

Fig. S1. Simultaneous-analysis (excluding *Maytenus abbottii*) parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch.

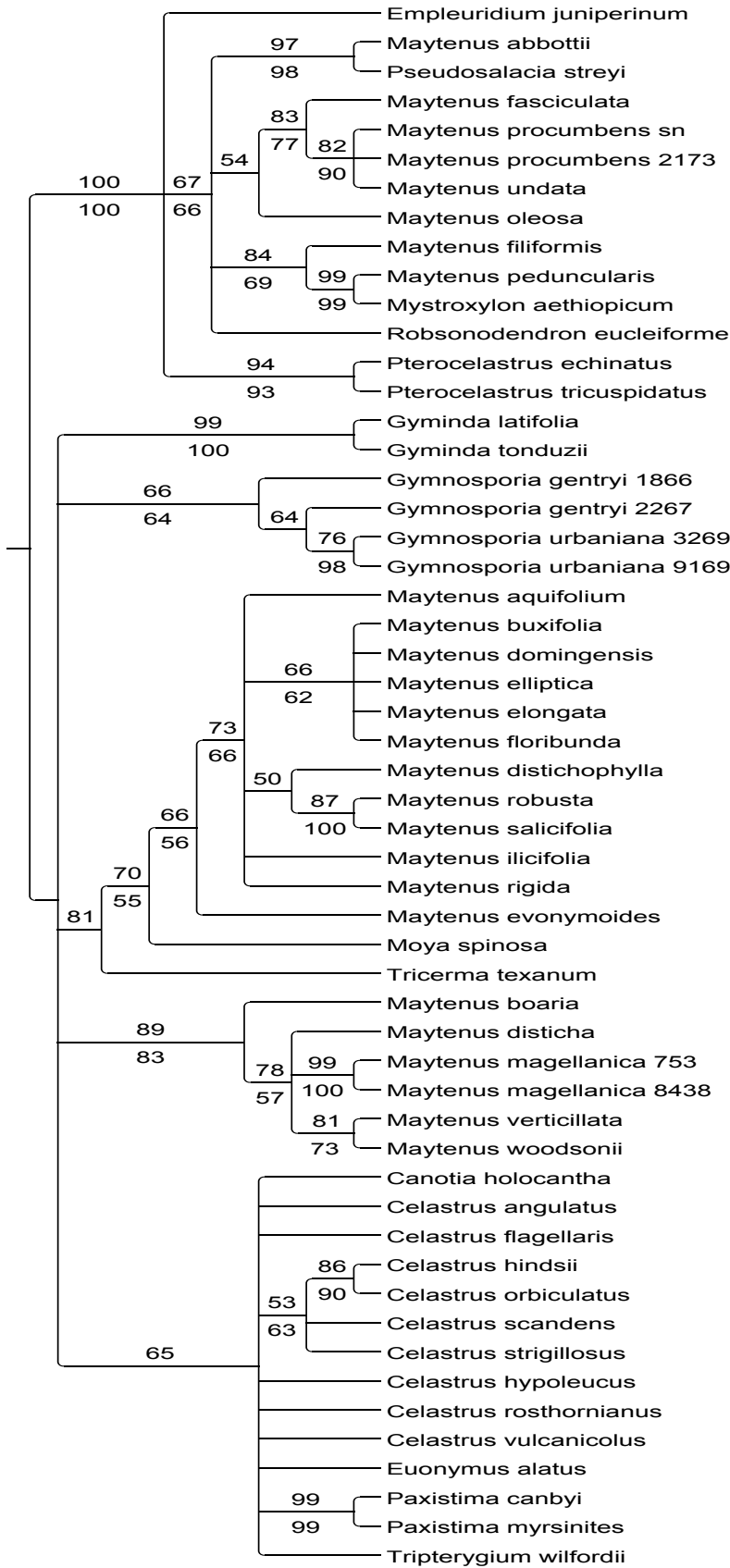


Fig. S2. 26S rDNA parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

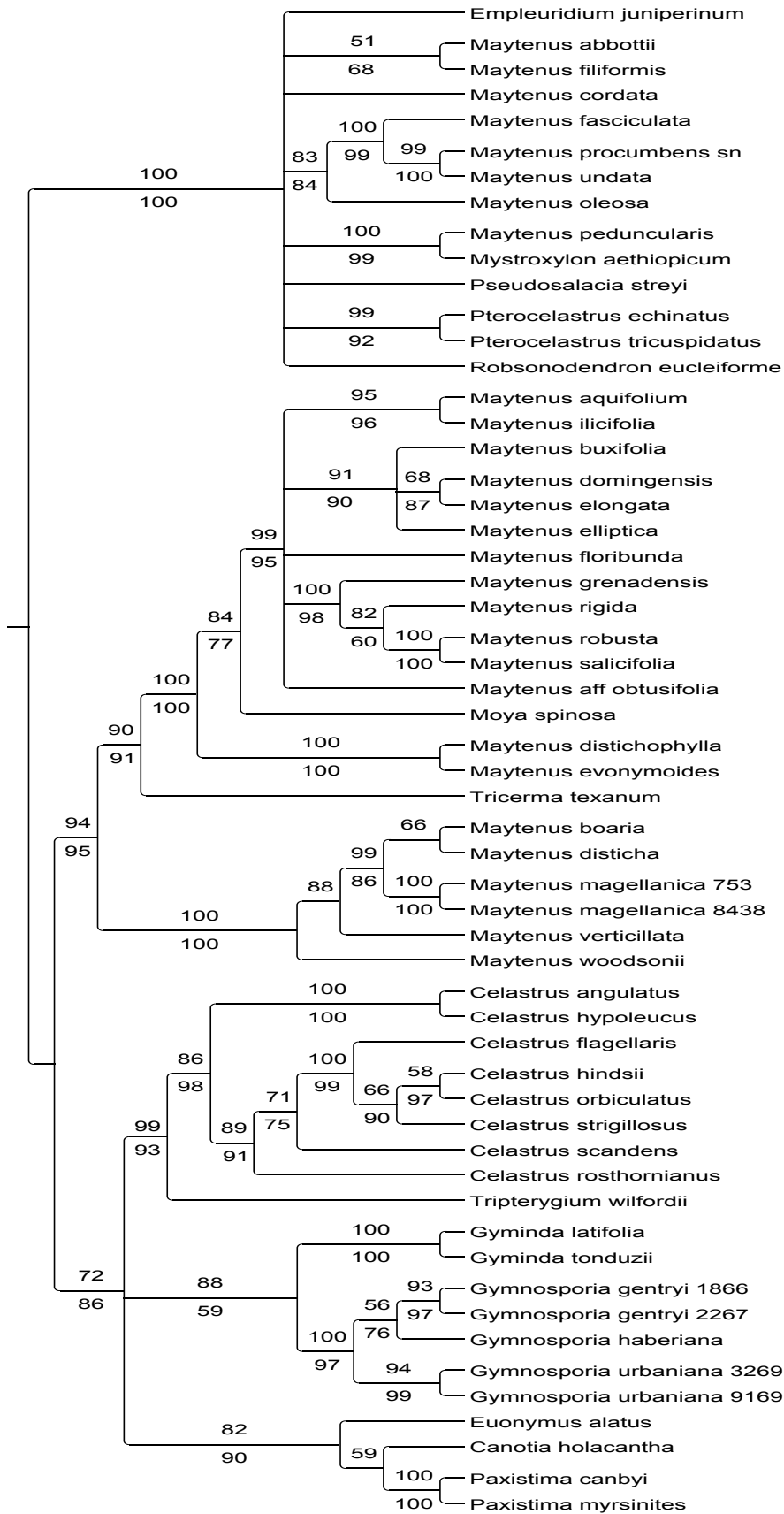


Fig. S3. ITS rDNA parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

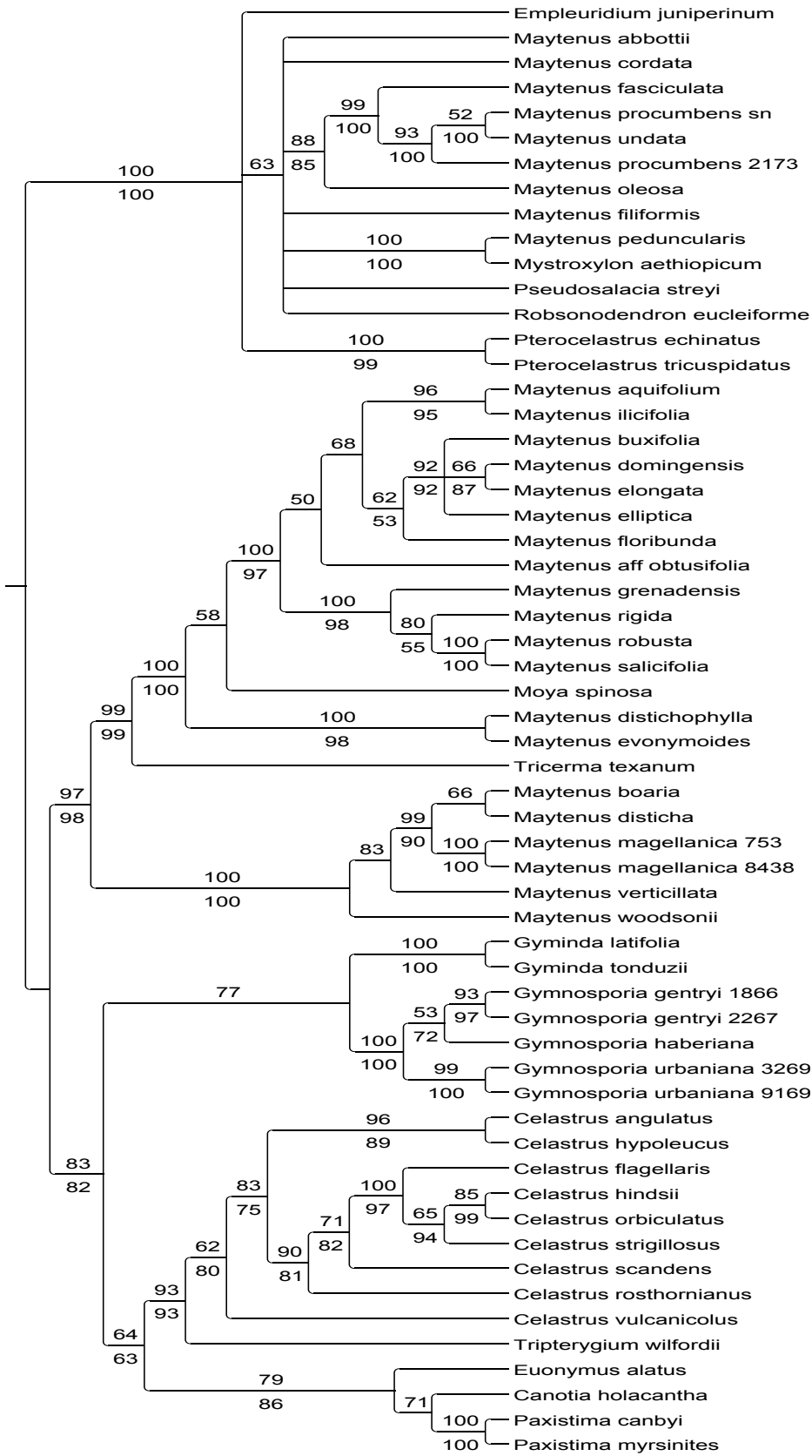


Fig. S4. Combined rDNA parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

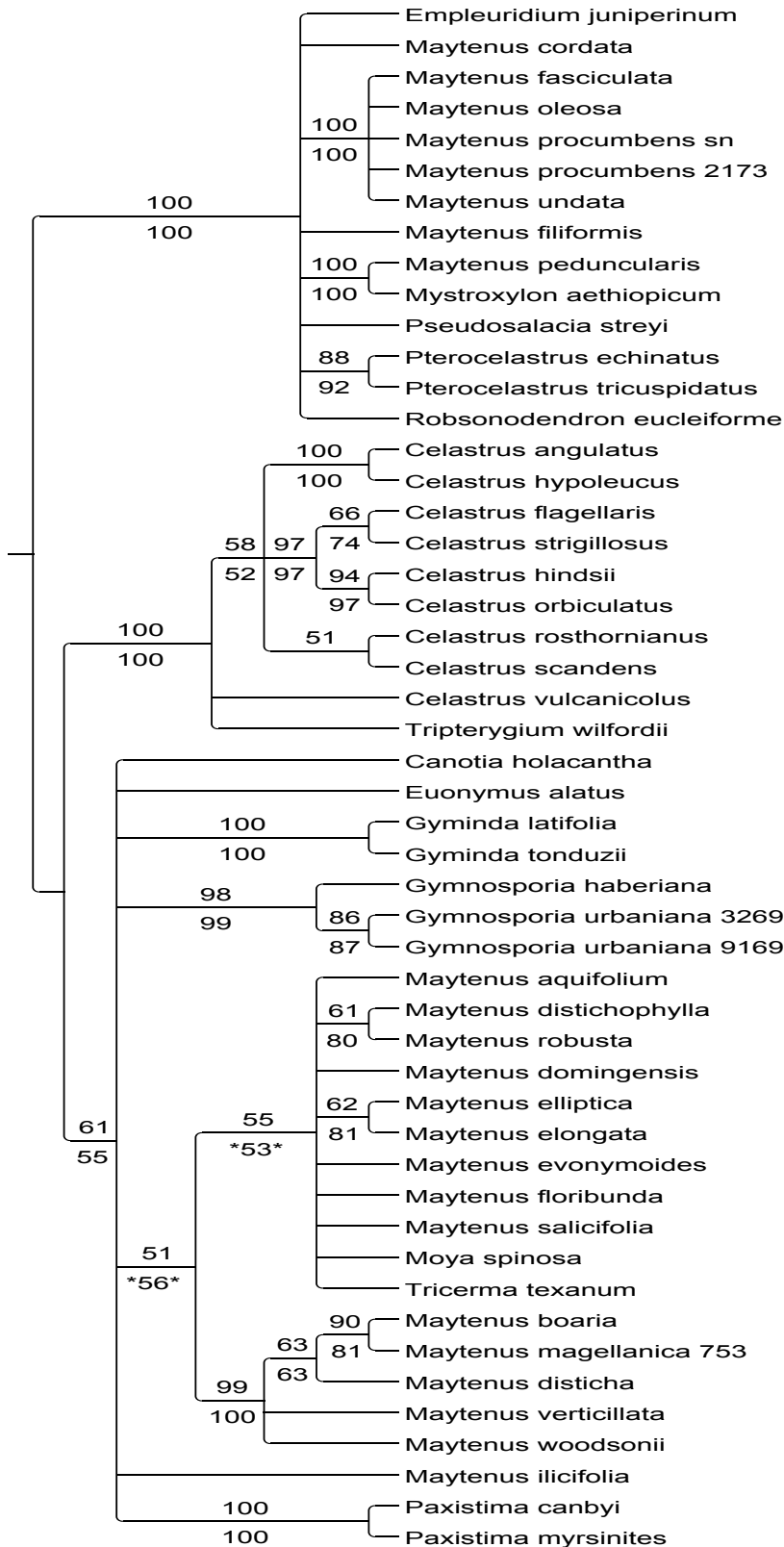


Fig. S5. *matK* parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch. Clades in the parsimony JK tree that were contradicted by clades in the likelihood BS tree are indicated by *XX*, with BS support for the highest contradictory likelihood clade listed.

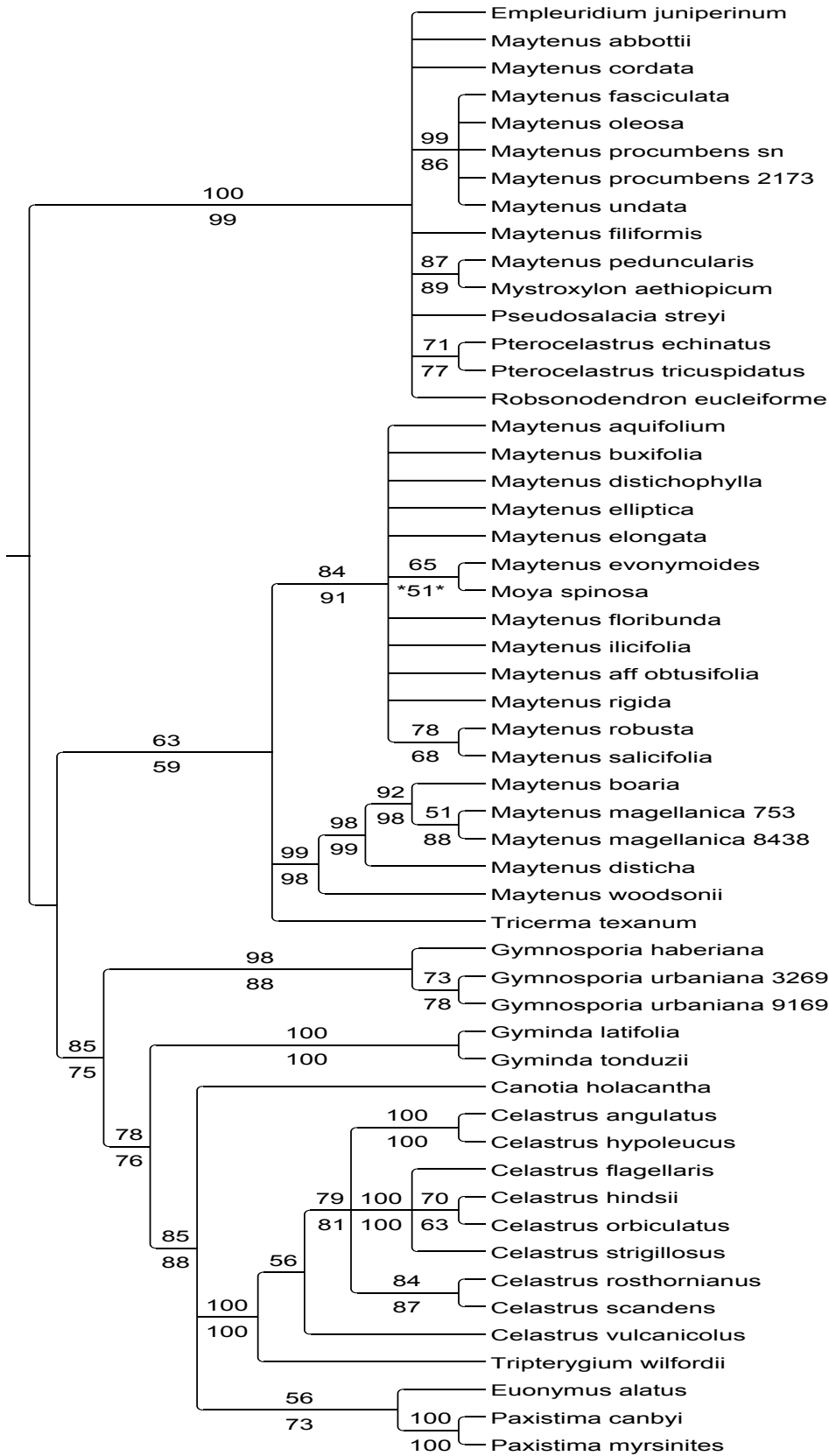


Fig. S6. *trnL-F* parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch. Clades in the parsimony JK tree that were contradicted by clades in the likelihood BS tree are indicated by *XX*, with BS support for the highest contradictory likelihood clade listed.

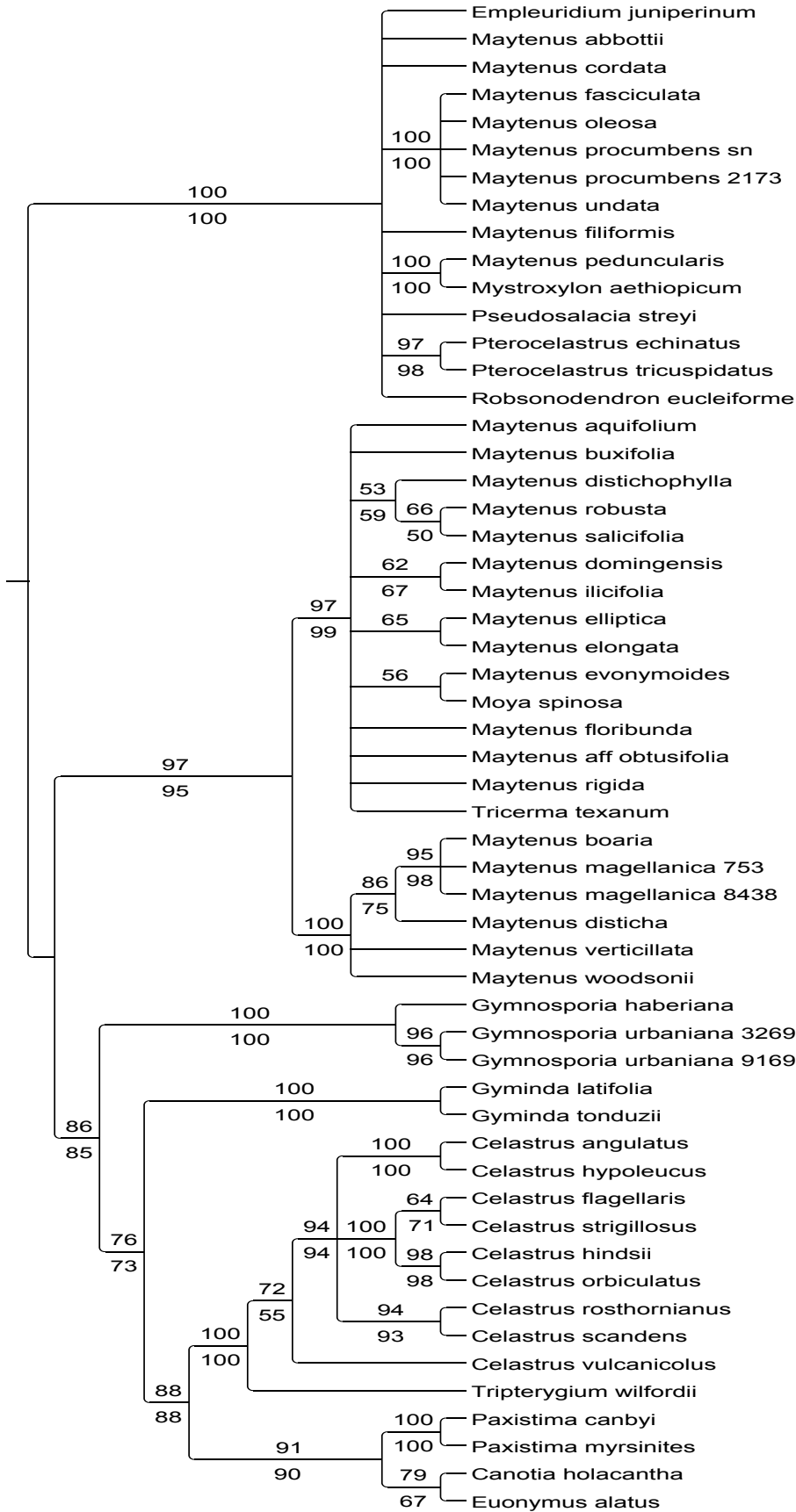


Fig. S7. Plastid parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

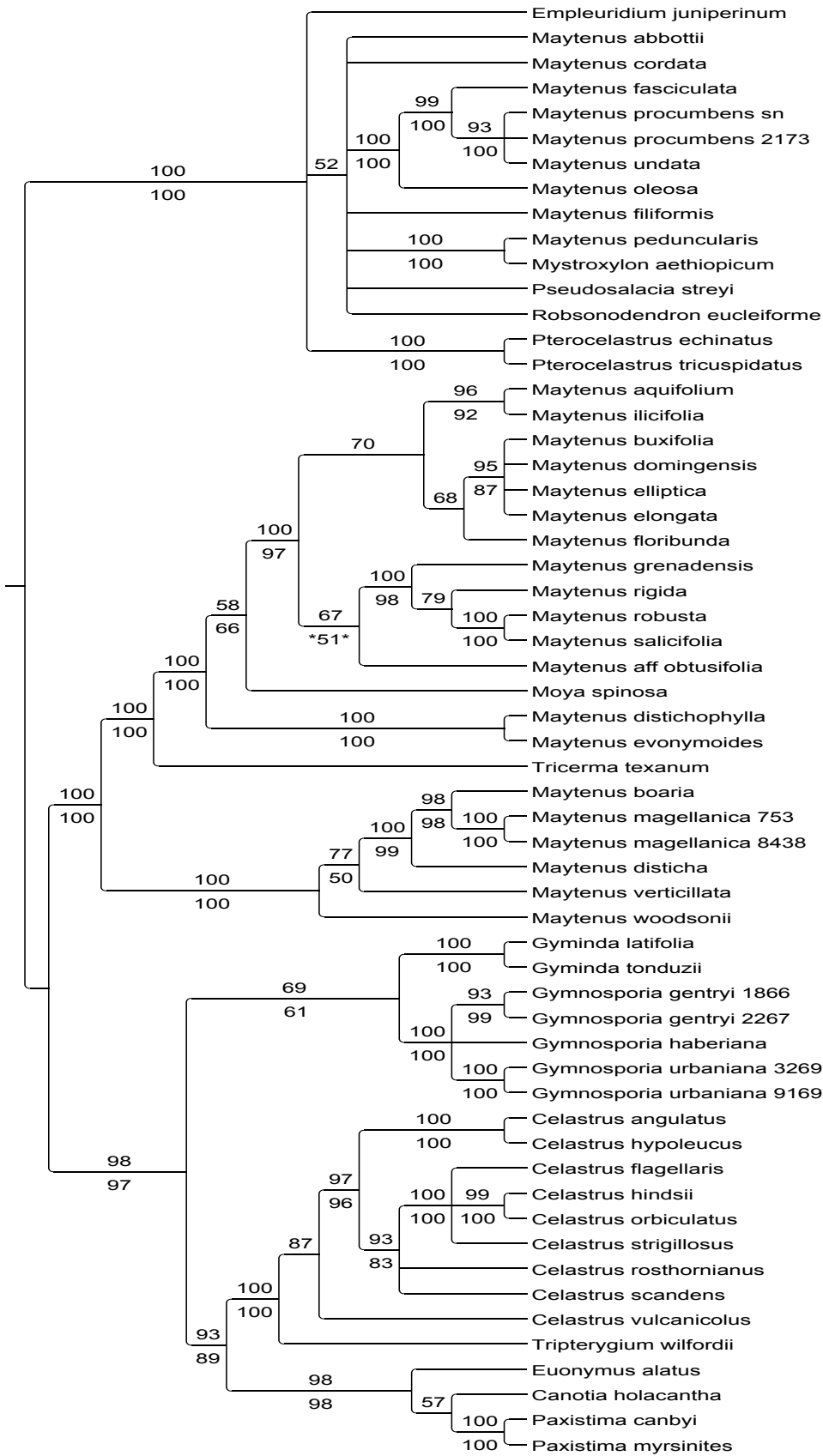


Fig. S8. Combined molecular parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch. Clades in the parsimony JK tree that were contradicted by clades in the likelihood BS tree are indicated by *XX*, with BS support for the highest contradictory likelihood clade listed.

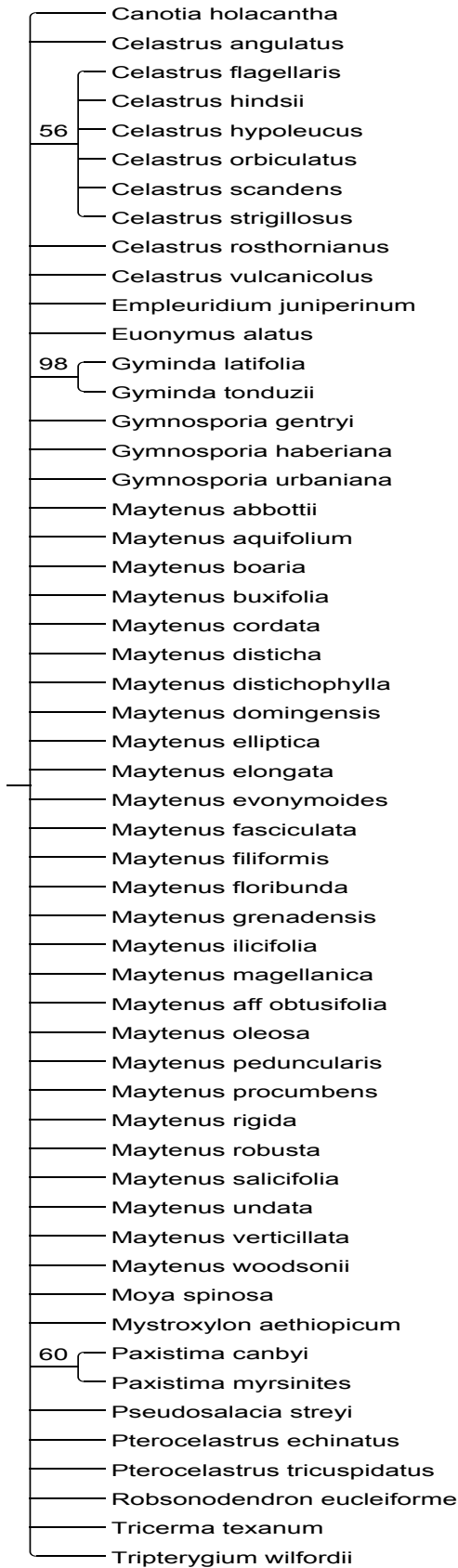


Fig. S9. Morphology parsimony JK tree of the American and African *Maytenus* clades with parsimony JK values $\geq 50\%$ above each branch.

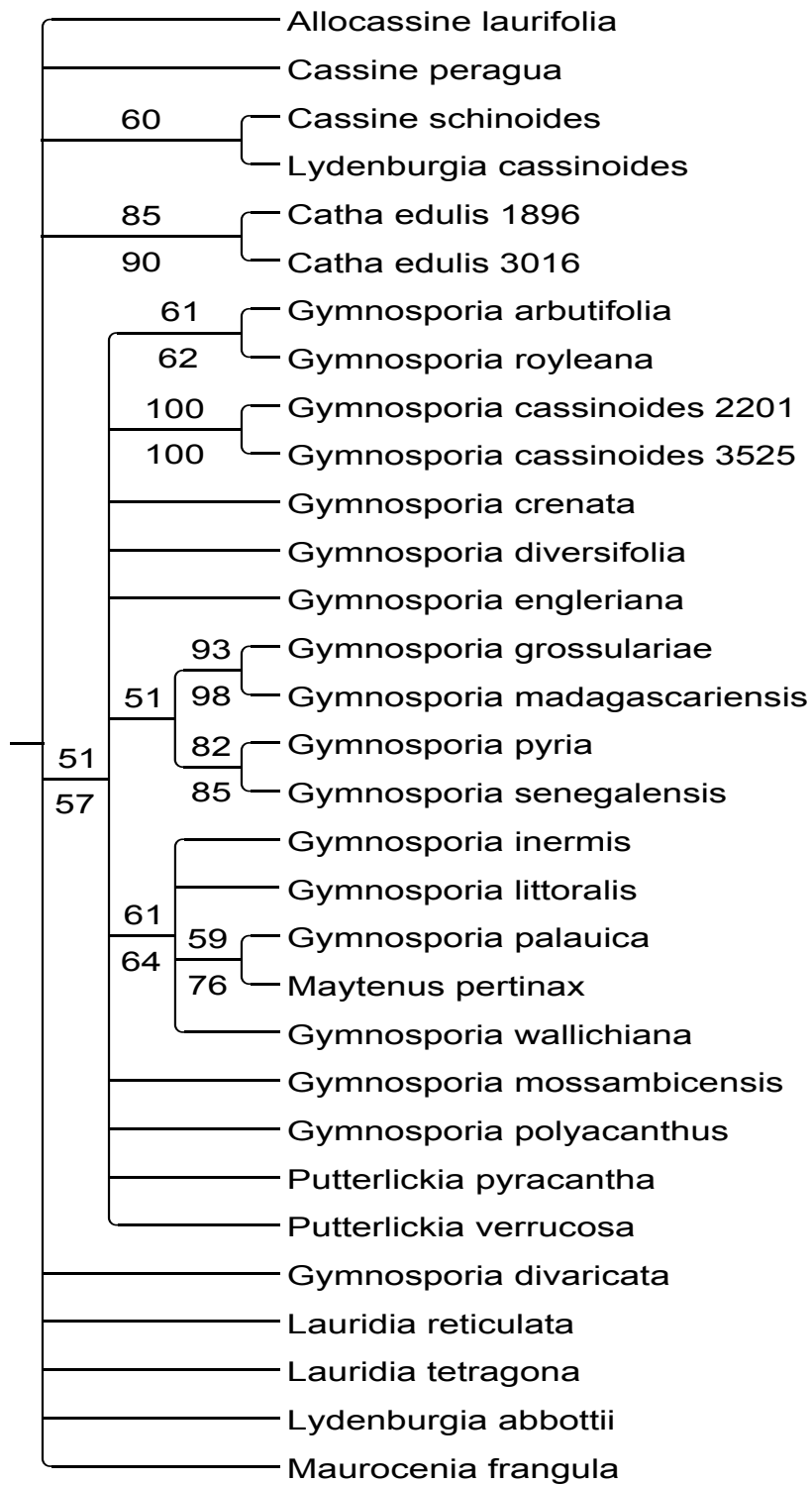


Fig. S10. 26S rDNA parsimony JK tree of the *Gymnosporia* clade with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

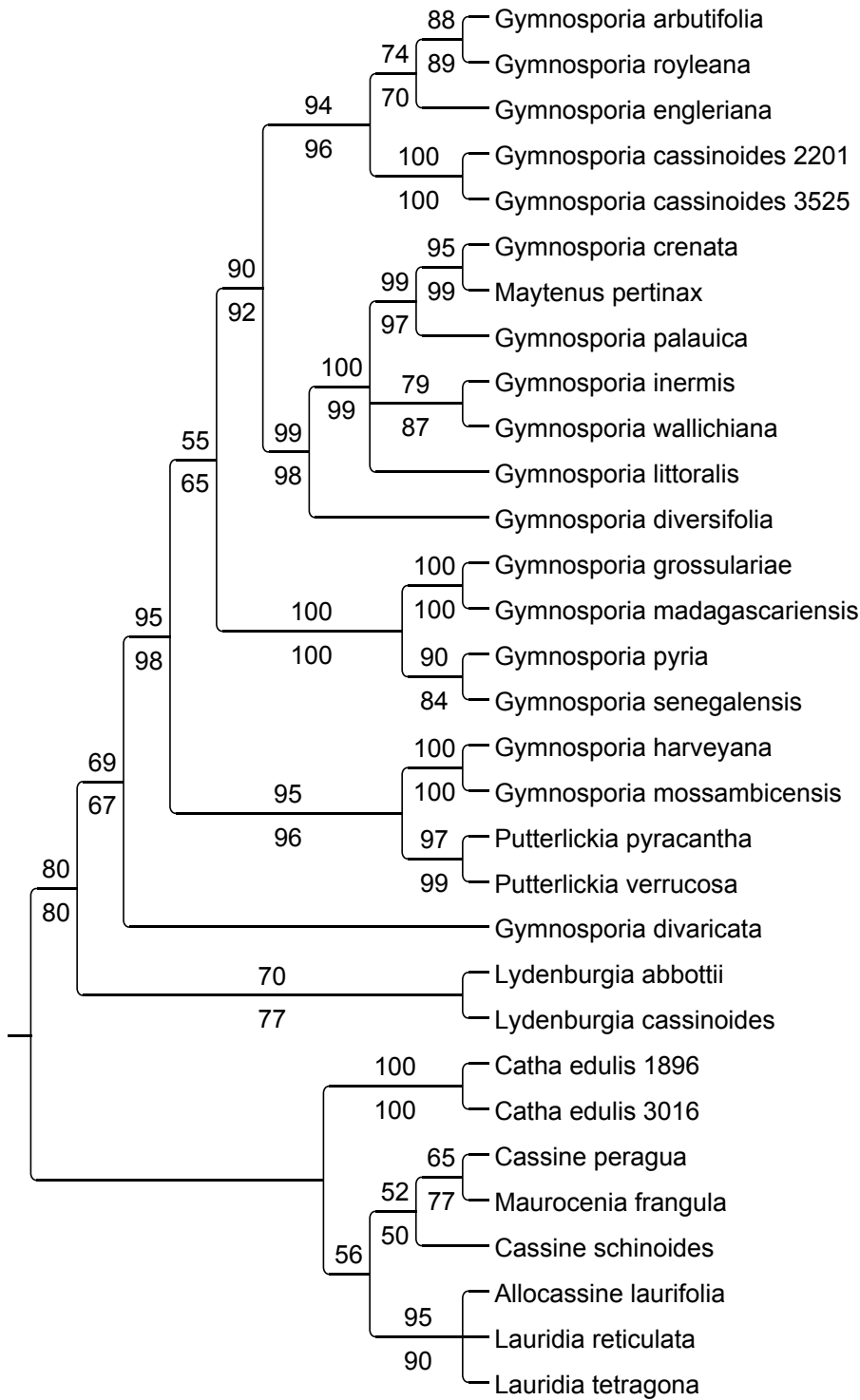


Fig. S11. ITS rDNA parsimony JK tree of the *Gymnosporia* clade with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

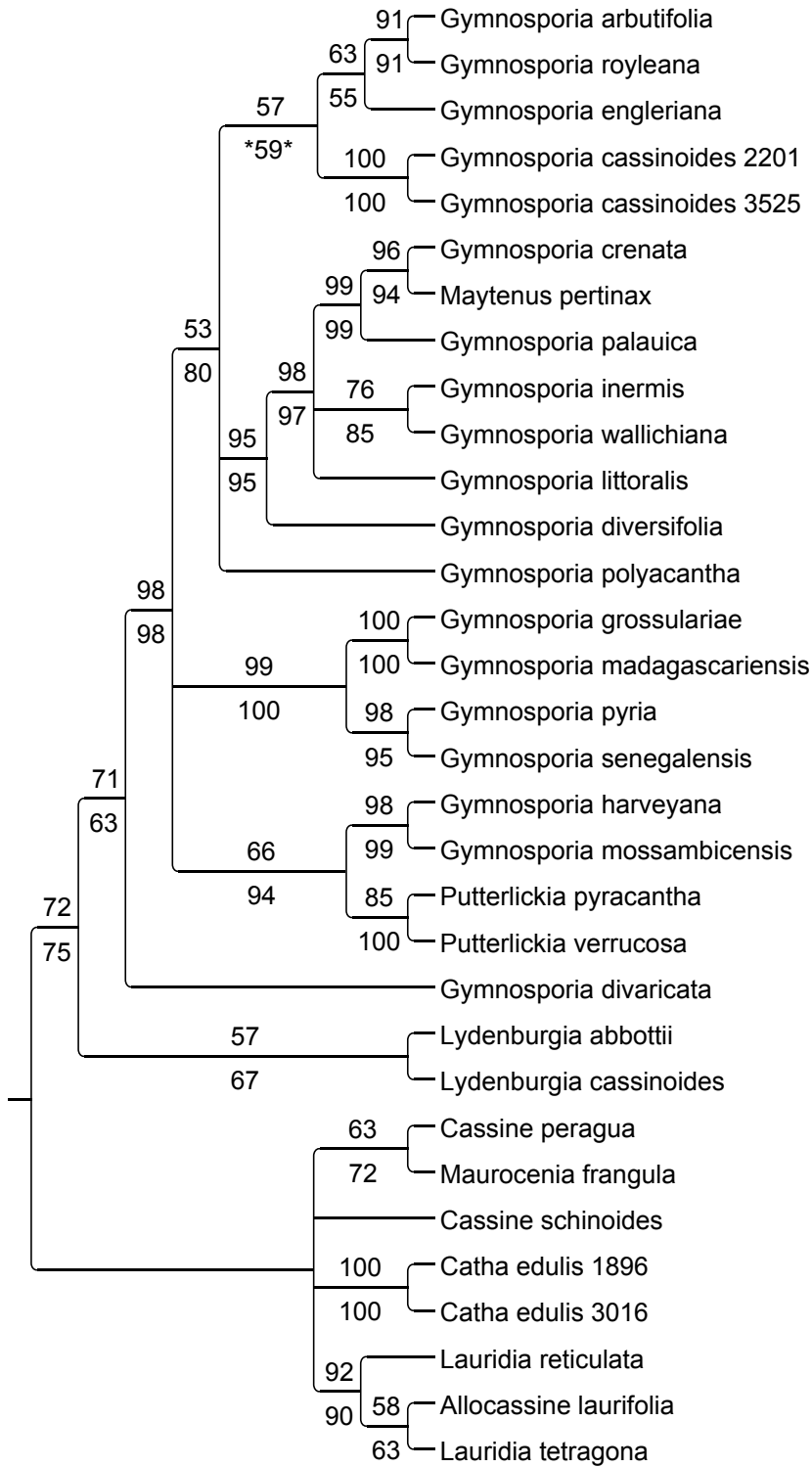


Fig. S12. Combined rDNA parsimony JK tree of the *Gymnosporia* clade with parsimony JK values \geq 50% above each branch, and likelihood BS values \geq 50% below each branch. Clades in the parsimony JK tree that were contradicted by clades in the likelihood BS tree are indicated by *XX*, with BS support for the highest contradictory likelihood clade listed.

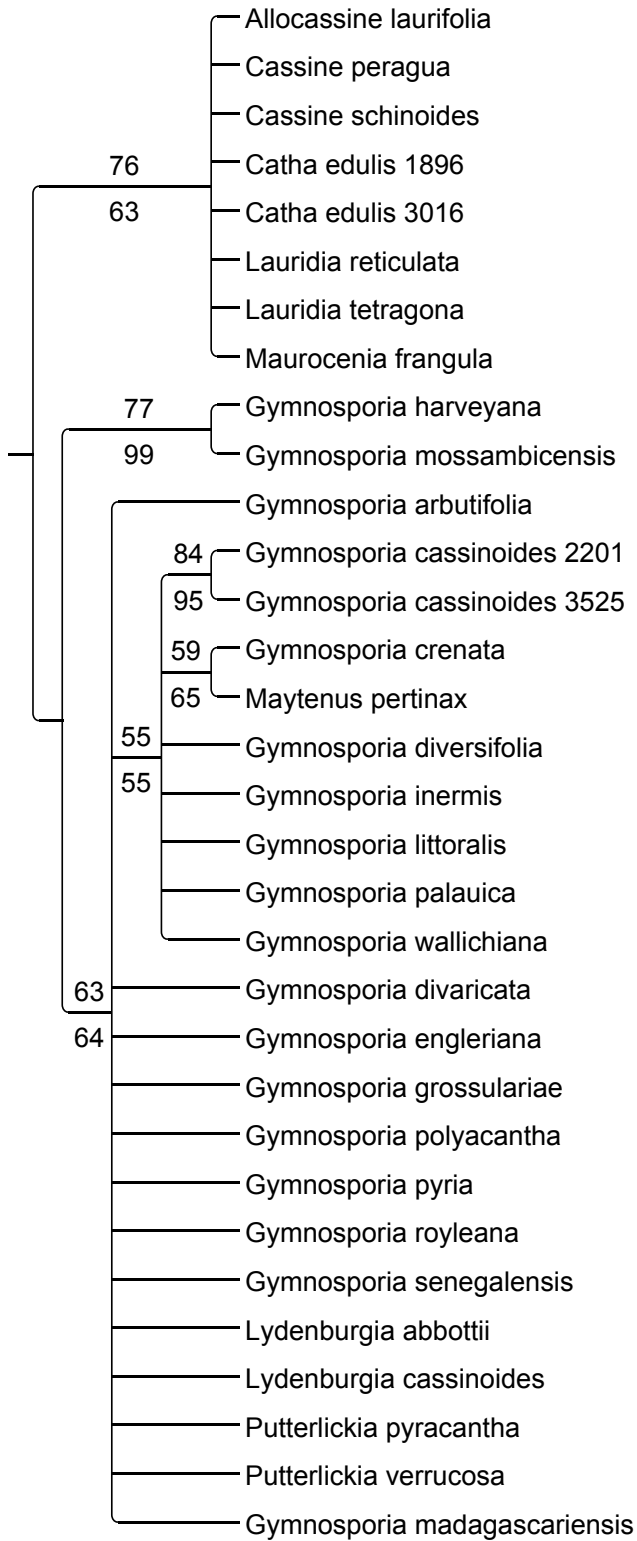


Fig. S13. *matK* parsimony JK tree of the *Gymnosporia* clade with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

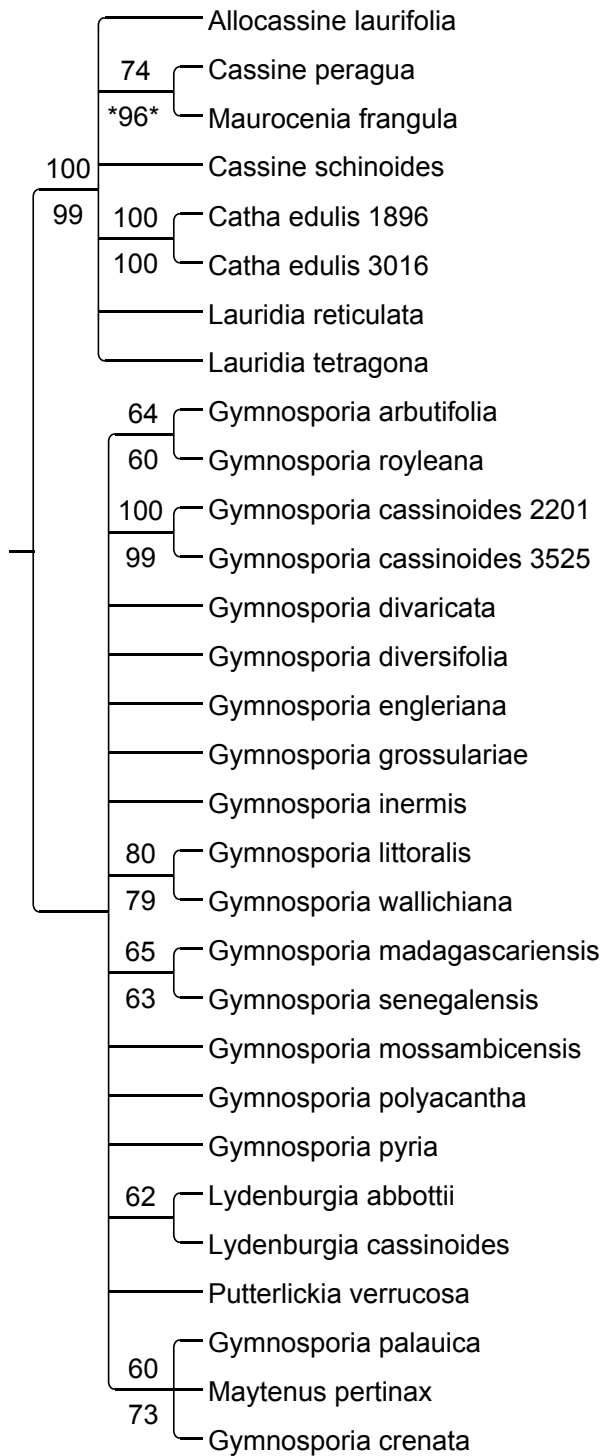


Fig. S14. *trnL-F* parsimony JK tree of the *Gymnosporia* clade with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch. Clades in the parsimony JK tree that were contradicted by clades in the likelihood BS tree are indicated by *XX*, with BS support for the highest contradictory likelihood clade listed.

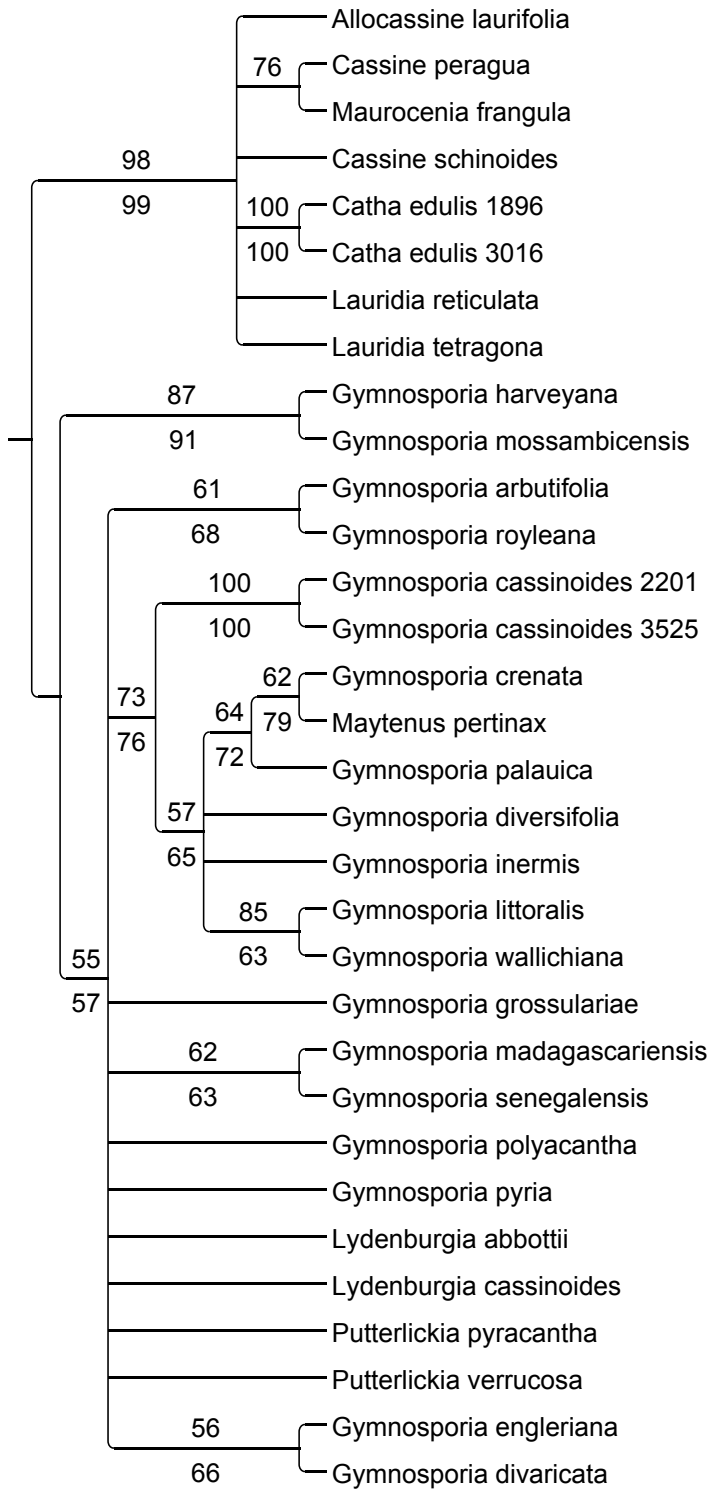


Fig. S15. Plastid parsimony JK tree of the *Gymnosporia* clade with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

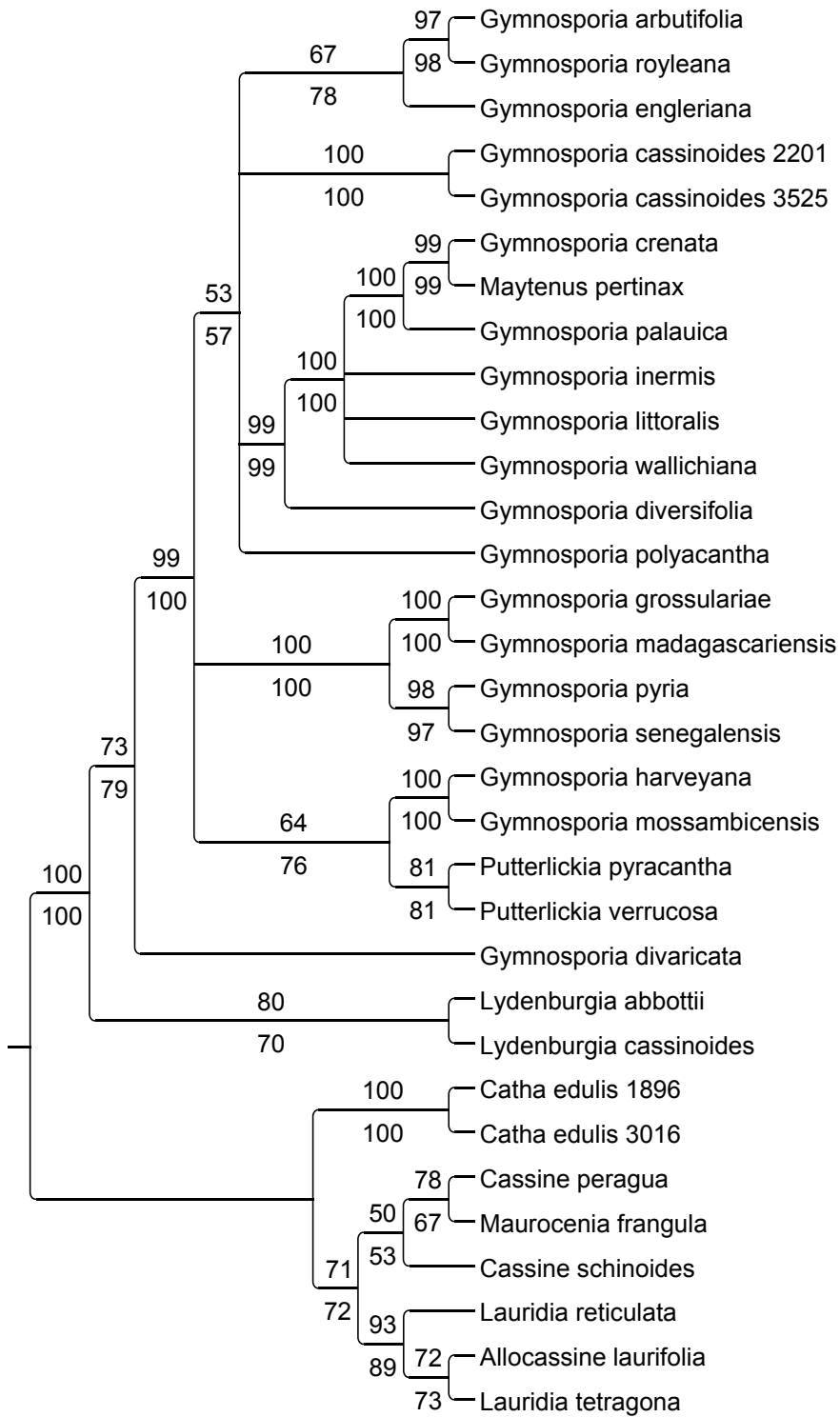


Fig. S16. Combined molecular parsimony JK tree of the *Gymnosporia* clade with parsimony JK values $\geq 50\%$ above each branch, and likelihood BS values $\geq 50\%$ below each branch.

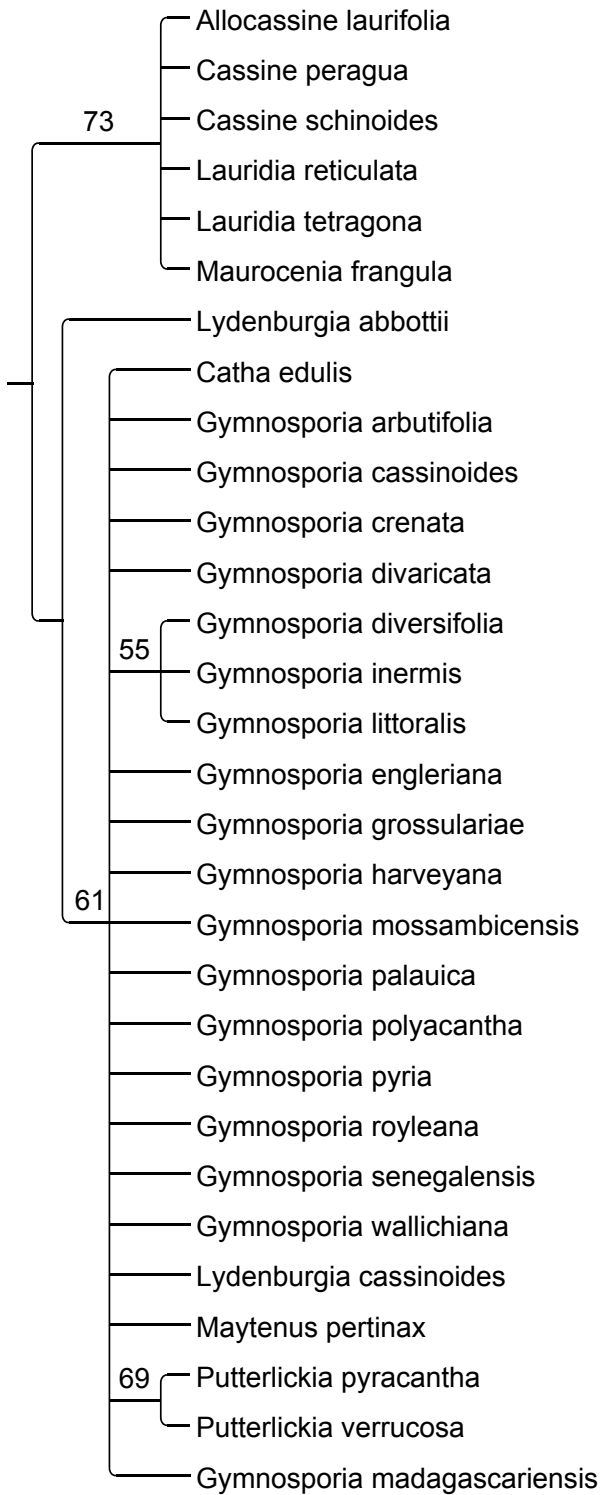


Fig. S17. Morphology parsimony JK tree of the *Gymnosporia* clade with parsimony JK values $\geq 50\%$ above each branch.

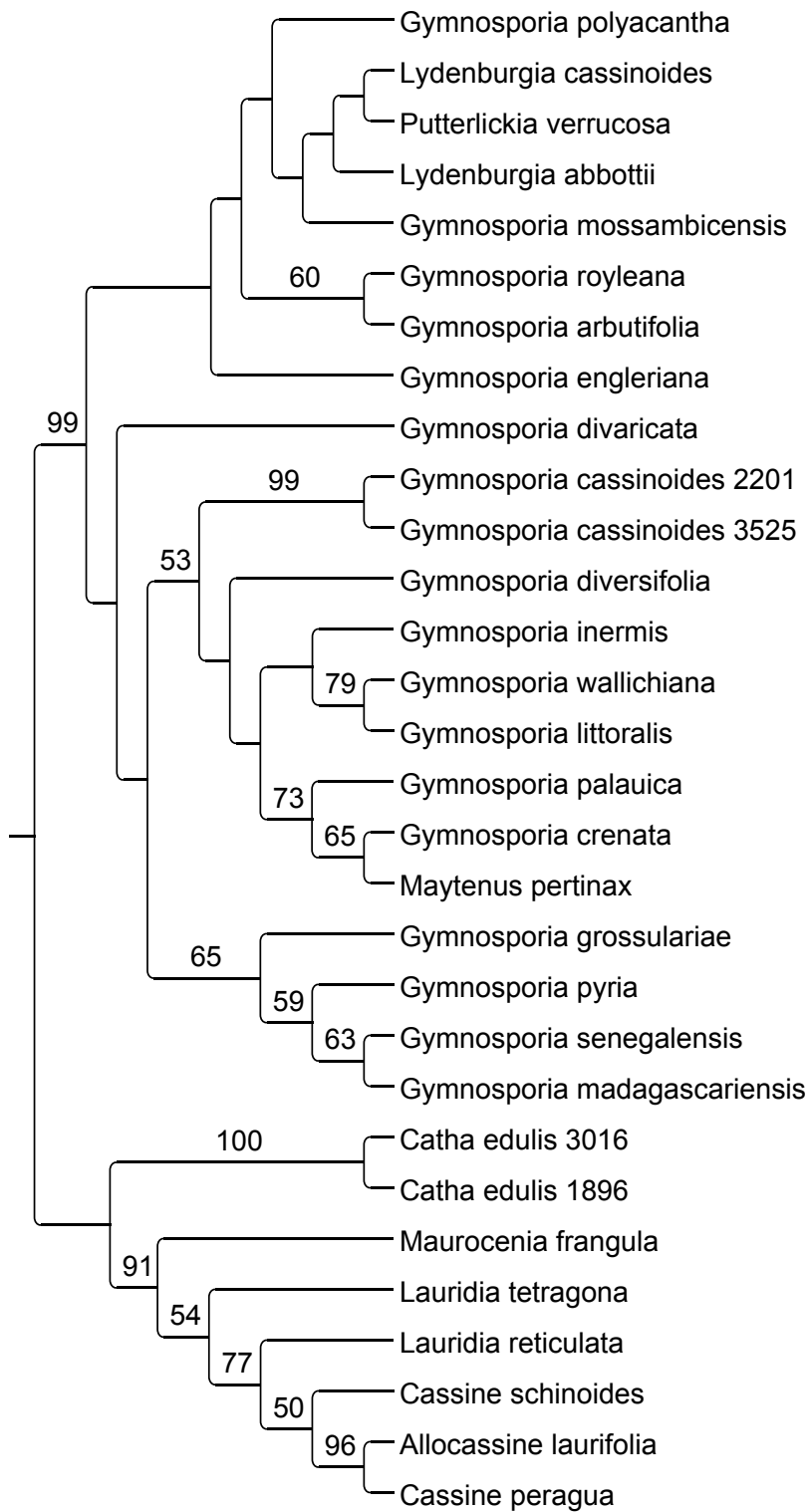


Fig. S18. The most optimal tree found by RAxML for *trnL-F* of the *Gymnosporia* clade with likelihood BS values $\geq 50\%$ above each branch.

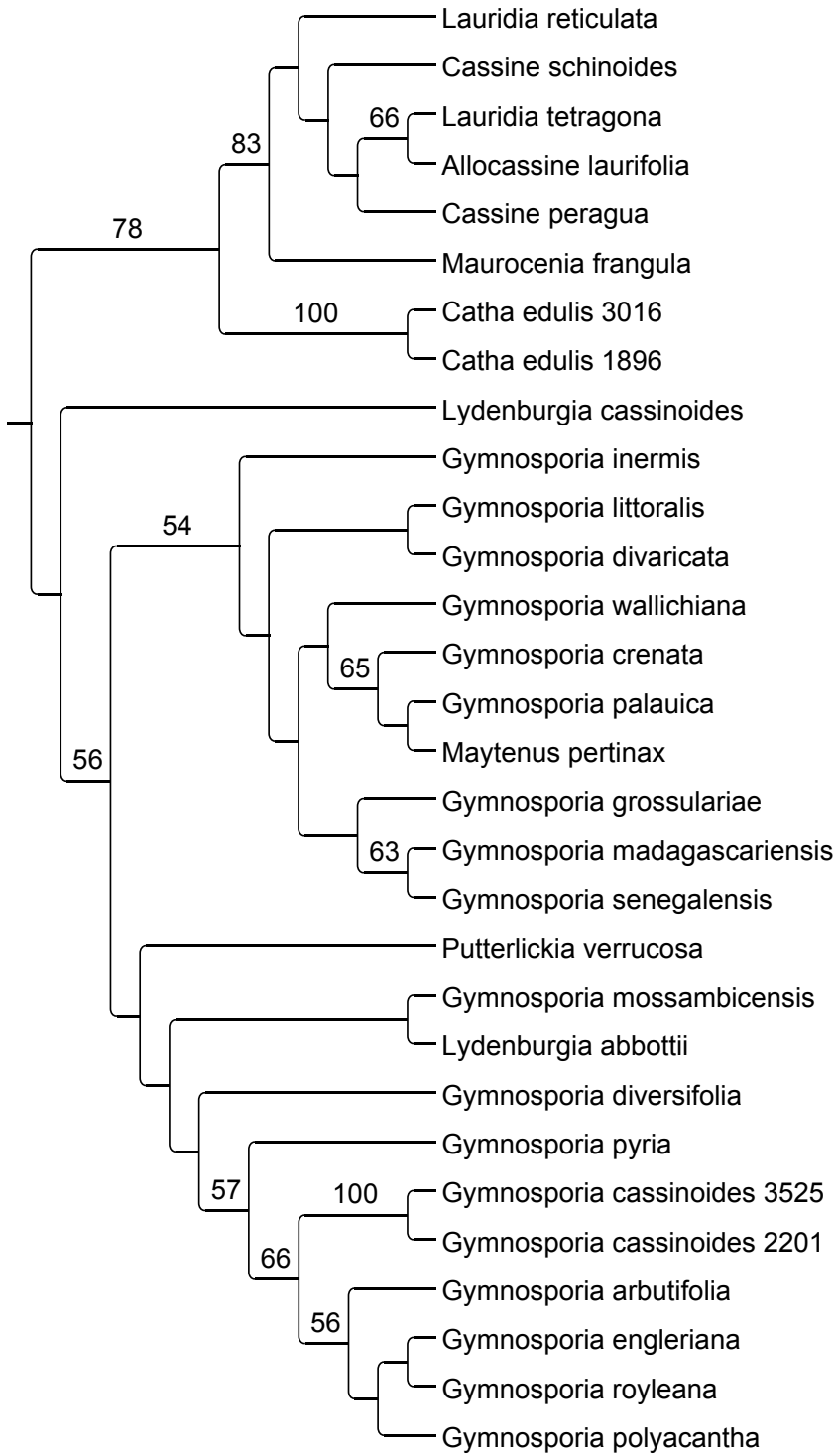


Fig. S19. The most optimal tree found by RAxML for the *trnL* intron of the *Gymnosporia* clade with likelihood BS values $\geq 50\%$ above each branch.

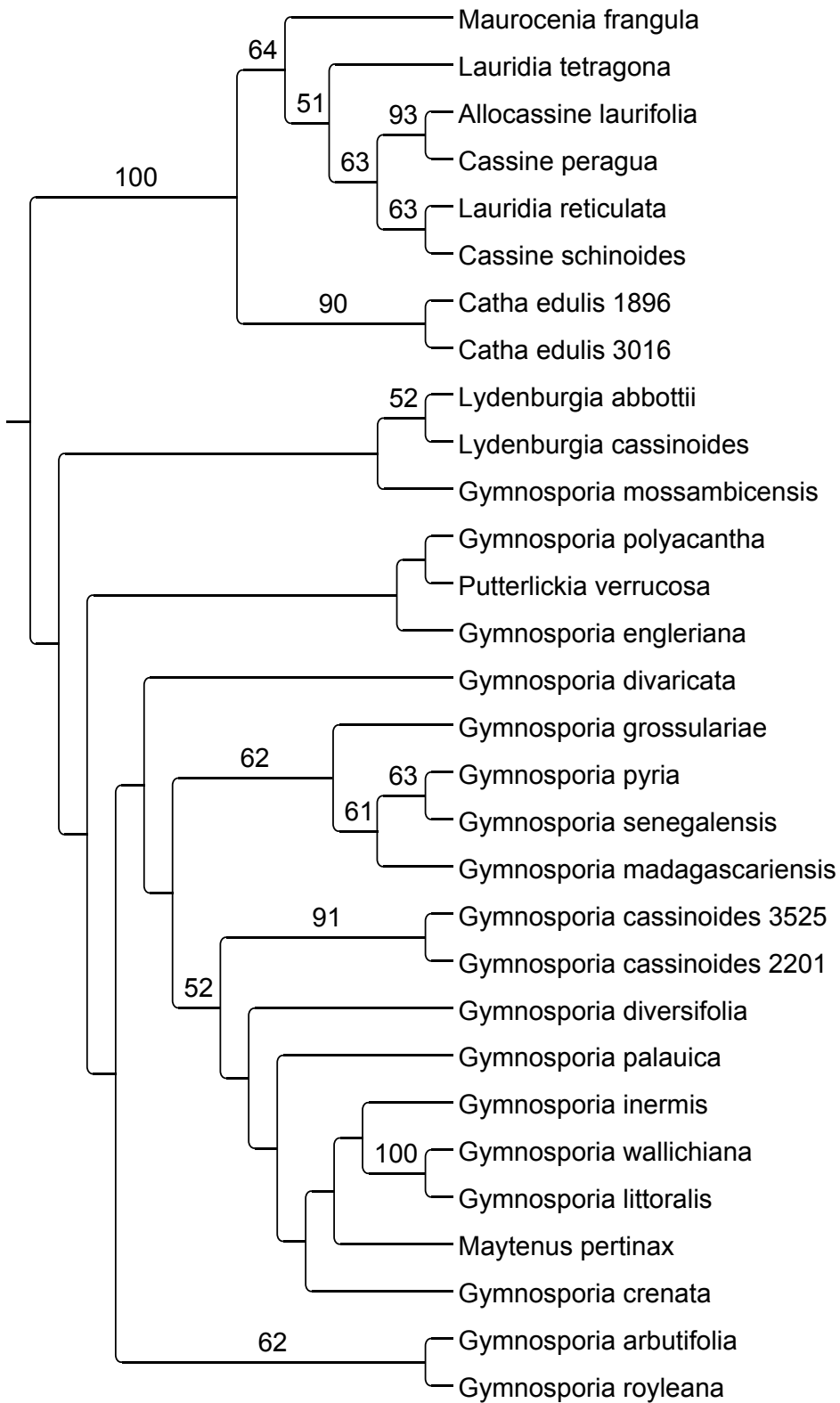


Fig. S20. The most optimal tree found by RAxML for the *trnL-F* intergenic spacer of the *Gymnosporia* clade with likelihood BS values $\geq 50\%$ above each branch.