

Supplementary Materials: Phylogenetic Structure of Foliar Spectral Traits in Tropical Forest Canopies

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Hierarchical Procedure for DNA Sequence Selection

Individuals with both *matK* and *rbcL* sequences available were the default selection for species where they were available. If no individuals of a given species had complete data for both markers, the most complete *rbcL* and *matK* sequences were chosen independently from all individuals of a species, and concatenated into one combined *rbcL* + *matK* sequence. If a given species had only one DNA marker available, this marker was concatenated with an empty vector for the length of the missing sequence (either *rbcL* or *matK*). For species with multiple combined *rbcL* + *matK* sequences available, or alternately with multiple single biomarkers of either *rbcL* or *matK*, the longest sequence was chosen by default. The suitability of selected sequences as a representative of their species was assessed by visually comparing the resulting combined phylogeny to the single-marker phylogenies, which included all other potential representative sequences for each species. If a sequence was found to improperly locate a species within the combined phylogeny, it was omitted and the hierarchical procedure selected the next most suitable strategy. This procedure resulted in the omission of 13 *matK* sequences and retained all *rbcL* sequences.

Table S1. Pairwise Pearson's correlation coefficients for species' standardized mean foliar trait values (lower diagonal) and phylogenetic independent contrasts (PICs) of trait values utilizing the DNA-based phylogeny (upper diagonal). Levels of significance are indicated with asterisks. LMA = leaf mass per area; Chl = chlorophyll.

	Nitrogen	Phosphorus	Calcium	LMA	Lignin	Cellulose	Phenols	Tannins	Chl
Nitrogen		0.63 ***	-0.34 ***	-0.71 ***	0.16 *	0.06	-0.22 **	-0.21 **	0.60 ***
Phosphorus	0.43 ***		-0.05	-0.27 ***	-0.11	0.09	-0.13 *	0.02	0.02
Calcium	-0.05	0.32 ***		-0.10	-0.42 ***	-0.14 *	0.07	0.26 ***	0.03
LMA	-0.57 ***	-0.38 ***	-0.19 **		-0.24 ***	-0.12 *	0.02	-0.16 *	-0.81 ***
Lignin	0.04	-0.22 **	-0.55 ***	0.11		-0.15 *	0.43 ***	0.40 ***	0.43 ***
Cellulose	-0.17 *	-0.16 *	-0.30 ***	0.09	0.36 ***		-0.58 ***	-0.23 **	-0.07
Phenols	-0.38 ***	-0.22 **	-0.30 ***	0.19 **	0.26 ***	-0.09		0.73 ***	-0.13 *
Tannins	-0.31 ***	-0.15 *	-0.31 ***	0.16 *	0.28 ***	-0.05	0.90 ***		-0.09
Chl	0.56 ***	0.29 ***	0.23 ***	-0.71 ***	-0.10	-0.15 *	-0.21 **	-0.18 *	

* $p < 0.05$; ** $p < 0.001$; *** $p < 1 \times 10^{-5}$.

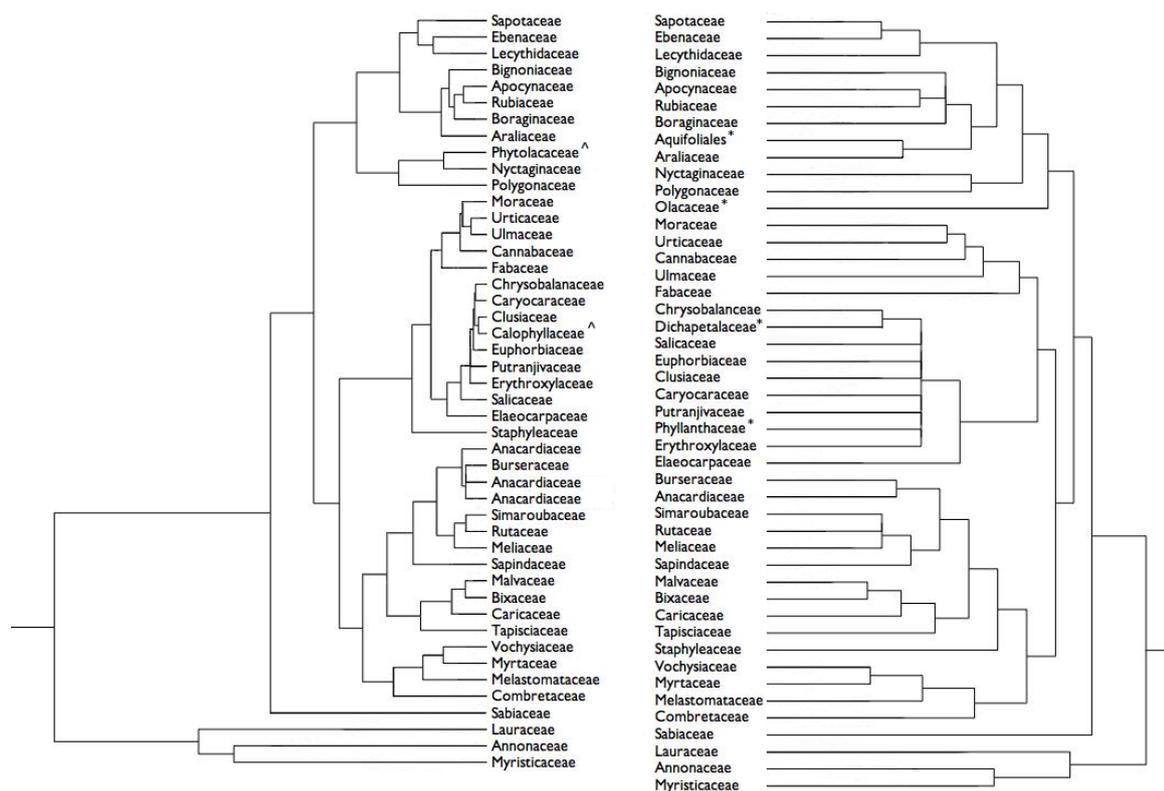


Figure S1. Comparison of the branching patterns of the DNA-based phylogeny (**left**-hand tree) and *Phylomatic* phylogeny (**right** hand tree) to the family level for all taxa included in the study. ^: families included only in the DNA-based phylogeny; *: families included only in the *Phylomatic* phylogeny.

Community Phylogenies (Figures S2–S7)

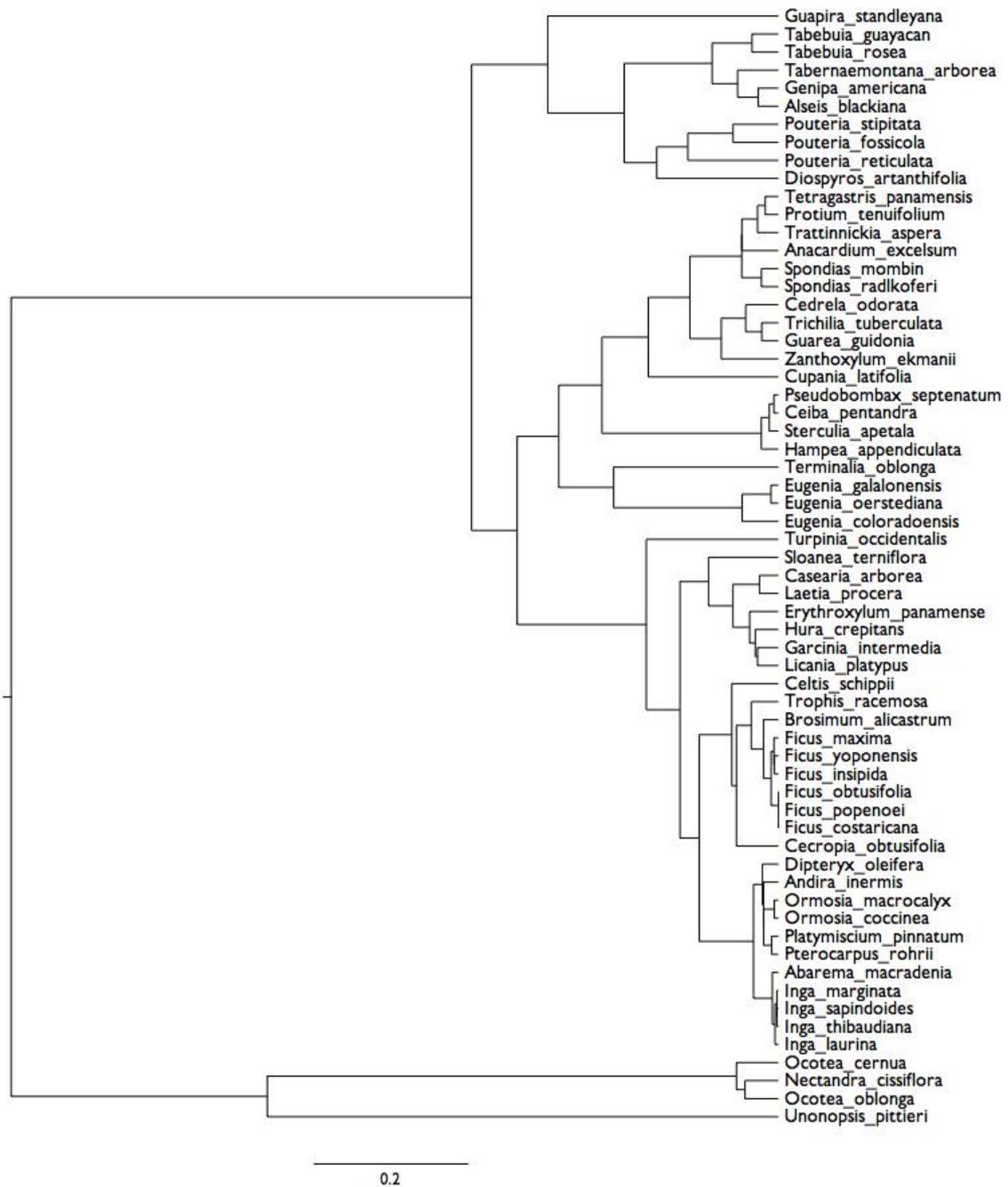


Figure S2. DNA phylogeny for BCI, representing 62 species with available genetic sequences.

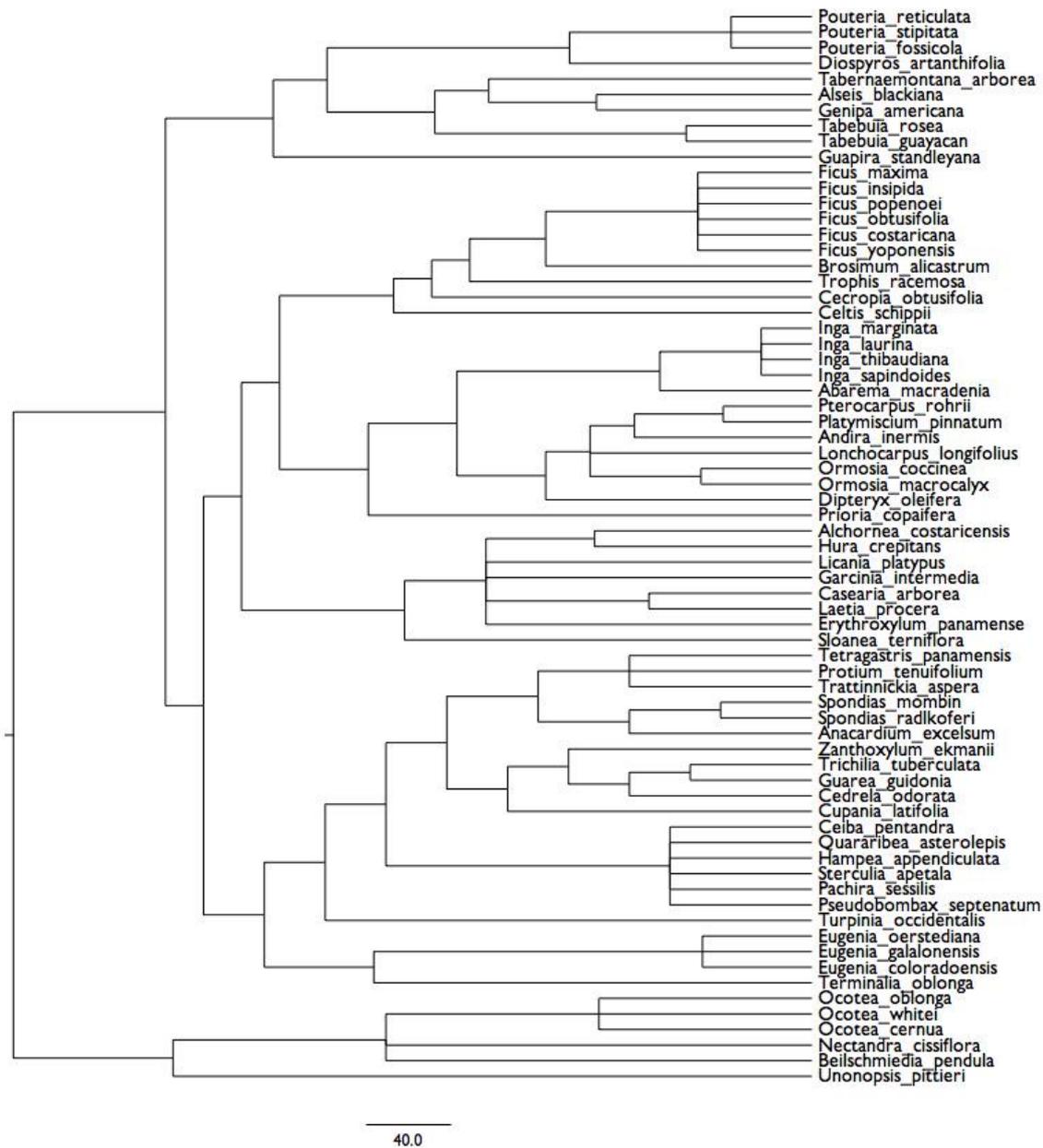


Figure S3. *Phylogenetic* phylogeny for BCI, representing 69 species included in the APG megatree.

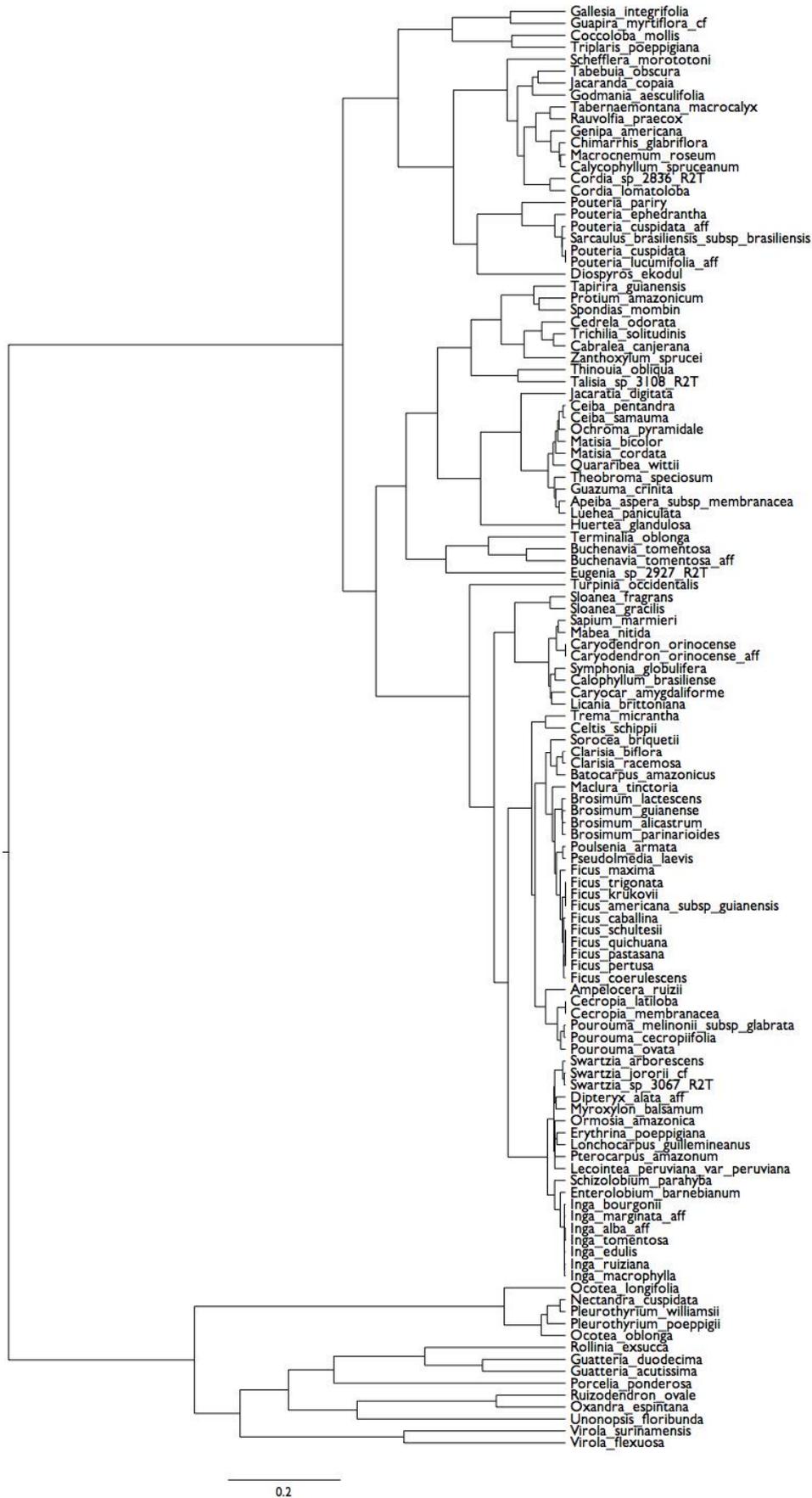


Figure S4. DNA phylogeny for Tam-I, representing 121 species with available genetic sequences.

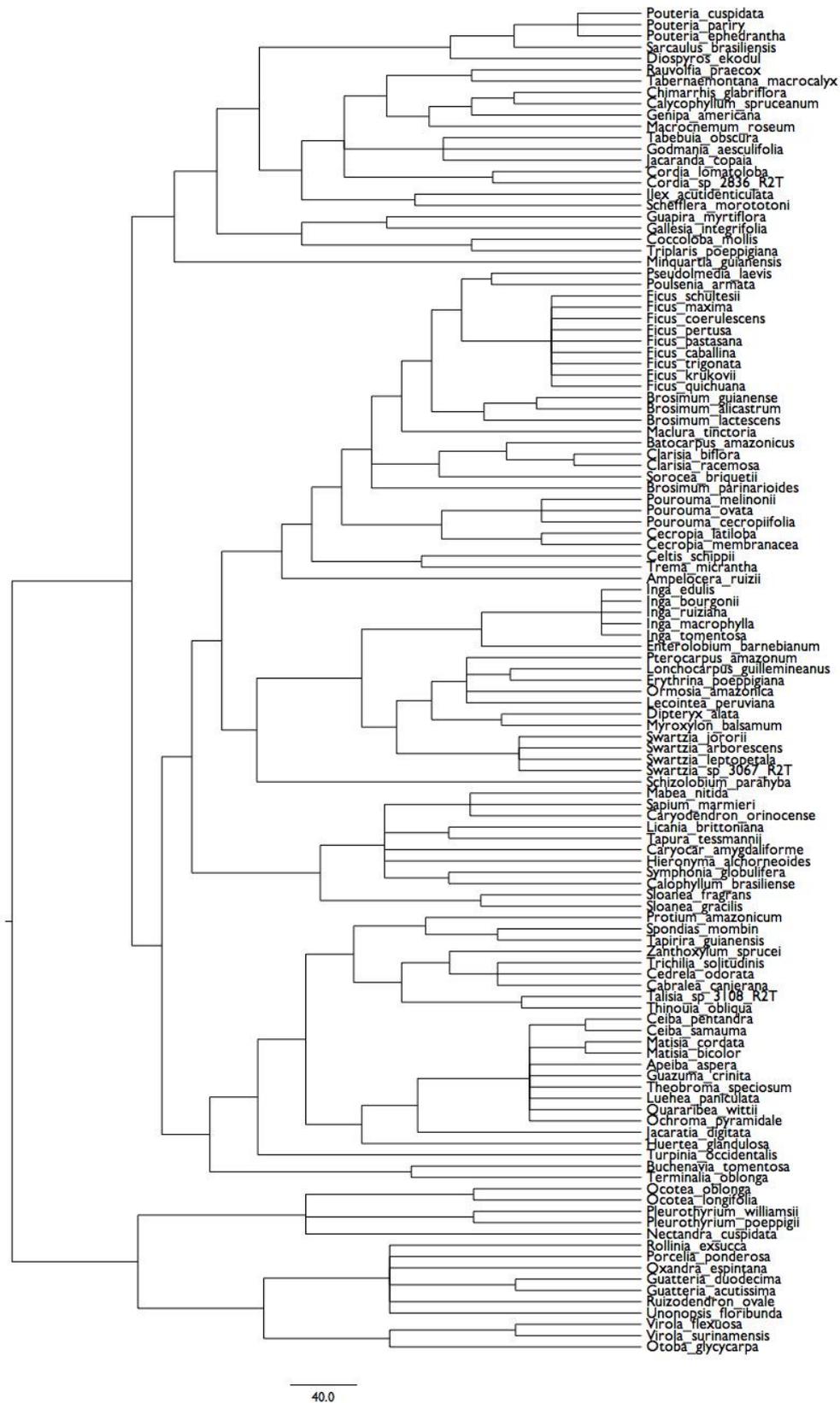


Figure S5. *Phylocom* phylogeny for Tam-I, representing 115 species included in the APG megatree.

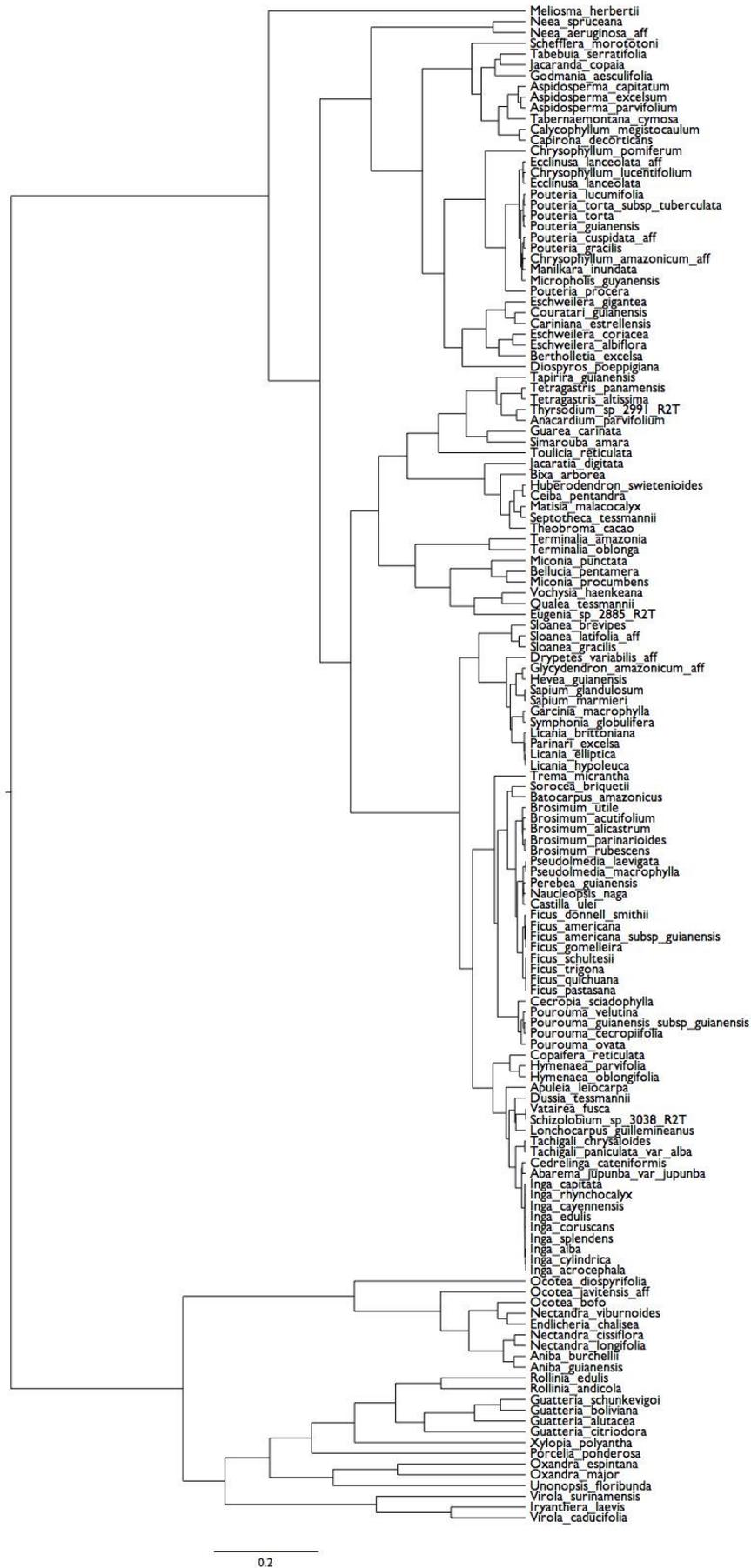


Figure S6. DNA phylogeny for Tam-U, representing 141 species with available genetic sequences.

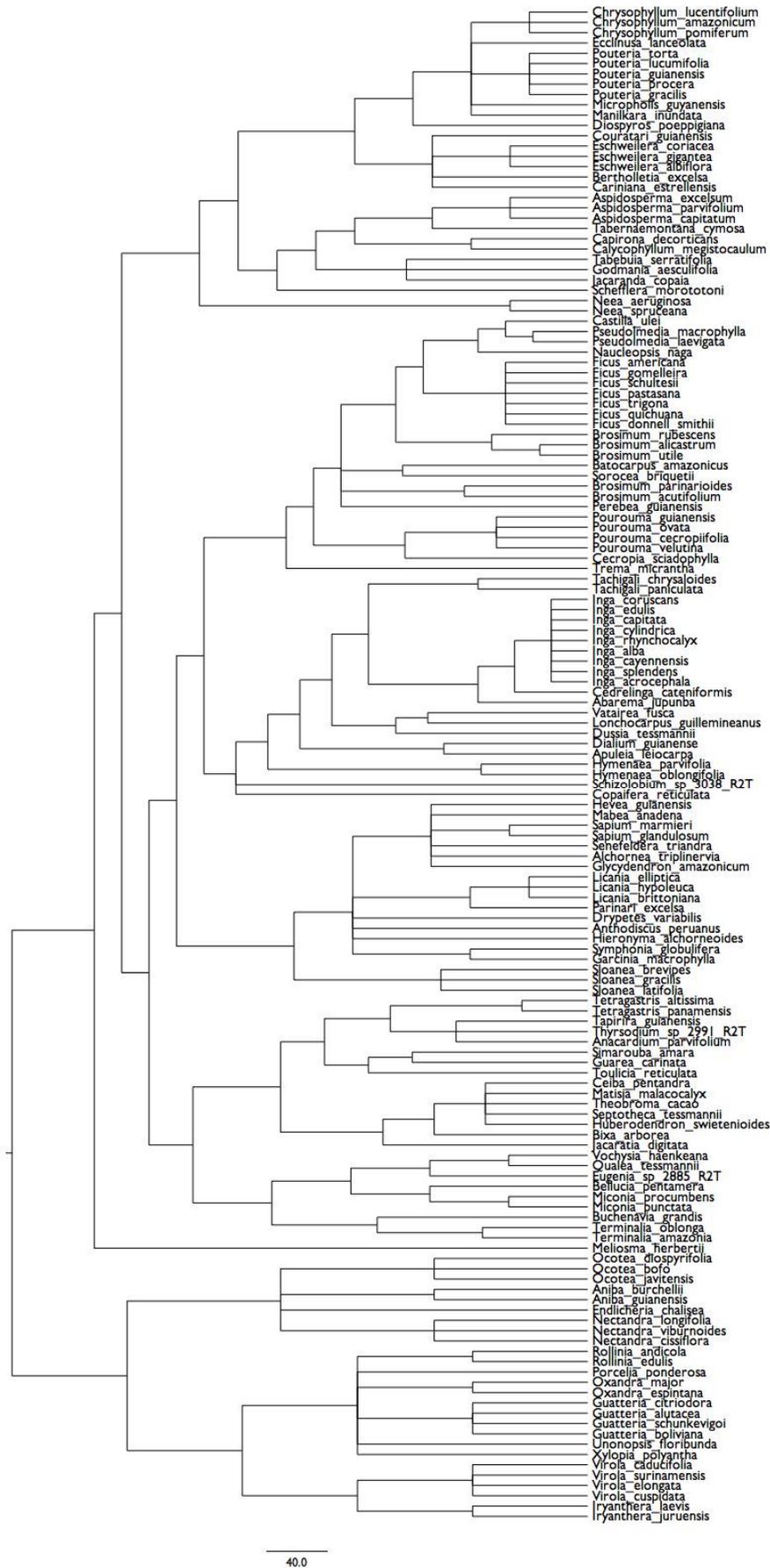


Figure S7. *Phylostatic* phylogeny for Tam-U, representing 144 species included in the APG megatree.

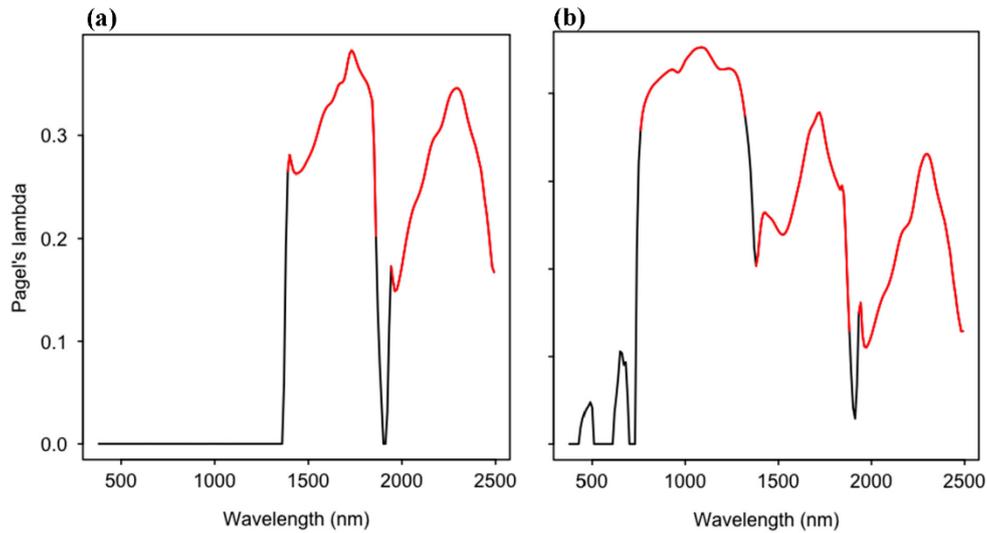


Figure S8. Phylogenetic signal, as Pagel’s lambda, of species reflectance coefficients for all species at all sites included in the study, utilizing (a) the DNA-based phylogeny and (b) the *Phylomatic* phylogeny.

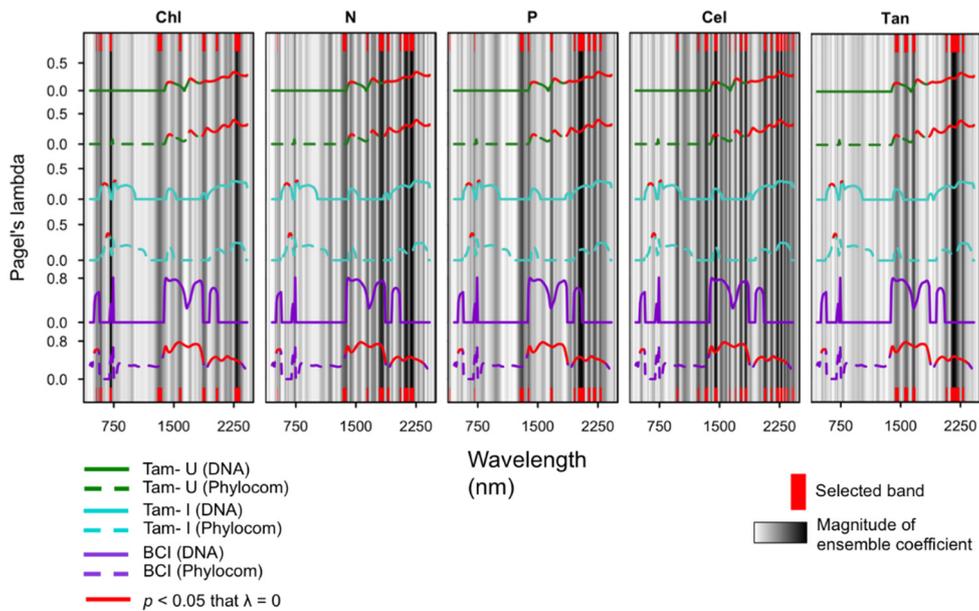


Figure S9. Phylogenetic signal, as Pagel’s lambda, of species reflectance coefficients at each site for five functional traits, overlaid on the multi-model ensemble regression coefficients (grey bars) as measures of band importance to each trait model. Site-specific lambda spectra are indicated by color: BCI = purple; Tam-I = cyan; Tam-U = green; and phylogeny used to generate lambda is indicated by line style: DNA = solid lines; Phylocom = dashed lines. Red bars (**top and bottom**) indicate bands selected by the ensemble as most important to the relationship between reflectance and chemical concentration/trait variation. Chl = chlorophyll; N = nitrogen; P = phosphorus; Cel = cellulose; Tan = tannins.

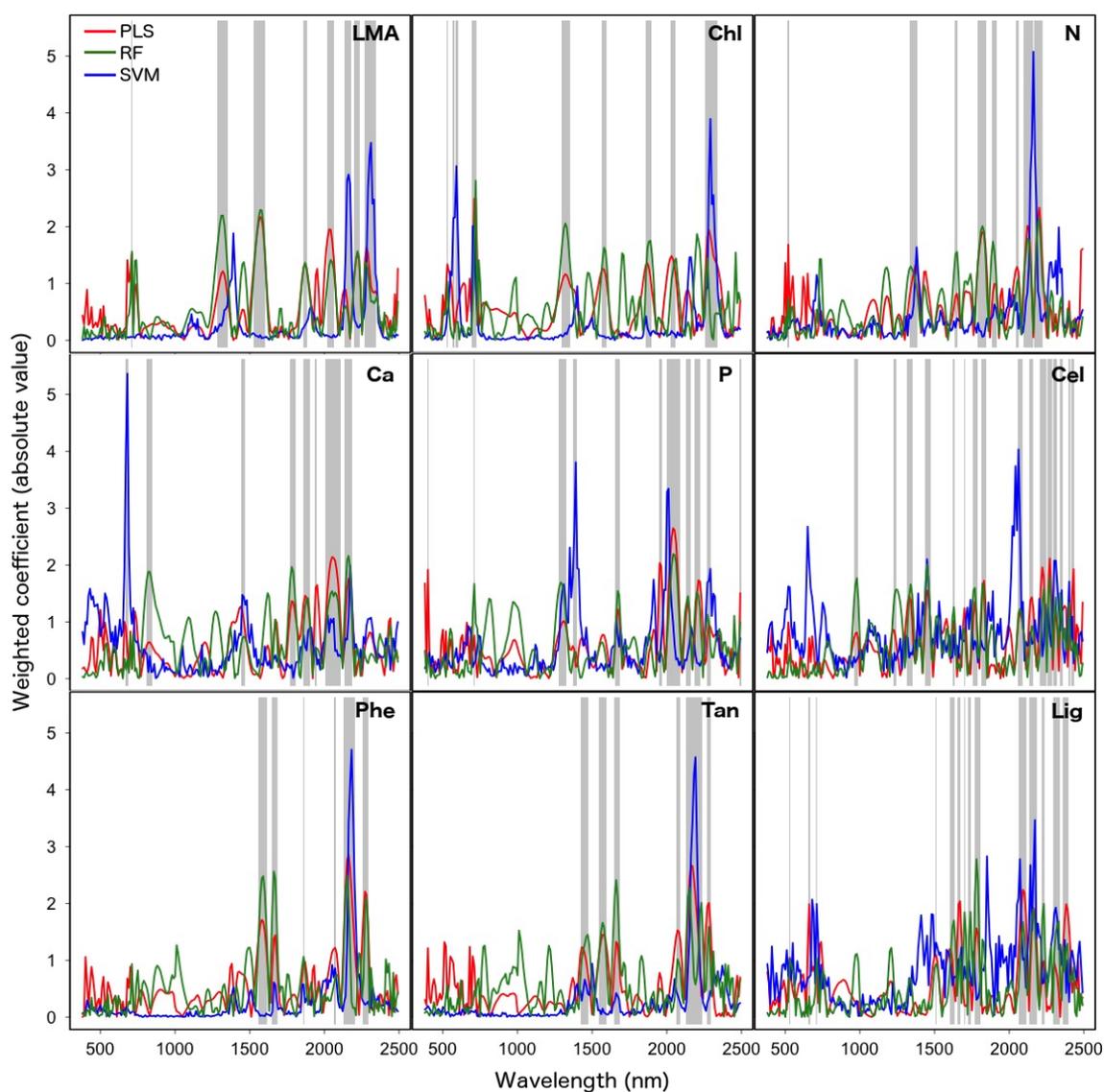


Figure S10. Spectral coefficients for three regression models that comprise the multi-model ensemble, weighted by individual model fit statistic (R^2). For each wavelength, the ensemble coefficient is equal to the sum of the three individual model coefficients. Bands selected as most influential for each biochemical trait by the ensemble are indicated by grey bars. LMA = leaf mass per area; Chl = chlorophyll; N = nitrogen; Ca = calcium; P = phosphorus; Cel = cellulose; Phe = phenols; Tan = tannins; Lig = lignin.



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