

# COVID-19 outbreak in Malaysia: Decoding D614G mutation of SARS-CoV-2 virus isolated from an asymptomatic case in Pahang

*Aini Syahida Mat Yassim<sup>a</sup>, Mohd Fazli Farida Asras<sup>a</sup>, Ahmad Mahfuz Gazali<sup>a,d</sup>, Martin S. Marcial-Coba<sup>b</sup>, Ummu Afeera Zainulabid<sup>c</sup>, Hajar Fauzan Ahmad<sup>a,d,\*</sup>*

<sup>a</sup>Faculty Industrial Sciences and Technology, Lebuhraya Tun Razak, 26300 Gambang, Pahang, Malaysia

<sup>b</sup>Pontifical Catholic University of Ecuador, 170143 Quito, Ecuador

<sup>c</sup>Kulliyyah of Medicine, International Islamic University Malaysia, 25200 Kuantan, Pahang, Malaysia

<sup>d</sup>Centre for Research in Advanced Tropical Bioscience (Biotropic Centre), Lebuhraya Tun Razak, 26300 Gambang, Pahang, Malaysia

## ABSTRACT

SARS-CoV-2 is a very transmissible and pathogenic coronavirus which detected in Malaysia in January 2020. Nevertheless, the sample from Malaysia is still under-sequenced. Hence lacking clarity of the circulating strain in Malaysia leads to a deadlock in understanding the virus infectivity. This study aimed to investigate the genome identity of circulating COVID-19 strains in Pahang and understand disease epidemiology during the pandemic. This study leveraged high-throughput sequencing analysis for the whole genome sequencing and implemented bioinformatic technique for the analysis. Here we reported that the virus with D614G mutation in Spike protein circulates in a few Malaysia states before the Sivagangga cluster announced in Kedah in July 2020. This mutated virus includes our virus sample isolated in April 2020 from an asymptomatic patient in Pahang. Based on the phylogenetic analysis, we discovered the origin of our sample Pahang/IIUM91 was not related to Sivagangga cluster. Here, we have generated 3D structure model of Pahang/IIUM91 Spike protein. D614G mutation in Pahang/IIUM91 Spike protein increases viral stability and flexibility, hence render higher infectivity. Collectively, our results suggest for the establishment of a complete SARS-CoV-2 genome database in Malaysia. Hence, more research should be established to learn the behaviour of this virus.

**KEYWORDS:** SARS-CoV-2, Mutation, D614G, Spike protein, Malaysia, Pahang

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