

A Contribution to the Phylogeny of the Ciidae and its Relationships with Other Cucujoid and Tenebrionoid Beetles (Coleoptera: Cucujiformia)

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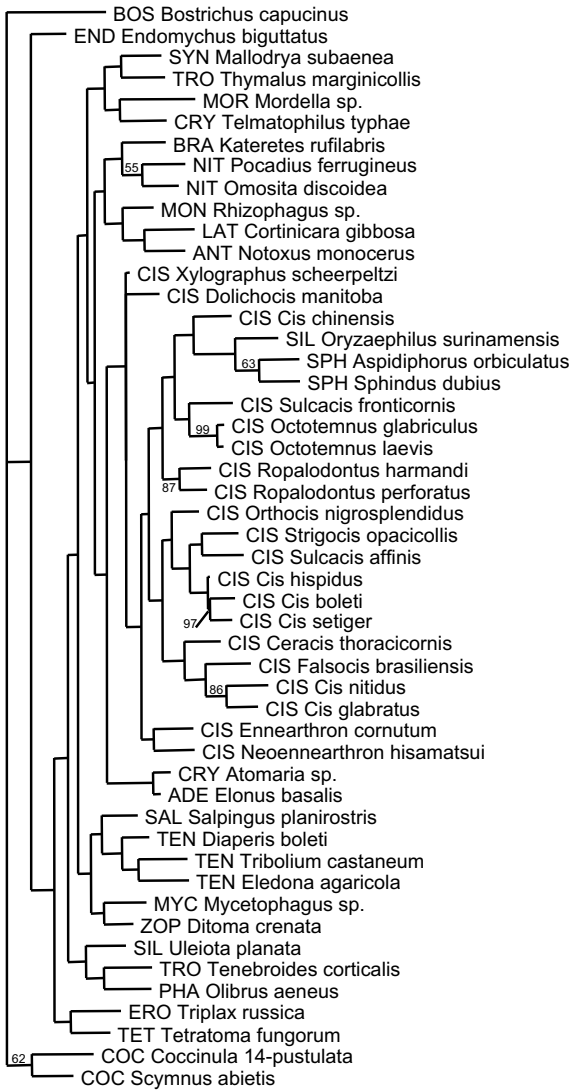
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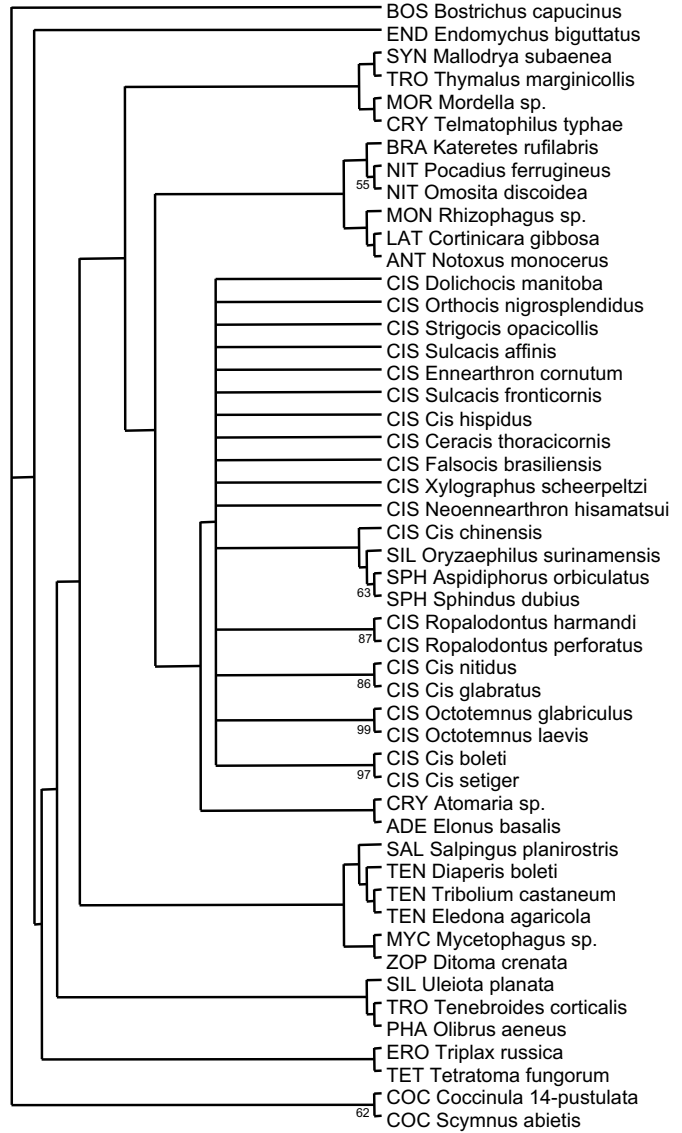
Figure captions for Electronic Supplement

EFigs. E1–E25. Phylogenetic trees resulting from the various analyses. The trees are designated according to the used taxon sample (E-sample; R-sample; C-sample), the used analytical method (MPew and MPdw = maximum parsimony based on fixed alignment, under equal resp. differentiated weighting of characters; ML = maximum likelihood; MB = MrBayes; DO = partial direct optimization, with gap cost either 2x or 4x that of nucleotide changes), and the included gene fragments (18S, COI, COII, the latter also including part of tRNA-Lys). See chapter 2 for details and Tab. 3 for tree statistics. The last specification, in parentheses, indicates the nature of the tree: (1/N) = one out of N most parsimonious trees, (1/1) meaning the single most parsimonious tree is shown; (sct) = strict consensus tree; (50%) = 50% majority rule tree. Bootstrap values and posterior probabilities of branches are indicated if $\geq 50\%$. The scale for branch lengths gives a measure for the amount of evolutionary changes (in % of aligned sequences); it is attached to the figures where such measurement is applicable (all but consensus trees and trees derived from DO analyses).

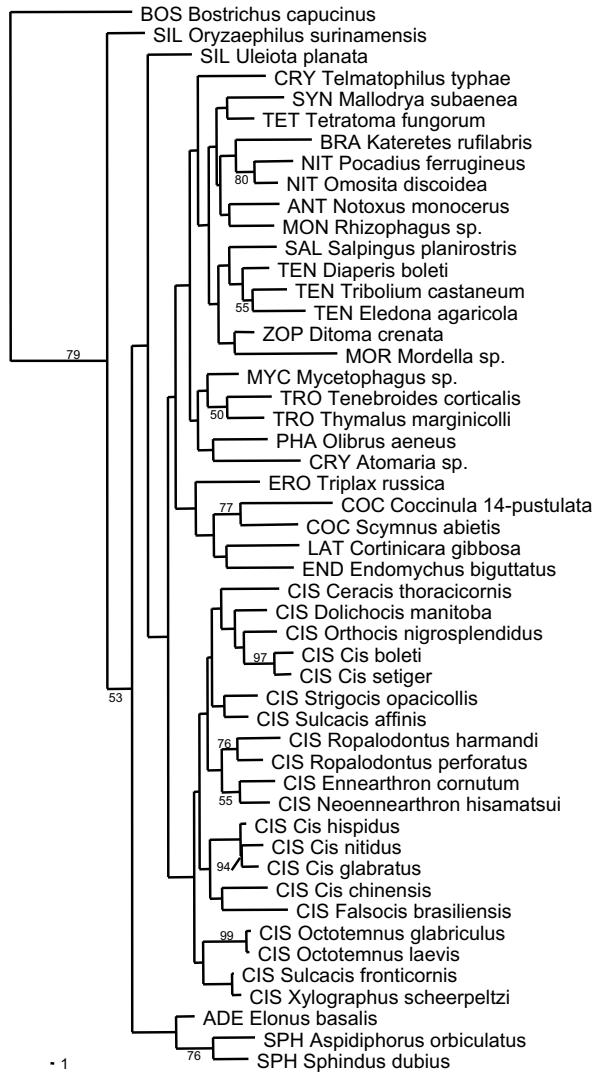


- 10

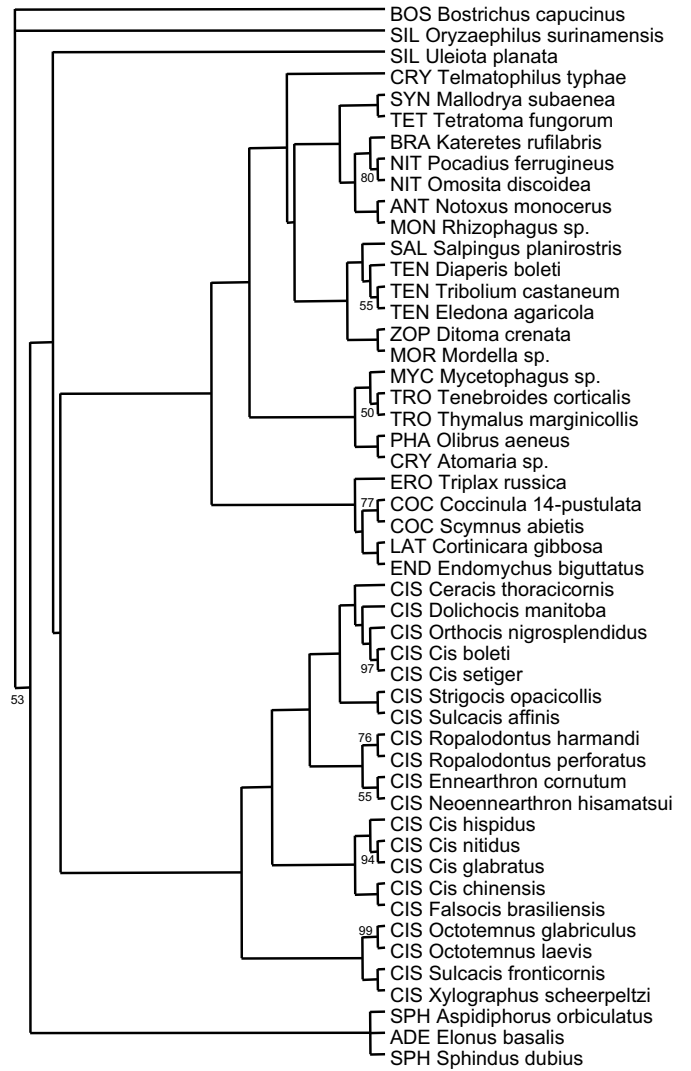
EFig. E1: E-sample-MPew[COI,18S](1/24)



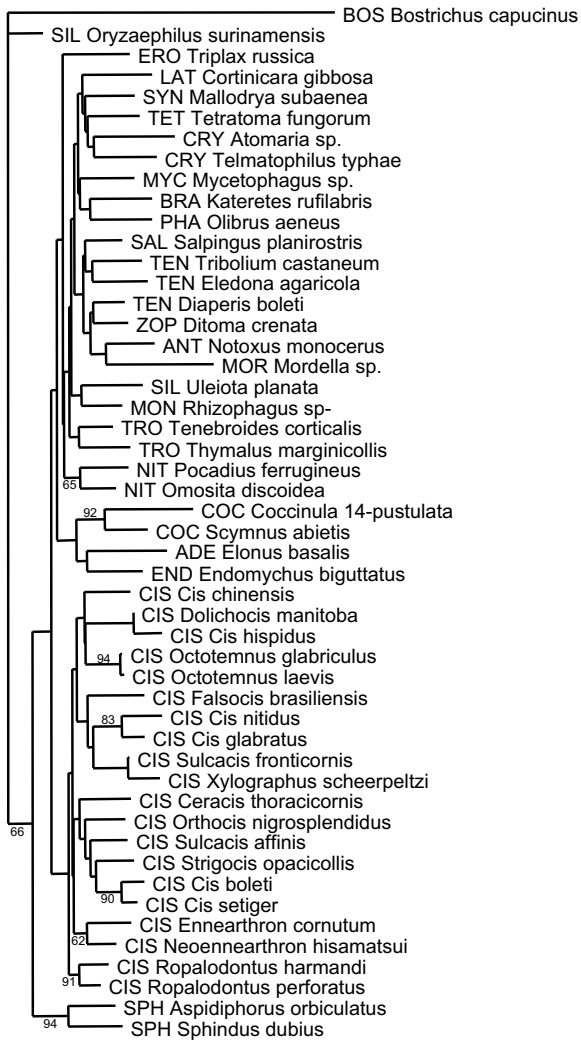
EFig. E2: E-sample-MPew[COI,18S](sct)



EFig. E3: E-sample-MPdw[COI,18S](1/3)

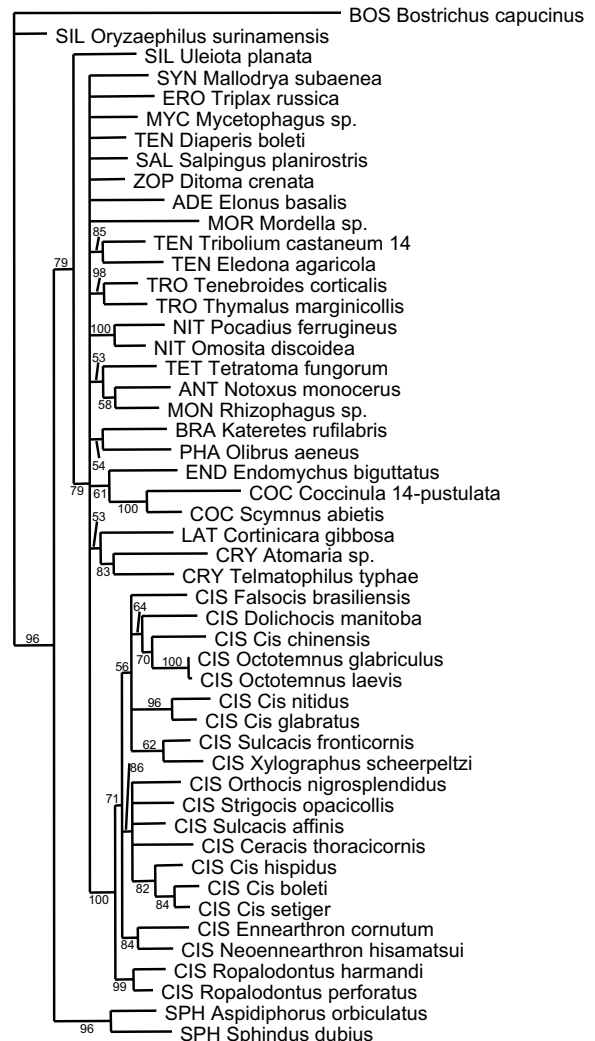


EFig. E4: E-sample-MPdw[COI,18S](sct)



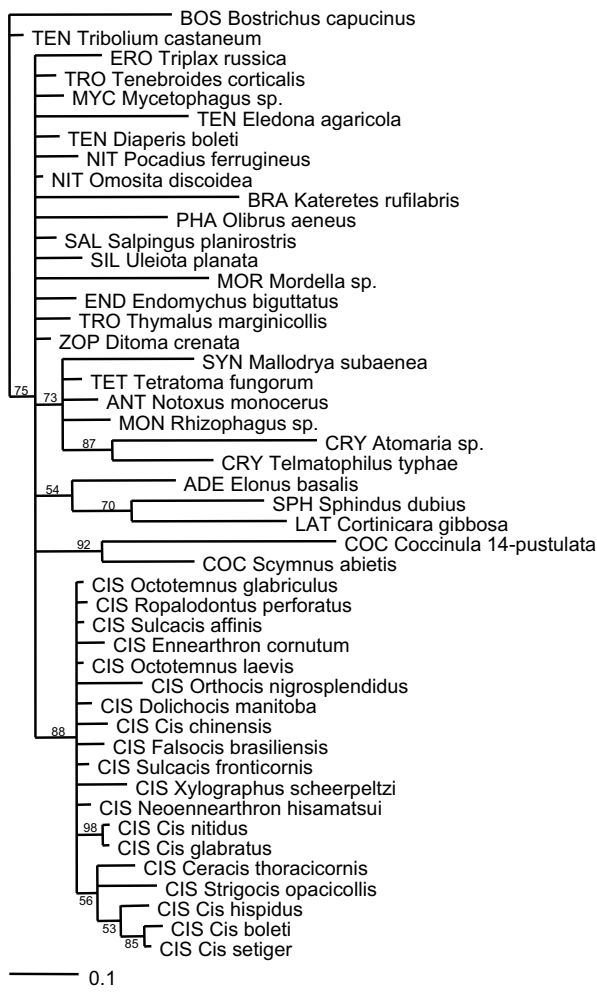
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EFig. E5: E-sample-ML[COI,18S](1/1)

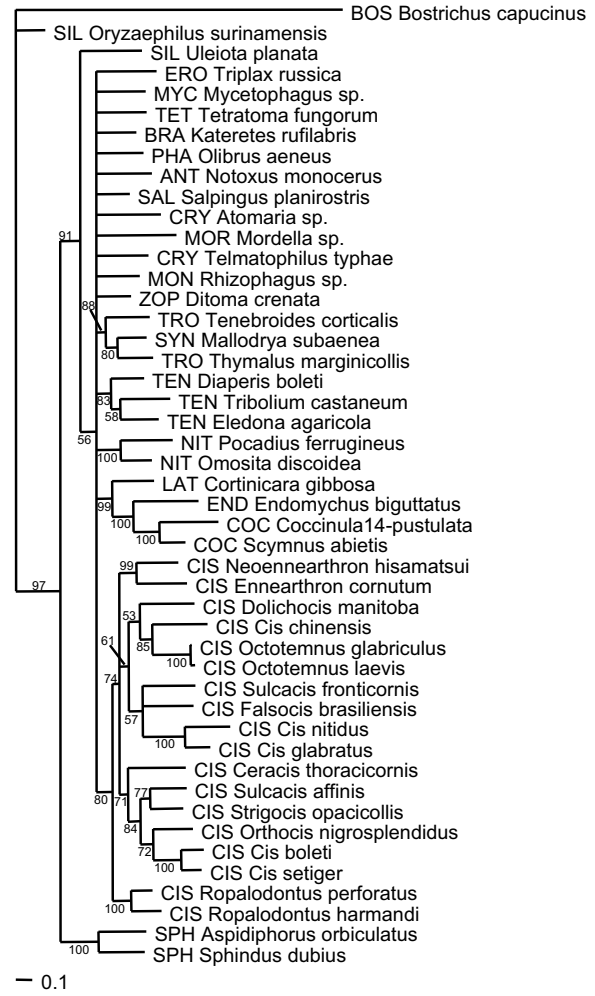


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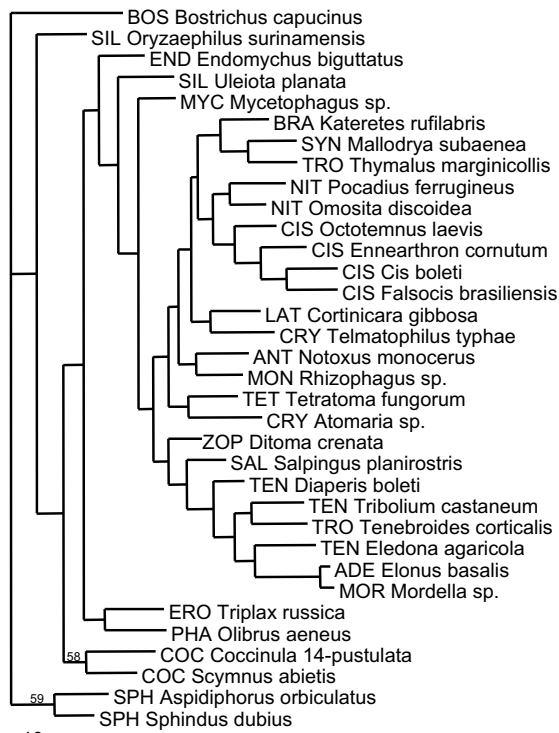
EFig. E6: E-sample-MB[COI,18S](50%mr)



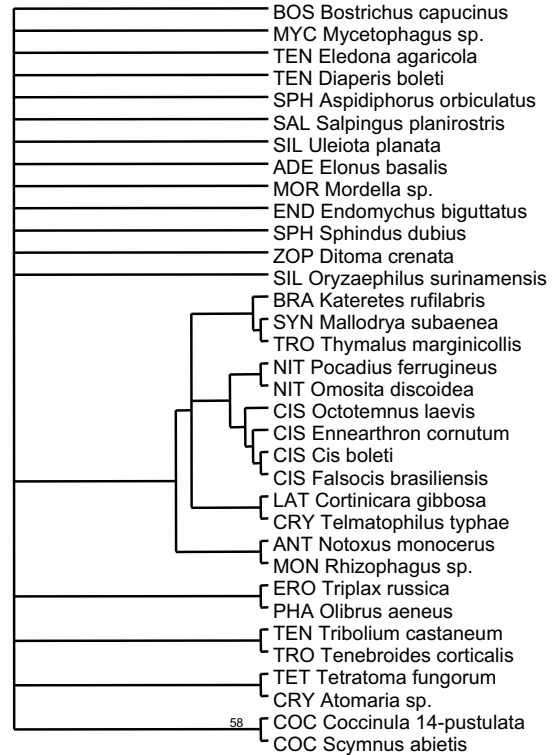
EFig. E7: E-sample-MB[18S](50%mr)



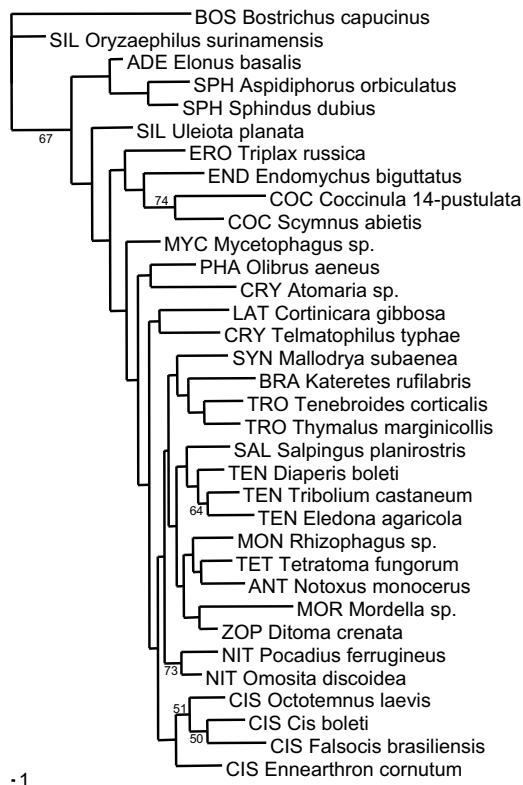
EFig. E8: E-sample-MB[COI](50%mr)



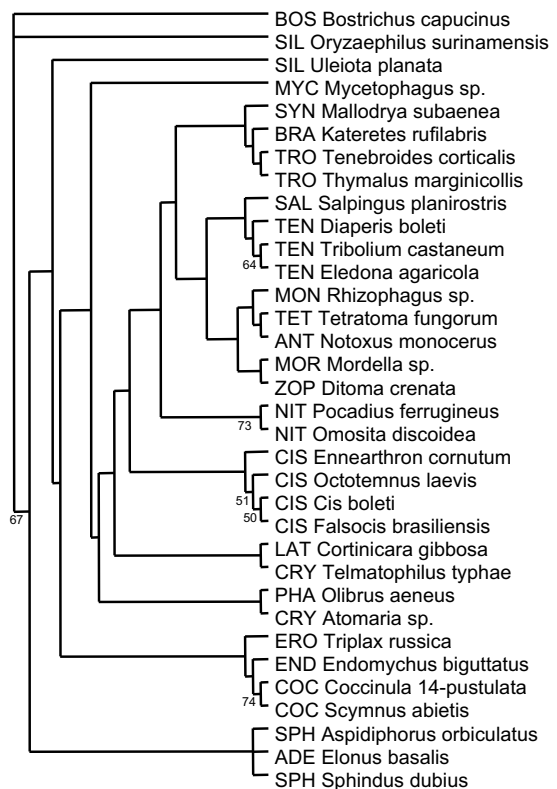
EFig. E9: R-sample-MPew[COI,18S](1/22)



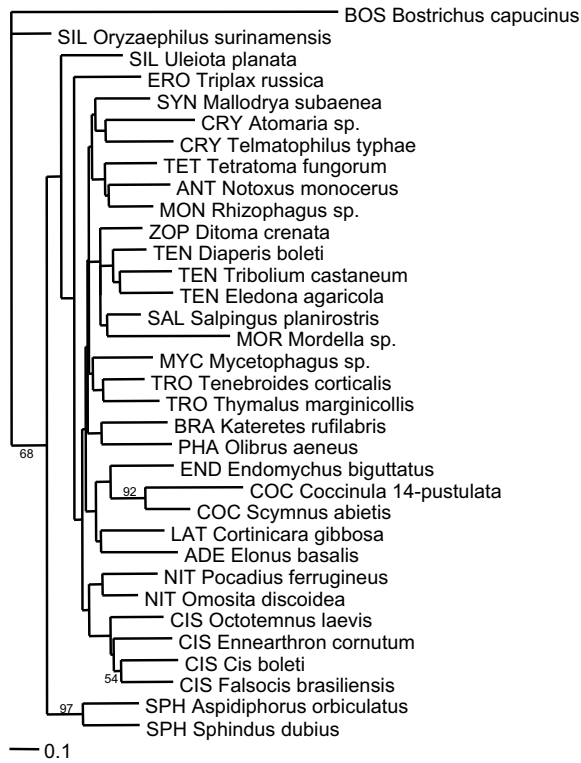
EFig. E10: R-sample-MPew[COI,18S](sct)



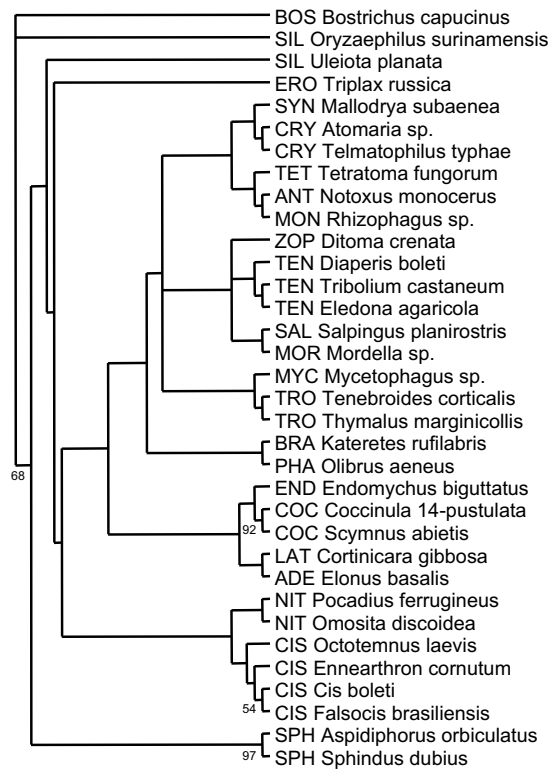
EFig. E11: R-sample-MPdw[COI,18S](1/3)



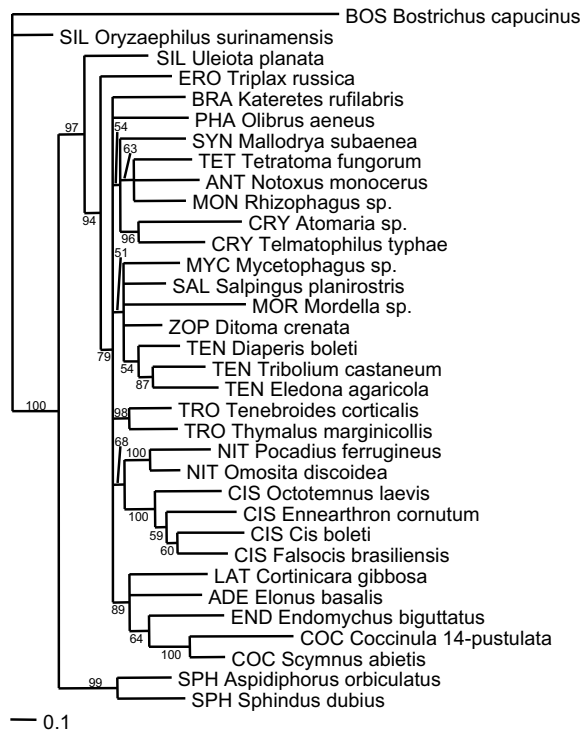
EFig. E12: R-sample-MPdw[COI,18S](sct)



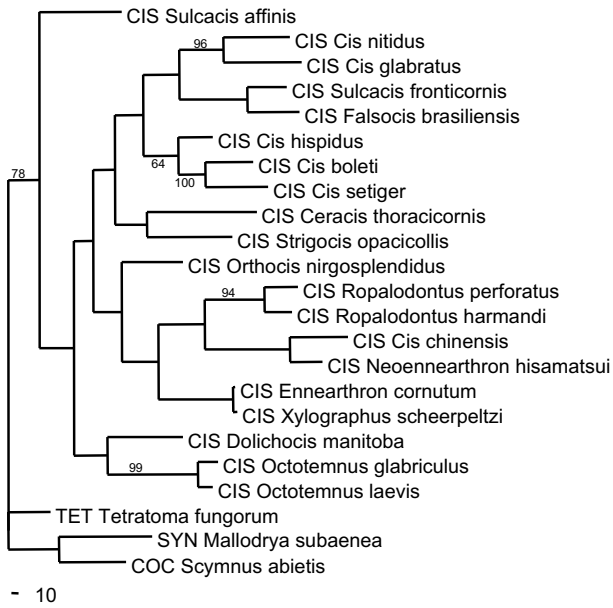
EFig. E13: R-sample-ML[COI,18S](1/5)



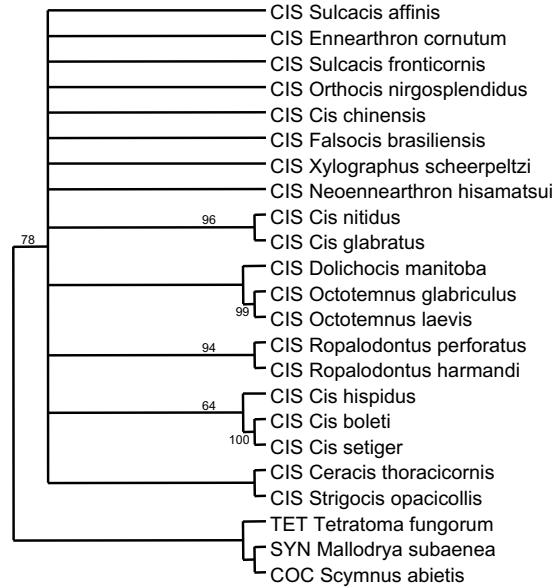
EFig. E14: R-sample-ML[COI,18S](sct)



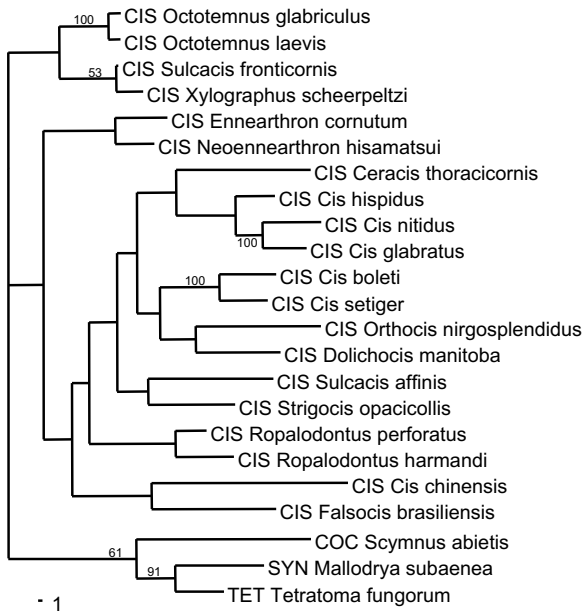
EFig. E15: R-sample-MB[COI,18S](50%mr)



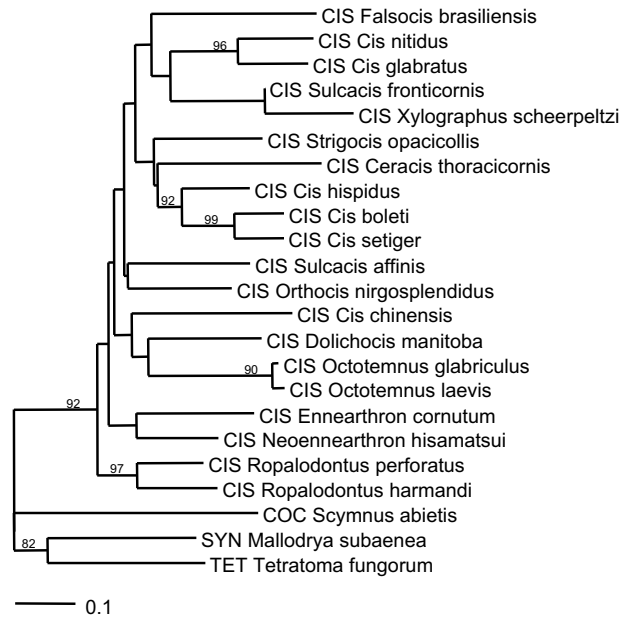
EFig. E16: C-sample-MPew[COI,COII,18S](1/10)



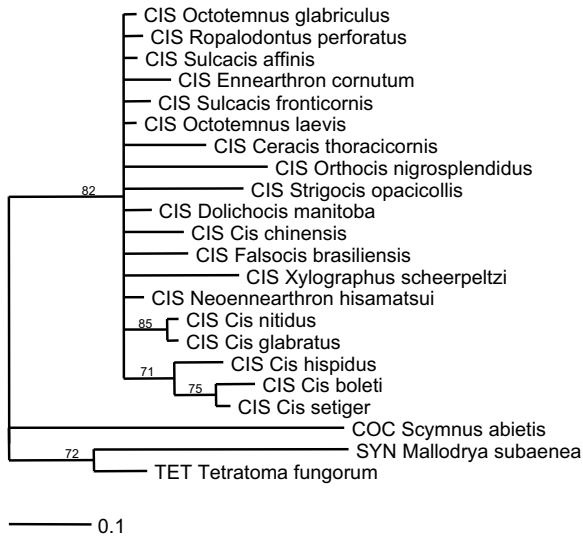
EFig. E17: C-sample-MPew[COI,COII,18S](sct)



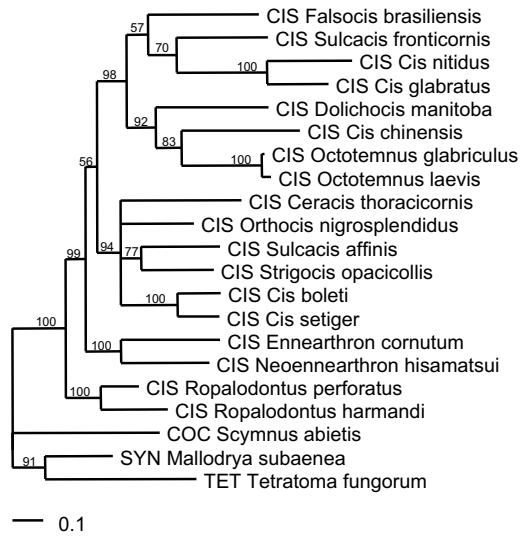
EFig. E18: C-sample-MPdw[COI,COII,18S](1/1)



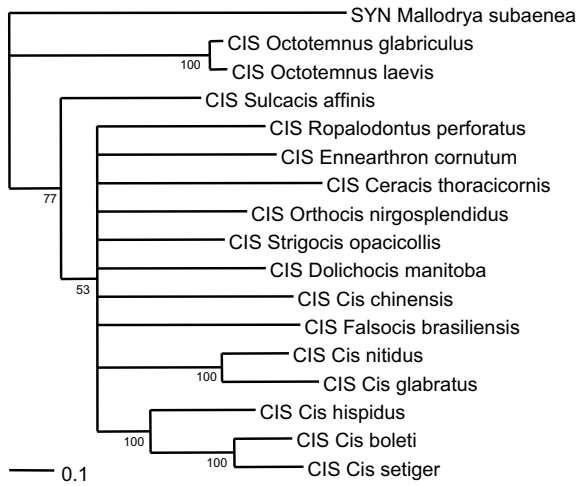
EFig. E19: C-sample-ML[COI,COII,18S](1/1)



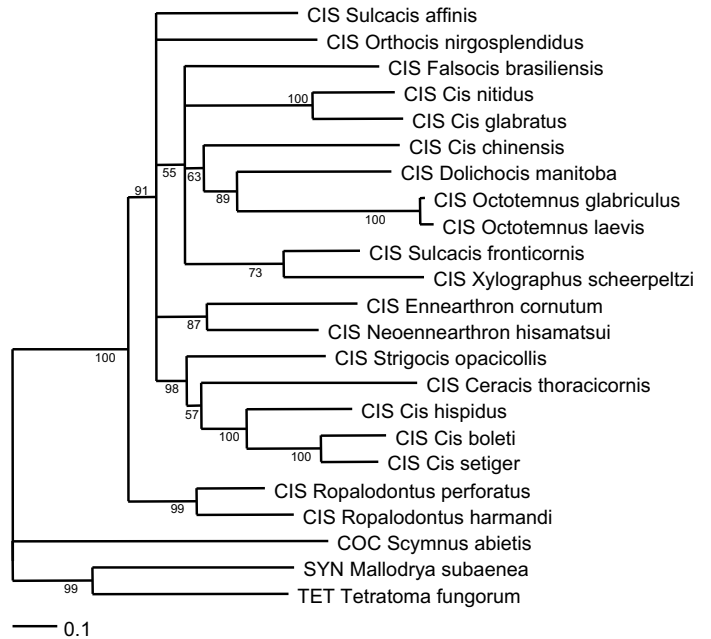
EFig. E20: C-sample-MB[18S](50%mr)



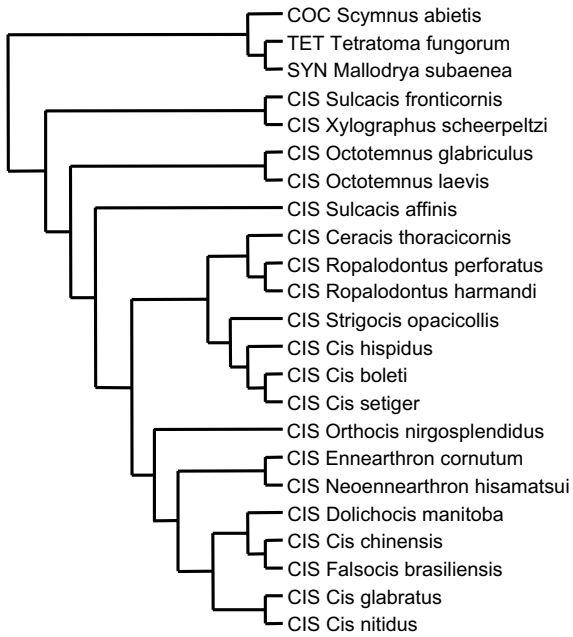
EFig. E21: C-sample-MB[COI](50%mr)



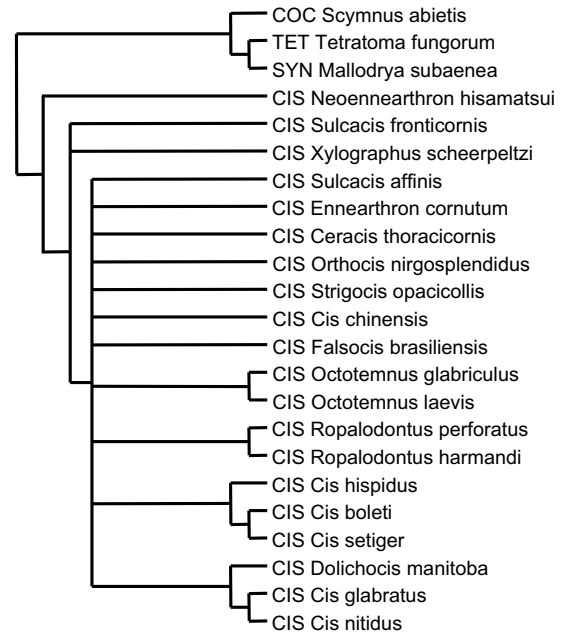
EFig. E22: C-sample-MB[COII](50%mr)



EFig. E23: C-sample-MB[COI,COII,18S](50%mr)



EFig. E24: C-sample-DOgap2x[COI,COII,18S](sct)



EFig. E25: C-sample-DOgap4x[COI,COII,18S](sct)