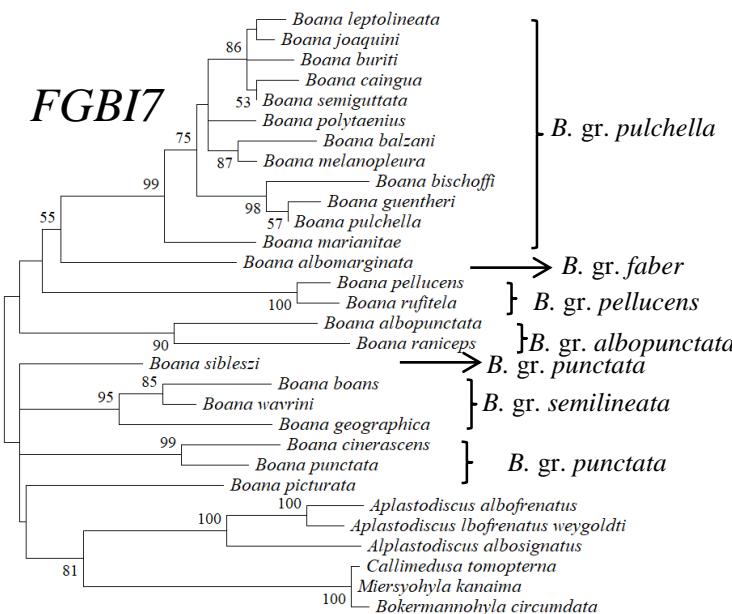
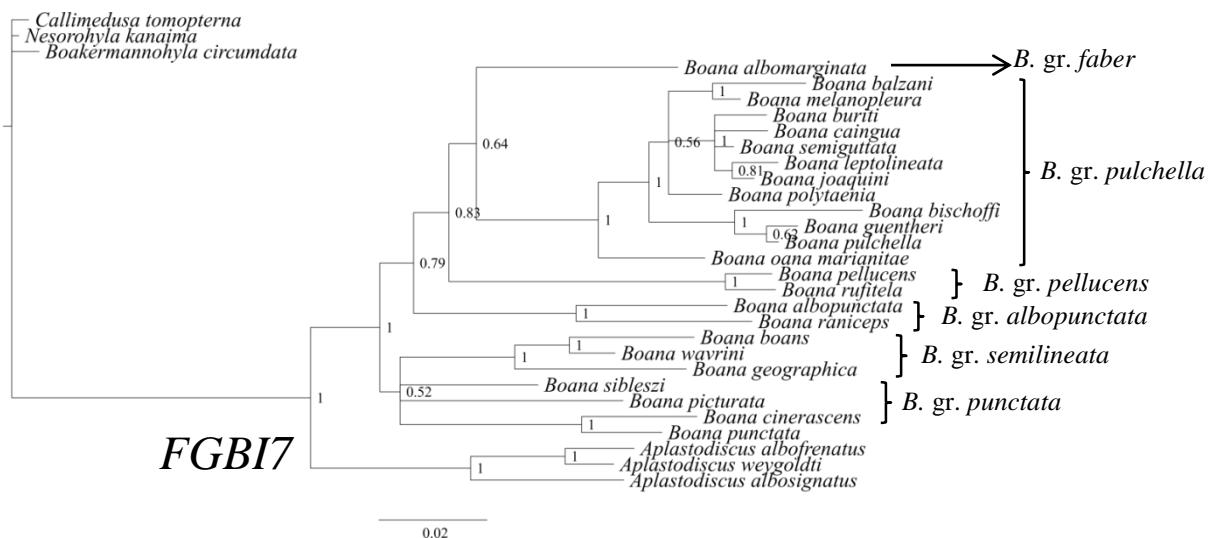
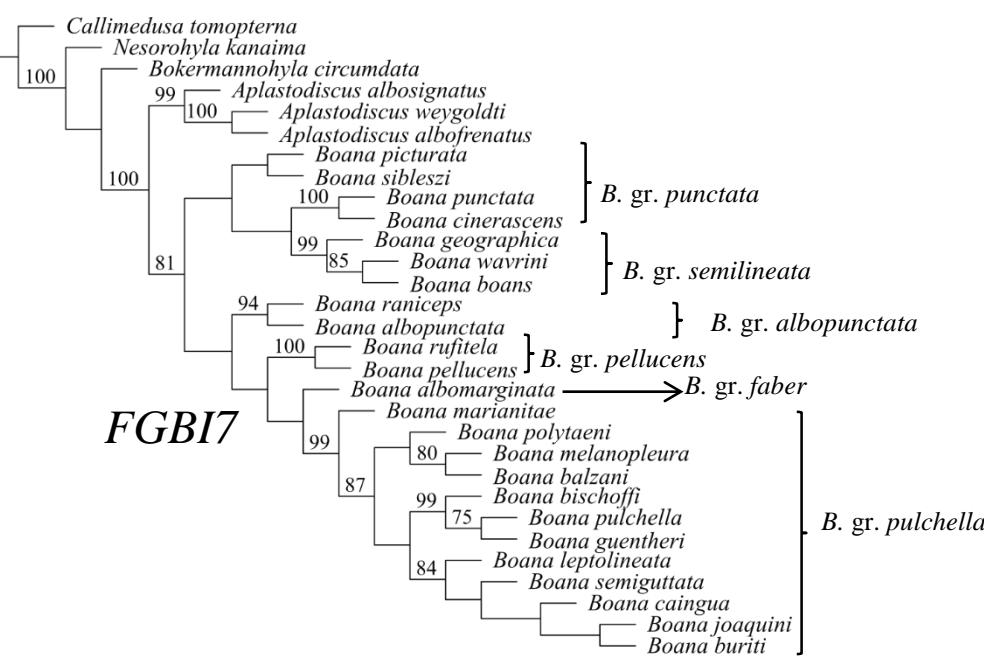
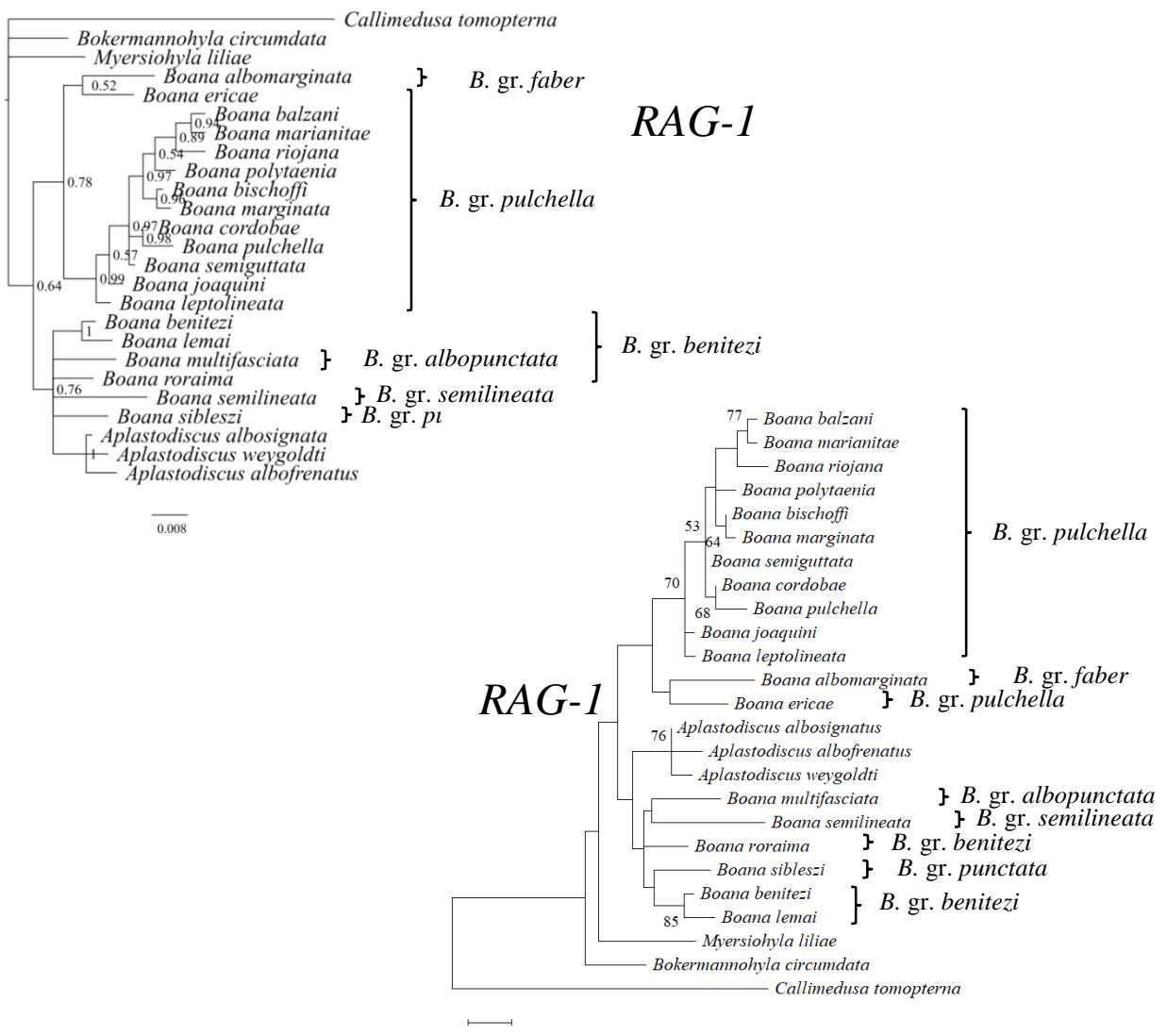
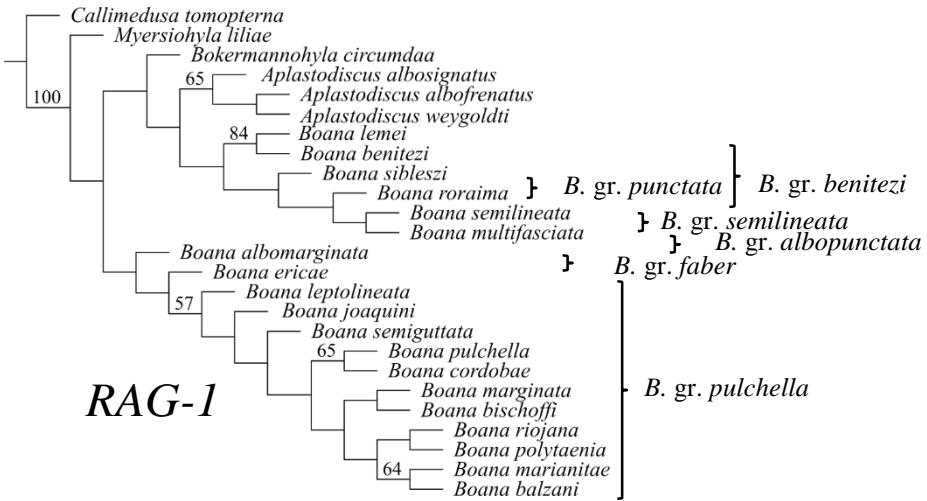


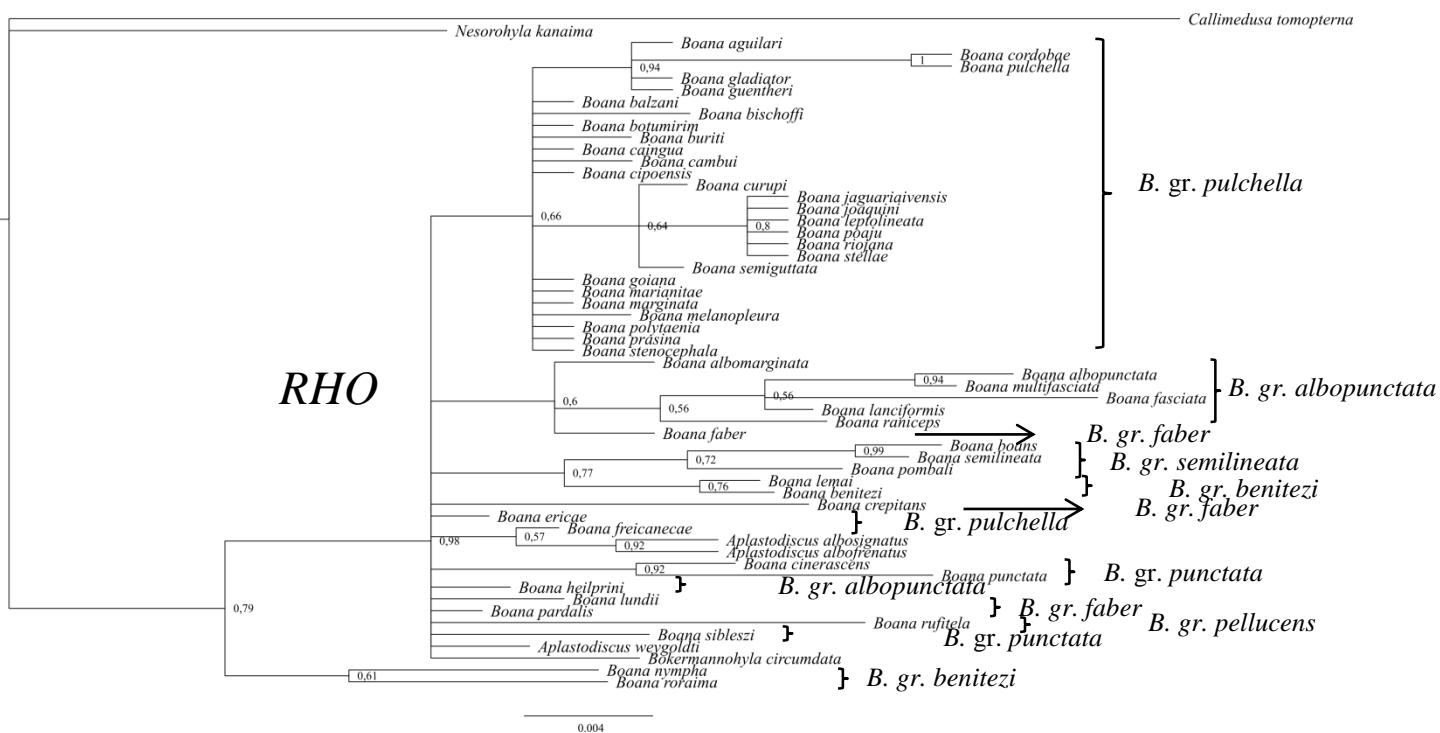
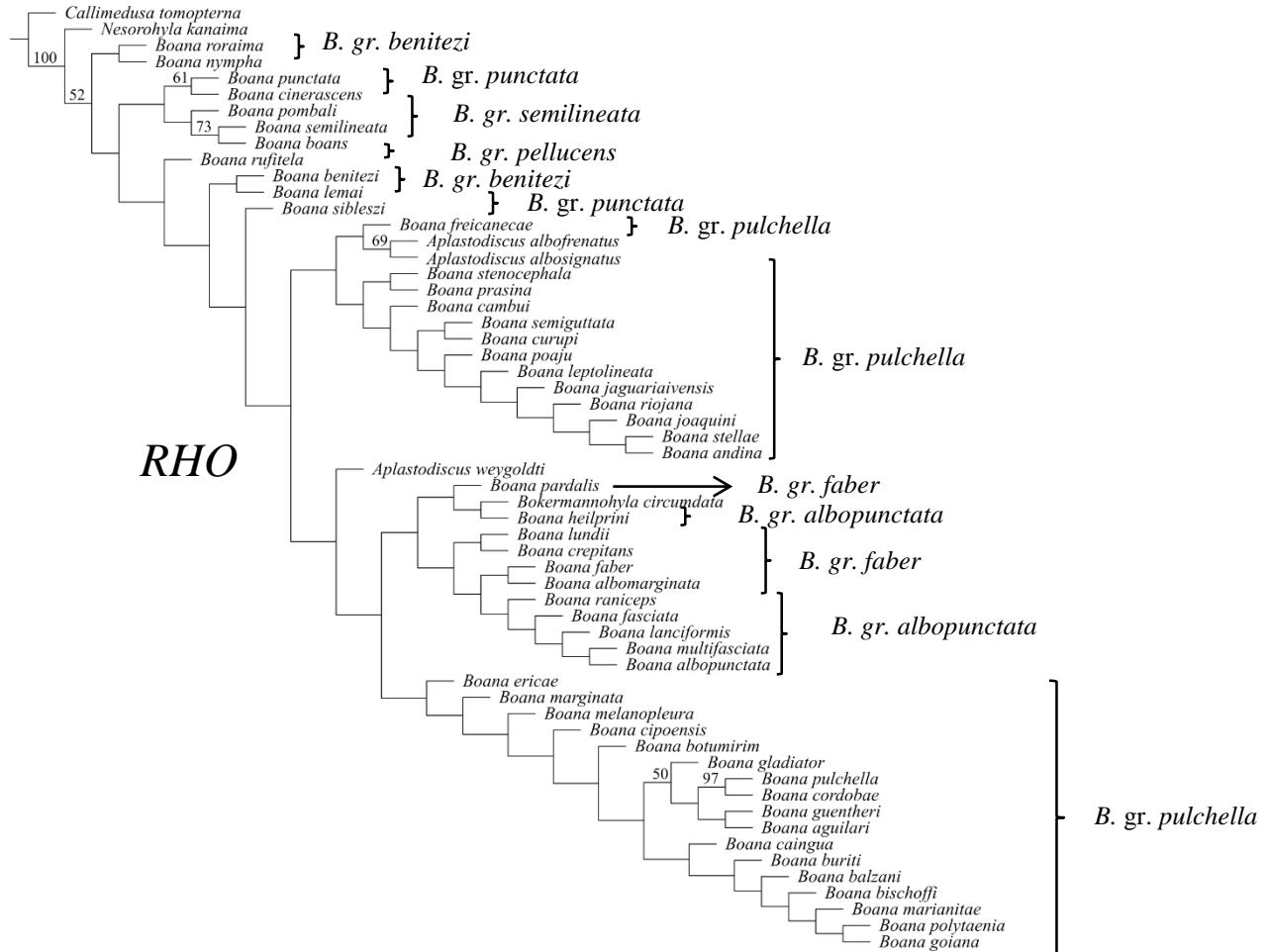
a.



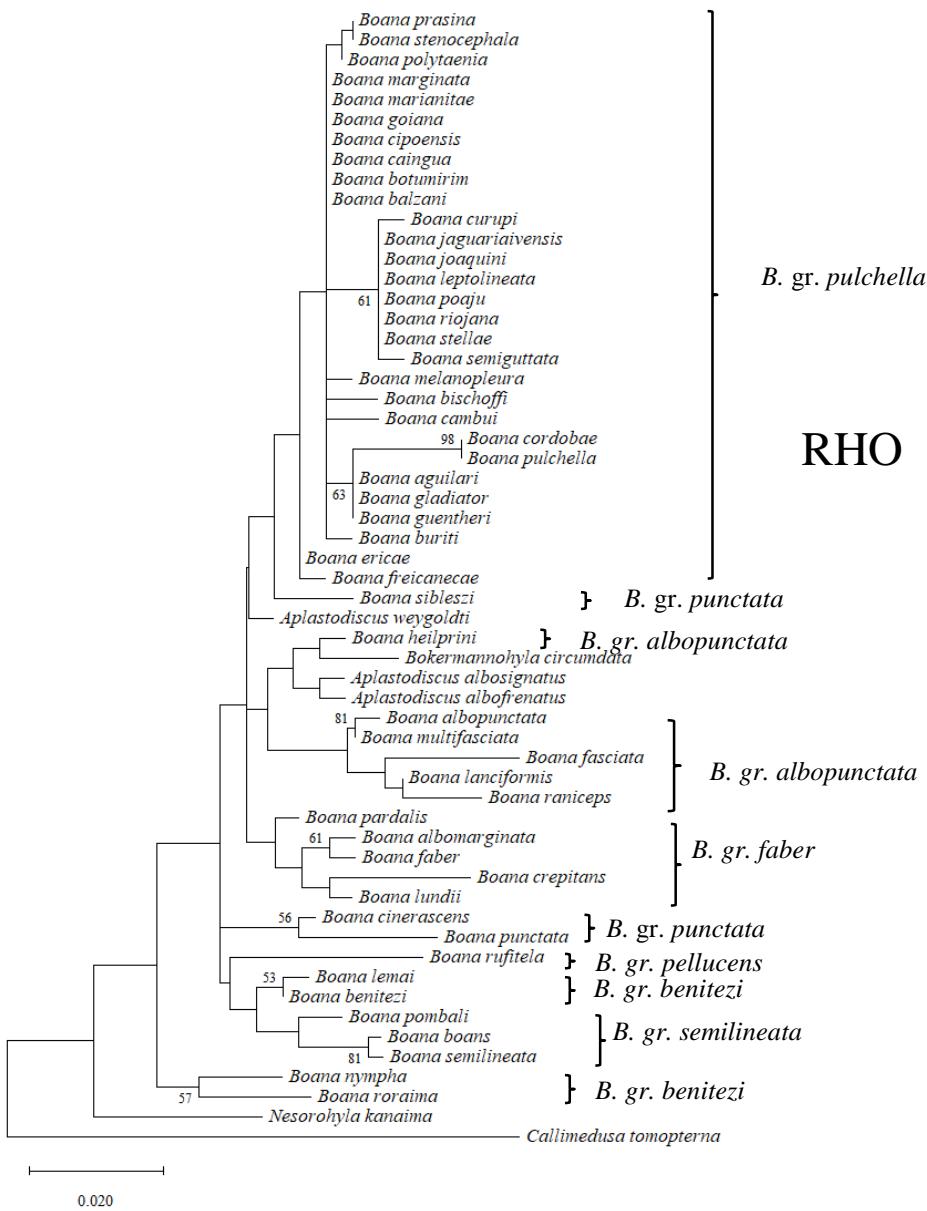
b.



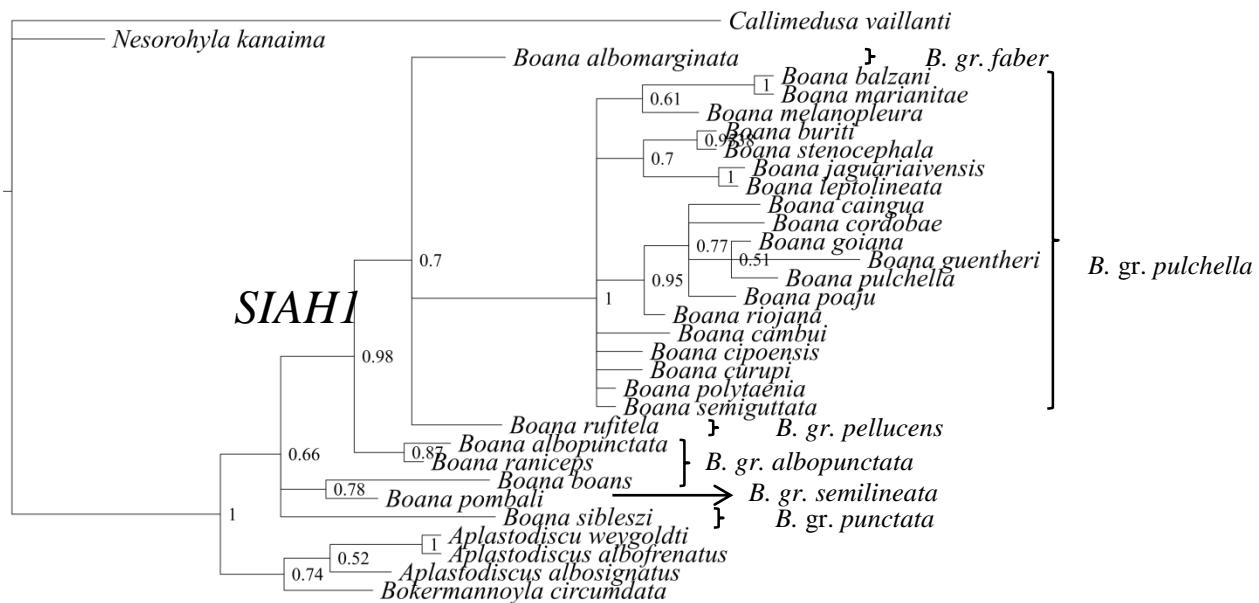
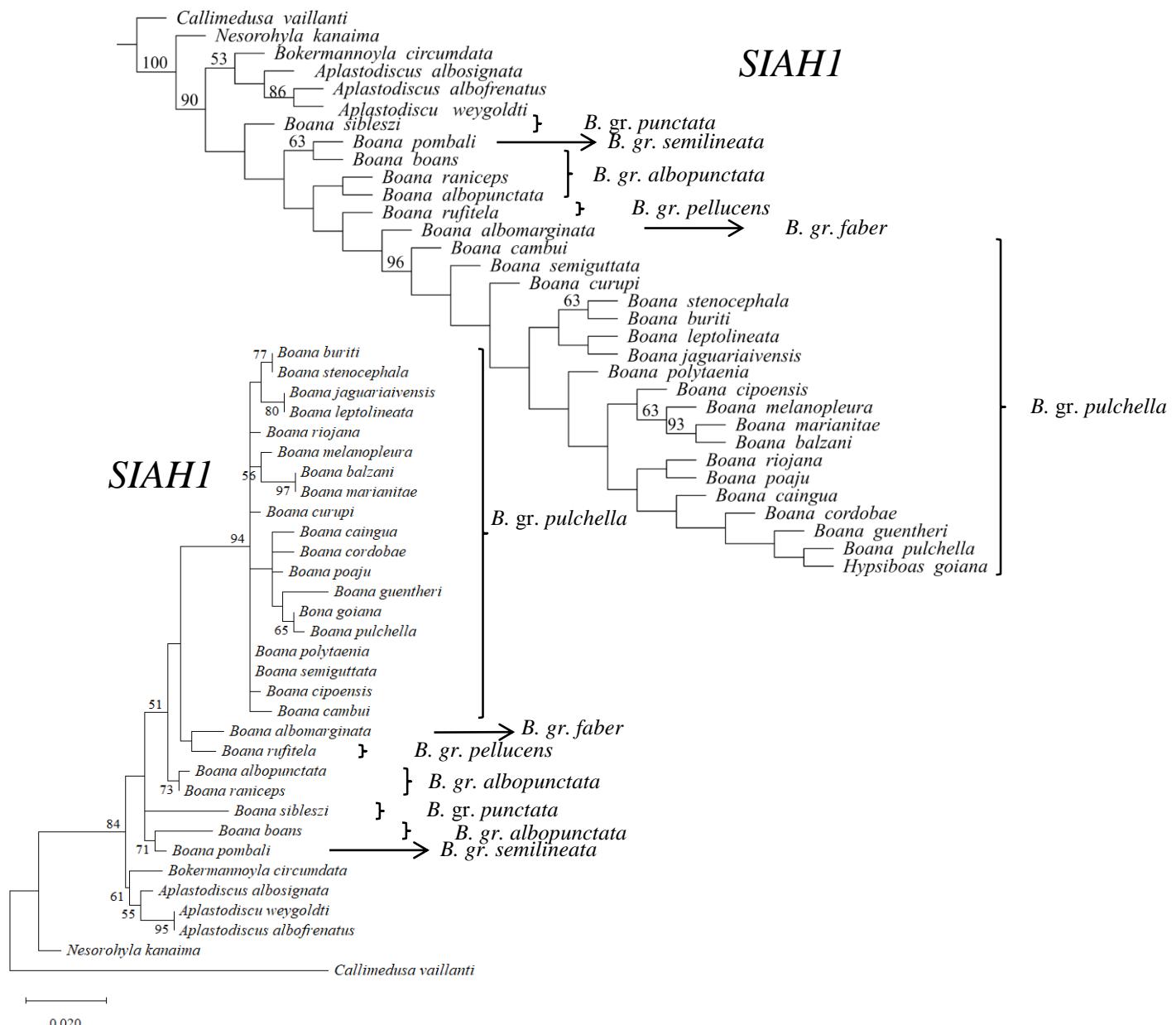
C₆



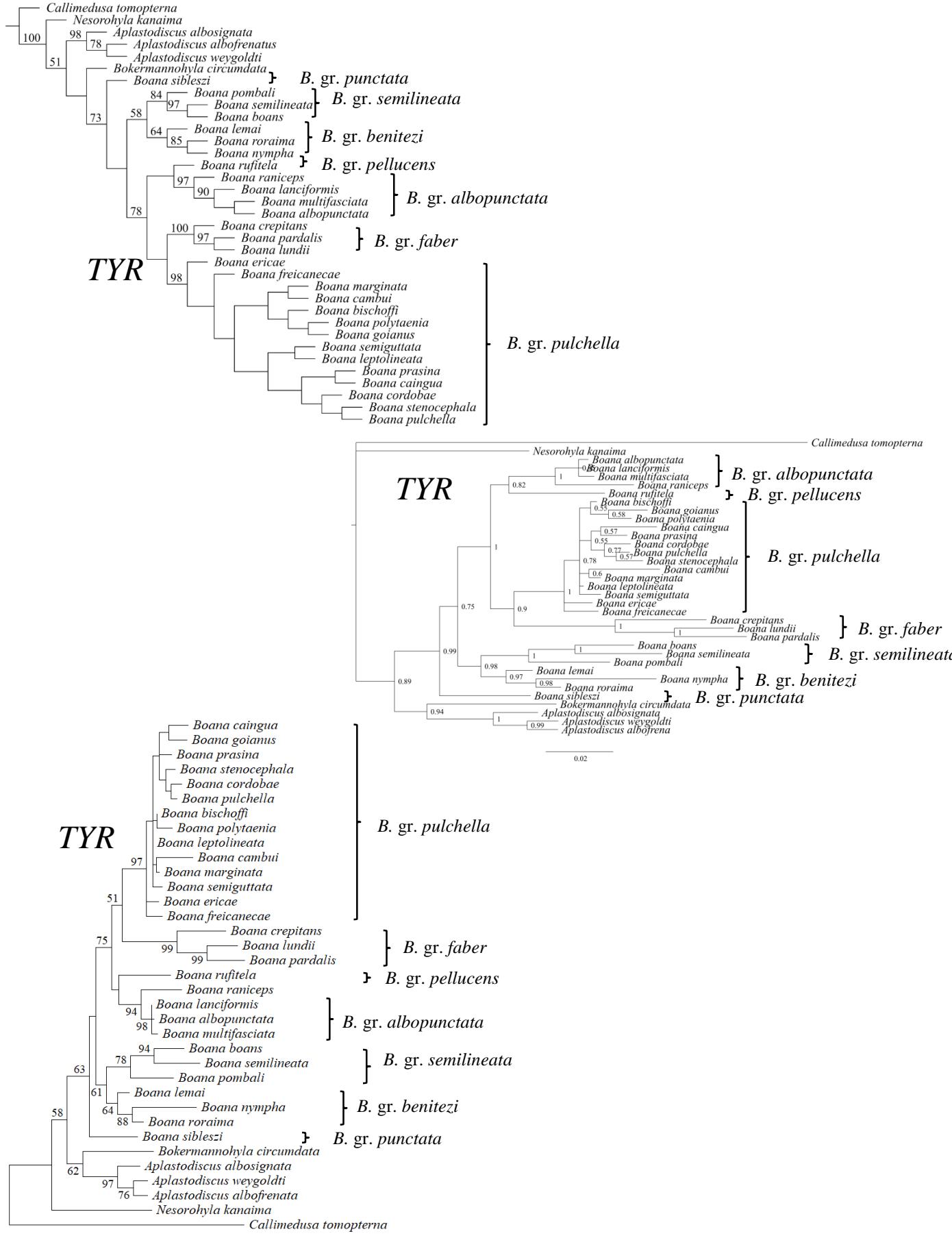
d.



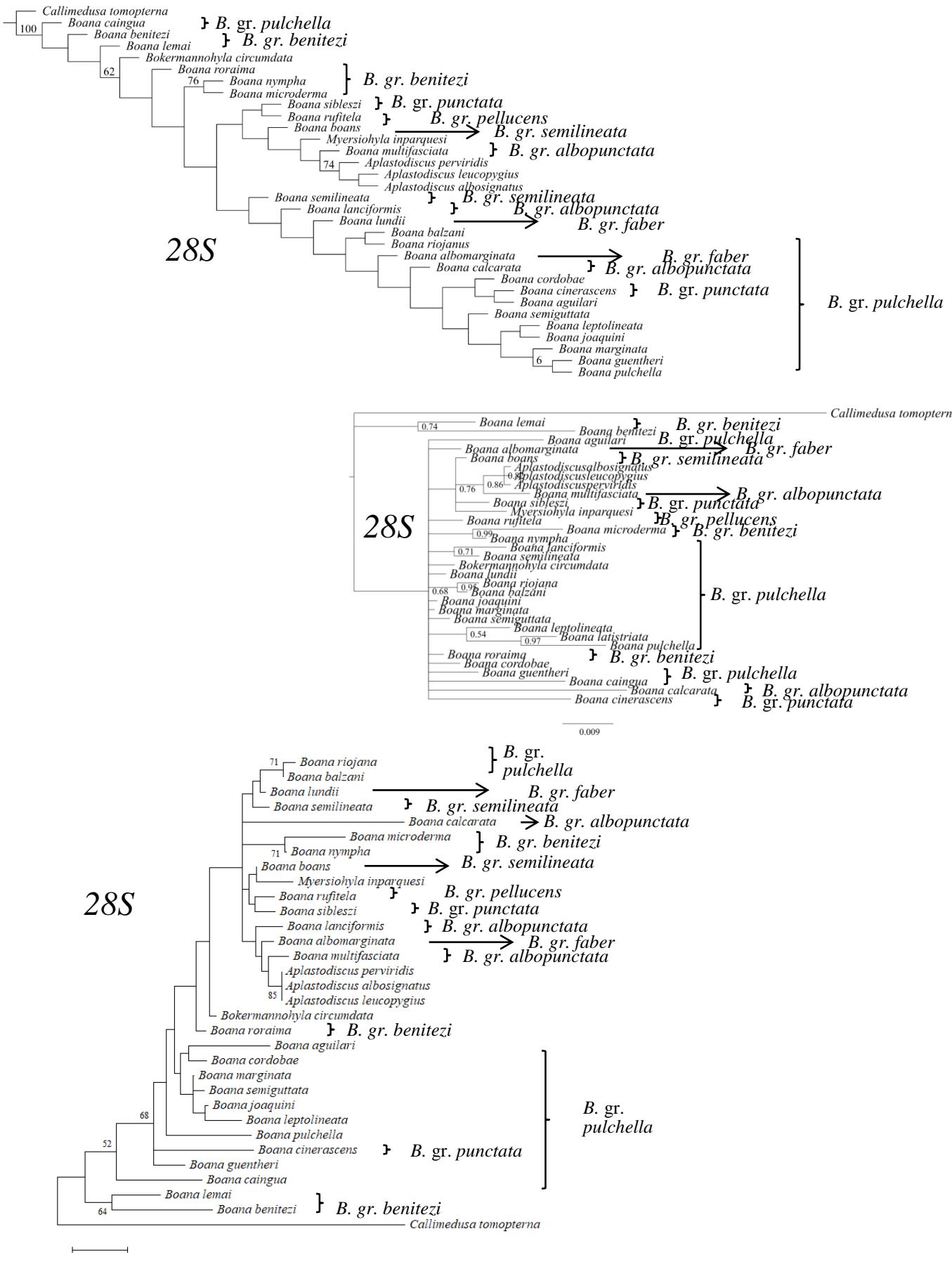
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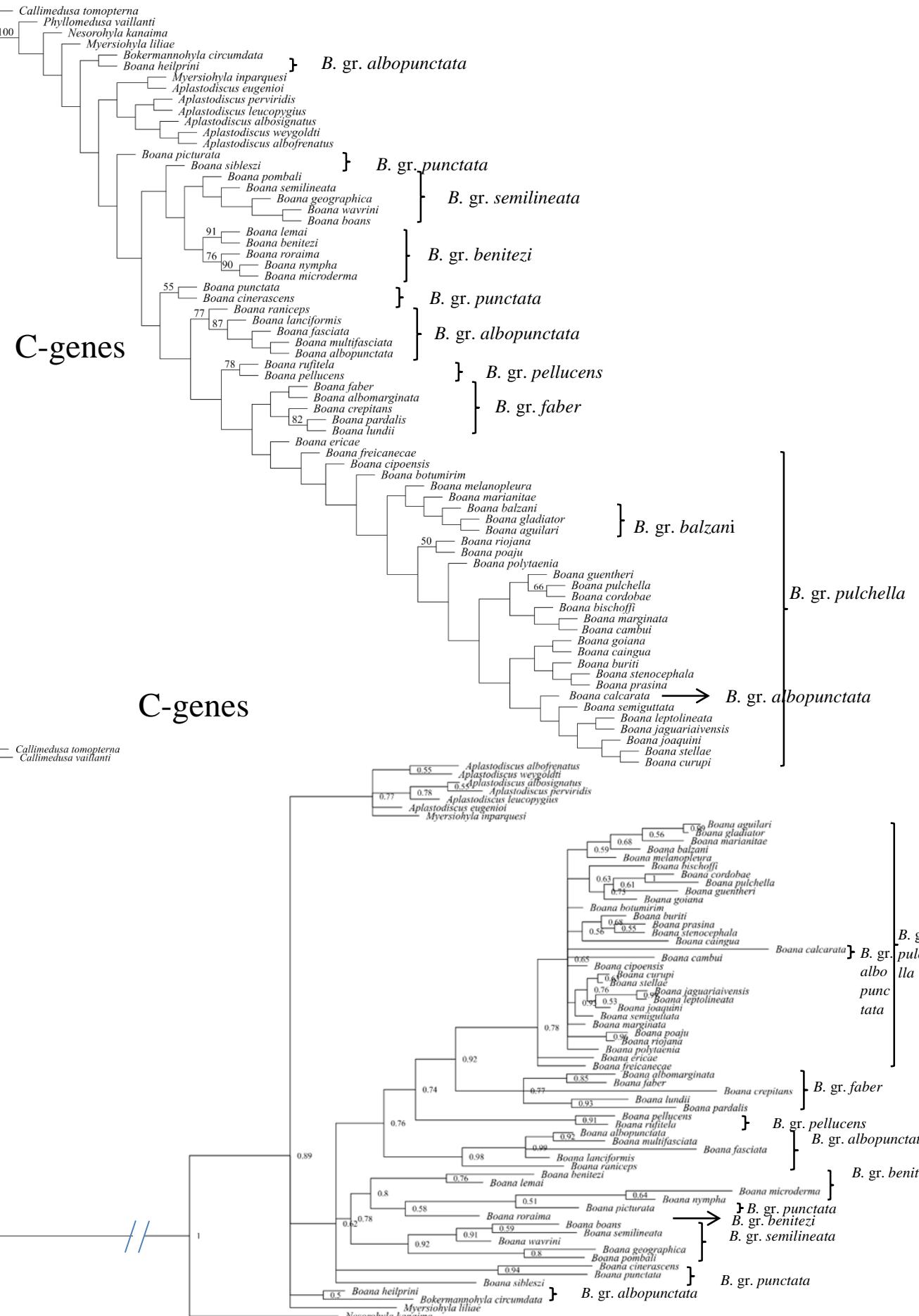
e.



C.

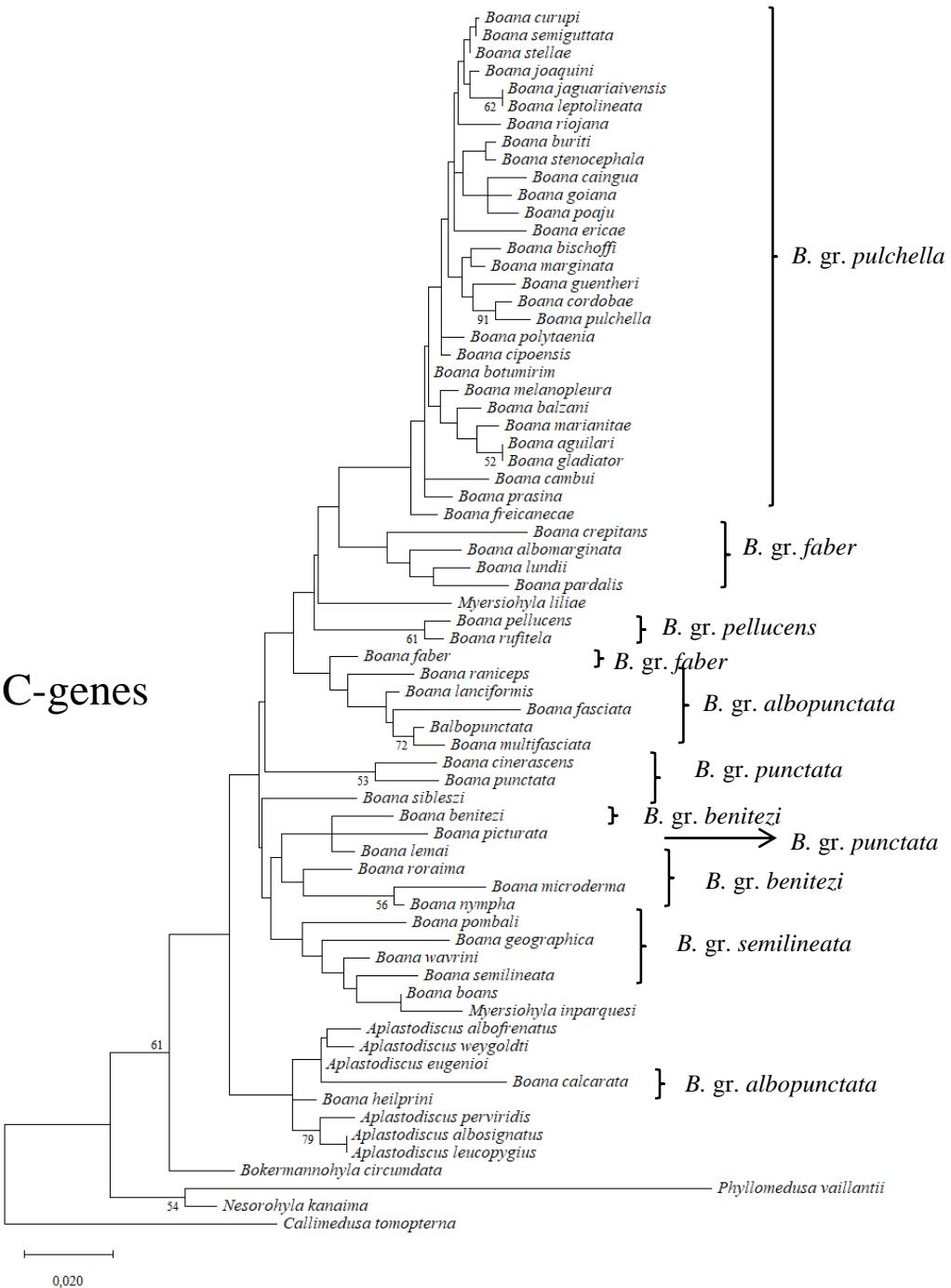


g.

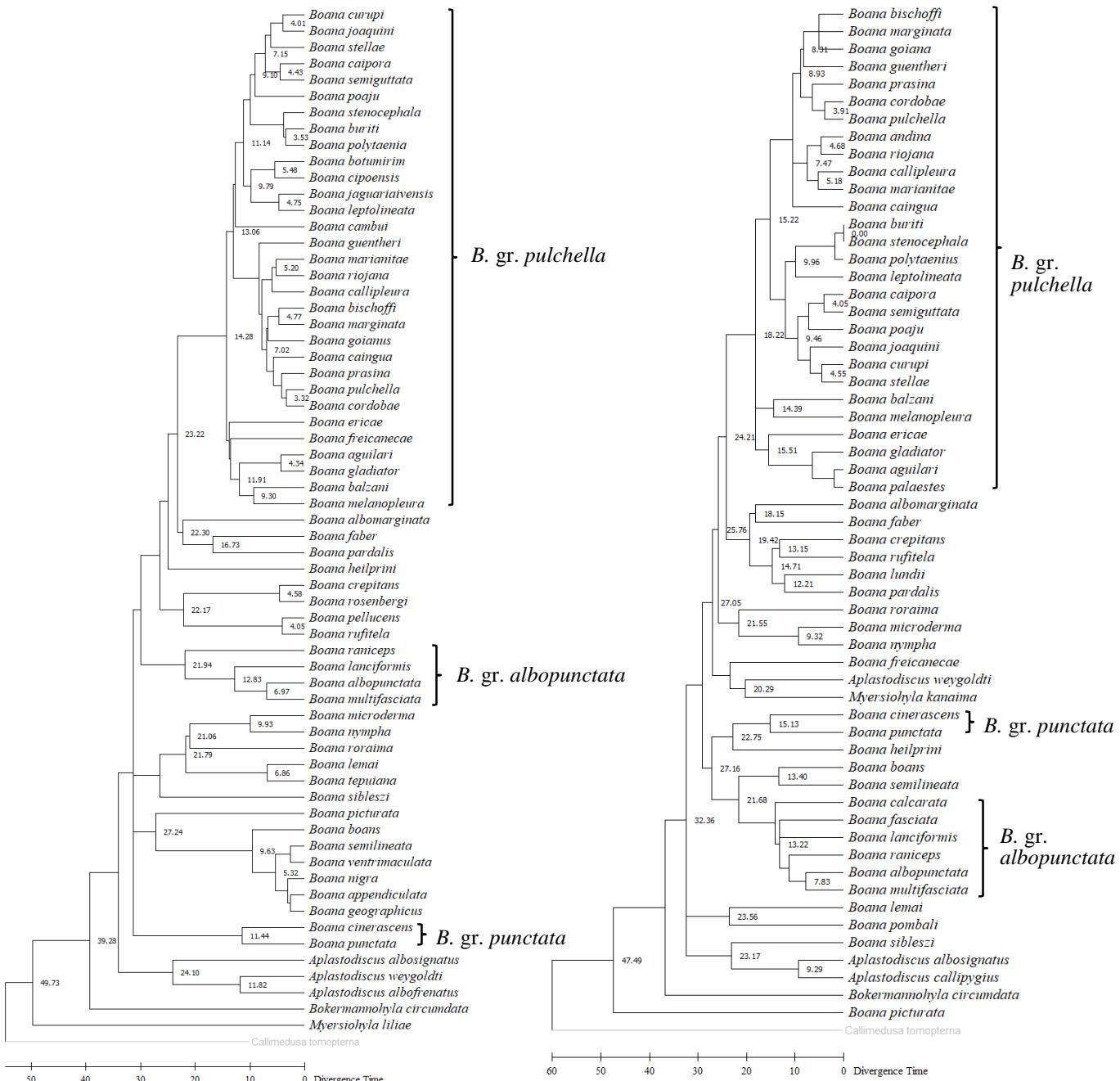


h.

C-genes

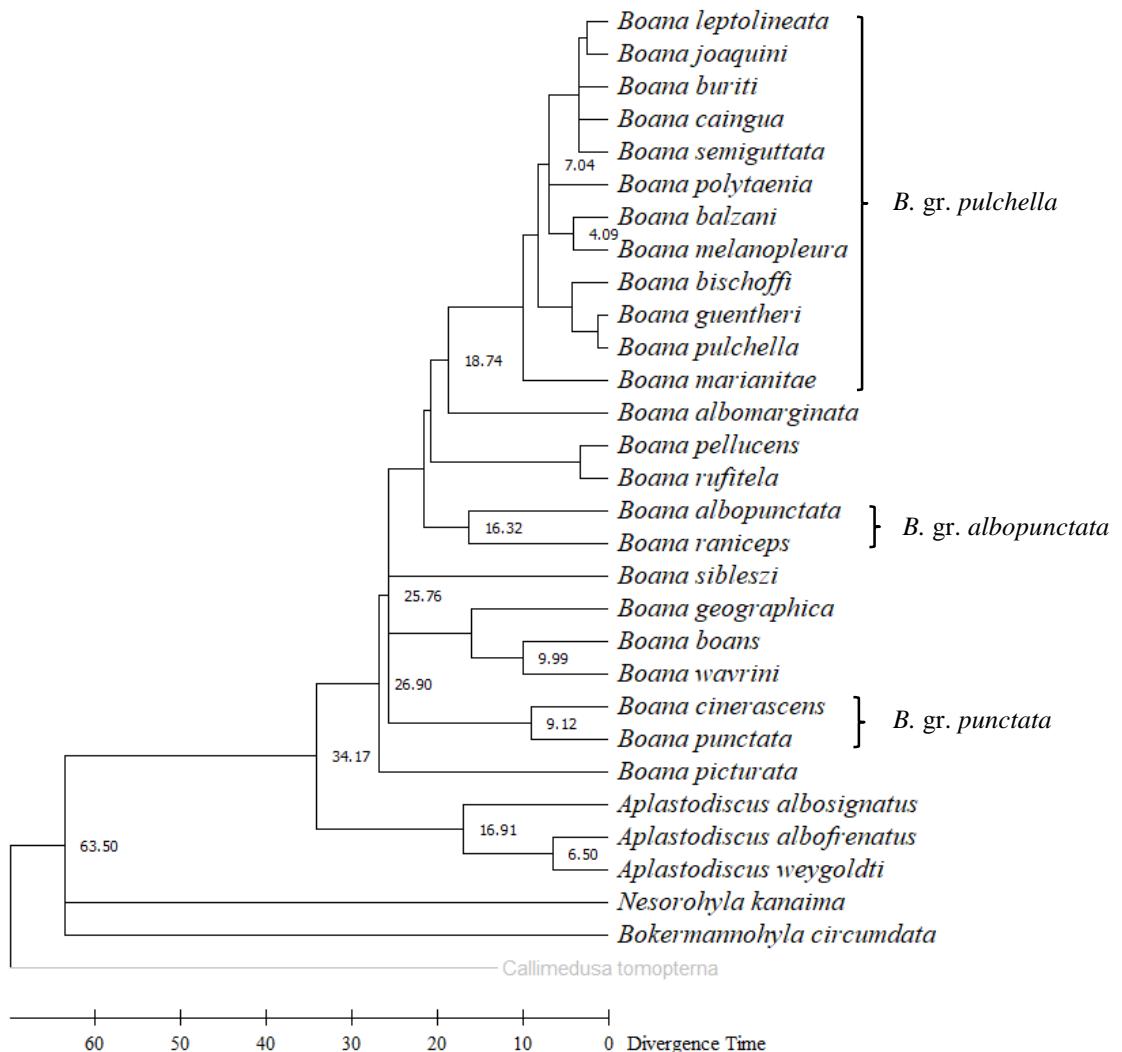


Supplementary Figure S1. Appendix 2. Phylogenetic trees corresponding to the studied markers (a. CXCR4, b. FGBI7, c. RAG-1, d. RHO, e. TYR f. SIAH1, g. 28S and C-genes), and the methods used—MP, MB, and ML, corresponding to the 1st, 2nd, and 3rd trees for each marker, respectively). For Jackknife support values from the MP method, and bootstrap support values for the ML method, values below 50% were not presented.



a.

b.



C.

Figure S2. Molecular dating of gene trees. a. *ND1*. b. *CYT B*, and c. *FGBI7* using the RelTime method in MEGA X.