

ELECTRONIC APPENDIX

This is the Electronic Appendix to the article

Reverse taxonomy: an approach towards determining the diversity of meiobenthic organisms based on ribosomal RNA signature sequences

by

Melanie Markmann and Diethard Tautz

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Electronic appendices are refereed with the text; however, no attempt is made to impose a uniform editorial style on the electronic appendices.

Reverse taxonomy: an approach towards determining the diversity of meiobenthic organisms based on ribosomal RNA signature sequences

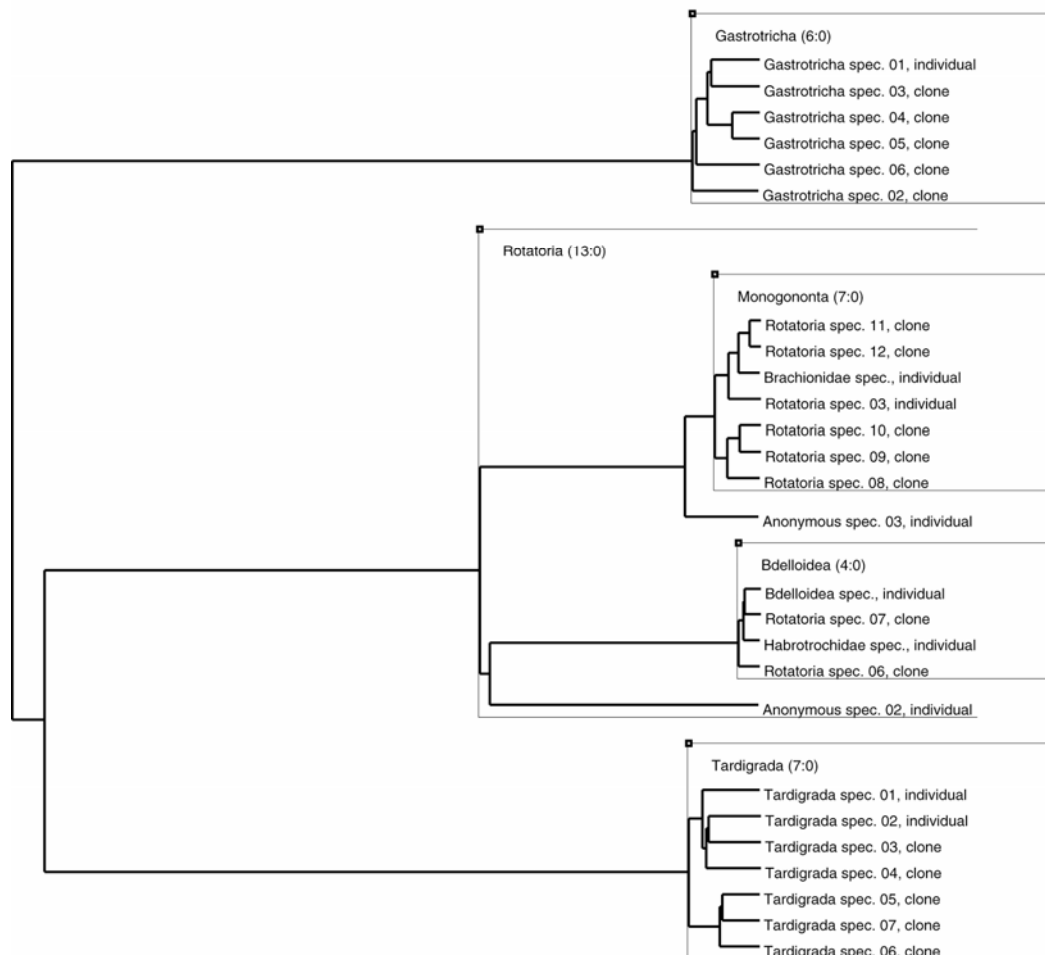
Melanie Markmann and Diethard Tautz

Supplementary data

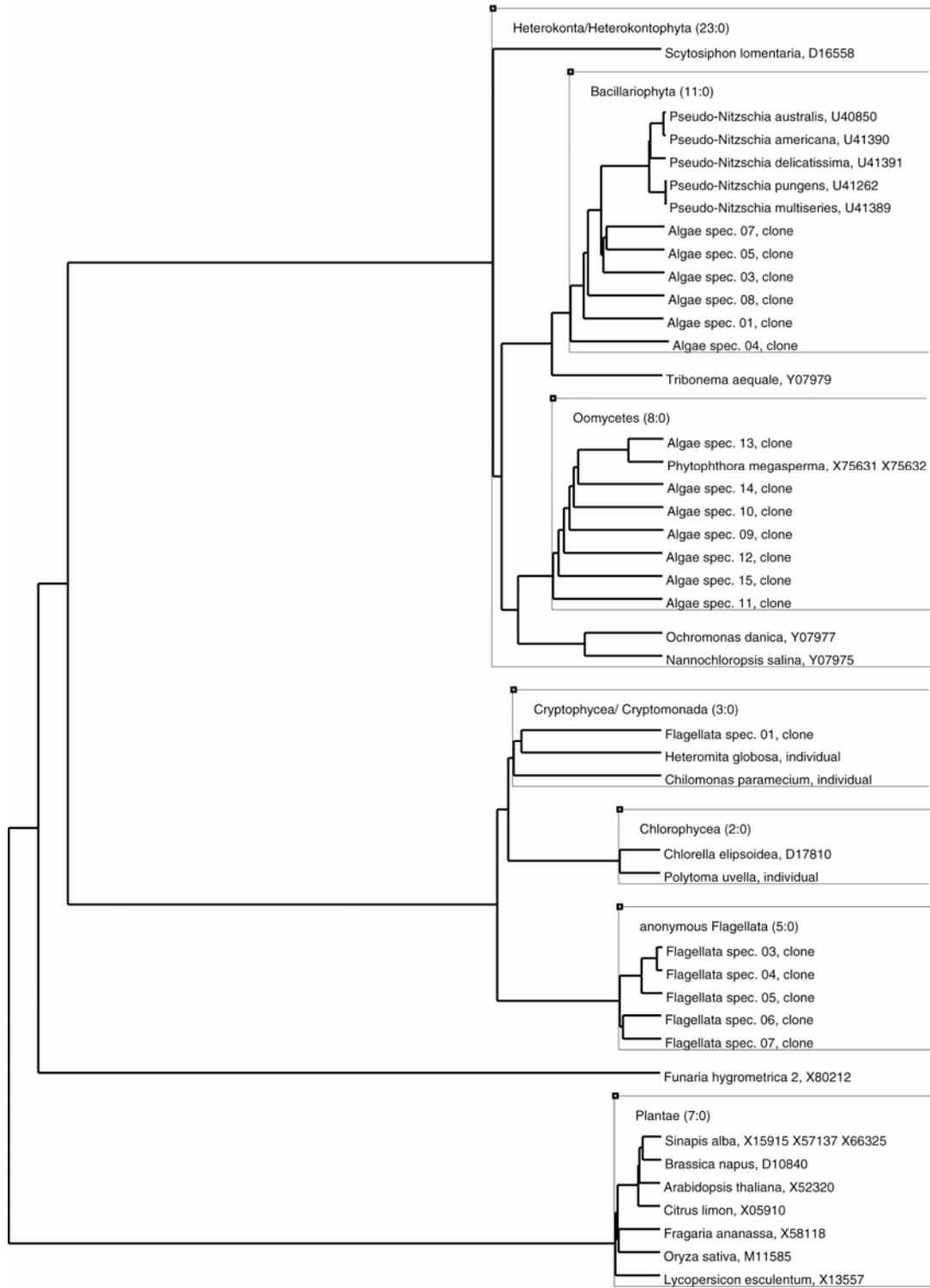
Phylogeny reconstruction to identify taxon groups

A neighbour joining tree was constructed that includes the newly determined sequences, as well as database sequences. The former are differentiated into sequences obtained from clones from the batch approach ("clone") or from PCR fragments obtained from single animals ("individuals"). The database sequences are flagged with their accession numbers. Each page presents a major taxon group.

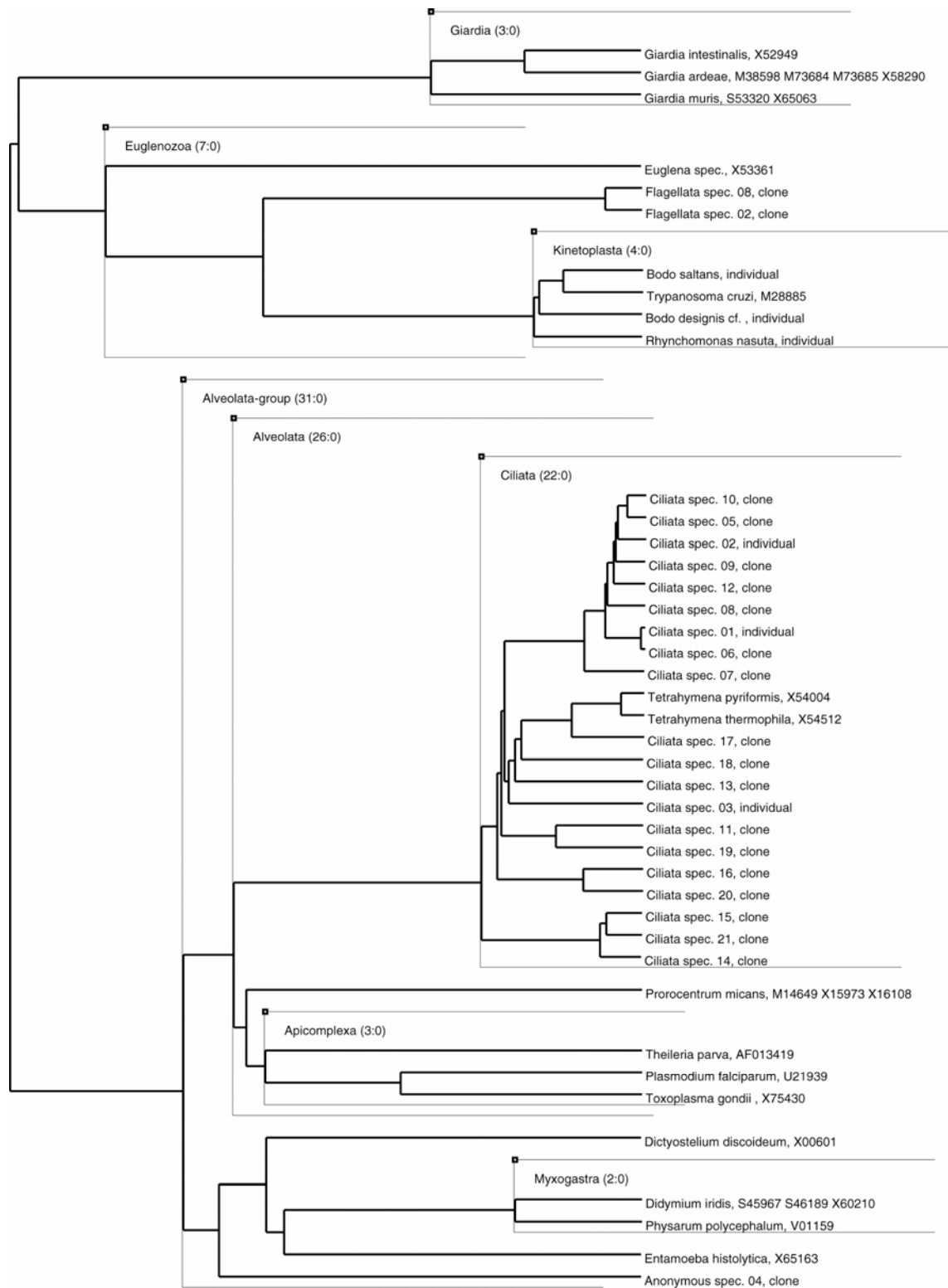
Gastrotricha, Rotatoria, Tardigrada



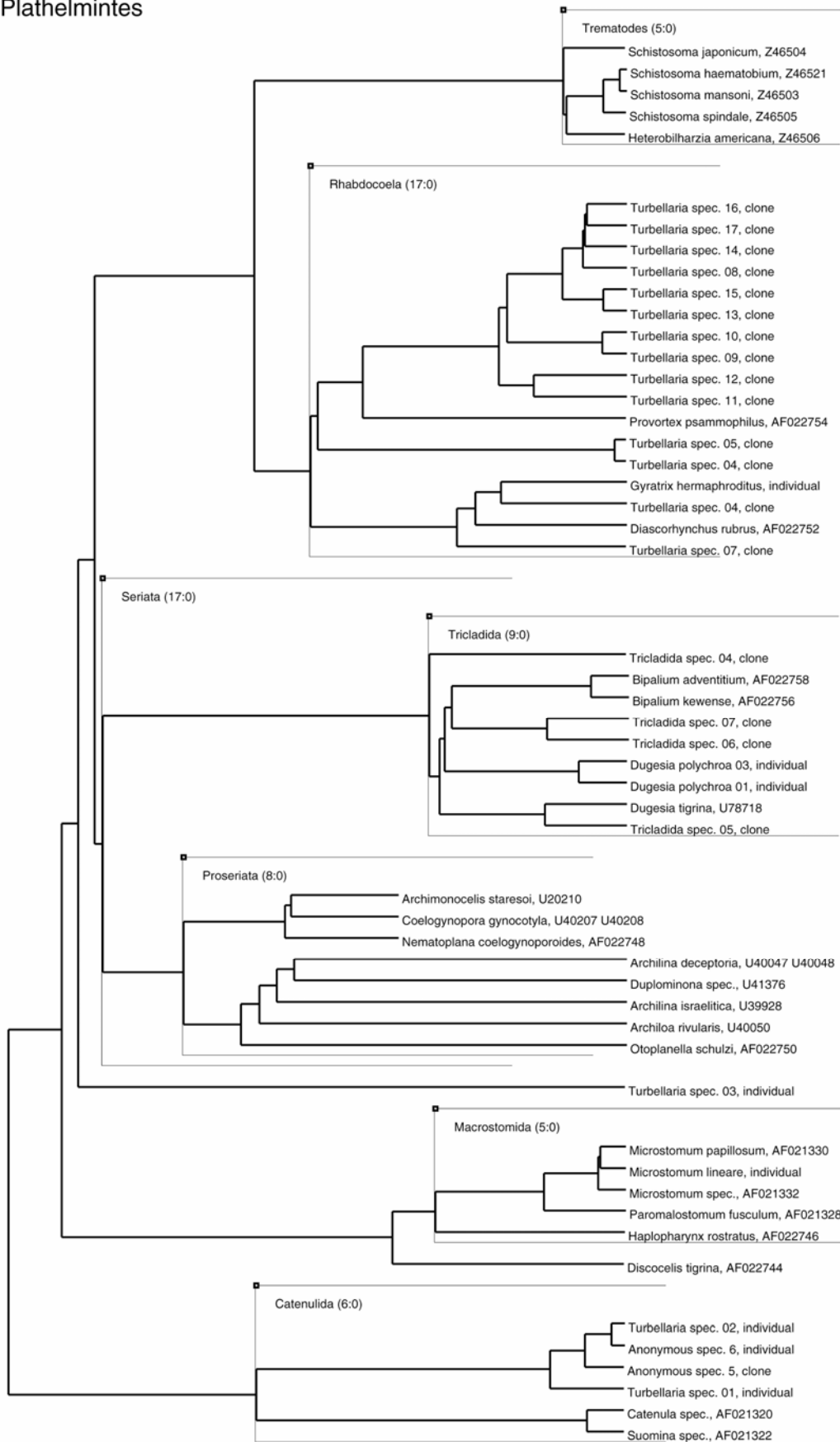
algae, flagellates, plants



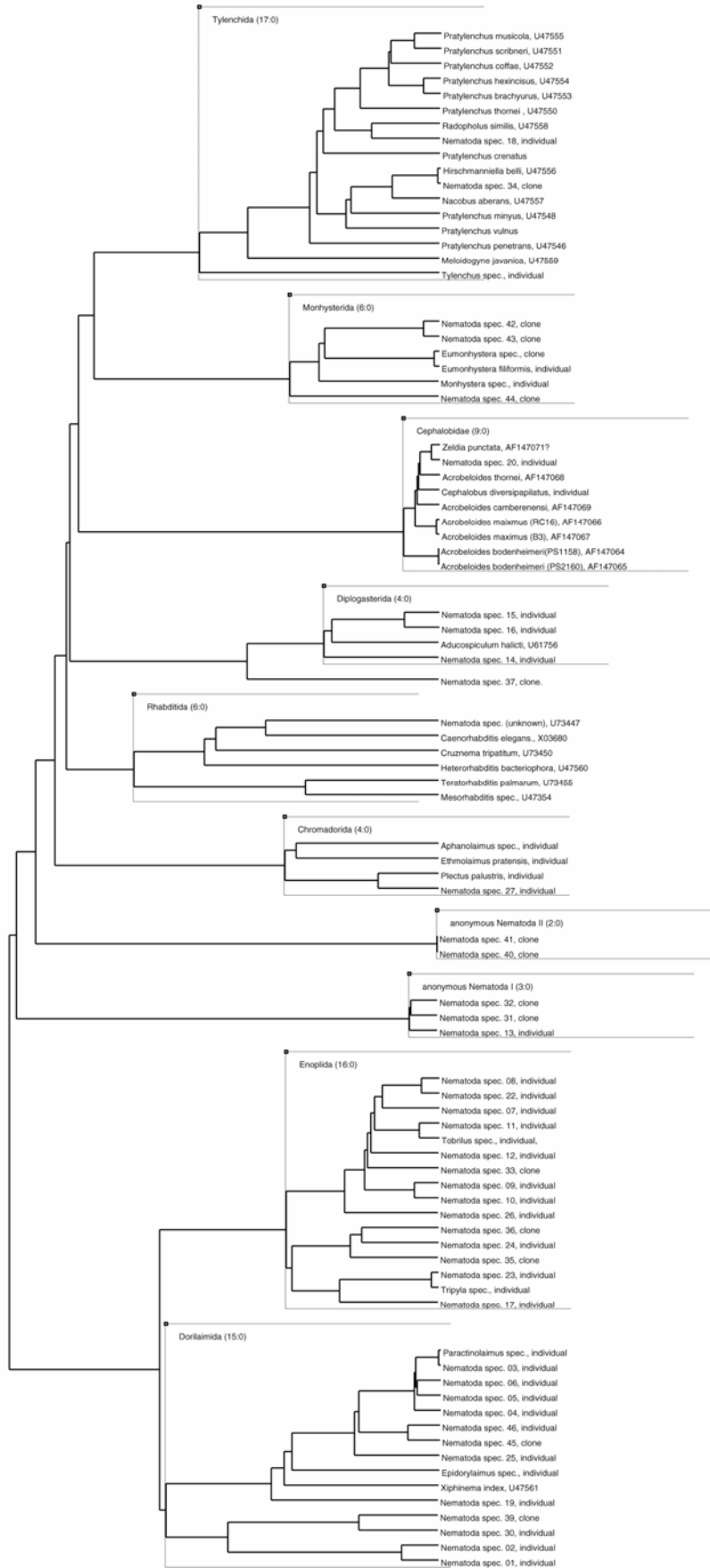
Alveolata group, Giardia, Euglenozoa



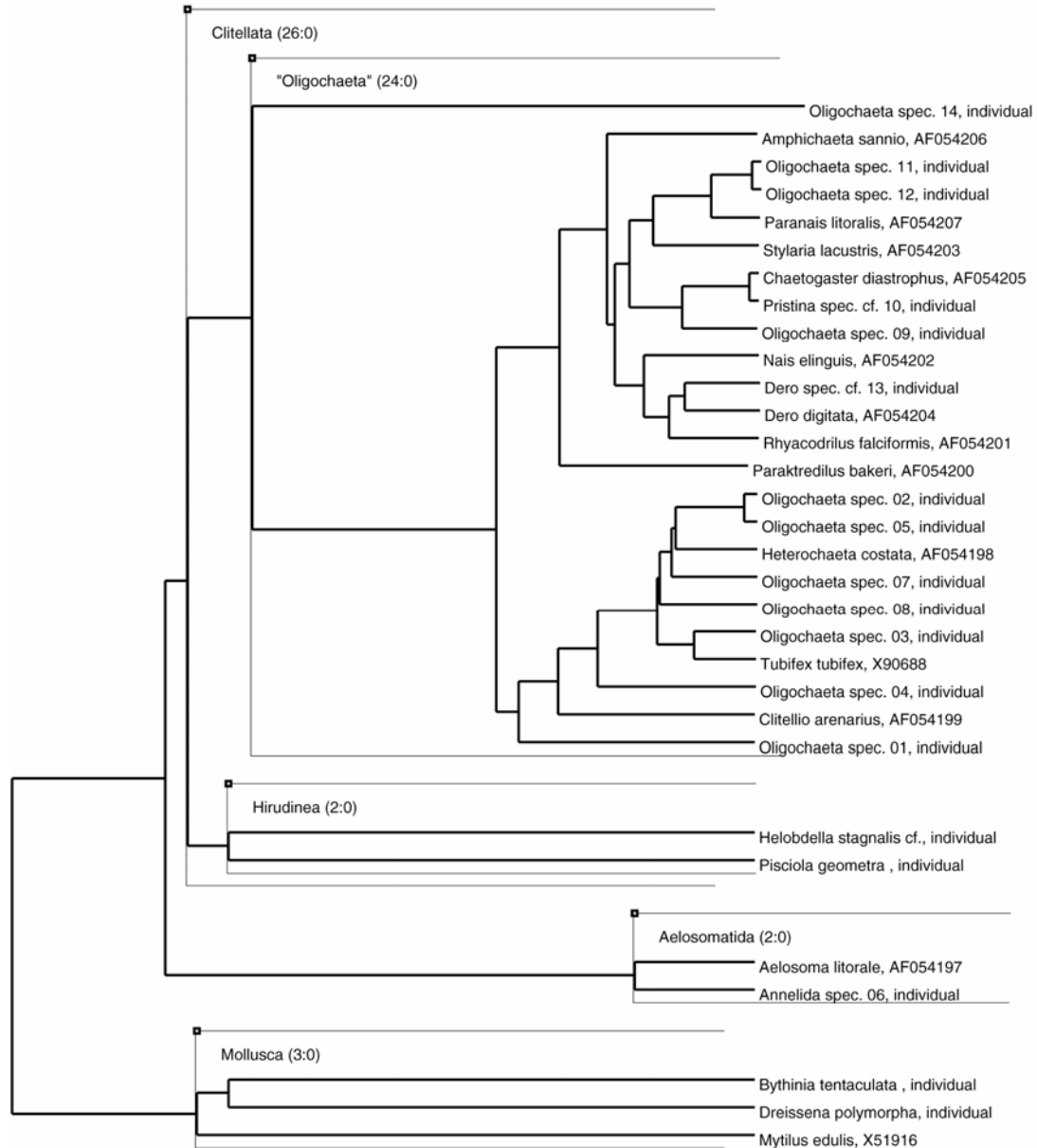
Plathelminthes



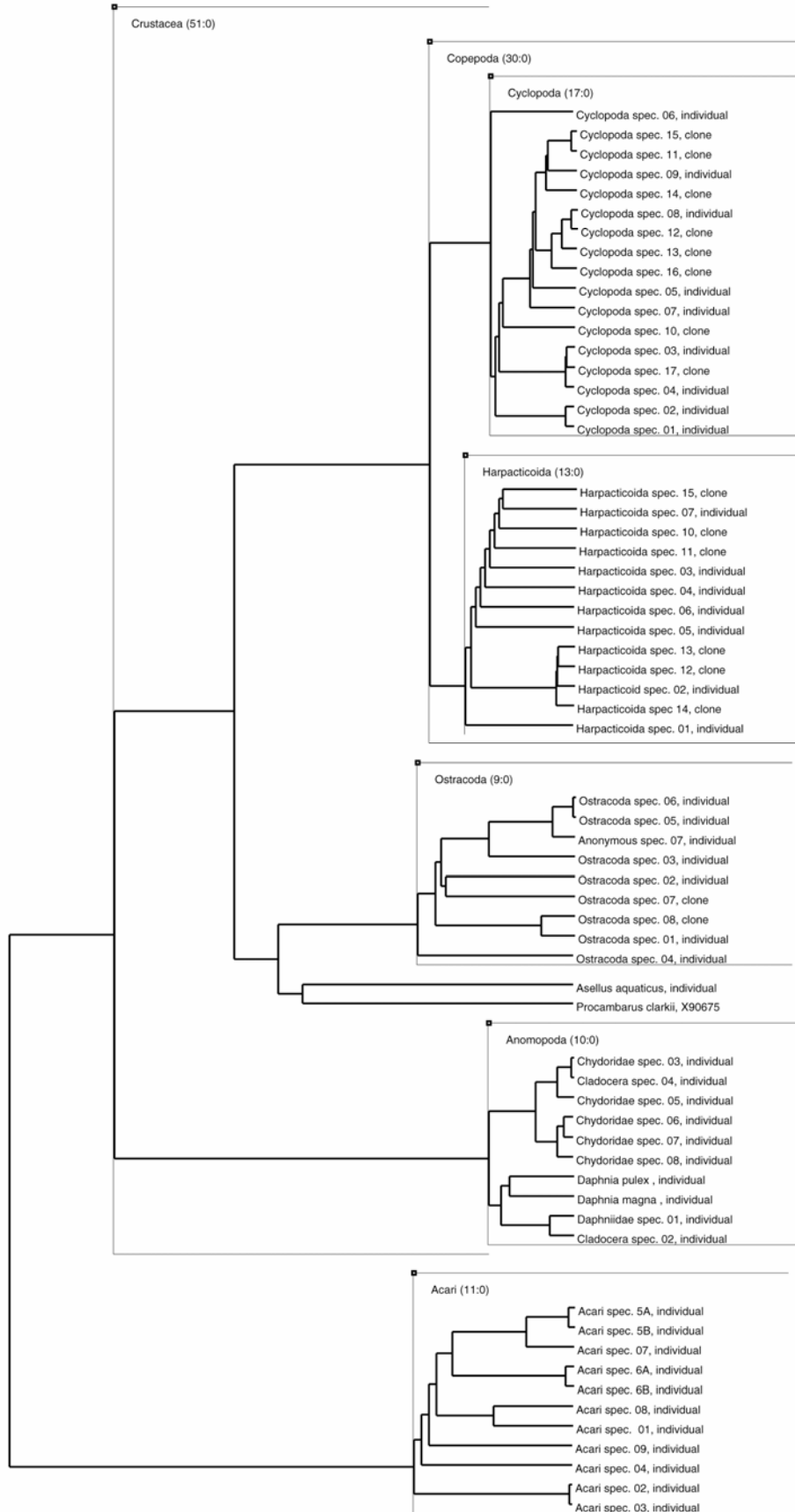
nematodes



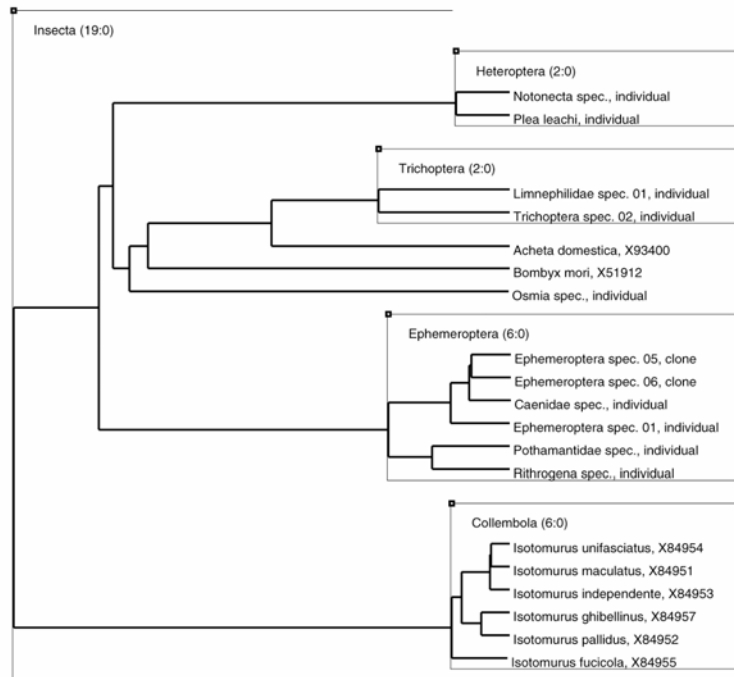
Annelids, molluscs



arthropods without insects



insects without Diptera



Diptera

