

PHYLOGENETIC RELATIONSHIPS OF MONOCOTS BASED ON THE HIGHLY INFORMATIVE
PLASTID GENE *ndhF*: EVIDENCE FOR WIDESPREAD CONCERTED CONVERGENCE

THOMAS J. GIVNISH,^{1,14} J. CHRIS PIRES,^{2,15} SEAN W. GRAHAM,³ MARC A. MCPHERSON,^{4,16} LINDA M. PRINCE,⁵
THOMAS B. PATTERSON,¹ HARDEEP S. RAI,³ ERIC H. ROALSON,⁶ TIMOTHY M. EVANS,⁷ WILLIAM J. HAHN,⁸
KENDRA C. MILLAM,¹ ALAN W. MEEROW,⁹ MIA MOLVRAY,¹⁰ PAUL J. KORES,¹⁰ HEATH E. O'BRIEN,^{11,17}
JOCELYN C. HALL,¹² W. JOHN KRESS,¹³ AND KENNETH J. SYTSMA¹

¹Department of Botany, University of Wisconsin, Madison, Wisconsin 53706-1381, USA; ²Department of Agronomy, University of Wisconsin, Madison, Wisconsin 53706-1597, USA; ³UBC Botanical Garden and Centre for Plant Research, University of British Columbia, Vancouver, British Columbia V6T 1Z4, Canada; ⁴Department of Agricultural, Food, and Nutritional Sciences, University of Alberta, Edmonton, Alberta T6G 2E9, Canada; ⁵Rancho Santa Ana Botanic Garden, Claremont, California 91711-3157, USA; ⁶School of Biological Sciences, Washington State University, Pullman, Wash. 99164-4236, USA; ⁷Department of Biology, Hope College, Holland, Michigan 49422-9000, USA; ⁸Department of Biology, Georgetown University, Washington, D.C. 20057-1003, USA; ⁹USDA-ARS-SHRS, National Germplasm Repository, and Fairchild Tropical Garden, Miami, Florida 33156, USA; ¹⁰Department of Biological Sciences, Moorpark College, Moorpark, California 93021-1695, USA; ¹¹Department of Biology, Duke University, Durham, North Carolina 27708, USA; ¹²Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, Massachusetts 02138, USA; ¹³National Museum of Natural History, Department of Botany, Smithsonian Institution, Washington, D.C. 20013-7012, USA
¹⁴Corresponding author (givnish@facstaff.wisc.edu)

ABSTRACT

We used *ndhF* sequence variation to reconstruct relationships across 282 taxa representing 78 monocot families and all 12 orders. The resulting tree is highly resolved and places commelinids sister to Asparagales, with both sister to Liliales–Pandanales in the strict consensus; Pandanales are sister to Dioscoreales in the bootstrap majority-rule tree, just above Petrosaviales. Acorales are sister to all other monocots, with Alismatales sister to all but Acorales. Relationships among the four major clades of commelinids remain unresolved. Relationships within orders are consistent with those based on *rbcL*, alone or in combination with *atpB* and 18S nrDNA, and generally better supported: *ndhF* contributes more than twice as many informative characters as *rbcL*, and nearly as many as *rbcL*, *atpB*, and 18S nrDNA combined. Based on functional arguments, we hypothesized that net venation and fleshy fruits should both evolve—and thus undergo concerted convergence—in shaded habitats, and revert to parallel venation and dry, passively dispersed fruits in open, sunny habitats. Our data show that net venation arose at least 26 times and disappeared 9 times, whereas fleshy fruits arose 22 times and disappeared 11 times. Both traits arose together at least 15 times and disappeared together 5 times. They thus show a highly significant pattern of concerted convergence ($P < 10^{-9}$) and are each even more strongly associated with shaded habitats ($P < 10^{-10}$ to 10^{-23}); net venation is also associated, as predicted, with broad-leaved aquatic plants. Exceptions to this pattern illustrate the importance of other selective constraints and phylogenetic inertia.

Key words: adaptation, biomechanics, correlated evolution, DISCRETE, seed dispersal, submersed plants, tropical forests.

INTRODUCTION

Monocotyledons—with roughly 60,000 species, 92 families, and 12 orders—are the most diverse, morphologically varied, and ecologically successful of the early-divergent angiosperms. Over the past ten years, molecular systematics has revolutionized our understanding of higher-level relationships within the monocots and made them among the best understood in the angiosperms (Chase et al. 1993, 1995a, b, 2000, 2006; Givnish et al. 1999; Bremer 2000,

2002; Kress et al. 2001; Caddick et al. 2002a, b; Hahn 2002; Patterson and Givnish 2002; Pires and Sytsma 2002; Michelangeli et al. 2003; Zanis et al. 2003; Graham et al. 2006; McPherson et al. submitted). Such studies have laid the groundwork for rigorous studies of adaptive radiation, geographic diversification, and the evolution of development, independent of phenotypic convergence among distantly related groups or divergence among close relatives.

Based on a cladistic analysis of more than 500 *rbcL* sequences, Chase et al. (1995a, b) identified six major clades of monocotyledons: commelinids (including Poales, Commelinales, Zingiberales, Dasygogonales, and Arecales), Asparagales, Liliales, Pandanales, Dioscoreales, and Alismatales, with *Acorus* L. sister to all other monocots. However, even when Chase et al. (2000) complemented these data with sequences of *atpB* plastid DNA and 18S nrDNA for a subset

Present addresses: ¹⁵ Division of Biological Sciences, 371 Life Sciences Center, University of Missouri, Columbia, Missouri 65211-7310, USA; ¹⁶ Department of Biology, Duke University, Box 90338, Durham, North Carolina 27708, USA; ¹⁷ Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Alberta T6G 2P5, Canada.

of 140 species—more than tripling the number of nucleotides scored per taxon—relationships among many major clades remained unresolved or weakly supported, and evolutionary ties among several groups of commelinids and asparagoids remained unclear.

To contribute to efforts to resolve these higher-level relationships and investigate the possibility of widespread concerted convergence and plesiomorphy in ecologically significant traits across the monocots, we decided to produce a well-resolved, highly inclusive monocot phylogenetic analysis based on sequences of the plastid gene *ndhF*. This gene provides abundant data for phylogenetic reconstruction: it is more than 50% larger than *rbcL* (ca. 2200 base pairs [bp] vs. ca. 1428 bp) and has substantially more variable positions (Gaut et al. 1997; Patterson and Givnish 2002). Our *ndhF* tree is also ideally suited for analyzing patterns of repeated convergence and divergence among the monocots: it entails many more characters, better resolution, and higher levels of support for individual clades than phylogenetic trees based on *rbcL* alone (albeit for fewer taxa), while incorporating many more taxa than the existing three-gene tree (Chase et al. 2000) based on *rbcL*, *atpB*, and 18S nuclear ribosomal DNA (nrDNA), or the 7- and 17-gene trees now in preparation (Chase et al. 2006; Graham et al. 2006).

Concerted convergence (Givnish and Sytma 1997a, b; Givnish and Patterson 2000; Patterson and Givnish 2002) is the independent rise in different lineages under similar ecological conditions of two or more traits that are genetically, developmentally, and functionally unrelated; *concerted plesiomorphy* involves the retention of the same suite of traits in different lineages under similar conditions (Patterson and Givnish 2002). These phenomena might result from adaptations of unrelated traits to the same environmental conditions, or (possibly more likely) to different components of the shared *set* of conditions. They should be challenging to detect and study using analyses based on phenotypic data, given that multiple (and seemingly independent) characters would carry the same, misleading “signal” regarding evolutionary relationships.

Patterson and Givnish (2002) demonstrated that concerted convergence and plesiomorphy occur among the monocots in the order Liliales. Phylogenetic reconstruction demonstrated that (1) visually showy flowers, capsular fruits, wind-dispersed seeds, narrow leaves, parallel venation, and bulbs arose upon invasion of open seasonal habitats, and (2) visually inconspicuous flowers, fleshy fruits, animal-dispersed seeds, broad thin leaves, net venation, and rhizomes persisted in lineages inhabiting ancestral forest understories. For each trait, the observed variation in phenotype with environment across lineages appeared to be functionally adaptive (Givnish and Patterson 2000; Patterson and Givnish 2002).

Two of these patterns of concerted convergence and plesiomorphy may hold throughout the monocots. Specifically, we predict that net venation and vertebrate-dispersed fleshy fruits should frequently evolve and be retained with each other under shady conditions in forest understories, and that parallel venation and nonfleshy fruits (dispersed by wind, water, or gravity) should frequently evolve and be retained with each other in open habitats. These predictions are based on the biomechanical economy of branched vs. unbranched support networks in thin leaves adapted to shady conditions,

and on the efficiency of dispersal via vertebrates vs. more passive means in less windy forest understories.

Shady conditions favor thin, broad leaf laminae, which cannot support themselves mechanically (especially after small losses of turgor pressure), and therefore require longitudinal and lateral reinforcement from primary and secondary veins (Givnish 1979, 1987). The cost per unit length of such veins scales like their diameter squared, whereas their strength scales like diameter cubed, favoring the coalescence of nearby, subparallel veins into one or few branching ribs of lower cost (Givnish 1979, 1995). Thus, the broader and thinner a lamina or its divisions, the greater should be the advantage of net venation and the greater the advantage of a single midrib. Givnish et al. (submitted) argue that soft, thin, broad leaves are also favored in fast-growing, emergent aquatic plants with access to abundant moisture and nutrients (e.g., *Sagittaria* L.), and in filmy-leaved submerged species adapted for photosynthesis underwater (e.g., *Aponogeton* L. f.). Net venation should thus also be selectively favored in such plants. In addition, whereas wind dispersal of seeds is likely to be effective in open, windy habitats, animal dispersal of fleshy fruits should be more effective below closed habitats (Croat 1978; Givnish 1998). In Neotropical rain forests, up to 95% of the woody understory species (mostly dicots) bear fleshy fruits dispersed by birds, bats, or nonvolant mammals (Gentry 1982).

In this paper, we evaluate these hypotheses by deriving a well-resolved monocot phylogenetic tree based on *ndhF* sequence variation. We compare the resulting clades with those previously resolved based on *rbcL*, *atpB* and 18S nrDNA sequence variation. Finally, we use the *ndhF* tree to test whether fleshy fruits, net venation, and occurrence in shady forest understories show significant patterns of concerted convergence under shady conditions.

MATERIALS AND METHODS

Phylogenetic Analyses

We included 282 monocot species in our analysis, representing as broad and representative a group of taxa as possible, including members of 78 of 92 families and all 12 orders (Table 1). Families and orders follow APG II (2003), except that we recognize Dasypogonales as equaling Dasypogonaceae (see Givnish et al. 1999; Doweld 2001; Reveal and Pires 2002), and Petrosaviales (Cameron et al. 2003). Most of the families unsampled are small, and several are nonphotosynthetic (e.g., Corsiaceae) or occur in wet or submerged habitats (e.g., Anarthriaceae, Posidoniaceae). The families not represented comprise only 1.2% of all monocot species. Only four (Burmanniaceae, Cyclanthaceae, Hydrocharitaceae, Potamogetonaceae) involve substantial numbers of taxa (100–225 species per family). We used *Ceratophyllum* L. as the outgroup, given its position sister to the monocots in several recent analyses (Soltis et al. 1997, 2000; Graham and Olmstead 2000; Zanis et al. 2002; Borsch et al. 2003). Total DNAs were extracted from fresh, deep-frozen, or silica gel-dried leaf material. We amplified and sequenced *ndhF* for most taxa ourselves following standard techniques (see Patterson and Givnish 2002), obtaining both forward and reverse strands in most cases. New sequences were uploaded to GenBank and accession numbers obtained; se-

Table 1. Classification, GenBank accession numbers, vouchers, and authors for the 283 *ndhF* sequences included in this study. Nomenclature follows Bremer et al. (2002) for orders and families (including “bracketed” taxa), and the International Plant Name Index (2004) for generic names, specific epithets, and taxonomic authorities. Specimens sampled include herbarium vouchers, accessions of living plants provided by various botanical gardens, and, in a few instances, initial citations. Material from curated living collections is designated by institution, followed by accession number. Abbreviations are as follows: ADBG (Adelaide Botanical Garden), ADU (University of Adelaide), NYBG (New York Botanical Garden), SEL (Marie Selby Botanical Garden), SIRG (Smithsonian Institution Research Greenhouses), and UCBG (University of California—Berkeley Botanical Garden).

Order and family	Species	GenBank	Voucher, accession, or citation	Author
Acorales				
Acoraceae	<i>Acorus calamus</i> L.	AY007647.2	Denver Botanic Garden, no voucher (RGO 97-149 DNA)	H. O'Brien
	<i>A. gramineus</i> Aiton	AF546992	<i>Rothwell & McPherson/Williams s. n.</i> , ALTA	H. O'Brien
Alismatales				
Alismataceae	<i>Alisma plantago-aquatica</i> L.	AF546993	<i>Buzgo 1013</i> , ALTA	L. Rollins
	<i>Sagittaria latifolia</i> Willd.	AY007657.2	<i>Barrett s. n.</i> , TRT	H. O'Brien
Aponogetonaceae	<i>Aponogeton elongatus</i> Benth.	AY191195	<i>Hahn s. n.</i> , WIS	J. C. Pires
Araceae	<i>Arisaema fraternum</i> Schott	AF546995	<i>Buzgo 953</i> , ALTA	L. Rollins
	<i>Gymnostachys anceps</i> R. Br.	AY191196	<i>Chase 3841</i> , K	J. C. Pires
	<i>Spathiphyllum wallisii</i> Hort.	AY007658.2	<i>Chase 210</i> , NCU	H. O'Brien & S. Graham
Butomaceae	<i>Butomus umbellatus</i> L.	AF546997	<i>Chase 6414</i> , K	L. Rollins
Cymodoceaceae	<i>Halodule wrightii</i> Asch.	AY191197	<i>Kolterman s. n.</i> , WIS	J. C. Pires
Juncaginaceae	<i>Triglochin maritimum</i> L.	AF546998	<i>Buzgo 1011</i> , ALTA	L. Rollins
Limnocaritaceae	<i>Hydrocleys</i> Rich. sp.	AY191198	U Wisconsin—Madison Botanical Garden	J. C. Pires
Scheuchzeriaceae	<i>Scheuchzeria palustris</i> L.	AF547007	<i>Waterway & Graham 97-60</i> , ALTA	M. A. McPherson
Tofieldiaceae	<i>Tofieldia glutinosa</i> (Michx.) Pers.	AF547023	<i>Morton & Venn 9282</i> , ALTA	M. A. McPherson & H. O'Brien
Zosteraceae	<i>Zostera angustifolia</i> (Hornem.) Rchb.	AF547022	<i>Chase 2795-W2</i> , K	H. Rai & L. Rollins
Petrosaviales				
Petrosaviaceae	<i>Japonolirion osense</i> Nakai	AY191199	<i>Chase 3000</i> , K	J. C. Pires
Dioscoreales				
Dioscoreaceae	<i>Dioscorea bulbifera</i> L.	AY007652.2	EPO Biology, U Colorado—Boulder, no voucher (RGO 97-151 DNA)	H. O'Brien
	<i>Tacca chantieri</i> André	AY191200	<i>Hahn 6977</i> , WIS	J. C. Pires
	<i>Trichopus sempervirens</i> (H. Perrier) Caddick & Wilkin	AF546996	<i>Caddick 304</i> , K	L. Rollins
Nartheciaceae	<i>Aletris farinosa</i> L.	AY191201	<i>Smith et al. 2263</i> , WIS	J. C. Pires
	<i>Narthecium ossifragum</i> Huds.	AY191202	<i>Chase 610</i> , K	J. C. Pires
Pandanales				
Pandanaceae	<i>Pandanus utilis</i> Bory	AY191203	<i>Hahn 6898</i> , WIS	J. C. Pires
Stemonaceae	<i>Croomia japonica</i> Miq.	AF547002	<i>Rothwell & Stockey 43</i> , ALTA	M. A. McPherson
	<i>Stemona tuberosa</i> Lour.	AF547009	<i>Rothwell & Stockey 46</i> , ALTA	M. A. McPherson
	<i>Stichoneuron caudatum</i> Ridl.	AF547010	<i>Rothwell & Stockey 45</i> , ALTA	M. A. McPherson
Velloziaceae	<i>Vellozia</i> Vand. sp.	AF546999	<i>Kubitzki & Feuerer 97-3</i> , HBG	L. Rollins
	<i>Talbotia elegans</i> Balf.	AF547011	<i>Rothwell & Stockey 48</i> , ALTA	M. A. McPherson
Liliales				
Alstroemeriaceae	<i>Alstroemeria</i> L. sp.	AF276011	<i>Anderson 13653</i> , MICH	T. B. Patterson
Calochortaceae	<i>Calochortus albus</i> Dougl. ex Benth.	AF275994	<i>Patterson 13</i> , WIS	T. B. Patterson
	<i>C. apiculatus</i> Baker	AF275995	<i>Patterson 1060</i> , WIS	T. B. Patterson
	<i>C. weedii</i> Wood	AF275998	<i>Patterson 18</i> , WIS	T. B. Patterson
	<i>Prosartes maculata</i> A. Gray	AF276015	<i>Foster s. n.</i> , Messiah Coll.	T. B. Patterson
	<i>Scoliopus bigelovii</i> Torr.	AF276017	<i>Kalt 9278</i> , WIS	T. B. Patterson
	<i>Streptopus amplexifolius</i> DC.	AF276019	<i>Foster s. n.</i> , Messiah Coll.	T. B. Patterson
	<i>S. lanceolatus</i> (Aiton) J. L. Reveal	AF276020	<i>Foster s. n.</i> , Messiah Coll.	T. B. Patterson
	<i>Tricyrtis affinis</i> Makino	AF276021	<i>Chase 2777</i> , K	T. B. Patterson
	<i>T. latifolia</i> Maxim.	AF276022	<i>Patterson 1070</i> , WIS	T. B. Patterson
Campynemataceae	<i>Campynema lineare</i> Labill.	AF276013	<i>Walsh 3488</i> , MEL	T. B. Patterson
Colchicaceae	<i>Androcymbium ciliolatum</i> Schltr. & K. Krause	AF276012	<i>Chase 272</i> , NCU	T. B. Patterson
	<i>Disporum flavens</i> Kitagawa	AY438618	<i>Millam 1307</i> , WIS	K. C. Millam
	<i>Uvularia sessilifolia</i> J. F. Gmel.	AF276023	<i>Patterson 10</i> , WIS	T. B. Patterson
	<i>Wurmbea pygmaea</i> (Endl.) Benth.	AF547012	<i>Case 77</i> , PERTH	M. A. McPherson

Table 1. Continued.

Order and family	Species	GenBank	Voucher, accession, or citation	Author	
Liliaceae	<i>Cardiocrinum giganteum</i> Makino	AF275999	Chase 3689, K	T. B. Patterson	
	var. <i>yunnanense</i> Makino	AF276000	Chase 935, K	T. B. Patterson	
	<i>Clintonia borealis</i> Raf.	AF276001	Patterson s. n., WIS	T. B. Patterson	
	<i>Erythronium albidum</i> Nutt.	AF276002	Patterson 1069, WIS	T. B. Patterson	
	<i>Fritillaria meleagris</i> L.	AF276003	Patterson 1068, WIS	T. B. Patterson	
	<i>Gagea wilczekii</i> Braun-Blanquet & Maire	AF276004	Chase 748, K	T. B. Patterson	
	<i>Lilium kelleyanum</i> Lemmon	AF276005	Felson 13, WIS	T. B. Patterson	
	<i>L. superbum</i> L.	AY007655.2	Chase 112, NCU	H. O'Brien	
	<i>Lloydia serotina</i> Sweet	AF276006	Jones s. n., K	T. B. Patterson	
	<i>Medeola virginiana</i> L.	AF276007	Patterson 1065, WIS	T. B. Patterson	
	<i>Nomocharis pardanthina</i> Franch.	AF276008	Chase 934, K	T. B. Patterson	
	<i>Notholirion bulbiferum</i> (Lingelsh.) Stearn	AF276009	Patterson s. n., WIS	T. B. Patterson	
	<i>Tulipa pulchella</i> Fenzl	AF276010	Patterson 1066, WIS	T. B. Patterson	
	<i>Trillium flexipes</i> Raf.	AY191205	Givnish, no voucher	J. C. Pires	
	Melianthaceae	<i>Veratrum viride</i> Aiton	AF276024	Chase 551, K	T. B. Patterson
		<i>Xerophyllum tenax</i> (Pursh) Nutt.	AY191204	Pires 99-072, WIS	J. C. Pires
<i>Philesia buxifolia</i> Lam. ex Poir.		AF276014	Chase 545, K	T. B. Patterson	
Philesiaceae	<i>Philesia buxifolia</i> Lam. ex Poir.	AF276014	Chase 545, K	T. B. Patterson	
Ripogonaceae	<i>Ripogonum elseyanum</i> F. Muell.	AF276016	Chase 187, NCU	T. B. Patterson	
Smilacaceae	<i>Smilax hispida</i> Muhl.	AF276018	Givnish s. n., WIS	T. B. Patterson	
Asparagales					
Agapanthaceae	<i>Agapanthus africanus</i> Beauverd	AF508405	UCBG 45.0288, UC	J. C. Pires	
Agavaceae	<i>Agave celsii</i> Hook.	AF508398	UCBG 65.1883, UC	J. C. Pires	
	<i>A. parviflora</i> Torr.	AF508399	UCBG 67.0582, UC	J. C. Pires	
	<i>Anemarrhena asphodeloides</i> Bunge	AY191162	Chase 1022, K	J. C. Pires	
	<i>Anthericum liliago</i> Linn.	AF508402	UCBG 93.0946, UC	J. C. Pires	
	<i>Behnia reticulata</i> Didr.	AY191168	Goldblatt 9273, MO	J. C. Pires	
	<i>Camassia quamash</i> (Pursh) Greene	AF547001	Coxson & Kuijt 5060, ALTA	M. A. McPherson	
	<i>Chlorophytum alismaefolium</i> Baker	AF508400	UCBG 86.949, UC	J. C. Pires	
		AY191163	ADBG G951045, ADU	J. C. Pires	
	<i>Herreria salsaparilha</i> Mart.	AY191178	Chase 2154, K	J. C. Pires	
	<i>Hosta ventricosa</i> (Salisb.) Stearn	AF508401	UCBG 87.0576, UC	J. C. Pires	
	<i>Yucca glauca</i> Nutt.	AF547014	Addicott, McPherson, & Hurlburt, no voucher (SWG 00121DNA)	M. A. McPherson	
Alliaceae	<i>Allium haematochiton</i> S. Watson	AY191160	UCBG 90.0117, UC	J. C. Pires	
	<i>A. textile</i> A. Nels. & J. F. Macbr.	AF547000	McPherson 990704-79, ALTA	M. A. McPherson	
	<i>Ipeion dialystemon</i> Guaglianone	AF508406	UCBG 93.0448, UC	J. C. Pires	
	<i>Leucocoryne coquimbensis</i> F. Phil.	AF508407	UCBG 94.1335, UC	J. C. Pires	
Amaryllidaceae	<i>Amaryllis paradisiicola</i> D. A. Snijman	AY191161	van Jaarsveld 13263, NBG	J. C. Pires	
	<i>Boophone disticha</i> (L. f.) Herb.	AY434486	Malan 121, NBG	A. W. Meerow	
	<i>Cyrtanthus herrei</i> (Leighton) R. A. Dyer	AY434484	van Zyl 104, NBG	A. W. Meerow	
	<i>Eustephia darwinii</i> Vargas	AY434479	Meerow 2436, FTG	A. W. Meerow	
	<i>Griffinia parviflora</i> Ker Gawl.	AY434478	Meerow 2389, FTG	A. W. Meerow	
	<i>Hippeastrum reticulatum</i> Herb.	AY434481	Meerow 2407, FTG	A. W. Meerow	
	<i>Hymenocallis tubiflora</i> Salisb.	AY434482	Meerow 2240, FTG	A. W. Meerow	
	<i>Leucojum aestivum</i> L.	AF547024	Graham 00-4-2, ALTA	M. A. McPherson	
	<i>Narcissus elegans</i> (Haw.) Spach	U79216	Barrett 1434, TRT	S. W. Graham	
	<i>Paramongaia weberbaueri</i> Velarde	AY434480	Meerow 2303, FTG	A. W. Meerow	
	<i>Proiphys cunninghamiana</i> (Lindl.) Habb.	AY434487	Meerow 1188, FTG	A. W. Meerow	
	<i>Scadoxus membranaceus</i> (Baker) Friis & Nordal	AY434485	Meerow 2240, FTG	A. W. Meerow	
	<i>Sternbergia lutea</i> Spreng.	U79224	Barrett 1434, TRT	M. A. McPherson	
	<i>Ungernia flava</i> Boiss. & Haussk. ex Boiss.	AY434483	Meerow 2436, FTG	A. W. Meerow	
	Aphyllanthaceae	<i>Aphyllanthes monspeliensis</i> L.	AY191167	Chase 614, K	J. C. Pires
		<i>Asparagus falcatus</i> L.	AF508403	Hahn 6881, WIS	J. C. Pires
	Asparagaceae	<i>Asparagus falcatus</i> L.	AF508403	Hahn 6881, WIS	J. C. Pires
	Asteliaceae	<i>Astelia banksii</i> A. Cunn.	AY191164	Chase 1072, K	J. C. Pires
		<i>A. fragrans</i> Colenso	AY191165	ADBG G900014, ADU	J. C. Pires
		<i>Collospermum hastatum</i> (Colenso) Skottsb.	AY191166	ADBG G87567, ADU	J. C. Pires

Table 1. Continued.

Order and family	Species	GenBank	Voucher, accession, or citation	Author
Asphodelaceae	<i>Asphodelus</i> L. sp.	AF508409	<i>Pires 99-132</i> , WIS	J. C. Pires
Blandfordiaceae	<i>Blandfordia punicea</i> (Labill.) Sweet	AY191169	<i>Chase 519</i> , K	J. C. Pires
Boryaceae	<i>Alania endlicheri</i> Kunth	AY191170	<i>Conran 707</i> , ADU	J. C. Pires
	<i>Borya septentrionalis</i> F. Muell.	AY225959	<i>Chase 2205</i> , K	J. C. Pires
Hemerocallidaceae	<i>Arnocrinum preissii</i> Lehm.	AY191172	<i>Conran 953</i> , ADU	J. C. Pires
	<i>Caesia calliantha</i> R. J. F. Henderson	AY191173	<i>Conran 826</i> , ADU	J. C. Pires
	<i>Dianella ensifolia</i> (L.) DC.	DQ058413	<i>Hahn 6869</i> , WIS	J. C. Hall
	<i>Geitonoplesium cymosum</i> R. Br.	AY191174	ADBG G880709, ADU	J. C. Pires
	<i>Hensmania turbinata</i> (Endl.) W. Fitzg.	AY191175	<i>Conran 946</i> , ADU	J. C. Pires
	<i>Johnsonia pubescens</i> Lindl.	AY191176	<i>Chase 2213</i> , K	J. C. Pires
	<i>Phormium cookianum</i> Le Jolis	AY191177	ADBG G881651, ADU	J. C. Pires
	<i>Tricoryne elatior</i> R. Br.	AY191206	<i>Conran 827</i> , ADU	J. C. Pires
Hyacinthaceae	<i>Albuca pendula</i> B. Mathew	AF508390	<i>Hannon 94565</i> , RSA	J. C. Pires
	<i>A. setosa</i> Jacq.	AF508391	UCBG 53.0370, UC	J. C. Pires
	<i>Hyacinthus orientalis</i> Linn.	AF508393	<i>Hahn 6861</i> , WIS	J. C. Pires
	<i>Muscari comosum</i> (L.) P. Miller	AF547006	<i>Harder 000419-1</i> , ALTA	M. A. McPherson
	<i>Ornithogalum caudatum</i> Aiton	AF508394	Hort. UW Botany	J. C. Pires
	<i>O. juncifolium</i> Jacq.	AF508395	UCBG 96.0458, UC	J. C. Pires
	<i>O. longibractatum</i> Jacq.	AF508396	UCBG 47.0533, UC	J. C. Pires
	<i>Scilla natalensis</i> Planch.	AF508397	UCBG 77.0338, UC	J. C. Pires
Hypoxidaceae	<i>Hypoxis juncea</i> Sm.	AJ535775	<i>Chase DNA 5946</i> , K	J. C. Pires
Iridaceae	<i>Gladiolus</i> L. spp.	AY191180	<i>Hahn 6970</i> , WIS	J. C. Pires
	<i>Iris missouriensis</i> Nutt.	AF547003	<i>McPherson 000707-5a-7</i> , ALTA	M. A. McPherson
	<i>I. tenax</i> Dougl.	AY191181	<i>Pires 99-077</i> , WIS	J. C. Pires
	<i>Sisyrinchium montanum</i> Greene	AF547008	<i>McPherson 990704-71</i> , ALTA	M. A. McPherson
Ixioliriaceae	<i>Ixiolirion tataricum</i> (Pall.) Herb. & Traub	AY191182	<i>Chase 489</i> , K	J. C. Pires
Lanariaceae	<i>Lanaria lanata</i> Druce	AY191183	<i>Goldblatt 9410</i> , MO	J. C. Pires
Laxmanniaceae	<i>Arthropodium cirratum</i> R. Br.	AY191184	<i>Chase 651</i> , NCU	J. C. Pires
	<i>Cordyline fruticosa</i> (L.) A. Chev.	AY225023	<i>Hahn 6932</i> , WIS	J. C. Pires
	<i>Eustrephus latifolius</i> R. Br.	AY191185	<i>Chase 193</i> , NCU	J. C. Pires
	<i>Lomandra longifolia</i> Labill.	AF547004	<i>Vitt 27411</i> , ALTA	M. A. McPherson
Orchidaceae	<i>Diuris laxiflora</i> Lindl.	AJ535765	<i>Kores & Molvray 209</i> , K	P. Kores & M. Molvray
	<i>Epipactis helleborine</i> (L.) Crantz	AJ535763	<i>Chase 199</i> , K	P. Kores & M. Molvray
	<i>Neuwiedia veratifolia</i> Blume	U20633	Kew DNA O-460	R. Neyland
	<i>Ridleyella paniculata</i> (Ridl.) Schltr.	AJ535768-70	Hort. Botanicus Leiden 31692	P. Kores & M. Molvray
	<i>Spiranthes cernua</i> (L.) L. C. Rich.	AJ535761	<i>Chase 81941 402</i> , K	P. Kores & M. Molvray
	<i>Tropidia effusa</i> Rchb. f.	AJ535766-7	<i>Kores & Molvray 301</i> , K	R. Neyland
Ruscaceae	<i>Convallaria majalis</i> L.	AF508404	<i>Hahn 6867</i> , WIS	J. C. Pires
	<i>Dracaena aubryana</i> Brongn. ex E. Morr.	AY191186	<i>Chase 1102</i> , K	J. C. Pires
	<i>Maianthemum racemosum</i> (L.) Link	AF547005	<i>McPherson 990704-97</i> , ALTA	M. A. McPherson
	<i>Nolina interrata</i> Gentry	AY191188	ADBG W920633, ADU	J. C. Pires
	<i>Ophiopogon wallichianus</i> (Kunth) Hook. f.	AY191189	<i>Chase 2865</i> , K	J. C. Pires
	<i>Polygonatum hookeri</i> Baker	AY191190	<i>Chase 492</i> , K	J. C. Pires
	<i>P. pubescens</i> Pursh	AY191191	<i>Chase 481</i> , K	J. C. Pires
Tecophilaeaceae	<i>Cyanastrum cordifolium</i> Oliv.	U79228	<i>Graham & Barrett 2</i> , TRT	M. A. McPherson
	<i>Cyanella hyacinthoides</i> L.	AY191192	ADBG G870862, ADU	J. C. Pires
	<i>Tecophilaea violiflora</i> Bertero ex Colla	AY191193	<i>Chase 1498</i> , K	J. C. Pires
Themidaceae	<i>Bessera elegans</i> Schult. f.	AF508351	<i>Pires 99-153</i> , WIS	J. C. Pires
	<i>Brodiaea elegans</i> Hoover	AF508357	<i>Pires 96-045</i> , WIS	J. C. Pires
	<i>Dichelostemma congestum</i> Kunth	AF508366	<i>Pires 96-030</i> , WIS	J. C. Pires
	<i>Milla biflora</i> Cav.	AF508371	<i>Rodriguez 2634</i> , IBUG	J. C. Pires
	<i>Muilla maritima</i> S. Watson	AF508375	<i>Pires 98-028</i> , WIS	J. C. Pires
	<i>Triteleia grandiflora</i> Lindl.	AF508380	<i>Hufford 2776</i> , WIS	J. C. Pires
Xanthorrhoeaceae	<i>Xanthorrhoea semiplana</i> F. Muell	AY191207	ADBG W922097, ADU	J. C. Pires
Xeronemataceae	<i>Xeronema callistemon</i> W. R. B. Oliv.	AY191194	ADBG G850899, ADU	J. C. Pires

Table 1. Continued.

Order and family	Species	GenBank	Voucher, accession, or citation	Author
Arecales				
Arecaceae				
	<i>Areca vestiaria</i> Giseke	AY044535	Hahn 6363, WIS	W. Hahn
	<i>Allagoptera arenaria</i> (Gomes) Kuntze	AY044564	Hahn 7047, WIS	W. Hahn
	<i>Bactris humilis</i> (Wall.) Burret	AY044558	Hahn 7384, WIS	W. Hahn
	<i>Beccariophoenix madagascariensis</i> Jum. & H. Perrier	AY044563	Hahn 7077, WIS	W. Hahn
	<i>Calamus caesius</i> Blume	AY044523	Hahn 6390, WIS	W. Hahn
	<i>Caryota mitis</i> Lour.	AY044531	Hahn 6627, WIS	W. Hahn
	<i>Chamaedorea seifrizii</i> Burret	AY044540	Hahn 6897, WIS	W. Hahn
	<i>Drymophloeus litigiousus</i> (Becc.) H. E. Moore	AY044537	Hahn 6370, WIS	W. Hahn
	<i>Elaeis oleifera</i> (Kunth) Cortés	AY044562	Hahn 7085, WIS	W. Hahn
	<i>Leopoldinia pulchra</i> Mart.	AY044547	Hahn 7642, WIS	W. Hahn
	<i>Manicaria saccifera</i> J. Gaertn.	AY044548	Hahn 7641, WIS	W. Hahn
	<i>Nypa fruticans</i> Wurmbr.	AY044525	Hahn 7106, WIS	W. Hahn
	<i>Phoenix dactylifera</i> L.	AY044529	Hahn 6899, WIS	W. Hahn
	<i>Ravenea hildebrandtii</i> C. D. Bouché	AY044544	Hahn 6392, WIS	W. Hahn
	<i>Reinhardtia simplex</i> (Wendl.) Drude ex Dammer	AY044551	Hahn 7811, WIS	W. Hahn
	<i>Serenoa repens</i> (W. Bartram) Small	AY191210	Hahn 7057, WIS	J. C. Pires
Dasypogonales				
Dasypogonaceae				
	<i>Calectasia intermedia</i> Sond.	AY191208	Chase 456, K	J. C. Pires
	<i>Dasypogon bromeliifolius</i> R. Br.	AY191209	Rudall 29, K	J. C. Pires
Commelinales				
Commelinaceae				
	<i>Amischotolype monosperma</i> (C. B. Clarke) I. M. Turner	AY198178	Bogner 1811	T. M. Evans
	<i>Aneilema calceolus</i> Brenan	AY198180	Faden & Faden 77/565, US	T. M. Evans
	<i>Cartonema phillyroides</i> F. Muell.	AY198181	Hort. Munich Bot. Gard. s. n.	T. M. Evans
	<i>Spatholirion longifolium</i> Dunn	AY198179	Chase 593, K	T. M. Evans
Haemodoraceae				
	<i>Anigozanthos flavidus</i> DC.	AF546994	Neyland 1884, MCN	H. O'Brien
	<i>Lachnanthes</i> Ell. sp.	AY191211	Hahn 6973, WIS	J. C. Pires
	<i>Xiphidium caeruleum</i> Aubl.	AF547013	SDSU greenhouse (coll. M. Simpson) SWG 5.7.94 DNA	M. A. McPherson
Hanguanaceae				
	<i>Hanguana</i> Blume sp.	AY125006	Kress 99-6325, US	L. M. Prince
	<i>H. malayana</i> (Jack) Merr.	AY007654	<i>Sirirugsa</i> s. n., SONG	S. W. Graham
		AY191212	<i>Sirirugsa</i> s. n., SONG	J. C. Pires
Philydraceae				
	<i>Philydrum lanuginosum</i> Gaertn.	U41622	Graham & Barrett 1, TRT	S. W. Graham
Pontederiaceae				
	<i>Eichhornia crassipes</i> (Mart.) Solms	U41599	Barrett 814, TRT	S. W. Graham
	<i>Heteranthera limosa</i> (Swartz) Willd.	U41608	Barrett 1054, TRT	M. A. McPherson
	<i>Hydrothrix gardneri</i> Hook. f.	U41606	Barrett 1414, TRT	M. A. McPherson
	<i>Monochoria korsakovii</i> Reg. & Maack	U41615	Barrett 1415, TRT	M. A. McPherson
Zingiberales				
Cannaceae				
	<i>Canna polymorpha</i> Lodd. ex Loud.	AY191214	Hahn 6912, WIS	J. C. Pires
Costaceae				
	<i>Costus pulverulentus</i> Presl	AY191215	Sytsma s. n., WIS	J. C. Pires
	<i>Dimerocostus strobilaceus</i> Kuntze	AY124997	Kress 94-3601, US	L. M. Prince
	<i>Tapeinochilos</i> Miq. sp.	AY124996	Kress 90-2984, US	L. M. Prince
Heliconiaceae				
	<i>Heliconia latispatha</i> Benth.	AY191216	Hahn 6921, WIS	J. C. Pires
Lowiaceae				
	<i>Orchidantha fimbriata</i> Holttum	AY191217	Kress & Beach 87-2159, US	J. C. Pires
Marantaceae				
	<i>Calathea foliosa</i> Rowlee ex Woodson & Schery	AY125003	Duke 287935	L. M. Prince
	<i>Maranta leuconeura</i> E. Morr.	AY191218	Kress 94-3724, US	J. C. Pires
	<i>Marantochloa purpurea</i> (Ridley) Milne-Redhead	AY125004	Kress 78-0894, US	L. M. Prince
	<i>Thaumatococcus daniellii</i> (Benn.) Benth. & Hook. f.	AY125005	Kress 98-6288, US	L. M. Prince
Musaceae				
	<i>Ensete ventricosum</i> (Welw.) E. E. Cheesm.	AY124993	Kress 94-5321, US	L. M. Prince
	<i>Musa</i> L. sp.	AY191219	Sytsma 7203, WIS	J. C. Pires
	<i>Musella lasiocarpa</i> (Fr.) Wu ex H. W. Li	AY124992	Kress 94-3709, US	L. M. Prince

Table 1. Continued.

Order and family	Species	GenBank	Voucher, accession, or citation	Author
Strelitziaceae	<i>Phenakospermum guyanense</i> Endl.	AY124995	<i>Kress 86-2099D</i> , US	L. M. Prince
	<i>Ravenala madagascariensis</i> J. F. Gmel.	AY124994	<i>Kress 92-3504</i> , US	L. M. Prince
Zingiberaceae	<i>Strelitzia</i> Aiton sp.	AY191220	<i>Sytsma 7204</i> , WIS	J. C. Pires
	<i>Alpinia galanga</i> (L.) Willd.	AY125002	SIRG 94-753	L. M. Prince
	<i>Globba curtisii</i> Holttum	AY125001	<i>Kress 99-6347</i> , US	L. M. Prince
	<i>Hedychium flavescens</i> Carey ex Rosc.	AY124998	<i>Kress 99-6590</i> , US	L. M. Prince
	<i>Riedelia</i> Trin. ex Kunth sp.	AY125000	SIRG 98-025	L. M. Prince
	<i>Siphonochilus kirkii</i> (Hook.) B. L. Burt	AY124999	<i>Kress 94-3692</i> , US	L. M. Prince
	<i>Zingiber officinale</i> Roscoe	AY191221	<i>Sytsma 7205</i> , WIS	J. C. Pires
Poales				
Bromeliaceae	<i>Aechmea haltonii</i> H. Luther	L75844	SEL 85-1447	R. G. Terry et al.
	<i>Ananas ananassoides</i> (Baker) L. B. Sm.	L75845	<i>Brown 3129</i> , RM	R. G. Terry et al.
	<i>Brewcaria reflexa</i> (L. B. Sm.) B. K. Holst	AY208982	Givnish et al. 1997	K. C. Millam
	<i>Brocchinia acuminata</i> L. B. Sm.	L75859	SEL 81-1937	R. G. Terry et al.
	<i>B. paniculata</i> Schult. F.	AY208981	<i>Fernandez 8236</i> , PORT	K. C. Millam
	<i>Bromelia</i> Adans. sp.	L75860	<i>Brown 3128</i> , RM	R. G. Terry et al.
	<i>Canistrum giganteum</i> (Baker) L. B. Sm.	L75861	<i>Brown 3183</i> , RM	R. G. Terry et al.
	<i>Catopsis wangerini</i> Mez & Werckle	L75855	<i>Palací 1235</i> , RM	R. G. Terry et al.
	<i>Cryptanthus beuckeri</i> E. Morren	L75856	SEL 89-499	R. G. Terry et al.
	<i>Deuterochonia longipetala</i> Mez	AY208984	Hort. Marnier-Lapostelle s. n.	K. C. Millam
	<i>Dyckia</i> Schult. f. sp.	L75857	<i>Brown 3131</i> , RM	R. G. Terry et al.
	<i>Encholirium</i> Mart. ex Schult. sp.	L75862	SEL 1984-0364	R. G. Terry et al.
	<i>Fosterella penduliflora</i> (C. H. Wright) L. B. Sm.	L75863	SEL 69-1976-12	R. G. Terry et al.
	<i>Glomeropitcairnia penduliflora</i> Mez	L75864	<i>Givnish s. n.</i> , WIS	R. G. Terry et al.
	<i>Guzmania monostachya</i> Rusby	L75865	SEL 82-225	R. G. Terry et al.
	<i>Hechtia lundelliorum</i> L. B. Sm.	AY208985	SEL 85-1005	K. C. Millam
	<i>Hohenbergia disjuncta</i> L. B. Sm.	L75906	SEL 83-393	R. G. Terry et al.
	<i>Mezobromelia pleiosticha</i> J. F. Utley & H. Luther	L75891	SEL 81-1986	R. G. Terry et al.
	<i>Navia saxicola</i> L. B. Sm.	AY208983	Givnish et al. 1997	K. C. Millam
	<i>Nidularium selleanum</i> (Baker) E. Pereira & Leme	L75894	<i>Leme 1830</i> , HB	R. G. Terry et al.
	<i>Pitcairnia carinata</i> Mez	L75902	<i>Brown 3173</i> , RM	R. G. Terry et al.
	<i>Puya aequatorialis</i> André	L75903	SEL 93-211	R. G. Terry et al.
	<i>Tillandsia complanata</i> Benth.	L75899	SEL 79-0519	R. G. Terry et al.
<i>Vriesea viridiflora</i> (Regel) J. R. Grant	L75910	SEL 78-757	R. G. Terry et al.	
Cyperaceae	<i>Carex dioica</i> L.	AF191808	Royal Botanic Garden, Edinburgh 19851401	A. C. Yen
	<i>Cladium californicum</i> (S. Watson) O'Neill	AY129249	<i>Swearingen 1596</i> , RSA	E. H. Roalson
	<i>Dulichium arundinaceum</i> (L.) Britt.	AY129250	<i>Williams 1441</i> , RSA	E. H. Roalson
	<i>Eleocharis elegans</i> (Kunth) Roem. & Schult.	AY129258	<i>Roalson 1458</i> , WS	E. H. Roalson
	<i>Gahnia deusta</i> (R. Br.) Benth.	AY129253	<i>Overton 2708</i> , RSA	E. H. Roalson
	<i>Mapania paradoxa</i> Raynal	AY129256	<i>Granville 13232</i> , US	E. H. Roalson
	<i>Rhynchospora corniculata</i> (Lam.) A. Gray	AY129252	<i>Roalson 1276</i> , WS	E. H. Roalson
	<i>Scirpus nevadensis</i> S. Watson	AY129254	<i>Helmkamp s. n.</i> , RSA	E. H. Roalson
	<i>Ecdiocolea monostachya</i> F. Muell.	AY438617	<i>Hopper 8531</i> , K	M. A. McPherson
	Eriocaulaceae	<i>Eriocaulon compressum</i> Lam.	AF547017	<i>Unwin 241</i> , MU
<i>Tonina fluviatilis</i> Aubl.		AY198182	<i>Givnish 3109</i> , WIS	T. M. Evans
Flagellariaceae	<i>Flagellaria indica</i> L.	U22008	<i>Clark & Zhang 1305</i> , ISC	J. F. Wendel
Joinvilleaceae	<i>Joinvillea ascendens</i> Gaudich.	U21973	NYBG 800379	J. F. Wendel
Juncaceae	<i>Juncus effusus</i> L.	AF547015	<i>Rai 1004</i> , ALTA	H. Rai

Table 1. Continued.

Order and family	Species	GenBank	Voucher, accession, or citation	Author
Mayacaceae	<i>Mayaca fluviatilis</i> Aubl.	DQ058414	Berry 3004, WIS	J. C. Hall
Poaceae	<i>Anomochloa marantoidea</i> Brongn.	U21992	Clark 1299, ISC	J. F. Wendel
	<i>Arundo donax</i> L.	U21998	Clark s. n., ISC	J. F. Wendel
	<i>Avena sativa</i> L.	U22000	Zhang 8400174, ISC	J. F. Wendel
	<i>Bambusa stenostachya</i> Hack.	U21967	Zhang 8400174, ISC	J. F. Wendel
	<i>Brachyelytrum erectum</i> (Schreb.) P. Beauv.	U22005	Clark 1330, ISC	J. F. Wendel
	<i>Chusquea circinata</i> Soderstr. & C. E. Calderón	U21990	Quail Botanical Garden	J. F. Wendel
	<i>Coix lacryma-jobi</i> L.	AF117403	USDA Plant Identification Number (MIN)	R. Spangler et al.
	<i>Guaduella marantifolium</i> Franch.	AF164777	Kobayashi et al. 1539, ISC	L. G. Clark et al.
	<i>Hordeum vulgare</i> L.	U22003	Wise, no voucher, ISU	J. F. Wendel
	<i>Lithachne pauciflora</i> (Sw.) P. Beauv.	U21978	Clark 1298, ISC	J. F. Wendel
	<i>Olyra latifolia</i> L.	U21971	Londoño & Clark 911, ISC	J. F. Wendel
	<i>Oryza sativa</i> L.	NC.001320	Hiratsuka et al. 1989	H. Shimada & M. Sugiura
	<i>Panicum virgatum</i> L.	U21986	Clark 1164, ISC	J. F. Wendel
	<i>Phaenosperma globosa</i> Munro	U22006	Clark 1292, ISC	J. F. Wendel
	<i>Pharus lappulaceus</i> Aubl.	U21994	Clark 1329, ISC	J. F. Wendel
	<i>Phyllostachys edulis</i> Mazel ex J. Houz.	U21970	Clark 1289, ISC	J. F. Wendel
	<i>Poa pratensis</i> L.	U21980	Clark 1156, ISC	J. F. Wendel
	<i>Schizachyrium scoparium</i> Nash	AF117420	Kellogg V48, GH	R. Spangler et al.
	<i>Sorghastrum nutans</i> Nash	AF117421	Clark 1641, ISC	R. Spangler et al.
	<i>Sporobolus indicus</i> (L.) R. Br.	U21983	Clark 1293, ISC	J. F. Wendel
	<i>Tripsacum dactyloides</i> Schltr.	AF117433	Kellogg V49, GH	R. Spangler et al.
	<i>Zea mays</i> L.	NC.001666	Maier et al. 1995	G. Strittmatter & H. Kossel
Rapateaceae	<i>Zoysia matrella</i> Druce	U21975	Clark 1174, ISC	J. F. Wendel
	<i>Amphiphylum rigidum</i> Gleason	AF207638	Fernández, Stergios, Givnish, & Funk 8061, PORT	T. M. Evans & M. L. Zjhra
	<i>Cephalostemon flavus</i> (Link) Steyerm.	AF207624	Smith, Sytsma, & Givnish 303, WIS	T. M. Evans
	<i>Epidryos guayanensis</i> Maguire	AF207632	Berry & Brako 5539, WIS	T. B. Patterson
	<i>Guacamaya superba</i> Maguire	AF207636	Smith, Sytsma, & Givnish 301, WIS	T. M. Evans
	<i>Kunhardtia rhodantha</i> Maguire	AF207635	Smith, Sytsma, & Givnish 300, WIS	T. M. Evans
	<i>Marahuacaea schomburgkii</i> (Maguire) Maguire	AF207633	Fernández, Stergios, Givnish, & Funk 8205, PORT	T. B. Patterson & M. L. Zjhra
	<i>Maschalocephalus dinklagei</i> Gilg & K. Schum.	AF207628	Assí s. n., Côte d'Ivoire 5/95	T. M. Evans
	<i>Monotrema bracteatum</i> Maguire	AF207625	Smith, Sytsma, & Givnish s. n., WIS	T. M. Evans
	<i>Potarophytum riparium</i> Sandwith	AF207627	Givnish 94-3100, WIS	T. M. Evans
	<i>Rapatea paludosa</i> Aubl.	AF207623	Sytsma, Smith, & Givnish 5157, WIS	T. M. Evans
	<i>Saxofridericia regalis</i> Schomb.	AF207637	Hahn 4675, WIS	T. M. Evans & M. L. Zjhra
	<i>Schoenocephalum cucullatum</i> Maguire	AF207634	Sytsma, Smith, & Givnish 5116, WIS	T. M. Evans & M. L. Zjhra
	<i>Spathanthus bicolor</i> Ducke	AY438615	Givnish 89-125, WIS	K. C. Millam
	<i>S. unilateralis</i> Desv.	AY438613	Berry & Bachhuber 10 July 2000, WIS	J. C. Hall
	<i>Stegolepis hitchcockii</i> subsp. <i>morichensis</i> Maguire	AF207629	Smith, Sytsma, & Givnish 297, WIS	T. M. Evans
Restionaceae	<i>Elegia fenestrata</i> Pillans	AF547016	NYBG 1697/95, NY	H. Rai
Thurniaceae	<i>Prionium serratum</i> E. Mey.	AF547019		H. Rai
	<i>Thurnia sphaerocephala</i> Hook. f.	AY208986	Hahn 3999, US	H. Rai
Typhaceae	<i>Sparganium</i> L. sp.	AY191213	Givnish s. n., WIS	J. C. Pires
	<i>Typha angustifolia</i> L.	U79230	Graham 1040, TRT	S. W. Graham
Xyridaceae	<i>Orectanthe sceptrum</i> (Steyerm.) Maguire	AY438616		K. C. Millam & T. M. Evans
	<i>Xyris jupicai</i> Rich.	AF547017	Goldman 1766, BH	H. Rai

quences from previous studies were downloaded from GenBank to complete the data matrix (Table 1). Sequences were visually aligned using MacClade vers. 4 (Maddison and Maddison 2002). Almost all of the 54 indels detected were in-frame and straightforward (albeit laborious) to align, given their general restriction to single species or small sets of close relatives. The aligned data matrix (including 2518 aligned bases) is available upon request from the three senior authors.

Phylogenetic analyses based on maximum parsimony (MP) were conducted using PAUP* vers. 4.0b8 (Swofford 2002). One hundred replicate searches were conducted using tree-bisection-reconnection (TBR) and random stepwise-addition to maximize the chances of detecting multiple islands of trees if they exist. Bootstrap percentages were obtained via TBR searches on 500 random resamplings of the nucleotide data, saving up to 50 trees per replicate. For comparative purposes, an additional MP search was conducted including both nucleotide and indel data; individual indels were treated as equally weighted characters and scored to minimize the number of additional evolutionary events following Baum et al. (1994). We merged our nucleotide data with those analyzed by Chase et al. (2000) to conduct an MP search involving 88 monocot genera for which sequence data are available for 18S nrDNA, *rbcL*, *atpB*, and *ndhF*, using *Acorus* as an outgroup. Based on this analysis, the numbers of informative and variable characters contributed by each of these sequences were calculated.

Calibration of Molecular Phylogenetic Trees Against Time

As previously shown for *rbcL* (Gaut et al. 1992, 1997), *ndhF* displays substantial variation in rates of nucleotide evolution across different groups of monocots, precluding the use of simple molecular clocks to place phylogenetic events and character-state changes on a time line. We therefore used the computer program r8s to transform one of the most-parsimonious *ndhF* trees into ultrametric form—with equal branch lengths from the root after discarding the outgroup *Ceratophyllum*—using cross-verified penalized likelihood (Sanderson 2002). We calibrated this tree against absolute time by fixing the age of the divergence of Acorales from other monocots at 134 million years ago (Mya) (Bremer 2000), while setting the minimum ages of the stem groups of six clades (Poaceae–Joinvilleaceae–Flagellariaceae–Restionaceae, Typhaceae–Sparganiaceae, Zingiberales, Arecales, Araceae, and Tofieldiaceae) equal to 69.5 Mya, 69.5 Mya, 83 Mya, 89.5 Mya, 69.5, and 83 Mya, respectively, based on the estimated ages of the oldest known Cretaceous fossils for these groups (Bremer 2000).

Tests of Concerted Convergence

We used selected *ndhF* trees to test whether fleshy fruits, net venation, and occurrence in shaded understories show correlated evolution employing DISCRETE (Pagel 1994, 1999). DISCRETE uses a continuous Markov model to analyze the evolution of binary characters, incorporating branch lengths and weighting gains and losses equally. We executed separate tests of correlated evolution between (1) fleshy fruits and life in shady habitats; (2) net venation and shady habitats; (3) fleshy fruits and net venation; (4) net

venation and shady habitats, emergent broad-leaved aquatics, or submersed broad-leaved aquatics; and (5) fleshy fruits and net venation, excluding emergent and submersed broad-leaved aquatics. DISCRETE produces a likelihood ratio for which the distribution converges on that of χ^2 with 4 degrees of freedom. We tested for correlated evolution—and hence, concerted convergence—by comparing the observed likelihood ratio against critical values of χ^2 , a conservative approach (Pagel 1999). We conducted each test on four fully resolved trees, chosen randomly from among the maximum-parsimony trees to represent each of the four resolutions of the major polytomy at the base of the commelinids. The other unresolved nodes are unlikely to have any substantial effect on inferences regarding the correlated evolution of fleshy fruits, net venation, or life in shaded understories. We ran each test using branch lengths (inferred number of substitutions) as measures of the amount of molecular evolution down each branch, reflective of time discounted by the rate of molecular evolution inherent to different lineages. Rates of phenotypic transitions were fitted to a gamma distribution, based on median rates in quartiles across monocots. We conducted each test five times independently because DISCRETE can fit slightly different likelihood models to the data from each random starting point, as a result of nearly flat response surfaces and/or large numbers of species. In a few instances, the first step of a DISCRETE run—which evaluates a model assuming *no* correlated evolution between the given pair of traits—returned a log-likelihood substantially below that of other runs. We discarded such cases *a priori* because they represent a much worse fit of the independent model than is possible and would bias the dependent test toward higher significance of correlated evolution. This procedure would, if anything, create a bias *against* acceptance of a significant pattern of correlated evolution.

We considered “net venation” to include branching support structures within leaves, including cases of reticulate venation, simple leaves in which the veins diverge from a massive central rib regardless of whether they branch anatomically (e.g., *Musa*), and compound leaves with a branching rachis (palms). “Fleshy fruits” include berries, drupes, and seeds with showy, massive, nutritional arils dispersed by vertebrates. *Proiphys* Herb. (Amaryllidaceae) has brightly colored capsules that seem to mimic fleshy fruits (Meerow and Snijman 1998) and were scored as such. Seeds dispersed by ants, bearing small arils (elaiosomes), occur in forest and nonforest habitats and can serve as adaptations for purposes not directly related to dispersal (e.g., placement in nutrient-rich ant nests, shelter from frequent fire) (Beattie and Culver 1983; Beattie 1985; Hughes and Westoby 1992; Boyd 2001). The fruits of *Acorus* are anatomically berries, but are minute, have a relatively thick, dry coat, and lack the sweet or oily composition usually associated with adaptation for ingestion and dispersal by vertebrates. Other features of its morphology and (especially) its geographic pattern of genetic variation suggest that *Acorus* is water-dispersed (Liao and Hsiao 1998). Thus, we did not score either ant-dispersed seeds or the dry berries of *Acorus* as fleshy fruits. Species were classified as occurring primarily in open, sunny habitats (e.g., tundra, chaparral, desert) or closed, shady habitats (forest understories). For species growing in seasonally deciduous forests, the timing of leaf activity and fruit production rela-

tive to canopy closure was used to categorize the habitats occupied as sunny or shady (see Patterson and Givnish 2002). Assigning species to these two classes was occasionally problematic: light regimes occupied by different species can vary continuously (e.g., see Leach and Givnish 1999; Givnish et al. 2004b) and most published accounts of ecological distributions are qualitative. However, no matter how one slices the light availability gradient, taxa like *Schizanthyrium* Nees and *Strelitzia* Aiton occur in brightly lit sites, while *Trillium* L. and *Cyanastrum* Cass. occur in shaded understories.

For illustrative purposes, we overlaid net venation, fleshy fruits, and life in shady habitats on an ultrametric tree using MacClade. Accelerated transformation was employed to minimize the number of apparently independent origins of each trait. A complete matrix of venation, fruit, and ecological character states is available upon request from the first author.

RESULTS

Phylogenetic Relationships

Maximum parsimony produced one island of 880 trees, each 16,489 steps in length based on 1727 variable characters, of which 1408 are potentially phylogenetically informative (Fig. 1A–D). Across monocots, *ndhF* strongly supports (85–100% bootstrap) the monophyly of nine of the twelve orders identified by previous molecular studies (Chase et al. 1995a, b, 2000); support is only modest for Commelinales (52%) and Asparagales (65%), and Petrosaviales are represented by only a single taxon (*Japonolirion* Nakai). Several nodes previously unresolved or weakly supported are resolved in the *ndhF* phylogenetic tree. Our analysis demonstrates that (1) Asparagales are sister to the commelinids; (2) both of these groups are sister to Liliales plus Pandanales; (3) *Japonolirion* (Petrosaviales) and/or Dioscoreales are sister to all preceding groups; (4) Alismatales are strongly supported (99% bootstrap) as sister to the preceding orders; and (5) *Acorus* (Acorales) is sister to all other monocots.

Bootstrap support for individual clades is often substantially higher than that based on *rbcL*, considered alone or in combination with *atpB* and 18S nrDNA (see Chase et al. 1995a, b, 2000). Even so, support values are still only modest at several points along the backbones of the asparagoid portion of the tree and the monocot tree as a whole (Fig. 1A–D). In a four-gene analysis, *ndhF* contributes 2.2 times as many informative characters as *rbcL*, and 87% as many as *rbcL*, *atpB*, and 18S nrDNA combined. Only nine nodes are unresolved in the *ndhF* strict consensus tree. Of these, only two—involving a four-way polytomy at the base of the commelinids, and a trichotomy involving four families of Zingiberales—involve substantial numbers of taxa. The commelinid polytomy involves unresolved relationships among Poales (P), Zingiberales plus Commelinales (ZC), Dasypogonales (D), and Arecales (A). Each of these clades is strongly supported individually (79–100%), as are the commelinids as a whole (85%). Among the most-parsimonious trees based on *ndhF* sequence variation, we found four different patterns of relationship among the major commelinid clades: ((P,A),(ZC,D)); (P,(ZC,A,D)); ((P,(ZC,D)),A); and ((P,D),A),ZC).

Within Poales, *ndhF* places Bromeliaceae sister to Typhaceae–Sparganiaceae at the base of the order, with this overall group sister to an unresolved trichotomy involving (1) Rapateaceae, (2) the sedge alliance—Cyperaceae–Juncaceae–Thurniaceae, Eriocaulaceae–Xyridaceae, and Mayacaceae, and (3) the grass alliance—Poaceae, Joinvilleaceae, Ecdeiocoleaceae, Flagellariaceae, and Restionaceae (Fig. 1A–B). Rapateaceae are sister to the grass and sedge alliances in the bootstrap consensus (54% support), and are sister to these groups in the strict consensus tree as well if *Ecdeiocolea* F. Muell. is excluded or if nucleotide characters are sequentially reweighted based on their consistency index. Poaceae and Poaceae–Joinvilleaceae–Ecdeiocoleaceae have 100% bootstrap support, with *Elegia* L. (Restionaceae) and/or Flagellariaceae sister to these other elements of the grass alliance. Thurniaceae are sister to Cyperaceae–Juncaceae (93% bootstrap) at the core of the sedge alliance. Eriocaulaceae and Xyridaceae are monophyletic (100% and 84% bootstrap support, respectively) and each other's closest relatives at the base of the sedge alliance minus Mayacaceae (Fig. 1A). The four major subclades of Poales—the grass alliance, sedge alliance, Rapateaceae, and Bromeliaceae—show as much sequence divergence from each other as that seen among the remaining orders of monocots. Members of the grass and sedge alliances show the highest rates of *ndhF* evolution among monocots; bromeliads display unusually low rates, and rapateads are intermediate in this respect (Fig. 1A–D). Resolution of relationships within the latter two families by highly informative *ndhF* indicates that both require new internal classifications, including five new subfamilies and re-circumscription of an additional two (Givnish et al. 2004a, in press).

Commelinales and Zingiberales are both resolved as sister clades (79% bootstrap support). In Zingiberales, *ndhF* resolves three pairs of sister families—Zingiberaceae–Costaceae (61%), Marantaceae–Cannaceae (80%), and Strelitziaceae–Lowiaceae (89%). Within Commelinales, Pontederiaceae and Haemodoraceae both have 100% bootstrap support as sister taxa. Philydraceae are sister to the rest of Commelinales, but this position is weakly supported (Fig. 1B). One indel supports their placement with Pontederiaceae and Haemodoraceae, and a combined analysis of *ndhF* indels and nucleotides (not shown) places *Philydrum* Banks ex Gaertn. in an unresolved trichotomy with Pontederiaceae–Haemodoraceae and Commelinaceae–Hanguanaceae. *Hanguana* is strongly supported (90%) as being sister to Commelinaceae; *Cartonema* R. Br. is sister to all other members of the latter. Our analysis places the climbing rattan *Calamus* Auct. ex L. sister to the rest of Arecales (98% bootstrap), with the mangrove palm *Nypa* Steck next-divergent. *Dasyopogon* R. Br. and *Calectasia* R. Br. are resolved as forming the monophyletic order Dasypogonales (100% bootstrap).

An important finding of this study is that *ndhF* places Asparagales sister to the commelinids rather than Liliales in the strict consensus tree (Fig. 1C). Asparagales are composed of a ladder of eight clades, with Orchidaceae sister to the rest (Fig. 1C). The sequence of families is broadly similar to that seen in recent studies (see Discussion). Hyacinthaceae are sister to Agavaceae rather than Themidaceae,

ndhF monocot phylogeny

L = 16,489 steps

CI = 0.211

CI' = 0.192

RI = 0.696

A. Poales I

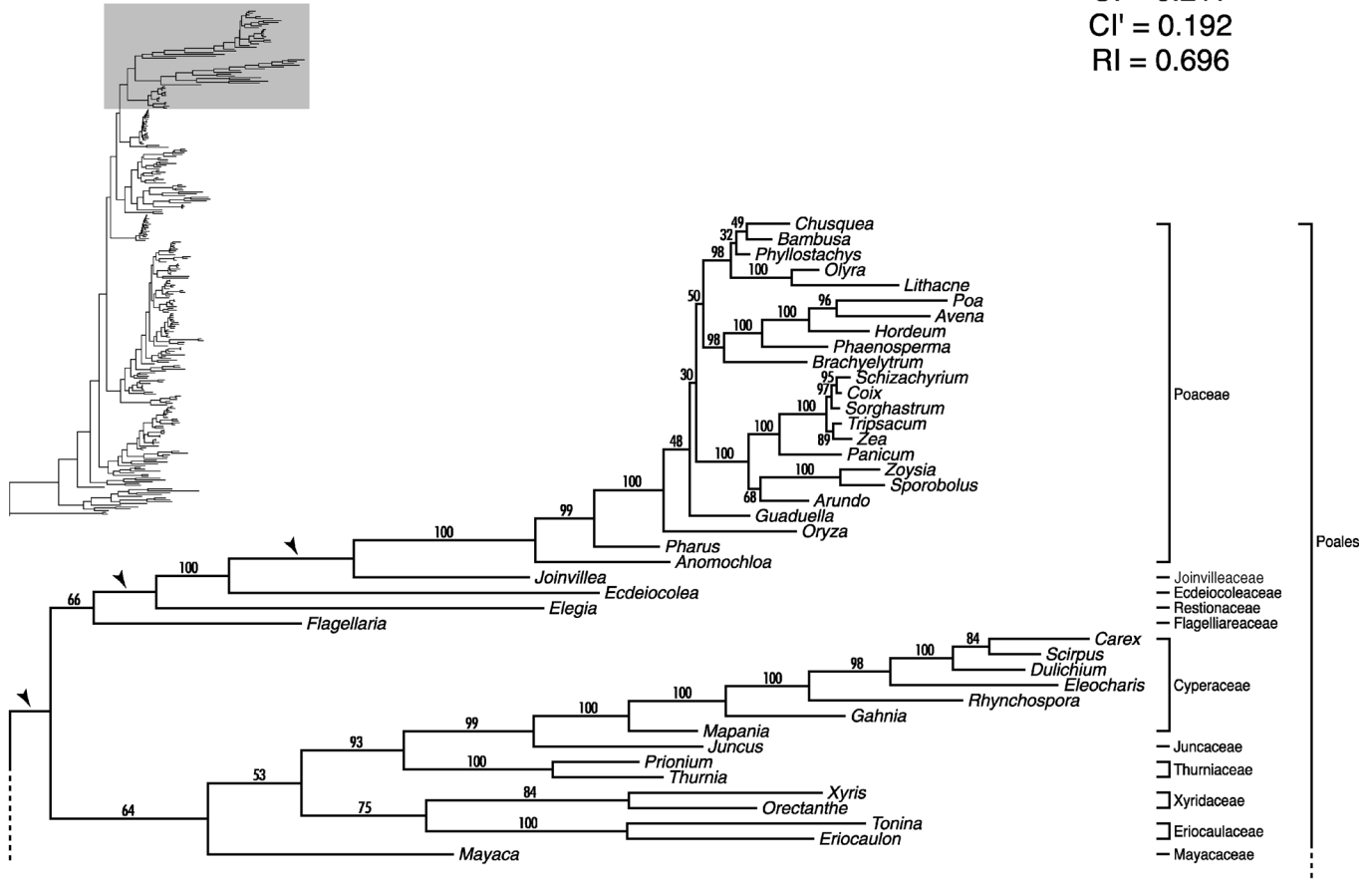


Fig. 1A–D.—Phylogram of one of 874 most parsimonious trees produced by cladistic analysis of *ndhF* sequence variation. CI = consistency index including all variable characters; CI' = consistency index for informative characters only; RI = retention index. Arrowheads indicate nodes that collapse in the strict consensus tree. Bootstrap values are indicated above each node.—A. Poales I.—B. Poales II, Zingiberales, Commelinales, Dasypogonales, and Arecales.—C. Asparagales.—D. Liliales, Pandanales, Dioscoreales, Petrosaviales, Alismatales, and Acorales.

with which they share bulbs and a similar habit. Agapanthaceae are sister to Amaryllidaceae–Alliaceae. Orchidaceae are strongly supported as monophyletic (100% bootstrap), and are placed sister to all other Asparagales with moderate support (Fig. 1C).

In Liliales, *ndhF* identifies *Campynema* Labill. as earliest divergent, followed successively by Melanthiaceae, Colchicaceae–Alstroemeriaceae, Philesiaceae–Ripogonaceae, Smilacaceae, and Liliaceae (Fig. 1D). The last consists of Calochortaceae and Liliaceae sensu Tamura (1998a, b), with *Calochortus* Pursh itself embedded in a lineage containing *Prosartes* D. Don, *Scoliopus* Torr., *Streptopus* Michx., and *Tricyrtis* Wall. *Disporum* Salisb. is sister to *Uvularia* L. in Colchicaceae. *Clintonia* Dougl. ex Lindl. and *Medeola* L., with fleshy fruits and broad, net-veined leaves, are strongly supported as each other's closest relatives, forming subfamily Medeoloideae of Liliaceae (Tamura 1998b); this group is sister, in turn, to subfamily Lilioideae, characterized by capsular fruits and narrow, parallel-veined leaves excepting forest-dwelling, net-veined *Cardiocrinum* Lindl.

Pandanales are sister to Liliales in the *ndhF* strict consen-

sus tree (Fig. 1D), and to Dioscoreales in the bootstrap majority-rule tree. Among the families sampled, Velloziaceae are sister to Pandanaceae–Stemonaceae in Pandanales, and Nartheciaceae are sister to Dioscoreaceae of Dioscoreales. *Japonolirion* of Petrosaviales is part of an unresolved trichotomy involving itself, Dioscoreales, and commelinids–Asparagales–Liliales–Pandanales; together, these groups form a strongly supported clade (100% bootstrap) consisting of all monocots except Alismatales and Acorales (Fig. 1D).

Araceae (100% bootstrap) are sister to Tofieldiaceae and the remaining Alismatales. The latter form a clade with 100% bootstrap support and two well-marked subclades, including Alismataceae–Limnocharitaceae–Butomaceae (95%), and Aponogetonaceae–Juncaginaceae–Scheuchzeriaceae–Cymodoceaceae–Zosteraceae. Juncaginaceae and Scheuchzeriaceae are resolved as sister groups based on *ndhF* sequence variation. Tofieldiaceae are weakly supported (69%) as sister to the families of the former Najadales (Dahlgren et al. 1985). Finally, *ndhF* provides 100% bootstrap support for the position of *Acorus* sister to all other monocots (Fig. 1D).

B. Poales II – Arecales

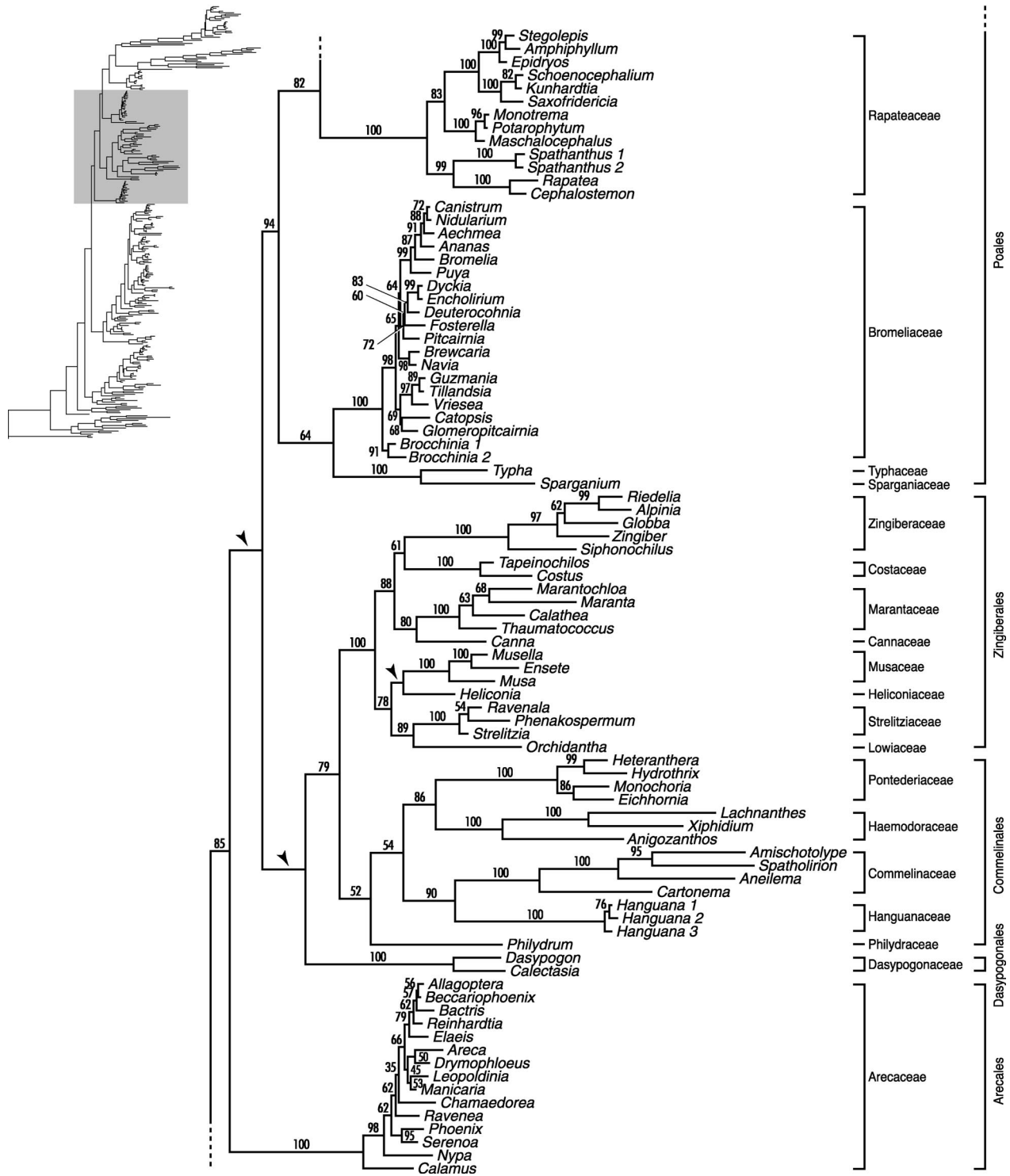


Fig. 1A–D.—Continued.

Concerted Convergence

Based on our *ndhF* data, fleshy fruits appear to have arisen at least 21 times and been lost 11 times, whereas net venation has arisen at least 26 times and been lost 9 times (Table

2; Fig. 2). As predicted, these traits have undergone concerted convergence. They have done so in highly significant fashion ($P < 10^{-9}$, log-likelihood test), with both traits arising together (at the same or adjacent nodes) 15 times and disappearing together 5 times (Table 2; Fig. 2). Fleshy fruits

C. Asparagales

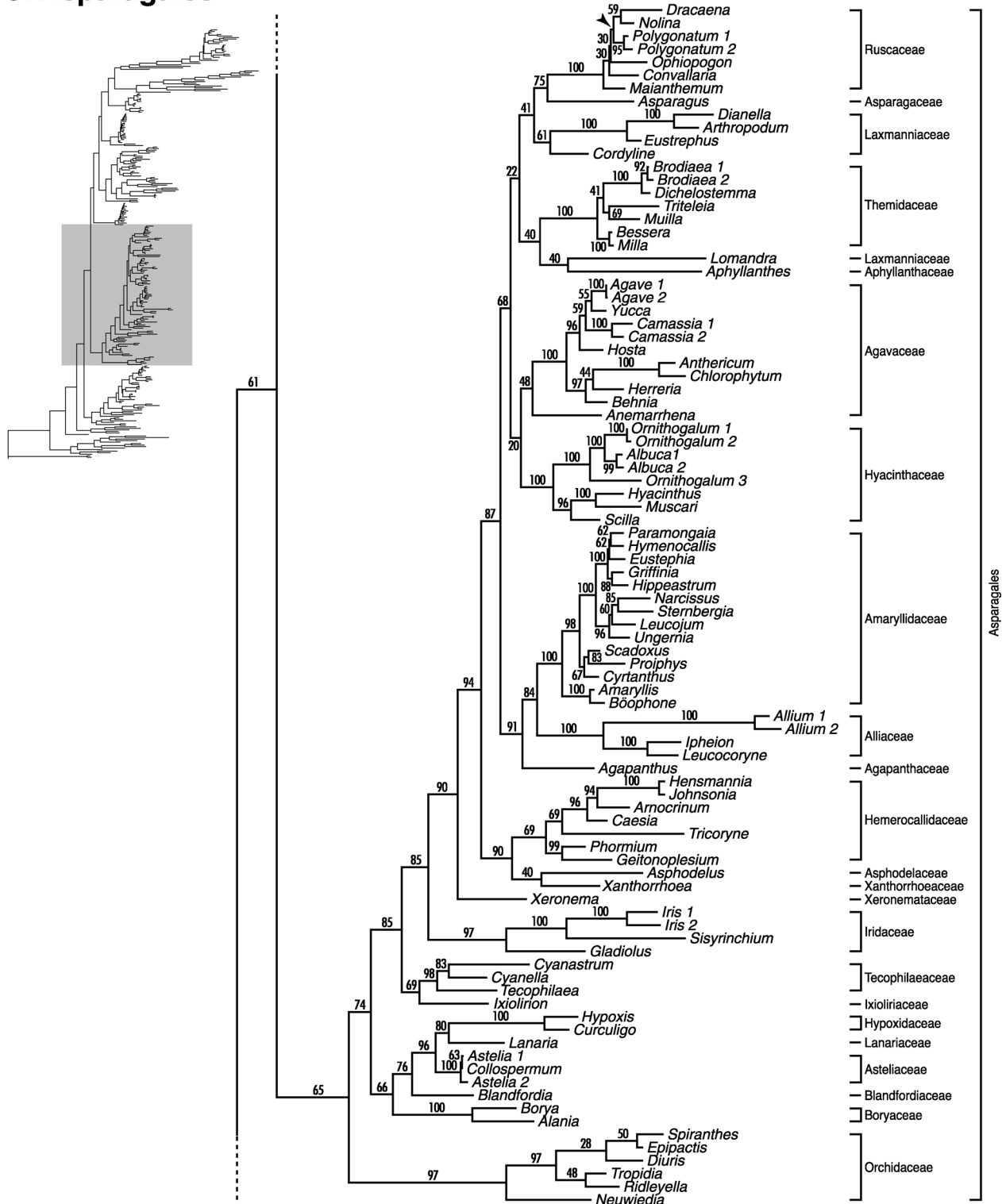


Fig. 1A–D.—Continued.

and net venation arose together in Joinvilleaceae, Flagellariaceae, Hanguanaceae, Arecales, Zingiberales, *Behnia* Didr., two groups of Amaryllidaceae, *Geitonoplesium* A. Cunn., *Curculigo* Gaertn., the core Liliales, *Trillium*, and Araceae, and are associated with each other in Ruscaceae–Laxman-

niaceae, *Disporum*, and *Tacca* Forst., with the evolution of fleshy fruits slightly lagging that of net venation among close relatives and inferred ancestors in the last two lines (Fig. 2). Fleshy fruits and net venation were lost together in *Arthropodium* R. Br., *Hypoxis* L.–*Lanaria* Aiton., Lilioideae, and

D. Liliales – Acorales

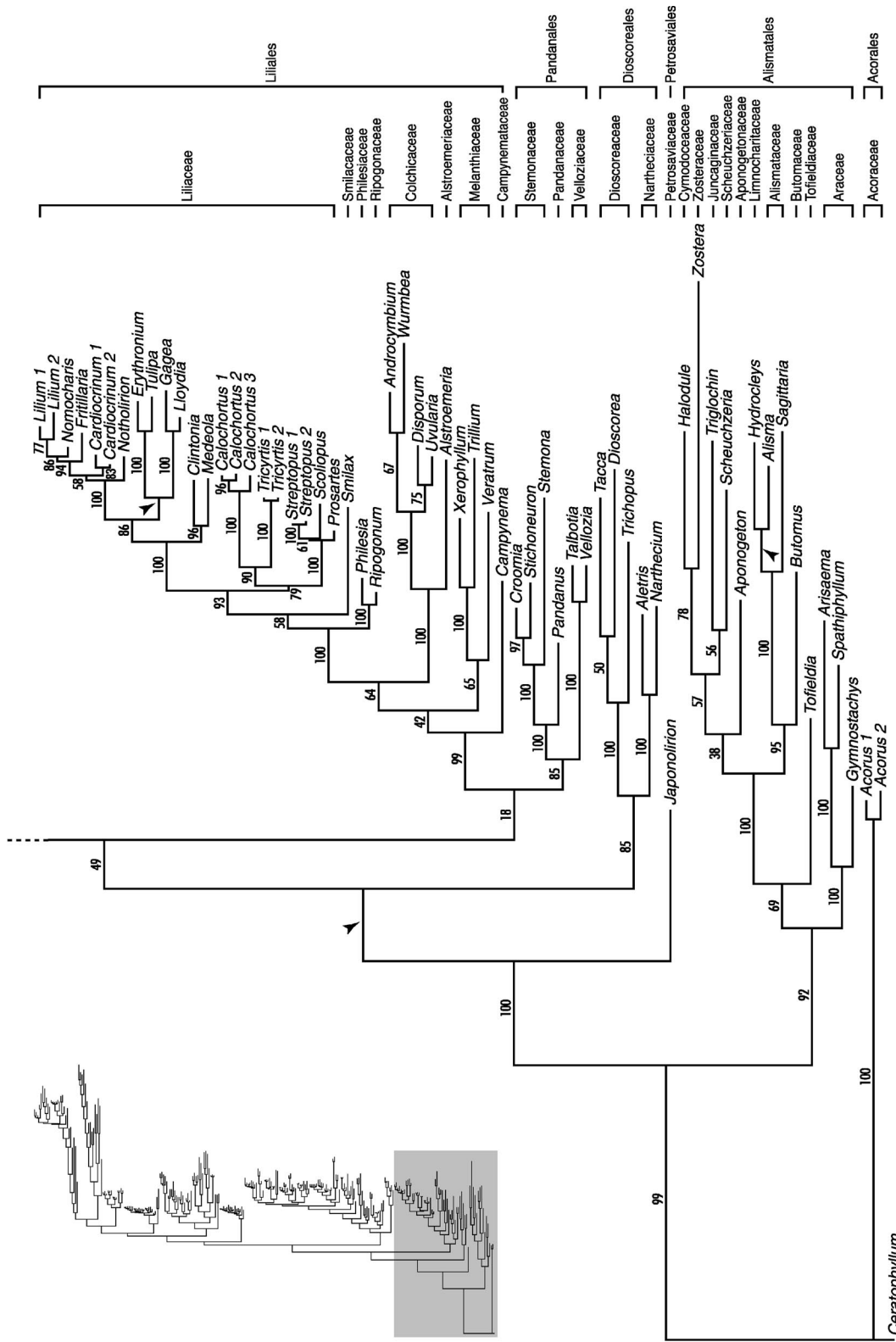


Fig. 1A–D.—Continued.

Table 2. Inferred evolutionary origins of net venation, fleshy fruits, and life in shady habitats, and of parallel venation, passively dispersed fruits and/or seeds, and life in sunny habitats. Most instances of the evolution of the former character states represent initial transitions from the latter, while most instances of the origin of the latter represent reversals from the former. Transitions on the same line occurred at the same node or (in a few cases) adjacent nodes. Instances where all three character states underwent transition at the same or adjacent nodes—involving concerted convergence—are underlined. All calls are based on overlaying characters on a single most-parsimonious tree using accelerated transformation in MacClade (Maddison and Maddison 2002).

Net venation	Fleshy fruits	Shade
Bambusoideae		Bambusoideae
<u>Joinvillea + early-divergent Poaceae</u>	<u>Joinvillea</u>	<u>Joinvillea + early-divergent Poaceae</u>
<u>Flagellaria</u>	<u>Flagellaria</u>	<u>Flagellaria</u>
		Monotremeae
	Bromelioideae	Bromelioideae
<u>Hanguanaceae</u>	<u>Hanguanaceae</u>	(<u>Hanguanaceae</u> + Commelinaceae)
	<u>Amischatolype</u>	
<u>Zingiberales + Philydraceae^a</u>	<u>Zingiberales</u>	<u>Zingiberales</u>
<u>Arecaceae</u>	<u>Arecaceae</u>	<u>Arecaceae</u>
<u>Hosta</u>		<u>Hosta</u>
<u>Behnia</u>	<u>Behnia</u>	<u>Behnia</u>
		<u>Chlorophytum</u>
<u>Ruscaceae + Laxmanniaceae</u>	<u>Ruscaceae + Laxmanniaceae</u>	<u>Ruscaceae + Laxmanniaceae</u>
<u>Griffinia</u>	<u>Hippeastrum</u>	<u>Griffinia + Hippeastrum</u>
<u>Hymenocallis</u>		<u>Hymenocallis</u>
<u>Proiphytis–Scadoxus</u>	<u>Proiphytis–Scadoxus</u>	<u>Proiphytis–Scadoxus</u>
<u>Geitonoplesium</u>	<u>Geitonoplesium</u>	<u>Geitonoplesium</u>
<u>Cyanastrum</u>		<u>Cyanastrum</u>
<u>Curculigo</u>	<u>Curculigo</u>	<u>Curculigo</u>
	<u>Asteliaceae + Blandfordiaceae</u>	<u>Asteliaceae + Blandfordiaceae</u>
	<u>Neuwiedia</u>	<u>Neuwiedia</u>
		<u>Epipactis</u>
		<u>Tropidia</u>
<u>Cardiocrinum</u>	[<u>Cardiocrinum</u>] ^b	<u>Cardiocrinum</u>
<u>Liliales above</u>	<u>Liliales above</u>	<u>Liliales above</u>
<u>Alstroemeria</u>	<u>Ripogonum</u>	<u>Ripogonum</u>
		<u>Calochortus albus</u>
<u>Disporum–Uvularia</u>	<u>Disporum</u>	<u>Disporum–Uvularia</u>
<u>Trillium</u>	<u>Trillium</u>	<u>Trillium</u>
Stemonaceae		Stemonaceae
	Pandanaceae	
<u>Dioscoreaceae</u>	<u>Tacca</u>	<u>Dioscoreaceae</u>
Alismataceae ^a		Alismataceae ^a
<u>Zostera^a</u>		
<u>Aponogeton^a</u>		
<u>Araceae</u>	<u>Araceae</u>	<u>Araceae</u>

Nolina Michx., with the loss of fleshy fruits in the last lagging that of net venation by one node.

Both fleshy fruits and (especially) net venation show even stronger patterns of correlated evolution with shady conditions than with each other. In almost every case, the evolution of net venation and fleshy fruits is associated with life

Table 2. Continued.

Parallel venation	Passively dispersed fruits	Sun
Higher Poaceae	Poaceae	Higher Poaceae <i>Cartonema</i>
	Costaceae	
	Cannaceae ^a	Cannaceae Strelitziaceae
	Lowiaceae	
	<i>Nypa</i>	<i>Nypa</i> <i>Phoenix</i>
<u>Dracaena + Nolina</u>	<u>Nolina</u>	<u>Dracaena + Nolina</u>
<u>Ophiopogon</u>		
<u>Asparagus</u>		<u>Asparagus</u>
<u>Arthropodium</u>	<u>Arthropodium</u>	<u>Arthropodium</u>
<u>Hypoxis–Lanaria</u>	<u>Hypoxis–Lanaria</u>	<u>Hypoxis–Lanaria</u>
<u>Lilioideae</u>	<u>Lilioideae</u>	<u>Lilioideae</u>
<u>Calochortus</u>	<u>Calochortus + Tricyrtis^b</u>	<u>Calochortus</u>
	<u>Scolopus</u>	
<u>Androcymbium–Wurmbea</u>		

^a Associated with broad-leaved emergent or submersed aquatic habit.

^b Associated with retention or origin of passively dispersed fruits adapted to dispersal in autumn under an open canopy in temperate deciduous forests, while leaves have net venation adapted for activity in summer under a closed canopy.

in forest understories, whereas their loss is associated with open habitats. Specifically, 19 of 21 gains of fleshy fruits are associated with invasion of—or life in—shady sites, whereas 7 of 11 losses are associated with the invasion of sunny conditions. For net venation, 22 of 26 gains are associated with shady conditions, whereas 8 of 9 losses are associated with sunny conditions. These patterns of origin and maintenance are highly significant ($P < 10^{-10}$ to 10^{-30}) when tested in DISCRETE, using branch lengths that are equal to the inferred total amounts of molecular evolution down each lineage, a function of time plus plant characteristics such as generation time; Table 3). These results support our hypotheses about adaptation and establish the existence of a highly significant pattern of concerted convergence across the monocots.

Net venation shows an even more marked association with shade if we factor out the four lineages (Alismataceae, Aponogetonaceae, Philydraceae, Zosteraceae) in which it arose in broad-leaved aquatic plants, mostly near the base of the monocots in Alismatales (Tables 2, 3). All origins of net venation are associated with either shady conditions (85%) or broad leaves in aquatic emergents or submersed species (15%). Fleshy fruits also show a stronger association with net venation if we exclude aquatic plants with broad leaves and net venation, in which we have no a priori reason to expect the evolution of fleshy fruits.

The numerous origins of fleshy fruits and net venation are distributed rather evenly across lineages and time (Fig. 2). Both traits arose nearly 90 Mya ago in Araceae and Arecaceae. The former family is dominated by herbs, vines, and epiphytes of tropical rain-forest understories, together with some temperate forest herbs (e.g., *Arisaema* Mart., *Arum* L.)

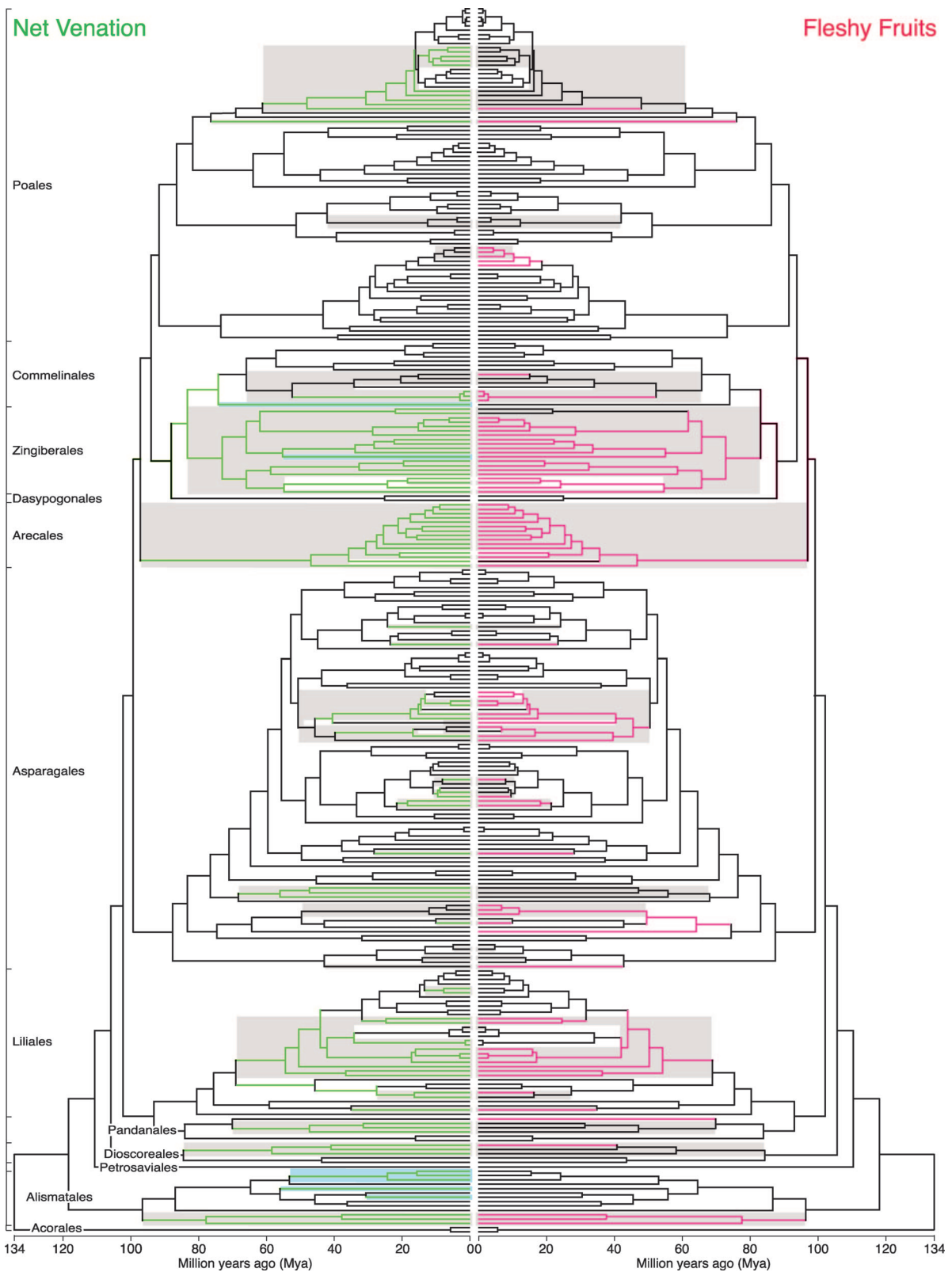


Fig. 2.—Concerted convergence of net venation (green), fleshy fruits (red), shaded habitats (sand boxes), and broad-leaved aquatic habit (blue boxes). Note that almost all transitions to net venation and fleshy fruits occur upon invasion of shaded habitats, and that almost all reversals to parallel venation and dry, passively dispersed seeds or fruits occur upon re-invasion of open, sunny habitats. The tree shown is ultrametric and has been calibrated against the age of six Cretaceous fossils using penalized likelihood, so that the tempo and taxonomic distribution of phenotypic transitions can be visualized. Both net venation and fleshy fruits show somewhat constant rates of ecological evolution over the past 90 million years, with an increase in the absolute number of origins toward the present and a decrease in the number of origins per clade present.

Table 3. Log likelihood ratios (LR) and significance levels (P) resulting from five different tests for correlated evolution across monocots in net venation, fleshy fruits, and life under shaded conditions, conducted on four representative trees using DISCRETE (Pagel 1994, 1999). Mean (\pm SE) LR represents the average value from five independent analyses per tree per test (see text).

	Tree A	Tree B	Tree C	Tree D	Mean	SE of mean	Significance
1. Fleshy fruits and net venation							
Mean LR	50.6	53.1	59.4	48.1	52.8		
Standard error	0.8	1.4	2.6	0.3	1.3	2.4	
Minimum	48.0	50.7	50.7	47.5	49.2	1.2	$P < 10^{-9}$
2. Fleshy fruits and shade							
Mean LR	74.0	73.4	72.4	66.3	71.5		
Standard error	3.9	2.5	1.4	1.7	1.3	1.8	
Minimum	63.9	65.7	66.8	59.7	64.0	2.2	$P < 10^{-11}$
3. Net venation and shade							
Mean LR	129.8	132.7	120.9	132.1	128.9		
Standard error	3.2	1.3	1.7	0.9	1.8	2.7	
Minimum	117.0	127.5	116.1	128.6	122.3	1.2	$P < 10^{-23}$
4. Net venation and shade + broad-leaved aquatics							
Mean LR	154.3	154.7	154.2	159.3	155.7		
Standard error	2.4	1.7	2.0	3.9	2.5	1.2	
Minimum	144.8	148.2	148.1	146.5	146.9	1.2	$P < 10^{-30}$
5. Fleshy fruits and net venation, excluding broad-leaved aquatics							
Mean LR	63.8	61.2	58.4	60.6	61.0		
Standard error	1.4	1.3	0.9	1.4	1.2	1.1	
Minimum	61.1	56.1	55.0	55.4	56.9	2.0	$P < 10^{-10}$

and broad-leaved submersed aquatics (e.g., *Anubias* Schott, *Cryptocoryne* Fisch. ex Wydler). The palms contain many rain-forest lineages, but have also invaded open subtropical savannas and scrub. The most recent instances of concerted convergence in fleshy fruits (or mimics thereof) and net venation occurred within the last 5 to 10 Mya, in *Griffinia* Ker Gawl. and *Proiphys-Scadoxus* Raf. of Amaryllidaceae and *Curculigo* of Hypoxidaceae. Fleshy fruits arose at least three times in Poales, twice in Commelinales, once in Zingiberales, once in Arecales, eight times in Asparagales, three times in Liliales, once in Pandanales, once in Dioscoreales, and once in Alismatales. Net venation arose at least three times in Poales, once in Commelinales, once in Zingiberales, once in Arecales, eleven times in Asparagales, four times in Liliales, once in Pandanales, once in Dioscoreales, and four times in Alismatales. During 10-Mya intervals, an average of 2.9 ± 0.5 lineages evolved net venation, whereas an average of 2.4 ± 0.4 lineages evolved fleshy fruits, implying a rather clocklike rate of adaptive evolution in both these traits across the monocots. It is important to note that many of the inferred reversals to parallel venation or passively dispersed, dry fruits appear to have occurred quite recently, with the exception of the reversal at the base of subfamily Lilioideae of Liliaceae (Fig. 2).

As might be expected given the relative numbers of origins of net venation and fleshy fruits, there are a number of groups of understory plants in which only net venation, not fleshy fruits, evolved. The net-venation-only syndrome characterizes the bambusoids, early-divergent grasses, Costaceae, *Hosta* Tratt., *Cyanastrum* Oliv., and Stemonaceae. *Cardiocrinum* and *Tricyrtis* of temperate deciduous forests both have net veins only, but are photosynthetically active under shady conditions in summer while releasing seeds af-

ter the canopy re-opens in autumn. Net veins also occur in the absence of fleshy fruits in four lineages of broad-leaved aquatics, including Alismataceae, Aponogetonaceae, and Zosteraceae of Alismatales and Philydraceae of Commelinales. Fleshy fruits arose without net venation under shady conditions in bromelioid bromeliads, *Amischotolype* Hassk., Asteliaceae and relatives, and the apostasioid orchid *Neuwiedia* Blume.

DISCUSSION

Phylogenetic Relationships

Cladistic analysis of *ndhF* sequence variation yields a highly resolved, well-supported phylogenetic tree for the monocots (Fig. 1). Relationships among orders are unclear in only two cases, involving the commelinids and the position of Dioscoreales and Pandanales close to the base of the monocots. The lack of resolution among the four major commelinid clades—Poales, Zingiberales plus Commelinales, Dasyogonales, and Arecales—may simply reflect a rapid initial diversification among the commelinids. Analyses based on seven genes (but many fewer taxa) resolve this polytomy by placing Dasyogonales sister to Poales, and Arecales sister to Zingiberales—Commelinales, but the bootstrap support for both relationships is weak ($\leq 51\%$) (Chase et al. 2006). Analyses based on 17 genes flip these relationships, placing Arecales as sister to Poales and Dasyogonales sister to Zingiberales—Commelinales, and bootstrap support for these relationships is also weak ($< 50\%$) (Graham et al. 2006). Here Pandanales are sister to Liliales in the *ndhF* strict consensus, but to Dioscoreales in the bootstrap consensus. The latter position is consistent with that obtained from an analysis based on 7 and 17 genes (Chase et al. 2006;

Graham et al. 2006). Alismatales are sister to a strongly supported clade (100% bootstrap) consisting of all other monocots except Acorales (Fig. 1). Petrosaviales or Dioscoreales are, in turn, sister to all other elements of this large clade; 7- and 17-gene analyses place Petrosaviales sister to all monocots except Alismatales and Acorales, and Dioscoreales sister to Pandanales (Chase et al. 2006; Graham et al. 2006).

Within commelinids, *ndhF* supports many relationships identified previously based on other sequence data (Givnish et al. 1999; Chase et al. 2000; Graham et al. 2003; Michelangeli et al. 2003), and resolves others for the first time. Bromeliaceae and Typhaceae–Sparganiaceae are sister to each other and earliest divergent within Poales, with Rapateaceae being next divergent in the bootstrap consensus and sequentially weighted analyses (see Fig. 1 and Results). Our findings for Poales differ somewhat from those of Michelangeli et al. (2003) based on morphology and sequence variation in *rbcL* and *atpA*. Those authors placed Rapateaceae sister to paraphyletic family Xyridaceae, including Eriocaulaceae and Mayacaceae, at the base of Poales; identified Bromeliaceae, then Typhaceae–Sparganiaceae as sister lineages to the remaining members of the order; and positioned *Flagellaria* L. as sister to two terminal clades, consisting of (1) *Anarthria* R. Br., *Aphelia* R. Br., and Restionaceae, and (2) *Joinvillea* Gaudich., *Ecdeiocolea*, and Poaceae. The nodes at which our results and those of Michelangeli et al. (2003) differ, however, are weakly supported (<50% bootstrap) in their analysis. These include (1) the positions of Bromeliaceae, Rapateaceae, and Typhaceae–Sparganiaceae relative to each other and to Eriocaulaceae, Mayacaceae, and Xyridaceae; (2) the supposed paraphyly of Xyridaceae; and (3) the position of *Flagellaria*, not Restionaceae, as sister to the remainder of the grass alliance. Our *ndhF* analysis resolves both Xyridaceae (including *Orectanthe*) and Eriocaulaceae as being monophyletic with 84–100% bootstrap, and identifies these two families as each other's closest relative (75% bootstrap). We resolve Bromeliaceae as sister to Typhaceae–Sparganiaceae with 64% bootstrap support, and place Rapateaceae as the next-divergent element with 79% support in the bootstrap majority-rule tree, consistent with its strongly supported position in the 7-gene tree (Chase et al. 2006). These relationships are similar to those derived by Bremer (2000) based on *rbcL*, but differ in the placement of the three earliest-divergent clades consisting of Bromeliaceae, Rapateaceae, and Typhaceae–Sparganiaceae. The placement of the last just inside Bromeliaceae–Rapateaceae by Bremer (2000) involves a very short branch, however. We were unable to amplify and sequence *ndhF* for DNAs of *Aphelia* (Centrolepidaceae) and *Trithuria* Hook. f. (Hydatellaceae) kindly provided by J. Davis and D. Stevenson, and so were unable to confirm their strongly supported finding that *Aphelia* is sister to Restionaceae or the more weakly supported association of *Trithuria* with Xyridaceae.

The strongly supported placement of *Thurnia* Hook. f.–*Prionium* E. Mey. sister to Cyperaceae–Juncaceae by *ndhF* is consistent with that of several recent molecular studies (Givnish et al. 1999; Bremer 2000; Chase et al. 2000; Michelangeli et al. 2003). The position of *Mayaca* Aubl. sister to all other elements of the sedge alliance, however, is more weakly supported and problematic. An earlier *ndhF* se-

quence of this taxon had placed it sister to Bromeliaceae (Givnish et al. 1999), but a new, higher quality sequence from Venezuelan material places it sister to the remainder of the sedge alliance, near Xyridaceae and Eriocaulaceae, which seems more plausible based on morphology and *atpA* and *rbcL* sequence data (Michelangeli et al. 2003); *rbcL* places *Mayaca* immediately sister to Xyridaceae and Eriocaulaceae (Bremer 2000). The possibility that *Mayaca* could act as a “wild card” much like *Ecdeiocolea* (see above) or *Aphyllanthes* Tourn. ex L. in Asparagales (see Fay et al. 2000), should not be overlooked.

The extensive divergence of the grass alliance, sedge alliance, rapateads, and bromeliads from each other is comparable to that among other groups of monocots already recognized at the ordinal level (Fig. 1). The remarkable isolation of both Bromeliaceae and Rapateaceae from other monocots in both morphology and sequence variation appears to reflect 15 to 40 million years between the origins of each group and when present-day lineages began to diverge from each other (Givnish et al. 2004a, in press). If support for the four major clades of Poales grows in future multigene analyses, and the position of Eriocaulaceae, Xyridaceae, and (especially) Mayacaceae becomes solidified, it would be prudent to revisit the issue of recognizing the four major clades in Poales—representing 31% of all monocot species—as orders in their own right.

The resolution of Commelinales and Zingiberales as sister taxa is consistent with previous molecular analyses (Givnish et al. 1999; Chase et al. 2000; Evans et al. 2003; Graham et al. 2003). Relationships among families within Zingiberales are largely consistent with a detailed analysis based on morphology and several rapidly evolving stretches of DNA (Kress et al. 2001). Our analysis, however, places Musaceae, Heliconiaceae, and Strelitziaceae–Lowiaceae in an unresolved trichotomy sister to the remaining “ginger” families, rather than in a ladder with Musaceae earliest-divergent as seen in Kress et al. (2001). Our *ndhF* tree identifies Haemodoraceae and Pontederiaceae as each other's closest relatives (Fig. 1B). They fail, however, to provide positive evidence that their immediate sister is Philydraceae, as have other molecular studies (Graham and Barrett 1995; Graham et al. 1998; Chase et al. 1995a, 2000; Givnish et al. 1999). However, inclusion of indels places *Philydrum* in a polytomy consistent with a tie to Haemodoraceae and Pontederiaceae (see Results), and thus consistent with previous studies based on morphology (Dahlgren et al. 1985) and molecular variation. Fleshy-fruited, net-veined *Hanguana* is strongly supported as being sister to Commelinaceae, consistent with previous molecular analyses (Givnish et al. 1999; Chase et al. 2000) but not with morphology, which tends to place this genus of southeast Asian rain forests with Zingiberales instead (Rudall et al. 1999).

The placement of *Calamus* as sister to the rest of Arecales, followed by *Nypa*, is consistent with relationships obtained using 5–7 kilobases (kb) of coding and noncoding plastid DNA (Asmussen and Chase 2001; Hahn 2002). Although bootstrap support for relationships within the rest of Arecales based on *ndhF* alone are low (35–95%), the fact that they are fully resolved based on a single gene is promising, given that many similar relationships are unresolved using *rbcL* alone (Uhl et al. 1995). Members of Arecales, Bro-

meliceae, and Zingiberales display unusually slow rates of plastid DNA evolution (Gaut et al. 1992; Givnish et al. 1999; Fig. 1A–D). It should thus not be surprising that relationships within these groups are much better resolved by *ndhF* than by *rbcL*, with or without *atpB* and 18S nrDNA (see Chase et al. 1995a, 2000). Although molecular data (*ndhF*; *rbcL*, *atpB*, 18S nrDNA; and 7- and 17-gene trees in development) do not resolve the relationships among the four major clades of commelinids, certain anatomical and chemical characteristics tend to link Commelinales–Zingiberales to Poales (Stevens 2003).

The placement of Asparagales sister to the commelinids rather than Liliales by *ndhF* (Fig. 1C) runs counter to the previous view that Asparagales and Liliales are sister to each other (Dahlgren et al. 1985). The arrangement of families within Asparagales generally supports that obtained in other recent studies (Fay et al. 2000; Pires et al. 2006; McPherson et al. submitted). Relationships within and near Amaryllidaceae are largely consistent with those obtained by Meerow et al. (1999) based on *rbcL* and the *trnL*–*trnF* region, except that *ndhF* places Agapanthaceae sister to Amaryllidaceae–Alliaceae, rather than Amaryllidaceae alone.

Relationships within Liliales are mostly consistent with those obtained by Vinnersten and Bremer (2001) based on *rbcL*, and by Patterson and Givnish (2002) based on *rbcL* and *ndhF*. Our results differ slightly from the *rbcL* tree, in which Alstroemeriaceae and Colchicaceae are sister to the rest of the order, and in which Liliaceae sensu Tamura (1998b), *Calochortus*, and *Scoliopus*–*Streptopus*–*Tricyrtis* form a trichotomy at the base of Liliaceae sensu Tamura (1998a). Analysis of the combined *rbcL* and *ndhF* data produces a tree identical to that based on *ndhF* alone (Patterson and Givnish 2002). The placement of *Prosartes* in Liliaceae and *Disporum* in Colchicaceae supports previous analyses based on *rbcL* (Shinwari et al. 1994a, b; Chase et al. 1995a, b), despite the striking morphological convergence in habit, net venation, and fleshy fruits in these two groups, formerly lumped in *Disporum*.

The position of Pandanales sister to Dioscoreales in the *ndhF* bootstrap majority-rule tree is consistent with analyses of placeholders involving 7 and 17 genes, as is the position of *Japonolirion* (or Dioscoreales) sister to monocots other than Alismatales and Acorales in the strict consensus tree (Chase et al. 2006; Graham et al. 2006). Attempts to sequence *ndhF* for representatives of Burmanniaceae (*Burmannia* L., *Thismia* Griff.) failed despite repeated attempts, preventing us from determining where this family belongs. *Tacca*–*Dioscorea* L. is sister to *Trichopus* Gaertn. within the dioscorealean taxa sequences surveyed, consistent with the findings of Caddick et al. (2002a, b) based on *rbcL*, *atpB*, and 18S nrDNA. The isolated position of *Japonolirion* supports the decision to recognize this genus (and achlorophyllous *Petrosavia* Becc.) as constituting Petrosaviales, one of the 12 monocot orders (Cameron et al. 2003).

Relationships among the families of Alismatales based on *ndhF* are broadly similar to those implied by *rbcL* (Les et al. 1997) but differ in detail. Mostly, the divergences between the two trees are not strongly supported in either case. The identification of Juncaginaceae and Scheuchzeriaceae as sister groups by *ndhF*, however, is probably significant, given that these morphologically similar families share a unique

cyanogenic glucoside (triglochinin) known in no other angiosperm family (see Haynes et al. 1998). Repeated attempts to amplify and sequence *ndhF* from several of the smallest, aquatic families of Alismatales failed, preventing as detailed an analysis of relationships in this group as desired (D. Les and S. W. Graham pers. comm.). Our results support the important conclusion of Les et al. (1997) that the “aquatic” families of Alismatales fall into two clades, one including Alismataceae, Limnocharitaceae, and Butomaceae, and the other a series of three independently evolved families of sea-grasses, with the Madagascar lace-plant family (Aponogonaceae) closely related to the latter clade.

As noted by Chase et al. (1995a) and Zomlefer (1999), several genera once placed in Melanthiaceae in Liliales—including *Japonolirion*, *Nartheicum* Huds., and *Tofieldia* Huds.—are now identified as belonging to three additional orders of monocots, including Petrosaviales, Dioscoreales, and Alismatales. Their growth form, marked by narrow equitant leaves, is also strikingly similar to that of *Acorus* at the base of the monocots (although *Japonolirion* differs from *Nartheicum* and *Tofieldia* in having bifacial leaves; M. W. Chase pers. comm.). Our results strongly support this position for *Acorus*, consistent with all recent molecular studies (e.g., Chase et al. 1993, 1995a, b, 2000, 2006; Bremer 2000; Fuse and Tamura 2000; Graham and Olmstead 2000; Soltis et al. 2000; Borsch et al. 2003; Zanis et al. 2003; Graham et al. 2006).

Concerted Convergence

The independent origin of net venation at least 26 times in the monocots, always in association with invasion of shady conditions (85%) or life as a broad-leaved aquatic plants—as well as the independent origin of fleshy fruits at least 21 times, 19 in association with shaded forest understories—is one of the most remarkable, widespread, and highly significant ($P < 10^{-30}$ to 10^{-30}) cases of convergent evolution ever documented. The joint evolution of fleshy fruits and net venation 15 times across the monocots, and their joint loss five times, is also—by far—the most striking case of concerted convergence and plesiomorphy thus far demonstrated. These patterns are not only highly significant, they have high explanatory value as well. Phylogenetically unstructured correlation coefficients (r) range from 0.54 for the coincidence of net venation and fleshy fruits, to 0.64 and 0.73 for the coincidence of fleshy fruits and net venation with shaded habitats, to 0.77 for the coincidence of net venation with shaded habitats or a broad-leaved aquatic habit, when all traits are scored as binary characters.

In many ways, the contrast between *Trillium* and its closest relatives in Melanthiaceae (represented in this and all other surveys by *Xerophyllum* Michx.) epitomizes the pattern of concerted convergence discussed in this paper. *Trillium* grows in the shaded understories of temperate mesic forests, has broad, thin, soft leaves, net venation, and fleshy fruits, while *Xerophyllum* grows in more open habitats (meadows, fireswept pine glades) and possesses narrow, thick, hard leaves with parallel venation and tiny, wind-dispersed seeds released from dry capsules. It would be difficult, based on gross morphology, to infer that these taxa are actually very close relatives; the demonstration that they are

is one of the triumphs of plant molecular systematics. The contrast between *Trillium* and *Xerophyllum* is paralleled by several other cases, most notably involving the contrast between *Hypoxis* (mostly grass-leaved, capsule-fruited herbs of meadows, prairies, and glades, occasionally found in woodlands) and *Curculigo* (broad-leaved, net veined, fleshy-fruited herbs of tropical forest understories). A few *Hypoxis* occur in tropical forest understories or have broad leaves, and a few *Curculigo* have rather narrow leaves. Fleshy-fruited, net-veined, forest-dwelling *Geitonoplesium* also contrasts sharply with all of its dry-fruited, parallel-veined relatives of open habitats (see Conran 1999). *Cyanastrum* of shady African rain forests and woodlands has broad, cordate leaves with net venation, while confamilial *Cyanella* L. of open South African fynbos and *Tecophilaea* Bert. ex Colla of the Chilean high Andes have narrow, rather fleshy, grasslike foliage that lack cross veins. The difference between forest-dwelling *Hosta* (with thin, broad, net-veined leaves) and *Agave* L., *Yucca* L., and other elements of Agavaceae (mostly with thick, succulent, parallel-veined leaves) to which *Hosta* is sister (Bogler and Simpson 1996) could hardly be more striking, although it does not entail the evolution of different fruit types.

In addition to such cases of divergence among close relatives, striking convergence among distant relatives also supports our case. Asian *Disporum* of Colchicaceae and North American *Prosartes* of Liliaceae both grow in the understories of temperate mesic forests and share net venation and fleshy fruits, as well as many other features of growth form (e.g., arching stems) and floral morphology. They are so similar that both were placed in the same genus, until Shinwari et al. (1994a, b) used molecular data to demonstrate that the North American taxa were closely related to *Streptopus*, while the Asian taxa were closely related to *Uvularia*. Both of these genera, in turn, are remarkably similar in many ways to *Polygonatum* Miller, *Disporopsis* Hance, and *Smilacina* Desf. (also native to temperate forest understories) of Rusaceae in order Asparagales; indeed, these genera were grouped with *Disporum* and *Prosartes* in the asparagoid tribe Polygonatae by Krause (1930), Therman (1956), Hutchinson (1959), and La Frankie (1986)!

The joint evolution of fleshy fruits and net venation is not lock-step: by no means is every invasion of forest understories associated with a gain of both traits, nor is every invasion of open sites associated with a loss of both traits. Nevertheless, this pattern is highly significant and some apparent exceptions are illuminating. Bromelioid bromeliads evolved fleshy fruits, but not net venation—which may be understandable, given that they also possess CAM photosynthesis and thus have thick, succulent leaves in which net venation would not be adaptive. CAM photosynthesis seems obviously adaptive in the open, dry habitats (Winter and Smith 1996) in which bromelioids evolved (Givnish et al. in press), but is also advantageous under the constantly damp, rain-forest-interior conditions where most other bromelioids grow because it allows CO₂ recycling when the leaf surfaces are occluded with raindrops (Pierce et al. 2002). Vanilloid orchids (not included in our survey) evolved net venation but not fleshy fruits, except *Vanilla* Plum. ex Mill. itself (Cameron and Chase 1998)—which may also be understandable, given that mycotrophy in general appears to favor tiny, ex-

ceedingly numerous seeds that are *independently dispersable*, presumably to maximize the chances of contacting a suitable fungal partner. Finally, the retention of net venation in several species of palms (Arecaceae) and yams (Dioscoreaceae) that have invaded open tropical and subtropical habitats speaks for the importance of phylogeny and genetic/developmental heritage, not ecology, in helping maintain this trait. It is true that even yams of open, hot savannas often have thin, soft-textured leaves; presumably this is related to their short leaf lifespans, the ephemeral period of abundant moisture in their savanna habitats, and the widespread trend for specific leaf mass (g m⁻²) to decline with leaf longevity across biomes and (mainly dicot) lineages (Reich et al. 1997; Ackerly and Reich 1999). However, palms of open savannas and oases often have tough, coriaceous foliage and a relatively compact, palmate form—and yet retain a branching support structure within leaves, strongly supporting a role of phylogenetic morphological conservatism.

There are a few additional cases involving the concerted convergence of net venation and fleshy fruits beyond the monocot taxa we included in our survey. Examples include *Palisota* Rchb. ex Endl. (Commelinaceae), *Vanilla* and *Selenipedium* Rchb. f. (Orchidaceae), *Eucharis* Planch. & Linden (Amaryllidaceae), and Cyclanthaceae of tropical rain-forest understories. Perhaps the most striking evidence that selection strongly favors both net venation and fleshy fruits under shaded conditions, however, is provided by *Gnetum* L. This genus of tropical vines and trees is characterized by fleshy fruits and broad, net-veined leaves that strongly resemble those of *Coffea* L. and other understory angiosperms—and yet *Gnetum* is a gymnosperm, closely related to the xeric-adapted *Ephedra* L. and *Welwitschia* Reichb. (Bowe et al. 2000; Chaw et al. 2000). The strong resemblance of *Gnetum* to certain angiosperms helped inspire the hypothesis that the angiosperms were derived from gymnosperms via Gnetales (Doyle and Donoghue 1986; Donoghue 1994). Molecular data do not support that hypothesis, however, indicating that the gymnosperms as a whole are sister to the angiosperms and that Gnetales arose from within the conifers (Bowe et al. 2000; Chaw et al. 2000; Soltis et al. 2002; but see Rydin et al. 2002). Won and Renner (2003) have recently discovered a horizontal transfer of a group II intron (a self-splicing RNA and putative spliceosomal ancestor) and adjacent exons of mitochondrial *nadI* from asterid angiosperms to a few Asian species of *Gnetum*. Although this might seem to open the possibility of a horizontal transfer of genes coding for net venation into *Gnetum*, such a scenario seems highly unlikely, given that the Asian species involved are nested well within *Gnetum*, all of whose species are characterized by net venation.

Phylogenetic analyses indicate that fleshy fruits have evolved repeatedly in association with forest understories in Lobeliaceae (Givnish 1998), Gesneriaceae (Smith 2001), and urticoid Rosales (Sytsma et al. 2002) among the dicots. Givnish (1979) observed that net venation occurs in several monocot groups with thin, broad leaves in forest understories, including *Arisaema*, *Smilax* L., *Trillium*, and various tropical ginger and their relatives. Conover (1983) and Chase et al. (1995a) independently noted similar, qualitative associations of net venation with broad-leaved forest vines; Cameron and Dickison (1998) noted a similar association of

net venation with achlorophyllous vanilloid orchids. The association of net venation with the climbing habit among monocots is well marked. We believe it arises for three reasons: (1) most vines are, perforce, growing in microsites shaded by the hosts they are climbing; (2) species growing directly on tree boles are likely to experience especially dense shade, given that the boles occlude half the sky (Givnish and Vermeij 1976); and (3) the vine habit, by its nature, entails low allocation to support tissue, resulting in more rapid rates of upward growth and self-shading of lower leaves than in self-supporting plants with the same photosynthetic rate, and favoring shorter leaf lifespans and thus thinner, softer leaves with lower specific leaf mass (Givnish 2002). Indeed, a survey of 52 European woody species grown in a common garden showed that climbers/scramblers (6 species) had the lowest specific leaf mass of the species surveyed (Castro-Diez et al. 2000). The association of net veins with the achlorophyllous vanilloid orchids most likely reflects initial adaptation of chlorophyllous ancestors to shady conditions, including the evolution of net venation (seen today in other shade-adapted orchid genera, such as *Goodyera* R. Br. and *Isotria* Raf.). Subsequently, evolution may have favored abandonment of the photosynthetic habit under such unproductive conditions and a focus on carbon input via mycotrophy, with further reduction in leaf size and thickness.

Given that both fleshy fruits and net venation each arose more than 20 times in the monocots, the question immediately arises as to whether the same developmental pathways and underlying genes were involved in each case, or whether these adaptations arose in different ways in different groups (as has occurred in different populations of rock pocket mice that have independently evolved dark pelage on dark-colored soils [Nachman et al. 2003]). The fact that both fleshy fruits and net venation have arisen without the other in some cases demonstrates that they are unlikely to be the pleiotropic effects of a single gene or supergene. Furthermore, given that several groups show obvious differences in the fine details of their pattern of net venation (e.g., see Shinwari et al. 1994a, b), and that “fleshy fruits” involve the elaboration of different tissues in different groups (e.g., arils vs. capsule walls), it seems unlikely that all of the multiple origins of net venation and fleshy fruits have each depended on the same genes and developmental pathways for each trait. Determining whether or not this has been the case should be a goal of new studies at the interface of ecology, evolution, and development (“eco-evo-devo”; Givnish 2003).

When Patterson and Givnish (2002) demonstrated that net venation, fleshy fruits, inconspicuous flowers, and rhizomes undergo concerted convergence under shady conditions in Liliales, they also showed that these patterns distorted phylogenetic inference based solely on morphology. When morphology was analyzed cladistically, two clades—characterized by the alternative suites of traits undergoing concerted convergence—emerged; when these traits were excluded from analysis, the relationships inferred were nearly identical to those deduced from DNA sequence variation. It would now be worthwhile to see if the same holds true for monocots as a whole: if both fruit and venation type are excluded, does an analysis of relationships across monocots based on morphology more closely approach that based on molecular

data? Chase et al. (1995a) have already noted that several of the groups placed at the base of the monocots by morphology alone (Stevenson and Loconte 1995) share reticulate venation. It would also be interesting to evaluate whether—as in Liliales—large, visually conspicuous flowers are mainly found in open habitats with strong illumination by broad-spectrum light, and if small, visually inconspicuous flowers are mainly found in shaded sites with low illumination by narrow-spectrum, greenish light. Many forest herbs in eastern North America accord with this prediction (Givnish and Patterson 2000). Across the angiosperms as a whole, this hypothesis may account for the striking increase with rainfall in the fraction of woody species with inconspicuous flowers in tropical forests documented by Gentry (1982), given that most of the tree diversity added in wetter forests are understory species (Givnish 1999a). Repeated shifts to visually inconspicuous flowers in shade to visually conspicuous flowers under bright, full-spectrum light may be analogous to the increased sexual selection for bright coloration in African rift-lake cichlids in clearer waters (Seehausen et al. 1997) and the likely role that an analogous process has played in the evolution of bright coloration in tropical coral-reef fish (Givnish 1999b).

ACKNOWLEDGMENTS

This study was partly supported by a University of Wisconsin–Madison Vilas research fellowship and NSF grants DEB 9623690 and IBN-9904366 to TJG, by NSERC Discovery grants to SWG, by NSF grant DEB 0129179 to AWM, and by a Smithsonian Institution grant to WJK and LMP. The authors would like to thank Mark Chase (Royal Botanic Gardens, Kew) for kindly providing access to DNA samples for a number of taxa. Several helpful comments on the manuscript were provided by Mark Chase and another anonymous reviewer.

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