The D614G Mutation in Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Spike Glycoprotein: A Mini-Report

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Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a quickly spreading virus that poses a major burden on global human health. Thus, it is essential to develop COVID-19 vaccines. Vaccine development might not be easy, as a consequence of mutations. This study aimed to demonstrate the D614G mutation in SARS-CoV-2 spike glycoprotein from Indonesia. 102 isolates from the GISAID EpiCoV database and the Wuhan-Hu-1 isolate (reference sequence) from GenBank, NCBI were used in this study. BioEdit employed to examine the D614G mutation in the spike glycoprotein of SARS-CoV-2. In this report, there are 56 D614G mutations among 102 SARS-CoV-2 isolates. In summary, this report might suggest that the D614G mutation implicates the COVID-19 pandemic in Indonesia. Nevertheless, this report was a preliminary study and this study recommends expanding molecular epidemiology and surveillance programs to monitor COVID-19.

Keywords: *COVID-19, D614G Mutation, SARS-CoV-2.*

Introduction

The Chinese government first reported a novel pneumonia-causing disease in Wuhan (end of December 2019)[1,2,3]. The causative agent was identified and named severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) by the International Committee on Taxonomy of Viruses (ICTV). This new virus has rapidly spread across China and to many other countries across the world, including Indonesia. The World Health Organization has named the disease caused by SARS-CoV-2 as coronavirus disease 2019 (COVID-19)[4,5,6,7].

According to an online interactive dashboard hosted by the Center for Systems Science and Engineering at Johns Hopkins University (Baltimore, USA), which tracks reported cases of COVID-19 in real-time, about 70 million people have been infected by SARS-CoV-2 worldwide, with approximately 600,000 cases in Indonesia alone (December 2020)[8]. Currently, there are three coronaviruses that cause illness in humans: severe acute respiratory syndrome coronavirus (SARS-CoV), Middle-East respiratory syndrome coronavirus (MERS-CoV), and SARS-CoV-2[9].

The coronavirus family is composed of four different genera: *Alphacoronavirus*, *Betacoronavirus*, *Deltacoronavirus*, and *Gammacoronavirus*. SARS-CoV-2 belongs to Coronaviridae[10,11]. The SARS-CoV-2 genome is a single-stranded positive-sense RNA of roughly 30,000 nucleotides. This genome encodes four structural proteins: membrane (M), envelope (E), nucleocapsid (N), and spike (S)[12]. The spike glycoprotein has recently emerged as the primary target antigen in the formulation of a SARS-CoV-2 vaccine[13]. Previous study identified the candidate for a peptide-based vaccine against COVID-19 based on the spike glycoprotein[14].

The molecular epidemiological data of the SARS-CoV-2 outbreak remains unclear. Furthermore, a vital tool for discovering new emerging viruses is research

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on molecular epidemiology[15,16]. In addition, D614G is a common amino acid mutation in the SARS-CoV-2 spike glycoprotein globally[17]. Zhang *et al*. reported that this spike glycoprotein mutation transmits more efficiently[17,18]. Thus, this study aimed to demonstrate the D614G mutation in SARS-CoV-2 isolates from Indonesia.

Methods

SARS-CoV-2 Isolates

SARS-CoV-2 spike glycoprotein gene (3822 bp) sequences were obtained from GenBank (National Center for Biotechnology Information, USA) and the Global Initiative on Sharing All Influenza Data (GISAID) EpiCoV database (Germany). This study used 102 SARS-CoV-2 isolates from Indonesia (end of December 2020).

Analysis of the D614G Mutation

In this report, the translation process of the genome performed by using BioEdit and then investigated the D614G missense mutation status of all isolates.

Results and Discussion

Coronaviruses infect both animals and humans and lead to many illnesses, including enteric, neurological, and respiratory diseases[3]. There are four distinct genera of coronaviruses. SARS-CoV, MERS-CoV, and SARS-CoV-2 are three highly pathogenic coronaviruses, capable of infecting humans, that emerged in 2002, 2012, and 2019, respectively[10]. Outbreaks of SARS-CoV-2 have led to a state of medical and economic emergency worldwide[15].

Many researchers worldwide have previously reported mutations in the SARS-CoV-2 genome[19,20]. In addition, Tang *et al*. have suggested that SARS-CoV-2 exhibits the characteristic high mutation rate of an RNA virus. Furthermore, the mutation rate of SARS-CoV-2 and other coronaviruses might be slightly lower than other RNA viruses because of its genome-encoded exonuclease[21]. The high mutation rate increases the potential of this zoonotic viral pathogen to adapt to efficient transmission from human to human and potentially allows it to become more virulent[15]. This report revealed that there are 56 D614G mutations among 102 SARS-CoV-2 isolates (Table 1).

Table 1. The Partial Results of D614G Mutation Analysis.

No	Isolate	D614G Mutation
1	Wuhan-Hu-1	No
2	JK-EIJK-0141	No
3	JK-EIJK-2444	No
4	JK-EIJK-0317	No
5	JK-EIJK-01	No
6	JK-EIJK-04	No
7	JK-EIJK-03	No
8	JK-EIJK-02	No
9	SA-EIJK-06	No
10	KI-EIJK-05	No
11	JK-EIJK-07	No
12	YO-UGM-202449	Yes
13	JB-TFRIC19-L4173	Yes
14	JI-ITD-853Sp	No
15	JI-ITD-1238Sp	No

This study is crucial for future investigations into the pathogenesis, prevention, and treatment of SARS-CoV-2. Development of this genomic data is vital work that will facilitate vaccine design, epidemiological investigations, viral detection, functional analysis, and evaluation of treatment options[22,15].

On the other hand, our molecular phylogenetic study reported the relationship of SARS-CoV-2 and other *Coronaviridae* based on the spike glycoprotein genes[14]. In line with this, SARS-CoV-2 is closest to *Rhinolophus affinis* coronavirus RaTG13, followed by pangolin coronavirus[13]. Therefore, Malayan pangolin is assumed to be the intermediate host before the virus began infecting humans.

Conclusion

In summary, there are 56 D614G mutations among 102 SARS-CoV-2 isolates. This report might suggest that the D614G mutation implicates the COVID-19 pandemic in Indonesia. Nevertheless, this report was a preliminary study and this study recommends expanding molecular epidemiology and surveillance programs to monitor COVID-19.

Conflict of Interest : The author declare that they have no conflict of interest.

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