Genome Sequences of SARS-CoV-2 Sublineage B.1.617.2 Strains from 12 Children in Chattogram, Bangladesh

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ABSTRACT We announce the complete genome sequences of 12 severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) sublineage B.1.617.2 strains (Delta variant) obtained from nasopharyngeal and oropharyngeal swab samples from 12 pediatric patients in Chittagong, Bangladesh, displaying COVID-19 symptoms. Oxford Nanopore MinION sequencing technology was used to generate the genomic sequences.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a single-stranded RNA virus that belongs to the genus Betacoronavirus of the family Coronaviridae. This causative agent of coronavirus disease 2019 was first reported in Bangladesh on 8 March 2020. The complete sequences of 12 SARS-CoV-2 isolates from 12 children are presented in this paper.

As part of the countrywide COVID-19 laboratory network, the International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b), 250 Bedded General Hospital, Chattogram, and the Chattogram Maa O Shishu Hospital have been testing for SARS-CoV-2 since April 2020. Due to the recent emergence of the SARS-CoV-2 delta variant in Bangladesh, we wanted to evaluate its presence in COVID-19-positive children. Between 1 June 2021 and 7 July 2021, we enrolled 12 children with symptoms of COVID-19 and collected nasopharyngeal and oropharyngeal swab samples (n = 12). The presence of SARS-CoV-2 was determined by real-time reverse transcriptase PCR using ORF1ab- and N gene-specific primers/probes (1).

The QIAamp viral RNA minikit (Qiagen) was used for extraction of the viral RNA. Sequencing libraries were prepared following the nCoV-2019 sequencing protocol v3 (LoCost) (2). Briefly, a batch of 24 amplified samples was barcoded prior to being pooled for purification and sequencing adapter ligation. The final libraries were quantified and loaded onto a FLO-MIN106D (R9.4.1) flow cell on an Oxford Nanopore MinION MK 1C platform for 8 h. In total, 2,890,603 reads (range, 71,821 to 170,241 reads per sample; average length, 499 bp) were generated by real-time base calling using Guppy 4.3.4 as released with ARTIC Nextclade r1.0.4 workflow on the cloud-based analysis platform EPI2ME Desktop Agent v3.3.0 with default parameters, based on

Consensus genome sequences were achieved with 99.55% coverage at a minimum coverage of 10X and maximum of 400X.

A phylogenetic tree was constructed on 3 August 2021 using the Nextclade v1.5.2 (https://clades.nextstrain.org/) with default parameters (3). All 12 of the genome sequences branched in clade 21A (Fig. 1). According to the GISAID database Basic Local Alignment Search Tool (BLAST) (4), the genomes share the highest levels of similarity with sequences uncovered from the Indian delta variant (GISAID accession number EPI_ISL_2029113). According to analysis using Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin) with default parameters (https://pangolin.cog-uk.io/) (5), 4 of the 12 sequences are reported to be from delta sublineage AY.4, while the rest are from lineage B.1.617.2.

The availability of genomic data for circulating SARS-CoV-2 strains from children of different parts of the world will serve as a valuable resource for monitoring the infection patterns of different variants among children. Overall, it will help with infection control and management of SARS-CoV-2 spread among children.

Data availability. The data from this study can be found at NCBI under the BioProject accession number PRJNA766295. The complete nucleotide sequences of these SARS-CoV-2 strains have been deposited in the GISAID database under the accession numbers EPI_ISL_2987440, EPI_ISL_2987441, EPI_ISL_2987442, EPI_ISL_2987443, EPI_ISL_2987444, EPI_ISL_2987445, EPI_ISL_2987446, EPI_ISL_2987447, EPI_ISL_2987448, EPI_ISL_2987449, and EPI_ISL_2987450. The Sequence Read Archive (SRA) and GenBank accession numbers are listed in Table 1.

Ethical approval. This study has been approved by the research review board of Chattogram Maa O Shishu Hospital Medical College (protocol number CMOSHMC/IRB/2021/17).

ACKNOWLEDGMENTS

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