Supporting Information

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SI Materials and Methods

Molecular Dating. To provide insight into the timing of divergences for the topologies presented, we applied the following three time constraints: (*i*) the most recent common ancestor of *Quercus* and *Cucumis* was set to a minimum of 85 mya based on the fossil *Bedellia* (Fagales) (1); (*ii*) the angiosperm crown group was set to a minimum age of 131.8 mya (2–5); and (*iii*) the eudicots crown was set to minimum age of 125 mya (3, 6). In each case, priors on fossils were treated as fitting an exponential distribution (7) with a mean of 1 and the offset set to the minimum age of the fossil. The exponential distribution is similar to that of a lognormal distribution, in that it has a long tail of diminishing probability toward older ages (7). We chose to use an exponential distribution to minimize the number of additional parameters being estimated from the data and because it may be a good alternative to a lognormal in the face of inadequate paleontological information (7). Finally, we treated the age of the root node as a uniform distribution between 290 and 310 my [*U*(290,310)] (8). These dates were chosen because they conservatively bracket the first appearance of an extant seed plant lineage. Reports of conifer leaves and shoots are known from 309.2 to 307.1 mya, but unequivocal conifers with well-preserved female cones (e.g., *Emporia lockardii*) (9) are first recorded from around the Carboniferous-Permian boundary (290 mya). Fossil cycad megasporophylls also first appear in the fossil record during the early Permian (290–281.5 mya) (10). We took a conservative approach to selecting fossil constraints: the *Bedellia* and gymnosperm constraints were chosen because they represent the geologically oldest fossils that could confidently be assigned to their respective clades. Using these constraints also enabled us to make a direct comparison with previous plastid genome-based molecular dating analyses that used similar constraints (11).

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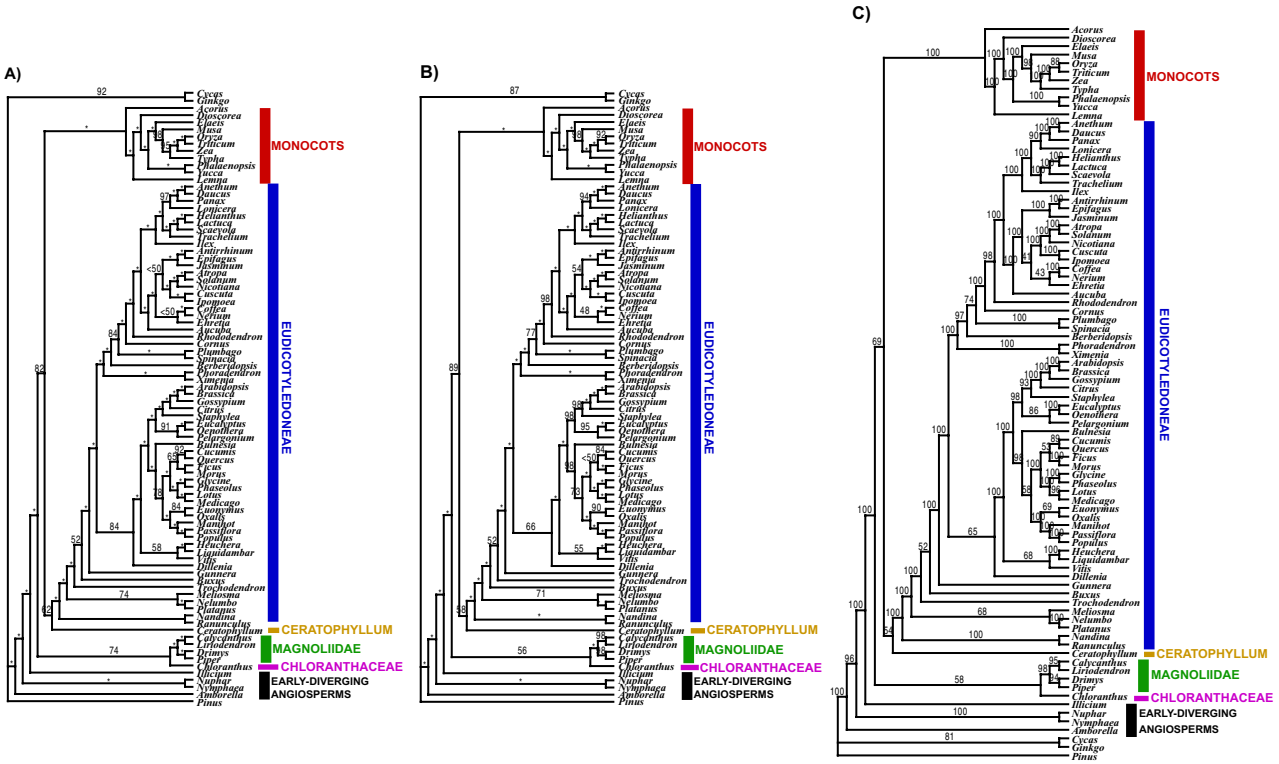

Fig. S1. (*A* and *B*) Cladograms of the best ML trees as determined by RAxML for the 83-gene combined data set, under the following partitioning schemes: (*A*) partitioned by gene but estimating a single set of branch lengths across partitions (ln L = −1090114.62); (*B*) partitioned by gene and with branch lengths allowed to vary by partition (ln L = −1070630.97). Numbers associated with branches are ML bootstrap support values. Asterisks indicate 100% BS support. (*C*) Cladogram showing results of two-stage ML bootstrap analysis for the 83-gene combined data set.

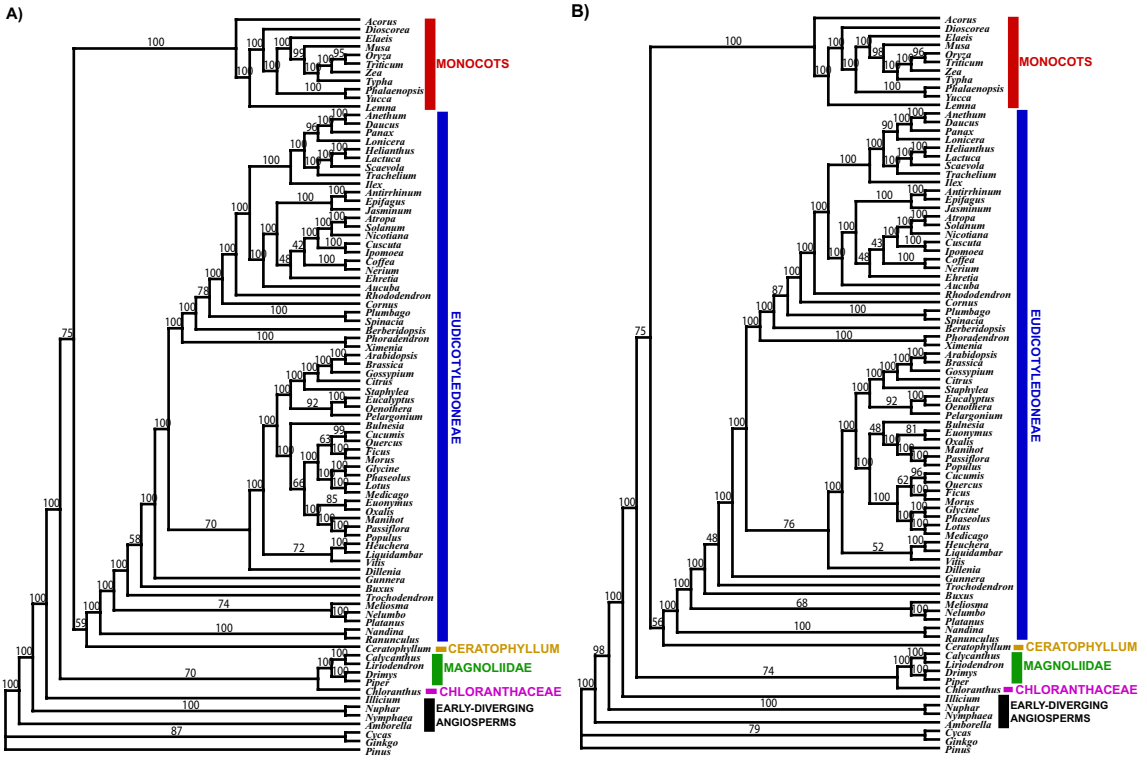

Fig. S2. Results of CodonPart and CodonPartBL analyses. Numbers associated with branches are ML bootstrap support values. (*A*) Cladogram of the best ML tree as determined by RAxML for the 83-gene combined data set, under the CodonPart partitioning scheme (ln L = −1098583.60). (*B*) Cladogram of the best ML tree as determined by RAxML for the 83-gene combined data set, under the CodonPartBL partitioning scheme (ln L = −1096911.47).

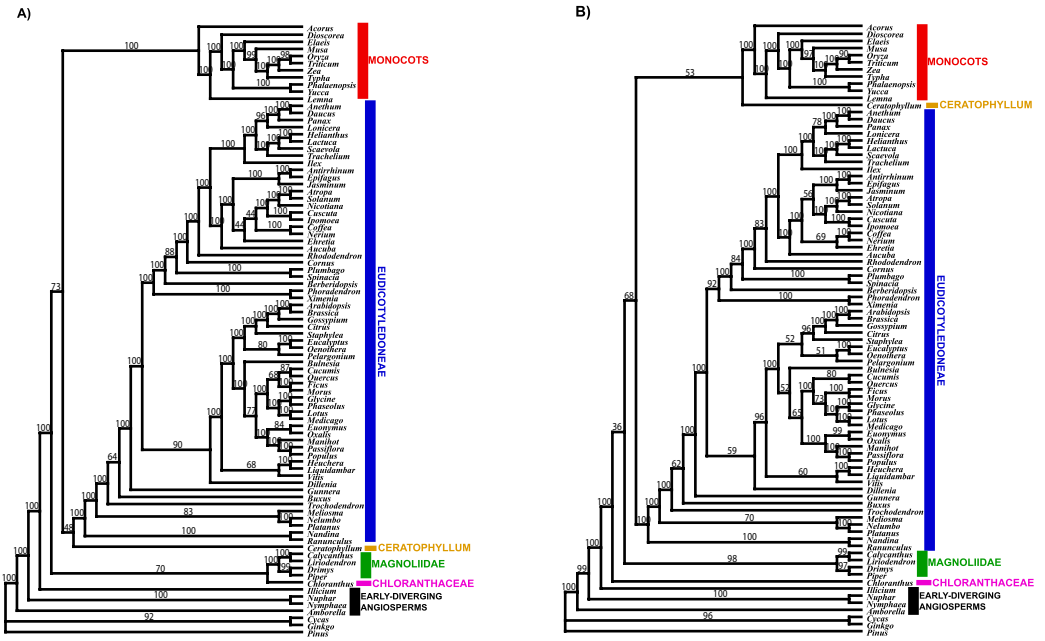

Fig. S3. Results of CodonGenePart and CodonGenePartBL analyses. Numbers associated with branches are ML bootstrap support values. (*A*) Cladogram of the best ML tree as determined by RAxML for the 83-gene combined data set, under the CodonGenePart partitioning scheme (ln $L = -1075855.59$). (*B*) Cladogram of the best ML tree as determined by RAxML for the 83-gene combined data set, under the CodonGenePartBL partitioning scheme (ln $L = -1040771.37$).

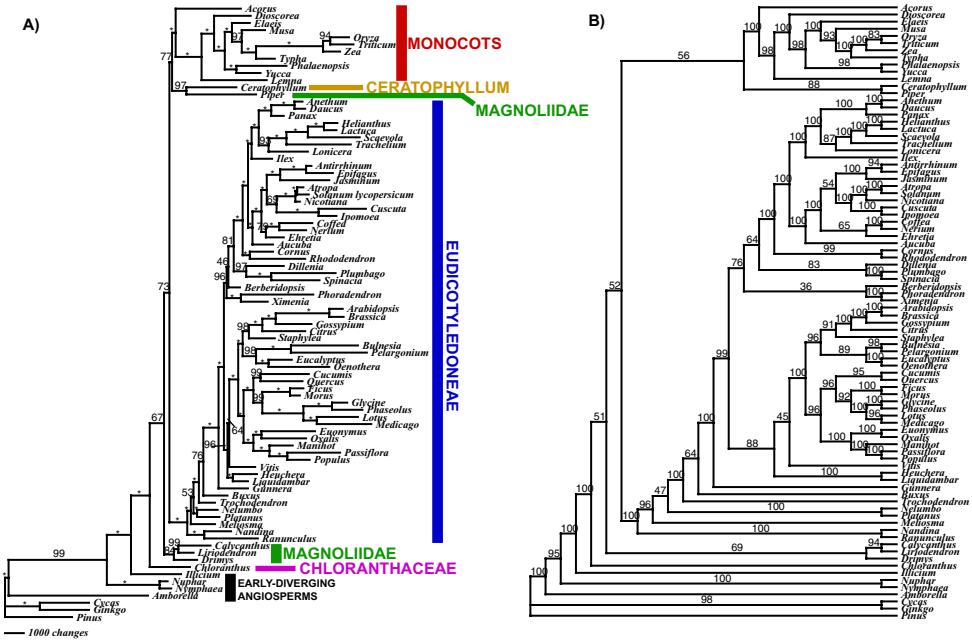

Fig. S4. Results of parsimony analyses on 83-gene data set. (*A*) Phylogram of the single MP tree (tree length = 212,546 steps; CI = 0.325; RI = 0.481) for the 83-gene combined data set. Numbers associated with branches are MP nonparametric bootstrap support values. Asterisks indicate 100% BS support. (*B*) Cladogram showing results of two-stage MP bootstrap analysis.

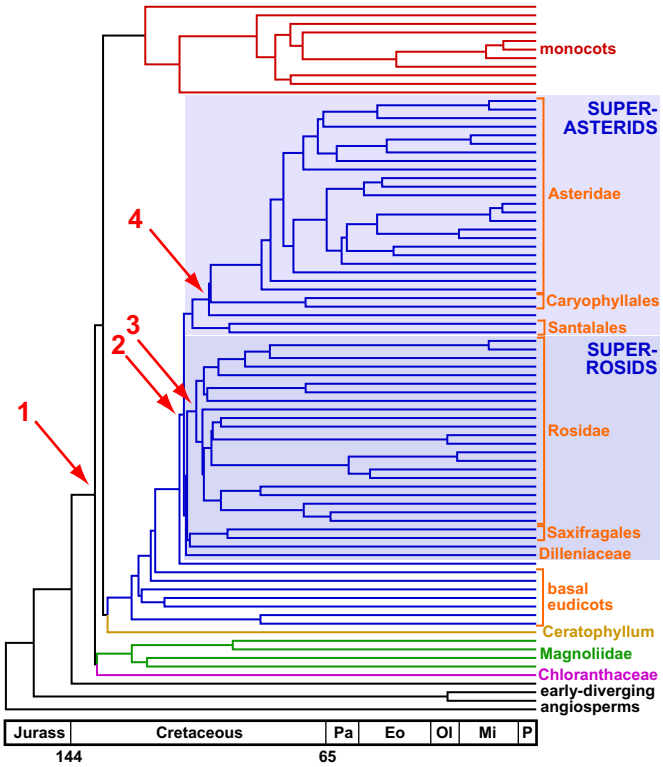

Fig. S5. Chronogram depicting angiosperm divergence times as estimated by the BEAST analysis using the 83-gene unpartitioned ML tree. A geologic timescale is provided at the bottom. Arrows indicate examples of rapid radiations within angiosperms that dating analyses suggest occurred in <5 million years: 1, basal Mesangiospermae diversification; 2, basal Pentapetalae radiation; 3, basal Rosidae radiation; 4, radiation of Berberidopsidales, Caryophyllales, and Asteridae. The gymnosperm outgroups have been removed from this figure.

Other Supporting Information

Table S1 (DOC)
Table S2 (DOC)
Table S3 (DOC)
Table S4 (DOC)