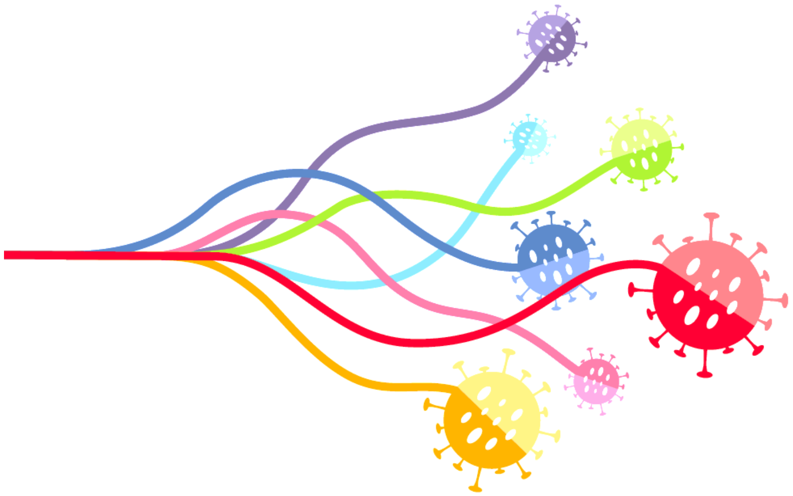
SARS-CoV-2 Variants in Bangladesh

Technical briefing 1

31 August 2021

This briefing provides an update on previous briefings 1 to 31 July 2021



IEDCR

icddr,b

ideSHi
institute for developing Science & Health initiatives

Child Health Research Foundation
CHRF Prevent Infections, Save Lives

BILL & MELINDA
GATES foundation

BACKGROUND

Who We Are

The National SARS-CoV-2 Variant Surveillance (NSVS) in Bangladesh is conducted by a consortium of four institutes: (1) Institute of Epidemiology, Disease Control and Research (IEDCR), a Bangladesh government research institute, under the Ministry of Health and Family Welfare (MoHFW), and also the Govt mandated institute for outbreak investigation and response and communicable disease surveillance; (2) International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b); (3) Child Health Research Foundation (CHRF), and Institute for Developing Science and Health Initiatives (ideSHi). These institutes are working closely to monitor genomic variants of SARS-CoV-2 across the country.

What We Do

Our overall goal is to identify variants of SARS-CoV-2 in Bangladesh through institutional collaborative efforts and systematic approach. The specific objectives are:

1. to build essential capacity for genomic surveillance through strategic enhancement of the existing genome sequencing and analysis capacity.
2. to implement strategic sequencing approach to maximize information regarding the virus evolution within the country by identifying SASR-CoV-2 variants across the country.
3. to share data with stakeholders who can use these data for a broad range of pathogen threats in the future, building a sustainable platform for epidemic surveillance in Bangladesh.

Why We Do

To support the country’s epidemic preparations, it is important to scale-up whole genome sequencing (WGS) capacity following a systematic approach to monitor the SARS-CoV-2 variants circulating in Bangladesh. Utilization and strategic strengthening of this capacity of the consortium institutes will maximize the information we can obtain about the epidemic and will help in country wide interpretation.

How We Do

The consortium will sequence 1800 genome over the period of 12 months. IEDCR-ideSHi will complete 500 genomes using nanopore MinION and MiSeq Illumina platforms. icddr,b will complete 800 genomes (MiSeq illumina platform) and CHRF will complete 500 genomes (NextSeq illumina platform).

The genomic surveillance data and the outcomes of the study will be disseminated by sharing the research findings with the national and international stakeholders; Institute of Epidemiology, Disease Control and Research (IEDCR), World Health Organization (WHO), Directorate General of Health Services (DGHS) of GoB. The report of the circulatory SARS-COV-2 variants will be submitted bi-weekly to GISAID.ORG database, which is an open platform from where all the stakeholders can avail genetic data of the contemporary variants as and when required.

SUMMARY

There are 4 current variants of concern (VOC) and 9 variants under investigation (VUI) are circulating globally. Among them, 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 July 2021.

Principal findings are:

- The Delta variant accounted for approximately 99.4% of the variants from 1 to 31 July 2021.
- We have identified different lineages of Delta variant such as Delta B.1.617.2-like, Delta AY.1, AY.4, AY.10, AY.12, AY.16, AY.19, AY.20, AY.21 and AY.25.
- A single Beta variant was identified in Mymensingh.
- No variant unique to Bangladesh has been detected.

SARS-CoV-2 variants: case numbers and proportion

1. Variants under surveillance

Table 1. World Health Organization nomenclature as of

Variants	Lineage	Designation	Status
Beta	B.1.351	VOC-20DEC-02	VOC
Delta	B.1.617.2, AY.1-AY.25	VOC-21APR-02	VOC
Mu	B.1.621	VOI-21JUL-1	VOI

VOC: variant of concern; VOI: variant of interest

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 variant and the Delta variant are both 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 labelled as an "emerging variant". A brief description of emerging variants circulating recently in Bangladesh is given below.

Beta (lineage B.1.351)

On 18 December 2020, lineage B.1.351, was first detected in South Africa and has been labelled as Beta variant by WHO. Scientists noted that the variant contains several mutations that allow it to attach more easily to human cells because of the following three mutations in the receptor-binding domain (RBD) in the spike glycoprotein of the virus: N501Y, K417N, and E484K.

Delta (lineage B.1.617.2)

The Delta variant, also known as B.1.617.2, was first discovered in India. It was first discovered 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.

Recently, several new variants of interest have been under extensive monitoring. For example, Mu.

Mu (lineage B.1.621)

The Mu variant, also known as lineage B.1.621, was first detected in Colombia in January 2021 and was designated by the WHO as a variant of interest (VOI) on 30 August 2021. There have been outbreaks of Mu variant in more than 40 countries including South and North America, East Asia and Europe.

2. Overall variant circulation in Bangladesh: from 1 July to 31 July 2021

The consortium has sequenced 179 samples collected between 01 July to 31 July 2021. These samples were collected from all 8 divisions of Bangladesh. Table 2 shows the total number of variants sequenced by region. 178 out of 179 samples were Delta (99.4%), and 1 (0.6%) was Beta variant. The Beta variant was detected in Mymensingh on 13 July 2021.

Table 2. Total number of confirmed cases by variant and region

Division	Beta	Delta-like	Delta-AY.4	Delta-AY.10	Delta-AY.12	Delta-AY.16	Delta-AY.19	Delta-AY.20	Delta-AY.21	Delta-AY.25	TOTAL
Dhaka		40			11	1		1	2		**55**
Chattogram		26		1	4			1	1	1	**34**
Sylhet		5			1						**6**
Rajshahi		29	1		2						**32**
Khulna		19	6		3		1				**29**
Barishal		7									**7**
Rangpur		5		1	1						**7**
Mymensingh	1	7			1						**9**
TOTAL	**1**	**138**	**7**	**2**	**23**	**1**	**1**	**2**	**3**	**1**	**179**

We have identified different lineages of Delta variants such as Delta B.1.617.2-like, Delta AY.1, AY.4, AY.10, AY.12, AY.16, AY.19, AY.20, AY.21 and AY.25. Figure 1 shows the percentage of geographical distribution of different SARS-CoV-2 variants including Delta lineages. Delta B.1.617.2-like lineage (77%) was the most predominant variant circulating across the country followed by Delay AY.12 (13%) and Delta Ay.4 (4%).

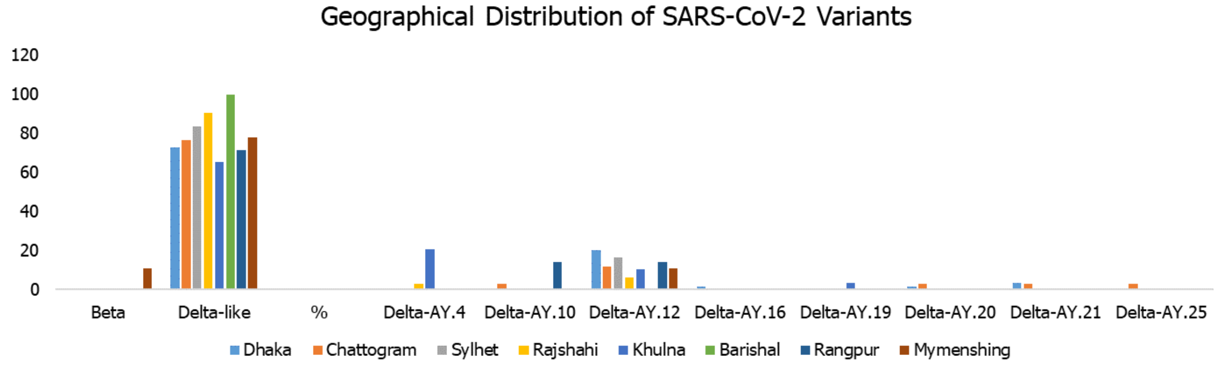


Figure 1. Geographical distribution percentage of SARS-CoV-2 variants in Bangladesh

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

A phylogenetic tree of the 179 complete genomes of Bangladesh variants (collected between 01-31 July 2021) sequenced by the consortium was constructed using NextClade (clades.nextsrain.org). Phylogenetic analysis reveals that there have been multiple introductions of Delta variants across the country (Figure 2). Till 31 July 2021, no variant unique to Bangladesh has been detected. Interestingly, 1 Beta variant which was mostly detected during March-June, 2021, still exists in one Division (Mymensingh).

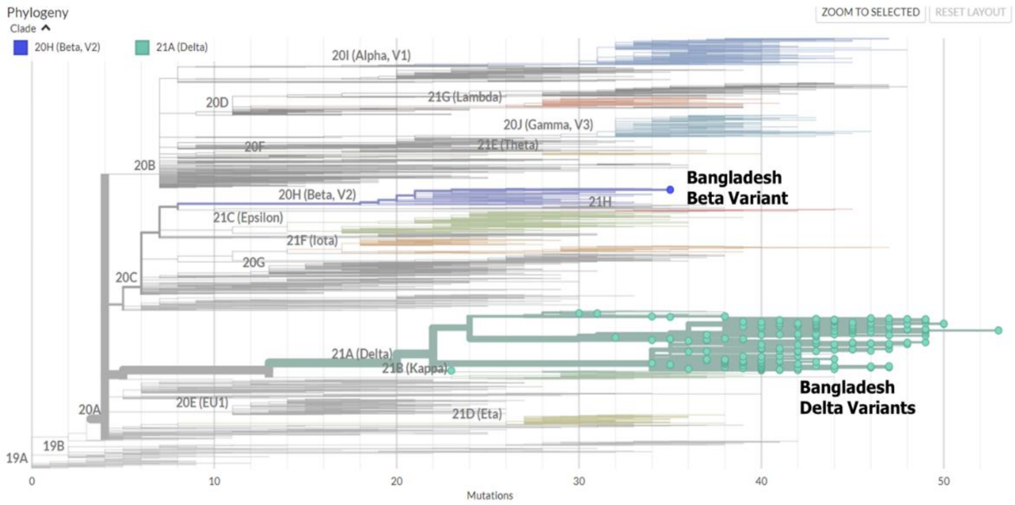


Figure 2. Phylogenetic tree of the 179 SARS-CoV-2 Bangladeshi variants (collected 01-31 July 2021) sequenced by the consortium.