

Laboratory Surveillance of COVID-19 Variants in Taiwan

Ji-Rong Yang*, Chuan-Yi Kuo, Yun-Tong Lin, Yu-Chi-Lin, Hsiao-Jung Chen,
Hsiang-Yi Huang, Bao-Shan Chen, Chih-Tsun Hsieh,
Jung-Jung Mu, Ming-Tsan Liu, Shu-Ying Li

Abstract

Since the novel coronavirus (SARS-CoV-2) first appeared in Wuhan, China in December 2019, it has rapidly spread to other countries around the world in a short period of time, leading to a global pandemic. In order to strengthen the efficacy of epidemic prevention and control, it is very important to grasp the genetic changes of the circulating viruses from virus-infected cases through genome sequence analysis in real time. The National Reference Laboratory in Taiwan Centers for Disease Control has completed the establishment of the viral genetic surveillance process through genome sequencing since the official publication of the whole genome sequence of the world's first SARS-CoV-2 strain. The analysis is performed on clinical specimens of confirmed COVID-19 cases or their virus isolates and the resultant data are handed over to the Central Epidemic Command Center to be released at the daily press conference in an open and transparent manner, which are applicable for optimizing national intervention strategies such as vaccines, drugs and pathogen diagnostic tools. It can also improve the efficiency of the causal investigation of various cluster events by exploring the genetic relationship of different SARS-CoV-2. This article describes in detail the entire laboratory monitoring process for SARS-CoV-2 genetic surveillance and the temporal identification results of various SARS-CoV-2 variants in Taiwan from 2020 to 2022.

Keywords: SARS-CoV-2, COVID-19, genome sequencing, virus variant

Center for Diagnostics and Vaccine Development,
Taiwan Centers for Disease Control,
Ministry of Health and Welfare, Taiwan
DOI: 10.6525/TEB.202208_38(15).0001

Corresponding author: Ji-Rong Yang*
E-mail: ggyang@cdc.gov.tw
Received: Jun. 14, 2022
Accepted: Jun. 14, 2022