Correspondence

To the Editors

New SARS-COV-2 variants and paediatric COVID-19 clinical manifestations

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Dear Editors,

COVID-19 variants are presently in focus. Basically, a COVID-19 variant may cause an antigenicity change[1]. Firstly, SARS Co-V2 variant B.1.1.7 emerged in UK and there are many reports on its possible clinical impact[2]. At present, there are also other important variants such as the South African variant, Brazilian variant and US variant.

In children, the effects of SARS-CoV2 variants are not clear. Paediatric COVID-19 is usually mild and self-limited[3]. Brookman S, *et al*[4] found that "*there was no evidence of more severe disease having occurred in children and young people during the second wave, suggesting that infection with the B.1.1.7 variant does not result in an appreciably different clinical course to the original strain*." This contrasts with a report by Eaaswarkhanth M, *et al*[2] that stated "*the S-D614G strains may be more virulent, increasing the severity in infected individuals, especially in Europe where this mutation is prominent*[2]." Zhang L, *et al*[5] proposed a similar observation of change of disease pattern due to the single point substitution. Therefore, the effect of mutation is still inconclusive.

Since those reports are based on epidemiological studies, there may be a confounding effect. The effect of genetic substitution, as a single parameter, may be a clue for molecular pathogenetic explanation. Theoretically, a mutant has a somewhat different molecular structure from the index type. If the change results in a less required molecular amount for completeness of a reaction between pathogen molecule and host receptor, it might result in more severe disease or infectivity[1]. Based on this principle, mutation should have clinical effects regardless of setting. For example, if D614G strains occur, the decreased molecular weight due to amino acid substitution, from D to G, should affect disease manifestation in Western or non-Western countries. Also, either paediatric or adult population should be similarly impacted by molecular change in each variant. On the same basis, a novel variant with many mutation points such as the USA mutant, which consists of many substitutions, should have more clinical impact than a variant with fewer substitutions.

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***Rujittika Mungmunpuntipantip[1]; Viroj Wiwanitkit[2]**
[1]*Private Academic Consultant, Bangkok Thailand*
[2]*Honorary Professor, Dr. DY Patil University, Pune, India*
**Correspondence:* rujittika@gmail.com

https://orcid.org/0000-0003-0078-7897