

Notes from the Field

Genome Characterization of the First Outbreak of COVID-19 Delta Variant B.1.617.2 — Guangzhou City, Guangdong Province, China, May 2021

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On May 20, 2021, 75-year-old female (Case A) went to a local hospital due to pharyngeal pain and low-grade fever in Liwan District, Guangzhou City, Guangdong Province. The oropharyngeal swab from Case A tested preliminarily positive for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)/coronavirus disease 2019 (COVID-19) virus using a quantitative real-time reverse transcription polymerase chain reaction (RT-qPCR) method after a hospital visit. In the early morning of May 21, 2021, the re-collected specimens were confirmed to be positive for COVID-19 for this patient with RT-qPCR tests by Guangdong Provincial CDC and Guangzhou City CDC. Subsequently, Guangdong Province began immediately taking a series of rigorous intervention measures including social distancing, community management, and lockdown to contain this outbreak. A total of 4 cases were confirmed with COVID-19 infections between May 23 and May 26 (Table 1). These patients were transported immediately to the local designated treatment hospital for isolated treatment by ambulance after COVID-19 virus infection was confirmed.

The viral ribonucleic acid (RNA) was extracted directly from 200-μL swab samples with Viral RAN/DNA Mini Kit (Invitrogen, USA). High-throughput sequencing was performed for 5 COVID-19 virus samples using Illumina (USA) and MGI Tech Co., Shenzhen, China. Nucleotide (nt) and amino acid (AA) differences between the 5 virus genome sequences from this study and the reference sequence Wuhan-Hu-1 were analyzed using the programs BioEdit and online tool “Nextclade” (<https://clades.nextstrain.org/>) (1).

The 5 specimens from Case A, Case B, Case C, Case D, and Case E were tentatively designated as XG5138-Case A-GZ-2021-05-21, XG5370-Case B-GZ-2021-05-23, XG5571-Case C-MM-2021-05-24, XG5647-Case D-GZ-2021-05-26, and XG5645-Case E-GZ-2021-05-26, respectively, in this study. Compared with the reference genome sequence Wuhan-Hu-1 (2–3), the genome sequences coverage of these 5 strains were 99.89%, 99.85%, 99.86%, 99.86%, and 99.87%, respectively. Based on the “Pango lineages” rule, the 5 virus strains from this study were assigned to delta (B.1.617.2), which was also known as variant of

TABLE 1. Demographic characteristics of the cases and specimen testing information.

Case ID	Sample number	Gender	Age (years)	Report city	Date of first positive detection of COVID-19 virus	Ct value (ORF1ab/N) by RT-qPCR			
						Specimen type	Daan	Bojie	Mingde
Case A	XG5138-Case A-GZ-2021-05-21	Female	75	Guangzhou	May 21, 2021	Nasopharyngeal swab	17/16	N/A	18/21
						Oropharyngeal swab	20/19	N/A	18/21
Case B	XG5370-Case B-GZ-2021-05-23	Male	75	Guangzhou	May 23, 2021	Nasopharyngeal swab	21/22	N/A	26/26
						Oropharyngeal swab	21/21	N/A	23/23
Case C	XG5571-Case C-MM-2021-05-24	Female	47	Maoming	May 25, 2021	Nasopharyngeal swab	16/13	14/15	N/A
						Oropharyngeal swab	20/18	19/20	N/A
Case D	XG5647-Case D-GZ-2021-05-26	Male	11	Guangzhou	May 26, 2021	Nasopharyngeal swab	16/13	N/A	16/15
Case E	XG5645-Case E-GZ-2021-05-26	Female	73	Guangzhou	May 26, 2021	Nasopharyngeal swab	19/17	N/A	19/19

Note: N/A=not applicable.

Abbreviation: RT-qPCR=quantitative real-time reverse transcription PCR.

concern (VOC) Delta (Figure 1) (4–6).

Compared with the reference genome sequence Wuhan-Hu-1, 5 strains shared 35 nucleotide variation sites (G210T, C241T, C1191T, C1267T, C3037T, C5184T, T6023C, C9598T, C9891T, T11418C, T12946C, C14408T, G15451A, C16466T, C18176T, A20262G, A21137G, C21618G, G21987A, T22917G, C22995A, A23403G, C23604G, G24410A, G25088T, C25469T, A25562G, T26767C, T27638C, C27739T, C27752T, A28461G, G28881T, G29402T, and G29742T) and 7 deletion mutations (22029–22035, 28248–28254, and 28274). Except for the mutations above, another variation site (C27092T) was observed in genome of the strain XG5571-Case C-MM-2021-05-24, XG5647-Case D-GZ-2021-05-26, and

XG5645-Case E-GZ-2021-05-26. XG5370-Case B-GZ-2021-05-23 had a unique variation site (T21673C), but not the C27092T variation.

By comparing deduced amino acid sequences, the 5 strains displayed 29 AA variation sites (M:I82T; N:D63G, R203M, D377Y; ORF1a:P309L, P1640L, Y1920H, A3209V, V3718A; ORF1b:P314L, G662S, P1000L, P1570L, K2557R; ORF3a:S26L, Q57R; ORF7a:V82A, L116F, T120I; ORF9b:T60A; S:T19R, G142D, R158G, L452R, T478K, D614G, P681R, D950N, and V1176F) and 4 deletion mutations (ORF8:D119del, F120del; S:F156del, and R157del).

The delta (B.1.617.2) was first identified in India in October 2020 and its spike protein had 9–10 characteristic mutations: T19R, (G142D), 156del, 157del, R158G, L452R, T478K, D614G, P681R, and

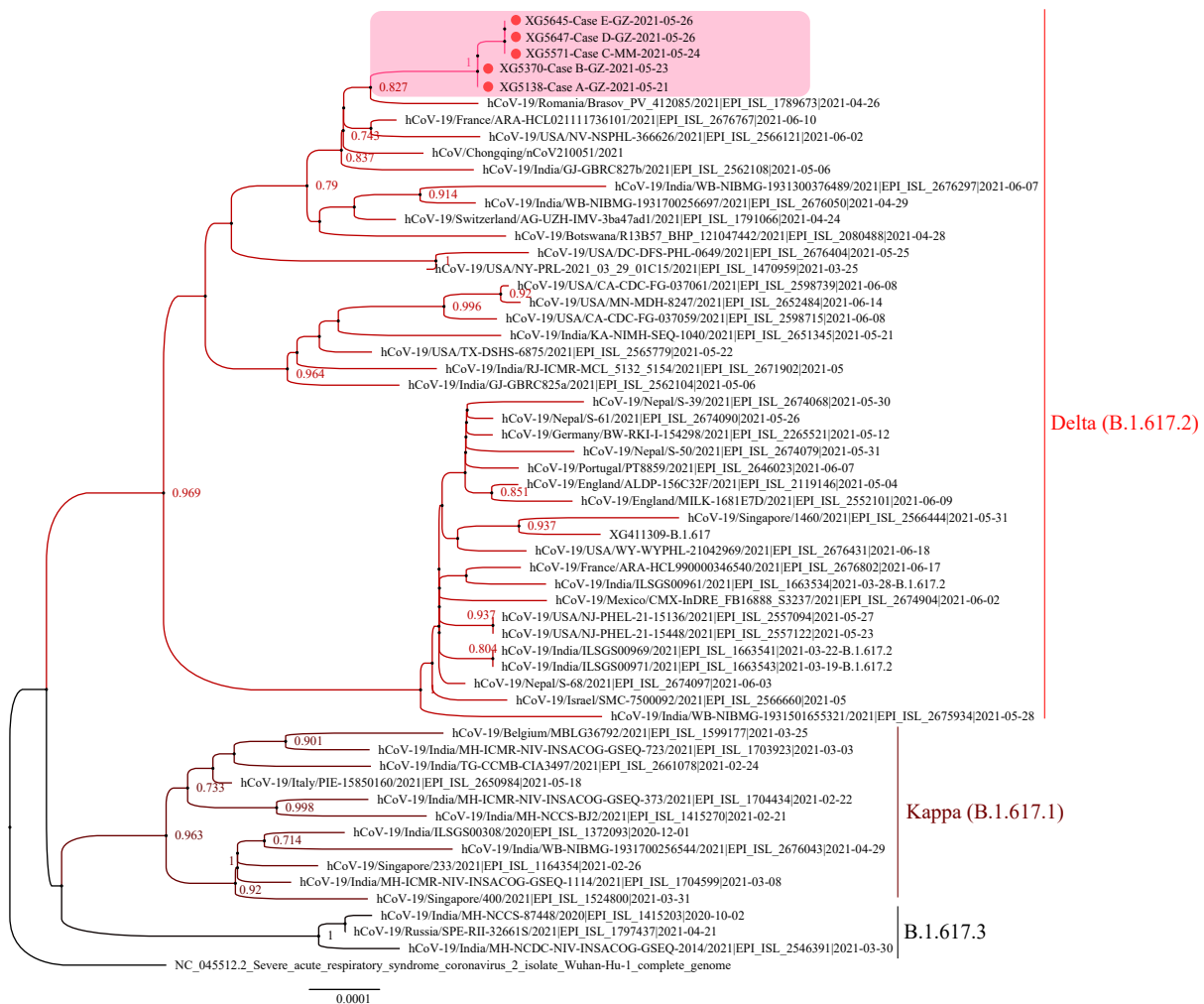


FIGURE 1. Neighbor-joining phylogenetic tree based on the whole-genome sequences of the delta (B.1.617.2) COVID-19 virus representative strains.

Note: The delta (B.1.617.2), kappa (B.1.617.1) and B.1.617.3 strains were marked on the right side. The five Guangzhou delta strains were indicated by red dots and highlighted by light red background. The tree was rooted using the Wuhan reference strain.

D950N (4–5,7). According to the current data of the World Health Organization (WHO), the delta (B.1.617.2) spread rapidly to 74 countries, areas, or territories (December 2019–June 8, 2021) (5). The epidemiological investigation showed that Case A was the index case and Case B (husband) was a close contact of Case A. Furthermore, Case C and Case E were at high risk of exposure due to Case A's activities (Case C as a waiter served Case A in a restaurant, and Case E went to same restaurant for dinner at the same time). Lastly, Case D was the grandson of Case E and was therefore a close contact. The whole gene sequencing results showed that Case C, Case D, and Case E added a common mutation site (C27092T) based on the sequence of Case A, and Case B possessed a new mutation site (T21673C) compared with Case A's sequence.

This Guangzhou outbreak is the first local transmission caused by delta (B.1.617.2) in China. The transmissibility and pathogenicity of these mutant variants urgently need more attention.

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