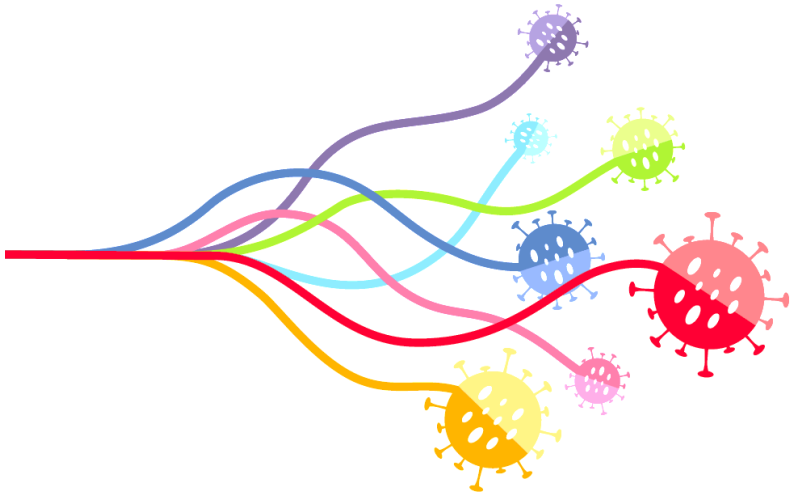
SARS-CoV-2 Variants in Bangladesh

Technical briefing 1

September 2021

This briefing provides an update on previous briefings 1 to 30 September 2021



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SUMMARY

There are 4 current variants of concern (VOC) and 5 variants under investigation (VUI) that are circulating globally. Among them, the Delta variant constitutes more than 90% of the new infections. This report has been published to share detailed SARS-CoV-2 variant surveillance in Bangladesh during September 2021. The cumulative data since July 2021 have been included at the end of this report.

Principal findings are:

- The Delta variant accounted for 100% from 1 to 30 September 2021.
- We have identified different lineages of Delta variant such as Delta B.1.617.2-like, Delta AY.5, AY.11, AY.15, AY.19, AY.20, AY.23.1, AY.26, AY.34, AY.35, and AY.39.
- In Pangoline sequence analysis, Scorpio call replaced lineage assignment AY.4 to Delta B.1.617.2-like. Therefore, all previous AY.4 are replaced with Delta B.1.617.2-like in our sequence analysis from 1 July to 30 September 2021.
- No variant unique to Bangladesh has been detected.
- No delta plus was identified.

1. Variants under surveillance worldwide

SARS-CoV-2, the virus that causes COVID-19, has many variants of particular importance due to their potential for increased transmissibility, increased virulence, or reduced effectiveness of vaccines against them. Early in the pandemic, there were few 'mutant' variant viruses because of the small number of people infected. As time went on, SARS-CoV-2 started evolving to become more transmissible. Notably, the Alpha, Beta, Gamma, and Delta variants are more transmissible than the original virus identified around Wuhan in China. Viruses generally acquire mutations over time, giving rise to new variants. When a new variant appears to be growing in a population, it can be labeled as an "emerging variant". A brief description of an emerging variant circulating recently in Bangladesh is given below.

The Delta variant also known as B.1.617.2, is now the most common worldwide. It was first discovered in India in October 2020 and has since spread internationally. In June 2021, reports began to appear of a variant of Delta with the K417N mutation. It has been nicknamed "Delta plus" from "Delta plus K417N". The name of the mutation, K417N, refers to an exchange whereby lysine (K) is replaced by asparagine (N) at position 417.

In mid-October 2021, the AY.4.2 Delta sublineage was expanding in England and USA, and being monitored and assessed. It contains mutations A222V and Y145H in its spike protein. It has been suggested that AY.4.2 might be 10-15% more transmissible than the original Delta variant. In the UK, it was reclassified as a "variant under investigation" (but not "of concern") in late October 2021.

2. Variant circulation in Bangladesh: September 2021

The consortium has sequenced 174 samples collected between 1 to 30 September 2021. These samples were collected from all 8 divisions of Bangladesh. Table 1 shows the total number of variants sequenced by region. The previously identified Delta AY.4 is considered as Delta-like lineage according to recent Pango nomenclature.

Table 1. Total number of confirmed cases by variant and region, September 2021

Division	Delta-like	Delta-AY.5	Delta-AY.11	Delta-AY.15	Delta-AY.19	Delta-AY.20	Delta-AY.23.1	Delta-AY.26	Delta-AY.34	Delta-AY.35	Delta-AY.39	TOTAL
Dhaka	48	1						1	1		3	**54**
Chattogram	20	1		1		2					2	**26**
Sylhet	11	1										**12**
Rajshahi	24	1	1		1						1	**28**
Khulna	28					1	1				1	**31**
Barishal	7									1	1	**9**
Rangpur	4											**4**
Mymensingh	10											**10**
TOTAL	**152**	**4**	**1**	**1**	**1**	**3**	**1**	**1**	**1**	**1**	**8**	**174**

All 174 samples were Delta (100%). Among those, Delta B.1.617.2-like (87%) was the most prominent lineage. We have also identified other lineages of Delta variants such as Delta AY.5, AY.11, AY.15, AY.19, AY.20, AY.23.1, AY.26, AY.34, AY.35, and AY.39. Figure 1 shows the percentage of the geographical distribution of different SARS-CoV-2 variants between 1 to 30 September 2021.

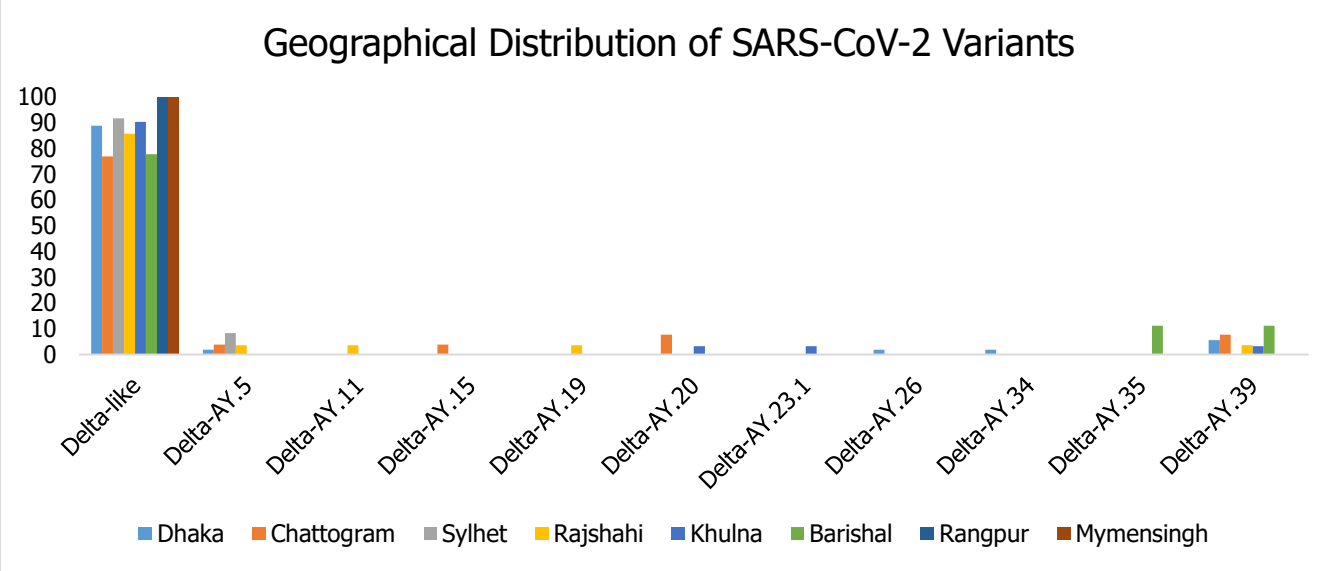

Figure 1. Geographical distribution percentage of SARS-CoV-2 variants in Bangladesh, September 2021

3. Metadata Analysis: September 2021

We have analyzed 76 metadata available by specific variables e.g. age, sex, blood group, comorbidity, vaccination, hospitalization, and death (Table 2). Out of 76, 50% of the patients were between 36-64 years, and 32% were between 18-35 years. Out of 66 patients, 98% reported positive blood groups: notably 24% A+, 39% B+ and 27% O+. 38% of patients were co-morbid, 53% 1st dose vaccinated, 43% full vaccinated, 12% hospitalized, and 4% deceased. One vaccinated and 2 unvaccinated patients had died of COVID-19. When compared metadata with sequencing data, no specific Delta lineage was found to be responsible for hospitalization or death.

Table 2. Total number of confirmed variants by specific variables (n=76 available), September 2021

Variables	Delta variants (%)
Age groups (years)	
=>65	8 (10%)
36-64	38 (50%)
18-35	24 (32%)
<18	6 (8%)
Male	41 (54%)
Blood group (n=66)	
A+	16 (24%)
B+	26 (39%)
AB+	5 (8%)
O+	18 (27%)
O-	1 (2%)
Co-morbidity present	29 (38%)
1st dose vaccinated	40 (53%)
Fully vaccinated	33 (43%)
Hospitalized	9 (12%)
Vaccinated and hospitalized	4 (5%)
Deaths	3 (4%)
Comorbidity present and deceased	3 (4%)
Vaccinated and deceased	1 (1%)
Hospitalized and deceased	3 (4%)

4. NextStrain build of SARS-CoV-2 variant distribution in Bangladesh (1-30 September 2021)

A phylogenetic tree of the 174 complete genomes of Bangladesh variants (collected between 1-30 September 2021) sequenced by the consortium was constructed using NextClade (clades.nextsrain.org). Phylogenetic analysis reveals that there have been multiple introductions of Delta variants (clade 21A, 21J, and 21I) across the country (Figure 2). Till 30 September 2021, no variant unique to Bangladesh has been detected. No delta plus was identified.

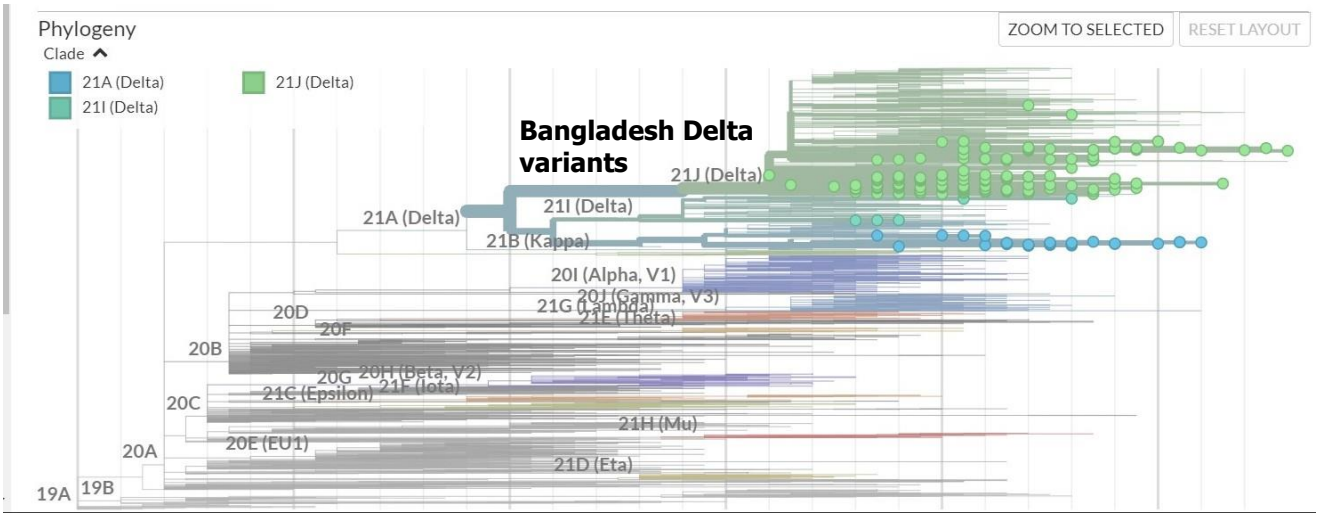

Figure 2. Phylogenetic tree of the 174 SARS-CoV-2 Bangladeshi variants (collected 1-30 September 2021) sequenced by the consortium.

5. Cumulative Variant circulation in Bangladesh: July-September 2021

The consortium has sequenced 539 samples collected between 1 July to 30 September 2021. These samples were collected from all 8 divisions of Bangladesh. Table 3 shows the total number of variants sequenced by region.

Table 3. Total number of confirmed cases by variant and region, Jul-Sep 2021

	Beta	Delta-like	Delta-AY.5	Delta-AY.10	Delta-AY.11	Delta-AY.15	Delta-AY.16	Delta-AY.19	Delta-AY.20	Delta-AY.23.1	Delta-AY.26	Delta-AY.33	Delta-AY.34	Delta-AY.35	Delta-AY.37	Delta-AY.38	Delta-AY.39	Delta-AY.41	TOTAL
Dhaka		139	1	1	2		4		1		8		1				8	1	**166**
Chattogram		65	1	3	1	1			4		5	1	1		1	1	8		**92**
Sylhet		21	1														1		**23**
Rajshahi		84	1	2	2			1				2					2		**94**
Khulna		83	1						2	1	4				1		4	1	**97**
Barishal		22		1							1			1			1		**26**
Rangpur		10		1							4	1							**16**
Mymensingh	1	22										1					1		**25**
TOTAL	**1**	**446**	**5**	**8**	**5**	**1**	**4**	**1**	**7**	**1**	**22**	**5**	**2**	**1**	**2**	**1**	**25**	**2**	**539**

All SARS-CoV-2 strains were Delta variants except one Beta variant (identified in July). The most predominant was Delta B.1.617.2-like (83%) followed by Delta AY.39 (5%) and Delta AY.26 (4%) (Figure 3).

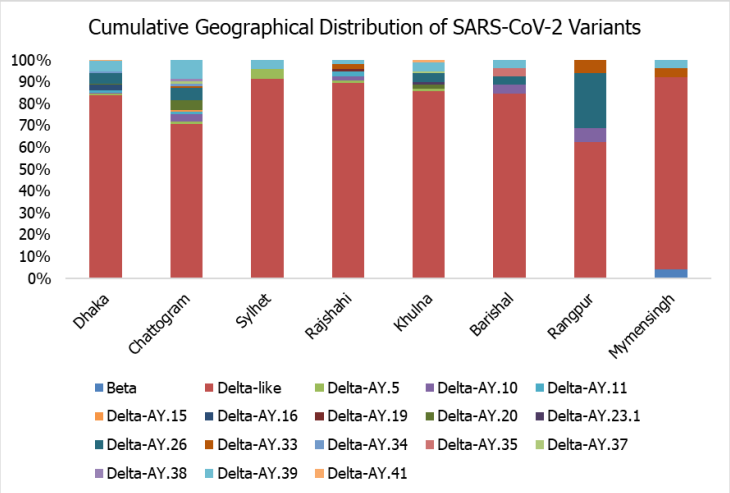

Figure 3. Geographical distribution percentage of SARS-CoV-2 variants in Bangladesh, Jul-Sep 2021

6. Metadata Analysis: July-September 2021

We have analyzed 326 metadata available by specific variables e.g. age, sex, blood group, comorbidity, vaccination, hospitalization, and death (Table 4). Out of 326, 50% of patients were between 36-64 years, and 33% were between 18-35 years. Out of 266 patients, 96% reported positive blood groups: notably 37% B+ and 29% O+. 36% of patients were co-morbid, 53% 1st dose vaccinated, 38% fully vaccinated, 17% hospitalized, and 5% deceased. One vaccinated and 15 unvaccinated patients had died of COVID-19. When compared metadata with sequencing data, no specific Delta lineage was found to be responsible for hospitalization or death.

Table 4. Total number of confirmed variants by specific variables (n=326 available), July-September 2021

Variables	Delta variants (%)
Age groups (years)	
=>65	30 (9%)
36-64	164 (50%)
18-35	106 (33%)
<18	26 (8%)
Male	166 (51%)
Blood group (n=266)	
A+	55 (21%)
B+	98 (37%)
AB+	26 (10%)
O+	77 (29%)
A-	2 (0.8%)
B-	2 (0.8%)
O-	5 (2%)
AB-	1 (0.4%)
Co-morbidity present	119 (36%)
1st dose vaccinated	174 (53%)
Fully vaccinated	123 (38%)
Hospitalized	55 (17%)
Vaccinated and hospitalized	18 (6%)
Deaths	16 (5%)
Comorbidity present and deceased	13 (4%)
Vaccinated and deceased	1 (0.3%)
Hospitalized and deceased	12 (4%)

7. NextStrain build of SARS-CoV-2 variant distribution in Bangladesh (1 July-30 September 2021)

A phylogenetic tree of the 539 complete genomes of Bangladesh variants (collected between 1 July-30 September 2021) sequenced by the consortium was constructed using NextClade (clades.nextsrain.org). Phylogenetic analysis reveals that there have been a single Beta (clade 20H) and multiple introductions of Delta variants (clade 21A, 21J and 21I) across the country (Figure 4). From 1 July to 30 September 2021, no variant unique to Bangladesh has been detected. No delta plus was identified.

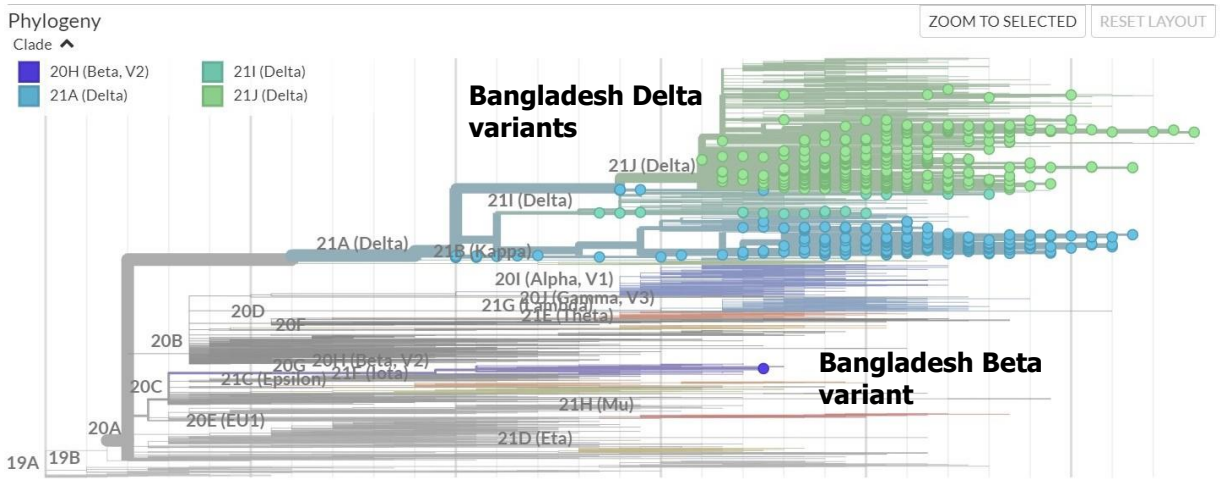

Figure 4. Phylogenetic tree of the 539 SARS-CoV-2 Bangladeshi variants (collected 1 July-30 September 2021) sequenced by the consortium.