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PHYLOGENETIC ANALYSES OF BASAL ANGIOSPERMS BASED ON NINE PLASTID, MITOCHONDRIAL, AND NUCLEAR GENES

Yin-Long Qiu,[1,*,†,‡] Olena Dombrovska,[*,†,‡] Jungho Lee,[2,†,‡] Libo Li,[*,†] Barbara A. Whitlock,[3,†] Fabiana Bernasconi-Quadroni,[‡] Joshua S. Rest,[4,*] Charles C. Davis,[*] Thomas Borsch,[§] Khidir W. Hilu,[‖] Susanne S. Renner,[5,#] Douglas E. Soltis,[**] Pamela S. Soltis,[††] Michael J. Zanis,[6,‡‡] Jamie J. Cannone,[§§] Robin R. Gutell,[§§] Martyn Powell,[‖‖] Vincent Savolainen,[‖‖] Lars W. Chatrou,[##] and Mark W. Chase[‖‖]

*Department of Ecology and Evolutionary Biology, University Herbarium, University of Michigan, Ann Arbor, Michigan 48109-1048, U.S.A.; †Biology Department, University of Massachusetts, Amherst, Massachusetts 01003-5810, U.S.A.; ‡Institute of Systematic Botany, University of Zurich, 8008 Zurich, Switzerland; §Nees-Institut für Biodiversität der Pflanzen, Friedrich-Wilhelms-Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany; ‖Biology Department, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 24061, U.S.A.; #Department of Biology, University of Missouri, St. Louis, Missouri 63121-4499, U.S.A.; **Department of Botany and the Genetics Institute, University of Florida, Gainesville, Florida 32611, U.S.A.; ††Florida Museum of Natural History and the Genetics Institute, University of Florida, Gainesville, Florida 32611, U.S.A.; ‡‡School of Biological Sciences, Washington State University, Pullman, Washington 99164, U.S.A.; §§Institute for Cellular and Molecular Biology, and Section of Integrative Biology, University of Texas, Austin, Texas 78712, U.S.A.; ‖‖Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3DS, United Kingdom; and ##National Herbarium of the Netherlands, Utrecht University, Heidelberglaan 2, 3584 CS Utrecht, The Netherlands

DNA sequences of nine genes (plastid: *atpB*, *matK*, and *rbcL*; mitochondrial: *atp1*, *matR*, mtSSU, and mtLSU; nuclear: 18S and 26S rDNAs) from 100 species of basal angiosperms and gymnosperms were analyzed using parsimony, Bayesian, and maximum likelihood methods. All of these analyses support the following consensus of relationships among basal angiosperms. First, *Amborella*, Nymphaeaceae, and Austrobaileyales are strongly supported as a basal grade in the angiosperm phylogeny, with either *Amborella* or *Amborella* and Nymphaeales as sister to all other angiosperms. An examination of nucleotide substitution patterns of all nine genes ruled out any possibility of analytical artifacts because of RNA editing and GC-content bias in placing these taxa at the base of the angiosperm phylogeny. Second, Magnoliales are sister to Laurales and Piperales are sister to Canellales. These four orders together constitute the magnoliid clade. Finally, the relationships among *Ceratophyllum*, Chloranthaceae, monocots, magnoliids, and eudicots are resolved in different ways in various analyses, mostly with low support. Our study indicates caution in total evidence approaches in that some of the genes employed (e.g., mtSSU, mtLSU, and nuclear 26S rDNA) added signal that conflicted with the other genes in resolving certain parts of the phylogenetic tree.

Keywords: basal angiosperms, *Amborella*, magnoliids, multigene analysis, synapomorphic substitutions, phylogeny.

Introduction

The past 20 years have witnessed significant progress in our understanding of the phylogeny of basal angiosperms from analyses of molecular and nonmolecular data (Dahlgren and Bremer 1985; Donoghue and Doyle 1989; Loconte and Stevenson 1991; Martin and Dowd 1991; Hamby and Zimmer 1992; Taylor and Hickey 1992; Chase et al. 1993; Qiu et al. 1993, 1999, 2000, 2001; Soltis et al. 1997, 2000; Nandi et al. 1998; Hoot et al. 1999; Mathews and Donoghue 1999, 2000; Parkinson et al. 1999; Renner 1999; Soltis et al. 1999*a*; Barkman et al. 2000; Doyle and Endress 2000; Graham and Olmstead 2000*b*; Savolainen et al. 2000; Nickrent et al. 2002; Zanis et al. 2002, 2003; Borsch et al. 2003; Hilu et al. 2003; Löhne and Borsch 2005). Specifically, it has become increasingly clear that *Amborella*, Nymphaeaceae, and Austrobaileyales (*sensu* APG II 2003) represent the earliest-diverging lineages of extant angiosperms. Furthermore, the magnoliids (*sensu* APG II 2003; see Qiu et al. 1993 for a review of the history of this term) have been identified as a monophyletic group in some analyses (Qiu et al. 1999, 2000; Zanis et al. 2002, 2003; Hilu et al. 2003), but their monophyly (Savolainen et al. 2000; Soltis et al. 2000) and especially relationships among their member orders (Magnoliales, Laurales, Piperales, and Canellales) need further evaluation

[1] Author for correspondence; e-mail ylqiu@umich.edu.
[2] Current address: School of Biological Sciences, Seoul National University, Shillim, Kwanak, Seoul, South Korea 151-747.
[3] Current address: Department of Biology, University of Miami, Miami, Florida 33124-0421, U.S.A.
[4] Current address: Department of Ecology and Evolution, University of Chicago, Chicago, Illinois 60637, U.S.A.
[5] Current address: Department of Biology, Ludwig Maximilians University Munich, Munich, Germany.
[6] Current address: Division of Biological Sciences, University of California, San Diego, La Jolla, California 92093, U.S.A.

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and resolution. Finally, all angiosperms excluding *Amborella*, Nymphaeaceae, and Austrobaileyales can be divided into five clades: *Ceratophyllum*, Chloranthaceae, magnoliids, monocots, and eudicots (tricolpates *sensu* Judd and Olmstead 2004; see also Walker and Doyle 1975; Crane 1989; Donoghue and Doyle 1989; Doyle and Hotton 1991; Chase et al. 1993). Relationships among these five lineages, however, are best interpreted as unresolved at present because analyses with different taxon and character-sampling schemes and phylogenetic methods have produced conflicting topologies that are generally only weakly supported (Barkman et al. 2000; Soltis et al. 2000; Zanis et al. 2002, 2003; Hilu et al. 2003).

Despite progress, more work is needed to further clarify relationships among basal angiosperms. In this study, we add sequence data of four new genes to a five-gene matrix assembled earlier (Qiu et al. 1999, 2000) and conduct parsimony, Bayesian, and maximum likelihood (ML) analyses to address several issues. First, we attempt to show that placement of *Amborella*, Nymphaeaceae, and Austrobaileyales at the base of angiosperm phylogeny is free of any analytical artifact. This is especially important in light of recent analyses of the entire plastid genome sequences of *Amborella* and *Nymphaea* that do not support them as basalmost angiosperms (Goremykin et al. 2003*a*, 2003*b*, 2004; but see Soltis and Soltis 2004; Soltis et al. 2004; Stefanovic et al. 2004). Second, we aim to evaluate the monophyly of magnoliids and to resolve the relationships among their members: Magnoliales, Laurales, Piperales, Canellales. Finally, we wish to resolve relationships among *Ceratophyllum*, Chloranthaceae, magnoliids, monocots, and eudicots.

Material and Methods

We included 100 terminals from 98 genera, representing all major lineages of gymnosperms and basal angiosperms. *Acorus* and *Ceratophyllum* were the only two genera for which two species each were sampled. Only two families of basal angiosperms were not included, Gomortegaceae (Renner 1999) and Hydnoraceae (Nickrent et al. 2002), because of many missing data entries. Most of the terminals consist of sequences derived from a single species (and frequently the same DNA sample) and occasionally from different species of the same genus (tables 1, 2). Eight gymnosperms covering all four extant lineages were used as outgroups.

The four new genes added in this study are: plastid *matK* (a group II intron-encoded maturase), mitochondrial SSU (small subunit) and LSU (large subunit) rDNAs, and nuclear 26S rDNA. With the five genes from our earlier analyses (mitochondrial *atp1* and *matR*, plastid *atpB* and *rbcL*, and nuclear 18S rDNA), the total of nine genes used in this study represents a sampling of a large number of characters from each of the three plant genomes. Furthermore, these genes encompass diverse functions, including energy metabolism, carbohydrate synthesis, RNA processing, and protein synthesis.

DNA extraction and sequencing methods follow Qiu et al. (2000). All primer sequences used for amplifying and sequencing the genes are available from the corresponding author on request. All sequences of mtLSU were newly generated in this study, whereas approximately half of the sequences were generated by us for mtSSU, *matK*, and nuclear 26S rDNA. For the five genes used in Qiu et al. (1999), several new sequences were produced to fill the missing entries in that matrix. The orthologous *atp1* was used to replace the copy we obtained earlier from *Amborella* (Qiu et al. 1999, 2000), which has been shown to be a xenolog horizontally transferred from an asterid (Barkman et al. 2000; Bergthorsson et al. 2003). For all nine genes we have taken sequences from GenBank when appropriate. Detailed source information for all sequences and correction to errors in table A1 of Qiu et al. (2000) are provided in tables 1 and 2. Of all taxa and all genes, only four taxa have missing data in one or two genes: *Metasequoia* (mtSSU and *matR*), *Hortonia* (*matR*), and *Dioscorea* and *Myristica* (nu26S) (tables 1, 2). Eight of the nine genes (all except mtSSU) were aligned using Clustal X (Thompson et al. 1997). Because of extraordinary length variation in several regions of mtSSU, this gene was manually aligned with the alignment editor AE2 (developed by T. Macke; Larsen et al. 1993). Although these regions typically had minimal sequence identity that could not be aligned based on sequence alone, they usually had similar structural elements that facilitated the alignment of these sequences. In addition, all of the computer-generated alignments were manually adjusted with the MacClade 4.05 (Maddison and Maddison 2002) alignment editor. All of the aligned positions were used in the phylogenetic analyses. We also eliminated the positions in regions with significant length variations in the four rDNAs from the phylogenetic analyses of the nine-gene matrix. These latter analyses yielded results not substantially different from those presented here (data not shown).

Three series of analyses were performed to address various issues. First, two separate matrices were assembled to reconstruct the overall phylogeny of basal angiosperms, one consisting of all nine genes and the other of five protein-coding genes. The decision to make a separate matrix using the five protein-coding genes was based on the following considerations: (1) all positions within the protein genes should evolve more independently than those of rDNAs, many of which evolve in a coupled fashion due to base pairing in stem regions in these genes (Soltis and Soltis 1998; Soltis et al. 1999*b*; O. Dombrovska and Y.-L. Qiu, unpublished data); (2) the protein-coding genes generally show fewer problems of paralogy and xenology compared to nuclear 18S and 26S rDNAs, for which nonorthologous copies were occasionally encountered; and (3) the protein-coding genes are free of alignment uncertainties compared to two mitochondrial rDNAs, which exhibit extraordinary length variations caused by insertions and deletions in a few regions. The parsimony, Bayesian, and maximum likelihood (ML) analyses were implemented separately on both matrices. To evaluate the informativeness of the two nuclear rDNAs further, the five-protein-gene matrix was combined with 18S and 26S rDNAs sequentially to form two more matrices. Only parsimony bootstrap analyses were conducted on these two matrices.

Second, three separate genome-specific matrices were constructed to address whether placement of *Amborella*, Nymphaeaceae, and Austrobaileyales as sisters to all other extant angiosperms is supported by data from the plastid, mitochondrial, and nuclear genomes separately. This type of analysis has only been conducted occasionally (Mathews and

Donoghue 1999, 2000; Graham and Olmstead 2000*b*; Savolainen et al. 2000; Zanis et al. 2002). A robust understanding of organismal phylogeny should be based on evidence from each of the three plant genomes (Qiu and Palmer 1999) except in cases of hybridization and horizontal gene transfer. Only parsimony bootstrap analyses were conducted on these data sets.

Third, we investigated the types of substitutions that provided phylogenetic signal for identifying *Amborella*, Nymphaeaceae, and Austrobaileyales as the earliest-diverging lineages of extant angiosperms. For an issue as critical as the rooting of angiosperm phylogeny, merely having high bootstrap numbers from an analysis is not enough to gain confidence in the result (Soltis et al. 2004). Some poorly understood molecular evolutionary phenomena, such as RNA editing (Steinhauser et al. 1999; Kugita et al. 2003; Dombrovska and Qiu 2004) and GC-content bias (Steel et al. 1993), both of which can occur in a genome-wide, lineage-specific fashion, can generate substitutions that lead to spurious groupings in phylogenetic analyses. Hence, it is important that we understand the types of substitutions that are behind those high bootstrap percentages. We examined the nine-gene matrix visually and identified the sites that contain apparently synapomorphic changes that separate gymnosperms-*Amborella*-Nymphaeaceae-Austrobaileyales from all other angiosperms. Sites were classified as apparently synapomorphic if they contained the same nucleotide in at least two of the four gymnosperm lineages (cycads, *Ginkgo*, conifer II [non-Pinaceae conifers], and Gnetales + Pinaceae; Bowe et al. 2000; Chaw et al. 2000) and at least two of the three basal angiosperm lineages (*Amborella*, Nymphaeaceae, and Austrobaileyales) but had a different and generally invariable nucleotide in all other angiosperms (hence a synapomorphy for euangiosperms, *sensu* Qiu et al. 1999). We then performed both a most parsimonious tree search and a parsimony bootstrap analysis with these sites removed to verify our identification. These synapomorphic substitutions were finally checked to determine if they could have been generated by RNA editing or GC-content bias. In addition, codon position and type of change (transition vs. transversion) were noted for these substitutions.

These last two series of analyses were designed to complement the analyses we performed earlier (Qiu et al. 1999, 2000, 2001), to ensure that the placement of *Amborella*, Nymphaeaceae, and Austrobaileyales as basal lineages is indeed based on historical signal recorded in the multiple genes from all three plant genomes rather than the result of yet poorly understood analytical artifacts. These analyses are particularly relevant in the ongoing debate over whether *Amborella* and *Nymphaea* are basal angiosperms (Goremykin et al. 2003*a*, 2003*b*, 2004; Soltis et al. 2004; Soltis and Soltis 2004; Stefanovic et al. 2004).

In parsimony searches we used equal weighting for all positions and character-state changes using PAUP* 4.0b10 (Swofford 1998). When searching for the shortest trees, a heuristic search was conducted using 1000 random taxon-addition replicates, one tree held at each step during stepwise addition, TBR branch swapping, steepest descent option off, MulTrees option on, and no upper limit of MaxTrees. For bootstrap analyses, 1000 resampling replicates were performed (except for the matrix of five protein genes plus two nuclear rDNAs where 5000 resampling replicates were used) with the same tree search procedure as described above except with simple taxon addition and the steepest descent option on.

For Bayesian and ML analyses, the optimal models of sequence evolution for the nine-gene and five-protein-gene data sets were estimated using ModelTest 3.6 (Posada and Crandall 1998) and DT-ModSel (Minin et al. 2003). The general time-reversible model (Rodríguez et al. 1990) including parameters for invariant sites and rate variation ($\mathrm{GTR} + \mathrm{I} + \Gamma$) best fits both data sets and was used to conduct the analyses.

Bayesian analyses were performed using MrBayes version 3.0b4 (Huelsenbeck and Ronquist 2001). For the nine-gene matrix, the data were partitioned according to codon positions (first, second, and third, for protein genes only), genomes (plastid, mitochondrial, and nuclear), and gene types within a genome (rRNA vs. protein genes). For the five-protein-gene matrix, the data were partitioned according to codon positions and genomes. Calculations of likelihood for searches of both matrices were implemented under the $\mathrm{GTR} + \mathrm{I} + \Gamma$ model of sequence evolution, assuming different stationary nucleotide frequencies. The posterior probability (PP) was estimated by sampling trees from the PP distribution using Metropolis coupled Markov Chain Monte Carlo methods. Two and four chains of 5,000,000 generations were run for the nine-gene matrix and five-protein-gene matrix, respectively. Chains were sampled every 100 generations. Likelihood scores converged on a stable value after 500,000 generations (the burn-in of the chain), and calculations of PP were based on the trees sampled after this generation.

Maximum likelihood analyses were performed separately on the nine-gene and five-protein-gene data sets using PHYML version 2.4.4 (Guindon and Gascuel 2003) under the optimal model of sequence evolution. For both data sets, the $\mathrm{GTR} + \mathrm{I} + \Gamma$ model was implemented with parameter values for the proportion of invariant sites (nine-gene = 0.19, five-gene-protein = 0.21) and the gamma distribution (nine-gene = 0.43, five-gene-protein = 0.68) as estimated by ModelTest 3.6 and DT-ModSel. The optimal rate of nucleotide substitution and transition/transversion ratios was estimated from the data during ML searches. Maximum likelihood support values were similarly estimated from 100 bootstrap replicates in PHYML.

Results

For the nine-gene data set, which contained 26,990 aligned nucleotides, two islands with two and four shortest trees (length = 51, 834 steps; consistency index [CI] = 0.47; retention index [RI] = 0.57) were found 259 and 315 times, respectively, out of 1000 random taxon-addition replicates in the parsimony search. One of the six trees is shown (fig. 1), with the nodes that are not present in the strict consensus of all six trees indicated by asterisks.

For the five-protein-gene data set, which contained 9351 aligned nucleotides, a single island of two shortest trees (length = 18, 839 steps; CI = 0.42; RI = 0.59) was found in all 1000 random taxon-addition replicates in the parsimony search. One of the two trees is shown (fig. 2), with the nodes

Table 1

Vouchers, Contributors, GenBank Accession Numbers, and References for the Sequences Used in This Study

Family and species	mt-SSU rDNA	mt-LSU rDNA	cp-*matK*	nu-*26S* rDNA
Acoraceae:				
Acorus calamus L.	Parkinson et al. 1999; AF193976	Qiu 94052; OD/FBQ/YQ DQ008817	Fuse and Tamura 2000; AB040154	Qiu 94052; OD/YQ; DQ008654
Acorus gramineus Soland.	Qiu 97131; JL/LL/YQ; DQ008668	Qiu 97131; OD/FBQ/YQ; DQ008818	Fuse and Tamura 2000; AB040155	Kuzoff et al. 1998; AF036490
Alismataceae:				
Alisma plantago-aquatica L.	Qiu 96177; JL/LL/YQ; DQ008669	Qiu 96177; OD/FBQ/YQ; DQ008812		Qiu 96177; LL/YQ; DQ008651
Alisma canaliculatum A. Br. & Bouché			Fuse and Tamura 2000; AB040179	
Amborellaceae:				
Amborella trichopoda Baill.	Parkinson et al. 1999; AF193987	B. Hall sn, IND, Qiu 97123*; OD/FBQ/YQ DQ008832	Hilu et al. 2003; B. Hall sn, BONN AF543721 (TB)	Zanis et al. 2003; AY095449
Annonaceae:				
Annona muricata L.	Qiu 90031; JL/LL/YQ; DQ008670	Qiu 90031; OD/FBQ/YQ; DQ008783	K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch 3460, BONN AF543722 (KH)	Sun & An 98130, KUN; OD/YQ; DQ008634
Cananga odorata (Lam.) Hook. f. & Thomson	Chase 219, NCU; JL/LL/YQ; DQ008671	Chase 219, NCU; OD/FBQ/YQ; DQ008784	Borsch & Löhne 3555, BONN AY437817	Chase 219, NCU; OD/YQ; DQ008635
Araceae:				
Orontium aquaticum L.	Qiu 97112; JL/LL/YQ; DQ008672	Qiu 97112; OD/FBQ/YQ; DQ008813	Hilu et al. 2003; Borsch 3457, BONN AF543744 (KH)	Qiu 97112; OD/YQ; DQ008652
Spathiphyllum × '*Clevelandii*'	Qiu 94140; JL/LL/YQ; DQ008673	Qiu 94140; OD/FBQ/YQ; DQ008814		
Spathiphyllum floribundum (Lind.& Andre) N.E.Br.			Hilu et al. 2003; Borsch 3408 BONN AF542575	
Spathiphyllum wallisii Hort.				Zanis et al. 2003; AY095473
Aristolochiaceae:				
Aristolochia macrophylla Lam.	Qiu 91019; JL/LL/YQ; DQ008674	Qiu 91019; OD/FBQ/YQ; DQ008796		Zanis et al. 2003; AY095450
Aristolochia Pistolochia L.			Hilu et al. 2003; Borsch 3257, FR AF543724 (TB)	
Asarum canadense L.	Kuhlman sn, IND, Qiu 96018*; JL/LL/YQ; DQ008676	Kuhlman sn, IND, Qiu 96018*; OD/FBQ/YQ; DQ008799		Kuhlman sn, IND, Qiu 96018*; OD/YQ; DQ008643
Asarum yakusimense Masam.			Hilu et al. 2003; Huber sn, BONN AF542571 (TB)	
Saruma henryi Oliv.	Qiu 91018; JL/LL/YQ; DQ008677	Qiu 91018; OD/FBQ/YQ; DQ008800	Murata et al. 2001; AB060736	Qiu 91018; OD/YQ; DQ008644
Thottea tomentosa Ding Hou	Chase 1211, K; JL/LL/YQ; DQ008675	Chase 1211, K; OD/FBQ/YQ; DQ008797	Murata et al. 2001; AB060738	Chase 1211, K; OD/YQ; DQ008642
Asparagaceae:				
Asparagus officinalis L.	Qiu 94063; JL/LL/YQ; DQ008678	Qiu 94063; OD/FBQ/YQ; DQ008807		Qiu 94063; OD/YQ; DQ008646
Asparagus filicinus			J. Yamashita et al., unpublished data; AB029805	

Atherospermataceae:				
Atherosperma moschatum Labill.	Qiu 92007; JL/LL/YQ; DQ008679	Qiu 92007; OD/FBQ/YQ; DQ008775	Qiu 92007; Kew; AJ966790	Qiu 92007; LL/YQ; DQ008628
Daphnandra micrantha (Tul.) Benth.	Whalen 132, NSW; JL/LL/YQ; DQ008680	Whalen 132, NSW; OD/FBQ/YQ; DQ008776	Whalen 132, NSW; Kew; AJ966791	Whalen 132, NSW; OD/YQ; DQ008629
Doryphora sassafras Endl.	Qiu 98109; JL/LL/YQ; DQ008681	Qiu 98109; OD/FBQ/YQ; DQ008777	Hilu et al. 2003; Borsch 3409, BONN AF542568 (TB)	Qiu 98109; OD/YQ; DQ008630
Austrobaileyaceae:				
Austrobaileya scandens C. T. White	Parkinson et al. 1999; AF193988	Qiu 90030; OD/FBQ/YQ; DQ008827	Hilu et al. 2003; Borsch 3464 BONN AF543726 (TB)	Zanis et al. 2003; AY095452
Berberidaceae:				
Mahonia bealei (Fortune) Carr.	Qiu 74; JL/LL/YQ; DQ008682	Qiu 74; OD/FBQ/YQ; DQ008754		Qiu 74; OD/YQ; DQ008613
Mahonia japonica			Hilu et al. 2003; Borsch 3405, BONN AF542585 (TB)	
Podophyllum peltatum L.	Qiu 92003; JL/LL/YQ; DQ008683	Qiu 92003; OD/FBQ/YQ; DQ008755	Hilu et al. 2003; Borsch 3393, BONN AF542586 (TB)	Qiu 92003; OD/YQ; DQ008614
Buxaceae:				
Buxus sempervirens L.		Qiu 97057; OD/FBQ/YQ; DQ008743	Qiu 97057; Kew; AJ966792	S. Kim et al., unpublished data; AF389243
Buxus sp.	Parkinson et al. 1999; AF193996			
Pachysandra procumbens Michx.	Chase 207, NCU; JL/LL/YQ; DQ008684	Chase 207, NCU; OD/FBQ/YQ; DQ008742		Qiu sn, Z (Qiu L99028*); OD/YQ; DQ008607
Pachysandra terminalis Sieb. & Zucc.			Hilu et al. 2003; Borsch 3407, BONN AF542581 (KH)	
Cabombaceae:				
Brasenia schreberi J. Gmelin	Qiu 91031; JL/LL/YQ; DQ008685	Qiu 91031; OD/FBQ/YQ; DQ008830	Les et al. 1999; AF092973	Qiu 91031; LL/YQ; DQ008661
Cabomba sp.	Parkinson et al. 1999; AF193982;	Qiu 97027; OD/FBQ/YQ; DQ008831		
Cabomba caroliniana A. Gray			Les et al. 1999; AF108719	Soltis et al. 2003; AF479239
Calycanthaceae:				
Calycanthus floridus L.	Parkinson et al. 1999; AF193989	Qiu 94155; OD/FBQ/YQ; DQ008780	K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch 3455 BONN AF543730 (KH)	
Calycanthus occidentalis Hook. & Arn.				Zanis et al. 2003; AY095454
Chimonanthus praecox (L.) Link	Qiu 9; JL/LL/YQ; DQ008686	Qiu 9; OD/FBQ/YQ; DQ008781	Hilu et al. 2003; Borsch 3396, BONN AF542569 (TB)	Qiu 9; OD/YQ; DQ008632
Canellaceae:				
Canella winterana (L.) Gaertn.	Qiu 90017; JL/LL/YQ; DQ008687	Qiu 90017; OD/FBQ/YQ; DQ008804	K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch 3466 BONN AF543731 (TB)	Zanis et al. 2003; AY095455
Cinnamodendron ekmanii Sleum.	Zanoni & Jimenez 47067; JL/LL/YQ; DQ008688	Zanoni & Jimenez 47067; OD/FBQ/YQ; DQ008805	Zanoni & Jimenez 47067; Kew; AJ966793	Zanoni & Jimenez 47067; MZ/DES/PSS AY095458

Table 1

(*Continued*)

Family and species	mt-SSU rDNA	mt-LSU rDNA	cp-*matK*	nu-*26S* rDNA
Ceratophyllaceae:				
Ceratophyllum demersum L.	Parks sn, IND, Qiu 95003*; JL/LL/YQ; DQ008689	Parks sn, IND, Qiu 95003*; OD/FBQ/YQ; DQ008766	Parks sn, IND, Qiu 95003*; Kew; AJ966794	Zanis et al. 2003; AY095456
Ceratophyllum submersum L.	Qiu 98088; JL/LL/YQ; DQ008690	Qiu 98088; OD/FBQ/YQ; DQ008767	Qiu 98088; Kew; AJ581400	Qiu 98088; OD/YQ; DQ008622
Chloranthaceae:				
Ascarina rubricaulis Solms	Thien 500, NO; JL/LL/YQ; DQ008691	Thien 500, NO; OD/FBQ/YQ; DQ008821	Thien 500, NO Kew; AJ966795	Thien 500, NO; OD/YQ; DQ008656
Chloranthus brachystachys Bl.			Hilu et al. 2003; Borsch 3467 BONN AF543733 (KH)	
Chloranthus multistachys Pei	K. Wurdack 92-0010, NCU; JL/LL/YQ; DQ008692	K. Wurdack 92-0010, NCU; OD/FBQ/YQ; DQ008819		Zanis et al. 2003; AY095457
Hedyosmum arborescens Sw.	Chase 338, NCU; JL/LL/YQ; DQ008693	Chase 338, NCU; OD/FBQ/YQ; DQ008822	Chase 338, NCU; Kew; AJ581402	
Hedyosmum bonplandianum L.				Zanis et al. 2003; AY095461
Sarcandra chloranthoides Gardner	Parkinson et al. 1999; AF193992	Qiu 92002; OD/FBQ/YQ; DQ008820	Qiu 92002; Kew; AJ966796	Qiu 92002; OD/YQ; DQ008655
Cycadaceae:				
Cycas revoluta Thunb.	Chaw et al. 2000; AB029356	Qiu 94051; OD/FBQ/YQ; DQ008840		Qiu 94051; OD/YQ; DQ008667
Cycas panzhihuaensis			Wang et al. 2000; AF143440	
Cyclanthaceae:				
Carludovica palmata Ruiz & Pavon	Qiu 97021; JL/LL/YQ; DQ008694	Qiu 97021; OD/FBQ/YQ; DQ008809	Hilu et al. 2003; Roth sn, BONN AF542578 (TB)	Qiu 97021; OD/YQ; DQ008648
Degeneriaceae:				
Degeneria vitensis	JM Miller 1189-63; JL/LL/YQ; DQ008695	JM Miller 1189-63; OD/FBQ/YQ; DQ008787	Azuma et al., unpublished data; AB055549	JM Miller 1189-63; OD/YQ; DQ008637
Didymelaceae:				
Didymeles perrieri Olivier	Andrianantoanina 387, MO; JL/LL/YQ; DQ008696	Andrianantoanina 387, MO; OD/FBQ/YQ; DQ008744	Andrianantoanina 387, MO; Kew; AJ581406	Andrianantoanina 387, MO; OD/YQ; DQ008608
Dioscoreaceae:				
Dioscorea sp.	Qiu 94044; JL/LL/YQ; DQ008697	Qiu 94044; OD/FBQ/YQ; DQ008806		
Dioscorea alata			Fuse and Tamura 2000; AB040208	
Eupomatiaceae:				
Eupomatia bennettii F. Muell.	Qiu 90022; JL/LL/YQ; DQ008698	Qiu 90022; OD/FBQ/YQ; DQ008785	Qiu 90022; Kew; AJ966797	Qiu 90022; OD/YQ; DQ008636
Eupteleaceae:				
Euptelea polyandra Sieb. & Zucc.	Parks sn, IND, Qiu 95098*; JL/LL/YQ; DQ008699	Parks sn, IND, Qiu 95098*; OD/FBQ/YQ; DQ008763	Parks sn, IND, Qiu 95098*; Kew; AJ581413	Zanis et al. 2003; AF389249
Fumariaceae:				
Dicentra sp.	Qiu 95026; JL/LL/YQ; DQ008700	Qiu 95026; OD/FBQ/YQ; DQ008764	Qiu 95026; Kew; AJ966798	
Dicentra exima Torrey				Zanis et al. 2003; AF389262

Ginkgoaceae:				
Ginkgo biloba L.	Chaw et al. 2000; AB029355	Qiu 94015; OD/FBQ/YQ; DQ008838	Hilu et al. 2003; Borsch 3469 BONN AF543736 (KH)	Qiu 94015; OD/YQ; DQ008665
Gnetaceae:				
Gnetum gnemon L.	Qiu 97141; JL/LL/YQ; DQ008701	Qiu 97141; OD/FBQ/YQ; DQ008833	Hilu et al. 2003; Borsch 3470 BONN AF542561 (KH)	Kuzoff et al. 1998; AF036488
Gyrocarpaceae:				
Gyrocarpus americana Jacq.	Chase 317, NCU; JL/LL/YQ; DQ008702	Chase 317, NCU; OD/FBQ/YQ; DQ008770	Chase 317, NCU; Kew; AJ581417	Chase 317, NCU; OD/YQ; DQ008624
Hernandiaceae				
Hernandia nymphaeifolia (Presl) Kub.				Zanis et al. 2003; AY095462
Hernandia ovigera L.	Qiu 01007; JL/LL/YQ; DQ008703	Qiu 01007; OD/FBQ/YQ; DQ008771	Qiu 01007; Kew; AJ966799	
Himantandraceae:				
Galbulimima belgraveana (F. Muell.) Sprague	Weston 929, NSW; JL/LL/YQ; DQ008704	Weston 929, NSW; OD/FBQ/YQ; DQ008788	Weston 929, NSW; Kew; AF465294	Zanis et al. 2003; AY095459
Idiospermaceae:				
Idiospermum australiense (Diels) S.T. Blake	Qiu 91042; JL/LL/YQ; DQ008705	Qiu 91042; OD/FBQ/YQ; DQ008782	Qiu 91042; Kew; AJ581425	Qiu 91042; OD/YQ; DQ008633
Illiciaceae:				
Illicium floridanum Ellis	Qiu 61; JL/LL/YQ; DQ008706	Qiu 61; OD/FBQ/YQ; DQ008825	K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch 3552, BONN AF543738 (TB)	Qiu 61; OD/YQ; DQ008659
Juncaginaceae:				
Triglochin maritima L.	Qiu 97106; JL/LL/YQ; DQ008707	Qiu 97106; OD/FBQ/YQ; DQ008811	Hilu et al. 2003 Borsch 3392 BONN AF542566 (TB)	Qiu 97106; LL/YQ; DQ008650
Lactoridaceae:				
Lactoris fernandeziana Phil.	Chase 1014, K; JL/LL/YQ; DQ008708	Chase 1014, K; OD/FBQ/YQ; DQ008798	L.W. Chatrou et al., unpublished data; AF465297	Zanis et al. 2003; AY095463
Lardizabalaceae:				
Akebia quinata Decne.	Qiu 91020; JL/LL/YQ; DQ008709	Qiu 91020; OD/FBQ/YQ; DQ008761	Hilu et al. 2003; Borsch 3412 BONN AF542587 (TB)	Qiu 91020; OD/YQ; DQ008619
Lardizabala biternata Ruiz & Pavon	Qiu 97135; JL/LL/YQ; DQ008710	Qiu 97135; OD/FBQ/YQ; DQ008760	Qiu 97135; TB/KH; AY437809	Qiu 97135; OD/YQ; DQ008618
Lauraceae:				
Cinnamomum camphora (L.) T. Nees & Eberm.	Qiu 102; JL/LL/YQ; DQ008711	Qiu 102; OD/FBQ/YQ; DQ008772	Qiu 102; Kew; AJ966800	Qiu 102; OD/YQ; DQ008625
Cryptocarya alba (Molina) Looser			Rohwer 2000; AJ247158	
Cryptocarya meisneriana Frodin	Qiu 98048; JL/LL/YQ; DQ008712	Qiu 98048; OD/FBQ/YQ; DQ008774		Qiu 98048; OD/YQ; DQ008627
Laurus nobilis L.	Parkinson et al. 1999; AF193990	Qiu 94209; OD/FBQ/YQ; DQ008773	Qiu 94209; Kew; AJ966801	Qiu 94209; OD/YQ; DQ008626
Magnoliaceae:				
Liriodendron chinense (Hemsl.) Sarg.	Parkinson et al. 1999; AF193993	Qiu 28; OD/FBQ/YQ; DQ008786		Zanis et al. 2003; AY095464
Liriodendron tulipifera L.			Azuma et al. 1999; AB021016	
Magnolia denudata Desr.				Zanis et al. 2003; AF389256
Magnolia grandiflora L.	Chaw et al. 2000; AF161089			

Table 1

(***Continued***)

Family and species	mt-SSU rDNA	mt-LSU rDNA	cp-*matK*	nu-*26S* rDNA
Magnolia tripetala L.		Qiu 3; OD/FBQ/YQ; DQ008741	Azuma et al. 1999; AB021001	
Menispermaceae:				
Cissampelos pareira L.	Chase 347, NCU; JL/LL/YQ; DQ008713	Chase 347, NCU; OD/FBQ/YQ; DQ008758	Chase 347, NCU; Kew; AJ966802	Chase 347, NCU; OD/YQ; DQ008616
Cocculus trilobus (Thunb.) DC	Qiu 91016; JL/LL/YQ; DQ008714	Qiu 91016; OD/FBQ/YQ; DQ008759		Qiu 91016; OD/YQ; DQ008617
Cocculus laurifolius DC.			Hilu et al. 2003; Borsch 3406 BONN AF542588 (TB)	
Monimiaceae:				
Hedycarya arborea J.R. & G. Forst.	Qiu 90028; JL/LL/YQ; DQ008716	Qiu 90028; OD/FBQ/YQ; DQ008769	Qiu 90028; Kew; AJ581436	Qiu 90028; LL/YQ; DQ008623
Hortonia floribunda Wight ex Arn.	Qiu 02002*; JL/LL/YQ; DQ008717	Qiu 02002*; OD/FBQ/YQ; DQ008778	Qiu 02002*; TB; AY437811	Zanis et al. 2003; AF264143
Peumus boldus Molina	Edinburgh BG 19870707; JL/LL/YQ; DQ008715	Edinburgh BG 19870707; OD/FBQ/YQ; DQ008768	Rohwer 2000; AJ247183	Zanis et al. 2003; AY095466
Myristicaceae:				
Mauloutchia chapelieri Warb.	Schatz 3847A, MO; JL/LL/YQ; DQ008719	Schatz 3847A, MO; OD/FBQ/YQ; DQ008790	Schatz 3847A, MO; TB; AY437812	Schatz 3847A, MO; OD/YQ; DQ008638
Myristica fragrans Houtt.	Qiu 92014; JL/LL/YQ; DQ008718	Qiu 92014; OD/FBQ/YQ; DQ008789	Qiu 92014; Kew; AJ966803	
Nelumbonaceae:				
Nelumbo lutea (Willd.) Pers.				Zanis et al. 2003; AF389259
Nelumbo nucifera Gaertner	Parkinson et al. 1999; AF193983	Qiu 91028; OD/FBQ/YQ; DQ008753	K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch & Summers 3220, FR AF543740 (TB)	
Nymphaeaceae:				
Nuphar sp.	Parkinson et al. 1999; AF193981	Qiu M114; OD/FBQ/YQ; DQ008829		Qiu M114; LL/YQ; DQ008660
Nuphar lutea L.			Hilu et al. 2003; Borsch 3337, FR AF543741 (TB)	
Nymphaea sp.	Chaw et al. 2000; AF161091	Qiu 91029; OD/FBQ/YQ; DQ008828		Zanis et al. 2003; AY095465
Nymphaea odorata Aiton			Hilu et al. 2003; Borsch & Wilde 3132, VPI & BONN AF543742 (TB)	
Papaveraceae:				
Sanguinaria canadensis L.	Qiu 91032; JL/LL/YQ; DQ008720	Qiu 91032; OD/FBQ/YQ; DQ008765	Qiu 91032; Kew; AJ966804	Qiu 91032; OD/YQ; DQ008621
Pinaceae:				
Pinus sp.	Qiu 94013; JL/LL/YQ; DQ008721	Qiu 94013; OD/FBQ/YQ; DQ008835		
Pinus douglasiana Martinez			L. G. Geada et al., unpublished data; AB063520	

Pinus wallichiana A. B. Jackson				I. Capesius, unpublished data; AJ271114
Piperaceae:				
Peperomia graveolens Rauh & Barthlott			Hilu et al. 2003; Prinsler s.n. BONN AF542574 (TB)	
Peperomia obtusifolia A. Dietr.	Qiu 94135; JL/LL/YQ; DQ008722	Qiu 94135; OD/FBQ/YQ; DQ008794		Qiu 94135; LL/YQ; DQ008641
Piper betle L.	Chaw et al. 2000; AF161088	Qiu 91048; OD/FBQ/YQ; DQ008795		Zanis et al. 2003; AY095467
Piper crocatum R. & P.			Hilu et al. 2003; Slotta s.n., VPI AF543745 (KH)	
Platanaceae:				
Platanus occidentalis L.	Chaw et al. 2000; AF161090	Qiu 94152; OD/FBQ/YQ; DQ008752	K.W. Hilu et al., unpublished data; AF543747	Fishbein et al. 2001; AF274662
Podocarpaceae:				
Podocarpus costalis Presl	Chaw et al. 2000; AF029369			
Podocarpus macrophyllus (Thunb.) Sweet		Qiu 95006; OD/FBQ/YQ; DQ008837	Wang and Shu 2000; AF228111	Qiu 95006; OD/YQ; DQ008664
Potamogetonaceae:				
Potamogeton berchtoldii Fieber	Qiu 96063; JL/LL/YQ; DQ008723	Qiu 96063; OD/FBQ/YQ; DQ008810		Qiu 96063; OD/YQ; DQ008649
Potamogeton distinctus Arth. Benn.			Tanaka et al. 1997; AB002581	
Proteaceae:				
Grevillea banksii R. Br.			Hilu et al. 2003; Borsch 3413 BONN AF542583 (TB)	
Grevillea robusta Cunn. & R. Br.	Parkinson et al. 1999; AF193995	Qiu 94087; OD/FBQ/YQ; DQ008751		Qiu 94087; OD/YQ; DQ008612
Persoonia katerae P. Weston & L. Johnson	Weston 1120, NSW; JL/LL/YQ; DQ008724	Weston 1120, NSW; OD/FBQ/YQ; DQ008750	Weston 1120, NSW; TB; AY437813	Weston 1120, NSW; OD/YQ; DQ008611
Petrophile canescens Cunn. ex R. Br.	Qiu 98018; JL/LL/YQ; DQ008725	Qiu 98018; OD/FBQ/YQ; DQ008749	Qiu 98018; Kew; AJ966805	Qiu 98018; OD/YQ; DQ008610
Ranunculaceae:				
Ranunculus sp.	Chaw et al. 2000; AF161093	Qiu 95024; OD/FBQ/YQ; DQ008756		
Ranunculus ficaria L.			Borsch 3554 BONN; TB; AY437814	
Ranunculus keniensis Milne-Redhead & Turrill				Zanis et al. 2003; AF389269
Xanthorhiza simplicissima Marshall	Qiu 91030; JL/LL/YQ; DQ008726	Qiu 91030; OD/FBQ/YQ; DQ008757	Hilu et al. 2003; Borsch 3394 BONN AF542567 (TB)	Qiu 91030; OD/YQ; DQ008615
Sabiaceae:				
Sabia sp.	Qiu 91025; JL/LL/YQ; DQ008727	Qiu 91025; OD/FBQ/YQ; DQ008747	Qiu 91025; Kew; AJ966806	
Sabia swinhoei Hemsl.				Zanis et al. 2003; AF389272
Meliosma squamulata Hance	B. Shih 3749, HAST; JL/LL/YQ; DQ008728	B. Shih 3749, HAST; OD/FBQ/YQ; DQ008748		B. Shih 3749, HAST; OD/YQ; DQ008609
Meliosma veitchiorum Hemsl.			Chase 2989, K; Kew; AJ581449	
Sargentodoxaceae:				
Sargentodoxa cuneata (Oliv.) Rehder & Wilson	Pan 93001, NCU; JL/LL/YQ; DQ008729	Pan 93001, NCU; OD/FBQ/YQ; DQ008762	Pan 93001, NCU; Kew; AJ966807	Pan 93001, NCU; OD/YQ; DQ008620

Table 1

(*Continued*)

Family and species	mt-SSU rDNA	mt-LSU rDNA	cp-*matK*	nu-26*S* rDNA
Saururaceae:				
Anemopsis californica (Nutt.) Hook. & Arn.	Qiu 97116; JL/LL/YQ; DQ008730	Qiu 97116; OD/FBQ/YQ; DQ008791	Borsch 3397 BONN; TB; AY437810	Qiu 97116; OD/YQ; DQ008639
Houttuynia cordata Thunb.	Qiu 92016; JL/LL/YQ; DQ008731	Qiu 92016; OD/FBQ/YQ; DQ008793	K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch 3481 BONN AF543737 (TB)	Qiu 92016; OD/YQ; DQ008640
Saururus cernuus L.	Qiu 97098*; JL/LL/YQ; DQ008732	Qiu 97098*; OD/FBQ/YQ; DQ008792	K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch & Wilde 3108, VPI & FR AF543749 (TB)	Zanis et al. 2003; AY095468
Schisandraceae:				
Kadsura japonica (L.) Dunal	Parkinson et al. 1999; AF193985	Parks sn, IND, Qiu 94159*; OD/FBQ/YQ; DQ008823	Hilu et al. 2003; Borsch 3411, BONN AF542565 (KH)	Parks sn, IND, Qiu 94159*; OD/YQ; DQ008657
Schisandra rubriflora			K.W. Hilu, K. Müller, and T. Borsch, unpublished manuscript; Borsch 3477; BONN AF543750 (KH)	
Schisandra sphenanthera Rehd. & Wils.	Parkinson et al. 1999; AF193984	Parks sn, IND, Qiu 94165*; OD/FBQ/YQ; DQ008824		Parks sn, IND, Qiu 94165*; OD/YQ; DQ008658
Siparunaceae:				
Siparuna decipiens (Tul.) A. DC.	Sothers 911, MO; JL/LL/YQ; DQ008733	Sothers 911, MO; OD/FBQ/YQ; DQ008779	Sothers 911, MO; Kew; AJ966808	Sothers 911, MO; OD/YQ; DQ008631
Stemonaceae:				
Croomia pauciflora Miq.	Qiu 97096*; JL/LL/YQ; DQ008734	Qiu 97096*; OD/FBQ/YQ; DQ008808	Qiu 97096*; TB; AY437815	Qiu 97096*; OD/YQ; DQ008647
Taxodiaceae:				
Metasequoia glyptostroboides Hu & Cheng		Qiu 95084; OD/FBQ/YQ; DQ008836	Gadek et al. 2000; AF152203	Qiu 95084; OD/YQ; DQ008663
Tetracentraceae:				
Tetracentron sinensis Oliv.	Parkinson et al. 1999; AF193998	Qiu 90009; OD/FBQ/YQ; DQ008745	Fishbein et al. 2001; AF274633	Fishbein et al. 2001; AF274670
Tofieldiaceae:				
Pleea tenufolia Michaux	Qiu 96128*; JL/LL/YQ; DQ008735	Qiu 96128*; OD/FBQ/YQ; DQ008815	L.W. Chatrou et al., unpublished data; AF465301	Zanis et al. 2003; AY095472
Tofieldia calyculata (L.) Wahlenb.	Qiu 97041; JL/LL/YQ; DQ008736	Qiu 97041; OD/FBQ/YQ; DQ008816		Qiu 97041; OD/YQ; DQ008653
Tofieldia racemosa			Fuse and Tamura 2000; AB040160	
Trimeniaceae:				
Trimenia moorei W.R. Philipson	ANBG 701680; JL/LL/YQ; DQ008737	ANBG 701680; OD/FBQ/YQ; DQ008826	ANBG 701680; Kew; AJ966809	Zanis et al. 2003; AY095470
Trochodendraceae:				
Trochodendron aralioides Sieb. & Zucc.	Qiu 49; JL/LL/YQ; DQ008738	Qiu 49; OD/FBQ/YQ; DQ008746	Fishbein et al. 2001; AF274634	Fishbein et al. 2001; AF274671

Welwitschiaceae:				
Welwitschia mirabilis Hook. f.	Chaw et al. 2000; AF161083	Qiu M44; OD/FBQ/YQ; DQ008834	Hilu et al. 2003; Borsch 3410, BONN AF542562 (TB)	Qiu M44; OD/YQ; DQ008662
Winteraceae:				
Drimys winteri J.R. & G. Forster	Parkinson et al. 1999; AF197162	Qiu 90016; OD/FBQ/YQ; DQ008801	Borsch 3479, BONN; TB AY437816	Kuzoff et al. 1998; AF036491
Takhtajania perrieri M. Baranova & J. Leroy	Rabenantoandro 219, MO; JL/LL/YQ; DQ008740	Rabenantoandro 219, MO; OD/FBQ/YQ; DQ008803	Rakotomalaza et al. 1342, MO; Kew; AJ581455	Rabenantoandro 219, MO; OD/YQ; DQ008645
Tasmannia insipida DC	Qiu 90032; JL/LL/YQ; DQ008739	Qiu 90032; OD/FBQ/YQ; DQ008802	Qiu 90032; Kew; AJ966810	Zanis et al. 2003; AY095469
Zamiaceae:				
Zamia floridana A. DC.	Chaw et al. 2000; AF029357	Qiu 95035; OD/FBQ/YQ; DQ008839		Qiu 95035; OD/YQ; DQ008666
Zamia furfuracea Aiton			S. Zhang et al., unpublished data; AF410170	

Note. Vouchers with numbers between Qiu 1 and Qiu 93999 are deposited in NCU, Qiu 94001–Qiu 97999 in IND, Qiu 98001–Qiu 99999 in Z, and Qiu 00001–Qiu 02999 in MICH. Vouchers by collectors other than Qiu are indicated with the herbaria where they have been deposited. Sequence contributors: DES, Douglas E. Soltis; FBQ, Fabiana Bernasconi-Quadroni; KH, Khidir Hilu; JL, Jungho Lee; LL, Libo Li; MZ, Michael Zanis; OD, Olena Dombrovska; PSS, Pamela S. Soltis; TB, Thomas Borsch; YQ, Yin-Long Qiu. Numbers labeled with asterisks are DNA numbers (no voucher or a voucher by someone without a number).

Table 2

Information on New Sequences and Replacements for the Five Genes Used by Qiu et al. (2000) and Correction of Errors in Table A1 of Qiu et al. (2000)

Family and species	mt-*atp1*	mt-*matR*	cp-*atpB*	cp-*rbcL*	nu-18S rDNA
Acoraceae:					
Acorus calamus L.		**Qiu 94052; OD/YQ; DQ007422**			
Acorus gramineus Soland.		**Qiu 97131; OD/YQ; DQ007423**			
Alismataceae:					
Alisma plantago-aquatica L.			**Qiu 96177; LL/YQ; DQ007417**		
Amborellaceae:					
Amborella trichopoda Baill.	**B. Hall sn, IND, Qiu 97123*; JL/YQ; DQ007412**				
Annonaceae:					
Cananga odorata (Lam.) Hook. f. & Thomson			**Chase 219, NCU; LL/YQ; DQ007418**		
Aristolochiaceae:					
Asarum canadense L.			Hoot et al. 1999; U86383		
Thottea tomentosa Ding Hou					**Chase 1211, K; LL/YQ; DQ007406**
Atherospermaceae:					
Daphnandra repandula F. Muell.				Renner et al. 1998; AF052195	
Doryphora aromatica (F.M. Bailey) L.S. Sm.				E. E. M. Ablett et al., unpublished data; L77211	
Cabombaceae:					
Brasenia schreberi J. Gmelin				Les et al. 1991; M77031	
Cabomba caroliniana A. Gray			Graham and Olmstead 2000*b*; AF187058	Les et al. 1991; M77027	
Calycanthaceae:					
Chimonanthus praecox (L.) Link					Soltis et al. 2000; AF503352
Canellaceae:					
Cinnamodendron ekmanii Sleum.				**Zanoni & Jimenez 47067; LL/YQ; DQ007428**	
Ceratophyllaceae:					
Ceratophyllum demersum L.			Savolainen et al. 2000; AJ235430		
Chloranthaceae:					
Ascarina rubricaulis Solms	Thien 500, NO; JL/FBQ/YQ; AF197667	Thien 500, NO; FBQ/JL/YQ; AF197755		Thien 500, NO; ZC/JL/YQ; AF197592	

Hedyosmum arborescens Sw.			Savolainen et al. 2000; AJ235491		
Cycadaceae:					
Cycas revoluta Thunb.			**Pryer et al. 2001; AF313558**		
Degeneriaceae:					
Degeneria vitensis	JM Miller 1189-63; JL/FBQ/YQ; AF293752	JM Miller 1189-63; FBQ/JL/YQ; AF197771	Savolainen et al. 2000; AJ235451	Qiu et al. 1993; L12643	Soltis et al. 2000; AF206898
Didymelaceae:					
Didymeles perrieri Olivier					Hoot et al. 1999; AF094541
Dioscoreaceae			Caddick et al. 2002; AF308014		
Eupomatiaceae:					
Eupomatia bennettii F. Muell.					Soltis et al. 1997; AF469771
Eupteleaceae:					
Euptelea polyandra Sieb. & Zucc.			Hoot et al. 1999; U86384		Soltis et al. 1997; L75831
Ginkgoaceae:					
Ginkgo biloba L.			Savolainen et al. 2000; AJ235481		
Gnetaceae:					
Gnetum gnemon L.			Graham and Olmstead 2000*b*; AF187060		
Gomortegaceae:					
Gomortega keule (Molina) I.M. Johnson			Soltis et al. 2000; AF209593	Ueda et al. 1997; AF206773	
Gyrocarpaceae:					
Gyrocarpus americana Jacq.	Chase 317, NCU; JL/FBQ/YQ; AF197701	Chase 317, NCU; FBQ/JL/YQ; AF197805	Savolainen et al. 2000; AJ235487	Qiu et al. 1993; L12647	Soltis et al. 2000; AF206923
Hernandiaceae:					
Hernandia ovigera L.	**Qiu 96255*; JL/YQ; DQ007413**	**Qiu 01007; LL/YQ; DQ007424**	**Qiu 01007; LL/YQ; DQ007419**	**Qiu et al. 1993; L12650**	**Qiu 96255*; FBQ/YQ; DQ007407**
Himantandraceae:					
Galbulimima belgraveana (F. Muell.) Sprague			Savolainen et al. 2000; AJ235478		
Juncaginaceae:					
Triglochin maritima L.				Les et al. 1997; U80714	
Lauraceae:					
Cryptocarya obovata				P. G. Martin and J. Dowd, unpublished data; L28950	
Monimiaceae:					
Peumus boldus Molina				Soltis et al. 2000; AF206807	

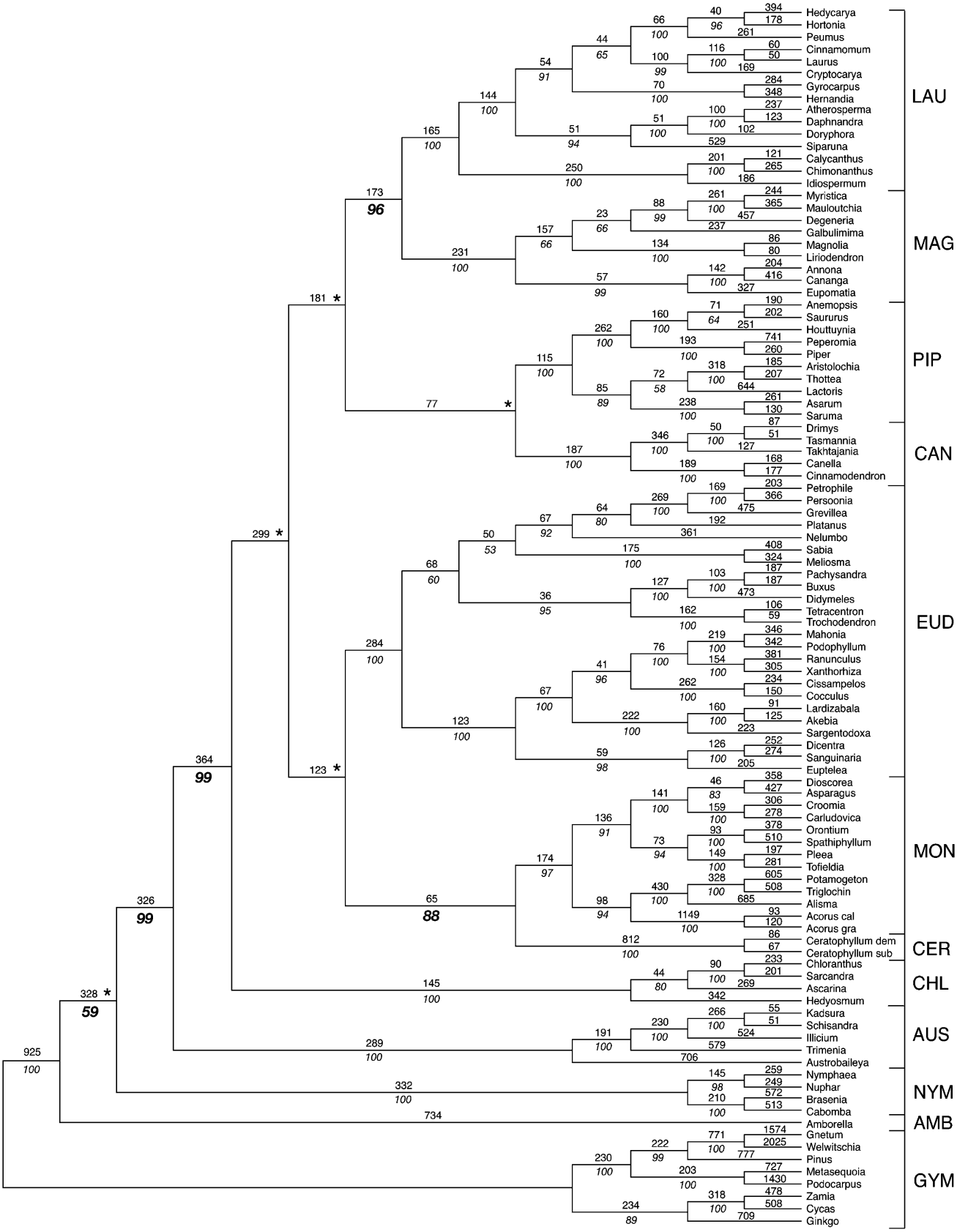
Table 2

(***Continued***)

Family and species	mt-*atp1*	mt-*matR*	cp-*atpB*	cp-*rbcL*	nu-18S rDNA
Hortonia floribunda Wight ex Arn.	**Qiu M166; JL/YQ; DQ007414**		**Qiu 02002*; LL/YQ; DQ007420**	**Renner 1998; AF040663**	**Qiu 02002*; LL/YQ; DQ007408**
Myristicaceae:					
Mauloutchia chapelieri Warb.					**Schatz3847A, MO; LL/YQ; DQ007409**
Nymphaeaceae:					
Nuphar variegata Durand				Les et al. 1991; M77029	
Nymphaea odorata Aiton				Les et al. 1991; M77034	
Piperaceae:					
Peperomia obtusifolia A. Dietr.			Savolainen et al. 2000; AJ235556		
Podocarpaceae:					
Podocarpus costalis Presl					Chaw et al. 1997; D38473
Podocarpus macrophyllus (Thunb.) Sweet		**Qiu 95006; FBQ/YQ; DQ007425**			
Potamogetonaceae:					
Potamogeton berchtoldii Fieber			Qiu 96063; FBQ/JL/YQ; AF197600		**Qiu 96063; LL/YQ; DQ007410**
Proteaceae:					
Persoonia lanceolata				G. M. Plunkett et al., unpublished data; U79178	
Petrophile circinata			Hoot and Douglas 1998; AF060401		
Sabiaceae:					
Meliosma squamulata Hance		**B. Shih 3749, HAST; OD/YQ; DQ007426**			
Saururaceae:					
Saururus cernuus L.					Soltis et al. 1997; U42805
Schisandraceae:					
Schisandra chinensis					Soltis et al. 1997; L75842
Siparunaceae:					
Siparuna brasiliensis (Spreng.) A. DC.			**J. Lombardi 2714, MO; LL/YQ; DQ007421**		
Siparuna decipiens A. DC.					**Sothers 911, MO; LL/YQ; DQ007411**
Stemonaceae:					
Croomia pauciflora Miq.					Caddick et al. 2002; AF309408
Croomia japonica Miq.			Caddick et al. 2002; AF308039		

Tofieldiaceae:					
Pleea tenufolia Michaux				Chase et al. 1993; AJ131774	
Trimeniaceae:					
Trimenia moorei W.R. Philipson	**ANBG 701680; JL/YQ;DQ007415**				
Welwitschiaceae:					
Welwitschia mirabilis Hook. f.			S.W. Graham et al., unpublished data; AF239795		Soltis et al. 2000; AF207059
Winteraceae:					
Takhtajania perrieri M. Baranova & J. Leroy	**Rabenantoandro 219, MO; LL/YQ; DQ007416**	**Rabenantoandro 219, MO; LL/YQ; DQ007427**	Soltis et al. 2000; AF209683		
Tasmannia insipida			Hoot et al. 1999; AF093424		
Zamiaceae:					
Zamia furfuracea Aiton			**Graham and Olmstead 2000*a*; AF188845**		
Zamia pumila L.					Nairn and Ferl 1988; M20017

Note. New sequences are given in boldface.


Hedycarya
Hortonia
Peumus
Cinnamomum
Laurus
Cryptocarya
Gyrocarpus
Hernandia
Atherosperma
Daphnandra
Doryphora
Siparuna
Calycanthus
Chimonanthus
Idiospermum
Myristica
Mauloutchia
Degeneria
Galbulimima
Magnolia
Liriodendron
Annona
Cananga
Eupomatia
Anemopsis
Saururus
Houttuynia
Peperomia
Piper
Aristolochia
Thottea
Lactoris
Asarum
Saruma
Drimys
Tasmannia
Takhtajania
Canella
Cinnamodendron
Petrophile
Persoonia
Grevillea
Platanus
Nelumbo
Sabia
Meliosma
Pachysandra
Buxus
Didymeles
Tetracentron
Trochodendron
Mahonia
Podophyllum
Ranunculus
Xanthorhiza
Cissampelos
Cocculus
Lardizabala
Akebia
Sargentodoxa
Dicentra
Sanguinaria
Euptelea
Dioscorea
Asparagus
Croomia
Carludovica
Orontium
Spathiphyllum
Pleea
Tofieldia
Potamogeton
Triglochin
Alisma
Acorus cal
Acorus gra
Ceratophyllum dem
Ceratophyllum sub
Chloranthus
Sarcandra
Ascarina
Hedyosmum
Kadsura
Schisandra
Illicium
Trimenia
Austrobaileya
Nymphaea
Nuphar
Brasenia
Cabomba
Amborella
Gnetum
Welwitschia
Pinus
Metasequoia
Podocarpus
Zamia
Cycas
Ginkgo
LAU
MAG
PIP
CAN
EUD
MON
CER
CHL
AUS
NYM
AMB
GYM

that are not present in the strict consensus of the two trees indicated by asterisks.

Because the tree topologies from the two parsimony searches are generally congruent, we describe them together. *Amborella*, Nymphaeaceae, and Austrobaileyales form successive sister lineages to the rest of the angiosperms, with generally strong bootstrap support (we regard bootstrap values of 50%–69% as weak, 70%–84% as moderate, and 85% and above as strong support; these cutoff values are designated for convenience of communication, but see Hillis and Bull 1993 for a discussion of phylogenetic implication of bootstrap values). However, the placement of *Amborella* as the sister to all other angiosperms is only weakly to moderately supported. Further, five strongly supported clades are recognized within the remaining angiosperms in the five-protein-gene analysis: monocots, Chloranthaceae, *Ceratophyllum*, magnoliids, and eudicots. In contrast, the monophyly of magnoliids did not receive support of >50% in the nine-gene analysis. *Ceratophyllum* was moderately supported as the sister to eudicots in the five-protein-gene analysis but strongly supported as the sister to monocots in the nine-gene analysis. No other higher-level relationships among the basal angiosperms received bootstrap support above 50%. Finally, within the magnoliids, the sister relationships between Magnoliales and Laurales, between Canellales and Piperales, and between these two larger clades are all strongly supported in the five-protein-gene analysis. In the nine-gene analysis, however, only the sister relationship between Magnoliales and Laurales received strong support. The bootstrap percentages of key nodes in the trees from analyses of nine genes, five protein genes, five protein genes plus 18S rDNA, and five protein genes plus 18S and 26S rDNAs are presented in table 3.

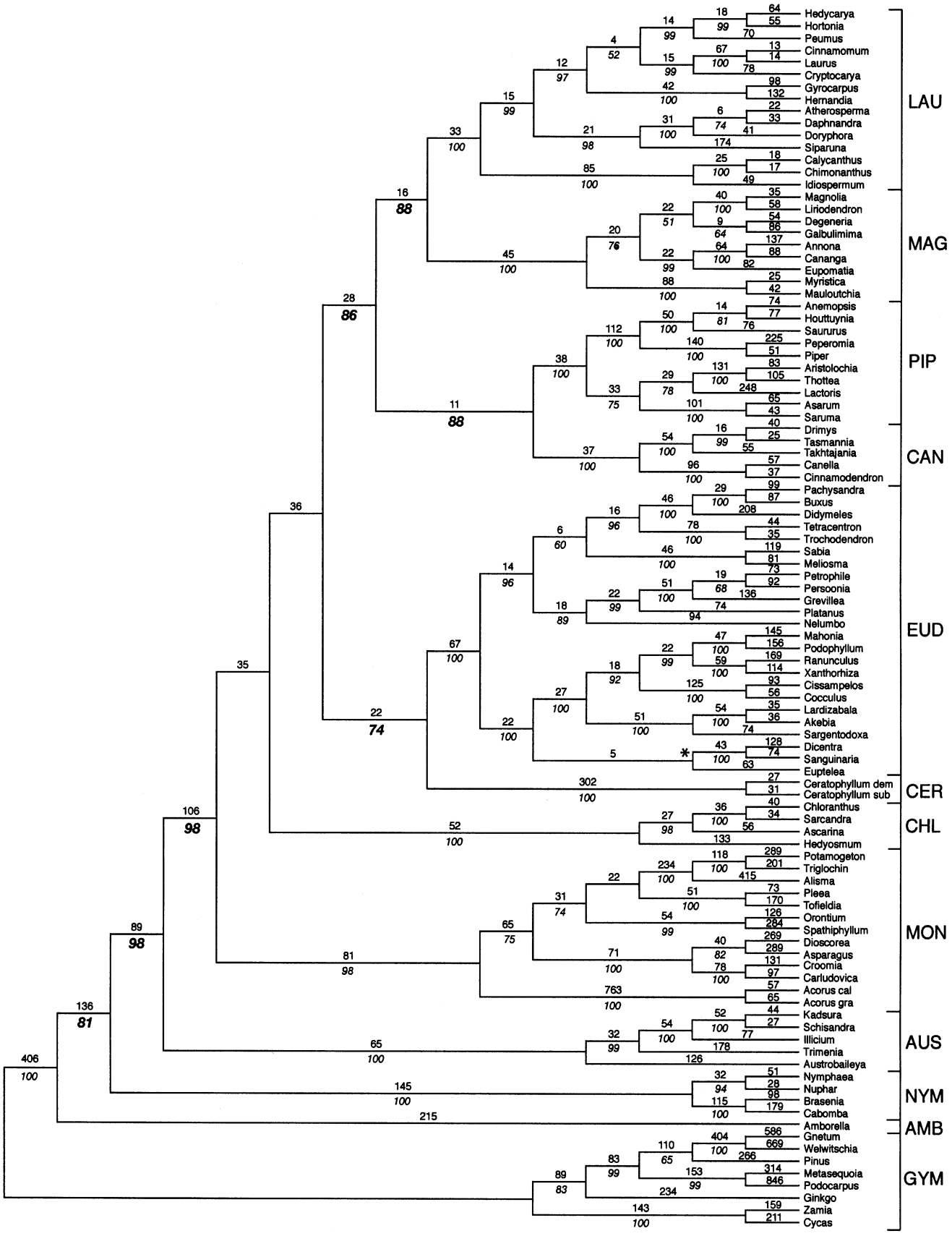
The Bayesian analyses of the nine-gene and five-protein-gene matrices produced similar topologies, with the sole difference being that monocots and eudicots switched position as the sister to magnoliids (fig. 3). There are two additional topological features that are seen in results of the Bayesian but not the parsimony analyses: *Ceratophyllum* is sister to Chloranthaceae (PP = 0.78 and 0.92 in the nine-gene and five-protein-gene analyses, respectively), and *Amborella* is sister to Nymphaeaceae (PP = 1.00 in both analyses). Otherwise, the topologies of the Bayesian and parsimony trees are similar.

The ML analyses of the nine-gene and five-protein-gene matrices also identified certain relationships that were recovered in the parsimony and Bayesian analyses, i.e., monophyly of magnoliids and placement of *Amborella*, Nymphaeales, and Austrobaileyales as successive sisters to all other extant angiosperms, but they differed on resolving relationships among *Ceratophyllum*, Chloranthaceae, magnoliids, monocots, and eudicots. Schematic presentations of the trees from both analyses and the bootstrap values are shown in figure 3.

The parsimony bootstrap analyses of three genome-specific matrices produced similar topologies but with different support for various relationships among basal angiosperms (fig. 4). The positions of *Amborella*, Nymphaeaceae, and Austrobaileyales were supported by all three genome-specific analyses, with the plastid data set giving strong support and the mitochondrial and nuclear data sets providing only moderate to weak support, respectively. Chloranthaceae, *Ceratophyllum*, and eudicots were each recovered with strong support in all three single-genome analyses. Monocot monophyly was strongly supported by plastid data, moderately supported by mitochondrial data, and not supported by a bootstrap value >50% by the nuclear data. The monophyly of magnoliids and relationships among the member clades (Magnoliales, Laurales, Canellales, and Piperales) received only weak support in the plastid genome analysis. The mitochondrial and nuclear data sets contained essentially no phylogenetic signal for recognizing this clade or for resolving relationships among its subclades, with the sole exception that the sister relationship between Magnoliales and Laurales is strongly supported by the mitochondrial data set.

In our examination of the nine-gene alignment, a total of 71 sites were identified that contain apparently synapomorphic substitutions that separate gymnosperms-*Amborella*-Nymphaeaceae-Austrobaileyales and all other angiosperms (fig. 5). With these sites removed, both the shortest tree search and a bootstrapping analysis of the nine-gene matrix identified *Ceratophyllum* as the sister to all other angiosperms, with 55% bootstrap support. *Amborella*, Nymphaeaceae, and Austrobaileyales formed a weakly (63%) supported clade as part of a trichotomy with monocots and a clade containing Chloranthaceae, magnoliids, and eudicots (data not shown). We also conducted a shortest tree search using the 71-site matrix (fig. 5), but because of limited information for resolving relationships among the shallow branches, the search did not finish because of the huge number of trees found and the corresponding computer memory shortage. However, in the trees recovered when the search was aborted, the angiosperms exclusive of *Amborella*, Nymphaeaceae, and Austrobaileyales did form a monophyletic group, with members of the latter three clades variously grouping with the gymnosperms (data not shown). These results confirm that our identification of the sites containing putatively synapomorphic substitutions was correct. The 71 sites are distributed throughout the entire length of each of the nine genes, with only 13 sites linked in five groups (fig. 5). They contain all six possible substitutional changes, with 38 sites exhibiting transitions between gymnosperms-*Amborella*-Nymphaeaceae-Austrobaileyales and all other

Fig. 1 One of the six shortest trees found in the parsimony analysis of the nine-gene matrix. Numbers above branches are branch lengths (ACCTRAN optimization); those below in italics are bootstrap percentages (only those >50% are shown; for branches related to *Amborella*, Nymphaeaceae, Austrobaileyales, *Ceratophyllum*, magnoliids, monocots, and eudicots, the bootstrap percentages are in boldface). The nodes labeled with asterisks are collapsed in the strict consensus of the six shortest trees. Abbreviations: GYM = gymnosperms; AMB = *Amborella*; NYM = Nymphaeaceae; AUS = Austrobaileyales; CHL = Chloranthaceae; CER = *Ceratophyllum*; MON = monocots; EUD = eudicots; CAN = Canellales; PIP = Piperales; MAG = Magnoliales; LAU = Laurales; *Acorus cal* = *Acorus calamus*; *Acorus gra* = *Acorus gramineus*; *Ceratophyllum dem* = *Ceratophyllum demersum*; *Ceratophyllum sub* = *Ceratophyllum submersum*.


Hedycarya
Hortonia
Peumus
Cinnamomum
Laurus
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Gyrocarpus
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Siparuna
Calycanthus
Chimonanthus
Idiospermum
Magnolia
Liriodendron
Degeneria
Galbulimima
Annona
Cananga
Eupomatia
Myristica
Mauloutchia
Anemopsis
Houttuynia
Saururus
Peperomia
Piper
Aristolochia
Thottea
Lactoris
Asarum
Saruma
Drimys
Tasmannia
Takhtajania
Canella
Cinnamodendron
Pachysandra
Buxus
Didymeles
Tetracentron
Trochodendron
Sabia
Meliosma
Petrophile
Persoonia
Grevillea
Platanus
Nelumbo
Mahonia
Podophyllum
Ranunculus
Xanthorhiza
Cissampelos
Cocculus
Lardizabala
Akebia
Sargentodoxa
Dicentra
Sanguinaria
Euptelea
Ceratophyllum dem
Ceratophyllum sub
Chloranthus
Sarcandra
Ascarina
Hedyosmum
Potamogeton
Triglochin
Alisma
Pleea
Tofieldia
Orontium
Spathiphyllum
Dioscorea
Asparagus
Croomia
Carludovica
Acorus cal
Acorus gra
Kadsura
Schisandra
Illicium
Trimenia
Austrobaileya
Nymphaea
Nuphar
Brasenia
Cabomba
Amborella
Gnetum
Welwitschia
Pinus
Metasequoia
Podocarpus
Ginkgo
Zamia
Cycas
LAU
MAG
PIP
CAN
EUD
CER
CHL
MON
AUS
NYM
AMB
GYM

Table 3

Bootstrap (and Jackknife When Indicated) Percentages for a Subset of the Major Clades in the Tree Shown in Figures 1 and 2, and in Several Previous Studies

Clade	3-gene (Soltis et al. 2000) (jack knife)	5-gene (Qiu et al. 2000)	5–11 gene (Zanis et al. 2002)	5-protein (this study)	5-protein + 18S (this study)	5-protein + 18S + 26S (this study)	9-gene (this study)
Amborella "basal"[a]	65	88	91	81	87	89	59
Amborella/Nymphaeaceae basal[b]	72	98	98	98	98	95	99
Amborella/Nymphaeaceae/ Austrobaileyales basal[c]	71	96	98	98	98	93	99
Magnoliids	<50	62	78	86	77	65	<50
Laurales + Magnoliales	...	60	98	88	89	83	96
Canellales + Piperales	...	80	75	88	90	75	<50
Eudicots + Ceratophyllaceae	53	...	...	74	73	...	...
Monocots + Ceratophyllaceae	...	<50	57	...	...	50	88

Note. <50 indicates a clade that was retrieved with a data set but received bootstrap support <50%; ellipsis dots indicate a clade that was not retrieved with the data set indicated.

[a] Monophyly of all angiosperms other than *Amborella*.

[b] Monophyly of all angiosperms other than *Amborella* and Nymphaeaceae.

[c] Monophyly of all angiosperms other than *Amborella*, Nymphaeaceae, and Austrobaileyales.

angiosperms (16 A ↔ G and 22 C ↔ T) and 33 sites showing transversions (8 A ↔ C, 8 A ↔ T, 6 C ↔ G, and 11 G ↔ T). This substitution pattern and frequency clearly contrast with what would be expected if RNA editing and GC-content bias had contributed signal to link *Amborella*-Nymphaeaceae-Austrobaileyales with the gymnosperms. RNA editing and reverse editing should result in far more changes of C ↔ T, A ↔ C, A ↔ T, C ↔ G, and G ↔ T than A ↔ G substitutions. The GC-content bias would predict many more changes of A ↔ G, A ↔ C, G ↔ T, and C ↔ T than those of A ↔ T, and C ↔ G. For the five protein genes, only mitochondrial *atp1* has all four sites located at the third codon positions, and the other four genes (plastid *atpB*, *matK*, *rbcL*, and mitochondrial *matR*) have sites at all three codon positions, with 11, 8, and 24 sites located at the first, second, and third codon positions, respectively. For the four rDNAs, all sites are located in well-aligned conservative regions. These results indicate that the phylogenetic signal in these nine genes that supports placement of *Amborella*, Nymphaeaceae, and Austrobaileyales as basal lineages is not likely due to any peculiar molecular evolutionary phenomena that may cause analytical artifacts, such as RNA editing and GC-content bias.

Discussion

Recent molecular analyses have converged on a topology of basal angiosperm relationships in which (1) *Amborella*, Nymphaeaceae, and Austrobaileyales represent the basal lineages of extant angiosperms; (2) two pairs of traditional magnoliid taxa, Magnoliales-Laurales and Canellales-Piperales, are sister to each other and form the magnoliid clade; and (3) *Ceratophyllum*, Chloranthaceae, monocots, magnoliids, and eudicots form a polytomy after the initial diversification that led to *Amborella*, Nymphaeaceae, and Austrobaileyales (Mathews and Donoghue 1999; Qiu et al. 1999, 2000; Graham and Olmstead 2000*b*; Soltis et al. 2000; Zanis et al. 2002, 2003; Borsch et al. 2003; Hilu et al. 2003; Löhne and Borsch 2005). This set of relationships has been used to formalize a classification system for angiosperms (APG II 2003) and to guide investigation of various aspects of early angiosperm evolution (e.g., Endress and Igersheim 2000; Friis et al. 2000; Thien et al. 2000; Williams and Friedman 2002; Ronse De Craene et al. 2003; Feild et al. 2004; Kramer et al. 2004). Work is still needed to establish firmly that the current consensus rests on a solid phylogenetic foundation and, more importantly, to resolve the polytomy among *Ceratophyllum*, Chloranthaceae, monocots, magnoliids, and eudicots. Attention to these pivotal issues in our understanding of the origin and early evolution of angiosperms is justified, especially given that three recent analyses using entire plastid genome sequences have failed to confirm that *Amborella* and *Nymphaea* are basal lineages in angiosperm phylogeny (Goremykin et al. 2003*a*, 2003*b*, 2004) and published molecular analyses have not obtained full resolution and strong support for most higher-level relationships among basal angiosperms. Below we discuss these issues.

Fig. 2 One of the two shortest trees found in the parsimony analysis of the five-protein-gene matrix. Numbers above branches are branch lengths (ACCTRAN optimization); those below in italics are bootstrap percentages (only those >50% are shown; for branches related to *Amborella*, Nymphaeaceae, Austrobaileyales, *Ceratophyllum*, magnoliids, monocots, and eudicots, the bootstrap percentages are in boldface). The node labeled with an asterisk is collapsed in the strict consensus of the two shortest trees. Abbreviations: GYM = gymnosperms; AMB = *Amborella*; NYM = Nymphaeaceae; AUS = Austrobaileyales; CHL = Chloranthaceae; CER = *Ceratophyllum*; MON = monocots; EUD = eudicots; CAN = Canellales; PIP = Piperales; MAG = Magnoliales; LAU = Laurales; *Acorus cal* = *Acorus calamus*; *Acorus gra* = *Acorus gramineus*; *Ceratophyllum dem* = *Ceratophyllum demersum*; *Ceratophyllum sub* = *Ceratophyllum submersum*.

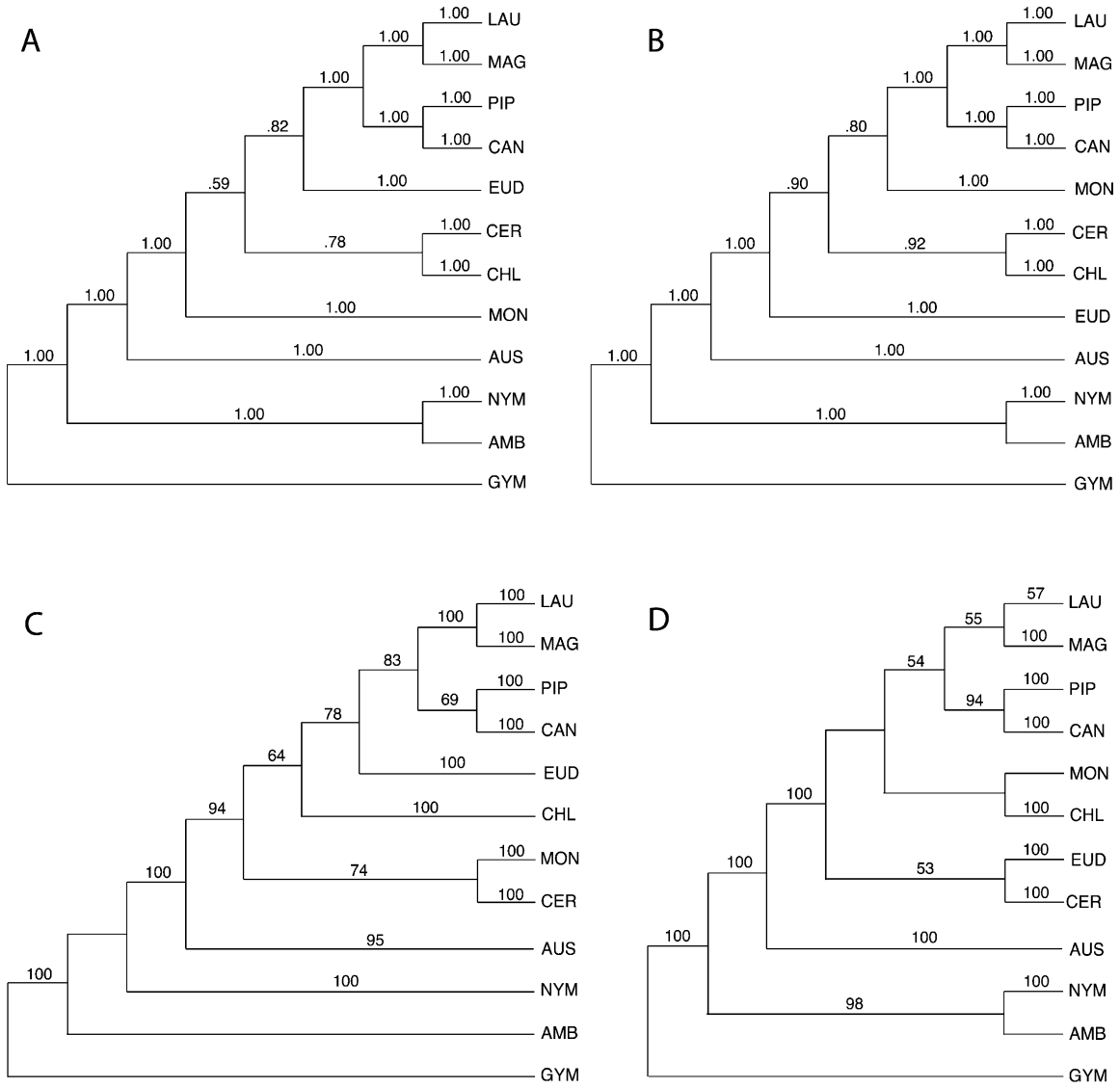

Fig. 3 Simplified presentation of the trees from Bayesian and fast maximum likelihood (ML) analyses of the nine-gene and five-protein-gene matrices. Taxa used in the analyses are the same as those used in figs. 1 and 2. *A*, Bayesian analysis of the nine-gene matrix. *B*, Bayesian analysis of the five-protein-gene matrix. *C*, ML analysis of the nine-gene matrix. *D*, ML analysis of the five-protein-gene matrix. The numbers above the branches are posterior probabilities for Bayesian analyses or bootstrap values for ML analyses. Abbreviations: GYM = gymnosperms; AMB = *Amborella*; NYM = Nymphaeaceae; AUS = Austrobaileyales; CHL = Chloranthaceae; CER = *Ceratophyllum*; MON = monocots; EUD = eudicots; CAN = Canellales; PIP = Piperales; MAG = Magnoliales; LAU = Laurales.

Amborella, Nymphaeaceae, and Austrobaileyales as the Basalmost Lineages of Extant Angiosperms

Several early studies hinted at the possibility that one or more of the three lineages now placed at the base of the angiosperm phylogenetic tree, *Amborella*, Nymphaeaceae, and Austrobaileyales, could represent the earliest-diverging lineages of extant angiosperms (Donoghue and Doyle 1989; Martin and Dowd 1991; Hamby and Zimmer 1992; Qiu et al. 1993; Soltis et al. 1997). However, lack of strong internal support and poor resolution in parts of the topologies prevented general acceptance of those results. In 1999–2000, several comprehensive analyses using extensive taxon and gene sampling as well as duplicate gene rooting strategy identified *Amborella*, Nymphaeaceae, and Austrobaileyales as the successive sister clades to all other angiosperms (Mathews and Donoghue 1999, 2000; Parkinson et al. 1999; Qiu et al. 1999, 2000; Soltis et al. 1999*a*; Barkman et al. 2000; Graham and Olmstead 2000*b*; Soltis et al. 2000). The impressively resolved overall topology with strong bootstrap support and a high degree of convergence of results from different research groups using different taxon and gene sampling schemes as well as different rooting strategies led to the realization that the earliest-diverging lineages of extant angiosperms had been identified. Subsequent analyses with different methods and

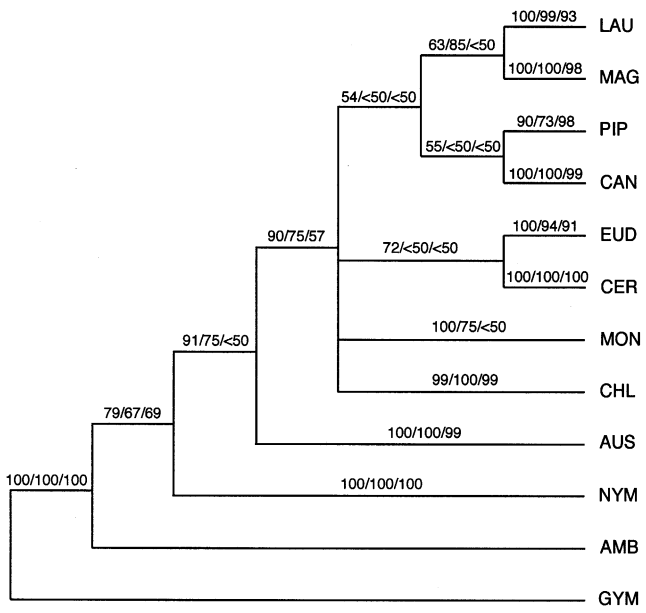

Fig. 4 Simplified presentation of parsimony bootstrap consensus trees of the three genome-specific analyses. Taxa used in the analyses are the same as those used in figs. 1 and 2. The three numbers above the branch separated by slashes are bootstrap values from plastid, mitochondrial, and nuclear genome-specific analyses, respectively. Abbreviations: GYM = gymnosperms; AMB = *Amborella*; NYM = Nymphaeaceae; AUS = Austrobaileyales; CHL = Chloranthaceae; CER = *Ceratophyllum*; MON = monocots; EUD = eudicots; CAN = Canellales; PIP = Piperales; MAG = Magnoliales; LAU = Laurales.

new data have further confirmed and reinforced this consensus (Qiu et al. 2001; Zanis et al. 2002, 2003; Borsch et al. 2003; Hilu et al. 2003; Löhne and Borsch 2005).

In contrast to this seemingly well-established earlier consensus, three recent analyses by Goremykin et al. (2003*a*, 2003*b*, 2004) using entire plastid genome sequences failed to place *Amborella* and *Nymphaea* as basal lineages of angiosperms. Although the scanty taxon sampling, particularly of monocots, which occupy the basalmost position among angiosperms in the trees obtained by these authors, raises doubt about the validity of their conclusions (Soltis and Soltis 2004; Soltis et al. 2004; Stefanovic et al. 2004), it is important that we scrutinize our own data and analyses to ensure that our conclusions are not biased by any analytical problem. Despite theoretical understanding of several longstanding issues in phylogenetics, such as long branch attraction (Felsenstein 1978) and the trade-off between taxon versus character sampling (Hillis 1996, 1998; Graybeal 1998; Soltis et al. 1998; Zwickl and Hillis 2002), it is still not clear how best to diagnose the effects of long branch attraction or inadequate taxon or character sampling in empirical studies. We have therefore conducted various kinds of analyses since our initial publications to detect any possible "misbehavior" of the data that might have contributed to the topology we obtained (cf. Qiu et al. 2000, 2001).

In this study, we further examined the substitutions separating gymnosperms-*Amborella*-Nymphaeaceae-Austrobaileyales from all other angiosperms and found that these changes are distributed in all nine genes from the three genomes and include all six possible substitutional changes at frequencies that do not seem to be biased by RNA editing or GC-content bias (fig. 5). This result, together with previously published tests (Qiu et al. 2000, 2001) that showed that the *Amborella*-Nymphaeaceae-Austrobaileyales rooting in our earlier analyses (Qiu et al. 1999) was unaffected by long branch attraction, suggests that the strategy of using multiple genes and dense "judicious" taxon sampling (Hillis 1998) is effective in tackling the recalcitrant problem of determining the earliest-diverging lineages of extant angiosperms.

In their most recent study, Goremykin et al. (2004) presented a comparison of putative synapomorphic substitutions between the Poaceae-basal or the *Amborella*-Nymphaeaceae-Austrobaileyales-basal topologies and found that there are more sites supporting the former than the latter. We note that their use of a single gymnosperm (*Pinus*) as the outgroup, use of Poaceae as the only representatives of monocots, and exclusion of the third codon positions could lead to misidentification and underdetection of synapomorphic sites. In our analysis, we applied a more stringent criterion to score a site as synapomorphic; namely, it had to be conserved in at least two of the four gymnosperm lineages and two of *Amborella*, Nymphaeaceae, and Austrobaileyales but with a largely invariable different nucleotide in all other angiosperms. Furthermore, conservation of the five linked sites in the mtSSU, GTGTG in gymnosperms-*Amborella*-Nymphaeaceae (fig. 5) actually extends to *Adiantum*, *Huperzia*, and *Lycopodium* (Duff and Nickrent 1999) and possibly throughout all nonflowering land plants (Oda et al. 1992; Duff and Nickrent 1999; Parkinson et al. 1999; Chaw et al. 2000). Moreover, 28 of 47 sites that contain synapomorphic substitutions in the five protein genes are located at the third codon positions. Thus, we argue that the sites we identified are free of the problems of insufficient taxon sampling and bias and probably represent many of the sites that contain phylogenetic signal for resolving the basalmost angiosperm issue.

Finally, the placement of *Amborella*, Nymphaeaceae, and Austrobaileyales as basal lineages is supported by all three single-genome analyses (fig. 4), passing the test that a robust understanding of organismal phylogeny should be supported by analysis of all genomes within the organism (Qiu and Palmer 1999). Additionally, both the nine-gene and five-protein-gene analyses using parsimony, ML, and Bayesian methods give strong support to this topology. In consideration of the variety of analyses we have conducted on our multigene data set in this and previous studies (Qiu et al. 1999, 2000, 2001), it is safe to conclude that the *Amborella*-Nymphaeaceae-Austrobaileyales-basal topology of the angiosperm phylogeny has been rigorously tested. Moreover, the congruent topologies inferred from functionally and structurally different coding genes in this study and others (e.g., phytochromes: Mathews and Donoghue 1999, 2000; floral MADS-box genes: Kim et al. 2004) and noncoding DNAs in the analyses of Borsch et al. (2003) and Löhne and Borsch (2005) should make sufficiently clear that locus-inherent specific patterns of molecular evolution have not led to a spurious conclusion of the rooting of angiosperm phylogeny.

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                                2233332331 31321331133 33332313 21213331311323 3333
                                           |          |          |          |
                Magnolia        GTGGCACCGT CTACCGCCCTC AGTCAAAC TTTTATATTATATA AGGA CGGGA CAAAAC TCACTTA TAATCC
                Pachysandra     .C....T... T.......A.. .T...... .............. ..A. ...AT ...... ....... ......
                Buxus           ..A...T... T.....G.A.. ........ ...T........... ..A. ..... ...... .T..... ....A.
                Didymeles       ......T.A. T..T....A.. ........ ...G........... ..A. ..... ...... C.G.... -....-
                Tetracentron    ......T.A. T.....G.--- ........ .............. ..C. ..... ...... .....C. ......
                Trochodendron   ......T.A. G.....G.--- ........ .............. ..C. ..... ...... .....C. ......
                Sabia           ......TA.. T.......A.. .C.....T ........G..... .TA. ..... G..... ....... ....A.
                Meliosma        ......T... --G..C..A.. .......T ..........C... ..A. ..... .....- ....... ....A.
                Petrophile      ...A..T... --..A.T.... ........ .............. ..A. ..... ...... .....C. -.....
                Persoonia       ...A..T... -...A.T.T.. ........ .............. ..A. ..... ...... .T..... ...-..
                Grevillea       ...A..T... --.T....... ..G..... .............. ..A. ..... G..... .....C. -...A.
                Platanus        ...A..T... T...T...... ........ .............. ..A. ..... ...... ....... ......
EUD             Nelumbo         .C.A..T... T......... G....... -............. ..A. ..... ...... ....... ...CA.
                Mahonia         ...A...T.. -....A..AAT ........ .............. ..A. ..... ...... ....... ....A.
                Podophyllum     ...A...T.. .....A..A.T ........ -............. ..A. ..... ...... ....... ....T.
                Ranunculus      .......... ----------. ........ .............. .AA- ..... ...... ....... ....T.
                Xanthorhiza     ...A...... ---..A..T.T ...A...A -............. ..A. ..... ...... .....C. ......
                Cissampelos     ...AG..... T.......A.T ........ ........G..... ..AT ..... ...... .....CG -...A.
                Cocculus        ...A...... ........A.T ........ -............. ..AT ..... ...... ....... ......
                Lardizabala     ....T...A. T.......A.. ........ .............. .TA. .TC.. A..... ......~ ....A.
                Akebia          ....T...A. -.......A.. ........ -............- .TA. .TC.. A..... ...... ......
                Sargentodoxa    ....T..... ........A.. ........ .............. .TA. .TC.. A..... ......~ ....A.
                Euptelea        ..A....... ......G.A.. .A...... -............- ..A. ..... ...... ....... ......
                Dicentra        .C........ ....TA..... ........ -............. ..A. ..... ...... ....... ...C..
                Sanguinaria     .C........ .....AT.A.. ........ .............. ..A. ..... ...... ....... ....A.
                Ceratophyllum_dem ...A...TA. T.......A.. .T...... ...GC......... ..A. ..... G..... ....C.. ....T.
CER             Ceratophyllum_sub ...A...TA. T.......A.. .T...... ...GC......... ..A. ..... G..... ....C.. ....T.
                Peumus          .......... .......... ........ -............- .... .....- G..... ......G ......
                Hedycarya       .......... .......... ........ .............. .... ...TC T..... .T....G G....-
                Gyrocarpus      .......... .....T.... ........ .............. .... ..... ...... ......G ......
                Hernandia       ....T..... ..C..CA.... ........ .......------ ..-- ..... ...... ....C.G ......
                Cinnamomum      .......... T.CA..G.... ........ ........A..... .... ..... G..... ....C.G ...C..
                Laurus          .......... T.CA..G.... ........ ........A..... .... ..... G..... ....C.G -..C.-
                Cryptocarya     .......... ..G...G.... ........ ...G........... .... ..... G..... ....C.G -.....
LAU             Atherosperma    .......... .......... ........ .............. .... ..... ...... ......G .....-
                Daphnandra      .......... .......... ........ .............. .... ..... ...... ......G -.....
                Doryphora       .......... .......... ........ -............- .... ..... ...... ......G -G...-
                Hortonia        .G........ .......... ........ ---------------- .... ..... T..... ......G .-----
                Siparuna        ....T..... T......... ....G... .............. .... ....-- .T.... .T.T..G -.....
                Calycanthus     ..A....... .......... ........ ........G..... .... ..... ...... ......G G.....
                Chimonanthus    ..A....... -......... ........ -.......G..... .... ..... ...... ......G G.....
                Idiospermum     ..A....... .......... ........ -.......G..... .... ..... ...... ......G -.....
                Annona          ---....... .........A. .....G.. .............. ..C. ..... ...... C....CG -..C..
                Cananga         .......... .........A. ........ .............. .... ..... ...... C....CG ......
                Eupomatia       .......... T......... T....... .............. .... ..... ...... C..... ......
MAG             Liriodendron    .......... .......... ........ -............. .... ..... ...... ....... ......
                Degeneria       .......... ....T..... ........ .............. .... ..... ...... ....... C.....
                Galbulimima     .......... .......... ........ .............. .... ..... ...... .T..... ......
                Myristica       .......... .......... ........ .............. .... ...TC ...... ....... ------
                Mauloutchia     .......... --........ ........ .............. .... ...TC .T.... C...C.. -..C..
                Anemopsis       .......T.. ...TT.T.... ...T.... .............. .CAC ..... G..... .T...CT -...A-
                Saururus        .......... ...TT...... ...T.... -............. .T.. ..... T..... .T...CT ....T.
                Houttuynia      ...-...T.. ...TT...... ...T.... ....T......... .T.. ..... G...C. .T...CT ....A-
                Peperomia       ...A..T... ...TTATG... ...T.... ...AT........- .AA. ..... TCT.TT .ATG.CT .CT.A-
                Piper           .C....TT.. ------..... ...T.... ....T......... .AA. ..... G...~. ...T.CT .C.--.
PIP             Aristolochia    .......... .......... ........ .............. .... ..... ...... .T..... ......
                Thottea         .......... ....T...A.. ........ -............- .... ..... ...... .T..... -.....
                Lactoris        ...A..TT.. ...T....T.. ........ .............. ...T A..T. T..... ..TT... ....A.
                Asarum          ...A...T.. .......... ........ .............. .... ..... ...... ....... .....-
                Saruma          .C.A...T.C .......... ........ .............. .... ..... ...... ....... ......
                Drimys          ...A...... ....A...A.T .A...... .............. .... ..... A..... ....... ......
                Tasmannia       .......... ......T...T .A...... .............. .... ...T. ...... ....... ......
CAN             Takhtajania     .......---- ........A.T ........ .............. .... ..... ----- ....... ......
                Canella         .......... .......... ...T.... .............. .... ..... ..CCT. ...T.C. ......
                Cinnamodendron  .......... .......... ...T.... -............. .... ..... ...... ....C.. ..T.G.
                Dioscorea       .N.A....A. ...G.A..G.. .AC..... -............. .... ..... ...... C.....G ------
                Asparagus       .CA...T... T......... GC.....T .............. .... ..... ...... C....C. -...T-
                Croomia         .C.A...T.. -....AT.... ........ ....T...A..... G... ..... A..... C.G.... -...A-
                Carludovica     .C.A...TA. .....A..... ........ -.......A..... .... ..... ...... C..... -...AT
                Potamogeton     ......T.T. ....TA....T ........ ....C......... .CTC ...TC G..... C..... ....T.
                Triglochin      ......TTT. T....A..T.T ...T...T ....C......... .CTC ...TC TC.... C....C. ....A.
MON             Alisma          .C.A...... .....A....T .T....CG -...CC........- .CTT ..... G..... .T..... C.G...
                Orontium        .......... .....A..T.T .T...... ....T......... .T.. ..... ...... ......~ C.--.
                Spathiphyllum   ..A.G..TA. ........T.T ...A.... ---.T........- .T.. ..... G..... .T....~ C.....
                Pleea           .......... ...-.AG...T ........ .............. .T.. ..... ...... C..... ......
                Tofieldia       ......T... ......G...T ........ .............. .T.. ..... G..... C..... ......
                Acorus_cal      .C....T... G.........T ........ ...C~A..~.A..- ..T. .TC.. ~~~~~A ..G..CG .....-
                Acorus_gra      .C....T... G.........T ........ ...C~A..~.A..- ..T. .TC.. ~~~~~A ..G..CG ......
                Chloranthus     .......... ...A...... ........ .............. ..A. ..... ...... ....... ....A.
CHL             Sarcandra       .......... ...A...... ........ .............. ..A. ..... ...... ....... ......
                Ascarina        .......... T......... ........ -............- ..A. ....-- G..... ....... ---A-
                Hedyosmum       ...A...... .....A.... ........ .............. ..C. .T... G...G. ....... ....T.
                Kadsura         T.A.TG.... TC.TATTGA.G GA.TGGGA C..G....~.CG.T G.TT G.... .....G C.GT.CT GTTGG.
                Schisandra      T.A.TG.... TC.TATTGA.G GA.TGGGA -..G....~.CG.- G.TT G.... .....G C.GT.CT GTTGG.
AUS             Illicium        T.A.TG.T.. TC.TATTGA.G GA.TGGGA C..G......CG.T GTTW G.... .....- C.GT.C. -TTGG-
                Trimenia        ---...T... ...TAT.GA.G G..Y.G.A -..G......CG.- G.-- G.... .....G C.GT..T CTTGG.
                Austrobaileya   T..A.G.... TCGTAT.GA.G G...GGGA C..GC...~.CG.T GTTT G.... .....G C.GT..T GTT.G.
                Nymphaea        TC.AAGTTA. TCGTATTGA.A GACTGGGA CCCGCATGGCCGCT GTTT GTCTC GTGTGG CTGT.CG GT..GT
NYM             Nuphar          TC.AAGTTAC TCGTATTGA.A GACTGGGA CCCGCATGGCCGCT GTTT GTCTC GTGTGG CTGT.CG GT.AG-
                Brasenia        TC.AAGTTAC TCGTATTGACA GACT.GGA CCCGCATGGCCGCT GTTW .TCTC GTGTGG CTGTCCG GC..G-
                Cabomba         --.AAGTTAC TCGTAT--ACA GACT.GGA CCCACATGGCCGCT GTTT GTCTC GTGTGG CTGTCCG GC.AGT
AMB             Amborella       TCAAA.TTAC TCGTATTGACA GAC.GGGA -CCGCATGGCCGC- GT-- GTCTC GTGTGG CTGTCCG G.TGGT
                Gnetum          TAAAA.TTA. ---A.ATA.C. GACT.G.A CC.GCATGGC-GC- GT.T GTC.G GTGTG. CTGTCCG G.TGGT
                Welwitschia     TAAAA.TTAC ---ATATGTCA GA.T...A -C.GCATGGC-GC- GATT GTC.G GTGTGG CTGTACG GTTGG.
                Pinus           TCAAAGTTAC ----ATT.ACA GACTGGGA -CCGCATGGC-GC- GTTT GTCTC GTGTGG C.GTCCC GTTGGT
GYM             Metasequoia     TCAAAGT--- T.GTA.TGACA GAGTG.G. ------------- G.TW -TC.. ------ C.G.CC- -TTGGT
                Podocarpus      T~AAAGT--- T.GTGT.GACA GACT.GGA --CGCATGGTCGC- G.TT GTCTC GTGTGG C.GTCCC GTTGGT
                Ginkgo          TCAAGG.TAC --GTATTGACA GACTGGGA CCCACATGGCCGCT GTT- GTCTC GTGTGT CTGT..G -TTAGT
                Zamia           TCAAGGTTAC TCGTATTGACA C.CTGGGA CCCACACGGCCGC- GTTW GTCTC GTGTGG CTGTCCG CTTAGT
                Cycas           ---AAGTTAC TCGTATTGACA GACTGGGA CCCA.ACGGCCGCT GTTW GTCTC GTGTGG CTGTCCG GTTGGT
                                  atpB       matK       rbcL       matR       atp1 mtLSU mtSSU nu18S  nu26S
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Monophyly of and Relationships within the Magnoliids

Initial support for the magnoliid clade (Qiu et al. 1999, 2000) was not strong, and morphological evidence was lacking (Doyle and Endress 2000). However, other analyses with different methods and data have consistently corroborated this finding (Mathews and Donoghue 1999; Barkman et al. 2000; Graham and Olmstead 2000*b*; Zanis et al. 2002, 2003; Borsch et al. 2003; Hilu et al. 2003). Recent analysis of the group II intron in *petD* also found a synapomorphic indel for the magnoliid clade (Löhne and Borsch 2005). The parsimony analysis of the five-protein-gene matrix in this study yielded strong bootstrap support for both monophyly of the magnoliids and relationships among the four member subclades (fig. 2). Further, Bayesian and ML analyses of both nine-gene and five-protein-gene matrices recovered this clade and resolved the same set of relationships, despite with varying PP and bootstrap values (fig. 3). Thus, it is reasonable to say that the magnoliids represent a major clade of basal angiosperms. The taxa included in this clade represent a majority of the traditional ranalian complex (Qiu et al. 1993). With *Amborella*, Nymphaeaceae, Austrobaileyales, *Ceratophyllum*, Chloranthaceae, Ranunculales, Papaverales, and *Nelumbo* removed, all other taxa of Cronquist's (1981) subclass Magnoliidae remain as magnoliids.

Identification of this large magnoliid clade significantly enhances clarification and will aid further resolution of relationships among basal angiosperms. It effectively reduces the options for placing Chloranthaceae, a family that has been placed previously with Laurales (Thorne 1992), Piperales (Cronquist 1981), and Canellales (Dahlgren 1989) and that is still uncertain for its phylogenetic affinity. Furthermore, placement of Piperales as sister to Canellales within the magnoliids removes the order from the list of taxa to be considered as potential sister lineages to monocots, as Burger (1977) suggested a close relationship between Piperales and monocots. Similarly, Magnoliales (termed as Annonales then) alone can no longer be entertained as a potential sister group to monocots, as proposed by Dahlgren et al. (1985), since they are embedded within the magnoliid clade.

The close relationship between Magnoliales and Laurales was clearly recognized in the premolecular systematics era (Cronquist 1981). Two genome-specific analyses (plastid and mitochondrial), the nine-gene analysis, and the five-protein-gene analysis all identified this relationship, generally with strong support (figs. 1–4). Winteraceae and Canellaceae (collectively classified as Canellales; APG II 2003), traditionally placed in Magnoliales (Cronquist 1981) and still associated with that order in a morphological cladistic analysis by Doyle and Endress (2000), consistently appear as the sister to Piperales. The two larger clades, Magnoliales-Laurales and Canellales-Piperales, are sister to each other in all analyses that recovered the magnoliid clade (Mathews and Donoghue 1999; Graham and Olmstead 2000*b*; Zanis et al. 2002, 2003; Borsch et al. 2003; Hilu et al. 2003). Hence, these relationships among the magnoliid lineages can be deemed robust. However, they are different from those depicted by a morphological cladistic analysis (Doyle and Endress 2000). Convergence at the morphological level may be a factor. Future investigations of the development of morphological characters using molecular genetic approaches (e.g., Buzgo et al. 2004; Kramer et al. 2004) and other nonmolecular characters may sort out homoplasy and identify proper synapomorphies for the several clades identified here.

Relationships among Ceratophyllum*, Chloranthaceae, Monocots, Magnoliids, and Eudicots*

The primary remaining challenge is to resolve relationships among *Ceratophyllum*, Chloranthaceae, monocots, magnoliids, and eudicots. The highly divergent nature of *Ceratophyllum* was noticed by Les and his colleagues as early as 1988 and 1991, based on both morphological and molecular evidence. The phylogenetic affinity of this genus remains elusive. Based on bootstrap support for the placement of *Ceratophyllum*, which is moderate at best, our nine-gene and five-protein-gene analyses present two alternative hypotheses on the placement of the genus, sister to monocots and eudicots, respectively (figs. 1, 2; fig. 3*C*, 3*D*). The relationship of *Ceratophyllum* to eudicots was reported by Soltis et al. (2000) with only 53% jackknife support, by Hilu et al. (2003) with 71% jackknife support, and by Graham et al. (forthcoming) with 82% bootstrap support. The 74% parsimony bootstrap value and 53% ML bootstrap value in our five-protein-gene analyses (fig. 2) support this relationship to eudicots. In contrast, the placement with the monocots supported by our nine-gene analysis using both parsimony and ML methods is undermined by a topological anomaly within the monocots, i.e., the sister relationship of *Acorus* to alismatids (fig. 1). The correct placement of *Acorus* is sister to all other monocots according to several analyses with a large monocot sampling (Chase et al. 2000, forthcoming; Soltis et al. 2000; Hilu et al. 2003). The erroneous position of *Acorus* here could indicate that the placement of *Ceratophyllum* in the nine-gene analysis is an artifact. Indeed, for all four mitochondrial genes we used (*atp1*, *matR*, mtSSU, and mtLSU), *Ceratophyllum*, *Acorus*, and alismatids have highly divergent sequences in comparison to other basal angiosperms, indicating that they could attract to each other as long branches. The relationship of *Ceratophyllum* to Chloranthaceae, shown by our Bayesian analyses of both the nine-gene

Fig. 5 "Synapomorphic substitutions" that separate gymnosperms-*Amborella*-Nymphaeaceae-Austrobaileyales (or just *Amborella* and Nymphaeaceae in some cases) from all other angiosperms in plastid *atpB*, *matK*, and *rbcL*, mitochondrial *matR*, *atp1*, mtLSU, and mtSSU, and nuclear 18S and 26S rDNAs. The numbers in the top row refer to codon positions in the protein genes. A hyphen indicates missing data; a tilde (~) indicates a gap; dots denote the same nucleotides as in *Magnolia* (the top sequence). The underlined sites are contiguous in the original alignment, and all other sites are distributed individually throughout the gene. Abbreviations: GYM = gymnosperms; AMB = *Amborella*; NYM = Nymphaeaceae; AUS = Austrobaileyales; CHL = Chloranthaceae; CER = *Ceratophyllum*; MON = monocots; EUD = eudicots; CAN = Canellales; PIP = Piperales; MAG = Magnoliales; LAU = Laurales.

(PP = 0.78) and five-protein-gene (PP = 0.92) matrices (fig. 3), has been reported only once before (Antonov et al. 2000) and is difficult to evaluate, particularly given the current controversy surrounding the confidence one can have in the PP in Bayesian phylogenetics (Suzuki et al. 2002; Douady et al. 2003; Felsenstein 2004; Simmons et al. 2004).

The placement of Chloranthaceae among other basal angiosperms has long been a subject of debate (Qiu et al. 1993). Our nine-gene and five-protein-gene analyses did not yield bootstrap support to place this family with confidence (figs. 1, 2). Clearly, more work is needed to determine the phylogenetic affinity of this family.

Relationships among magnoliids, monocots, and eudicots, the three lineages encompassing nearly 3%, 22%, and 75% of all angiosperm species diversity, respectively (Drinnan et al. 1994), continue to elude resolution despite several large-scale sequence analyses (Soltis et al. 2000; Savolainen et al. 2000; Hilu et al. 2003). Monocots were placed in a clade with magnoliids and Chloranthaceae with 56% jackknife support in Soltis et al. (2000), and this topology was also recovered by Hilu et al. (2003) using a different data set in a Bayesian analysis (but not in their parsimony analysis). Eudicots-*Ceratophyllum* were sister to this large clade. Our Bayesian analysis of the five-protein-gene matrix obtained a similar topology, with *Ceratophyllum* placed as a sister to Chloranthaceae instead of eudicots (fig. 3). Alternatively, the eudicots-*Ceratophyllum* clade is sister to the magnoliids in our five-protein-gene parsimony analysis, but without bootstrap support >50% (fig. 2). A similar topology was obtained in our earlier studies using a slightly different data set (Qiu et al. 1999, 2000) with the exception that *Ceratophyllum* was not placed with eudicots but rather with monocots. The third possible arrangement for these three large angiosperm lineages, with monocots and eudicots as sister to each other, has been seen in three analyses of plastid and nuclear genes (Mathews and Donoghue 1999; Graham and Olmstead 2000*b*; Graham et al., forthcoming). Thus, all three possible arrangements for monocots, magnoliids, and eudicots have been observed. It is clear that more data, in terms of both character and taxon sampling (particularly of monocots and eudicots), are needed before a firm conclusion can be reached on relationships among these three large angiosperm lineages.

Conclusions

Our analyses, as well as several earlier studies of the angiosperm phylogeny, revealed a steady increase in resolution and internal support for relationships as genes were added to initial single-gene matrices to form multigene data sets. For example, Soltis et al. (1998) revealed a steady increase in support for angiosperm relationships (including basal angiosperm relationships) as sequences from 18S rDNA and *atpB* were added to an *rbcL* data matrix to form two and three-gene data sets (also Soltis et al. 1999*a*, 2000; Savolainen et al. 2000; table 3). Similarly, Qiu et al. (1999, 2000) also observed an increase in the support for basal angiosperm relationships in an analysis of a five-gene data set (table 3). Support for many critical relationships among basal angiosperms continued to increase in the analyses of Zanis et al. (2002), which involved a matrix of five to 11 genes. In this study, phylogenetic analysis of the five protein-coding genes (*atpB*, *matK*, *rbcL*, *atp1*, and *matR*) yielded a topology and internal support for relationships generally comparable to those realized in the earlier multigene analysis of Zanis et al. (2002), with the exception of *Ceratophyllum*, which was placed differently in the two studies. Much of the increase in internal support from these five protein-coding genes compared to the five-gene analysis of Qiu et al. (1999), based on *atpB*, 18S, *rbcL*, *atp1*, and *matR*, involves the signal provided by *matK*. In fact, the rapidly evolving *matK* alone provides resolution and support comparable to that achieved with three more slowly evolving genes, *rbcL*, 18S, and *atpB* (Hilu et al. 2003). Our analyses indicate that the addition of the two nuclear rDNAs does not increase the support for most of the critical nodes we examined (table 3). For example, the addition of 18S did increase the support for the placement of *Amborella* as sister to all other flowering plants, but conversely, the support for the magnoliid clade was somewhat lower than that achieved with the five protein-coding genes. The addition of 26S slightly increased support for the placement of *Amborella*, but support for the monophyly of the magnoliid clade and Canellales + Piperales both decreased compared to the five-protein-gene analysis. The placement of *Ceratophyllum* also changed with the addition of 26S (table 3).

The most dramatic change in the internal support for clades resulted from the addition of the two mitochondrial rDNAs. The addition of these two genes resulted in a sharp drop in the support for *Amborella* as sister to all other angiosperms (to 59%), with support for the monophyly of magnoliids and also of Canellales + Piperales dropping below 50%. These two mitochondrial genes appear to be adding conflicting signal to that from the protein-coding and nuclear 18S rDNA. Conflict is also evident among data sets regarding the placement of *Ceratophyllum* as sister to either eudicots or monocots (table 3). The conflict introduced by mtSSU and mtLSU with regard to monophyly of magnoliids and relationships among their member clades seems to be caused by lineage-specific rate heterogeneity in these two genes (data not shown), whereas the drop in support for *Amborella* as the sister to all other angiosperms after addition of these two genes reflects a genuine uncertainty on the exact topology at the first node in the angiosperm phylogeny, as *Amborella* and Nymphaeaceae together are supported as the earliest-diverging lineage in three of the six analyses performed in this study (fig. 3; Barkman et al. 2000; Qiu et al. 2000; Stefanovic et al. 2004). More data are clearly needed to resolve this kind of conflict among different genes.

The comparisons we have conducted (table 3) provide a valuable lesson in the addition of genes. Although total evidence is a preferred approach (Soltis et al. 1998, 2000; Qiu et al. 1999; Savolainen et al. 2000), with some investigators advocating the combination of many genes (Rokas et al. 2003), it is important to stress that not all genes contain the same amount of information for phylogenetic reconstruction (Hilu et al. 2003) and that not all genes have the same history (Maddison 1997). These gene-specific effects are caused by differences in size and internal mutational dynamics and have to be considered in addition to well-known effects of different evolutionary histories caused by reticulations or

lineage sorting. Although total evidence is encouraged, it is important to evaluate the contribution and impact of individual genes. In our analyses, for example, the addition of two mitochondrial and nuclear 26S rDNAs had a negative impact on resolution and support for certain parts of the tree. Chase et al. (forthcoming) also observed that in a seven-gene combined analysis of monocots, the addition of 18S and partial 26S did not increase support and for some clades resulted in weaker support than a combined analysis of protein-coding plastid genes. Therefore, the total evidence approach needs to be taken with caution.

Besides amassing multigene sequence data for a large number of taxa, a different approach also promises to resolve the relationships among major angiosperm lineages, i.e., to search for informative genomic structural changes such as those reported for resolving the origin of and relationships within land plants (Manhart and Palmer 1990; Raubeson and Jansen 1992; Qiu et al. 1998; Lee and Manhart 2002; Dombrovska and Qiu 2004; Qiu and Palmer 2004; Quandt et al. 2004; Löhne and Borsch 2005). This approach is especially promising given that the entire plastid genome from an increasing number of angiosperms and other land plants has been sequenced (Goremykin et al. 2003*a*, 2003*b*; 2004), and more work is in progress. However, caution must be taken to ensure an appropriate taxonomic coverage so that homologous changes can be distinguished from homoplasious ones (Qiu and Palmer 2004).

Therefore, we recommend that future efforts be directed toward exploration of more data, for both sequences and gene/genome structural features, with proper attention paid to both quality and quantity of taxon and character sampling. The most effective and efficient ways to analyze the resulting large matrices remain parsimony methods, which have been shown to be robust even when data are heterogeneous (Kolaczkowski and Thornton 2004). Bayesian bootstrapping (Douady et al. 2003), when it can be practically implemented, will also be worth pursuing on these large matrices. The fast ML method developed by Guindon and Gascuel (2003) provides a third possibility for analyzing large data matrices as demonstrated in this study. Careful evaluation of support values using bootstrapping or jackknifing (internal support, Nei et al. 1998) as well as congruence with other evidence (external support, Chase et al. 1993; taxonomic congruence, Miyamoto and Fitch 1995) will be essential to ensure correct interpretation of analytical results.

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