I'm satisfied with all modifications to the new version of the manuscript. However, I can not understand the persistence of the authors to keep their phylogenetic analyses based on the non-accurate Neighbor-Joining (NJ) method.

I fully understand the difficulty to obtain the Bayesian inference, especially with highly divergent amino acid sequence alignments. Still, the same doesn't apply to the Maximum-Likelihood method. Nowadays, it's easy to compute a robust Maximum-Likelihood (ML) phylogenetic tree using a high number of sequences using user-friendly software i.e. IQ-TREE2. IQ-TREE2 not only a fast and easy to use software but also can automatically choose the best-fitting substitution model. Finally, a better Visualization of the phylogenetic trees is highly appreciated (Figures 3 and 4).

Overall, I appropriate the time and effort of the authors to complete this revised version. Then, I recommend the preprint after the authors provide the Maximum-Likelihood (ML) phylogenetic trees.
We have performed phylogenetic inference using the ML software IQ-TREE2, as recommended by the user. We have documented and referenced this in the Materials and Methods section and outlined the results in the Results section.