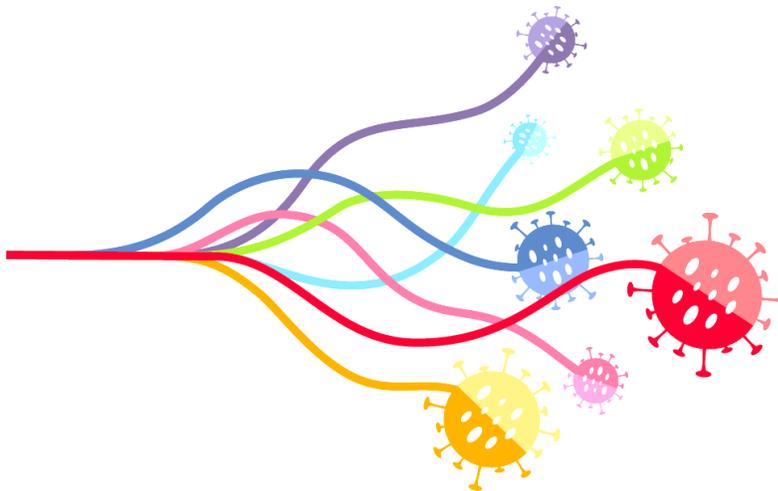


SARS-CoV-2 Variants in Bangladesh

Technical briefing 1

Report: December 2021

This briefing provides an update on variants identified from 1 to 31 December 2021



BILL & MELINDA
GATES foundation

SUMMARY

According to WHO, 5 variants of concern (VOC) and 6 variants under investigation (VUI) have been reported globally. The **Omicron variant** is the latest addition which has been designated as VOC because of its transmissibility, immune system evasion, and vaccine resistance. It has already spread to 159 countries including 63 cases in Bangladesh as of 23 January 2022 (GISAID.ORG).

This report shares data on SARS-CoV-2 variant surveillance in Bangladesh during 1-31 December 2022.

Principal findings are:

- **The Omicron variant accounted for 6%** and Delta 94% from 1 to 31 December 2021.
- Different lineages of Delta variants were identified.
- Delta AY.131 (37%), Delta B.1.617.2-like (17%) and Delta AY.127 (13%) were the most prominent lineages.
- Delta AY.131 emerged in December 2021 and became the most leading Delta lineages (37%).
- No variant unique to Bangladesh has been detected.
- **Out of 200 cases through our surveillance, 11 Omicrons were BA.1 and one BA.2 identified.**

2. Variants in Bangladesh: December 1-31, 2021

The consortium has sequenced 200 samples collected between 1 to 31 December 2021. These samples were collected from 7 divisions. Table 1 shows the total number of variants sequenced by region.

Table 1. Total number of confirmed cases by variant and region, Dec 1-31, 2021

Division	Omicron BA.1	Omicron BA.2	Delta-like	AY.102	AY.122	AY.127	AY.131	Other Delta	Total
Dhaka	7	1	14	7	5	8	36	11	89
Chattogram				5	1	1	2	3	12
Rajshahi			10	1	1	6	12	6	36
Khulna	3		5	6	5	7	20	4	50
Mymensingh	1					1	2	0	4
Rangpur			4			1	1	1	7
Sylhet				1		1	1	0	3
TOTAL	11	1	33	19	12	25	74	25	200

Out of 200 samples, 188 were Delta (94%) and 12 Omicron (6%). Among those, Delta AY.131 (37%), Delta B.1.617.2-like (17%) and Delta AY.127 (13%) were the most prominent lineages. Figure 1 shows the percentage of the geographical distribution of different SARS-CoV-2 variants between 1 to 31 December 2021.

National SARS-CoV-2 Variant Surveillance in Bangladesh

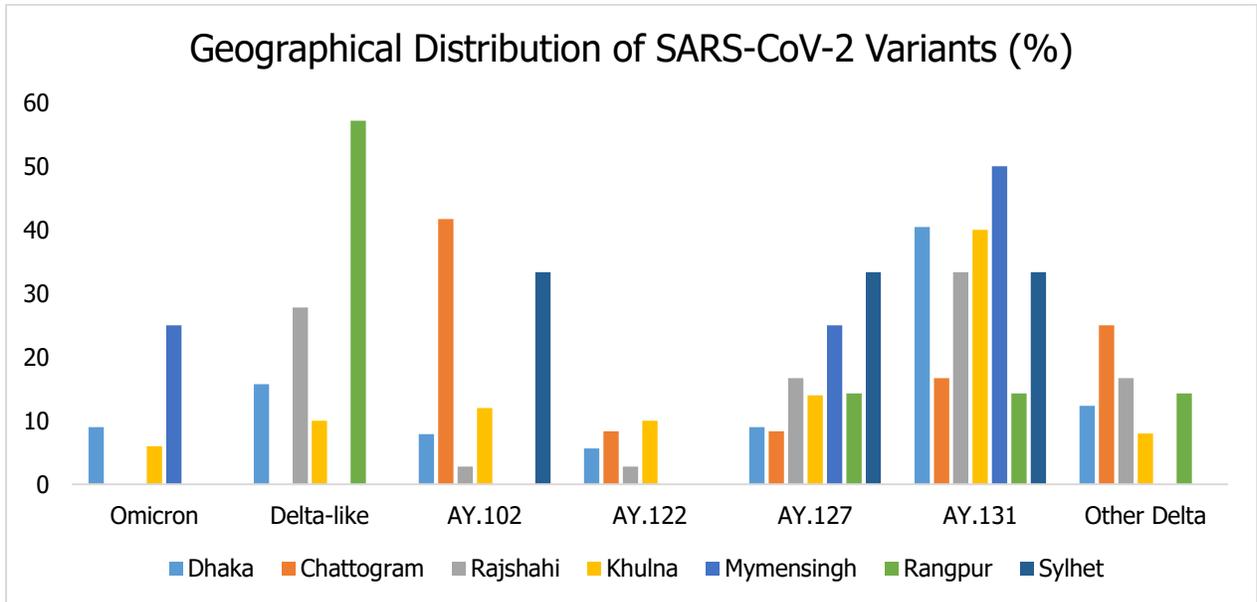


Figure 1. Geographical distribution percentage of SARS-CoV-2 variants in Bangladesh, 1-31 Dec 2021

3. NextStrain build of SARS-CoV-2 variant distribution in Bangladesh (1-31 December 2021)

A phylogenetic tree of the 200 complete genomes of Bangladesh variants (collected between 1-31 December 2021) sequenced by the consortium was constructed using NextClade (clades.nextstrain.org). Phylogenetic analysis reveals that there have been multiple introductions of Delta variants (clade 21A, 21J and 21I) across the country (Figure 2). From 1-31 December 2021, no variant unique to Bangladesh has been detected. 12 Omicron variants were identified through our surveillance.

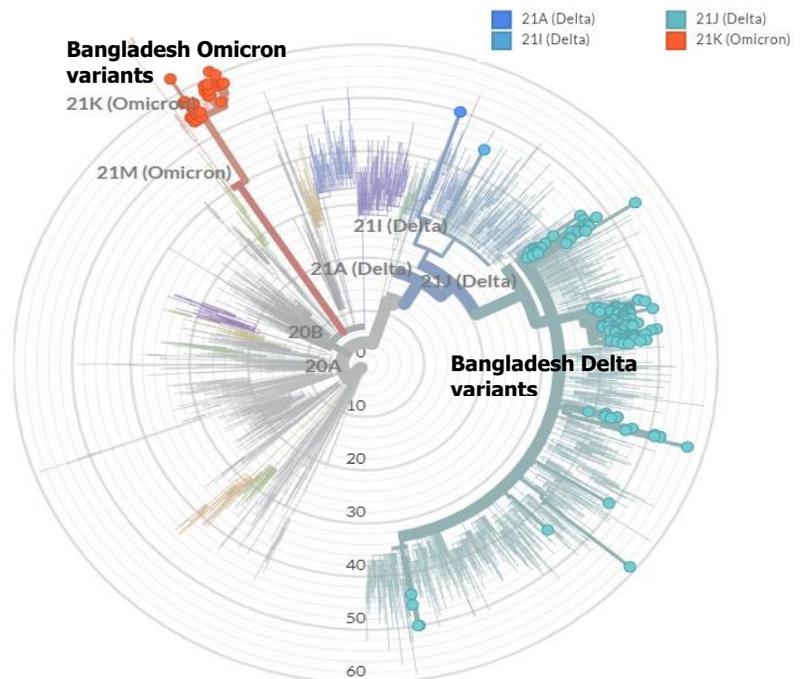


Figure 2. Phylogenetic tree of the 200 SARS-CoV-2 Bangladeshi variants in closed circle (collected 1-31 December 2021) sequenced by the consortium.

4. Cumulative Variants in Bangladesh: July-November 2021

The consortium has sequenced 1067 samples collected between 1 July to 31 December 2021. These samples were collected from all 8 divisions of Bangladesh. Table 2 shows the total number of variants sequenced by region.

Table 2. Total number of confirmed cases by variant and region, July-December 2021

	Beta	Omicron BA.1	Omicron BA.2	Delta-like	AY.4.4	AY.102	AY.122	AY.127	AY.131	Others	TOTAL
Dhaka		7	1	114	18	17	26	29	77	96	385
Chattogram				26	9	26	17	6	8	44	136
Rajshahi				88	7	13	27	17	23	27	202
Khulna		3		63	15	19	22	16	29	24	191
Sylhet				13	3		3	10	3	7	39
Barishal				14	6	10	1		8	9	48
Rangpur				10	3	2	4	4	3	8	34
Mymensingh	1	1		10	1	4	5	2	2	6	32
TOTAL	1	11	1	338	62	91	105	84	153	221	1067

12 SARS-CoV-2 strains were Omicron variants (identified in December), 1 Beta (identified in July) and the rest are Delta. The most predominant was Delta B.1.617.2-like (32%) (Figure 3).

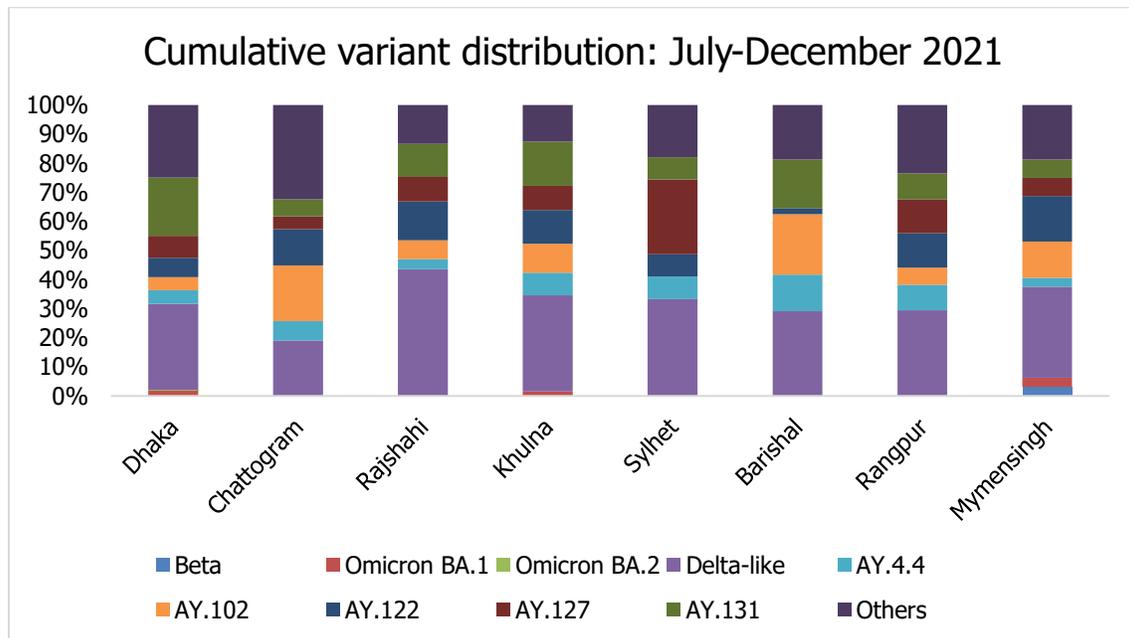


Figure 3. Geographical distribution percentage of SARS-CoV-2 variants in Bangladesh, July-December 2021

5. Metadata Analysis: July-December 2021

We have analyzed 702 metadata available by specific variables e.g. age, sex, blood group, comorbidity, vaccination, hospitalization, and death (Table 3). Out of 702, 50% of patients were between 36-64 years, and 32% were between 18-35 years. Out of 567 patients, 97% reported positive blood groups: notably 35% B+ and 33% O+. 34% of patients were co-morbid, 63% 1st dose vaccinated, 51% fully vaccinated, 13% hospitalized, and 3% deceased. Only 2 vaccinated patient (0.3%) and 20 unvaccinated patient had died. When compared metadata with sequencing data, no specific Delta lineage was found to be responsible for hospitalization or death.

Table 3. Metadata for specific variables (n=702 available), July-December 2021

Variables	Variants (%)
Age groups (years)	
=>65	63 (9%)
36-64	349 (50%)
18-35	226 (32%)
<18	64 (9%)
Male	375 (53%)
Blood group (n=567)	
A+	120 (21%)
B+	196 (35%)
AB+	46 (8%)
O+	186 (33%)
A-	5 (0.9%)
B-	4 (0.7%)
O-	7 (1%)
AB-	3 (0.5%)
Co-morbidity present	238 (34%)
Asthma	37 (5%)
Hypertension	115 (16%)
Diabetes	122 (17%)
Smoker	50 (7%)
1 st dose vaccinated	443 (63%)
Fully vaccinated	359 (51%)
Hospitalized	90 (13%)
Vaccinated and hospitalized	26 (4%)
Deaths	22 (3%)
Comorbidity present and deceased	18 (3%)
Vaccinated and deceased	2 (0.3%)
Hospitalized and deceased	16 (2%)

6. NextStrain build of SARS-CoV-2 variant distribution in Bangladesh (1 July-31 December 2021)

A phylogenetic tree of the 1067 complete genomes of Bangladesh variants (collected between 1 July-31 December 2021) sequenced by the consortium was constructed using NextClade (clades.nextstrain.org). Phylogenetic analysis reveals that there have been multiple introduction of Omicron variants (clade 21L and 21K), and Delta variants (clade 21A, 21J and 21I) across the country (Figure 3). From 1 July to 31 December 2021, no variant unique to Bangladesh has been detected. Only a single Beta (clade 20H) was identified in July 2021. **12 Omicron variants were identified through our surveillance.**

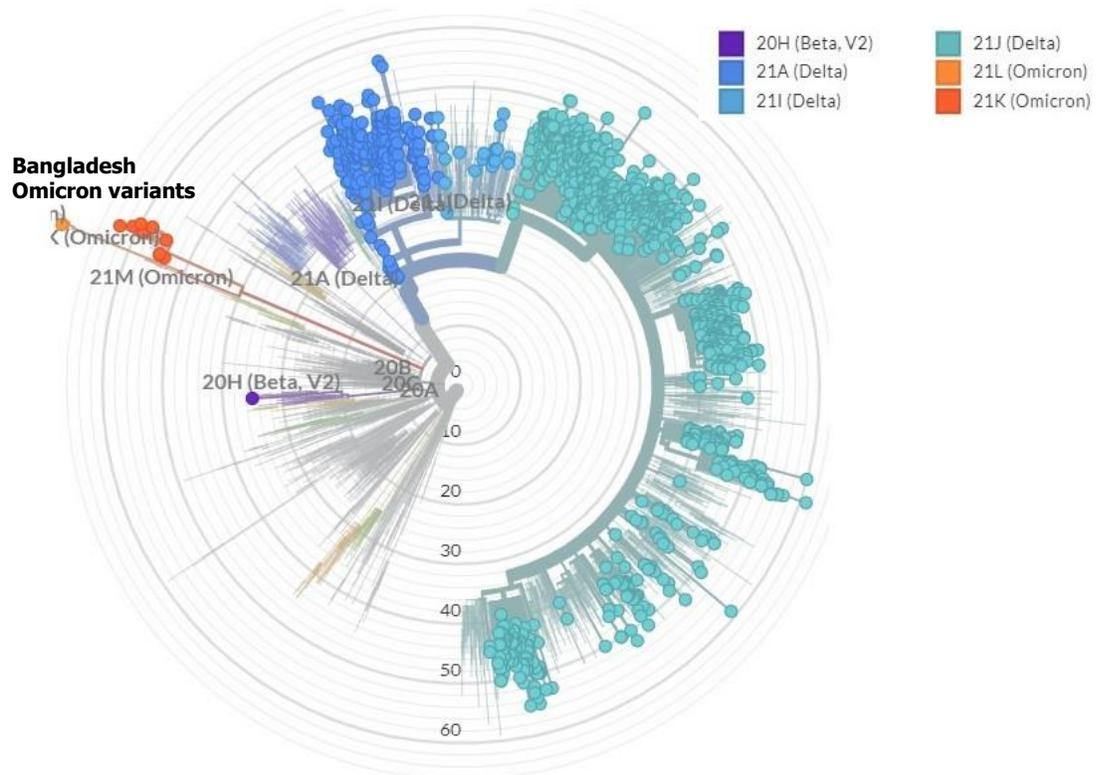


Figure 4. Phylogenetic tree of the 1067 SARS-CoV-2 Bangladeshi variants in closed circle (collected 1 July-31 December 2021) sequenced by the consortium.