



SARS CoV2 Variant Delta and Delta Plus, Molecular Change and Expected Impact of Response to COVID-19 Vaccine

Sora Yasri¹ , Viroj Wiwanitkit²

Dear Editor,

SARS CoV2 variant delta and delta plus, molecular change and expected impact of COVID-19 vaccine response- Dear Editor, COVID-19 is a newly emerging virus infection (1). Currently, several genetic mutations of the pathogen are registered. Of the several problematic variants, the delta variant is currently spreading worldwide (2). Ad-

ditionally, a newer variant, the delta plus variant, has already occurred and becomes the latest consideration in clinical medicine (3). Interestingly, the disease epidemiology and clinical features have changed due to new variants. For the delta variant, the mutation occur in the gene encoding the SARS-CoV-2 spike protein as T478K, P681R and L452R substitutions (2). Regarding the delta plus variant, additional mutations which are K417N, are observed (3). The present study aims at assessing the molecular change due to delta and delta plus variants.

The authors use a molecular quantum molecular calculation technique as used in previous studies (4, 5) for assessing the molecular change. Naïve or mutation-free type is used as a negative control. For a simulation process, new mutations corresponding to each variant are assigned to generate new variants. Molecular calculation is then performed to find the magnitude of change. The calculation result is presented as molecular weight change per molecule. The magnitude of the molecular change in the delta variant compared to the naïve type is greater than in the delta plus variant (Table 1).

In a previous study of an important VUI-202012/01, a significant molecular weight gain was observed, corresponding to a high transmissibility (5). It is suggested that the mutation that causes an increase in molecular weight can result in easier receptor binding, and less required pathogen molecules compared to the naïve virus type (5). On the other hand, such a variant can result in a drug or antibody molecule that is more necessary for biological interaction, implying an increased drug resistance or reduced vaccine efficacy (5). In the present study, it can show that both delta and delta plus variants manifest similar genetic characteristics, by inducing increased molecular weight. This might also mean increased transmissibility and reduced response to drugs and vaccines. Based on the present study, it can also be indicated that the delta variant should cause more problematic clinical outcomes than delta plus. This is in line with the fact that delta plus is detected still less than delta in the setting where delta is already widely spread.

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Table 1. Molecular change in naïve, delta variant and delta plus variant

Types	Mutations	Molecular change	
		Overall magnitude (g/mol)	Relative percentage of change to naïve (%)
Naïve	No	0	0
Delta variant	T478K, P681R and L452R	+129	+35.344%
Delta plus variant	T478K, P681R, L452R and K417N	+115	+22.50%

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¹KM Center, Bangkok, Thailand
²Honorary professor, Dr DY Patil University, Pune, India

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Correspondence
Sora Yasri,
KM Center, Bangkok, Thailand
Phone: +66 6624588925
e-mail:
sorayasri@outlook.co.th

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