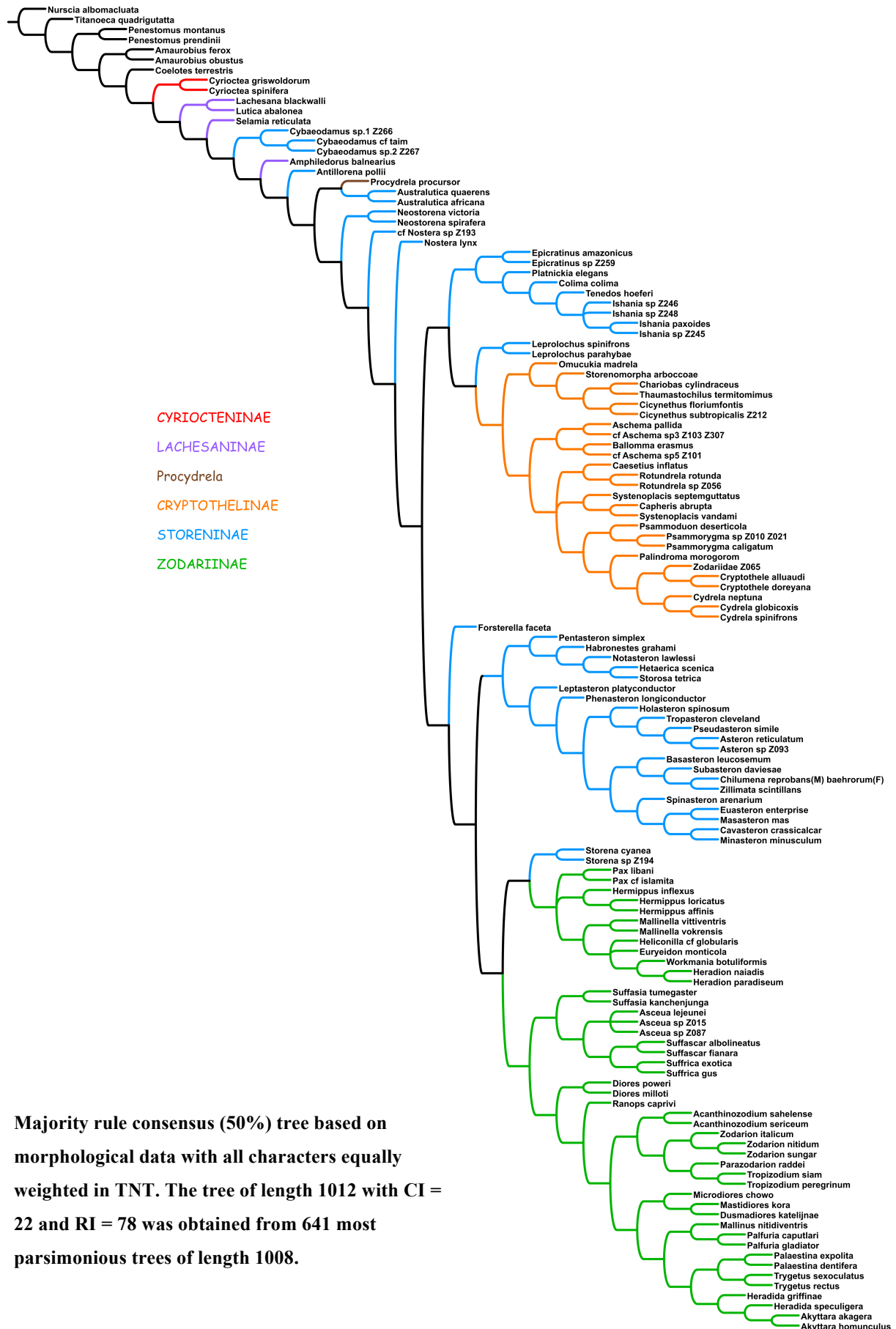


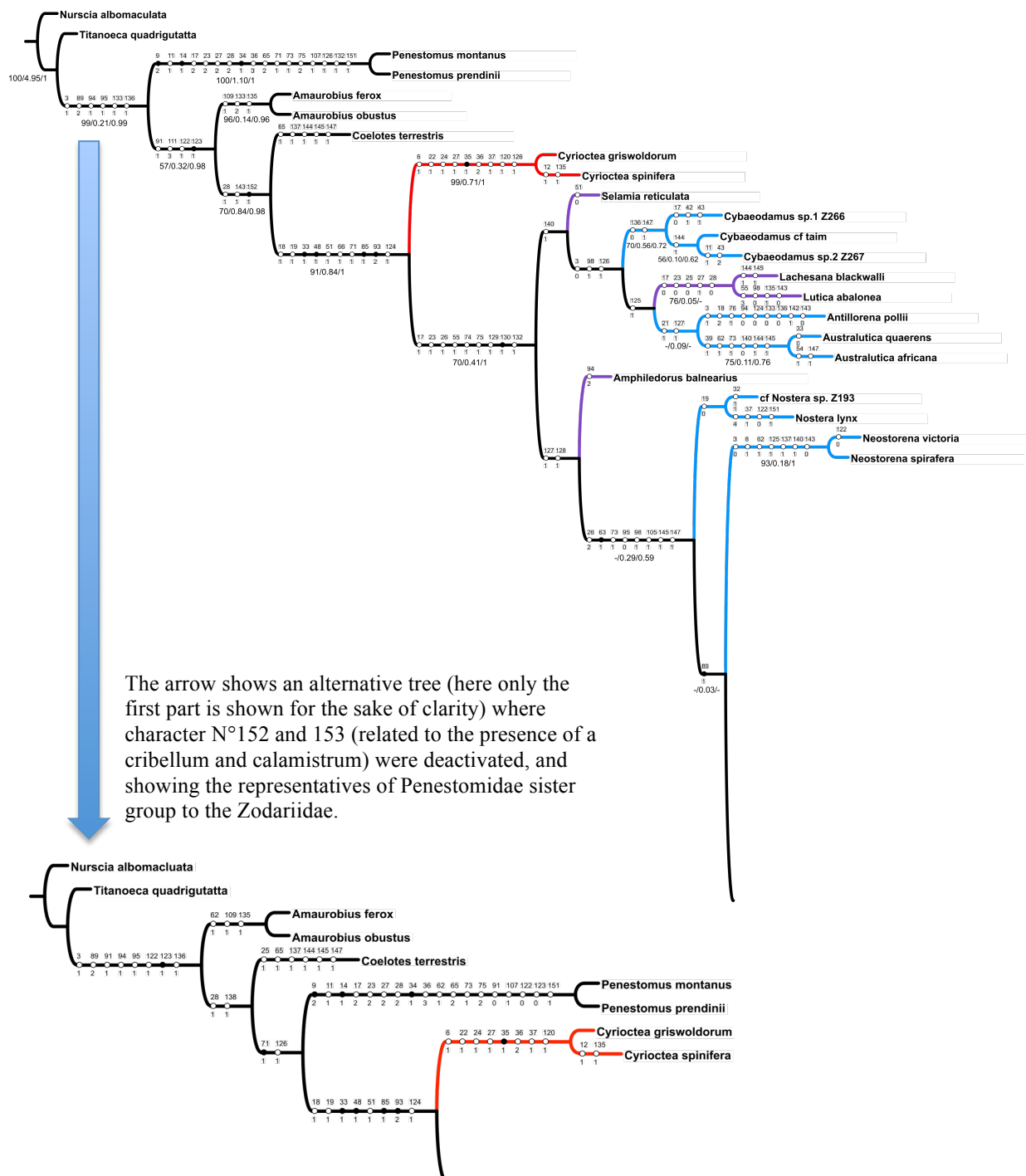
Appendix 6. Majority rule consensus tree (all characters equally weighted)



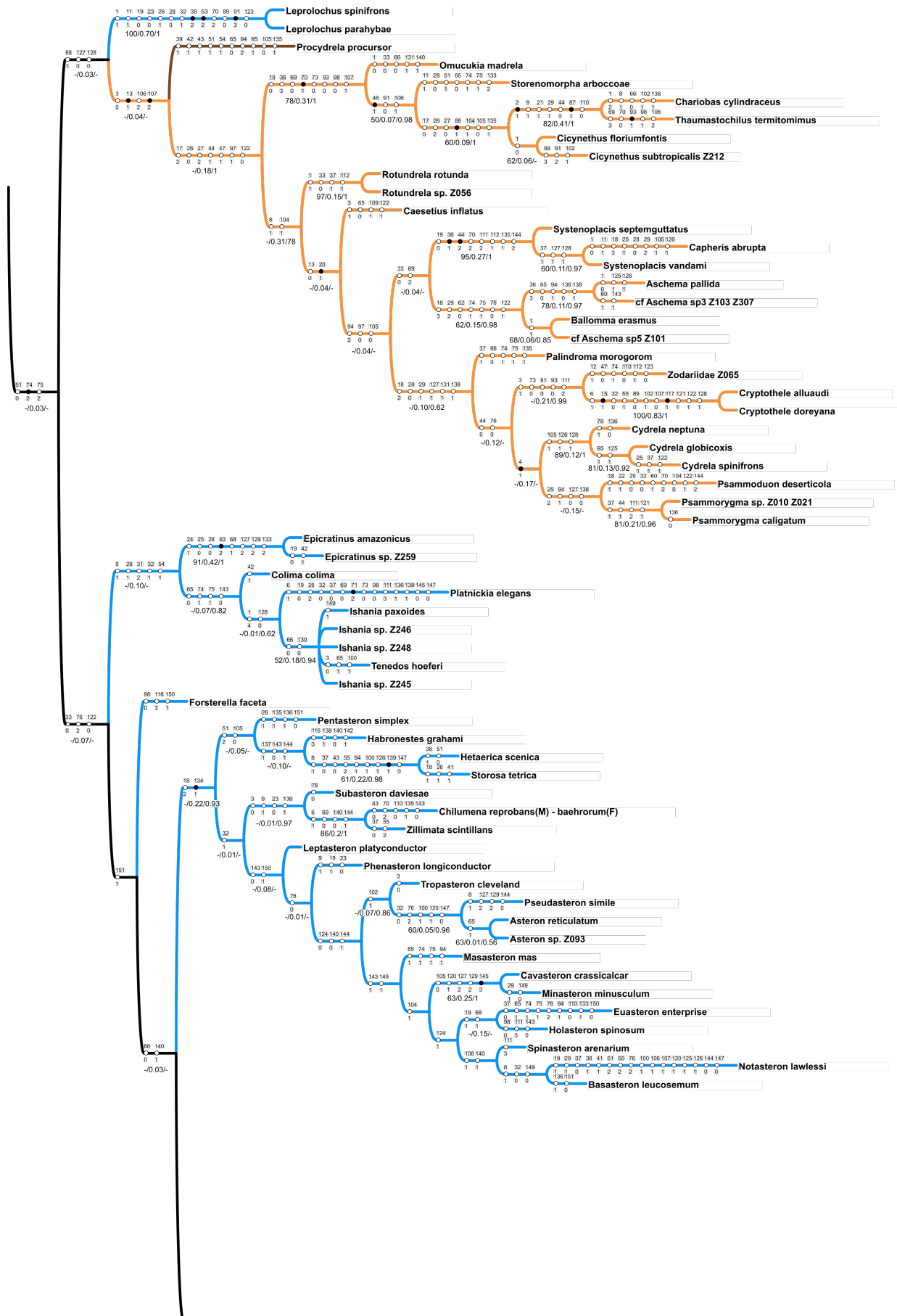
Majority rule consensus (50%) tree based on morphological data with all characters equally weighted in TNT. The tree of length 1012 with CI = 22 and RI = 78 was obtained from 641 most parsimonious trees of length 1008.

Appendix 7. Majority rule consensus tree (implied weighting k=4)

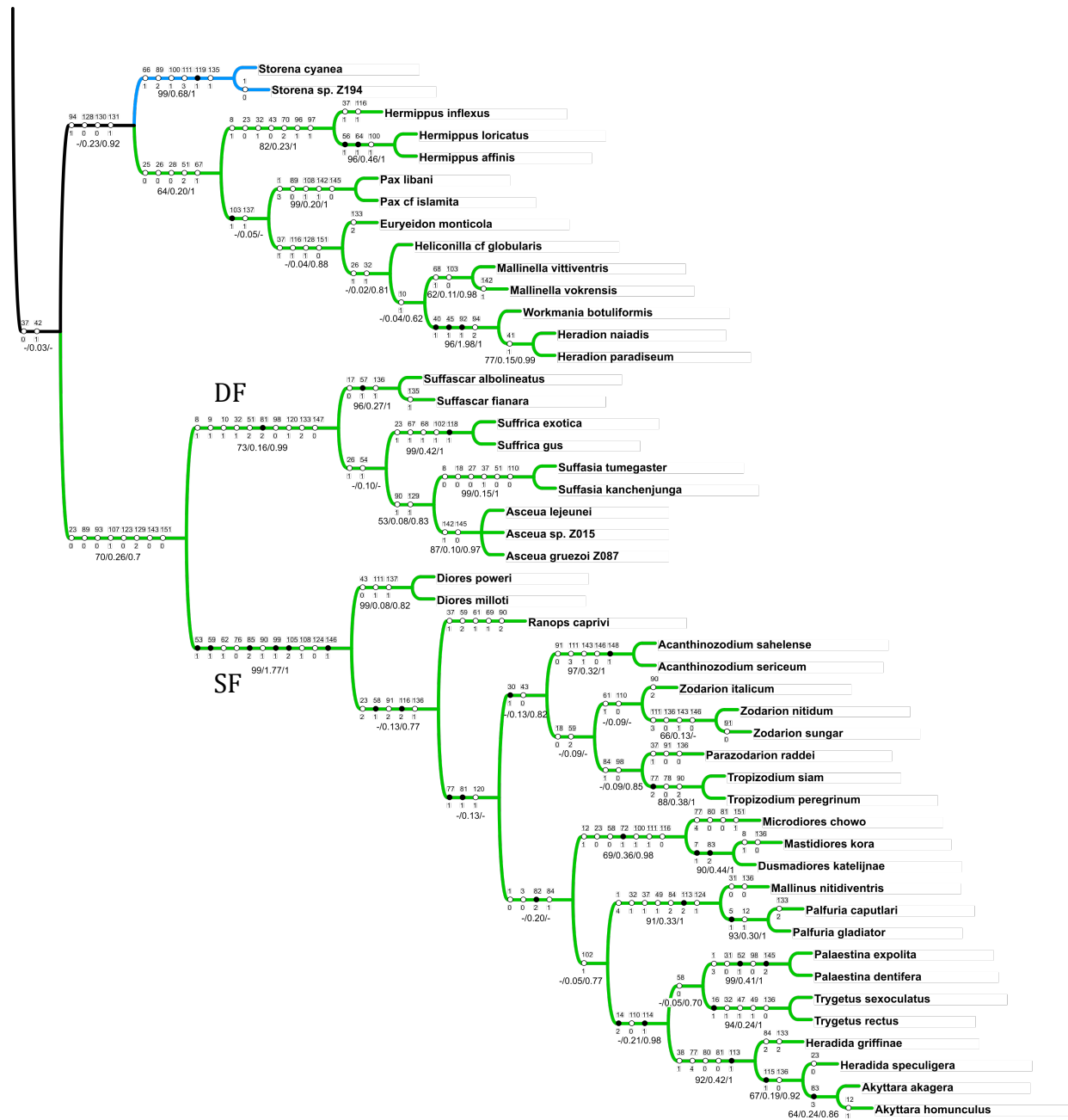
Majority rule consensus (50%) tree based on morphological data and calculated with implied weighting (k=4) in TNT. The tree of length 1043 (best score 60.68108) with CI = 22 and RI = 77 was obtained from 5 most parsimonious trees of length 1041 (best score 60.59795). Character numbers (unambiguous only) are placed above the circles and the states are shown under the circles. Black circles indicate non-homoplastic changes, and white circles homoplastic changes. The numbers below the branches indicate the Bootstrap value / Bremer support / Posterior probability (Bp/Br/PP). Branches with no support (Bp < 50; PP < 0.50) are indicated by an asterisk or not shown if both are below mentioned values. Clade colors represent the different subfamilies defined in this study: representative species of the Cyriocteininae are in red, Lachesaninae in violet, *Procydrela* in brown, Cryptothelinae in orange, Storeninae in blue and Zodariinae in green.



Appendix 7 – continued.



Appendix 7 - continued. SF = single femoral organ clade; DF = dual femoral organ clade



Appendix 8. Majority rule consensus Bayesian tree obtained with MrBayes (MB) on the morphological matrix.

The values at nodes indicate the posterior probabilities.

