Review of: "Evolution of new variants of SARS-CoV-2 during the pandemic: mutation-limited or selection-limited?"

Mauricio Alberto Realpe Quintero[1]

1 Universidad de Guadalajara

Potential competing interests: No potential competing interests to declare.

The study is very well designed, methods are adequate for achieving the goals, and the data analysis is sufficient for making the stated conclusions. The scope of the investigation is of global interest and it has a high significance across disciplines. Claims against mutation-limited hypothesis are well supported, however some precision could be of value.

Results of nonfit for the mutation-limited hypothesis are very interesting. It could be more supportive to match the simulation results with actual data from the same susceptible population. This is, figures 4 and 5 (pages 12-13), depicted from same country with variable Ro as a function of the interplay between both viral competing populations. Lower incidence might be associated with changes in the reproductive number upon declining of the previous variant and thus the hypothesis will be supported given that less viral variability will be needed to affect a slightly changing susceptible population of hosts assuming no immunity changes will be in place for the period of arrival of the new viral variant. Declining of immunity takes weeks. For instance, B117 virus has 70% more contagious (doi.org/10.1016/B978-0-323-85730-7.00041-2) or 3-fold higher transmissible as compared with previous strain. Mutation-limited hypothesis may be replaced by mutational entropy/activity increase hypothesis.