Response to the Reviewer

First of all, we thank the reviewer for the useful comments and suggestions. We have now addressed all the issues raised by the reviewer. We have revised the manuscript according to the comments given by the reviewer. Point by point responses are given below:

1. The paper is full of incorrect terminology, making it hard to follow what the authors are doing. My list was not exhaustive, but the authors appeared to not have bothered to check for any incorrect terminology themselves. They also have not corrected two of the mistakes I pointed out --- 'MERS' is still written as 'MARS' and the authors refer to their model as target-cell limited (it is not).

- We have corrected all the issues raised by the reviewers.

2. The references are sometimes not relevant to the corresponding statement. The specific papers I listed previously have been addressed, but there are still several references are not relevant to the corresponding statement.

- We have removed the irrelevant references and self-citations. We have also added some recent references for within host dynamics of SARS-CoV-2. Also, we have rewritten the INTRODUCTION with proper references. Some references and some paragraphs are modified accordingly.

3. There is also a lack of references for much of the introductory material. There isn't a single reference in the first paragraph. There are also many "statements of fact" in lines 76-108 that still don't have references.

- Proper references are provided in the revised manuscript.

4. The introduction is very muddled. The discussion of epidemiological models has not been removed. It is absolutely not relevant here and is simply there for self-citations. On the other hand, I still don't see a great discussion of SARS-CoV-2 in-host models. There have been a number of these published recently, including one that models monoclonal antibody treatment. Since the authors are also trying to model antibodies, it seems like that should be relevant.

In our introduction, we have tried to discuss the studies of SARS-CoV-2 infection at both the population and cellular levels. It is true that our study is based on cellular-level modeling. Still, we give these references to show the active participation of researchers in exploring different dynamics of SARS-CoV-2 infection at both micro and macro level.

5. The authors are not clear about which immune response they are modeling. This has been fixed.

- The model is based on the role of antibody responses.

6. I'm curious as to why removal of antibodies when they bind to virus is not included in the model. Saying that every model has limitations is a cop-out. Since you are trying to model antibodies, and presumably model them as realistically as possible, why is antibody loss to binding not considered? Have you tried it and it doesn't have a large effect? Do you not want to include it because it might make the drug look less effective?

- We numerically checked that it has no large effect for the set of parameters used but model would be more realistic if it is included.

7. The parameters presented in Table 1 do not have units. Units have been added to the table, although they are not all correct. Theta should have units of virus. alpha should have units of [virus]/[time][cell]. I'm also curious as to why uninfected cells are dying faster than infected cells (0.2/d for uninfected cells, only 0.189/d for infected cells). Being infected doesn't usually make cells live longer.

- The units and values of the parameters are checked and corrected. We have followed the following articles:

  - Hernandez-Vargas EA, Velasco-Hernandez JX. In-host mathematical modelling of COVID-19 in humans. Annual reviews in control. 2020 Jan 1;50:448-56.
  - Nikin-Beers, R. and Ciupe, S.M., 2015. The role of antibody in enhancing dengue virus infection. *Mathematical biosciences*, *263*, pp.83-92.
  - Ghosh, I., 2021. Within host dynamics of SARS-CoV-2 in humans: Modeling immune responses and antiviral treatments. *SN Computer Science*, *2*(6), pp.1-12.

8. The authors give no justification for the impulsive function on antibodies. I understand that antivirals are taken as multiple doses. I would like the authors to specifically list which antiviral causes an increase in antibodies. The only treatment I know of that directly increases antibodies is monoclonal antibody treatment and that is a single infusion, so no time lag. The manuscript has been submitted to an experimental/clinical journal; the authors should be clear about the actual clinical application of their work.

9. The authors assume a quasi-steady state approximation for antibodies to do their analysis. Is this really valid? I don't see any reference listed near where the authors make the quasi-steady state assumption. As I mentioned previously, the quasi-steady-state approximation is NOT valid over the rapidly-varying time frame of individual doses. It is also NOT valid over the 20–30-day phase of rising antibodies. So where is it valid? The authors should be able to justify this with actual calculations of the time scales.

- We agree with the reviewer's point of view. Actually, there are references that we followed for the analysis.
- We have now redone the whole analytical calculations without taking Quasi steady-state approximation (see the Section 3 and Appendix G and H, page 5-12).

  Hope this satisfies the reviewer's requirement.

10. In the analysis of the impulsive model, the authors assume only exponential decay of the antibodies between impulses; what happened to the growth term? First of all, it is not clear that the system was "linearized." Second, linearizing a system does not mean ignoring all the nonlinear terms; it means using the first order (linear approximation) of the nonlinear terms. So, this is not done correctly.

- We have checked that our analysis is okay. The same methodology were used in the following article:

  http://www.aimspress.com/aimspress-data/mbe/2021/2/PDF/mbe-18-02-075.pdf

- Here the growth term is ω in the impulsive system (3). In the numerical simulation, the original system (nonlinear model (3)) is used.

11. Line 371 states "The data are taken mainly from Wolfel et al. [36], and some are estimated." This sentence remains completely unchanged and I don't see any "clarification" that makes it accurate (there is NO PATIENT DATA in this paper).

- The line is removed as per the reviewer's suggestion. We now cited appropriate references for this research.

12. Figure 2: These figures make no sense. I'm not sure how this was addressed because these figures are unchanged.

- We agree with you and removed the figure.

13. Figure 4, should it be "Unstable for DFE" rather than "Unstable for EE"? This figure is also unchanged and therefore still incorrect.

- We agree with the reviewer. The figure is now modified as required (see Figure 3 in revised manuscript).

14. Figure 5 is labeled as showing variables over time, but there is no time in this figure. The authors have not checked and corrected the figures because this one is also unchanged.

- We have replotted the Figures. The issues is now not arising.