Rapid Reviews COVID-19

Review 2: "Impact of B.1.1.7 variant mutations on antibody recognition of linear SARS-CoV-2 epitopes"

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RR:C19 Evidence Scale rating by reviewer:

- **Reliable.** The main study claims are generally justified by its methods and data. The results and conclusions are likely to be similar to the hypothetical ideal study. There are some minor caveats or limitations, but they would/do not change the major claims of the study. The study provides sufficient strength of evidence on its own that its main claims should be considered actionable, with some room for future revision.

Review:

This study has used the established technique, serum epitope repertoire analysis (SERA) followed by protein-based immunome wide association studies (PIWAS) to assess whether serum from 579 COVID-19 patients, collected before the emergence of the SARS-CoV-2 B.1.1.7 variant, differentially recognizes spike and nucleocapsid from SARS-CoV-2 wave 1 Wuhan and B.1.1.7 lineages as a measure of B.1.1.7 immune escape from wave 1 induced antibody responses. The authors conclude that B.1.1.7 coding mutations in S and N would not result in immune evasion of linear epitopes for the large majority of the COVID patients studied. The study claims are justified by the methods and data. The results and conclusions are likely to be similar to the hypothetical ideal study. The only caveat is the nature of the technique, which must be confirmed by more classical neutralization studies, but as it stands the results are compelling and thus the study provides sufficient strength of evidence on its own that its main claims should be considered actionable, with some room for future revision, describing caveats of the method.