Respiratory Pathogen Genomic Surveillance in Bangladesh

Update on April-May 2023

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A. SUMMARY REPORT

During April-May 2023, influenza virus and SARS-CoV-2 circulation increased, whereas RSV gradually decreased significantly compared to the previous 6 months. This report is prepared to share respiratory pathogen genomic surveillance in Bangladesh during April-May 2023.

Principal findings are:

- RSV positivity was 7% for SARI cases and 2% for ILI cases. RSV was most prevalent in <6 months' infants followed by 6-11 months.
- SARS-CoV-2 positivity rate was 0.6% for SARI and 2.6% for ILI cases.
- Influenza positivity rate was 2% for both SARI and ILI cases.

B. Respiratory Surveillance: Samples were collected through 19 hospitals under HBIS and NISB platforms from all 8 divisions of Bangladesh between 1 April to 31 May 2023.

RSV circulation in Bangladesh:

We tested 652 SARI and 163 ILI (<5 years) for RSV using qPCR. Although the incidence was very high in April, RSV activity significantly decreased in May. RSV was responsible for most of the severe cases especially in children <6 months.

Table 2: Total number of confirmed RSV cases using qPCR: April-May 2023

Age groups	**April 2023**					
	SARI			**ILI**		
	Sample	**RSV (n)**	**RSV (%)**	**Sample (n)**	**RSV (n)**	**RSV (%)**
<6 months	104	82	**50.3**	18	2	11.1
6-11 months	86	28	31.1	27	7	25.9
12-23 months	66	12	20.7	31	4	12.9
2-<5 years	42	10	27.0	40	4	10.0
Total	**298**	**132**	**37.9**	**116**	**17**	**14.7**

Age groups	**May 2023**					
	SARI			**ILI**		
	Sample	**RSV (n)**	**RSV (%)**	**Sample**	**RSV (n)**	**RSV (%)**
<6 months	122	5	4.1	17	0	0.0
6-11 months	103	6	5.8	27	1	3.7
12-23 months	74	0	0.0	19	0	0.0
2-<5 years	55	0	0.0	21	0	0.0
Total	**354**	**11**	**3.1**	**84**	**1**	**1.2**

SARS-CoV-2 and Influenza virus circulation in Bangladesh

The consortium has tested 1865 SARI and 1337 ILI samples for influenza virus and SARS-CoV-2. Influenza virus shows low occurrence (0.2%-0.9%) during April-May, but COVID-19 has increased (from 1% to 4%) in May.

Table 1. Total number of confirmed influenza and COVID-19 using qPCR: April-May2023

Age groups	**April 2023**									
	SARI					**ILI**				
	Sample	**Flu (n)**	**Flu (%)**	**COVID (n)**	**COVID (%)**	**Sample (n)**	**Flu (n)**	**Flu (%)**	**COVID (n)**	**COVID (%)**
<1 Year	271	2	0.7	0	0.0	123	1	0.8	0	0.0
1-<5 Years	174	5	2.9	0	0.0	179	4	2.2	1	0.6
5-14 Years	114	2	1.8	1	0.9	97	3	3.1	2	2.1
15-24 Years	60	2	3.3	0	0.0	83	2	2.4	2	2.4
25-39 Years	61	3	4.9	0	0.0	65	1	1.5	2	3.1
40-59 Years	85	0	0.0	1	1.2	55	1	1.8	0	0.0
≥60 Years	102	2	2.0	0	0.0	34	0	0.0	0	0.0
Total	**867**	**16**	**1.8**	**2**	**0.2**	**636**	**12**	**1.9**	**7**	**1.1**

Age groups	**May 2023**									
	SARI					**ILI**				
	Sample	**Flu (n)**	**Flu (%)**	**COVID (n)**	**COVID (%)**	**Sample**	**Flu (n)**	**Flu (%)**	**COVID (n)**	**COVID (%)**
<1 Year	295	4	1.4	2	0.7	107	2	1.9	4	3.7
1-<5 Years	194	4	2.1	1	0.5	163	4	2.5	2	1.2
5-14 Years	142	3	2.1	1	0.7	139	1	0.7	7	5.0
15-24 Years	81	4	4.9	1	1.2	102	6	5.9	9	8.8
25-39 Years	69	1	1.4	2	2.9	83	1	1.2	5	6.0
40-59 Years	103	1	1.0	0	0.0	58	1	1.7	0	0.0
≥60 Years	114	3	2.6	2	1.8	49	2	4.1	1	2.0
Total	**998**	**20**	**2.0**	**9**	**0.9**	**701**	**17**	**2.4**	**28**	**4.0**

C. Genome Sequencing

Viruses	Oct-22	Nov-22	Dec-22	Jan-23	Feb-23	Mar-23	Apr-23	May-23	June-23	Total
RSV	22					42	18	6		**88**
Influenza				4	3	2	4	14		**27**
SARS-CoV-2	19	1		1				9	24	**54**

RSV

88 RSV qPCR-positive samples were sequenced using Paragon Genomics library preparation kit in Illumina MiSeq V3 system between October 2022 to June 2023.

- All were RSV B under B6 clade according to Nextstrain.

RSV Phylogeny

- Total 34 Bangladeshi RSV samples were taken randomly during the study period (March-May 2023).
- Based on WGS, global and Bangladeshi sequences clustered together in two lineages according to the clade in Nextclade build (figure 1).
- Bangladeshi sequences have created two clusters within the B6 clade (figure 1).

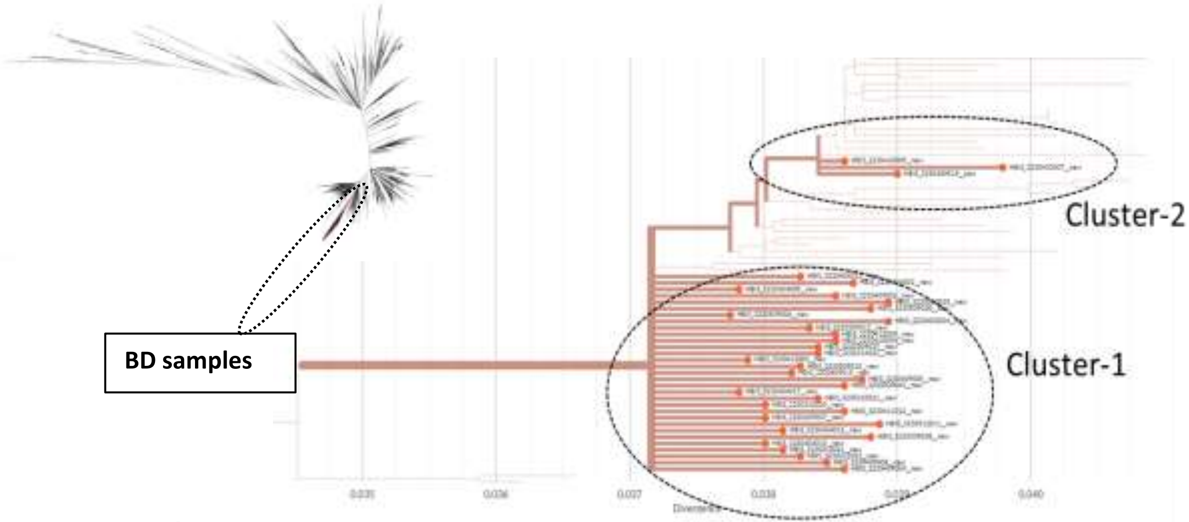

Figure 1: Phylogeny of RSV B viruses between March-May 2023

Influenza

27 were sequenced using Paragon Genomics library preparation kit in Illumina MiSeq V3 system between October 2022 to June 2023.

- 6 influenza A, and 21 influenza B Victoria.

Influenza virus phylogeny

- 15 Influenza B successfully passed the QC between March-May 2023.
- We have found two clades based on the HA region (V1A.3a.2 and V1A).
- Fourteen of the BD influenza B V1A.3a.2 sequences clustered with different global strains.
- Only one BD influenza B strain belongs to V1A cluster which is distantly related with other BD sequences.

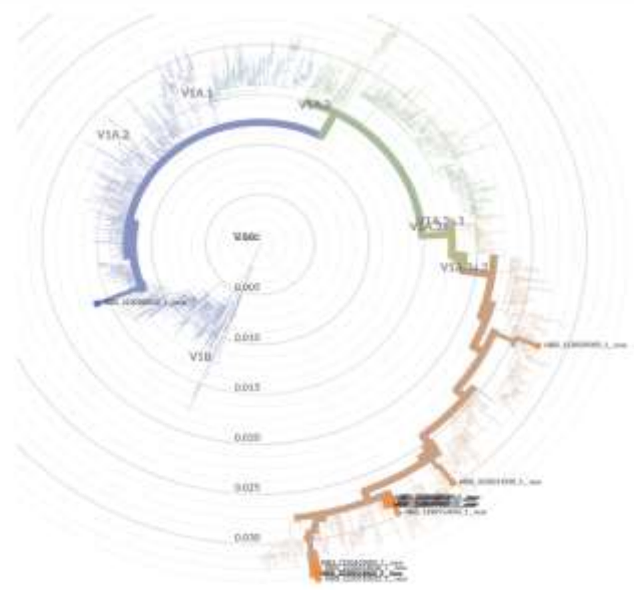

Figure 2: Phylogeny of influenza B viruses from March-May 2023

SARS-CoV-2

59 SARS-CoV-2 positive samples were sequenced in Oxford Nanopore platform.

- Four sub-lineages of the Omicron variant were identified. These are **XBB.1.16, XBB.2.3, FL.4 and XBB.3.**

SARS-CoV-2 phylogeny

- Represents 54 SARS-CoV-2 Omicron sequences reported from Bangladesh between October 2022 to June 2023.
- The tree has been represented as a mid-point rooted tree. Bootstrap support percentage of 95 or above are indicated in black dots. The circle indicates month of sample collection and the number represents age of the patient. The age caption 0 represents < 1-year-old baby.
- Omicron XBB.1, XBB.1.16 and XBB.2.3 sublineages were most predominant among the sequences.

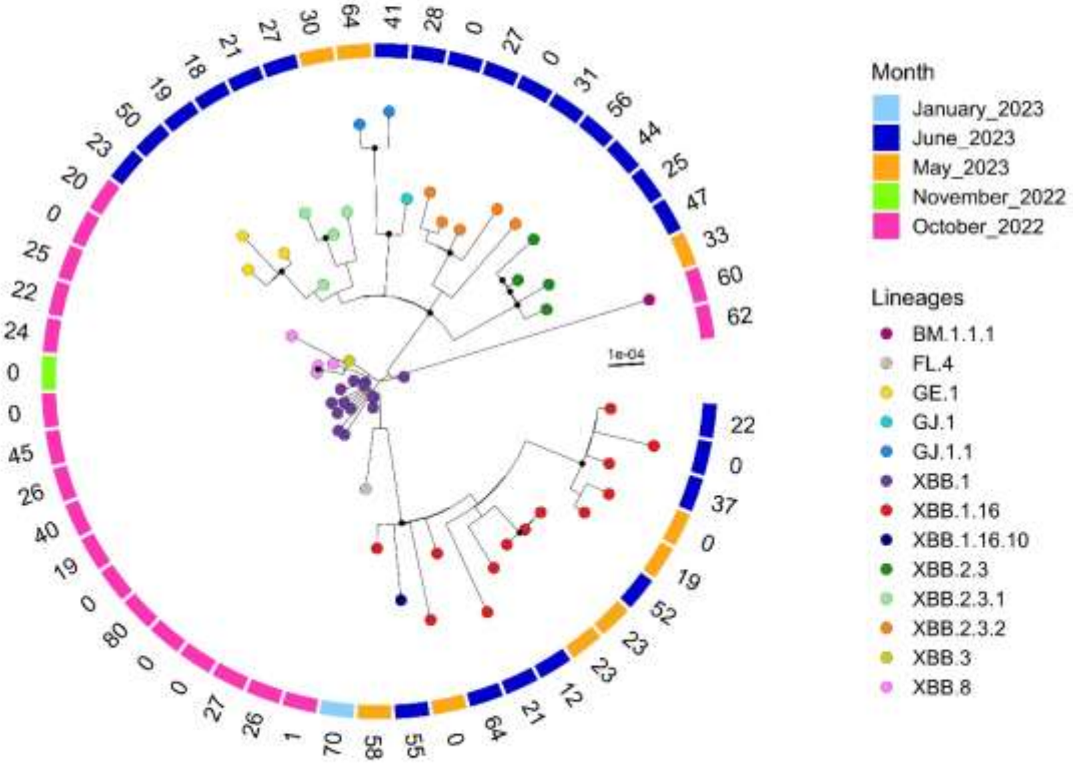

Figure 3: The maximum likelihood tree of 54 SARS-CoV-2 Omicrons that we have sequenced between October 2022-June 2023