

Peer Review File

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Reviewer 1

Comments

1. Could you provide more details on the implementation of the MLR models, GBTM, and high-dimensional transmission dynamics model? This would help readers better understand and reproduce the study. You could attach them in supplementary materials.

Reply: Thank you for your suggestion. We did miss some detailed descriptions on the models applied in the study. Now we have made clear statements on the models' principles as well as how to realize them in the programming tools. Additionally, we provided detailed results of our study so that it would be easier to check about the results given in the manuscript. All those information mentioned above could be checked in the Supplementary Material 1 and 2.

Changes in the text: We have made the description of our methods section (Line 79-134) more concise in the manuscript, with the detailed description of the models being placed in supplementary materials.

2. Have you considered the potential biases or limitations of studying a specific population of public health workers? How do you think the findings may differ in the general population? It is suggested to provide some other references for comparison.

Reply: Thank you for bringing this problem up. This study involves a follow-up serum antibody test, which could be difficult to conduct in general communities. What's more, in this study, our aim is to carry out a preliminary investigation to gather initial insights about impact of decay in antibody titers for three major antibodies on future COVID-19 epidemic trend and reinfection. As healthcare workers tend to be more obedient and are willing to cooperate, which is crucial in follow-up studies, we chose this population group. However, due to the limitation of experimental condition, random sampling is impossible for us, hence, convenience sampling is a practical way for us to collect data. However, as participants are chosen based on ease of access, it may not represent the broader population accurately, and these biases can skew results and limit the generalization of our findings. Now we are still working on with better way for collecting valid data and explore a more convincing result.

Changes in the text: We have made statements on the bias that may be result from our sampling in the data collection section in supplementary material 1, and discussion (Line 237-242, 297-299) as well as limitation sections (Line 329-338) in the manuscript. References which are used for make comparison are also added in Line 297-299.

3. It would be helpful to include a discussion on the implications of the study's findings for public health interventions and strategies.

Reply: Thank you for your mentioning about this. As a retrospective study, we aim at exploring potential risks and provide relevant strategies in decreasing the

impacts of the risks. Here we have added discussion on possible interventions that could reduce the impact of the factors on future infection and reinfection.

Changes in the text: We have made changes in discussion section line 278-280, 289-292, 311-315.

4. Line 250 “we considered that serum antibodies could persist for a 250 maximum of 73 days” , any reference?

Reply: Thank you for your question. We do have referred to a review on a longitudinal COVID-19 antibody dynamic study, which is the reference 6 in the references section in the manuscript. In this study, during the data collection section, we have noticed that some of the participants claimed that they had not been infection since December, 2022, and the last vaccination time that they had taken was 1 or 2 years ago, but the antibody titer of them showed extremely high IgM level, which did not make sense. Therefore, we applied a 73 day to be the maximum time interval between initial antibody appearing time and serum antibody testing time, to diminish potential bias caused by misinformation provided by the participant.

Changes in the text: Line 73 and 161, we have provided the statement with the reference.

5. Line 91, “we initiated data collection by distributing questionnaires to public health 91 workers in the Xiamen Center for Disease Control” ,how many health care workers in Xiamen Center for Disease Control? And how many questionnaires were dispatched?

Reply: Thank you so much for pointing this problem out. We are so sorry that we have made a mistake in our statement in the text. Actually, it was the staffs from the entire healthcare system in Xiamen City, instead of public health workers from Xiamen CDC. The participants are from hospitals, CDCs as well as primary healthcare organizations and were selected through convenience sampling. The questionnaire was sent out via QR code, the total dispatch amount was unclear, but there were a total of 1344 questionnaires were collected and 1191 of them were considered valid and included in the study.

Changes in the text: We have revised the words in Line 58-60, 70-72, 149-154.

6. Line 416-428, conclusion need to focus the significant or corresponding findings in current study.

Reply: Thank you for your advice, we have refined our conclusion according to your guide.

Changes in the text: Conclusion section in manuscript.

7. Languages need to be polished by native speakers.

Reply: Thank you for mentioning about that. We have noticed that there were some inaccurate uses in vocabularies and sentences, now we have refined the text and made it more readable.

Changes in the text: The whole text.

Reviewer 2

Comments

1. The paper lacks a clear description of the methodology, more details on data collection, analysis procedures, and model parameters would be helpful.

Reply: Thank you for your input. We have incorporated comprehensive descriptions of the models utilized in our study, outlining their core principles and the practical implementation using programming tools. Furthermore, we have furnished detailed results, enhancing the accessibility and verification of the information presented in the manuscript. For a comprehensive reference, all this supplementary information is available in Supplementary Material 1 and 2.

Changes in the text: We have made the description of our methods section (Line 79-134) more concise in the manuscript, with the detailed description of the models being placed in supplementary materials.

2. The authors should provide more recent studies in the field to support the paper's value and contextualize the findings.

Reply: Thank you for your insightful feedback. We appreciate your suggestion regarding the inclusion of more recent studies in the field. We recognize the importance of contextualizing our findings within the current landscape of research. We have reviewed recent literature to enhance the paper's value and provided a more comprehensive understanding of our study's significance.

Changes in the text: most of the discussion section.

3. What are the limitations of the models used in the study, and how do they impact the generalizability of the findings? It would be helpful to have a more explicit discussion of the limitations and uncertainties of the models, as well as the

implications and applications of the findings for COVID-19 prevention and control.

Reply: Thank you very much for your advice. We have added the limitation of the models in the text. The high-dimensional transmission dynamics model primarily accounts for population contact as a pivotal factor influencing the epidemic's peak. However, it's important to note that this model doesn't factor in virus mutations or potential immune escape by variants. This suggests the need for refinement in the model to enhance its predictive accuracy for future epidemic trends. In this retrospective study, our focus lies in uncovering potential risks and devising strategies to mitigate their impact. We've expanded our discussion to include interventions aimed at reducing the influence of these factors on future infections and reinfections.

Changes in the text: Limitation 336-340. Discussion section line 278-280, 289-292, 311-315.

4. Have you taken the potential impact of SARS-CoV-2 variants on antibody titers and reinfection risk into consideration? As new variants emerge and spread, the neutralizing activity and cross-protection of antibodies may vary.

Reply: Thank you for mentioning about this. We have previously overlooked the impact of mutant strains on our research content. We have reviewed some researches and it is indicated that immune escape is common in SARS-CoV-2 variants, therefore, there is a high chance that variants may affect the antibody

titers and reinfection risks. However, during our study period, the dominant strain the China were basically Omicron BA.5 and Omicron XBB, further studies should be conducted to investigate the impact of SARS-CoV-2 variants on antibody titer decay and reinfection.

Changes in the text: Line 38-40; Line 336-340