

New COVID-19 Variant, VUI-202012/01: Molecular Change, Epitope Alteration, and Implication for Vaccine Efficacy

Dear Editor,

COVID-19 is the new emerging coronavirus infection. The pandemic results in more than 75,000,000 people around the world (data on December 21, 2020). In clinical genetic, impact of genetic change on the infection is an interesting issue. The mutation might occur with the SARSCoV2 virus molecule. Recently, there is a report on new COVID-19 variant, VUI-202012/01. This new strain was firstly observed in UK and the relationship with increased transmissibility property is reported. The main genetic change is the genetic mutation N501Y inside the spike glycoprotein's receptor-binding domain, which is important molecular part binding to the ACE2 receptor in humans. In vaccinology, the impact of the mutation on vaccine efficacy is an important question.

Here, the authors use a standard bioinformatics analysis, as used in previous reports,^[1,2] for assessing the effect of molecular change in the VUI-202012/01. The online tool is accessible via <http://www.syfpeithi.de/bin/MHCServer.dll/EpitopePrediction.htm>. According to the analysis, there is a change of epitope pattern. At the mutation part, the identified epitope sequence change from "487F Q P T N G V G Y" in naïve case to "515C G P K K S T N L" in VUI-202012/01. It might expect that the VUI-202012/01 will be the new problem to prevent the successful COVID-19 containment by the newly available COVID-19 vaccines.

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Conflicts of interest

There are no conflicts of interest.

Beuy Joob, Viroj Wiwanitkit¹

Department of Community Medicine, Private Academic Consultant, Bangkok, Thailand, ¹Honoary Professor, Dr. D. Y. Patil University, Pune, India

Address for correspondence:

*Dr. Beuy Joob,
Sanitation 1 Medical Academic Center, Bangkok, Thailand.
E-mail: beuyjoob@hotmail.com*

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