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Article title: An integrated framework of plant form and function: The belowground perspective

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The following Supporting Information is available for this article:

Fig. S1 Results of the full quantitative literature review of 98 papers with 550 reported root-leaf-stem trait relationships presented as pie charts.

Fig. S2 Pairwise correlation of all traits used in the analysis based on the full dataset (*n* = 2510 species).

Fig. S3 Non-phylogenetically informed PCA on the core species set (*n* = 804) for the six core traits based on species mean trait data (corresponding to phylogenetically informed Fig. 3b, corresponding data in Table S5).

Fig. S4 Phylogenetically-informed PCA on the core species set (*n* = 804) separated for non-woody and woody plant species for the six core traits based on species mean trait data (corresponding to Fig. 3, corresponding data in Table S6).

Fig. S5 Three-dimensional representation of Fig. 4 added as separate file.

Fig. S6 PCA based on correlation matrix of species mean traits (*n* = 2510) expanding the six core traits (see Fig. 3) to a set of 14 leaf and root traits (corresponding data in Table S9).

Fig. S7 PCA based on correlation matrix based on species mean trait data of all traits (*n* = 2510, corresponding data in Table S10).

Fig. S8 Sensitivity analysis for data shown in Fig. 3 to test if using different combinations of

species numbers and traits would affect the results (corresponding data in Tables S11 and S12).

Fig. S9 Non-phylogenetically informed PCA of traits measured on the individual plant level (*n* = 455) for the six core traits (corresponding to phylogenetically-informed Fig. 5, corresponding data in Table S14).

Table S1 List of 140 papers and extracted information used for qualitative literature review. Available as separate file.

Table S2 List of additional data sources for the main database. Available as separate file.

Table S3 Quantitative description of all plant traits in the main database.

Table S4 Results of the phylogenetically-informed PCA on the core species set (*n* = 804) for the six core traits based on species mean trait data (as shown in Fig. 3).

Table S5 Results of the non-phylogenetically informed PCA on the core species set (*n* = 804) for the six core traits based on species mean trait data (as shown in Fig. S3).

Table S6 Results of the phylogenetically-informed PCA on the core species set (*n* = 804) for the six core traits based on species mean trait data of woody and non-woody species (as shown in Fig. S4).

Table S7 Results of the permutational multivariate analysis on the core species set (*n* = 804) including variation between different groups of species based on species mean trait data (as shown in Fig. 3).

Table S8 Results of the PCA based on the correlation matrix of all species (*n* = 2510) for the six core traits and plant height and rooting depth (as shown in Fig. 4).

Table S9 Results of the PCA based on the correlation matrix using complete pairwise data of all species (*n* = 2510) expanding the six core traits to a set of 14 leaf and root traits (as shown in Fig. S6).

Table S10 Results of the PCA based on the correlation matrix using complete pairwise data of all species (n = 2510) for all traits (as shown in Fig. S7).

Table S11 Results of the PCA based on the correlation matrix using complete pairwise data for species corresponding to the full data set (n = 804) for all traits (as shown in Fig. S8a).

Table S12 Results of the PCA based on the correlation matrix using complete pairwise data for all species (n = 2510) for only the six core traits (as shown in Fig. S8b).

Table S13 Results of the phylogenetically informed PCA of traits measured on the individual plant level (n = 455) for the six core traits (as shown in Fig. 5).

Table S14 Results of the non-phylogenetically informed PCA of traits measured on the individual plant level (n = 455) for the six core traits (as shown in Fig. S9).

Table S15 Results of the permutational multivariate analysis of traits measured on the individual plant level (n = 455) for the six core traits including variation between different mycorrhizal types (as shown in Fig. 5).

Methods S1 Detailed description of all methods for sections III, IV and V.

Methods S2 PRISMA flowchart of qualitative literature review.

Supporting information Figures:

Figure S1: Results of the full quantitative literature review of 98 papers with 550 reported root-leaf-stem trait relationships presented as pie charts where LN is leaf nitrogen concentration; LP is leaf phosphorus concentration; LTD is leaf tissue density or leaf dry matter content; Lth is leaf thickness; LMA is leaf mass per area; Lresp is leaf respiration; Llife is leaf lifespan; Amass is mass based leaf photosynthetic capacity; Height is maximum vegetative plant height; RN is root nitrogen concentration; RP is root phosphorus concentration; RTD is root tissue density or root dry matter content; RD is average root diameter; SRL is specific root length; Rresp is root respiration; Rlife is root lifespan; %M is arbuscular mycorrhizal colonisation intensity; Rdep is maximum rooting depth. * We use 1/LMA (equal to SLA) as this is most often reported in literature and expected to be positively correlated to SRL.

Pie content: grey (blue, green) = percentage of overall studies with non-significant (significantly negative, significantly positive) relationship, respectively. Green box color highlights the diagonal root-shoot-stem trait pairs which are assumed to be functional analogues and thus positively correlated. The outer ring color of the pie indicates the direction of hypothesized relationships based on our new framework of plant form and function (see Fig. 1); grey if no significant correlation was expected, blue for negative and green for positive expected correlations between trait pairs. Where the color of the outer ring matches the main color of the pie content our new framework is supported by a majority of studies in the literature. The size of the circle relates to the overall number of studies reporting a correlation between the trait pair: smallest size = no studies available, second size = 1-5 studies, third size = 6 - 10 studies, largest size = > 10 studies.

The full results corroborate our findings including only studies with more than 15 species in Fig. 1. It also visualized the strong focus on a select number of traits. Of the 90 possible root-shoot-stem trait pair correlations on the 19 selected traits, 34% (31 trait pairs) had no reported entry, 37% (33 trait pairs) had between one and five data points, 13% (12 trait pairs) had 6-10 studies, and 16% (14 trait pairs) had more than 10 studies reporting the respective pairwise correlation. Thus, only 29% (26 trait pairs) of the selected trait pairs provide a reliable breadth of studies and these are strongly biased towards 11 easily-accessible traits, notably chemistry and morphology. In addition, the 550 reported root-shoot-stem trait pair relationships comprise 317 (58%) non-significant, 158 (29%) significantly positive and 75 (14%) significantly negative correlations. Of the 59 root-shoot trait pairs where correlations have been reported, 36% (21 trait pairs) reported significant root-shoot pair correlations for at least half of the overall studies, while 41% (24 trait pairs) reported significant pairwise correlations for less than half of the studies, and 24% (14 trait pairs) reported no significant pairwise correlations. Thus, the majority of reported trait pairs (65%) is not consistently and significantly correlated.

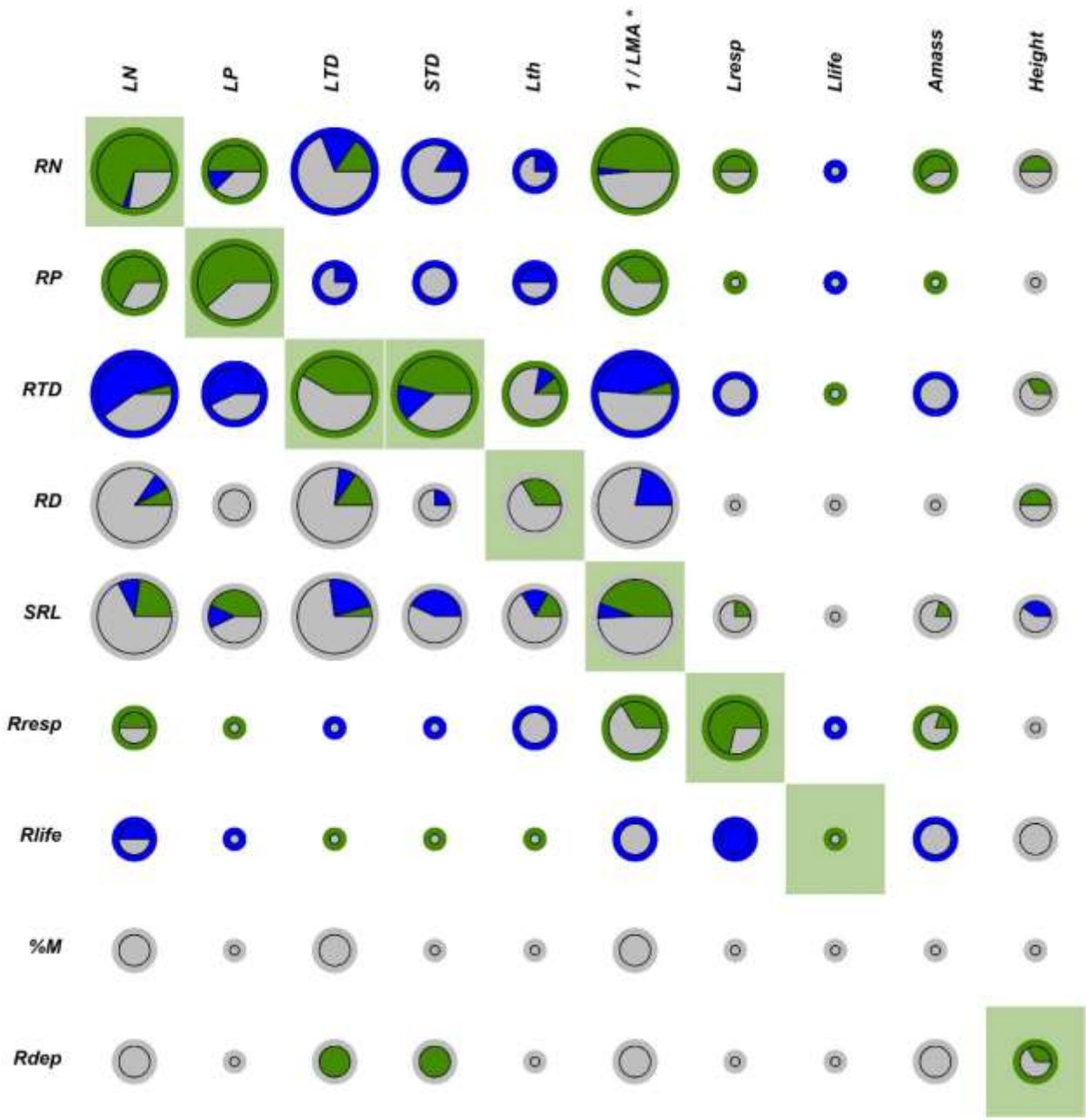

LN
LP
LTD
STD
Lth
1 / LMA *
Lresp
Llife
Amass
Height
RN
RP
RTD
RD
SRL
Rresp
Rlife
%M
Rdep

Figure S2: Pairwise correlation of all traits used in the analysis based on the full dataset (2510 species), where LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length. Scatterplots represent species mean trait correlations after correction for study design and publication identity. Regression lines represent significant correlations (blue) and significant phylogenetically-corrected bivariate relationships calculated by fitting Phylogenetic Generalized Least Square models (black). Correlation coefficients are presented for the data without (blue) and with (black) phylogenetic correction. We only included species in our analyses (n) if we were able to match at least one leaf trait measurement with at least one root trait measurement.

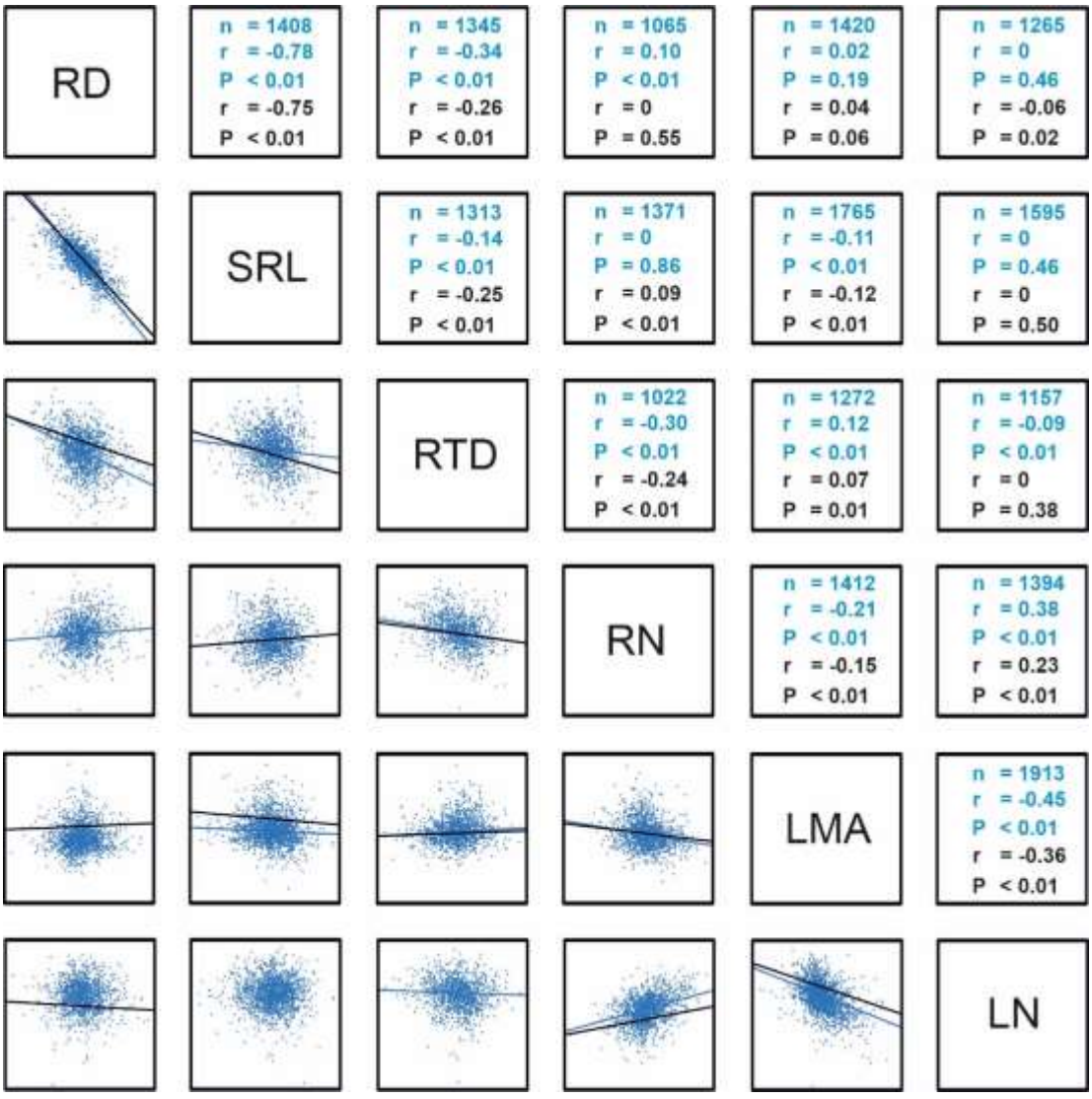


Figure S3: Non- phylogenetically informed principal component analysis of species mean traits (corresponding to phylogenetically informed **Fig. 3b,** data in **Table S5**), where LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length.

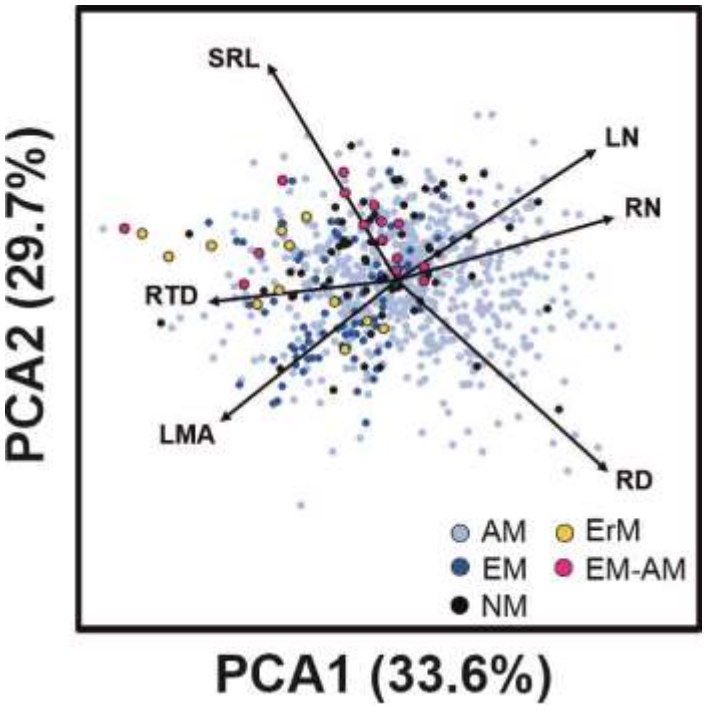


Figure S4: Phylogenetically-informed principal component analyses of the core species set of Fig. 3 (total 804 species) separated for (a) non-woody plant species (n = 324) and (b) woody plant species (n = 480) (corresponding data in **Table S6**), where LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length.

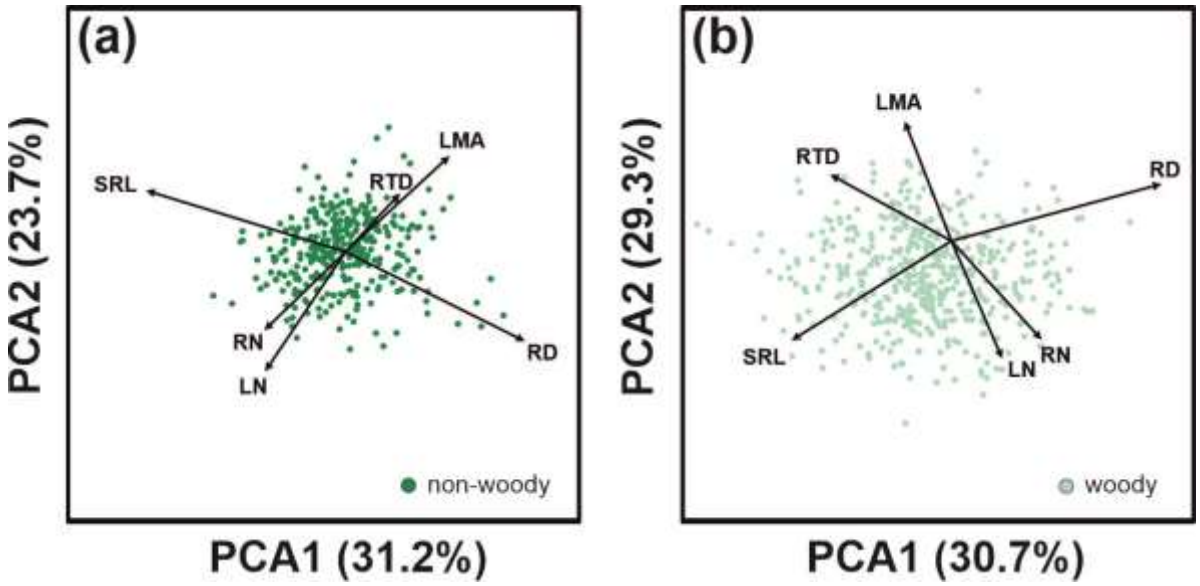


Figure S5 (provided as separate file): Animated three-dimensional representation of principal component analysis based on a correlation matrix of species mean values of root and leaf traits (species n = 2510) representing the six core traits together with overall plant size as in **Fig. 4** (corresponding data in **Table S8**). LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length; Height is maximum vegetative plant height; Rdep is maximum rooting depth.

Figure S6: Principal component analysis based on a correlation matrix of species mean values of root and leaf traits (species n = 2510) expanding the six core traits (see Fig. 3) to a set of 14 leaf and root traits (corresponding data in **Table S9)** where LMA is leaf mass per area; LN is leaf nitrogen concentration; LP is leaf phosphorus concentration; LL is leaf lignin concentration; Lth is leaf thickness; LTD is leaf tissue density; RN is root nitrogen concentration; RD is average root diameter; RP is root phosphorus concentration; RL is root lignin concentration; RTD is root tissue density; SRL is specific root length; %M is arbuscular mycorrhizal colonization intensity; CF is root cortex fraction, SSD is stem specific density. Six core traits are highlighted in larger font size.

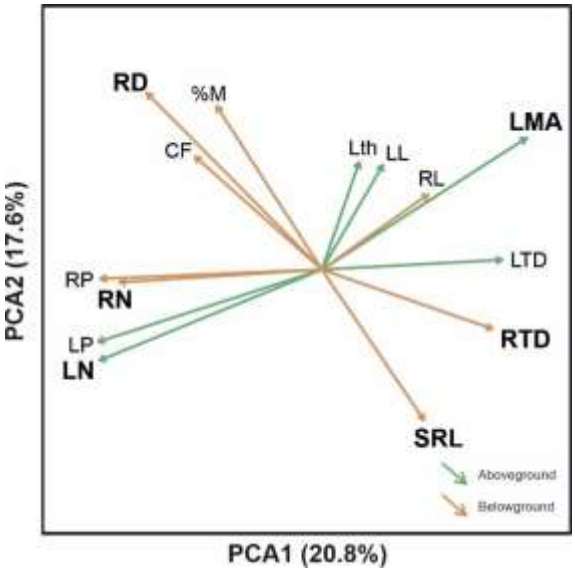


Figure S7: Principal component analysis based on a correlation matrix of species mean values of all traits (species n=2510, corresponding data in **Table S10**), where LMA is leaf mass per area; LN is leaf nitrogen concentration; LP is leaf phosphorus concentration; LL is leaf lignin concentration; Lth is leaf thickness; LTD is leaf tissue density; RN is root nitrogen concentration; RD is average root diameter; RP is root phosphorus concentration; RL is root lignin concentration; RTD is root tissue density; SRL is specific root length; %M is arbuscular mycorrhizal colonization intensity; CF is root cortex fraction; SSD is stem specific density; Height is maximum vegetative plant height; Rdep is maximum rooting depth. Core traits are highlighted in larger font size.

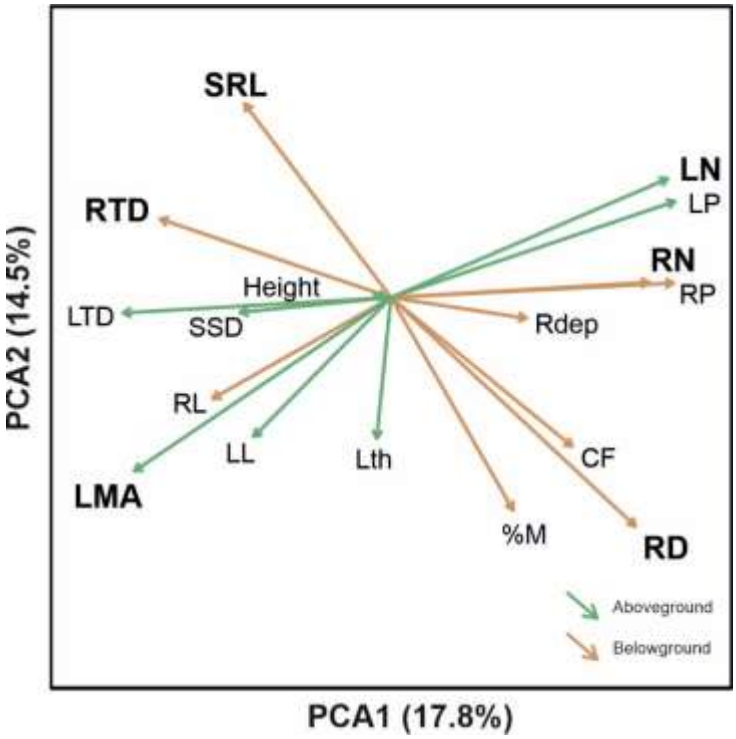


Figure S8: Sensitivity analysis for data shown in Fig. 3 to test if (a) using more traits but the exact same species set as in Fig. 3 or (b) using all species but the same number of traits as in Fig. 3 would change the outcome of or our main analysis (corresponding data in **Tables S11** and **S12)**, where LMA is leaf mass per area; LN is leaf nitrogen concentration; LP is leaf phosphorus concentration; LL is leaf lignin concentration; Lth is leaf thickness; LTD is leaf tissue density; RN is root nitrogen concentration; RD is average root diameter; RP is root phosphorus concentration; RL is root lignin concentration; RTD is root tissue density; SRL is specific root length; %M is arbuscular mycorrhizal colonization intensity; CF is root cortex fraction; SSD is stem specific density; Height is maximum vegetative plant height; Rdep is maximum rooting depth. Core traits are highlighted in larger font size. Principal component analysis was based on a correlation matrix of species mean values of root and leaf traits. Left: Trait selection as in Fig. S7 but only using the 804 species for which we also have full data coverage as in Fig. 3. The six core traits used in the main PCA are highlighted here in larger font size. Right: All species data (n = 2510) but only for the six core traits as in Fig. 3.

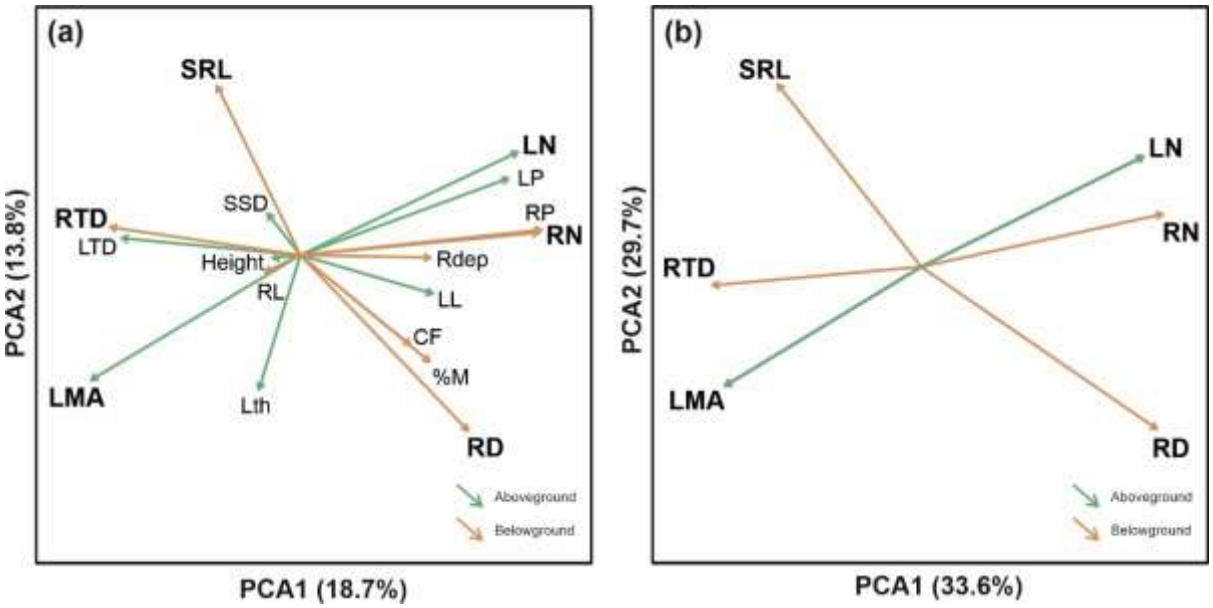
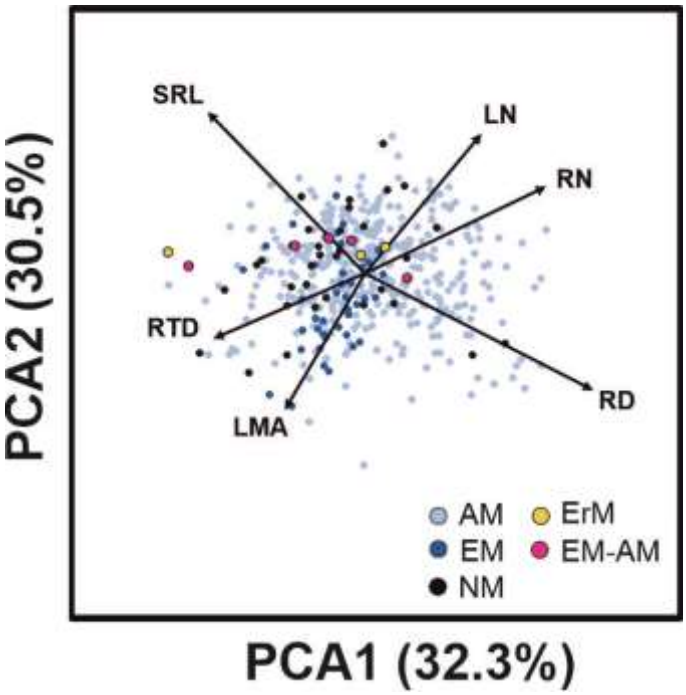


Figure S9: Non-phylogenetically informed principal component analysis of traits measured on the same individuals (Corresponding to phylogenetically informed **Fig. 5**, data in **Table S14**), where LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length.



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Supporting information Tables:

Table S1 List of 140 papers used for qualitative literature review together with an overview over the extracted information. **Provided as separate file.**

Table S2 List of additional publications and unpublished data sources for the main database and the individual based root and leaf trait data. **Provided as separate file.**

Table S3: Above- and belowground traits included in the full database where 'Obs.' is observation; 'Myc.' is mycorrhizal.

Traits	Units	Species no.	Obs no.	mean	1st Qu.	Median	3rd Qu.
Leaf mass per area	mg mm^{-2}	3989	119059	0.06	0.039	0.059	0.087
Leaf tissue density	g cm^{-3}	1652	12411	0.33	0.249	0.340	0.446
Leaf thickness	mm	1590	13037	0.24	0.159	0.212	0.295
Leaf nitrogen	mg g^{-1}	3259	37723	19.24	14.200	19.900	26.214
Leaf phosphorus	mg g^{-1}	2159	15797	1.38	0.970	1.400	2.070
Leaf lignin	mg g^{-1}	56	56	111.04	64.835	99.700	138.828
Maximum Height	m	4031	64321	0.707	0.200	0.503	1.980
Stem specific density	kg m^{-3}	1284	7397	0.502	0.360	0.508	0.646
Root tissue density	g cm^{-3}	1633	9996	0.18	0.117	0.195	0.330
Root nitrogen	mg g^{-1}	2004	10759	10.83	7.670	10.730	15.784
Root phosphorus	mg g^{-1}	810	3194	1.03	0.679	1.030	1.571
Root lignin	mg g^{-1}	287	722	168.69	120.000	160.000	210.000
Root diameter	mm	1773	10121	0.38	0.240	0.374	0.568
Specific root length	m g^{-1}	2242	11901	38.35	15.342	40.971	106.000
Myc. colonization	%	1955	5543	53.80	30.000	56.000	80.000
Cortex fraction	ratio	306	844	0.82	0.750	0.902	0.952
Maximum rooting depth	m	933	1793	1.21	0.700	1.280	2.200

Table S4: Analysis of the core species set with full information for the four root core traits and the two leaf core traits based on species mean trait data (n = 804) where LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length. Data are from the phylogenetically-informed principal component analyses of the global species set as shown in **Fig. 3**. Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Eigenvalue	1.804	1.648	1.107	0.792	0.553	0.096
Variance	0.301	0.275	0.184	0.132	0.092	0.016
LMA	0.420	0.568	-0.378	0.361	0.477	0.008
LN	-0.376	-0.597	0.474	0.001	0.527	-0.004
RN	-0.282	-0.559	-0.224	0.726	-0.174	0.007
RD	0.797	-0.548	-0.124	-0.074	0.013	-0.206
RTD	0.105	0.530	0.748	0.349	-0.117	-0.116
SRL	-0.872	0.274	-0.337	-0.087	0.057	-0.199

Table S5: Results of the non-phylogenetically informed principal component analyses of the core species set (n = 804) for the six core traits based on species mean trait data as shown in **Fig. S3.** LMA, leaf mass per area; LN, leaf nitrogen concentration; RN, root nitrogen concentration; RD, average root diameter; RTD, root tissue density; SRL, specific root length. Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Eigenvalue	2.014	1.784	0.988	0.700	0.439	0.075
Variance	0.336	0.297	0.165	0.117	0.073	0.013
LMA	0.380	-0.399	-0.313	-0.501	0.589	0.021
LN	-0.431	0.369	0.394	-0.018	0.723	-0.013
RN	-0.469	0.177	-0.126	-0.794	-0.321	0.016
RD	-0.457	-0.544	-0.063	0.132	0.031	-0.688
RTD	0.405	-0.062	0.761	-0.318	-0.157	-0.357
SRL	0.278	0.611	-0.384	-0.001	0.052	-0.631

Table S6: Results of the phylogenetically-informed PCA on the core species set (n = 804) for the six core traits based on species mean trait data of woody and non-woody species (as shown in **Fig. S4**). LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length. Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

		PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Woody	Eigenvalue	1.845	1.760	1.066	0.687	0.552	0.090
species	Variance	0.308	0.293	0.178	0.114	0.092	0.015
n = 480	LMA	0.201	0.672	-0.444	-0.275	-0.485	0.008
	LN	-0.219	-0.660	0.488	-0.043	-0.526	0.001
	RN	-0.389	-0.555	-0.320	-0.643	0.156	0.007
	RD	-0.920	0.325	-0.010	0.076	-0.025	-0.206
	RTD	0.524	0.374	0.622	-0.418	0.113	-0.109
	SRL	0.696	-0.565	-0.378	0.122	-0.056	-0.188
Non-woody	Eigenvalue	1.872	1.422	1.132	0.910	0.565	0.099
species	Variance	0.312	0.237	0.189	0.152	0.094	0.017
n = 324	LMA	0.450	0.540	0.178	-0.521	0.451	0.009
	LN	-0.348	-0.674	-0.392	0.023	0.520	-0.011
	RN	-0.348	-0.438	0.039	-0.786	-0.259	0.010
	RD	0.783	-0.509	0.292	0.013	-0.019	-0.202
	RTD	0.229	0.320	-0.890	-0.141	-0.134	-0.120
	SRL	-0.872	0.349	0.261	0.010	0.076	-0.208

Table S7: Permutational multivariate analysis on the core species set of 804 species displaying variation between plant growth form, mycorrhizal types and nitrogen fixing capacity for species mean trait data as shown in **Fig. 3**. AM is arbuscular mycorrhizal (*n* = 630); EM is ectomycorrhizal (*n* = 84); NM is non mycorrhizal (*n* = 63); ErM is ericoid mycorrhizal (*n* = 12); EM+AM is ecto- and arbuscular mycorrhizal (*n* = 15); N, nitrogen.

pairs	**Sums of squares**	***F***	***R²***	***P***
woody vs. non-woody	15123.04	17.61	0.0215	0.001
AM vs. ErM	14794.15	17.48	0.0266	0.001
AM vs. EM	28283.14	34.49	0.0462	0.001
AM vs. NM	5067.84	5.97	0.0086	0.002
AM vs. EM+AM	8440.93	9.98	0.0153	0.001
ErM vs. EM	3847.87	6.47	0.0644	0.004
ErM vs. NM	8803.28	10.99	0.1309	0.001
ErM vs. EM+AM	3454.45	5.51	0.1806	0.008
EM vs. NM	12041.31	17.36	0.1069	0.001
EM vs. EM+AM	6728.17	11.29	0.1043	0.001
NM vs. EM+AM	2606.98	3.28	0.0414	0.036
Non-N-fixing vs. N-fixing	39405.10	47.57	0.0560	0.001

Table S8: Results of the principal component analysis based on the correlation matrix of all species (n = 2510) for the six core traits and plant height and rooting depth as shown in **Fig. 4.** LMA is leaf mass per area; LN is leaf nitrogen concentration; Height is maximum vegetative plant height; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length; Rdep is maximum rooting depth. Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**
Eigenvalues	1.943	1.799	1.154	1.042	0.806	0.699	0.476	0.080
Variance	0.243	0.225	0.144	0.130	0.101	0.087	0.059	0.010
LMA	0.269	0.413	0.396		0.213	0.558	0.487	
LN	-0.374	-0.382	-0.388	-0.177	0.156		0.704	
Height			0.141	-0.872	-0.441	0.119		
RN	-0.454	-0.276			0.162	0.694	-0.450	
RD	-0.482	0.505		0.150	-0.149	-0.104		0.673
RTD	0.402	0.112	-0.496	-0.321	0.531		-0.249	0.354
SRL	0.330	-0.574	0.336		-0.171			0.641
Rdep	-0.278		0.551	-0.269	0.613	-0.411		

Table S9: Results of the principal component analysis based on the correlation matrix using complete pairwise data of all species (n = 2510) expanding the six core traits to a set of 14 leaf and root traits as shown in **Fig. S6.** LMA is leaf mass per area; LN is leaf nitrogen concentration; LP is leaf phosphorus concentration; LL, leaf lignin concentration; Lth, leaf thickness; LTD, leaf tissue density; RN is root nitrogen concentration; RD is average root diameter; RP is root phosphorus concentration; RTD is root tissue density; SRL is specific root length; %M is arbuscular mycorrhizal colonization intensity; RL is root lignin concentration; CF is root cortex fraction. Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

	PCA1	**PCA2**	**PCA3**	**PCA4**	**PCA5**	**PCA6**	**PCA7**	**PCA8**	**PCA9**
Eigenvalue	2.911	2.461	1.884	1.442	1.112	0.902	0.749	0.648	0.640
Variance	0.208	0.176	0.135	0.103	0.079	0.064	0.054	0.046	0.046
LMA	0.333	0.333		0.274	0.151		0.244	0.456	0.120
LN	-0.362	-0.230	-0.109		0.113	-0.216	0.610		-0.155
LP	-0.364	-0.183		-0.101	0.112	-0.426		0.517	0.334
LL		0.265	-0.550	0.122		-0.154	0.239	-0.166	0.136
Lth		0.271	0.264	0.583		-0.285	0.159	0.107	
LTD	0.293		-0.278	-0.394		0.420	0.262	0.392	
RN	-0.329		-0.236	0.299	0.220	0.424	0.261	-0.154	-0.300
RD	-0.285	0.447	0.215	-0.164		0.208			
RP	-0.360		-0.178	0.226	0.363	0.212	-0.445	0.282	
RTD	0.278	-0.150	0.157	-0.248	0.590	-0.293			-0.212
SRL	0.166	-0.381	-0.339	0.298	-0.365		-0.161		
%M	-0.171	0.414	-0.212	-0.158		-0.179		-0.357	0.466
RL	0.173	0.190	-0.457		0.239	-0.253	-0.340		-0.450
CF	-0.206	0.286		-0.237	-0.473	-0.187		0.288	-0.505

Table S10: Results of the PCA based on the correlation matrix using complete pairwise data of all species (n = 2510) for all traits including plant size (as shown **in Fig. S7**). LMA is leaf mass per area; LN is leaf nitrogen concentration; LP is leaf phosphorus concentration; LL is leaf lignin concentration; Lth is leaf thickness; LTD is leaf tissue density; RN is root nitrogen concentration; RD is average root diameter; RP is root phosphorus concentration; RL is root lignin concentration; RTD is root tissue density; SRL is specific root length; %M is arbuscular mycorrhizal colonization intensity; CF is root cortex fraction, SSD is stem specific density; Height is maximum vegetative plant height; Rdep is maximum rooting depth.

	PCA1	**PCA2**	**PCA3**	**PCA4**	**PCA5**	**PCA6**	**PCA7**	**PCA8**	**PCA9**
Eigenvalues	3.022	2.464	2.093	1.489	1.242	1.137	1.006	0.871	0.793
Variance	0.178	0.145	0.123	0.088	0.073	0.067	0.059	0.051	0.047
LMA	0.303	0.335	0.132	0.261	0.118	0.155			
LN	-0.327	-0.230	-0.198			0.132	-0.306	0.199	-0.214
LP	-0.336	-0.186	-0.164	-0.123	0.104			0.457	
LL	0.162	0.269	-0.506	0.170				0.118	-0.254
Lth		0.272	0.290	0.505	0.173		-0.231	0.269	-0.109
LTD	0.317		-0.217	-0.300	-0.219	0.213	0.183	-0.302	
RN	-0.305		-0.248	0.294		0.323		-0.392	
RD	-0.289	0.442	0.122	-0.227				-0.214	
RP	-0.334		-0.201	0.162	0.378	0.157	0.211	-0.173	0.351
RL	0.211	0.195	-0.382			0.116		0.300	0.479
RTD	0.273	-0.152	0.140	-0.316	0.343	0.156	-0.300	0.208	0.390
SRL	0.173	-0.375	-0.220	0.410	-0.196	-0.200	0.265	0.105	
%M	-0.144	0.411	-0.224	-0.149		-0.129	0.113	0.144	
CF	-0.214	0.288		-0.122	-0.454	-0.267		0.222	0.221
SSD	0.178		-0.343		-0.165	0.183	-0.598	-0.102	-0.213
Height				-0.116		0.681	0.438	0.340	-0.344
Rdep	-0.160		0.148	0.226	-0.576	0.333	-0.200		0.361

Table S11: Results of the PCA based on the correlation matrix using complete pairwise data for species corresponding to the full data set (*n* = 804) for all traits (as shown in **Fig. S8a**). LMA is leaf mass per area; LN is leaf nitrogen concentration; LP is leaf phosphorus concentration; LL is leaf lignin concentration; Lth is leaf thickness; LTD is leaf tissue density; RN is root nitrogen concentration; RD is average root diameter; RP is root phosphorus concentration; RL is root lignin concentration; RTD is root tissue density; SRL is specific root length; %M is arbuscular mycorrhizal colonization intensity; CF is root cortex fraction, SSD is stem specific density; Height is maximum vegetative plant height; Rdep is maximum rooting depth.

	PCA1	**PCA2**	**PCA3**	**PCA4**	**PCA5**	**PCA6**	**PCA7**	**PCA8**	**PCA9**
Eigenvalues	3.233	2.396	2.215	1.641	1.350	1.124	1.014	0.951	0.740
Variance	0.187	0.138	0.128	0.095	0.078	0.065	0.059	0.055	0.043
LMA	0.323	0.340	0.195	0.104	0.200		0.105	0.131	0.227
LN	-0.335	-0.281	-0.117				-0.162	0.160	
LP	-0.321	-0.209	-0.189		0.201	0.168	-0.176	-0.150	-0.119
LL	-0.204	0.105	0.597	-0.161			-0.147	-0.140	
Lth		0.366	0.173	0.424	0.187	0.207		0.223	-0.242
LTD	0.275			-0.452		-0.261	0.144	0.120	0.494
RN	-0.368		0.138		0.239	-0.113	0.171	0.352	0.340
RD	-0.259	0.478	-0.182			-0.196			
RP	-0.372			0.127	0.440			0.132	0.108
RL			0.243	-0.336	0.537	0.286		-0.221	
RTD	0.293				0.349		-0.644		
SRL	0.128	-0.461	0.255			0.294	0.388		
%M	-0.199	0.290		-0.467			-0.130	-0.136	
CF	-0.169	0.245	-0.194	-0.276	-0.141	0.406	0.279		-0.157
SSD		-0.113	0.262	-0.330	-0.115	-0.114		0.647	-0.508
Height					0.298	-0.628	0.409	-0.304	-0.443
Rdep	-0.201		0.482	0.177	-0.305	-0.231	-0.130	-0.328	0.102

Table S12: Results of the PCA based on the correlation matrix using complete pairwise data for all species (n = 2510) for only the six core traits (as shown in **Fig. S8b**). LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length. Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Eigenvalues	2.014	1.784	0.988	0.700	0.439	0.075
Variance	0.336	0.297	0.165	0.117	0.073	0.013
LMA	0.380	0.399	0.313	0.501	0.589	
LN	-0.431	-0.369	-0.394		0.723	
RN	-0.469	-0.177	0.126	0.794	-0.321	
RD	-0.457	0.544		-0.132		-0.688
RTD	0.405		-0.761	0.318	-0.157	-0.357
SRL	0.278	-0.611	0.384			-0.631

Table S13: Analysis of traits measured on the individual plant level with full information for the four root core traits and the two leaf core traits based on species mean trait data (n = 455) where LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length. Data are the phylogenetically-informed principal component analyses of the individual plants data set as shown in **Fig. 5.** Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Eigenvalue	1.952	1.623	1.005	0.791	0.565	0.064
Variance	0.325	0.271	0.167	0.132	0.094	0.011
LMA	0.518	-0.378	0.361	0.574	0.359	0.004
LN	-0.553	0.393	-0.506	0.127	0.517	0.001
RN	-0.396	0.572	0.043	0.621	-0.360	0.004
SRL	-0.833	-0.405	0.335	-0.009	0.037	-0.166
RTD	0.310	-0.557	-0.706	0.226	-0.184	-0.094
RD	0.655	0.724	0.073	-0.090	0.070	-0.167

Table S14: Results of the non-phylogenetically informed PCA of traits measured on the *individual trait pairs* (*n* = 455) with full information for the six core traits (as shown in **Fig. S9**). LMA is leaf mass per area; LN is leaf nitrogen concentration; RN is root nitrogen concentration; RD is average root diameter; RTD is root tissue density; SRL is specific root length. Displayed data are the eigenvalue as well as the proportion of variance explained by each principal component (PC) and the loadings of the root and leaf traits.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Eigenvalue	1.936	1.830	0.953	0.748	0.477	0.055
Variance	0.323	0.305	0.159	0.125	0.080	0.009
LMA	-0.203	-0.453	-0.262	-0.749	-0.351	-0.010
LN	0.297	0.465	0.437	-0.195	-0.683	-0.004
RN	0.463	0.291	0.037	-0.591	0.592	-0.014
SRL	-0.403	0.541	-0.355	-0.097	-0.010	0.640
RTD	-0.386	-0.217	0.780	-0.146	0.223	0.354
RD	0.587	-0.393	-0.072	0.143	-0.103	0.682

Table S15: Permutational multivariate analysis of individual plants on 455 species displaying variation between plant growth form, mycorrhizal types and nitrogen-fixing capacity as shown in **Fig. 5**. AM is arbuscular mycorrhizal (*n* = 372); EM is ectomycorrhizal (*n* = 42); NM is non mycorrhizal (*n* = 33); ErM is ericoid mycorrhizal (*n* = 5); EM+AM is ecto- and arbuscular mycorrhizal (*n* = 5); N, nitrogen.

pairs	**Sums of squares**	***F***	***R²***	***P***
woody vs. non-woody	2340.06	2.48	0.005	0.071
AM vs. NM	4856.18	5.12	0.013	0.008
AM vs. ErM	1758.84	1.87	0.005	0.139
AM vs. EM	11264.67	12.56	0.030	0.001
AM vs. EM+AM	2110.58	2.26	0.006	0.106
NM vs. ErM	414.62	0.37	0.011	0.676
NM vs. EM	3085.24	4.00	0.052	0.028
NM vs. EM+AM	329.21	0.31	0.009	0.748
ErM vs. EM	1343.97	2.31	0.051	0.106
ErM vs. EM+AM	24.81	0.02	0.004	0.974
EM vs. EM+AM	1655.28	3.00	0.063	0.071
Non-N-fixing vs. N-fixing	17692.00	19.47	0.041	0.001

Methods S1:

Here we provide a detailed description of methods for the literature review (section IV, including the PRISMA flowchart) and for the global analysis of above-belowground trait correlations (see sections V and VI).

Full methods on literature review (section IV main text)

To review the current status of literature on above-belowground functional trait linkages we searched the Web of Science (accessed on June 19th 2020) using the following string of keywords: TOPIC: (root trait OR root traits OR root economics OR root functional trait OR root functional traits OR root economics spectrum OR root and leaf traits) AND TOPIC: (leaf trait OR leaf traits OR leaf economics OR leaf economics spectrum OR plant economics spectrum OR plant economic spectrum OR plant and root trait). We screened 189 papers of which 98 could be included in the qualitative synthesis (see Methods S2 for PRISMA flowchart after Moher *et al*. (2009) and Table S1 for a full list of papers and extracted data).

We checked these 98 papers for trait correlations between organs (leaf, stem, root). We report the tendency of the correlations (positive, negative) and the significance ($P < 0.05$) as well as the number of tested species together with some information on plant types or ecosystems. We used phylogenetically-corrected results where these were provided. We indicated if correlations were calculated based on species-based comparisons or with community-level trait information (Table S1). Where appropriate data but no correlation analysis was provided, we calculated Pearson's r (indicated in comments in Table S1). We standardized and sometimes categorized trait names, e.g. we subsumed stem specific density (SSD), stem dry matter content (SDMC) and stem tissue density (STD) in a trait group "STD/SDMC" or leaf longevity and leaf lifespan as "leaf longevity". This approach was aimed at maximizing the inclusion of individual studies and at providing a larger number of observations for above- belowground trait comparisons (see Table S1 for original and new trait names). We selected core shoot and root traits according to the functional pairs described in the main paper and traits with key relevance representing *chemistry* (leaf nitrogen concentration, leaf phosphorus concentration, root nitrogen concentration, root phosphorus concentration), *morphology* (leaf tissue density, stem tissue density, leaf thickness, specific leaf area, root tissue density, root diameter, specific root length), *physiology* (photosynthetic capacity,

leaf and root respiration), *lifespan* (leaf and root lifespan) and *size* (maximum plant height, maximum rooting depth). For root traits, we additionally tested mycorrhization which subsumed information on arbuscular mycorrhizal colonisation rates, hyphal length, extraradical mycelium or presence of arbuscules and/or vesicles, also in an attempt to maximize study inclusion and observation numbers.

In summarizing our results, we counted: (1) the total number of studies reporting a correlation for the respective pair irrespective of significance of the relationship, (2) the number of studies showing a significantly positive relationship, (3) the number of studies showing a significantly negative relationship. We report the results for all 90 bivariate trait pairs as an overview of the available information (Fig. S1). For a more detailed review, however, we focused on the set of six above- and belowground traits which we expected to be functional analogues as detailed in the main paper (RN-LN, RP-LP, RTD-LTD, RD-LTh, SRL-SLA, maximum rooting depth -maximum plant height). The majority of these traits were also more easily accessible thus providing a more reliable breadth of studies. In addition to the selection of traits, we based the detailed review on a more conservative selection of studies including only those studies reporting trait relationships for a minimum of 15 species and excluding studies reporting trait relationships based on community weighted mean traits, e.g. trait means weighted by species abundances in a sampled plant community in the field. The 15-species cutoff is arbitrary but the overall outcome did not significantly change for cutoffs between 3 species (Fig. S1) or 20 species (*data not shown*).

Full methods for the global analysis linking above- and belowground traits (sections V and VI main text)

Main database: We took a three-step approach to link above and belowground traits in our multivariate analysis of the global trait data set. *First*, we focused on the traits defining the three known gradients of trait variation above- and belowground with two traits per gradient: the leaf conservation gradient (LMA, LN), the root conservation gradient (RTD, RN) and the root collaboration gradient (D, SRL, see Table 1). *In a second step*, we additionally represented the plant size gradient using maximum plant vegetative height and maximum rooting depth. *In a third step*, we broadened our perspective and included additional leaf traits (phosphorus concentration, lignin concentration, thickness, leaf tissue density) and root traits (phosphorus concentration,

lignin concentration, arbuscular mycorrhizal colonisation intensity, cortex fraction) to see if these traits aligned along the conservation or collaboration gradient.

Our analyses were based on two types of data sets. (1) We used species specific mean trait values based on global databases. Here we used mean trait data of fine-roots mobilized from the Global Root Trait database (GRooT) (Guerrero-Ramirez et al. 2020), which is a species-specific subset of the Fine-Root Ecology Database version 2.0 (FRED; Iversen *et al.*, 2017), combined with aboveground traits accessed from the Plant Trait Database (TRY; Kattge *et al.*, 2020). These data were further augmented with a limited number of additional contributors (see Table S2). We limited data from GRooT to living fine roots (excluding coarse roots and dead fine roots) of spermatophytes. (2) We used species-specific individual trait data where root and shoot traits were measured on the same plant individual or plot. This data set allowed us to verify and compare results from global trait means to those measured on individual plants where above-belowground correlations should be maximized. It is important to note, however, that we did not include intraspecific trait variation in our analysis (i.e., we selected representative individuals, see more on selection process below). This second data set was extracted from an additional set of 43 studies including both published and unpublished data (see Table S2). The final calculation of species-specific mean traits included data from the individual data set. Our full data set of species-specific mean traits included 2510 species with data on at least one measured trait aboveground and one measured trait belowground. Table S3 provides an overview over this final mean trait data set.

We focused our first step on the four root traits (RN, RTD, SRL, and RD) defined by the root economic space (RES, Bergmann *et al*., 2000) and on two leaf traits (LMA and LN) defining the leaf economic spectrum *sensu* Diaz *et al*. (2016). We performed this first analysis using only species where data on all six traits were available (i.e. full matrix without gaps). All trait data was checked for outliers, and we excluded all values of RTD exceeding 1.0 in further analyses. We performed this analysis for both the species mean trait data set (804 species) and the individual data set (455 species). To test for relationships among the six core traits in the full data set, we calculated bivariate trait relationships for all trait pairs.

In a second step, we included maximum plant height (H) and maximum rooting depth (Rdep) to represent plant stature. Plant height was taken from TRY while we used a recently-compiled data

set for rooting depth which included observations of rooting depth measured only under field conditions (Fan *et al*., 2017). We performed this analysis on the full data set of species with mean trait data for at least one aboveground trait and one belowground trait (2510 species).

In a third step, we broadened our trait spectrum to include additional leaf traits characterizing species on the "fast" (leaf phosphorus concentration (LP)) and "slow" (leaf lignin concentration (LL), leaf thickness (Lth)) side of the leaf conservation gradient as well as root traits characterizing species which align with the "fast" (root phosphorus concentration (RP)) and "slow" (root lignin concentration (RL)) end of the conservation gradient. Further, we added traits characterizing "outsourcing" species on the root collaboration gradient (arbuscular mycorrhizal colonization intensity (%M) and root cortex fraction (CF)). Categorical data from GRooT (via FRED and TRY) such as plant woodiness (woody, non-woody), mycorrhizal association (non-mycorrhizal, arbuscular mycorrhiza, ectomycorrhiza or other, e.g. ericoid mycorrhiza) and the ability of nitrogen fixation (fixers or non-fixers) were used in downstream analyses to test our conceptual framework. When no information on either mycorrhizal association or nitrogen fixation ability was available in GRooT, we used the FungalRoot Database (Soudzilovskaia *et al*., 2020) or nodDB Database (Tedersoo *et al*., 2018) respectively, to obtain additional information.

Data processing: All data processing and analyses were done using R 4.0.3 (R Core Team 2020). Our main goal was to analyse root vs. leaf trait relationships at the level of plant species. Our main data set for this analysis was the global data set (1) described in the previous section but we used the same string of data processing and analyses for data set (2) measured on individual plants. However, for data set (2) we did not calculate mean traits when multiple individuals per species were present as the main idea of this analysis was to maximize trait correlation within an individual plant. Instead of calculating species mean trait values over a number of plant individuals, we selected individuals and used the trait values of these plants as indicative of species traits. Individuals were selected either randomly (if there were only 2 individuals per species) or using the 'clhs' function of the 'clhs' package (if there were more than 2 individuals per species; (Roudier, 2011, Version 0.7.3) which uses a stratified random procedure and provides an efficient way of sampling variables from their multivariate distributions. Thus, when having more than 2 individuals per species, an individual was selected based on the proximity of its individual trait values to the mean species trait values.

Prior to analysis, we calculated species mean trait values for the global data set, as well as leaf mass per area (LMA) based on SLA (LMA = 1/ SLA) accessed from TRY. Data processing included log-transformation of all non-normally distributed traits except %M and CF, which were scaled from 0-1 and arcsine square root transformed. All trait records were standardized by calculating z-scores (z-score = (trait value – mean trait value) / standard deviation)). In order to correct for study design and source of publication, we calculated residuals using a linear mixed effect model for each trait (using the function 'lmer' from the package 'lme4', (Bates *et al.*, 2015, Version 1.1.23), with trait as the response variable, study design (e.g. *in situ* versus pot-grown plants) as a fixed factor and publication (as proxy for other design-related differences such as plant age, sampled fine-root pool, sample processing) as a random factor and used model residuals for further analysis. Scientific names for data in GRooT were standardized among data sets and updated using the Taxonomic Name Resolution Service version 4.0 (http://tnrs.iplantcollaborative.org/). Scientific names from TRY and individual studies were collapsed at the species-level and standardized using The Plant List (The Plant List, 2013). To increase the number of matches between species sets from TRY and GRooT we used the Leipzig Catalogue of Vascular Plants (LCVP, Freiberg *et al.*, 2020). This enabled us to identify more possible synonyms from both source lists as the LCVP provides a more updated synonym list compared to tools of taxonomic name resolution. Using the backbone phylogeny from Zanne *et al*. (2014) we constructed a phylogenetic tree including all species using the function 'phylomatic' from the package 'branching' (Chamberlain, 2020, Version 0.6.0). Due to an error with the function 'phylomatic' we needed to request phylogenetic information on family names from NCBI (NCBI Resource Coordinators *et al.*, 2018) using the function 'phylomatic_names' from the package ''rentrez' (Winter, 2017, Version 1.2.2) for all species before constructing the phylogenetic tree. Missing species were manually added using the function 'add.tips' from the package 'phangorn' (Schliep, 2011, Version 2.5.5). For the phylogenetic correction, we assigned missing species to a closely-related species from the same genus within the tree.

Statistical analysis: We used phylogenetically-informed methods for all analyses presented in the main paper and provide results for non-phylogenetically informed analysis in supporting figures (Fig. S3, S9) and supporting tables (Table S5, S14). First, we performed bivariate relationships among the six core traits (RD, SRL, RTD, RN, LMA and LN), based on the full data set (2510 species) where sample sizes ranged from 866 (for RTD vs. RN) to 1,497 (for SRL vs. LMA)

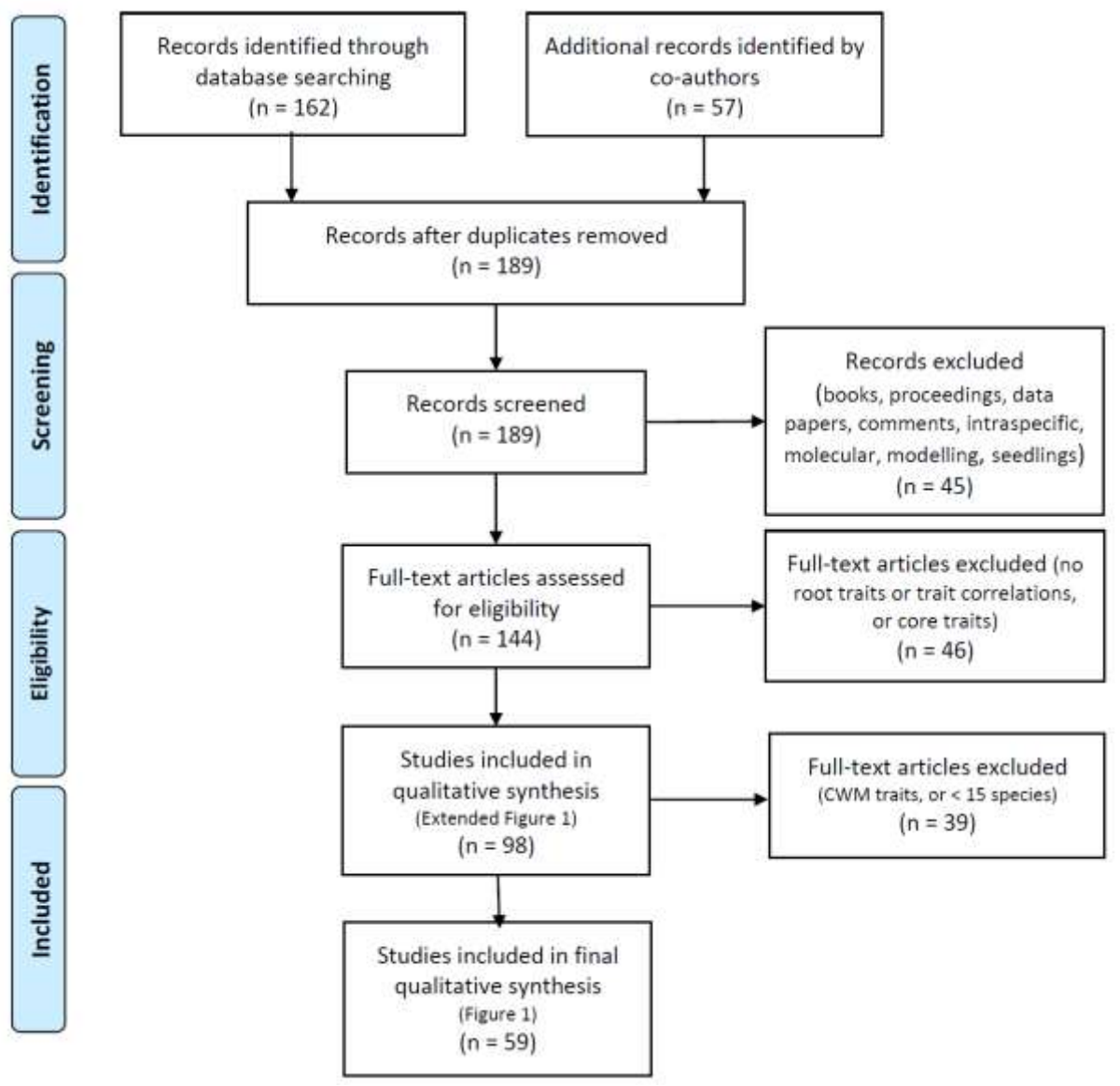
depending on the number of species with respective trait information. We fitted Phylogenetic Generalized Least Square models using the 'pgls' function in the R package 'caper' (Orme *et al.*, 2018, Version 1.0.1) to each pair of traits. We then calculated phylogenetically-corrected correlation coefficients (*r* values) by taking the square root of the adjusted model r^2, and by multiplying this with -1 if the regression coefficient was negative. In rare cases, when adjusted r^2 was below zero, we set the correlation coefficient to zero.

We performed one phylogenetically-informed Principal Component Analysis (PCA) for all six core traits (RD, SRL, RTD, RN, LMA and LN) using the 'phyl.pca' function of the 'phytools' package (Revell, 2012, Version 0.7.47). Additionally, an eigenanalysis was performed to use the correlation structure of the phylogeny to inform its estimates of eigenvalues and eigenvectors (Revell, 2009). In addition, we performed phylogenetically-informed PCAs for subsets of species with different mycorrhizal association types (arbuscular mycorrhiza, ectomycorrhiza, arbuscular mycorrhiza *and* ectomycorrhiza - i.e. intraspecific variation in mycorrhizal association type, ericoid mycorrhiza, and non-mycorrhiza), differences in woodiness (woody vs. non-woody) and differences in nitrogen-fixing ability (present or absent). To identify significant differences between these subsets of species in the global PCA, we used a Permutational Multiple Analysis of Variance (PERMANOVA), in which the first two PCA axes were treated as the response variables and mycorrhizal association type, woodiness or ability to fix nitrogen as the fixed factor. We used Euclidean pairwise distances in PCA space among species, and calculated 999 permutations, using the 'pairwise.adonis' function in the 'pairwiseAdonis' package (Arbizu, 2017, Version 0.0.1). To test for the significance of trait differences between different categories of mycorrhizal associations, we used false discovery rates (Benjamini & Hochberg, 1995) to reduce the likelihood of type I errors due to multiple testing. We performed this analysis for both the species mean trait data set (804 species) and the individual data set (455 species).

To investigate multiple trait relationships between root (RD, SRL, RTD, RN, RP, RL, CF and %M), leaf (LMA, LN, LL, LP, Lth, LTD), size traits (Max Height and Rdep), and a stem trait (SSD), we performed a PCA based on pairwise complete correlations using a regularized covariance matrix, where negative eigenvalues were set to small positive values using the 'princomp' function in the 'stats' package (R core team 2020, Version 4.0.3). We used mean trait

data of the full dataset, i.e. all 2510 species, to calculate the correlation matrix and subsequently perform a non-phylogenetically corrected PCA.

Methods S2: PRISMA flowchart of qualitative literature review after Moher et al. (2009). CWM is 'community weighted means'.



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