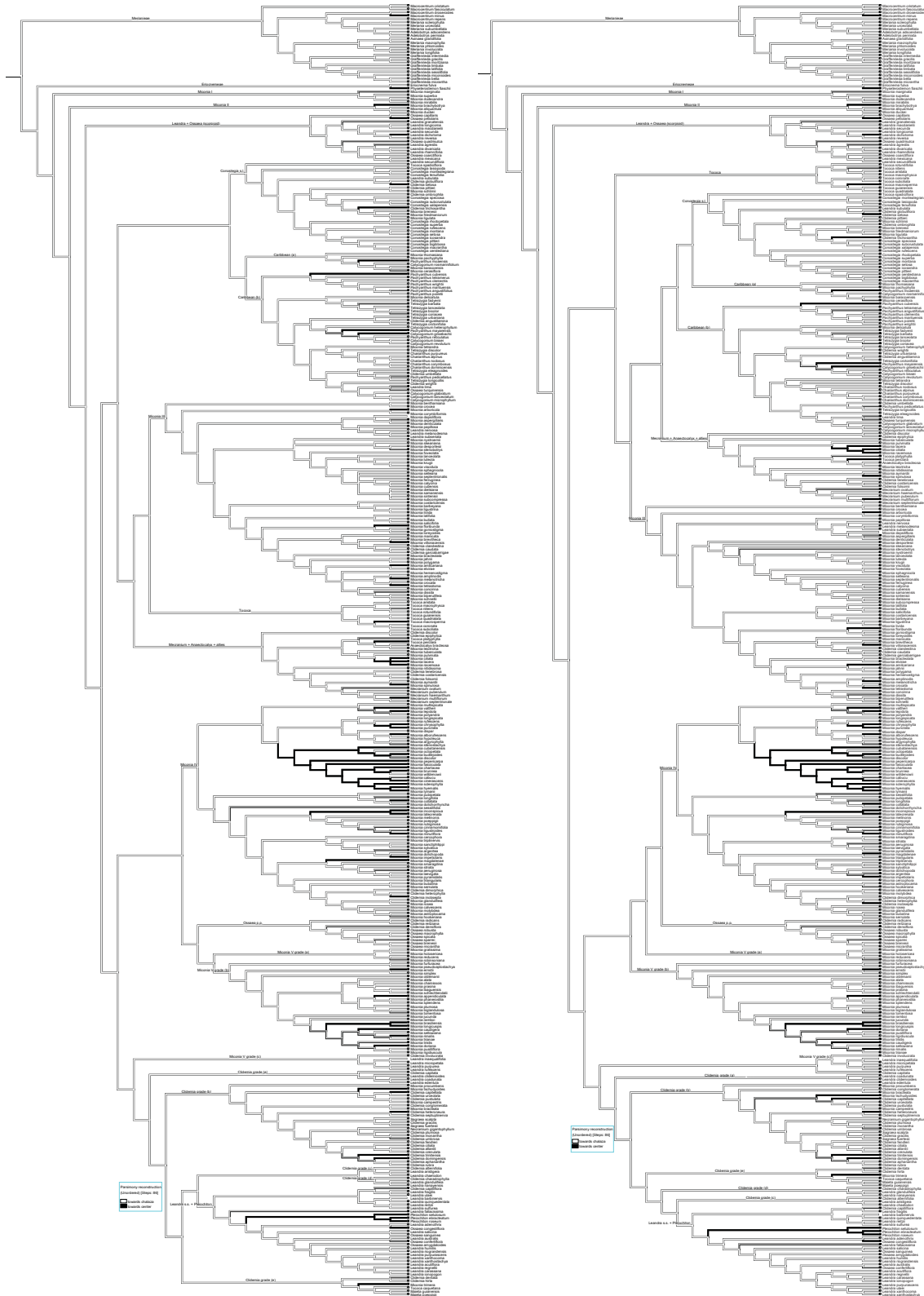


Figure S2. Ancestral character reconstruction of the 17 seed morphological characters used in this study. One of the most parsimonious trees (left) and the tree with the highest likelihood from the Bayesian run (right) derived from the analysis of a combined data matrix of ITS, ETS, *accD-psaI* and *psbK-psbI* DNA sequences are shown. Ancestral character reconstruction was performed using the parsimony criterion and considering the character states as unordered. Clade names were adopted, with some modifications, from Goldenberg et al. [25].

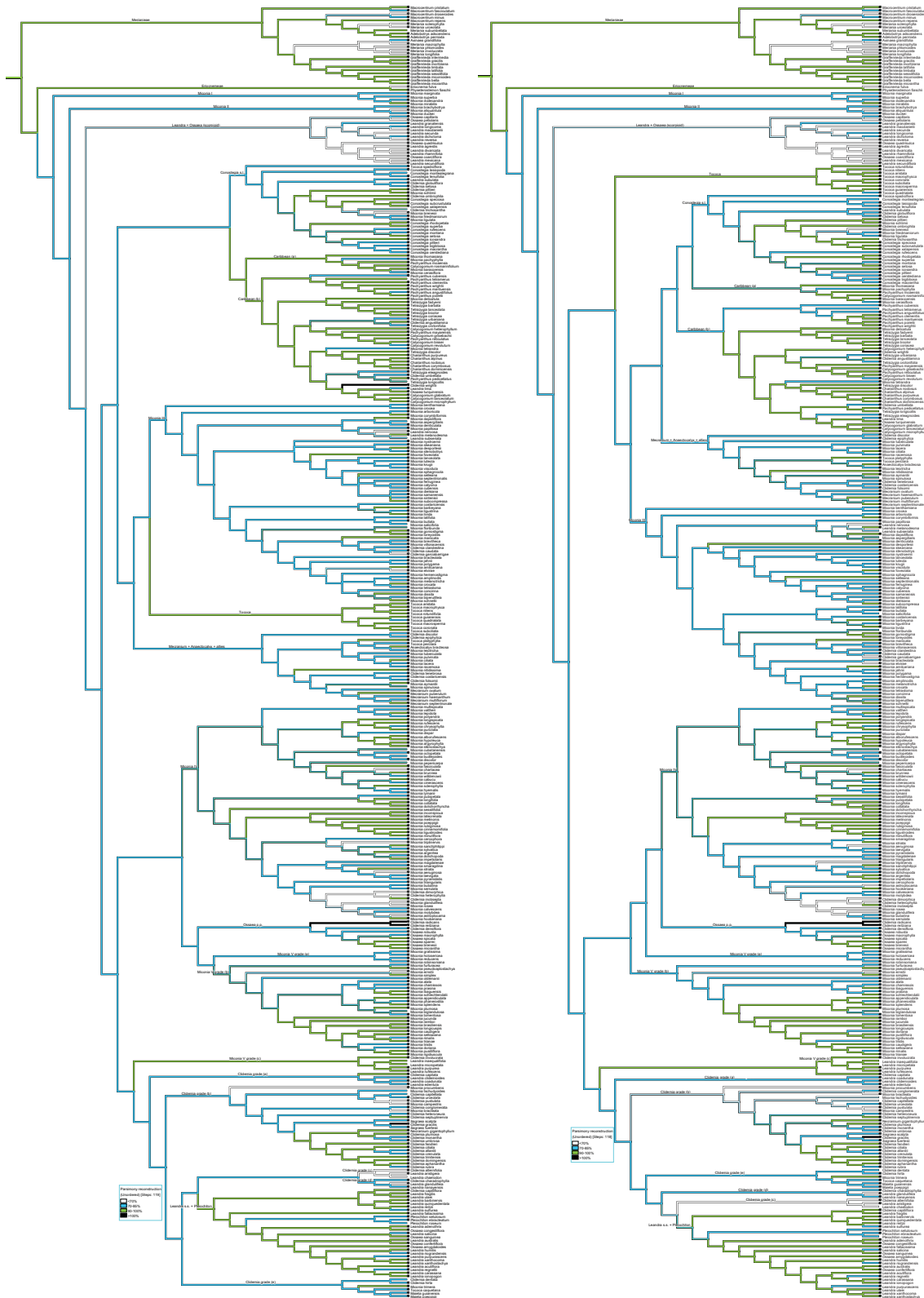




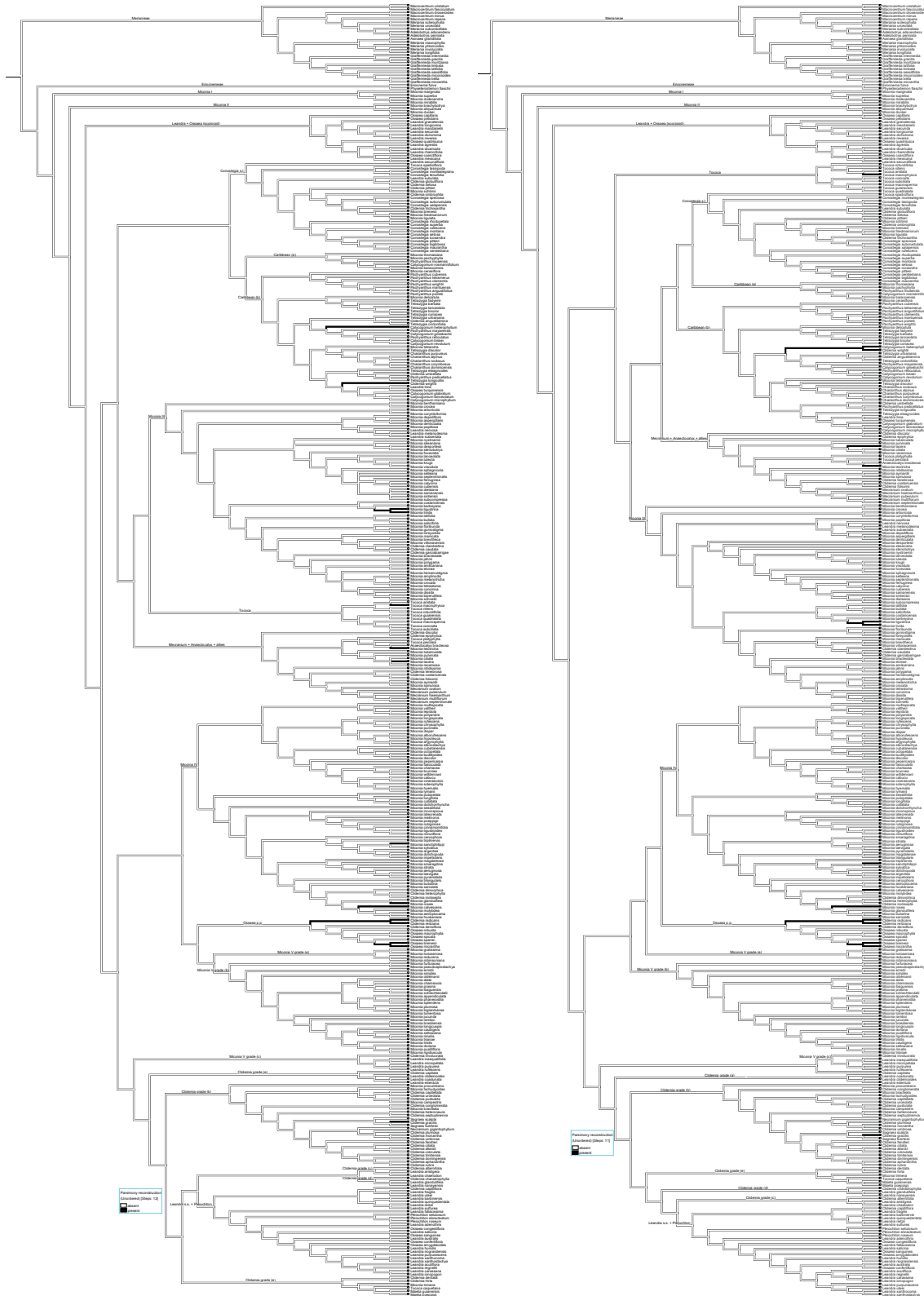


Character C. Location of the highest point perpendicular to the raphal zone.

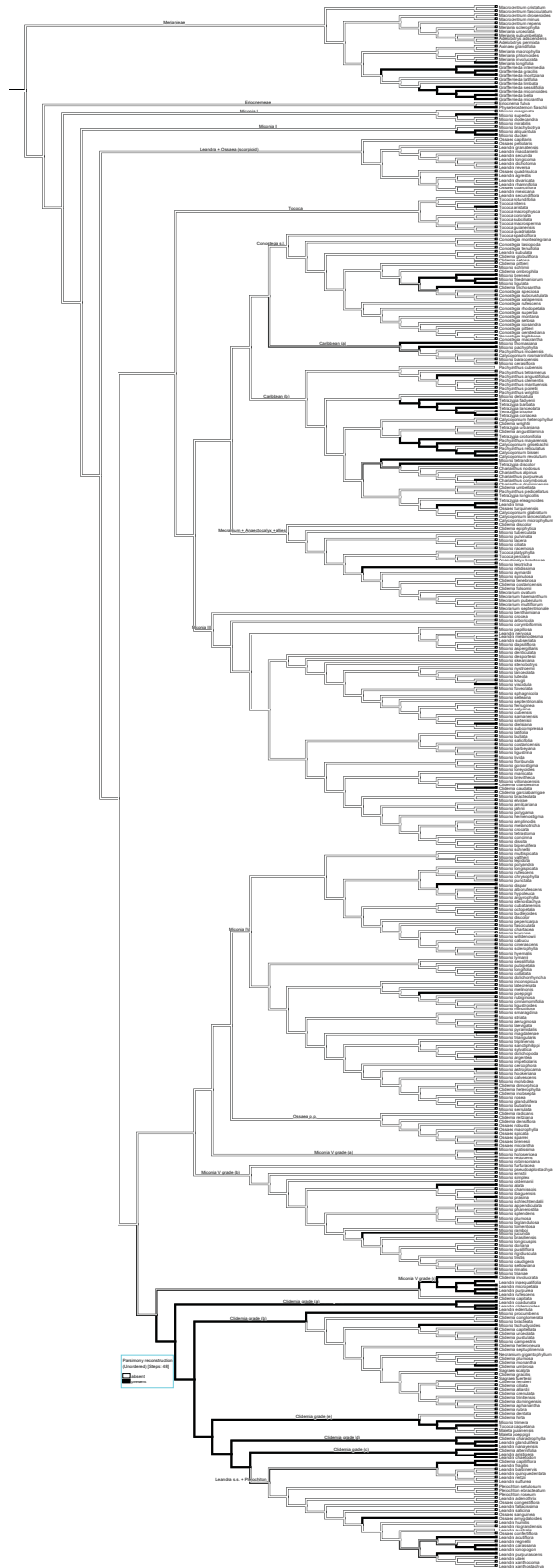
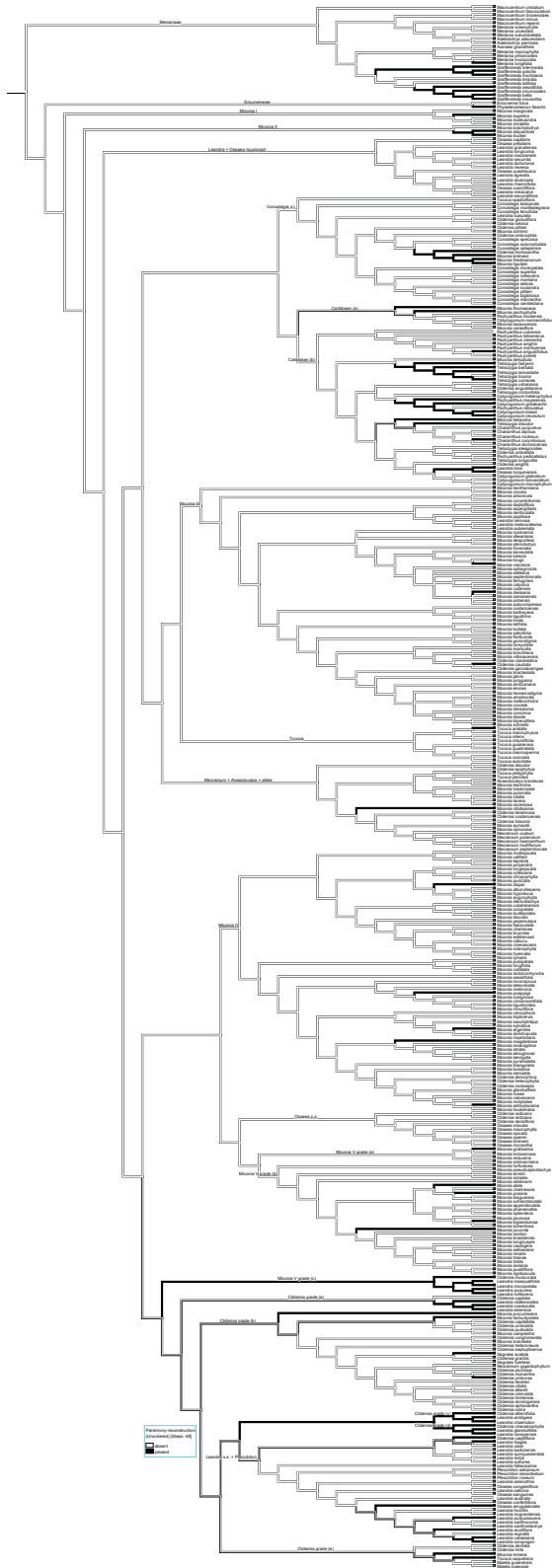




Character E. Length of the raphal zone proportional to the total length of the seed.



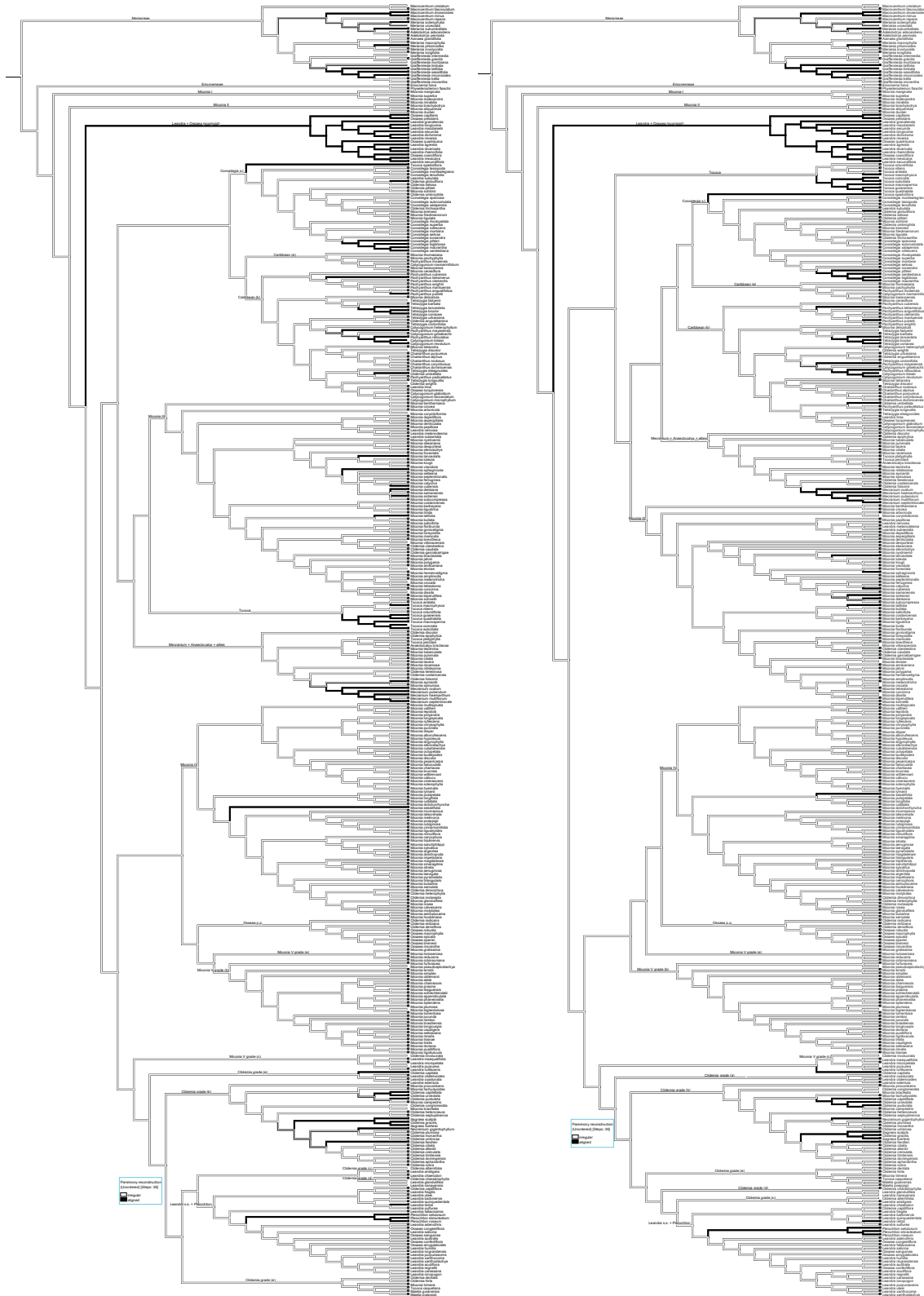
Character F. Ventrally-oriented expansion of the raphal zone.



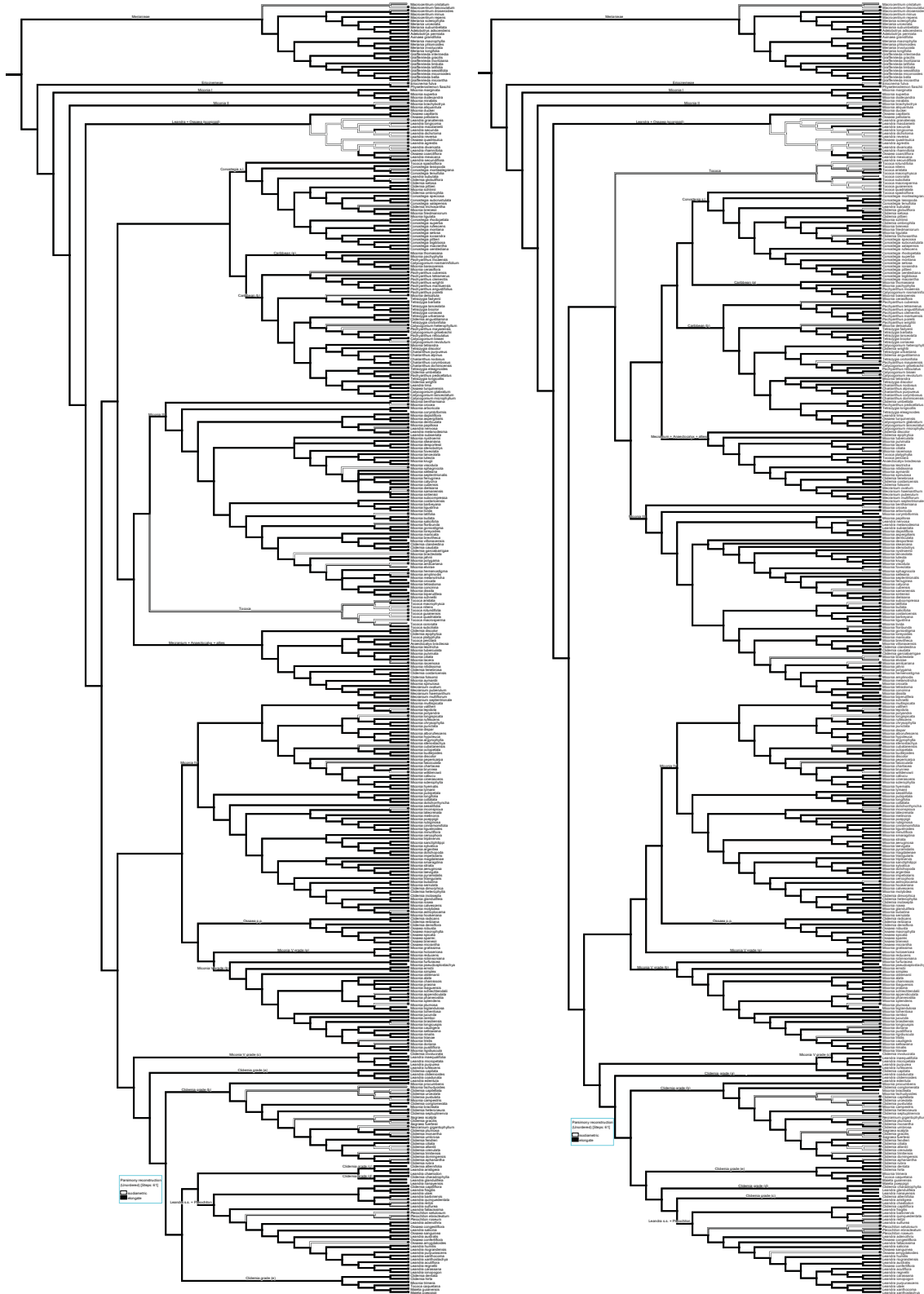
Character G. Appendix G.



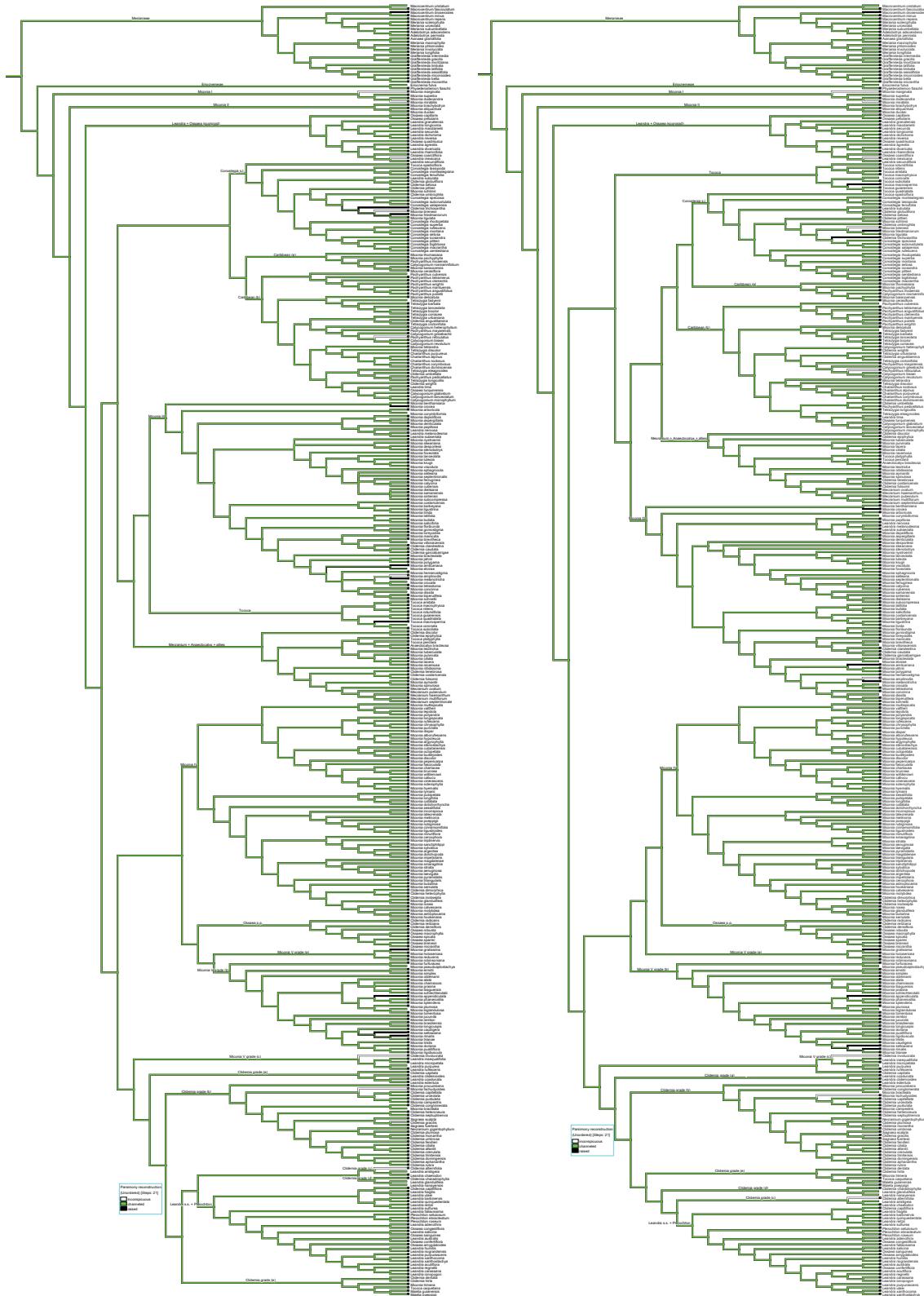




Character I. General arrangement of the cells with respect to each other.

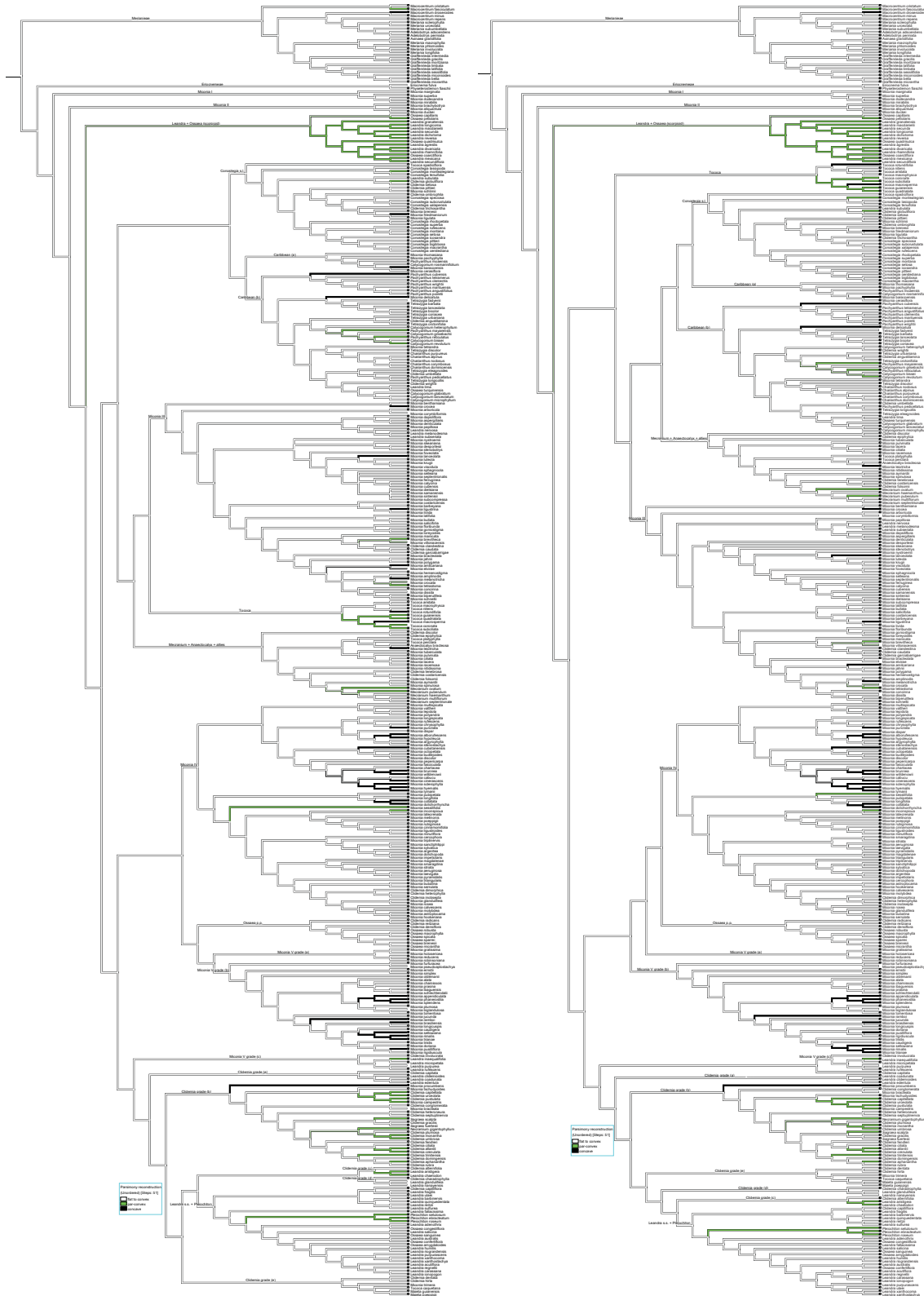


Character J. Cell shape.

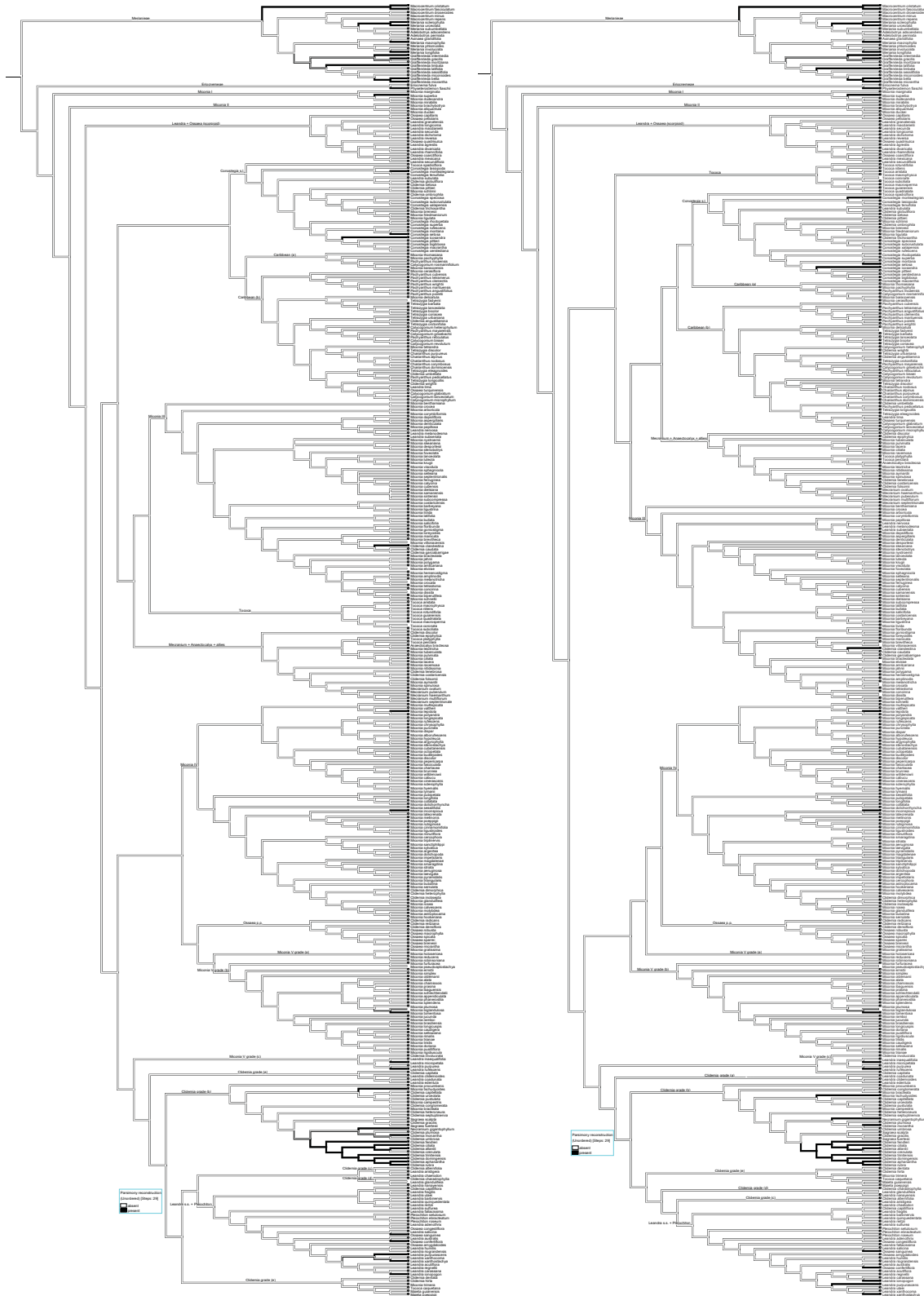


Character K. Relief of the anticlinal walls.

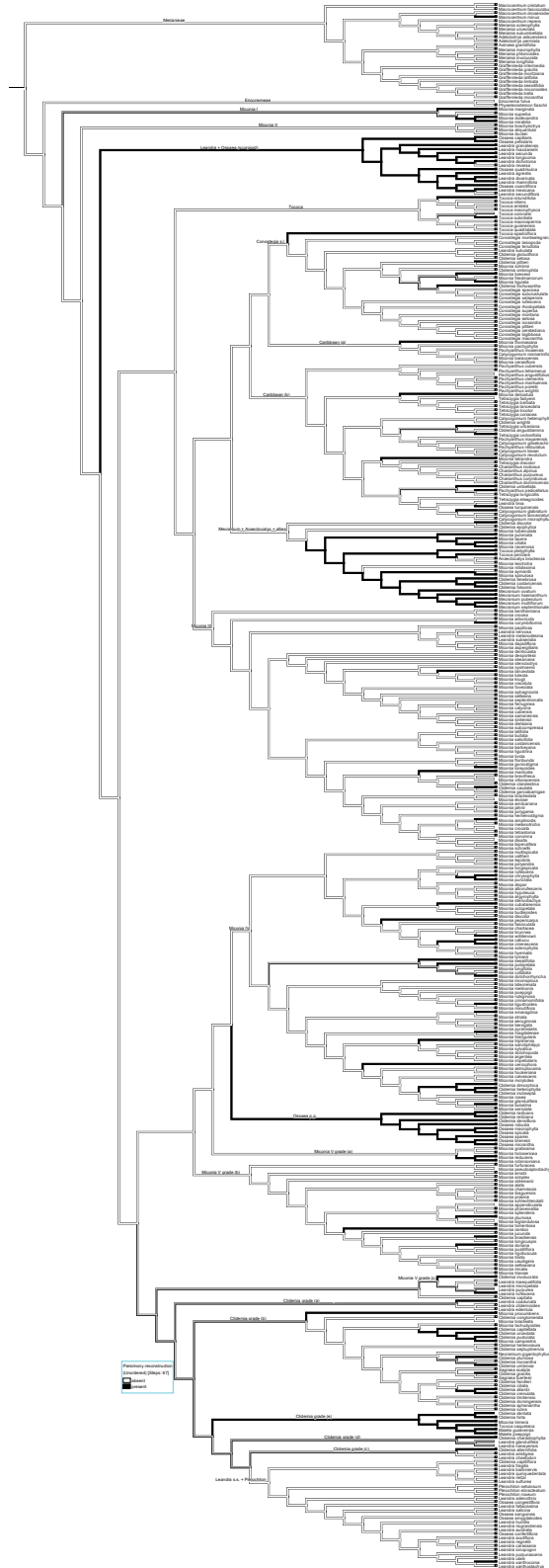
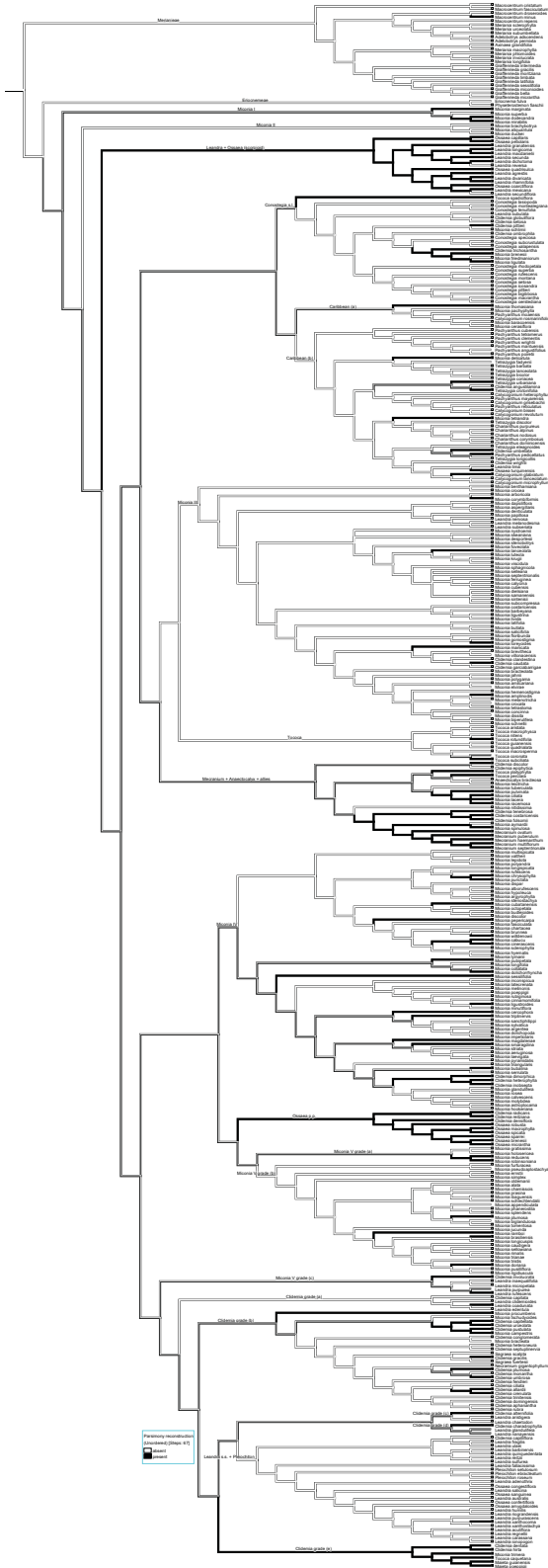




Character M. Relief of the periclinal walls.

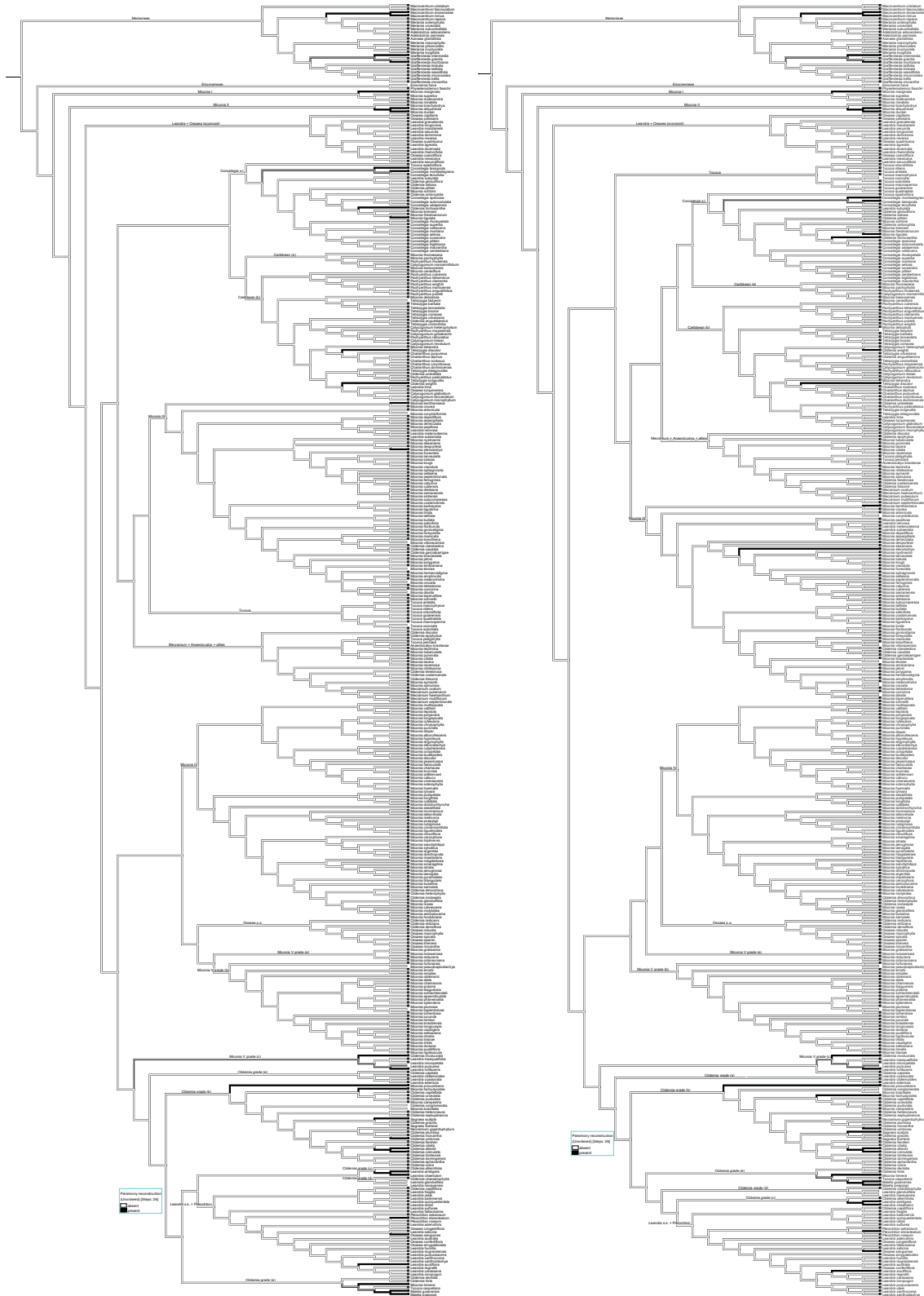


Character N. Periclinal walls dividing into two or more segments.

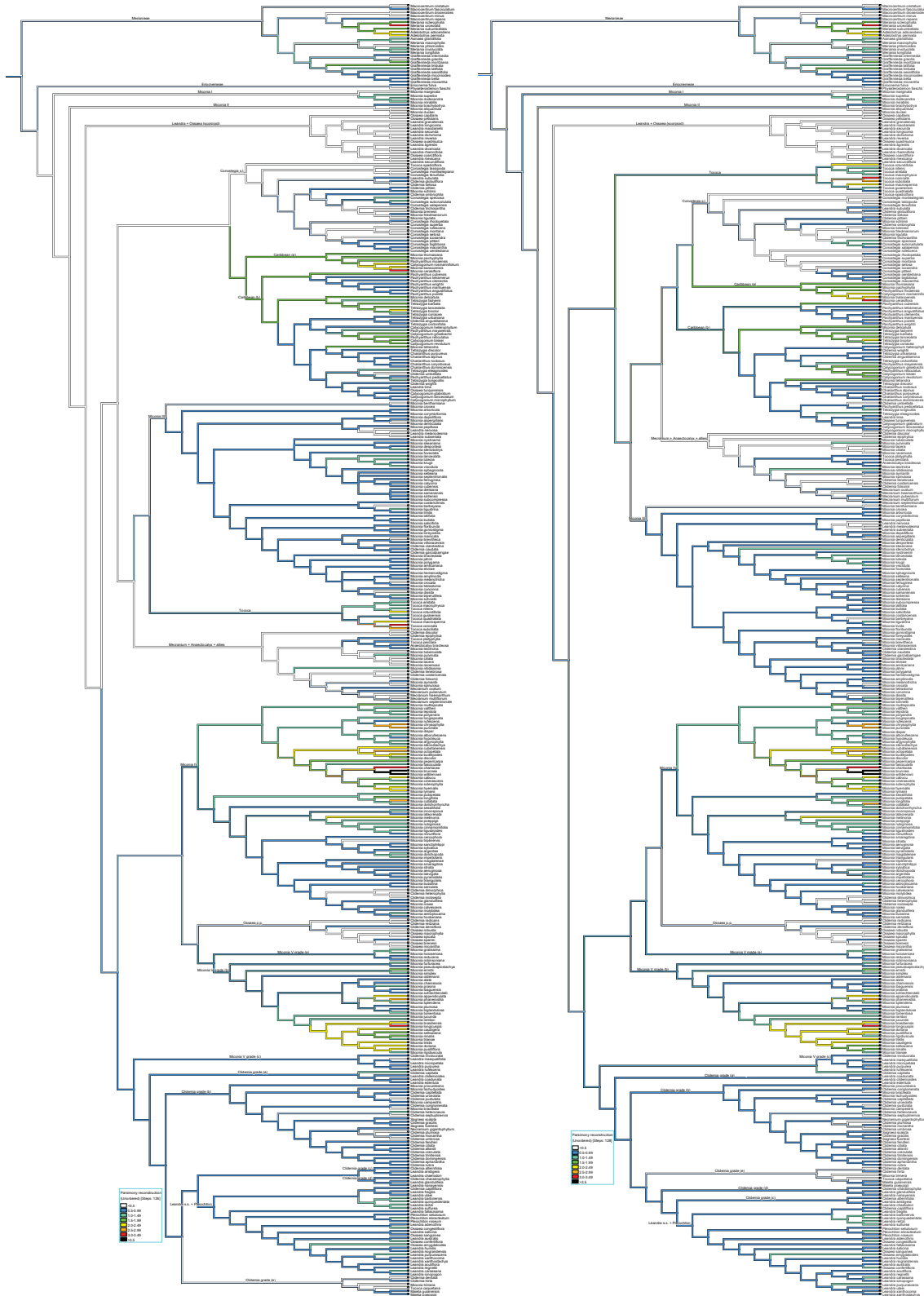


Character O. Microrelief of the periclinal walls.





Character P. Cells with features differing from the rest of the seed corpus.



Character Q. Length of the seed from antiraphal view (mm).