Dear Editor

Over the last few months, multiple lineages of the omicron (B.1.1.529) variant of SARS-CoV-2 have emerged. BA.1, BA.2, BA.3, BA.4 and BA.5 are the first five branches descending from an original Omicron ancestor. Recently the United States first detected Omicron sub-variant BA.2.12.1 which is the 12th lineage to branch off from BA.2 [1].

The Omicron variant contains more than 30 mutations and most of the mutations were reported in the spike protein which has been used as a key target for most of the available vaccines. Omicron variant is three times more infectious than the original SARS-CoV-2 strain [2]. It is the seventh month of 2022 and Bangladesh has already faced its record highest positivity of SARS-CoV-2 early in this calendar year. In recent days, BA.4, BA.5 and BA.5.1 along with BA.2.12.1 lineage of Omicron continues the emergence and evolution of a new SARS-CoV-2 epidemic Globally [3] along with South Asian countries [4] and in Bangladesh. On 28th January 2022 the positivity rate of SARS-CoV-2 infection was 33% which was the highest since 8th March 2020 when the first case was reported in Bangladesh and declined to below 1% on 16th March 2022 [4]. Though all the prohibiting orders have been revoked after the Delta outbreak at the end of 2021 as combatting SARS-CoV-2 has become a new normal, all the government and private service activities along with educational activities in institutes continue to be operative. Since then, the positivity rate maintained between 0-1% until 10th June 2022. All of a sudden the positivity rate tempted to surge forward. After 10th June 2022, a sharp incline of SARS-CoV-2 positivity rate has been noticed, which has raised to 16% on 26th June 2022 just in a difference of 15 days.

To determine the viral lineage of SARS-CoV-2, we performed whole genome sequencing analyses using SARS-CoV-2-positive samples collected at Novus Molecular lab, Poribag, Dhaka and sequenced at Child Health Research Foundation (CHRF), Dhaka. The Sequencing library was prepared using Illumina COVIDSeq Assay kit and sequencing was performed in Illumina iSeq100 platform.

The consensus genome was created by aligning the raw reads to reference genome MN908947.3 using https://github.com/czbiohub/sc2-illumina-pipeline. The genome was found to be BA.2.12.1 (according to Pangolin version 4.0.6 and pangolin-data version 1.9) with two characteristic mutations L454Q and S704L. The phylogenetic tree was created using https://github.com/neherlab/nextclade_data_workflows/tree/master/sars-cov-2.

Its prevalence in Bangladesh should be monitored closely because BA.2.12.1 can escape antibodies elicited by previous Omicron infection even after having been vaccinated with booster dose. World health organization emphasized to monitor BA.2.12.1 sub variants closely on May 4, 2022 [5]. Omicron BA.2.12.1 sub variants spread very fast, which led to the resurgence of the epidemic in many parts of the united states and cases have been reported in at least 79 countries all over the world.

In the current situation, there is very few evidence of the tenable threats associated with the emergence of the newly Omicron BA.2 lineage. As already countries along with many...
South Asian countries emerged by newer Omicron sub variant, Bangladesh is in an alarming period of the new wave [3]. A pick high infectivity could lead to an even more destructive situation over the countries system and it will be tough to control and provide care as more people will get infected/sick. Rapid screening and monitoring of newly coming BA.2.12.1 lineage of SARS-CoV-2 and genomic surveillance is essential for early detection of any other emerging variants to take proper measures of prevention. Evolution of next generation vaccines could be the effective prevention of concurrently evolving and emerging newer SARS-CoV-2 variants and lineages. It is the foremost sub variant of Omicron to be conscious of the evolutionary process at present. Though this is the first reported BA.2.12.1 from Bangladesh, epidemiologists must investigate to monitor their prevalence (see Fig. 1).

**Conflicts of interest**

There are no conflicts of interest.

**Credit authorship contribution statement**

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