

An Imported Case of COVID-19 Delta Variant B.1.617.2—Guangxi Zhuang Autonomous Region, China, June 8, 2021

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Abstract

A male passenger arriving at Nanning Wuxu Airport in Guangxi on an international flight from Jakarta, Indonesia, was found to be positive for SARS-CoV-2 nucleic acid on a routine test at the airport on June 8 2021. The passenger was sent to Fourth People's Hospital of Nanning immediately for further isolation and observation. On the day of admission, the test for SARS-CoV-2 nucleic acid of nasopharyngeal swabs, pharyngeal swabs and sputum specimens were positive (CT values of N gene and ORF1ab gene were between 20 and 30). After 8 weeks of hospitalization, the patient's test for SARS-CoV-2 nucleic acid of all specimens turned to negative. We isolated a SARS-CoV-2 variant strain from the nasal swab of the patient, and then we found that the genome sequence of the variant strain had 13 base deletions and 38 nucleotide mutations compared with that of the Novel Coronavirus Wuhan strain after sequencing, comparison and analysis. The deletions and mutations of the variant strain resulted in four amino acid deletions and 30 amino acid mutations. Furthermore, we found that the variant strain was similar to those from Indonesia, South Korea and The United Kingdom after conducting BLAST analysis on GISAID platform, among them, hCoV-19 /Indonesia/ Ji-ITD-43591N /2021 was the most similar, with 99.98% similarity and only 8 base differences. The maximum likelihood phylogenetic tree was constructed taking the Wuhan strain as the root and including most the reference sequence contained most of the epidemic strains. The result showed that the strains isolated in our laboratory belonged to Delta strain.

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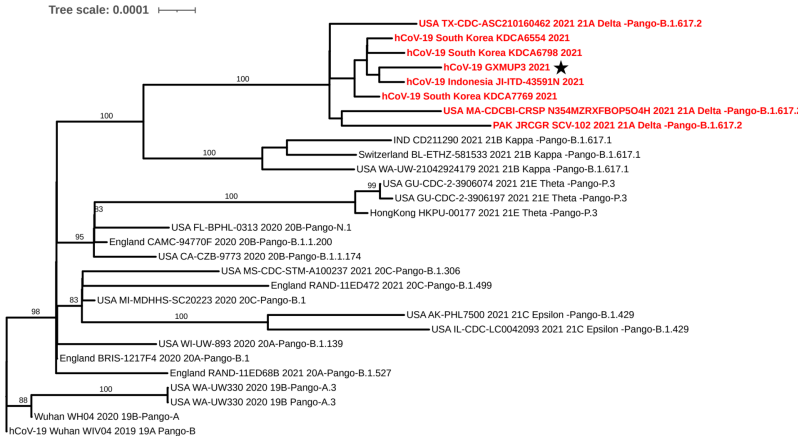


Figure 1. Phylogenetic tree based on the whole genome of SARS-CoV-2

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