Antiquities of the rainforest: evolution of mycoheterotrophic angiosperms growing on Glomeromycota

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Citation

Mennes, C. B. (2015, October 6). *Antiquities of the rainforest: evolution of mycoheterotrophic angiosperms growing on Glomeromycota*. Retrieved from https://hdl.handle.net/1887/35731

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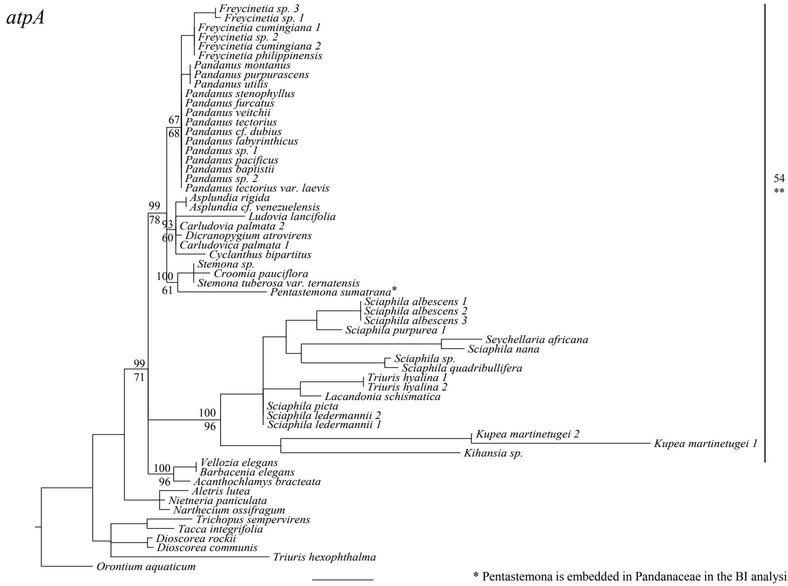
Title: Antiquities of the rainforest : evolution of mycoheterotrophic angiosperms growing on Glomeromycota
Issue Date: 2015-10-06

Appendix B: Supplementary Figures.

* This clade is not recovered in the ML analysis

Fig. S1. Phylogeny of Pandanales based on an ML analysis of the 18S rDNA dataset. Values above branches are Bayesian posterior probabilities (expressed as percentages); those below branches are bootstrap support percentages. The scale bar shows the number of substitutions per site. Clades which are not recovered in the ML analysis, but only in the BI analysis are indicated by a vertical bar.



* Pentastemona is embedded in Pandanaceae in the BI analysis
** This clade is not recovered in the ML analysis

Fig. S2. Phylogeny of Pandanales based on an ML analysis of the mitochondrial *atpA* dataset. Values above branches are Bayesian posterior probabilities; those below branches are bootstrap support percentages. The scale bar shows the number of substitutions per site. Clades which are not recovered in the ML analysis, but only in the BI analysis are indicated by a vertical bar.

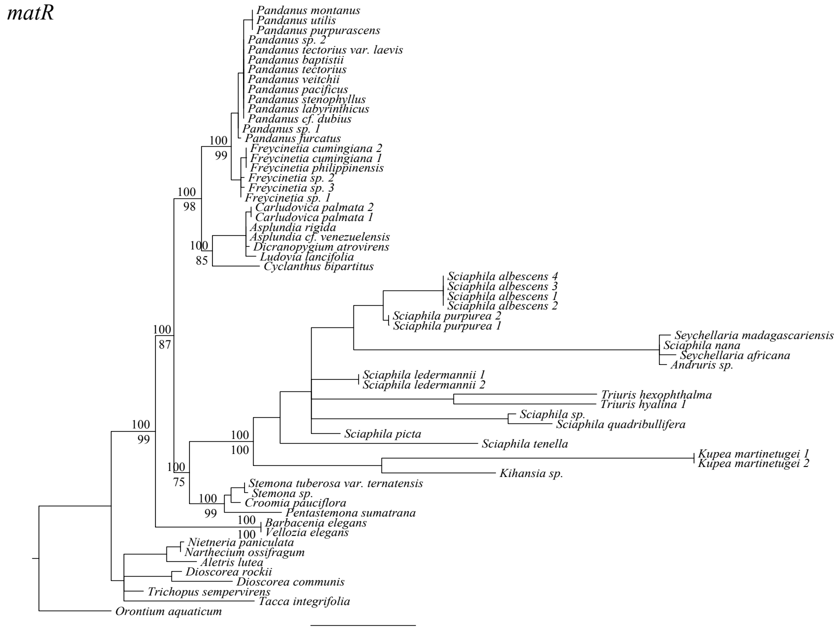


Fig. S3. Phylogeny of Pandanales based on an ML analysis of the mitochondrial *matR* dataset. Values above branches are Bayesian posterior probabilities; those below branches are bootstrap support percentages. The scale bar shows the number of substitutions per site.

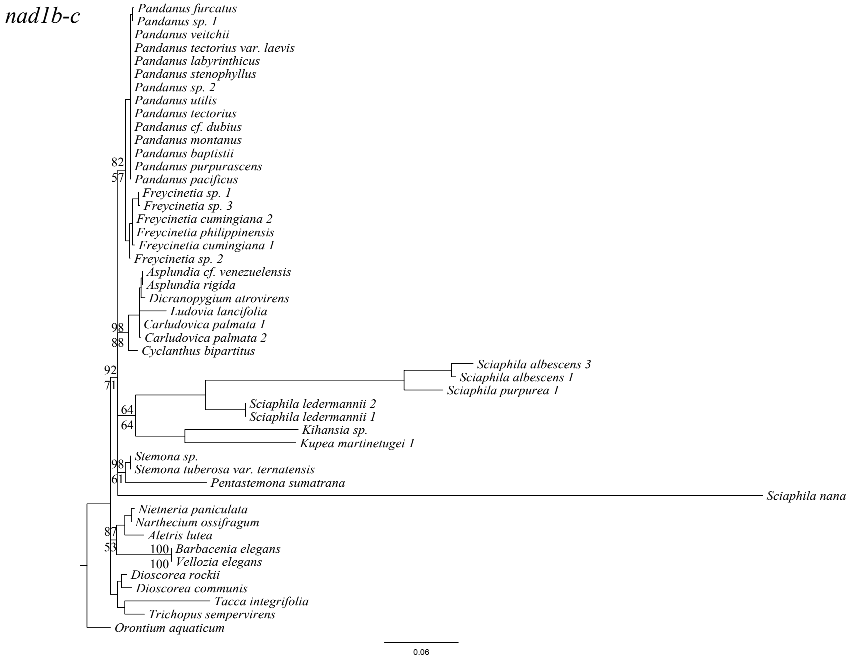
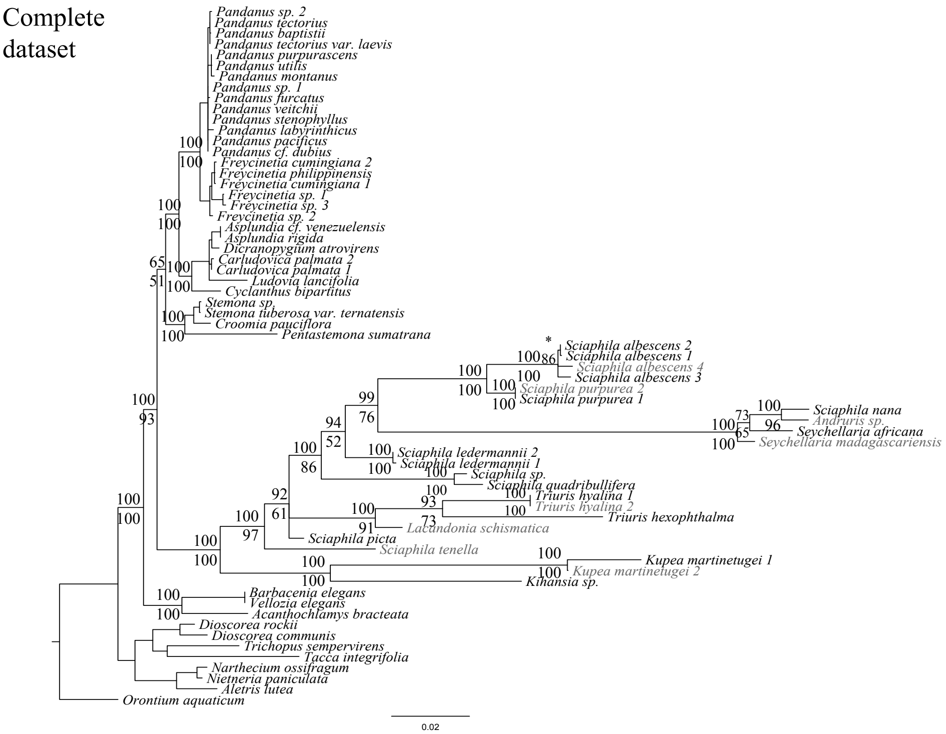


Fig. S4. Phylogeny of Pandanales based on an ML analysis of the mitochondrial *nad1 b-c* intron dataset. Values above branches are Bayesian posterior probabilities; those below branches are bootstrap support percentages. The scale bar shows the number of substitutions per site.



* This clade is not recovered in the BI analysis

Fig. S5. A four-gene ML analysis of Triuridaceae and relatives including several Triuridaceae taxa (in grey) with less than three genes (a portion of this is shown in Fig. 6). Values above branches are Bayesian posterior probabilities; those below branches are Bootstrap support percentages. The scale bar shows the number of substitutions per site.

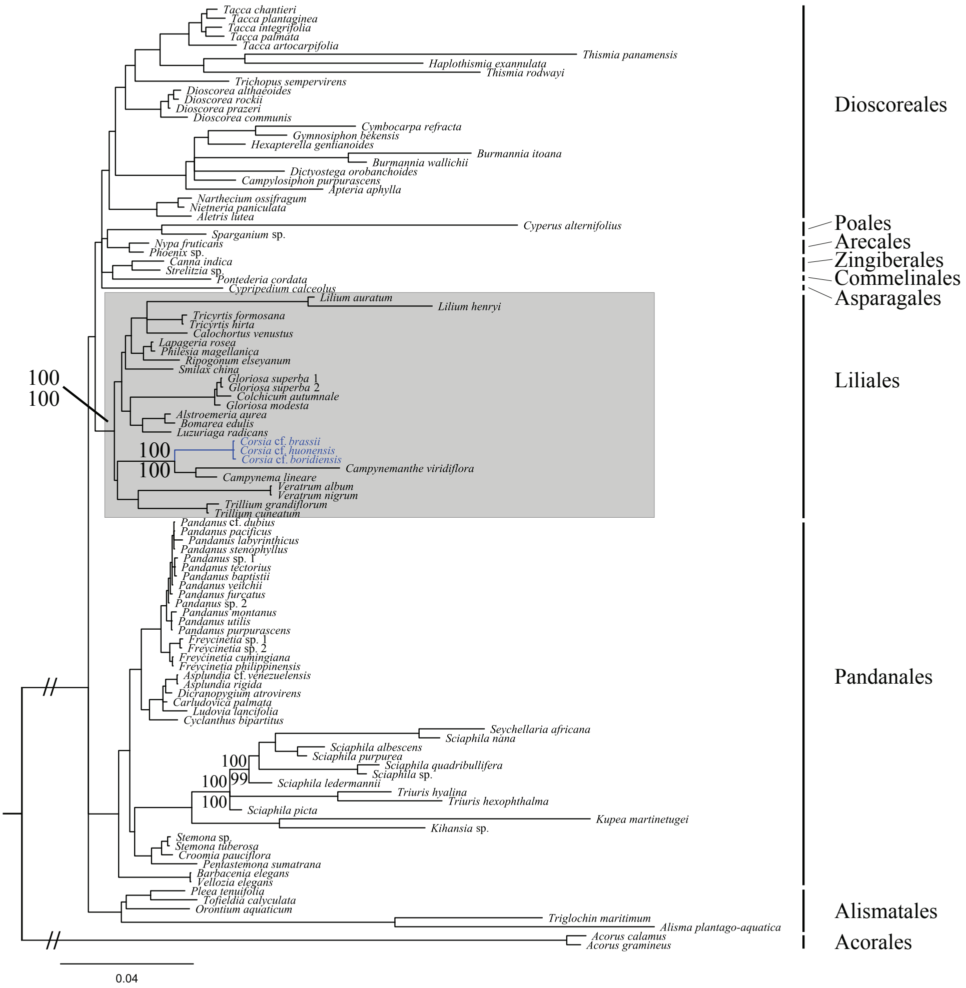


Fig. S6. Phylogeny of Liliales and related monocot orders based on a Bayesian-inference (BI) analysis of a three-locus molecular dataset (nuclear 18S rDNA and mitochondrial *atp*A and *mat*R), including only *Corsia* spp. (blue) from Corsiaceae. The grey shaded area shows the Liliales taxa. Values above branches are posterior probabilities (expressed as percentages) resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the maximum-likelihood (ML) analysis. Support values are only given for Corsiaceae and the slightly conflicting Triuridaceae taxa. The scale bar indicates the number of substitutions per site.

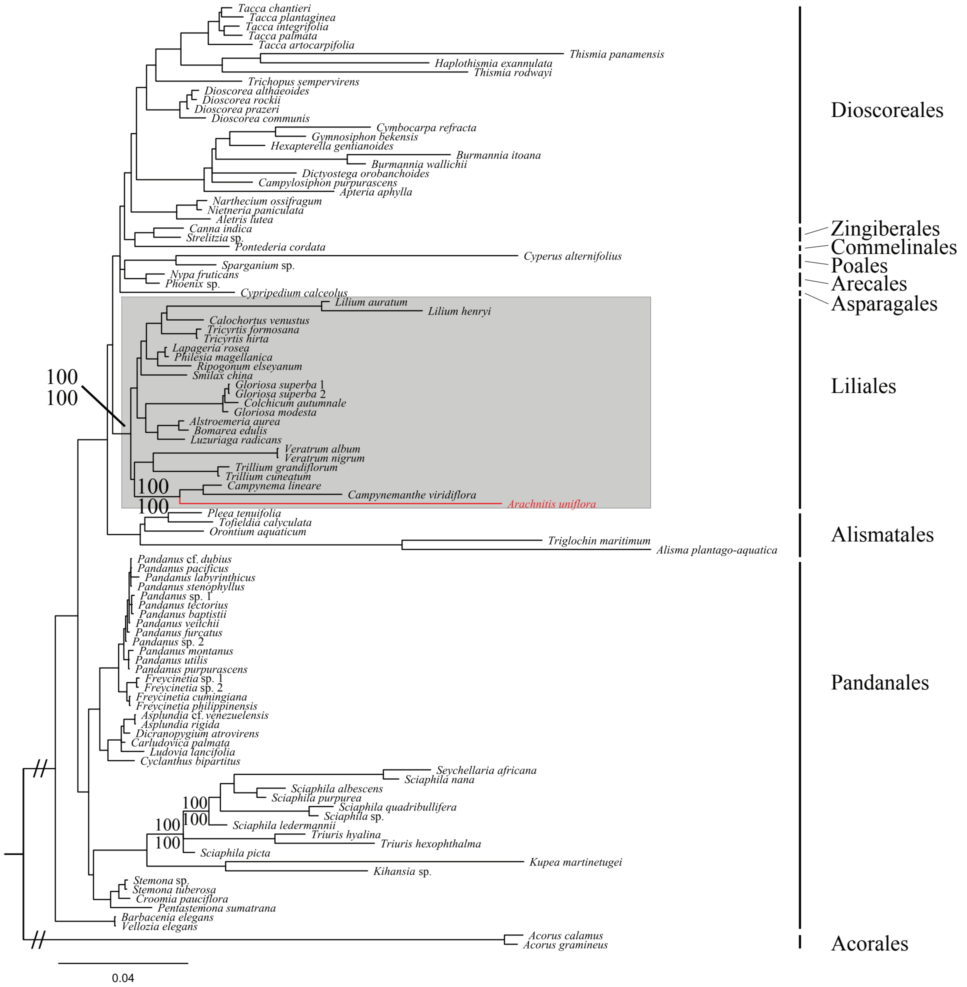
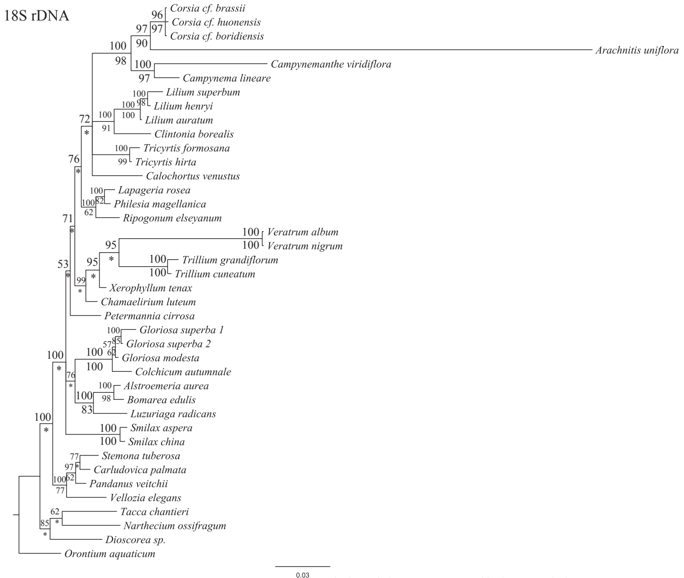
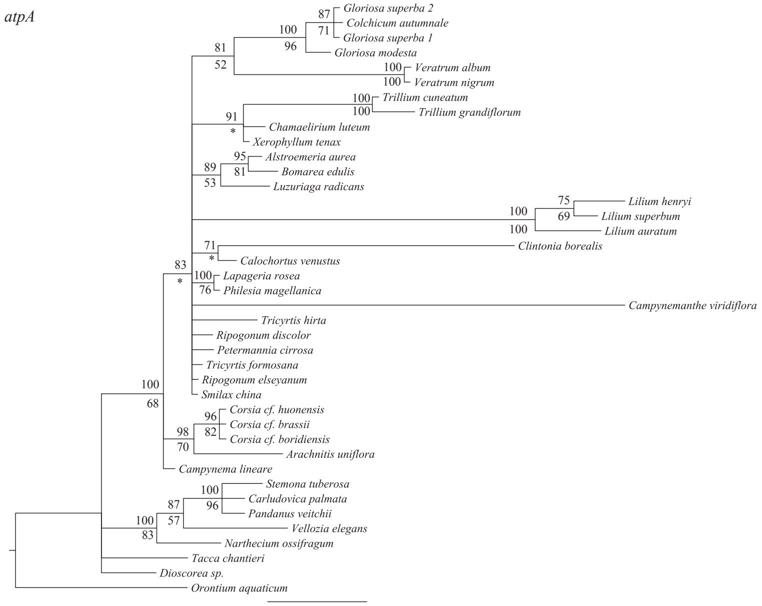


Fig. S7. Phylogeny of Liliales and related monocot orders based on a Bayesian-inference (BI) analysis of a three-locus molecular dataset (nuclear 18S rDNA and mitochondrial *atp*A, and *mat*R), including only *Arachnitis uniflora* (red) from Corsiaceae. The grey shaded area shows the Liliales taxa. Values above branches are posterior probabilities (expressed as percentages) resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the maximum-likelihood (ML) analysis. Support values are only given for Corsiaceae and the slightly conflicting Triuridaceae taxa. The scale bar indicates the number of substitutions per site.


18S rDNA

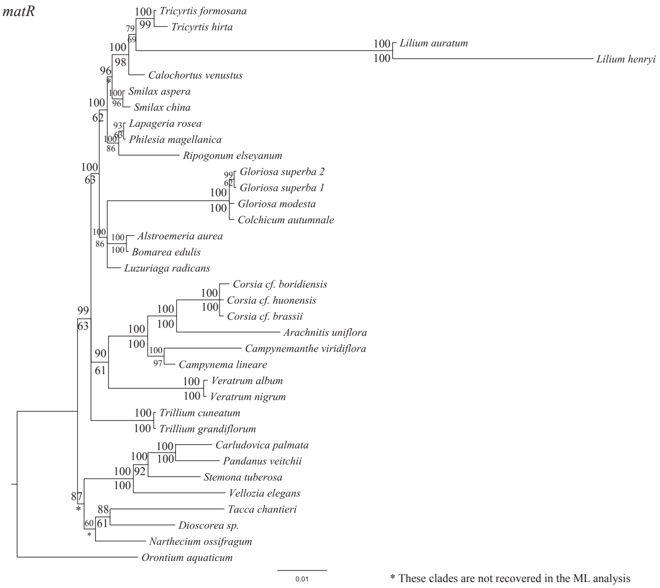
* These clades are not recovered in the ML analysis

Fig. S8. Phylogeny of Liliales based on a Bayesian-inference (BI) analysis of a single-locus molecular dataset (nuclear 18S rDNA). Values above branches are posterior probabilities (expressed as percentages) resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the maximum-likelihood (ML) analysis. The scale bar indicates the number of substitutions per site.


atpA

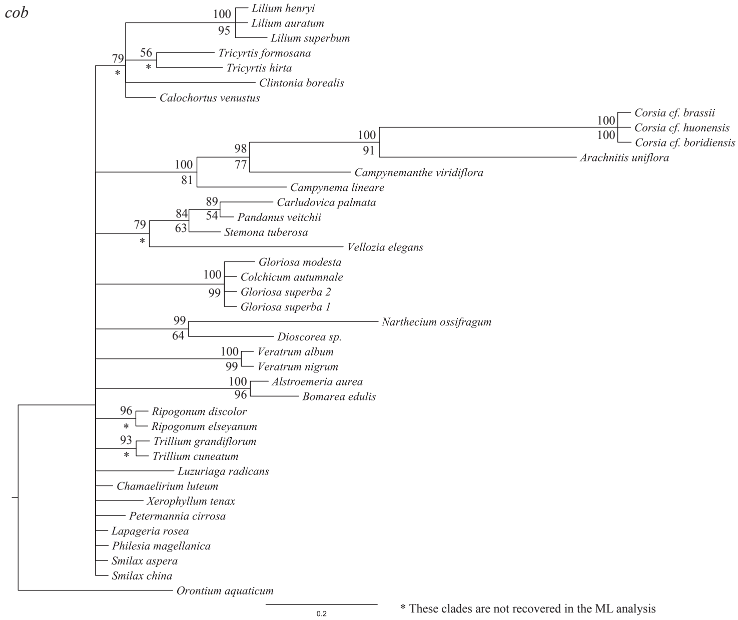
* These clades are not recovered in the ML analysis

Fig. S9. Phylogeny of Liliales based on a Bayesian-inference (BI) analysis of a single-locus molecular dataset (mitochondrial *atp*A). Values above branches are posterior probabilities (expressed as percentages) resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the maximum-likelihood (ML) analysis. The scale bar indicates the number of substitutions per site.



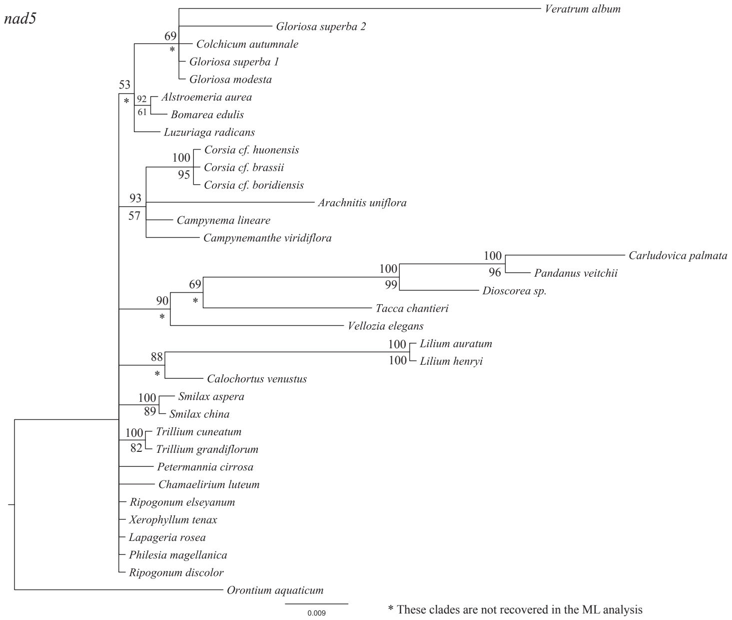
* These clades are not recovered in the ML analysis

Fig. S10. Phylogeny of Liliales based on a Bayesian-inference (BI) analysis of a single-locus molecular dataset (mitochondrial *mat*R). Values above branches are posterior probabilities (expressed as percentages) resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the maximum-likelihood (ML) analysis. The scale bar indicates the number of substitutions per site.



* These clades are not recovered in the ML analysis

Fig. S11. Phylogeny of Liliales based on a Bayesian-inference (BI) analysis of a single-locus molecular dataset (mitochondrial *cob*). Values above branches are posterior probabilities (expressed as percentages) resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the maximum-likelihood (ML) analysis. The scale bar indicates the number of substitutions per site.



* These clades are not recovered in the ML analysis

Fig. S12. Phylogeny of Liliales based on a Bayesian-inference (BI) analysis of a single-locus molecular dataset (mitochondrial *nad*5). Values above branches are posterior probabilities (expressed as percentages) resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the maximum-likelihood (ML) analysis. The scale bar indicates the number of substitutions per site.

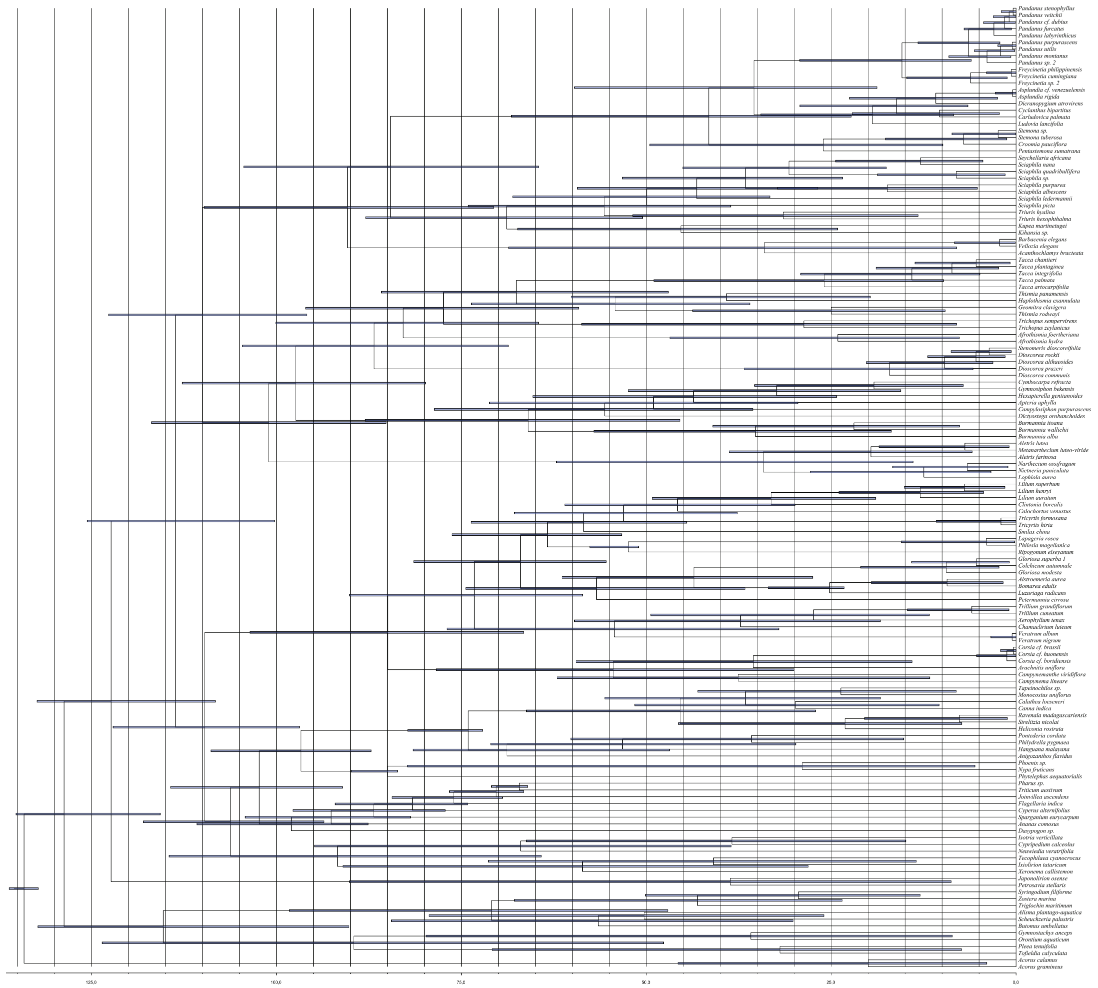
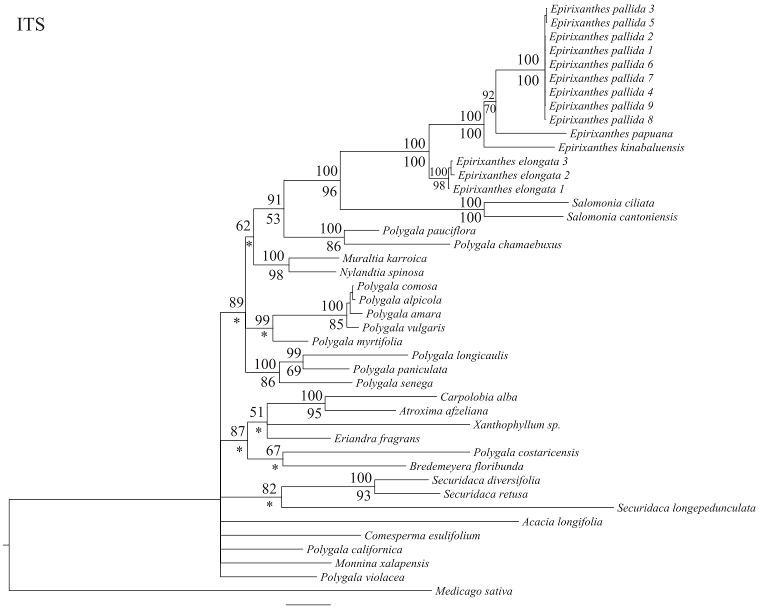
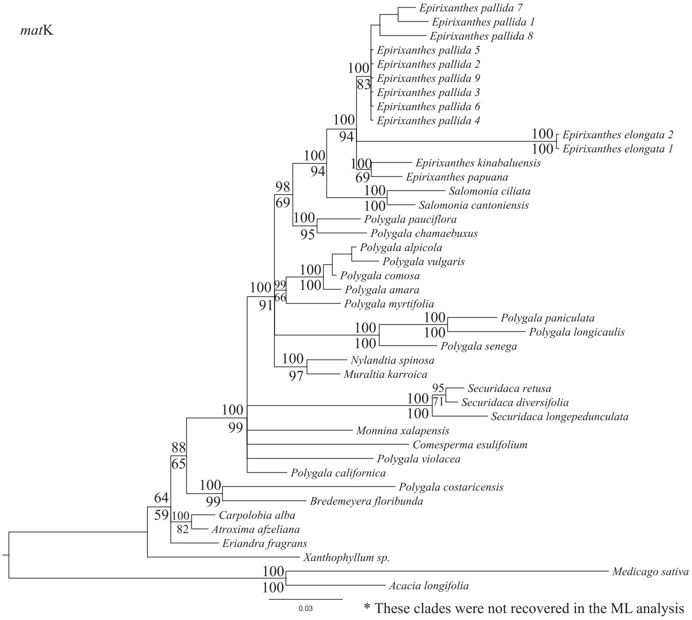


Fig. S13. Maximum clade credibility tree resulting from the divergence-time estimation of monocots inferred using the uncorrelated lognormal relaxed-clock method, based on a two-locus molecular dataset (nuclear 18S rDNA and mitochondrial atpA), six fossil calibration points, and assuming a Yule process of speciation (see text). The scale bar and the numbers in the figure both represent time (million years ago; Ma); bars around nodes represent 95% confidence intervals.



* These clades were not recovered in the ML analysis

Fig. S14. Phylogeny of Polygalaceae based on a Bayesian Inference (BI) analysis of the separate ITS dataset. Values above branches are posterior probabilities resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the Maximum Likelihood (ML) analysis. The scale bar indicates the number of substitutions per site.



* These clades were not recovered in the ML analysis

Fig. S15. Phylogeny of Polygalaceae based on a Bayesian Inference (BI) analysis of the separate *matK* dataset. Values above branches are posterior probabilities resulting from the BI analysis; those below branches are bootstrap support percentages resulting from the Maximum Likelihood (ML) analysis. The scale bar indicates the number of substitutions per site.