Results of Shimodaira Approximately Unbiased (AU) tests for differences among topologies, based on 10000 bootstrap replicates. For each data set, two alternative topologies were tested. Within columns are the -lnL scores corresponding to each topology using that specific data set. The AU tests were done under the GTR+I+gamma model for the nucleotide data set, and the LG+I+gamma model for the amino acid data set, with parameter values estimated from the data prior to the AU tests. Boldface font indicates the best tree. Topologies marked by “\*” are significantly different.

|  |  |  |
| --- | --- | --- |
|  | Data set | |
| topology | Concatenated plastid nucleotide (Fig. 2a) | Concatenated plastid amino acid (Fig. 2b) |
| Concatenated plastid nucleotide (Fig. 2a) | **878882.40197** | 238206.02947\* |
| Concatenated plastid amino acid (Fig. 2b) | 879859.37477\* | **238064.11712** |

\* p<0.05

In summary, each data set supports ‘its own’ topology over the alternative, and the difference is statistically significant in both cases.