

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/302396816>

# Puglisi et al 2016 elec supp

Dataset · May 2016

---

READS

18

5 authors, including:



**Tze Leong Yao**

Forest Research Institute Malaysia (FRIM)

19 PUBLICATIONS 54 CITATIONS

SEE PROFILE



**Richard Ian Milne**

The University of Edinburgh

61 PUBLICATIONS 1,970 CITATIONS

SEE PROFILE



**Michael Moeller**

Royal Botanic Garden Edinburgh

165 PUBLICATIONS 2,028 CITATIONS

SEE PROFILE



**David John Middleton**

Singapore Botanic Gardens

134 PUBLICATIONS 525 CITATIONS

SEE PROFILE

# TAXON

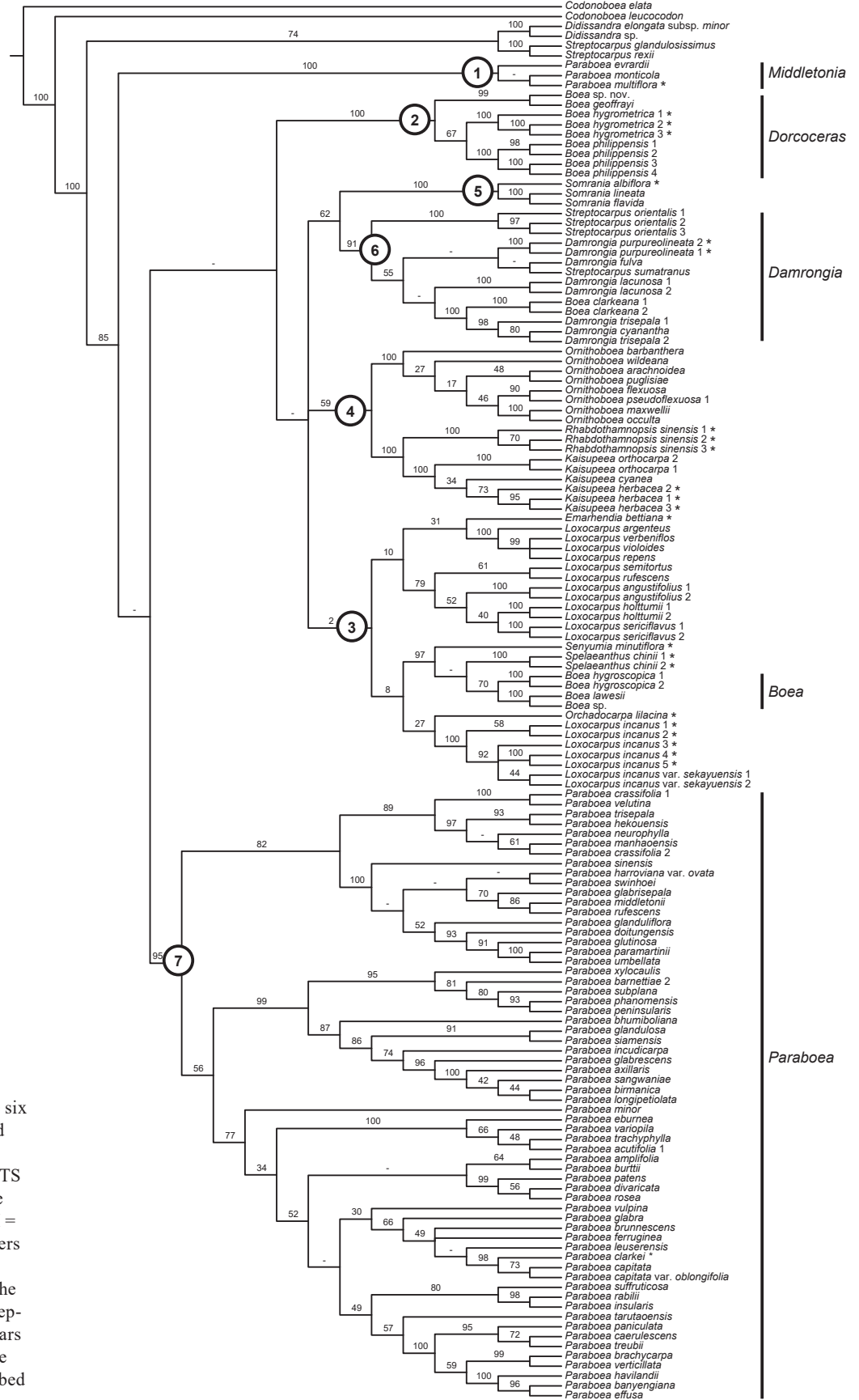
International Journal of Taxonomy, Phylogeny and Evolution

Electronic Supplement to

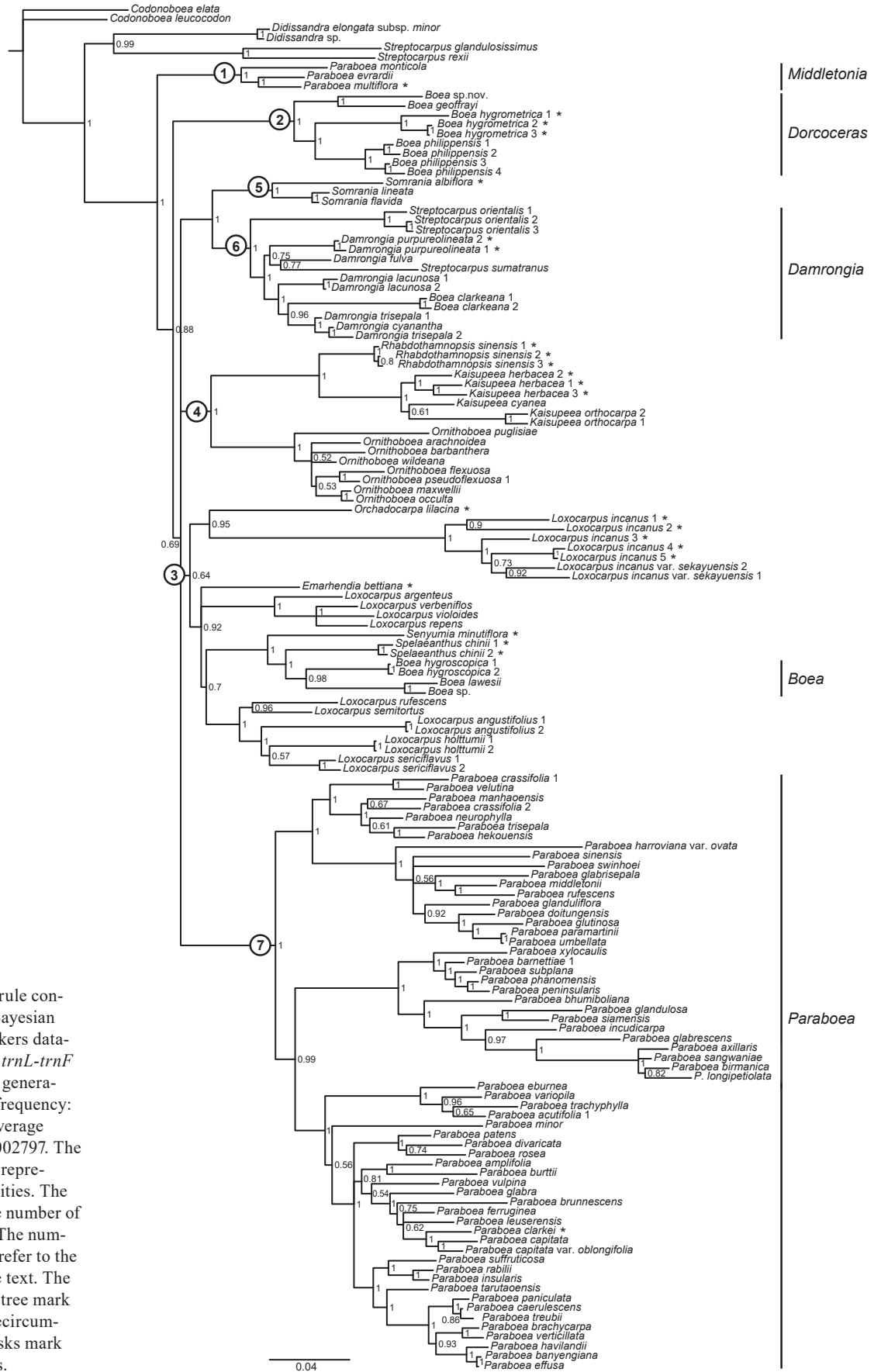
**Generic recircumscription in the Loxocarpinae  
(Gesneriaceae), as inferred by phylogenetic and  
morphological data**

**Carmen Puglisi, Tze Leong Yao, Richard Milne, Michael Möller & David J. Middleton**

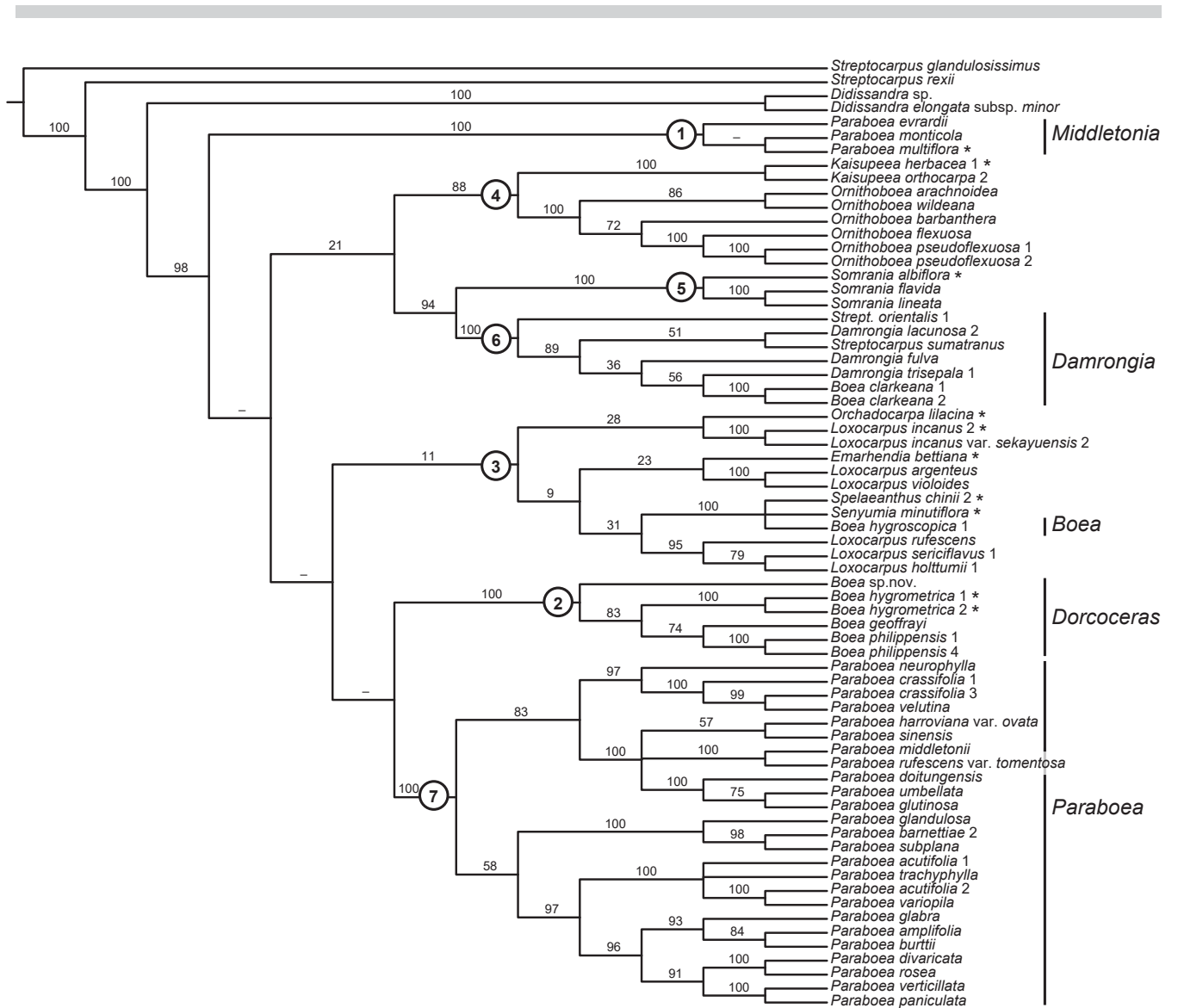
*Taxon* 65: 277–292



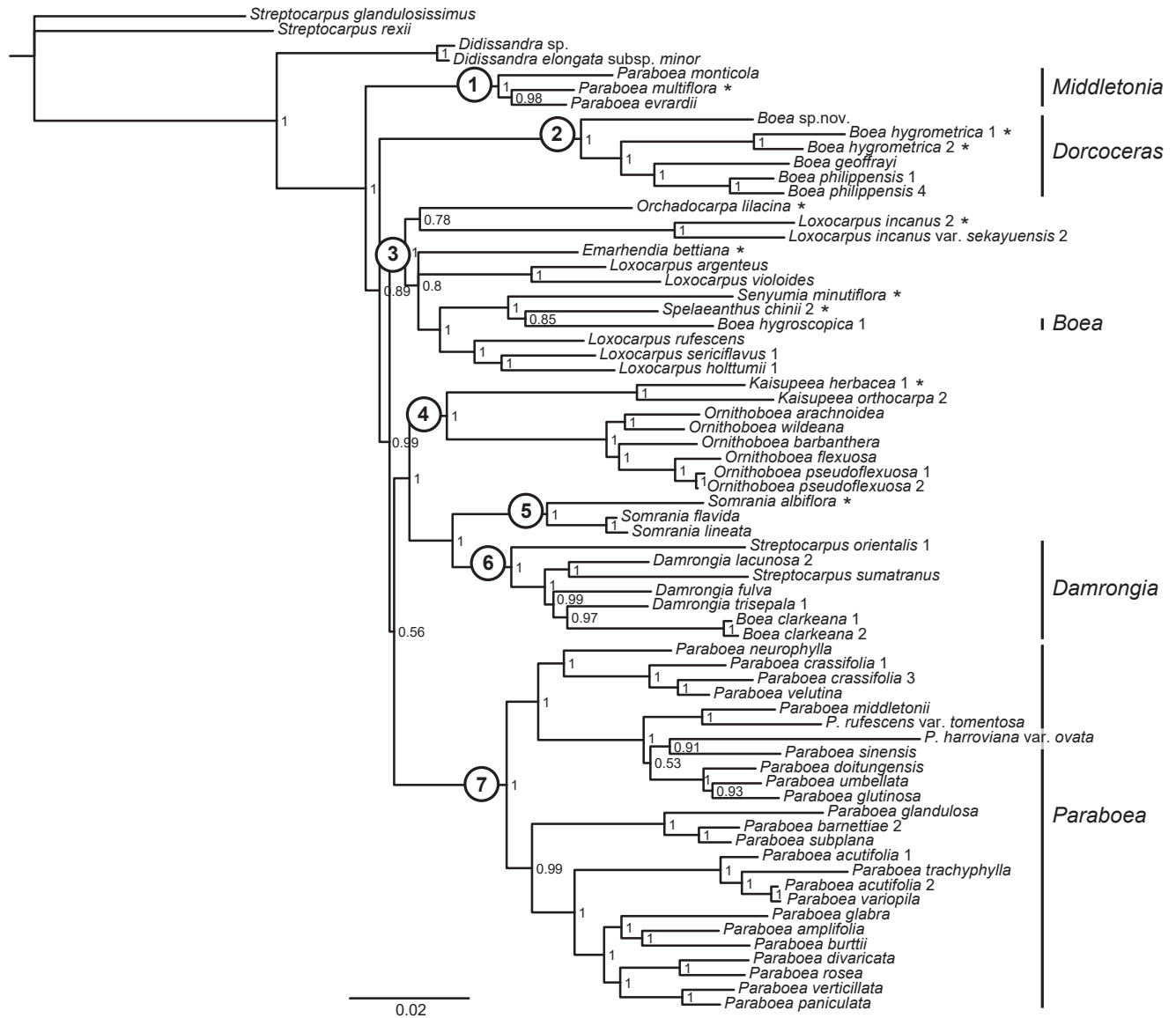
**Fig. S1.** Strict consensus of the six most parsimonious trees based on parsimony analysis of the 2-markers dataset, including ITS and *trnL-trnF* sequences. Tree length = 4049, CI = 0.3779, HI = 0.6221, RI = 0.7310. The numbers inside the circles refer to the clades as treated in the text. The numbers above the branches represent bootstrap values. The bars at the right of the tree mark the placement of the recircumscribed genera. Asterisks mark accessions of the types.



**Fig. S2.** 50% majority-rule consensus tree based on Bayesian inference of the 2-markers dataset, including ITS and *trnL-trnF* sequences. Number of generations: 10 mln, sample frequency: 1000, burn-in: 2000, average standard deviation: 0.002797. The numbers beside nodes represent posterior probabilities. The scalebar represents the number of substitutions per site. The numbers inside the circles refer to the clades as treated in the text. The bars at the right of the tree mark the placement of the recircumscribed genera. Asterisks mark accessions of the types.



**Fig. S3.** Strict consensus of the eight most parsimonious trees based on parsimony analysis of the 3-markers dataset, including ITS, *trnL-trnF* and *ndhF-trnL<sup>UAG</sup>* sequences. Tree length = 4271, CI = 0.5273, HI = 0.4727, RI = 0.6824. The numbers inside the circles refer to the clades as treated in the text. The numbers above the branches represent bootstrap values. The bars at the right of the tree mark the placement of the recircumscribed genera. Asterisks mark accessions of the types.



**Fig. S4.** 50% majority-rule consensus tree based on Bayesian inference of the 3-markers dataset, including ITS, *trnL-trnF* and *ndhF-trnL<sup>UAG</sup>* sequences. Number of generations: 10 mln, sample frequency: 1000, burn-in: 2000, average standard deviation: 0.001572. The numbers beside nodes represent posterior probabilities. The scalebar represents the number of substitutions per site. The numbers inside the circles refer to the clades as treated in the text. The bars at the right of the tree mark the placement of the recircumscribed genera. Asterisks mark accessions of the types.