Supplementary Information

Molecular thresholds of ITS2 and their implications for molecular evolution and species identification in seed plants

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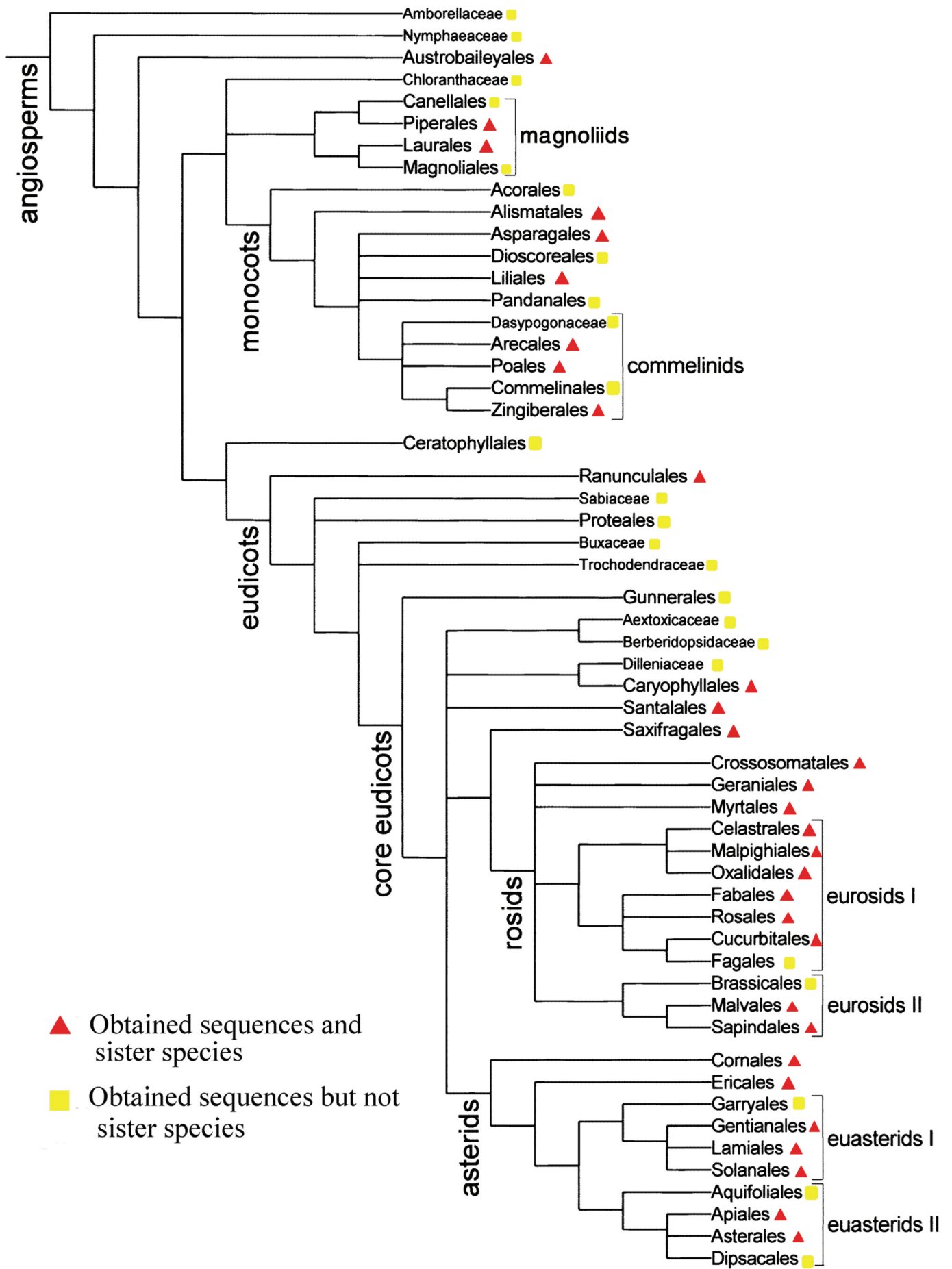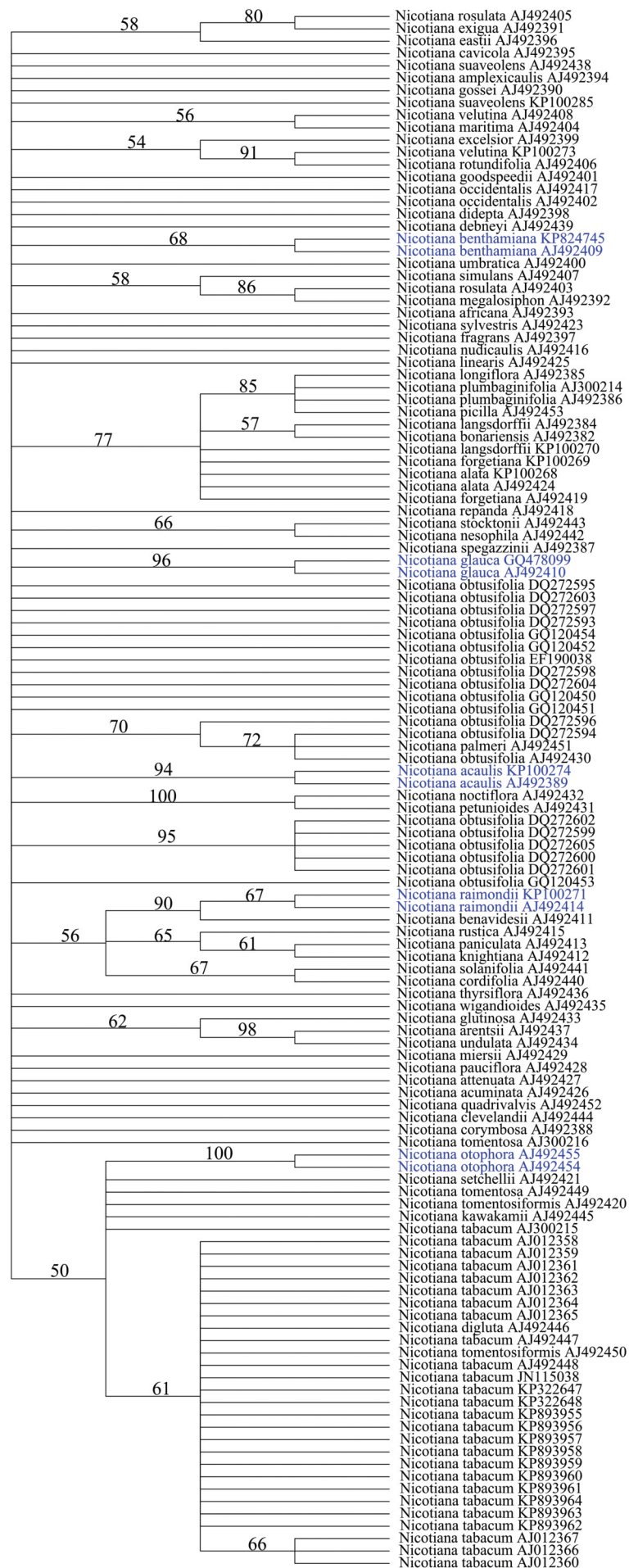
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Supplementary Figure 1

Supplementary Figure 2

Supplementary Table 7

(Supplementary Tables 1-6 and Dataset 1 are large datasets and included as separate Excel documents)

Supplementary Figure S1. The phylogenetic position of investigated taxa in the APG framework

Figure S2. A neighbor joining tree of *Nicotiana* plants based on ITS2 sequence. Bootstrap values （＞50%） are shown above the branches. Numbers followed taxon names are GenBank accession numbers. Successfully identified species are highlighted in blue.

Supplementary Table S7. Comparison of ITS2 genetic distance for the selected groups of species-rich orders

Taxon	Average value	95% Confidence interval	Variation	N
Asparagales	3.28%	[2.02%,4.54%]	[0.37%,13.49%]	31
Fabales	5.08%	[2.59%,7.57%]	[0.09%,43.45%]	37
Apiales	2.52%	[1.55%,3.49%]	[0.60%,6.10%]	15
Pinales	1.65%	[0.96%,2.33%]	[0.40%,3.23%]	9
All	3.13%	[2.63%,4.82%]	[0.09%,43.45%]	92