We used TREESPACE (Jombart et al., 2017) to visualize the variability of posterior trees among genes in 2-to 3-dimensional Euclidean space. In this approach, the pairwise distances between posterior trees were computed (as Robinson Foulds unweighted metric, Robinson and Foulds 1981) from the package phangorn, and decomposed into a low-dimensional Euclidean space using metric multidimensional scaling (MDS). Before applying MDS, TREESPACE transformed the unweighted Robinson Foulds tree distances into Euclidean distances using Cailliez’s transformation (Cailliez, 1983). The analysis was performed on posterior trees from 37 genes comprising entire set of Chlorophycean taxa (68 spp.) sampled in the study. TREESPACE was performed on the collections 3800 posterior trees (representing 100 randomly sampled trees/gene) obtained from MrBayes MCMC analysis.

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