

Supplementary material:

FIG. S1. Photos of *Maytenus megalocarpa* Groppo & Lombardi. All photos taken in type locality (Bahia: Ilhéus, Rodovia Itabuna-Ilhéus, área do CEPLAC (Comissão Executiva do Plano da Lavoura Cacaueira), Arboretum at Quadra I). A. Three individuals. B. Trunk. C. Wood. D. Leaves. E. Flowers. F. Seedling with cotyledons. G. Branch with immature fruits. H. Fruits on a tree. I and J. Fruits fallen to the ground. Photos by M.G., except C, E, and H by J.L.

FIG. S2. 26S rDNA parsimony strict consensus tree with jackknife values $\geq 50\%$ above each branch.

FIG. S3. ITS parsimony strict consensus tree with jackknife values $\geq 50\%$ above each branch.

FIG. S4. rDNA (26S + ITS) parsimony strict consensus tree with jackknife values $\geq 50\%$ above each branch.

FIG. S5. *matK* parsimony strict consensus tree with jackknife values $\geq 50\%$ above each branch. Lack of gene-tree resolution is caused by *Maytenus ilicifolia*, *Plenckia populnea* 8611, and *P. populnea* 12780 sequences lacking the 5' end of the gene and *M. magellanica* 753 and *M. verticillata* sequences lacking the 3' end of the gene. There is as little as 30-bp overlap between these five sequences.

FIG. S6. *matK* parsimony strict consensus tree after exclusion of four terminals (*Maytenus magellanica* 753, *M. verticillata*, *Plenckia populnea* 8611, *P. populnea* 12780) with jackknife values $\geq 50\%$ above each branch.

FIG. S7. *trnL-F* parsimony strict consensus tree with jackknife values $\geq 50\%$ above each branch. Lack of gene-tree resolution in the upper clade of *Maytenus* is caused by differential sampling of some terminals for the *trnL* intron or the *trnL-F* intergenic spacer.

FIG. S8. Plastid (*matK* + *trnL-F*) parsimony strict consensus tree with jackknife values $\geq 50\%$ above each branch. Lack of resolution is caused by differential sampling of some terminals for part or all of *matK* and/or *trnL-F*.

FIG. S9. Plastid (*matK* + *trnL-F*) parsimony strict consensus tree after exclusion of four terminals (*Plenckia populnea* 8611 and *P. populnea* 12780, which are only sampled for the 3' end of *matK*; *Maytenus* aff. *obtusifolia* and *M. rigida*, which are only sampled for the *trnL-F* intergenic spacer) with jackknife values $\geq 50\%$ above each branch.

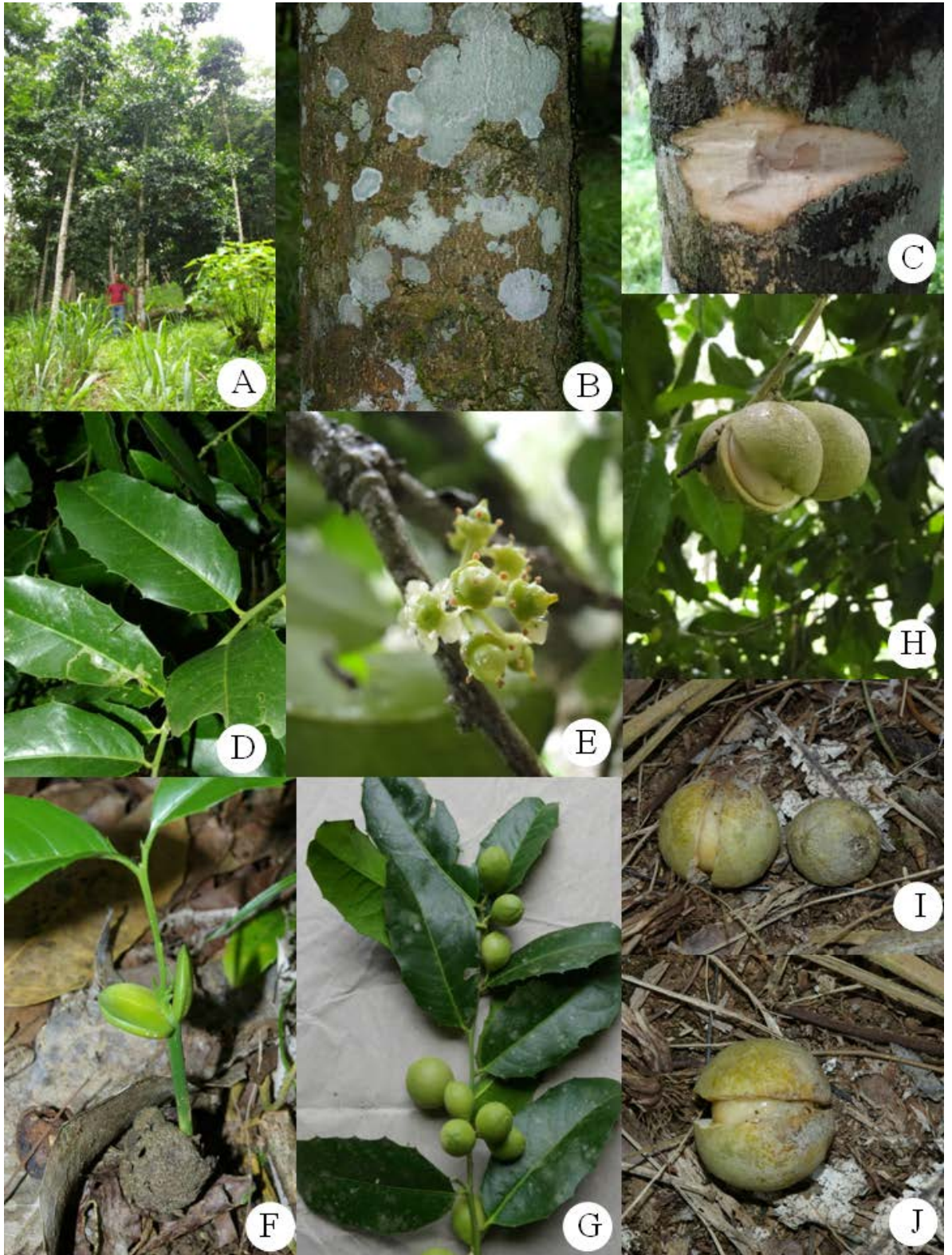


FIG. S1.

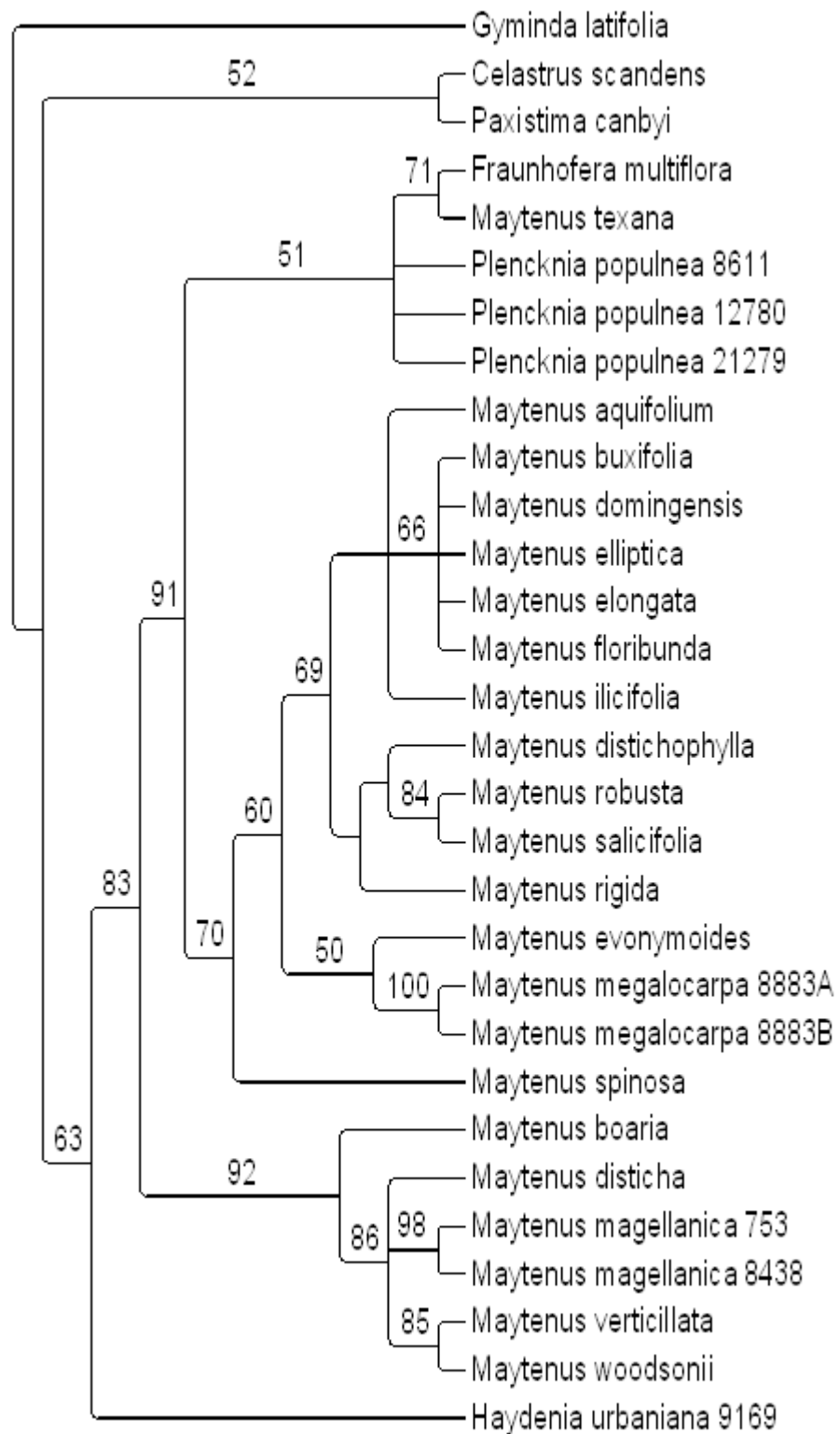


FIG. S2.

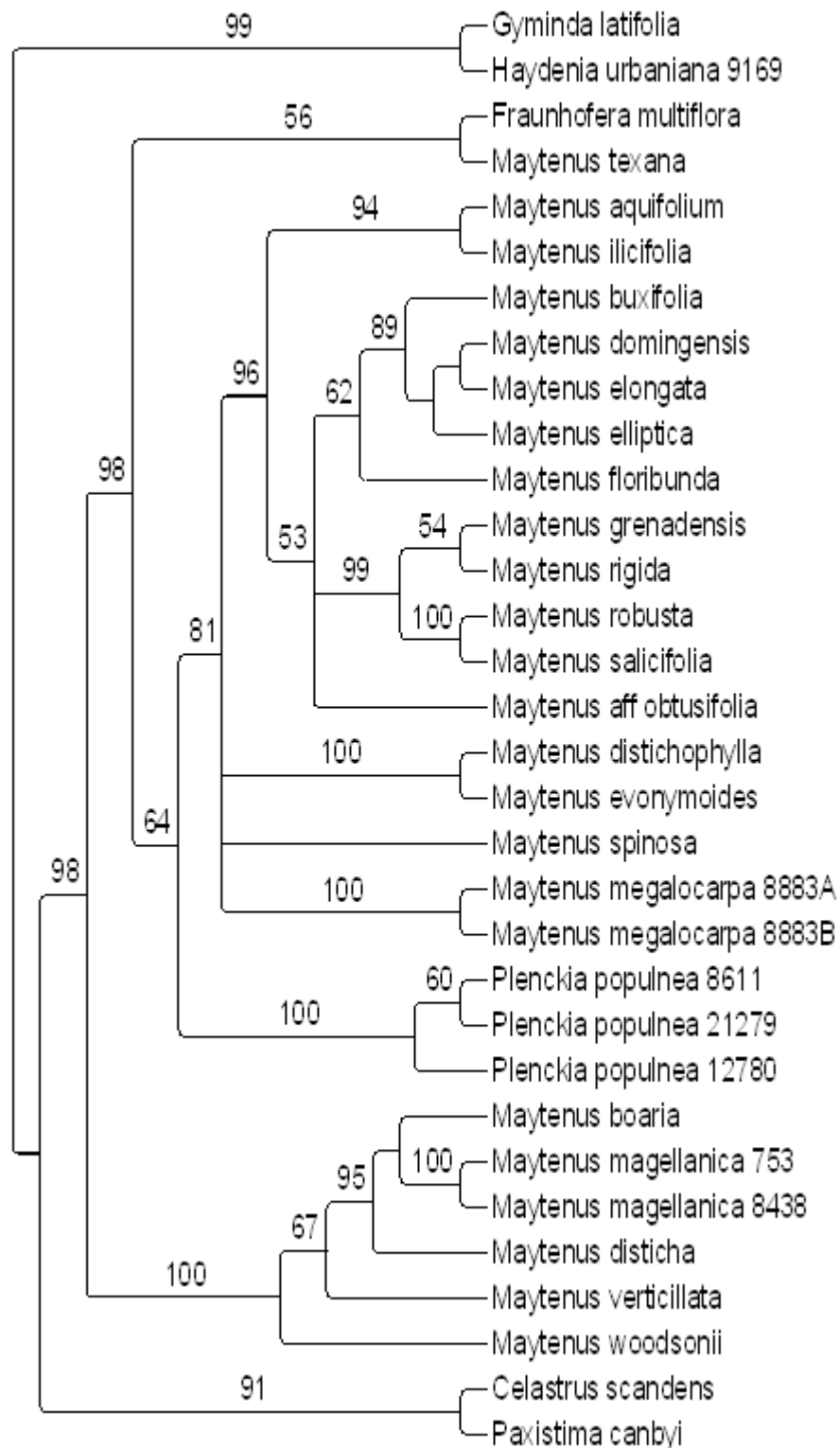


FIG. S3.

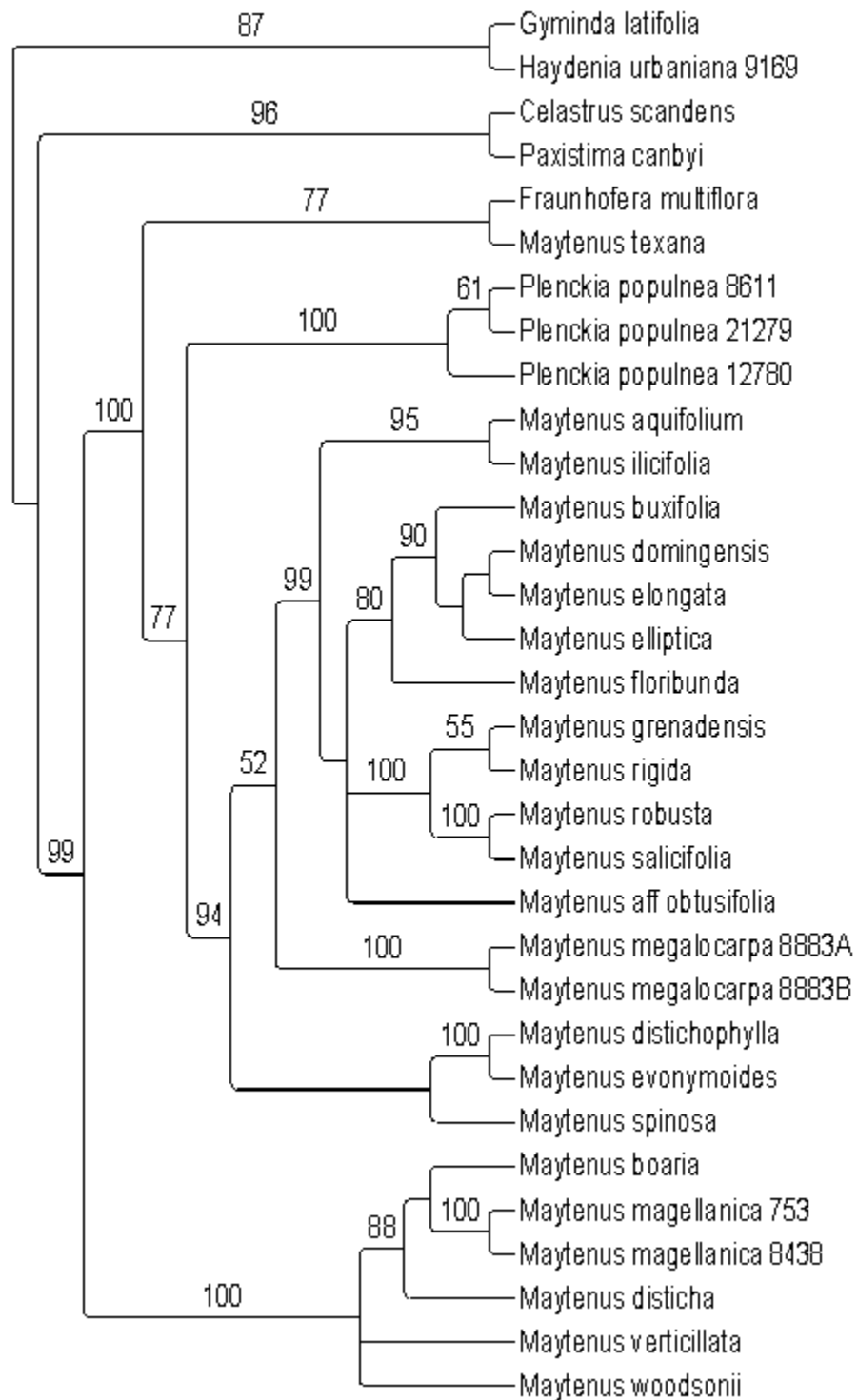


FIG. S4.

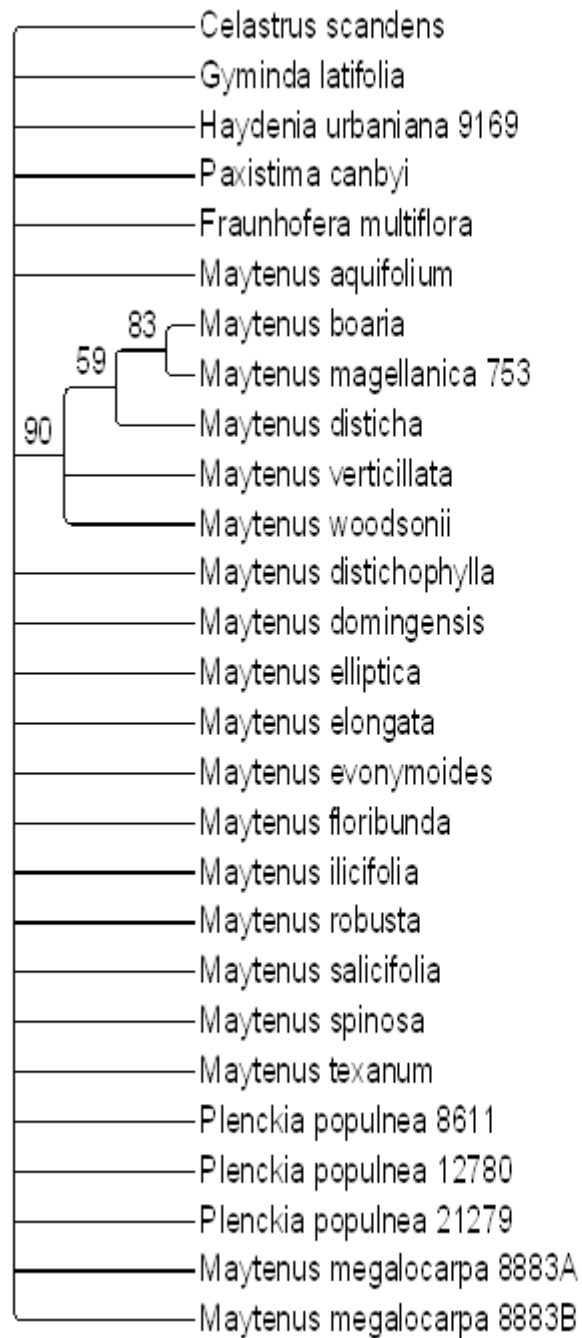


FIG. S5.

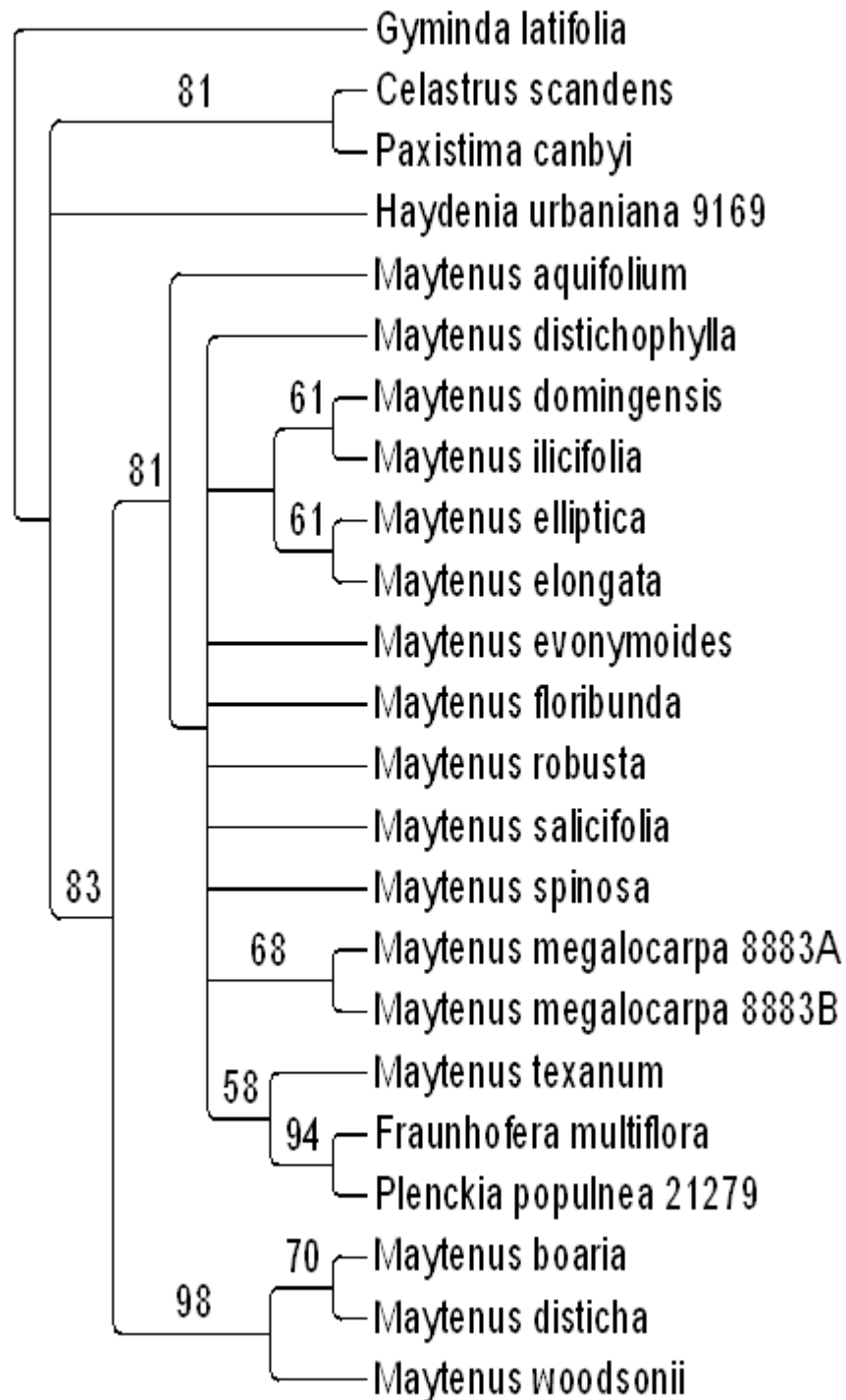


FIG. S6.

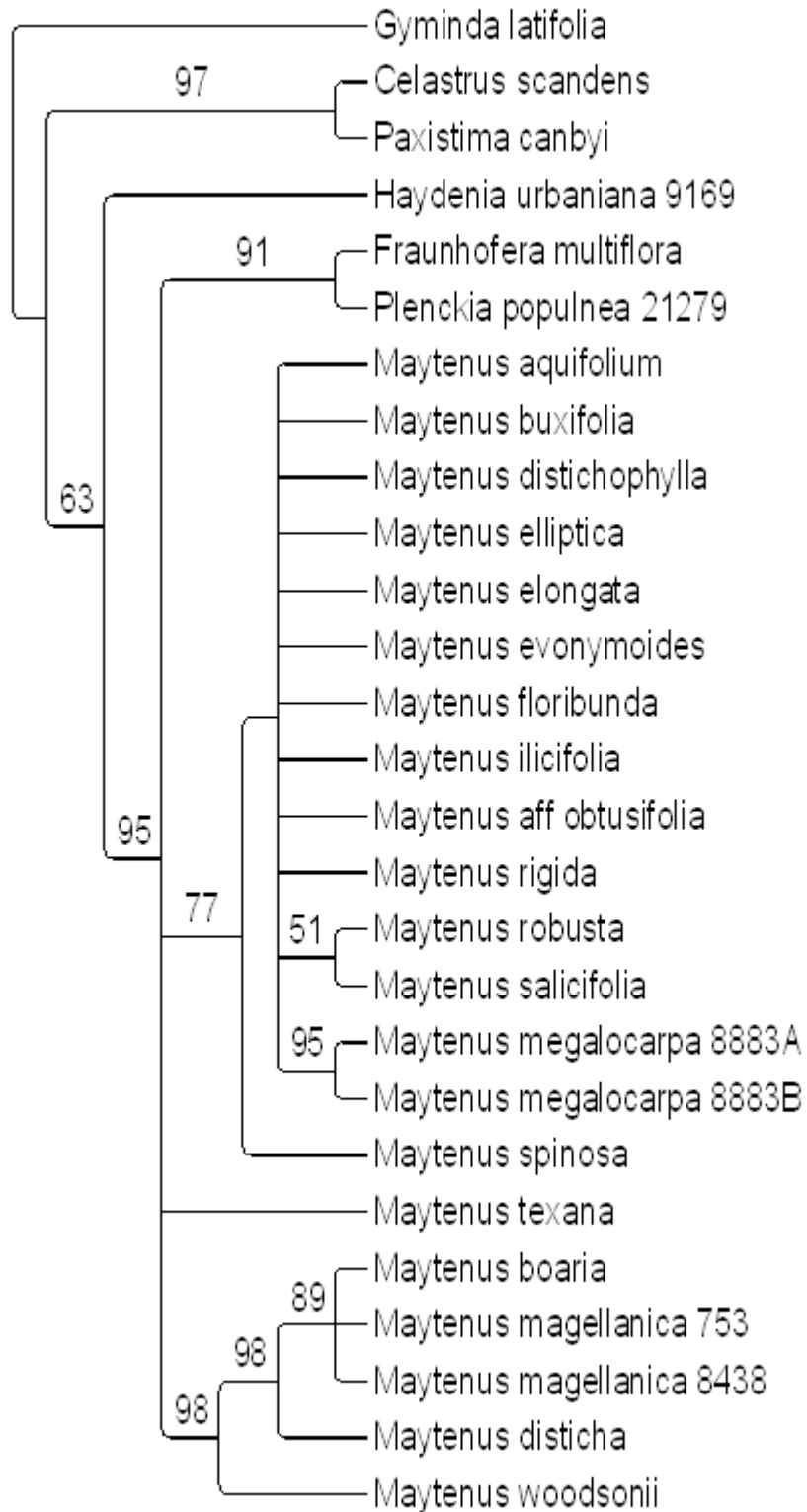


FIG. S7.

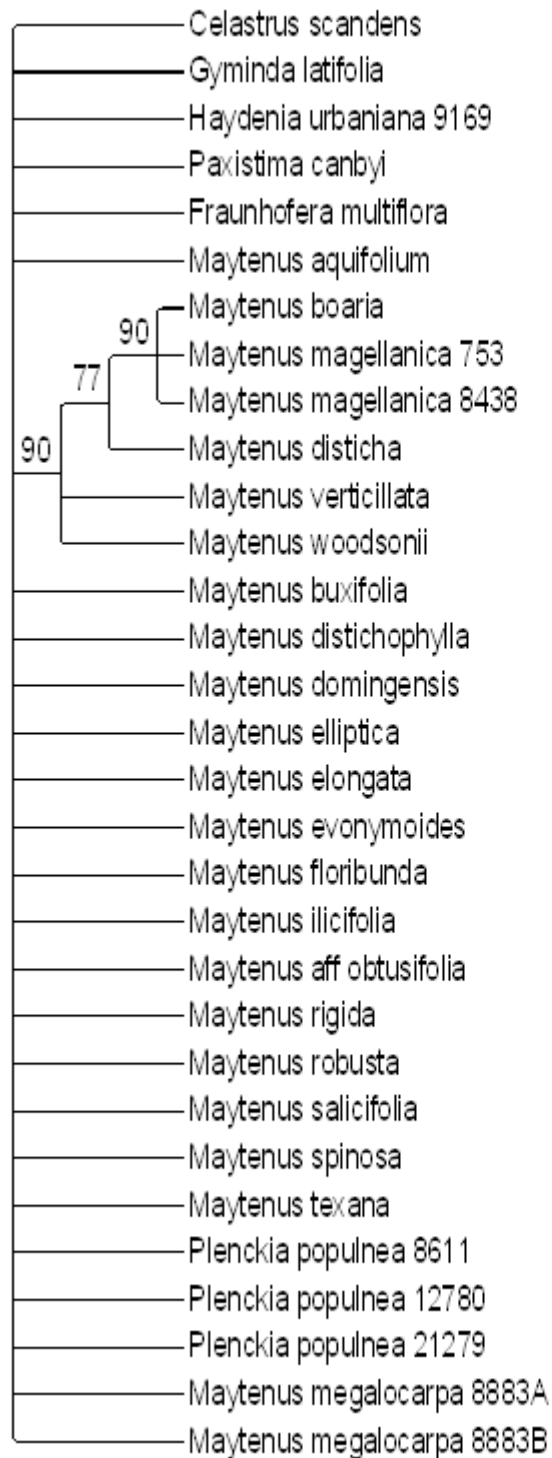


FIG. S8.

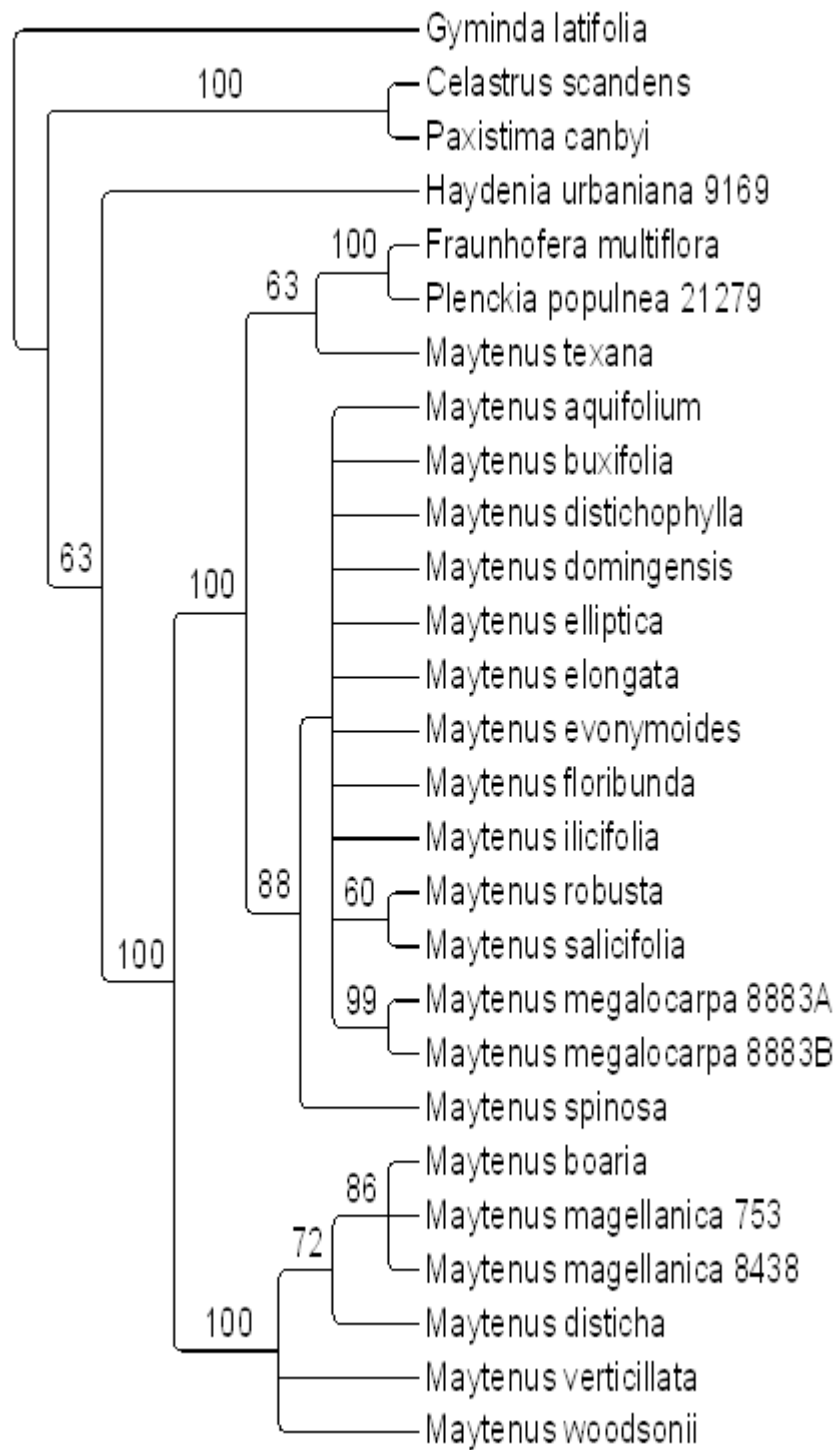


FIG. S9.