

Supplementary material

File S1: References for trait-trait and trait-environment relationships depicted in Figures 1 and 2:

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Table S1: Principal component analysis of functional traits. Eigenvalues, explained variation and trait loadings for first four principal components (PC1-4). “26 traits”: dataset with almost all continuous traits (not included was LChl). “14 traits”: dataset without root and stomatal traits to allow for the inclusion of species without observations on these traits.

	26 traits				14 traits			
	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4
explained variation (%)	26	18	12	9	28	22	14	9
Eigenvalue	6.84	4.77	3.19	2.37	3.94	3.07	1.96	1.20
Trait								
Hmax	-0.19	-0.30	0.71	0.24	-0.35	0.38	0.79	0.05
SLA	0.50	0.54	0.08	-0.37	0.78	-0.43	-0.14	-0.19
LDMC	-0.50	-0.20	0.67	-0.04	-0.29	-0.75	0.18	0.42
Lth	-0.02	-0.21	-0.79	0.33	-0.35	0.84	-0.20	-0.10
LAmx	-0.07	-0.19	0.77	0.30	-0.23	0.33	0.82	0.22
LCC	-0.58	-0.41	0.05	-0.43	-0.64	-0.39	0.08	-0.34
LNC	0.66	0.22	0.35	-0.42	0.78	-0.28	0.24	-0.22
LPC	0.76	0.31	0.07	-0.10	0.77	0.27	0.16	0.03
LKC	0.70	0.46	0.08	0.24	0.64	0.46	0.20	0.15
LMgC	0.62	-0.06	-0.34	0.22	0.49	0.47	-0.35	0.17
LCaC	0.46	-0.28	-0.33	0.13	0.16	0.65	-0.16	0.12
δ15N	0.35	0.47	0.24	-0.19	0.60	-0.02	0.35	-0.11
δ13C	-0.32	-0.25	-0.49	0.35	-0.55	0.42	-0.31	-0.12
RCC	-0.57	0.48	-0.17	-0.15	NA	NA	NA	NA
RNC	0.81	0.14	0.08	-0.21	NA	NA	NA	NA
RPC	0.79	-0.28	0.01	-0.15	NA	NA	NA	NA
RKC	0.75	-0.55	0.01	-0.03	NA	NA	NA	NA
RMgC	0.78	-0.47	-0.04	0.02	NA	NA	NA	NA
RCaC	0.67	-0.18	0.16	0.31	NA	NA	NA	NA
SD	-0.18	-0.39	-0.13	-0.71	NA	NA	NA	NA
SL	0.21	0.51	0.37	0.56	NA	NA	NA	NA
PSCA	-0.22	0.20	0.09	-0.34	NA	NA	NA	NA
SRL	0.12	0.88	-0.26	-0.14	NA	NA	NA	NA
RD	0.13	-0.93	0.19	0.02	NA	NA	NA	NA
RTD	-0.50	0.63	0.10	0.28	NA	NA	NA	NA
SSD	-0.02	0.11	0.02	0.29	0.03	-0.19	-0.26	0.82

Table S2: Principal component analysis of CWMs functional traits. Eigenvalues, explained variation and trait loadings for first four principal components (PC1-4) for crown and stem communities (see Materials and Methods).

	Crown				Stem			
	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4
explained variation (%)	32	25	13	9	27	23	13	13
Eigenvalue	8,88	7,08	3,76	2,63	7,49	6,56	3,77	3,51
Trait								
H _{max}	0,19	0,28	0,63	-0,22	-0,08	-0,42	0,65	0,41
SLA	0,41	-0,69	0,08	-0,10	0,75	-0,23	0,14	-0,08
LDMC	0,09	-0,73	0,56	-0,19	0,33	-0,77	0,27	0,13
L _{th}	-0,27	0,75	-0,51	0,21	-0,57	0,66	-0,32	-0,13
LA _{max}	0,28	0,43	0,78	-0,24	-0,25	-0,08	0,83	0,15
SPAD	0,58	-0,41	0,38	-0,32	0,47	0,20	0,29	-0,10
LCC	-0,35	-0,70	-0,43	-0,20	0,26	-0,57	-0,58	-0,08
LNC	0,59	-0,65	-0,10	-0,16	0,90	-0,05	-0,01	0,04
LPC	0,76	0,35	0,33	0,19	0,29	0,71	0,42	-0,15
LKC	0,36	0,87	0,19	0,03	-0,41	0,75	0,34	-0,13
LMgC	0,73	0,45	-0,14	-0,03	0,17	0,49	0,19	0,43
LCaC	0,73	-0,16	0,06	0,44	0,77	0,40	0,22	-0,17
δ ¹⁵ N	0,22	-0,02	0,52	0,41	0,33	0,35	0,58	-0,51
δ ¹³ C	-0,29	0,61	-0,39	-0,55	-0,62	0,04	-0,47	0,54
ph_pathway_C3	0,19	-0,46	0,17	0,71	0,58	-0,01	0,37	-0,59
RCC	-0,61	0,30	0,25	0,44	-0,32	0,07	-0,25	-0,69
RNC	0,66	-0,16	-0,33	0,36	0,55	0,53	-0,40	-0,24
RPC	0,62	-0,02	-0,61	0,24	0,42	0,68	-0,46	0,16
RKC	0,95	0,10	-0,18	-0,01	0,65	0,68	-0,01	0,18
RMgC	0,93	0,15	-0,23	0,00	0,68	0,50	-0,33	0,27
RCaC	0,74	0,45	-0,06	0,17	0,09	0,79	0,15	0,34
SD	0,09	-0,93	-0,06	0,00	0,68	-0,63	-0,13	-0,16
SL	-0,08	0,86	0,38	0,10	-0,64	0,61	0,41	0,10
PSCA	-0,08	-0,60	0,55	0,10	0,49	-0,42	0,23	-0,19
SRL	-0,73	-0,17	-0,06	0,61	-0,15	0,10	-0,23	-0,83
RD	0,86	0,06	0,00	-0,43	0,57	0,02	0,04	0,70
RTD	-0,82	0,28	0,31	-0,06	-0,84	-0,17	0,30	-0,20
SSD	0,55	0,21	0,13	0,28	-0,10	0,52	-0,13	-0,24

Table S3: Results of ANOVAs and pairwise comparisons of CWMs of different traits on tree species for crown and trunk assemblages. “variances”: states whether variances were homogenous (“homo”, $p > 0.05$) or heterogeneous (“hetero”, $p < 0.05$) according to Bartlett’s test. In the first case, F- and p-values are the results of regular ANOVA, followed by Tukey’s test, in the second case the results of Welch’s ANOVA, followed by max-t tests for multiple comparisons. p-values for pairwise comparisons between tree species: A-B, A-C etc.; A: *Aspidosperma*, B: *Brosimum*, C: *Calophyllum*, M: *Manilkara*. **p-values < 0.05 are in bold.** PP_C3 relates to the relative abundance of individuals belonging to C₃ species. For a full list of traits see Table 1.

trait	variances	crown								variances	trunk							
		F	p	A-B	A-C	A-M	B-C	B-M	C-M		F	p	A-B	A-C	A-M	B-C	B-M	C-M
SLA	homo	3.40	0.02	0.04	0.10	1.00	0.08	0.06	1.00	homo	1.48	0.24	0.40	0.78	0.20	0.93	0.98	0.73
LDMC	hetero	5.37	<0.01	0.02	0.73	0.81	0.001	0.25	0.28	homo	2.53	0.07	0.07	0.16	0.55	0.99	0.42	0.67
L _{th}	hetero	6.65	<0.01	<0.01	0.89	0.56	<0.001	0.12	0.17	homo	2.09	0.12	0.09	0.31	0.17	0.93	0.96	0.99
LA	homo	6.88	<0.001	0.02	0.97	<0.01	0.07	0.83	0.01	homo	0.17	0.92	0.97	0.91	0.99	0.99	0.99	0.96
H _{max}	hetero	4.89	<0.01	0.10	0.98	0.04	0.05	0.88	0.02	homo	0.88	0.46	0.99	0.97	0.78	0.85	0.87	0.41
LChl	homo	9.78	<0.001	<0.001	1.00	0.40	<0.001	0.01	0.39	homo	3.39	0.03	0.58	0.87	0.64	0.96	0.02	0.14
LCC	homo	1.30	0.28	0.92	1.00	0.35	0.88	0.72	0.32	hetero	0.49	0.70	0.98	1.00	1.00	0.72	0.81	1.00
RCC	homo	4.20	0.01	<0.01	0.47	0.35	0.23	0.26	1.00	homo	1.27	0.30	0.40	0.86	0.30	0.85	1.00	0.76
LNC	homo	8.77	<0.001	<0.001	0.84	0.98	<0.01	<0.001	0.96	homo	3.01	0.04	0.06	0.99	0.48	0.09	0.46	0.62
RNC	hetero	7.11	<0.01	0.04	0.08	1.00	0.76	<0.01	<0.01	homo	1.08	0.37	0.97	0.69	0.97	0.31	0.70	0.82
LPC	hetero	4.91	<0.01	0.02	0.43	0.01	0.21	0.91	0.23	homo	1.91	0.14	0.80	0.62	1.00	0.10	0.53	0.59
RPC	homo	3.77	0.01	0.10	0.18	0.98	1.00	0.04	0.09	homo	0.91	0.45	0.89	0.89	1.00	0.39	0.66	0.92
LKC	homo	2.51	0.06	0.80	0.63	0.04	0.99	0.27	0.51	homo	1.22	0.31	0.65	0.28	0.87	0.85	0.94	0.52
RKC	homo	6.79	<0.001	<0.001	0.13	0.17	0.17	0.08	0.99	homo	1.48	0.24	0.62	0.93	1.00	0.21	0.44	0.89
LCaC	hetero	3.61	0.02	0.40	0.84	0.78	0.03	0.01	1.00	hetero	1.62	0.23	0.46	1.00	1.00	0.58	0.13	0.99
RCaC	homo	1.86	0.14	0.24	0.61	0.14	0.94	0.99	0.82	hetero	0.44	0.72	0.97	0.87	0.99	0.86	0.99	0.75
LMgC	homo	1.42	0.24	0.22	0.88	0.48	0.68	0.96	0.92	hetero	0.18	0.91	0.90	0.92	0.88	1.00	1.00	1.00

RMgC	homo	7.03	< 0.001	< 0.001	0.04	0.20	0.37	0.07	0.87	hetero	0.97	0.43	0.71	1.00	0.99	0.41	0.39	0.99
SD	homo	2.94	0.04	0.37	1.00	0.56	0.33	0.02	0.69	homo	1.47	0.24	0.23	0.58	0.88	0.92	0.44	0.88
SL	homo	3.95	0.01	0.40	0.90	0.32	0.85	0.01	0.09	homo	1.24	0.31	0.30	0.49	0.80	0.99	0.66	0.88
PSCA	homo	2.17	0.10	0.77	0.39	1.00	0.06	0.72	0.43	homo	1.94	0.14	0.26	0.97	1.00	0.44	0.14	0.98
SRL	homo	12.45	< 0.001	< 0.001	0.03	< 0.001	0.05	0.65	0.44	hetero	0.97	0.43	0.46	0.79	0.65	0.64	0.84	0.95
RD	homo	14.03	< 0.001	< 0.001	0.01	0.001	0.03	0.13	0.90	hetero	1.94	0.16	0.27	0.85	0.65	0.22	0.29	0.89
RTD	homo	7.22	< 0.001	< 0.001	0.06	0.77	0.42	0.01	0.36	hetero	1.27	0.32	0.41	0.97	0.89	0.42	0.34	0.98
SSD	homo	1.88	0.14	0.13	0.96	0.96	0.37	0.32	1.00	hetero	2.72	0.08	0.38	0.23	0.94	0.76	0.18	0.12
$\delta^{13}\text{C}$	hetero	3.30	0.03	0.86	0.78	0.22	0.41	0.02	0.94	hetero	0.36	0.79	0.86	0.97	1.00	0.99	0.77	0.94
$\delta^{13}\text{C}_2$	hetero	8.83	< 0.001	0.01	0.65	0.72	< 0.001	0.09	0.05	homo	1.10	0.36	0.59	0.99	0.87	0.37	0.90	0.69
$\delta^{15}\text{N}$	homo	0.95	0.42	0.86	0.79	1.00	0.34	0.79	0.86	homo	0.51	0.68	0.83	0.63	0.75	0.97	1.00	0.98
PP_C3	hetero	4.14	0.01	1.00	1.00	1.00	0.18	0.05	0.12	homo	0.72	0.55	1.00	1.00	0.78	1.00	0.65	0.64

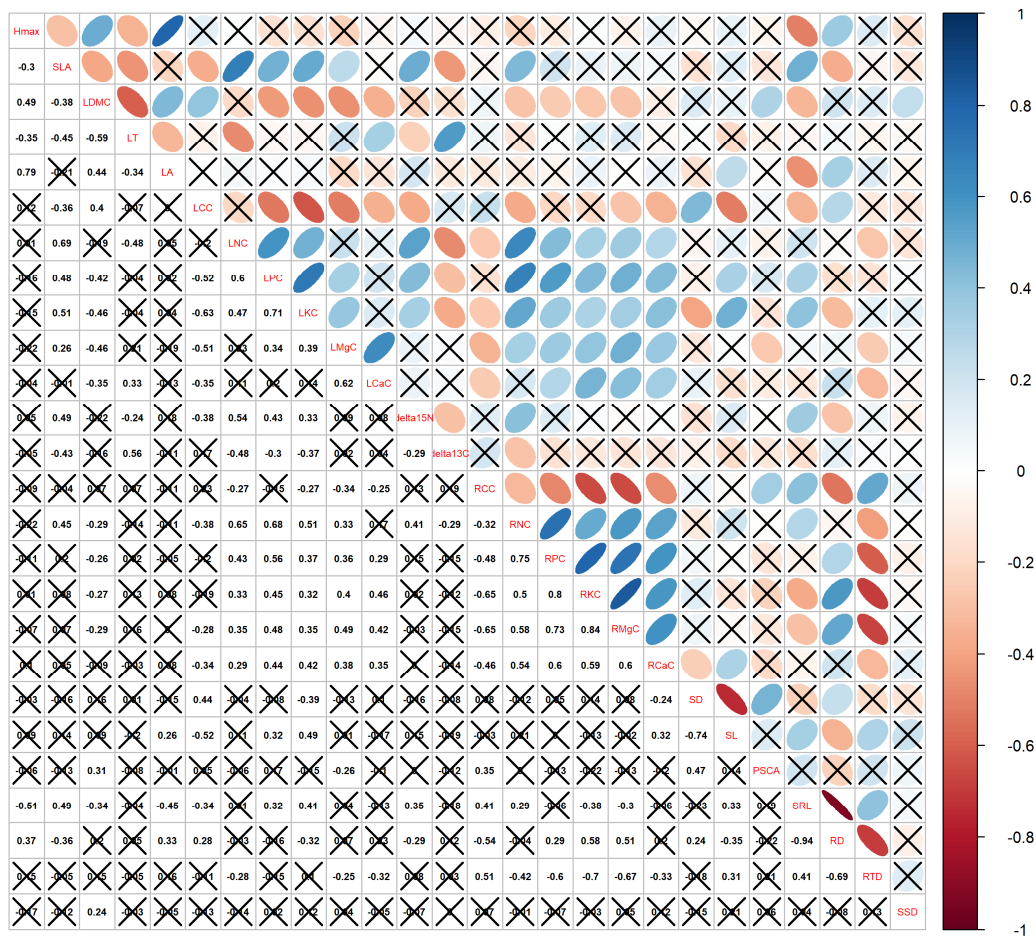


Figure S1: Correlation matrix for 26 traits. Pearson's correlation coefficients are given in the lower diagonal and are visually symbolized in the upper diagonal. Non-significant correlations ($p > 0.05$) are crossed.

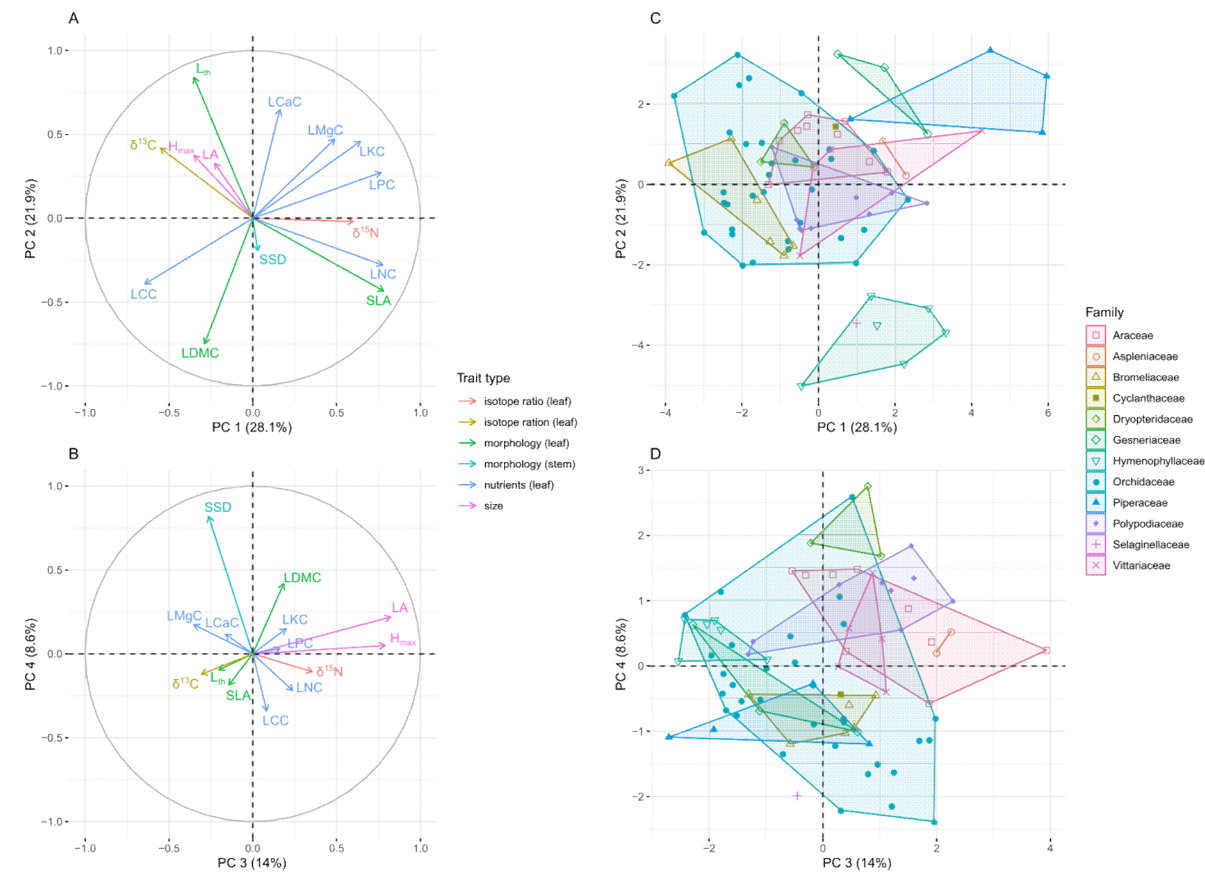


Figure S2: Principal component analysis of functional traits (excluding stomatal and root traits) of the epiphytic community at study site. Analysed were species averages for 13 functional traits of 81 epiphytic species (9 species not included in PCA for Figure 1). A and B: Variable correlation plots for the 1st and 2nd principal component (A) and the 3rd and 4th principal component (B), respectively. Colors refer to trait type. C and D: Epiphyte species within the ordination space. C: 1st and 2nd principal component, D: 3rd and 4th principal component. Plant families are differentiated by color and enclosed by convex hulls.

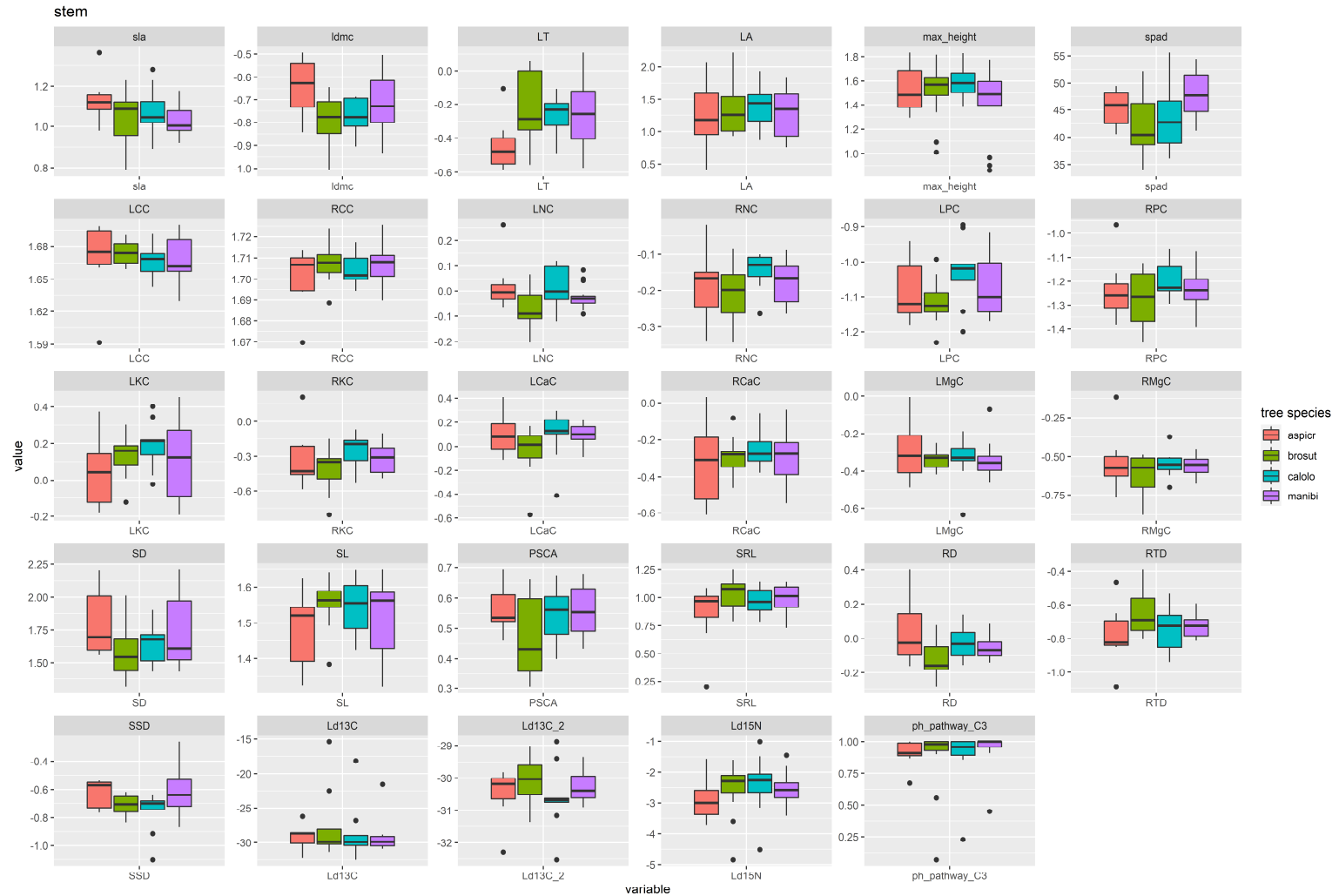


Figure S3: CWMs of different traits on stems of focal tree species. For units of trait values see table 1. Most traits were \log_{10} -transformed (see methods).
“ $\delta^{13}\text{C}_2$ ” refers to CWMs based on C_3 species only.

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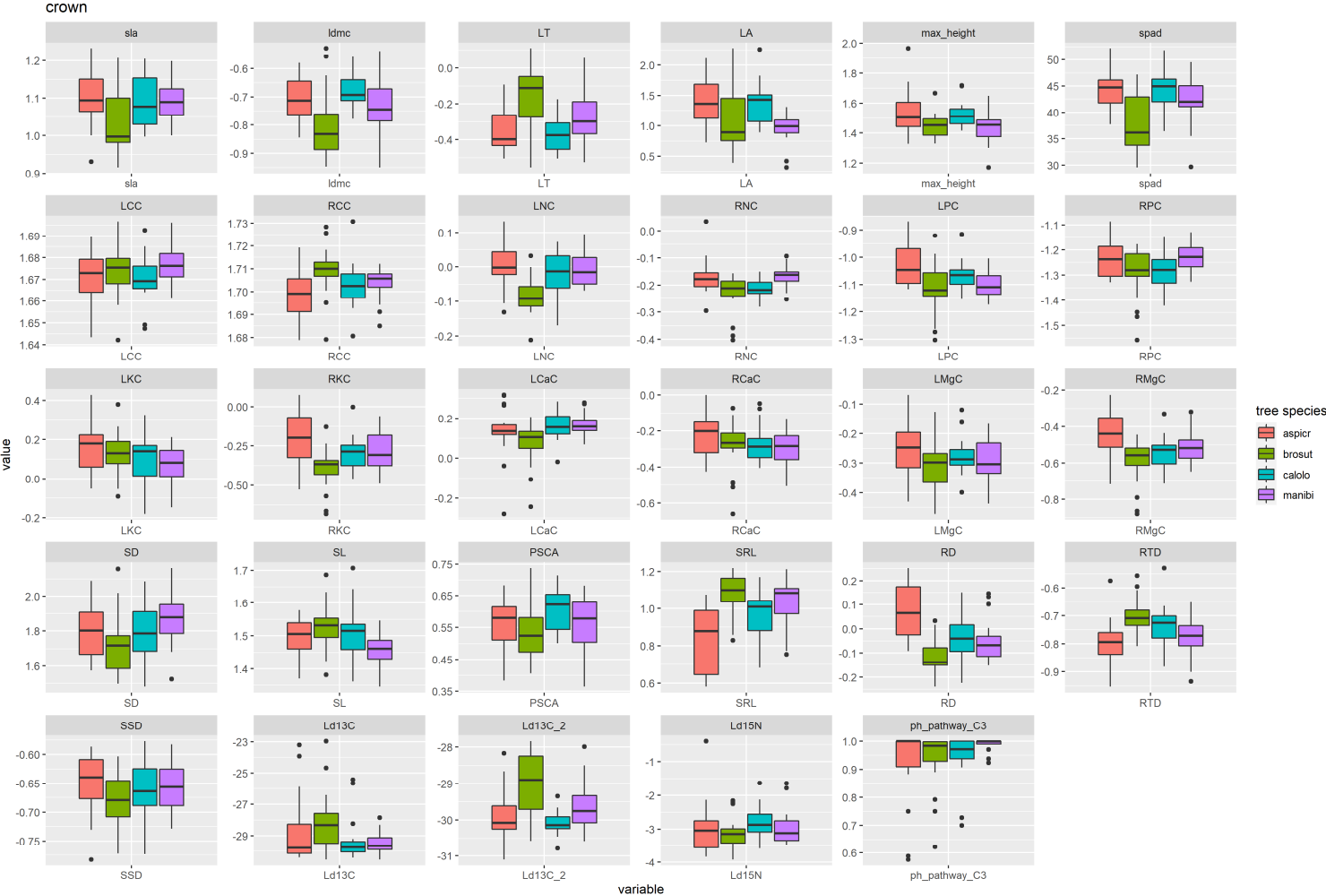


Figure S4: CWMs of different traits in crowns of focal tree species. For units of trait values see table 1. Most traits were log₁₀-transformed (see methods). “ $\delta^{13}\text{C}_2$ ” refers to CWMs based on C₃ species only.

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