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(Article begins on next page)
Molecular phylogenetics of Phyllanthaceae: evidence from plastid matK and nuclear PHYC sequences

ROSABELLE SAMUEL, HASHEENDRA KATHRIARACHCHI, PETRA HOFFMANN, MICHAEL H. J. BARFUSS, KENNETH J. WURDACK, CHARLES C. DAVIS, AND MARK W. CHASE

Phyllanthaceae are a morphologically diverse pantropical family of about 2000 species in c. 60 genera. They have been segregated along with Pandaceae, Picrodendraceae, and Putranjivaceae from Euphorbiaceae sensu lato (s.l.), following recent molecular work (Savolainen et al., 2000; APG II, 2003). The molecular systematics of Phyllanthaceae have been investigated as part of a larger multiflume study on the systematics of Euphorbiaceae s.l. The largest sampling used plastid rbcL sequences, and over 350 Euphorbiaceae s.l. sequences including 76 (74 taxa) of Phyllanthaceae, to assess subfamilial and tribal relationships (i.e., Wurdack and Chase, 1999; Wurdack, 2002; Wurdack et al., in press). Two clades of Phyllanthaceae found in these molecular analyses (Wurdack et al., in press, and here) are nearly identical to the suprageneric classification of Webster (1994) and Radelcliffe-Smith (2001), but the remaining clades do not correspond to previous tribal classifications. For a more detailed history of Phyllanthaceae classification, see Wurdack et al. (in press).

The matK gene is one of the most rapidly evolving plastid protein-coding regions (Wolfe, 1991). It is approximately 1550 base pairs (bp) long and encodes a matrase involved in splicing type II introns from RNA transcripts (Wolfe et al., 1992). Recent studies have shown the usefulness of this gene for resolving intergeneric or interspecific relationships among flowering plants, e.g., Malpighiaceae (Cameron et al., 2001), Poaceae (Li and Hilu, 1996), Cornaceae (Xiang et al., 1998), Nicotiana (Aoki and Ito, 2000; Clarkson et al., in press), Chrysosplenium (Soltis et al., 2001), Hypochaeris (Samuel et al., 2003), Orchidaceae (Goldman et al., 2001; Salazar et al., 2003) and most recently across all angiosperms (Hilu et al., 2003).

Low-copy nuclear protein-coding genes remain underutilized in phylogenetic studies, despite the need for nuclear comparisons with trees produced from plastid regions (Doyle, 1992, 1997). The nuclear regions most commonly used in phylogenetic studies are from high-copy ribosomal loci, such as ITS (Baldwin et al., 1995), 18S rRNA (Quail, 1991) and mediate diverse developmental responses throughout the life cycle of a plant. In angiosperms, five related sequences coding for phytochrome proteins designated PHYA-PHYE have been characterized in Arabidopsis thaliana (Sharrock and Quail, 1989; Clark et al., 1994). A simple way to sample putatively orthologous loci in the phytochrome gene family is to use locus-specific amplification primers. Phytochrome sequence data have provided a high degree of resolution within basal angiosperms (Mathews and Donoghue, 1999), Fabaceae (Mathews et al., 1995), Poaceae–Andropogoneae (Mathews et al., 2002), Malpighiaceae (Davis et al., 2002), and Malpighiaceae (Davis and Chase, 2004) and may be useful for resolving relationships within Phyllanthaceae. The overall rate of evolution of the PHY lineage is about 10 times faster than rbcL (Mathews et al., 1995).
This study analyzes the nuclear gene PHYC and the plastid gene matK to infer phylogenetic relationships within Phyllanthaceae and determine congruence of these two regions. We aim furthermore to evaluate the phylogenetic patterns obtained with rbcl sequence data (Wurdack et al., in press) with additional genetic markers as the basis for creating a revised tribal classification of Phyllanthaceae.

**MATERIALS AND METHODS**

**Plant material**—Forty-seven species (49 different accessions) from 30 genera (of the 60 genera recognized by Radcliffe-Smith [2001]) for Euphorbiaceae-Phyllanthoideae, representing five of 10 tribes, and six of 11 subtribes of Antideae and Phyllantheae were included in the analyses (see Supplemental Data accompanying the online version of this article http://ajbsupp.botany.org/8B). The taxon set used in the matK analysis included 41 ingroup species (43 accessions) and excluded Keayodendron, whereas the analysis of PHYC included 44 ingroup species (45 accessions) and excluded Uapaca. Outgroup taxa for these analyses included representatives from several other families of Malpighiales (APG II, 2003) including: Clusiaceae, Euphorbiaceae sensu stricto (s.s.), Hamiandraeae, Ochnaceae, Picrodendraceae, and Putranjivaeae (see Appendix 1 in supplemental data accompanying the online version of this article http://ajbsupp.botany.org/8B). Forty-one species (42 accessions) representing all 30 sampled genera were analyzed in combination. Because of our focus on Phyllanthaceae, and due to the limited sampling of other Malpighianae lineages, no close relationship among outgroup families should be inferred from our results. Most samples were obtained from the DNA Bank of the Royal Botanic Gardens, Kew, UK (http://www.rbgkew.org.uk/data/dnabank/homepage.html). In addition, silica gel dried specimens collected in Madagascar and Sri Lanka were included.

**DNA extraction and amplification**—Total DNA was extracted from material stored in silica gel following the 2 × CTAB (cetyltrimethyl ammonium bromide) procedure of Doyle and Doyle (1987). Most of the DNA samples obtained from herbarium specimens were purified by cesium chloride/ethidium bromide gradient (1.55 g/mL). Polymerase chain reaction (PCR) amplification was carried out using PCR ready mix (AB-0619/LD from Abgene, Vienna, Austria) and 2–8 ng (1 µL of 2–8 ng/µL) of template total DNA for a 50 µL reaction mixture. The PCR profile consisted of an initial 2-min pre-melt at 94°C and 35 cycles of 1-min denaturation at 94°C, 1-min annealing at 48°C, and 1-min extension at 72°C followed by a final extension of 10-min at 72°C. Amplified fragments were checked with 1% agarose gel, and the double-stranded DNA fragments were purified using QIAquick gel purification kit (Qiagen, Margaritella, Vienna, Austria).

We designed new amplification primers for matK spanning the entire region plus part of the trnK intron 5 Intron (trnK 570F) and trnK3' (1710R) (Table 1). Figure 1 shows the positions of the trnK intron in which matK is embedded and the positions of the primers used in this study. Degraded DNA from herbarium specimens was amplified in 5 or 6 fragments that were sequenced separately and then combined into a single contig.

For the PHYC gene, we designed our own primers from the available sequences in GenBank. Initially PCR products were cloned by ligation into pGEM-T Vector Systems (Promega GmbH, Mannheim, Germany); XL1-Blue competent cells were transformed according to the manufacturer’s protocol (Strategene Europe, Amsterdam, The Netherlands). Resulting colonies were screened for plasmids with inserts, and five positive clones were amplified and then sequenced using the same primers. To avoid time-consuming cloning, another set of primers from the aligned cloned sequences of some species was designed PHYC-F [5'-CCAGCTACTGATATACTCAGGCTC-3'] and PHYC-R [5'-CCAGCTTTCCATAGGCTTACGTA-3'], which enabled us to directly sequence a fragment of approximately 600 bp. This fragment is in the first exon of the PHYC gene starting from 800 bp downstream. The entire gene is 3571 bp long in Arabidopsis thaliana and has two introns, 136 and 98 bp in length. Primer positions of the sequences used in this study are shown in Fig. 2.

**Sequencing**—The purified fragments were directly sequenced on an ABI 377 automated sequencer (Applied Biosystems, ABI, Vienna, Austria) using dye terminator chemistry following the manufacturer’s protocol. Cycle sequencing reactions were performed for each template using each of the two primers used for PCR amplification and internal primers for matK if required. Both strands were sequenced. The programs Sequence Navigator and AutoAssembler (ABI) were used to edit and assemble the complementary sequences. These sequences have been deposited in GenBank (Appendix 1 in Supplemental Data that accompanies the online version of this article http://ajbsupp.botany.org/8B).

**Sequence alignment and phylogenetic analyses**—Alignments were obtained using the program Clustal V (Higgins et al., 1992) and improved by visual refinement. In the matK sequences, large gaps (in multiples of three) were often needed. Individual and combined parsimony analyses of matK and PHYC sequences, respectively, were performed using PAUP* 4.0b10 and the same settings, in accordance with previous analyses (Soltis et al., 2004; Soltis et al., 2005a). For both analyses, all possible trees were computed. The branch and bound search option was used to determine the most parsimonious trees. In the case of matK analysis, 7 trees were found, each having a consistency index (CI) of 0.88 and a rescaled consistency index (RC) of 0.83. In the case of PHYC analysis, 8 trees were found, each having a CI of 0.74 and an RC of 0.67. In addition, we performed bootstrapping analysis (1000 replicates) using the same settings, in accordance with previous analyses (Soltis et al., 2004; Soltis et al., 2005a). In the case of matK analysis, both the branch and bound search option and the bootstrap analysis found the same tree with a CI of 0.95 and an RC of 0.91. In the case of PHYC analysis, the branch and bound search option found the same tree with a CI of 0.75 and an RC of 0.69, whereas the bootstrap analysis found the same tree with a CI of 0.72 and an RC of 0.65.

**Fig. 1. Location of the matK gene in the trnK intron. Arrowheads indicate the location and direction of the primers. The trnK 3914F primer is from Johnson and Soltis (1994); all others are new to this study.**

**Fig. 2. PHYC (55716–59286) in the fifth chromosome of Arabidopsis thaliana (Genbank accession number AB005236). Arrowheads (PHYC F and PHYC R) indicate positions of our primers.**

### Table 1. Primer sequences used in this study for the amplification and sequencing of the trnK intron and matK gene.

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>trnK 570F</td>
<td>5'-TCC AAA ATC AAA AGA GCG ATT GG-3'</td>
</tr>
<tr>
<td>80F</td>
<td>5'-CTA TAC CCA CTT ATC TTT CGG GAG T-3'</td>
</tr>
<tr>
<td>390F</td>
<td>5'-CGA TCT ATT CAT TCA ATA TTT C-3'</td>
</tr>
<tr>
<td>800F</td>
<td>5'-CAT GCA TTA TGT TAG ATG TAC AGG-3'</td>
</tr>
<tr>
<td>1200F</td>
<td>5'-GA (CT) TCT GAT ATT ATC AAC CGA TTT G-3'</td>
</tr>
<tr>
<td>190R</td>
<td>5'-ATT CGA GTA ATT AAA CTT TTT ACA A-3'</td>
</tr>
<tr>
<td>530R</td>
<td>5'-GTG CCA ATT CCA ATC ATG CTT GAG-3'</td>
</tr>
<tr>
<td>950R</td>
<td>5'-AAA AT (AG) ACA TGG ACA TAA ATT GAC AA (AG) G-3'</td>
</tr>
<tr>
<td>1300R</td>
<td>5'-CGA AGT ATA TTA (CT) TT (CT) ATT CTA GCA TAC A-3'</td>
</tr>
<tr>
<td>1710R</td>
<td>5'-GCT TGG ATT TTT CAT TGC ACA CG-3'</td>
</tr>
</tbody>
</table>
Analysis of the matK gene—The aligned matK matrix consisted of 1612 bp, of which 840 positions were variable, and 602 (37%) were potentially parsimony informative. Heuristic searches generated three equally parsimonious trees with 1845 steps. One of the equally parsimonious trees with Fitch lengths (DELTRAN, delayed transformation, optimization) above each branch and bootstrap percentages (BP > 50) below each branch is shown in Fig. 3.

Phyllanthaceae are weakly supported (BP 60) as monophyletic and are split into two strongly supported (both BP 100) clades T and F (tanniferous and fasciculate clade, respectively). The first major clade (T) corresponds to tribes Antidesmeae + Bischofieae sensu Radcliffe-Smith (2001) and contains four subclades. One strongly supported (BP 100) subclade within clade T includes Aporosa and Baccarea (Antidesmeae-Scepinae); a second (BP 100) includes Apodiscus (Antidesmeae-Scepinae) as sister to the members of Antidesmeae Antidesmeinae included in this analysis, Antidesma + Thecacoris (BP 100); the third and fourth Uapaca (monogenic Antidesmeae-Uapacinae) and Bischofia (monotypic Bischofieae), respectively, are weakly placed relative to one another and to the other two subclades within clade T. Each of the two representative species of Baccarea and Thecacoris are moderately well supported (BP 82 and 87, respectively) as sister taxa.

The second major clade (F) is split into four well-supported (BP 100) subclades (F1, F2, F3, F4). The first (F1) comprises all members of Phyllanthaceae-Flueggeinae sensu Webster (1994) included in this analysis. Flueggea is sister to the weakly supported (BP 60) clade containing the remaining members of clade F1. Margaritaria is then sister to a strongly supported (BP 100) clade containing all genera with phyllanthoid branching (Webster, 1956). Phyllanthus is not monophyletic and falls into two clades each with BP 100. The first contains Phyllanthus calycinus (subgenus Isocladas) and P. cf. fuscoluridus + P. cf. mansakariva (both subgenus Kirkangelia section Antisonema, supported as sisters with BP 100). In the second, Phyllanthus nummularifolius (subgenus Kirangelia section Pentandra sensu Webster [1967] or subgenus Tenellanthus nov. invalidum sensu Brunel [1987]) is sister to the well-supported (BP 99) clade comprising Glochidion plus (Breynea + Sauropus). The latter two genera are strongly supported as sisters with BP 100. The two species of Breynea and Flueggea were each identified as monophyletic with BP 100 and 94, respectively.

Subclades F2, F3, and F4 are united in a weakly supported clade (BP 52). The second subclade (F2) is well supported (BP 100) and consists of Bredelia, Cleistanthus (both tribe Bredleiaceae), Pseudolachnostylis (Phyllanthaceae-Pseudolachnostylidinae), Gonatogyne, Lachnostylis, and Savia pro parte (all Wielandieae). Lachnostylis is sister to a clade (BP 100) of the remaining members of F2, which are split into two subclades; one with Gonatogyne + Savia dictyocarpa (BP 100), and the other with Bredelia, Cleistanthus and Pseudolachnostylis (BP 99). Cleistanthus is not monophyletic. Cleistanthus oblongifolius is more closely related to Bredelia (BP 100) than it is to Cleistanthus perrieri.

The third strongly supported (BP 100) subclade (F3) includes Actephila (Wielandieae), Leptopus (Phyllanthaceae-Leptopinae), Meineckia, Zimmermannia, Zimmermanniospis (Phyllanthaceae-Pseudolachnostylidinae), and Poranthera (Antidesmeae-Porantherinae). Poranthera is strongly supported (BP 100) as sister to a well-supported clade (BP 97) clade constituting the remaining members of clade F3. Within this clade, Actephila + Leptopus form a strongly supported (BP 100) subclade. The two sampled species of Leptopus (both Old World species) are also supported by BP 100. The other subclade (BP 100) contains Meineckia + Zimmermannia + Zimmermanniospis, with Meineckia sister to the other two taxa (BP 86). Heywoodia (Wielandieae) is weakly supported (BP 52) as sister to subclade F3.

The fourth well-supported subclade (F4; BP 100) includes all lineages of the western Indian Ocean Wielandieae. Wielandia is weakly supported as sister to all other species in this subclade (BP 57).

Analysis of the PHYC gene—The aligned PHYC matrix consisted of 601bp of which 485 were variable and 391 (65%) were potentially parsimony informative. Heuristic searches on this data set resulted in 1816 equally most parsimonious trees with 1861 steps. One of the equally parsimonious trees with Fitch lengths (DELTRAN optimization) above each branch and bootstrap percentages (BP > 50) below each branch is shown in Fig. 4.

The monophyly of Phyllanthaceae is weakly supported (BP < 50), and the two major clades, T and F; found in matK were recovered with weak support (BP 67 and 54, respectively; see Fig. 4). The composition of clades T and F1–F4 is identical to those uncovered using matK (with the omission of Uapaca from clade T, and the addition of Keayodendron to clade F2 due to sampling differences). The topology of subclade T was identical between PHYC and matK for all similarly sampled taxa, but there are some differences in the placement of individual taxa in subclades F1–F4.

Clade F1 is moderately supported (BP 82). In contrast to the matK analysis, Margaritaria is sister to the remaining members of clade F1. Flueggea is monophyletic (BP 100), and is well-supported (BP 90) as sister to the clade (BP 94) characterized by phyllanthoid branching (Webster, 1956). Phyllanthus is not monophyletic; species of Phyllanthus occur in at
Fig. 3. One of the three most parsimonious trees obtained from the maximum parsimony analysis of the *matK* gene (length = 1845, CI = 0.63, RI = 0.82). Branch lengths (DELTRAN optimization) and bootstrap percentages (>50) are indicated above and below the branches, respectively. Arrowheads indicate nodes not present in the strict consensus tree. Hyphens (-) indicate BP < 50.
Fig. 4. One of the most parsimonious trees obtained from the maximum parsimony analysis of the PHYC (length = 1861 steps, CI = 0.45, RI = 0.65). Branch lengths (DELTRAN optimization) and bootstrap percentages (>50) are indicated above and below the branches, respectively. Arrowheads indicate nodes not present in the strict consensus tree. Hyphens (-) indicate BP < 50.
least two clades. The first (BP 88) includes P. calycinus (subgenus Isocladus), plus a well-supported (BP 99) clade consisting of three taxa of subgenus Kirganelia section Anisone-ma. The second clade (BP 96) is a polytomy comprised of several species of Phyllanthus [P. lokoensis (subgenus Phyllanthus), plus two accessions of P. nummulariformis (Kirganelia-Pentandra or Tenellanthus) and P. epiphyllanthus (subgenus Xylophylla)], plus the well-supported (BP100) clade Glochidion (Breynia + Saurous). Within the last subclade, Saurous + Breynia are weakly supported as sisters (BP 54), and support for the two species of Breynia is moderate (BP 87).

Bridelia and Cleistanthus (both Bridelieae), Keayodendron and Pseudolachnostylis (both Phyllanthaceae-Pseudolachnostylidinae), Gonatogyne, Savia and Lachnostylis (all Wielandieae) form a strongly supported (BP 100) clade F2. As with matK, Gonatogyne + Savia on the one hand, and Bridelia, Cleistanthus and Pseudolachnostylis on the other hand form well-supported (BP 80 and 83) clades. Cleistanthus appears non monophyletic as in matK. Cleistanthus oblongifolius clusters with Bridelia again (BP 97), but C. perrieri forms a well-supported (BP 97) clade with Pseudolachnostylis, Keayodendron, which was not sampled in the matK analysis, is weakly supported as sister to all other members of clade F2.

Clade F3 is weakly supported (BP 76) and consists of two sister clades: one containing Actephila and Leptopus, and the other Poranthera and Meineckia (Zimmermannia + Zimmermanniopsis). Each of these clades is supported with BP > 50. The two species of Leptopus are united by BP 100. Meineckia (Zimmermannia + Zimmermanniopsis) is supported by BP 100, and the sister-group relationship of Zimmermannia and Zimmermanniopsis has weak support (BP 56). The position of Heywoodia is weakly supported as sister to F3, a placement identical to that inferred from matK.

The western Indian Ocean Wielandieae again group in the highly supported (BP 100) clade F4. No further bootstrap supported resolution is obtained with PHYC in this clade.

**Parsimony and Bayesian analysis of combined data—**

Since the consensus trees obtained with the individual gene matrices were topologically congruent, the two data sets were combined for further analysis. The aligned combined matK and PHYC matrix consisted of 2277bp. The heuristic search on this data set resulted in six equally most parsimonious trees with 3440 steps (Fig. 5). Bayesian analyses of the combined matrix produced a tree (not shown) that is nearly identical to the parsimony tree. All clades with high posterior probabilities (PP 1.0) are also present and receive at least moderate bootstrap support in the parsimony analysis.

The most notable result of this combined parsimony analysis is the high support (BP 100) for Phyllanthaceae. The two major clades (T and F) are well-supported (both with BP 100). The topology of clade T is identical with that in the matK tree, with similarly high bootstrap percentages. Clades F1–F4 are all well supported (BP 100) and resolved into F1, F2, and (F4 (Heywoodia + F3)).

Clade F1 is strongly supported (BP 100). The positions of Flueggea and Margaritaria equal those in the PHYC analysis. The topology of all other nodes agrees with both single-gene analyses, but bootstrap percentages vary slightly.

Clade F2 is well-supported in the combined analysis (BP 100). The topology of the strict consensus tree is identical to that of the PHYC analysis, having low support for internal nodes. Clade F3 shows an identical topology and similarly high bootstrap percentages in the combined and matK analyses. Placement of Heywoodia as sister of the F3 clade is moderately supported (BP 86), compared to the weak support in the single-region analyses. Clade F4 is supported by BP 100 in all three analyses, but support for internal nodes does not increase in the combined analysis as in clade F2.

**DISCUSSION**

matK and PHYC—The utility of matK for resolving generic or species level relationships is similar or greater than that of nuclear rDNA ITS (Solits et al., 1996). Indels are likely to be present in a matK data matrix of any taxonomic breadth. In our analysis matK resolves clades well at the tribal and generic levels and provides high bootstrap percentages for the different clades (Fig. 3). Although there was a greater percentage of potentiomorphically informative sites in PHYC (65%) than in matK (37%), the latter gene provided higher bootstrap percentages for the major clades and appears to be of greater phylogenetic utility.

**Comparison with rbcL—**

For ease of reference, the clades recovered in this study are named in concordance with the rbcL analysis of Wurdack et al. (in press). Sampling for the rbcL study (Wurdack et al., in press) was more comprehensive than in this study. All genera included here were also included in the rbcL study, with the exception of Keayodendron (clade F2) and Zimmermanniopsis (clade F3). This study is also the first to include representatives of Phyllanthus subgenus Kirganelia section Anisone-ma (clade F1). The topologies of the combined matK/PHYC (presented here) and rbcL trees are consistent with one another. Major clades of Phyllanthaceae (T, F1–F4) recovered with rbcL were also found with matK and PHYC. A single inconsistency in the topologies of the three genes is the placement of Cleistanthus perrieri (clade F2). The position of this species in the rbcL tree is identical to that in the matK tree (sister to Pseudolachnostylis (Bridelia + Cleistanthus oblongifolius)) but differs from the PHYC tree and the combined matK/PHYC tree (sister to Pseudolachnostylis only). It is possible that there is conflicting signal for the position of Pseudolachnostylis. Paraphyly of Cleistanthus was already reported and discussed in Wurdack et al. (in press).

The combined matK/PHYC tree shows higher support for individual clades and better resolution than that obtained from rbcL. It should be noted that outgroup sampling in these studies is not identical and may affect support for the Phyllanthaceae node. Most prominently, monophyly of Phyllanthaceae is supported with BP 100 (rather than just BP 73 with rbcL). The two major clades (T and F) have slightly improved support (BP 100 for both vs. BP 98 and 91 in rbcL). Support for the subclades F1–F4 has increased from BP 95–100 to BP 100 for all four clades in the combined analysis.

Monophyly of Thecacoris is confirmed in the matK and combined analysis with moderate support (BP 87 and 86, respectively). The sampled species represent the two major groups, Thecacoris s.s. and Cyathogyne, recognized at generic rank by some authors (e.g., Pax and Hoffmann, 1922; Léonard, 1995). Their relationship received BP < 50 in the rbcL analysis.

Two more instances of improved resolution are noted here with the caveat that sampling in the rbcL analysis was more comprehensive in these clades: Antidesma + Thecacoris are
Fig. 5. One of the six most parsimonious trees of the combined analysis of matK and PHYC (length = 3440, CI = 0.59, RI = 0.75). Branch lengths (DELTRAN optimization) and bootstrap percentages (≥50) are indicated above and below the branches, respectively. Arrowheads indicate nodes not present in the strict consensus tree. Hyphens (−) indicate BP < 50.
strongly supported sister taxa with *Apodiscus* sister to both, whereas with *rbcL* no further resolution was obtained for these three taxa. *Antidesma* and *Thecacoris* closely resemble each other, and the genera lack distinguishing generic characters in staminate specimens (both are dioecious). In pistillate specimens, the unilocular drupes of *Antidesma* are clearly different from the trilocular schizocarps of *Thecacoris*. In the *matK* and combined analyses, *Leptopus* and *Actephila* are grouped together (BP 98), which is biogeographically plausible (both are distributed in Asia and Australia) even though it contradicts wood anatomical (Menenge, 1987) and embryological (Webster, 1994) arguments used to distance *Actephila* (previously in Wielandieae) from *Leptopus* (Phyllanthaceae-Leptopinae).

**Drypetes madagascariensis**—The high genetic divergence of the two accessions of *Drypetes madagascariensis* (Putranjivaceae, outgroup for this study) may indicate heterogeneity of the species in its present circumscription. Most species of the dioecious genus *Drypetes* have few distinguishing morphological characters, and *D. madagascariensis* is noted for its remarkable variability (McPherson, 2000). The accession here marked as *D. cf. madagascariensis* differs from the majority of specimens solely by the lack or poor development of the fifth sepal but agrees in all other macro-morphological characters (the specimen is in fruit) with *D. madagascariensis*.

**Position of Zimmermanniopsis**—Zimmermanniopsis *uzungwaensis* has been variously accepted at generic rank (Radcliffe-Smith and Harley, 1990; Webster, 1994; Radcliffe-Smith, 2001) or included in *Meineckia* as section *Zimmermanniopsis* (Radcliffe-Smith, 1997; Govaerts et al., 2000). Placement in all analyses presented here confirms the close relationship of *Zimmermanniopsis* to *Zimmermannia*, and to *Meineckia* but more sampling is needed to determine the status of these taxa. A more comprehensive study of subclade F3 is presently underway at the Royal Botanic Gardens, Kew. One objective of this study is to clarify the taxonomy of the *Meineckial/Zimmermannnia/Zimmermanniopsis*-complex.

**Placement of Keayodendron**—The monotypic genus *Keayodendron* has not previously been included in molecular phylogenetic analyses. Initially described as a species of *Casearia* (formerly Flacourtiaceae; Salicaceae-Samydeae in Chase et al., 2002), Leandri (1959) transferred it correctly to Euphorbiaceae and described the new genus *Keayodendron*. He positioned it near *Drypetes* (now Putranjivaceae) because of the general resemblance of leaves and inflorescences, but also pointed out similarities to *Bridelia* in floral and embryo morphology, most strikingly the extrastaminal staminate disc in *Bridelia* and *Keayodendron* (vs. a central staminate disc in *Drypetes*). He furthermore compared his new genus to *Pseudolachnostylis* and *Securinea*. The resemblance between *Keayodendron* and *Bridelia* had already been noted in the basionym *Casearia brideloides* Gilg ex Engl. However, emphasis placed on the valvate sepals in tribe Bridelieae previously obscured the close relationship of those taxa. Webster (1994: 41–42) placed *Keayodendron* in Phyllanthaceae-Pseudolachnostylidinae “for lack of a better alternative,” stating that “...it is quite possible that *Pseudolachnostylis* and *Keayodendron* may not be closely related to the rest of the genera.” He compared its fruits and aspect to *Bridelia*, but the lack of petals and the imbricate sepals in *Keayodendron* deterred him from formally associating it with Bridelieae. Radcliffe-Smith (2001) followed Webster’s lead.

The molecular data place both *Keayodendron* and *Pseudolachnostylis* with *Bridelia* and *Cleistanthus* (Wurdack et al., in press, for *Pseudolachnostylis* only; this study). Stuppy (1996) came to the same conclusion and united these four genera in his *Bridelia* group according to their seed coat anatomy. *Bridelia*, *Cleistanthus*, and *Keayodendron* share a double disc in pistillate flowers (Radcliffe-Smith, 2001). This double disc is also described and illustrated in *Pseudolachnostylis* (Pax and Hoffmann, 1922, and P. Hoffmann’s own observations). It is a potential synapomorphy of this subclade because it is not present in *Gonatogyne* and *Savia* (P. Hoffmann, unpublished data). The position of *Keayodendron* within clade F2 is at present unclear.

**Phyllanthus subgenus Kig ranelia is not monophyletic**—*Phyllanthus* subgenus *Kig ranelia* was proposed by Webster (1956) based on *Kig ranelia* A. Juss. to accommodate species with phyllanthoid branching, five stamens, corolate pollen grains, and 3–10 carpels. He considered this variable subgenus to be primitive, comprising *P. sections Anisonema* and *Floribundia*. The latter section includes *P. nummulariifolius* and *P. tenellus* (Webster, 1957). Webster (1967) later described the new *P.* section *Pentandra* in subgenus *Kig ranelia* to accommodate *P. nummulariifolius* and *P. tenellus* along with the type, *P. pentandra*. He stated (Webster, 1967: 334) that “...this section is significant phylogenetically because most of its taxa have precisely the habit and appearance of species of subg. *Phyllanthus*, from which they scarcely differ in anything more than the five-merous rather than three-merous androe- cium. Since *P. tenellus* is the only herbaceous diplloid species with phyllanthoid branching, it and closely related taxa such as *P. capillipes* Schum. [= *P. nummulariifolius*] may be regarded as the nearest living equivalents of the taxa ancestral to subg. *Phyllanthus.*” Both of Webster’s studies focused on the Americas and dealt with few species of this predominantly Old World group.

Brunel (1975, 1987) studied the genus *Phyllanthus* extensively in continental Africa. He remarked on the heterogeneity of subgenus *Kig ranelia* and proposed to segregate the species related to *Phyllanthus tenellus* Roxb. in a new subgenus *Tenellanthus* (Brunel, 1987) which was never validly published.

Our study included for the first time species of both *P.* subgenus *Kig ranelia* section *Anisonema*, as well as *P.* subgenus *Kig ranelia* section *Pentandra* (*P.* subgenus *Tenellanthus* section *Tenellanthus*, nomen invalidum; Brunel, 1987). The three sampled taxa of section *Anisonema* belong to a morphologi- cally homogeneous group with a center of diversity in Madagascar. All closely resemble *P.* casturicum, and characters of the constituent taxa overlap. Species identification is provi- sional pending a taxonomic revision (M. Ralimanana and P. Hoffmann, unpublished data).

Placement of these taxa in our analyses corroborates Bru- nel’s (1975, 1987) view that subgenus *Kig ranelia* is hetero- geneous, as well as Webster’s (1967) comparison of his *P.* section *Pentandra* with subgenus *Phyllanthus*. *Phyllanthus nummulariifolius* is found in a subclade with *Breynia*, *Glo- chidion*, and *Saurups*, which in the *PHYC* analysis also contains *Phyllanthus epiphyllanthus* (subgenus *Xylophylla*) and *P.* lokoensis (subgenus *Phyllanthus*). Two accessions of *P.* num- mulariifolius were sequenced to confirm this placement. The three accessions of subgenus *Kig ranelia* section *Anisonema*
(P. cf. decipiens, P. cf. fuscoluridus and P. cf. mantsakariva) form a monophyletic group as predicted by their similar morphology. This clade is sister to Phyllanthus calycinus of subgenus Isocladus in this study with limited sampling in the largest genus of Phyllanthaceae (c. 800 species).

Western Indian Ocean Wielandiae—The centre of diversity for the taxa united here in clade F4 is Madagascar, with few species also represented in the Seychelles, the Comoro Islands, and the East coast of Kenya. They are morphologically similar despite being currently placed in the four different genera Blotta, Petalodiscus, Savia and Wielandia. The type of Savia is from Hispaniola and belongs in clade F2 as sister to S. dictyocarpa sampled here (Wurdack et al., in press). This shows the degree of taxonomic confusion surrounding this poorly known group. The lack of support for the internal nodes in this clade indicates that generic boundaries are in need of revision. The entire clade is revised in a forthcoming publication (Hoffmann and McPherson, in press).

Conclusions—Results of DNA sequence analyses using matK and PHYC correspond well with each other and with those separately obtained from analysis of rbcL (Wurdack et al., in press). Inclusion of missing genera and sampling of more taxa in problematic genera, namely Cleistanthus and Phyllanthus, as well as increasing the number of plastid markers analyzed and sequencing a longer fragment of low-copy nuclear PHYC may refine the phylogenetic hypothesis presented here.

Note added in proof: The high level of sequence divergence observed in the two accessions of Drypetes madagascariensis (outgroup taxa) may possibly be due the amplification of different PHY paralog, PHYE (in one of the accessions), instead of PHYC, which is otherwise used in our analyses.

LITERATURE CITED

Radcliffe-Smith, A., and M. M. Harley. 1990. Notes on African Eu-


