**Response to the editor and reviewer**

We greatly appreciate the editor and the reviewer for the efforts and the valuable suggestions and hope that deficiencies pointed out in the original submission are overcome in the revised version. Our responses of the Referee’s Report are given below.

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**General comments**

*1. p2, l7-8 It is not clear here if better estimates of divergence times have been obtained in the referenced papers or if this is simply an expectation*

**Author’s Response:**

Thanks for your correction.

I’m very sorry for my mistakes. After carefully reviewing the original manuscript, the typos and spelling mistakes are corrected as follows:

*2. p6, l44-45 On a dataset with sampling-through-time, the leaf node does not have to be the younger child. Does the operator still work in that case or is it a requirement that tO > tY ?*

**Author’s Response:**

Thank you for your professional suggestion.

*3. There is a mismatch between Figures 12 and 13 which show results for S3 and Table 5 which contains the standard deviation of the clock, which according to Figure 11 is S1. Similarly p9, l26 it is unclear which of S1 or S3 was actually measured.*

*4. p9 l33-34 I suggest adding some details on why configuration 1 was chosen as a comparison.*

*5. p10, l16 I don't understand what "the sampled trees were filtered by the shared common ancestor of each taxa" means. Later l22 it appears that the authors discarded the trees which did not match the reference topology, but it's unclear if that is the same thing as the previously mentioned filtering or an entirely different step of the process.*

*6. p10, l37-42 Is it really unexpected that the results obtained using the new operators would be consistent with the correlations enforced by these new operators ? Overall it's unclear what the conclusions from this section are.*

*7. p11, l8-23 It is very unclear what was actually done in this section. For instance, were the assigned divergence times and rates fixed in the analysis ? If so, how were they calculated, and if not, what are the values shown in figure 17 ? How were the summary trees obtained ?*

*8. Figures 12 and 13 are identical.*

*9. Figure 16b I suggest adding a legend showing the range of plotted values.*

*10. I would put a time axis on figure 17, as the credible intervals shown are not very meaningful without it.*

**Minor comments**

**Author’s Response:**

Thanks for your correction.

In the revised manuscript, we have corrected the mistakes that the reviewer has found as errors. The details are following:

*1. p1, l30 It is noticed that -> Note that*

*2. p2, l39 Prelimiaries -> Preliminaries*

*3. p4, l37 max(tj, tk) -> max(tL, tR)*

*4. p4, l53 the total genetic distance dL and dR -> the total genetic distance dL + dR*

*6. p6, l54 what happens if tO' < min(tG1, tG2) ?*

*7. p9, l26 MCMC simulation -> MCMC inference*

*8. p10, l48 becomes -> become*

*9. Figure 1 remove the box which only contains =*

*10. Figure 1 H3,R and H4,R should be H3,L and H4,L*

*11. Figure 11 substituion tree -> substitution tree*

*12. Figure 16 compare -> comparison*

**We greatly appreciate the reviewer for the valuable suggestions. We try our best to overcome the deficiencies pointed out in the original submission. If there are any problems in the revised version, please do not hesitate to point out. We will revise the submission according to reviewer’s suggestions.**