**Supplementary Information**

Appendix I. Relationships between characters in each step-matrix complex employed during the study (see explanation in materials and methods).

Summary:

7 Complexes of linked/inapplicable characters

Complex 0 (top 0): 0, 1,

Complex 1 (top 6): 6, 8,

Complex 2 (top 15): 15, 16,

Complex 3 (top 17): 17, 19, 22, 24,

Complex 4 (top 28): 28, 29, 30,

Complex 5 (top 32): 32, 33, 34, 35, 36, 37,

Complex 6 (top 38): 38, 39, 40, 41,

**Complex 0 (2 characters)**, conditions:

Char. 1 Stem\_core\_tracheids\_(only\_protosteles\_s.\_l.)

is inapplicable...

when

ch. 0 Stem\_core\_tracheids has

absent

**Complex 1 (2 characters)**, conditions:

Char. 8 Stele\_internal\_invaginations\_into\_metaxylem\_cylinder

Can only have state(s):

none

when

ch. 6 Stele\_leaf\_gaps\_(peripheral\_invaginations/dissections) has

absent

**Complex 2 (2 characters)**, conditions:

Char. 16 Cortex\_sclerenchymatic\_outer\_layer

is inapplicable...

when

ch. 15 Cortex\_sclerenchymatous\_outer\_cortical\_layer has

absent

**Complex 3 (4 characters)**, conditions:

Char. 19 Number\_of\_leaf-trace\_protoxylem\_strands\_upon\_departure\_from\_stele

Can only have state(s):

two more\_than\_

when

ch. 17 Number\_of\_initial\_protoxylem\_poles\_per\_leaf\_trace has

two

Char. 19 Number\_of\_leaf-trace\_protoxylem\_strands\_upon\_departure\_from\_stele

Can only have state(s):

more\_than\_

when

ch. 17 Number\_of\_initial\_protoxylem\_poles\_per\_leaf\_trace has

more\_than\_

Char. 22 Number\_of\_leaf-trace\_protoxylem\_strands\_in\_central\_part\_of\_cortex

Can only have state(s):

two more\_than\_

when

ch. 17 Number\_of\_initial\_protoxylem\_poles\_per\_leaf\_trace has

two

Char. 22 Number\_of\_leaf-trace\_protoxylem\_strands\_in\_central\_part\_of\_cortex

Can only have state(s):

more\_than\_

when

ch. 17 Number\_of\_initial\_protoxylem\_poles\_per\_leaf\_trace has

more\_than\_

Char. 24 Number\_of\_leaf-trace\_protoxylem\_strands\_upon\_departure\_from\_stem

Can only have state(s):

two more\_than\_

when

ch. 17 Number\_of\_initial\_protoxylem\_poles\_per\_leaf\_trace has

two

Char. 24 Number\_of\_leaf-trace\_protoxylem\_strands\_upon\_departure\_from\_stem

Can only have state(s):

more\_than\_

when

ch. 17 Number\_of\_initial\_protoxylem\_poles\_per\_leaf\_trace has

more\_than\_

**Complex 4 (3 characters)**, conditions:

Char. 29 sclerenchyma\_in\_trace\_concavity\_special\_states

is inapplicable...

when

ch. 28 sclerenchyma\_in\_leaf-trace\_concavity\_adaxially has

absent

Char. 30 origination\_of\_sclerenchyma\_associated\_with\_leaf\_trace

is inapplicable...

when

ch. 28 sclerenchyma\_in\_leaf-trace\_concavity\_adaxially has

absent

**Complex 5 (6 characters)**, conditions:

Char. 33 Sclerenchyma\_ring\_of\_petiole\_base

is inapplicable...

when

ch. 32 Sclerenchyma\_ring has

absent

Char. 34 Abaxial\_arch\_differentiating\_into\_ring

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

Char. 34 Abaxial\_arch\_differentiating\_into\_ring

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

Char. 35 Abaxial\_arch\_differentiating\_into\_two\_masses

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

Char. 35 Abaxial\_arch\_differentiating\_into\_two\_masses

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

Char. 36 Abaxial\_arch\_or\_two\_masses\_differentiating\_into\_three\_masses

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

Char. 36 Abaxial\_arch\_or\_two\_masses\_differentiating\_into\_three\_masses

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

Char. 37 Two\_masses\_differentiating\_further\_into\_adaxial\_arch

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

Char. 37 Two\_masses\_differentiating\_further\_into\_adaxial\_arch

is inapplicable...

when

ch. 33 Sclerenchyma\_ring\_of\_petiole\_base has

homogenous

**Complex 6 (4 characters)**, conditions:

Char. 39 Scattered\_sclerenchyma\_clusters\_in\_stipular\_expansions

is inapplicable...

when

ch. 38 Stipular\_wings\_or\_spines has

absent

OR

ch. 38 Stipular\_wings\_or\_spines has

spines

Char. 41 Elongate\_shape\_or\_arrangement\_of\_distinct\_sclerenchyma\_masses\_in\_stipu

is inapplicable...

when

ch. 38 Stipular\_wings\_or\_spines has

absent

AND

ch. 40 Distinct\_sclerenchyma\_clusters\_in\_stipular\_expansions has

absent

Syntax for the employed complexes, character and character state numbers correspond to those of the matrix in TNT format:

**xlinks**

**0 :0 < 1 - >**

**6 :0 < 8 0 >**

**15 :0 < 16 - >**

**17 :1 < 19 1 2 >**

**17 :2 < 19 2 >**

**17 :1 < 22 1 2 >**

**17 :2 < 22 2 >**

**17 :1 < 24 1 2 >**

**17 :2 < 24 2 >**

**28 :0 < 29 - >**

**28 :0 < 30 - >**

**32 :0 < 33 - >**

**33 :0 < 34 - >**

**33 :0 < 34 - >**

**33 :0 < 35 - >**

**33 :0 < 35 - >**

**33 :0 < 36 - >**

**33 :0 < 36 - >**

**33 :0 < 37 - >**

**33 :0 < 37 - >**

**38 :0 | 38 :2 < 39 - >**

**38 :0 & 40 :0 < 41 - >**

**;**

**Table S1.** Topological congruence between phylogenies inferred under different analytical approaches. The Robinson-Foulds distance is normalised so that “0.0” minimises distance (i.e., maximises congruence) and “1.0” maximises distance (i.e., minimises congruence). The proportion of common nodes is estimated relative to the maximum number of possible nodes for the smallest tree in each pairwise comparison. Pairwise comparisons against the reference topologies (under equal weighting and no dependencies; “ew-nondep”) entail topologies inferred with dependencies included under: equal weighting (“ew-dep”), and no dependencies under extended implied weighting with concavity 5 (“k5-nodep”), concavity 10 (“k10-nodep”), concavity 15 (“k15-nodep”) and concavity 20 (“k20-nodep”).

| **Comparison** | **RF distance** | **Proportion of common nodes** |
| --- | --- | --- |
| ew-nondep vs ew-dep | 0.67 | 0.48 |
| ew-nondep vs k5-nodep | 0.72 | 0.21 |
| ew-nondep vs k10-nodep | 0.71 | 0.21 |
| ew-nondep vs k15-nodep | 0.46 | 0.23 |
| ew-nondep vs k20-nodep | 0.68 | 0.20 |

**Fig. S1.** Reduced consensus trees from topologies inferred under equal and extended implied weighting and using or excluding character dependencies. Subfamilies highlighted in each tree in colour: (blue) Thamnopteroideae, (light blue) Itopsidemoideae, (green) Guairoideae, and (red) Osmundoideae. Groups in black are either incertae sedis or non-osmundalean fossils.

