

Review of: "Omicron Variant Could be an Antigenic Shift of SARS-CoV-2"

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Potential competing interests: No potential competing interests to declare.

Abstract:

1. Please spell out COVID-19 as coronavirus disease 2019 and VOC as variants of concern
2. I would use the word mutational and/or antigenic shift rather than heavy mutations as these affect the RBD/ACE2 interface.

Introduction:

1. Delta variant 97-100% more virulent. Please state the source citation that compares this between variants.
2. I would use the word affected the immune response. Lowering implies decreasing scale and there are many facets to the immune response cells like B, T cells and Interferon. This could be inferred by the overall decrease in mortality since the 2020/2021 variants.
3. Vaccine efficacy section. Please state source citations below or either of these could be cited/supplementary data. [Vaccines | Free Full-Text | An Immunological Review of SARS-CoV-2 Infection and Vaccine Serology: Innate and Adaptive Responses to mRNA, Adenovirus, Inactivated and Protein Subunit Vaccines \(mdpi.com\)](#) [Results - longer articles and adhoc publications from ONS — Nuffield Department of Medicine \(ox.ac.uk\)](#)
4. When describing this part you say Coronvac decreased antibody titers by 17x - 22x. This is incorrect. Antibody titers vary with time but there would be an initial 2-3 month increase and the assay scales are being evaluated by the WHO to this effect.
5. You refer to neutralising activity. You could chose to expand on this and differentiate into non-neutralising and neutralising antibodies or even polyclonal antibodies as the immune response is generally a clonal selection process generating polyclonal antibodies of predominant 3 types (IgG, IgM, IgA, IgE, IgD).
6. The variants of concern section looks fine. Please mention XBB1.5 and EG5.1, but this tracker is derived from nextstrain data will be current. [Profile - raj.rajnarayanan | Tableau Public](#) Please state limitations section on genomic sequencing as the surveillance requires genomic analyse based on PCR sample number globally in order to determine the prevalence which is very variable globally. I would check the image citation permissions.

Neutralization Resistant Mutations

1. I would use affected a,b,c
2. You could further transmissability and infection rate using the R0 terms and alsI IFR which is epidemiological

terminology. I think the initial estimates were around r_0 2.75 for D614G but others may be unknown.

3. Generally this sections looks ok, but please mention antibody epitopes affected by the amino acid mutations. The bloom lab but also [Report on Omicron Spike mutations on epitopes and immunological/epidemiological/kinetics effects from literature - SARS-CoV-2 coronavirus / nCoV-2019 Genomic Epidemiology - Virological](#) i found particularly relevant.
4. BA2.86 you could choose to update manuscript with.
5. You mention anti-RBD IgM as 297 mAbs. To what does this number refer to? Also please ensure the comparisons with different monoclonals have a cited source.

Discussion and Conclusion

1. You mention actual titre of Ab reactivity correlates with conferred protection. Please cite a source for this. T cells are equally and possibly more important with many phenotypes.
2. You could chose to include a limitations section as many of the cited studies use in vitro cell culture lines. e.g., PHAE, ACE2 recombinant cultures.

Overall an interesting manuscript to read. It is well written but does need further editing and updating.