Reviewer 4:

The article is well written, easy to follow and interesting work related to molecular dating analyses for origin and evolution of Omicron sub-lineages. I enjoyed reading it. The work uses a comprehensive dataset to support its conclusions, and is presented in an appropriate manner. I recommend it for publication. There are a couple of minor suggestions as follows.

Comment 1: Line 53, "the former carries genetic changes" should be changed to "the former carries some peculiar genetic changes"

Reply: Thank you for suggesting this change. We have introduced this change in Line 53.

Comment 2: Line 385 to 389, the sentence "This study also advocates…" is very long. I suggest breaking that sentence into two.

Reply: We have made correction as suggested.

Comment 3: Line 83-84: Continued evolution of SARS-CoV-2 Omicron VOC has already generated at least five sub-lineages, however, it is not clear to me why the authors preferred only the two sub-lineages of Omicron VOC for deciphering its possible origin and evolution.

Reply: We sincerely thank the reviewer for this point. For molecular clock phylogenetics inferences in this study, we focus especially on the Omicron BA.1 and BA.2 sub-lineages, which quickly spread concurrently in several countries throughout the world, and were the first recognized as the Omicron VOC. These are the following two reasons of not including BA.4 and BA.5 sub-lineages for molecular clock phylogenetics inferences:

(a) BA.1 and BA.2 have quite distinct spike proteins, however, BA.4 and BA. 5 have identical spike proteins, most similar to BA.2.
(b) Bayesian analyses of BA.4 and BA.5 sequences have already identified the most common recent ancestor in the mid-November 2021 (Tegally et al., 2022, doi: 10.1038/s41591-022-01911-2), corresponding to BA.2's the most common recent ancestor (in our study).

Based on these inferences, we believe that BA.1 and BA.2 sub-lineages, that appeared initially could actually provide more concrete inferences on the basis of Bayesian analyses.

Comment 4: Line 163-164: Performing Bayesian analyses on a large dataset is computing-intensive. I would suggest that the authors should mention here the computing facility employed for Bayesian analyses. This would make it easier for readers to follow and understand.

Reply: We thank the reviewer this point. We have now incorporated the statement for using supercomputer facility, which can be read as 'All these analyses were performed on the Hokusai BigWaterfall supercomputer of the Institute of Physical and Chemical Research (RIKEN), Japan' in the revised manuscript.

Comment 5: Line 394-395: What can a reader deduce from 'Omicron signature mutational profiles'? Is it a spike protein signature mutational profile?

Reply: Here, 'Omicron signature mutational profiles' refer to Omicron’s spike protein signature mutational profile. We have corrected it in the revised manuscript.