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Diversity begets diversity in competition for space

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Supplementary Table 1: Competitive outcomes for each isolate. Isolate names are used as unique identifiers, and refer to the collection numbers used by the USFS Forest Products Laboratory. See Supplementary data files for detailed outcomes.

Species	Isolate Name	% Wins	% Losses	% Draws
Armillaria gallica Marxm. & Romagn	FP-102531-T	0	24	76
Armillaria gallica Marxm. & Romagn	EL-8(T-2)	0	27	73
Armillaria gallica Marxm. & Romagn	FP-102534-T	0	24	76
Armillaria gallica Marxm. & Romagn	FP-102535-T	0	24	76
Armillaria gallica Marxm. & Romagn	FP-102542-T	0	16	84
Armillaria gallica Marxm. & Romagn	HHB-12551(T-1)	0	30	70
Armillaria gallica Marxm. & Romagn	OC-1(T-3)	0	27	73
Armillaria gallica Marxm. & Romagn	SH-1(T-1)	3	16	81
Armillaria sinapina Brub & Dessur.	PR-9(ST-3)	0	16	84
Armillaria tabescens (Scop.) Emel	FP-102622-T	3	19	78
Armillaria tabescens (Scop.) Emel	TJV-93-261-T	0	30	70
Fomes fomentarius (L.) J.J. Kickx	TJV-93-7-T	0	22	78
Hyphoderma setigerum (Fr.) Donk	HHB-12156-Sp	16	14	70
Hyphoderma setigerum (Fr.) Donk	FP-150263	43	16	41
Hyphodontia crustosa (Pers.) J. Eriksss.	HHB-13392-Sp	19	16	65
Laetiporus caribensis Banik & D.L. Lindner	GDL-1	3	5	92
Laetiporus conifericola Burds. & Banik	HHB-15411(Ta)	0	22	78
Laetiporus gilbertsonii Burds.	CA-6(Tb)	19	16	65
Laetiporus huroniensis Burds. & Banik	HMC-1 (Ta)	3	22	76
Lentinus crinitus (L.) Fr.	PR-2058	3	27	70
Merulius tremellosus Schrad.	FP-102301-Sp	22	19	59
Merulius tremellosus Schrad.	FP-150849	38	5	57
Resinicium meridionale Burds. & Nakasone	FP-150352	46	5	49
Phellinus gilvus (Schwein.) Pat.	HHB-11977-Sp-A	27	22	51
Phellinus hartigii (Alesch. & Schnabl.) Pat.	DMR-94-44-T	68	0	32
Phellinus robiniae (Murrill) A. Ames	FP-135708-T	3	11	86
Phellinus robiniae (Murrill) A. Ames	AZ-15-T	3	8	89
Phlebia rufa (Pers.) M.P. Christ.	MR-4280	0	8	92
Phlebia rufa (Pers.) M.P. Christ.	DR-60-Sp	5	8	86
Phlebiopsis flavidoalba (Cooke) Hjortstam	FP-102185	3	27	70
Phlebiopsis flavidoalba (Cooke) Hjortstam	FP-150451	73	3	24
Porodisculus pendulus (Schwein.) Schwein.	HHB-13576	68	3	30
Pycnoporus sanguineus (L.) Murrill	PR-SC-95	22	3	76
Schizophyllum commune (Fr.)	TJV-93-5-Sp	24	11	65
Schizophyllum commune (Fr.)	PR-1117	16	11	73
Tyromyces chioneus (Fr.) P. Karst.	HHB-11933-Sp	35	0	65
Xylobolus subpileatus (Berk. & M.A. Curtis) Boidin	FP-102567-Sp	0	5	95

Supplementary Table 2: Mixed-effect model results linking trait and phylogenetic distances to probability of competitive exclusion. Shown are the model coefficients for the fixed effects, with distance coefficients standardized (i.e., beta-coefficients) to represent the change in log-odds of competitive exclusion for a one standard deviation change from the mean distance. All models included species as random effects to account for correlation among pairwise competitions (see Methods, Statistical Modelling), and all models are adjusted for differences in initial starting positions. Models (1)-(6) give the results for each trait or phylogenetic metric included as the sole independent variable. Model (7) has all trait metrics included simultaneously, and model (8) has all traits and phylogeny included. N=615 for all models after removing intraspecific competition and missing data. Numbers give the coefficient estimates, with the corresponding standard errors given in parentheses below.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Phylogeny	0.449** (0.155)							−0.007 (0.131)
Growth rate		0.814*** (0.123)					0.742*** (0.175)	0.765*** (0.136)
Density			0.681*** (0.185)				0.347 (0.219)	0.349 (0.230)
Enzyme profile				0.408*** (0.117)			0.376** (0.115)	0.366** (0.128)
Decomposition					0.255* (0.113)		0.064 (0.117)	0.062 (0.120)
All traits						0.715*** (0.154)		
Initial diff.	0.169 (0.105)	0.167 (0.108)	0.202 (0.104)	0.229* (0.104)	0.195 (0.104)	0.254* (0.110)	0.194 (0.110)	0.195 (0.109)
Intercept	−2.702 (2.976)	−1.950 (2.513)	−2.789 (3.392)	−1.046 (2.798)	−2.400 (2.926)	−1.850 (3.078)	−3.011 (2.902)	−3.204 (3.046)
Observations	615	615	615	615	615	615	615	615
Akaike Inf. Crit.	678.565	650.517	675.316	676.312	683.495	657.712	643.633	645.633
Bayesian Inf. Crit.	793.527	765.479	790.278	791.274	798.457	772.674	771.860	778.282

Note: $^{*}p<0.05$; $^{**}p<0.01$; $^{***}p<0.001$

Supplementary Table 3: Model results predicting pairwise competitive exclusion as a function of four different phylogenetic distance metrics. Model (1) is the main pairwise substitution method (identical to the results of Table 2). Model (2) is the TimeTree method in MEGA. Method (3) is the 'chronos' method in the *ape* package in R, and model (4) gives the UPGMA method. See Methods for details of each model. Regardless of distance metric, all models showed near-identical coefficients. Numbers give the coefficient estimates, with the corresponding standard errors given in parentheses below.

	(1)	(2)	(3)	(4)
Phylogeny	0.449**	0.678***	0.537**	0.578***
	(0.155)	(0.180)	(0.169)	(0.169)
Initial diff.	0.169	0.179	0.171	0.158
	(0.105)	(0.107)	(0.105)	(0.106)
Intercept	−2.702	−3.256	−3.105	−2.718
	(2.976)	(3.037)	(3.057)	(2.983)
Observations	615	615	615	615
Akaike Inf. Crit.	678.565	668.017	677.649	673.035
Bayesian Inf. Crit.	793.527	782.979	792.611	787.997

Note: *p<0.05; **p<0.01; ***p<0.001

Supplementary Table 4: Model results predicting proportional loss of species as a function of (1) phylogenetic dissimilarity, (2) functional dissimilarity, (3) intransitivity, and (4) variation in competitive ranking. All models include species richness as well as the interaction between richness and the main effect. Numbers give the coefficient estimates, with the corresponding standard errors given in parentheses below. Note that species-specific coefficients are omitted.

	(1)	(2)	(3)	(4)
PD	−0.102			
	(0.087)			
FD		0.079		
		(0.089)		
Intransitivity			−2.632***	
			(0.416)	
Variation in ranking				0.535***
				(0.082)
Species richness	−1.281***	−1.770***	1.529***	−1.231***
	(0.092)	(0.100)	(0.150)	(0.091)
PD x Species richness	0.080***			
	(0.018)			
FD x Species richness		0.078***		
		(0.016)		
Intransitivity x Species richness			−2.117***	
			(0.125)	
Variation in ranking x Species richness				−0.001
				(0.015)
Intercept	−1.058***	−1.113***	−0.820***	−1.156***
	(0.087)	(0.087)	(0.228)	(0.103)
Observations	7,263	7,263	7,263	7,263
Akaike Inf. Crit.	6,774.597	6,705.568	4,759.624	6,683.010
Bayesian Inf. Crit.	6,953.751	6,884.722	4,938.779	6,862.165

Note: $^{*}p<0.05$; $^{**}p<0.01$; $^{***}p<0.001$

Supplementary Table 5: Model results giving proportional loss of species using all variables and their pairwise interactions. Model (1) includes all interactions regardless of significance; model (2) was trimmed using backward BIC selection. There were significant pairwise interactions among most variables, highlighting that loss of species depends on complex interactions among community-level properties. Numbers give the coefficient estimates, with the corresponding standard errors given in parentheses below.

	All pairwise interactions (1)	After BIC trimming (2)
Species richness	1.937^{***}	1.909^{***}
	(0.174)	(0.172)
FD	0.081	−0.083
	(0.132)	(0.120)
PD	−0.012	0.224^{**}
	(0.127)	(0.072)
Intransitivity	-3.570^{***}	-3.604^{***}
	(0.489)	(0.490)
Variation in ranking	-0.368^{***}	-0.333^{**}
	(0.106)	(0.105)
Species richness x FD	0.106^{***}	0.075^{***}
	(0.022)	(0.018)
Species richness x PD	0.019	
	(0.026)	
Species richness x Intransitivity	-2.593^{***}	-2.582^{***}
	(0.136)	(0.136)
Species richness x Variation in ranking	-0.290^{***}	-0.296^{***}
	(0.025)	(0.025)
FD x PD	−0.048	
	(0.038)	
FD x Intransitivity	-0.615^{*}	
	(0.241)	
FD x Variation in ranking	-0.129^{**}	-0.118^{**}
	(0.039)	(0.039)
PD x Intransitivity	0.314	
	(0.269)	
PD x Variation in ranking	0.299^{***}	0.303^{***}
	(0.038)	(0.037)
Intransitivity x Variation in ranking	2.838^{***}	2.826^{***}
	(0.202)	(0.201)
Intercept	-1.389^{***}	-1.419^{***}
	(0.265)	(0.265)
Observations	7,263	7,263
Akaike Inf. Crit.	4358.8	4361.7
Bayesian Inf. Crit.	4620.6	4596.0
Note:		$^{*}p<0.05$; $^{**}p<0.01$; $^{***}p<0.001$

Supplementary Table 6: Model results predicting the proportional loss of species richness in the patch-occupancy models using four different phylogenetic distance metrics. In all cases, PD was calculated using mean pairwise distance among all species in the community (see Methods, Analytical models). In model (1) pairwise distances were calculated using the pairwise substitution method (identical to the results of Table 3). Model (2) used the TimeTree method in MEGA. Method (3) used the the 'chronos' method in the *ape* package in R, and model (4) used the UPGMA method. See Methods for details of each model. Regardless of distance metric, all models showed near-identical coefficients and patterns. Numbers give the coefficient estimates, with the corresponding standard errors given in parentheses below.

	(1)	(2)	(3)	(4)
PD	−0.102	−0.018	−0.083	−0.088
	(0.087)	(0.086)	(0.097)	(0.088)
Species richness	−1.281***	−1.458***	−1.413***	−1.346***
	(0.092)	(0.092)	(0.090)	(0.090)
PD x Species richness	0.080***	0.034*	0.110***	0.065***
	(0.018)	(0.017)	(0.019)	(0.018)
Intercept	−1.058***	−1.088***	−1.101***	−1.090***
	(0.087)	(0.086)	(0.087)	(0.086)
Observations	7,263	7,263	7,263	7,263
Akaike Inf. Crit.	6,774.597	6,790.555	6,768.044	6,786.657
Bayesian Inf. Crit.	6,953.751	6,969.709	6,947.198	6,965.811

Note: *p<0.05; **p<0.01; ***p<0.001

Supplementary Table 7: Model results predicting loss of phylogenetic and functional dissimilarity as a function of initial species richness and richness-squared. Numbers give the coefficient estimates, with the corresponding standard errors given in parentheses below. Note that N=6,763 after removing communities with only one unique species, since FD and PD are not defined for S=1.

	Prop. change in PD	Prop. change in FD
Species richness	0.123^{***}	0.131^{***}
	(0.002)	(0.002)
Species richness^2	-0.007^{***}	-0.008^{***}
	(0.0002)	(0.0002)
Intercept	-0.685^{***}	-0.704^{***}
	(0.005)	(0.006)
Observations	6,763	6,763
Akaike Inf. Crit.	-19,665.33	-19,377.92
Bayesian Inf. Crit.	-19,638.06	-19,350.65

Note: $^{*}p<0.05$; $^{**}p<0.01$; $^{***}p<0.001$

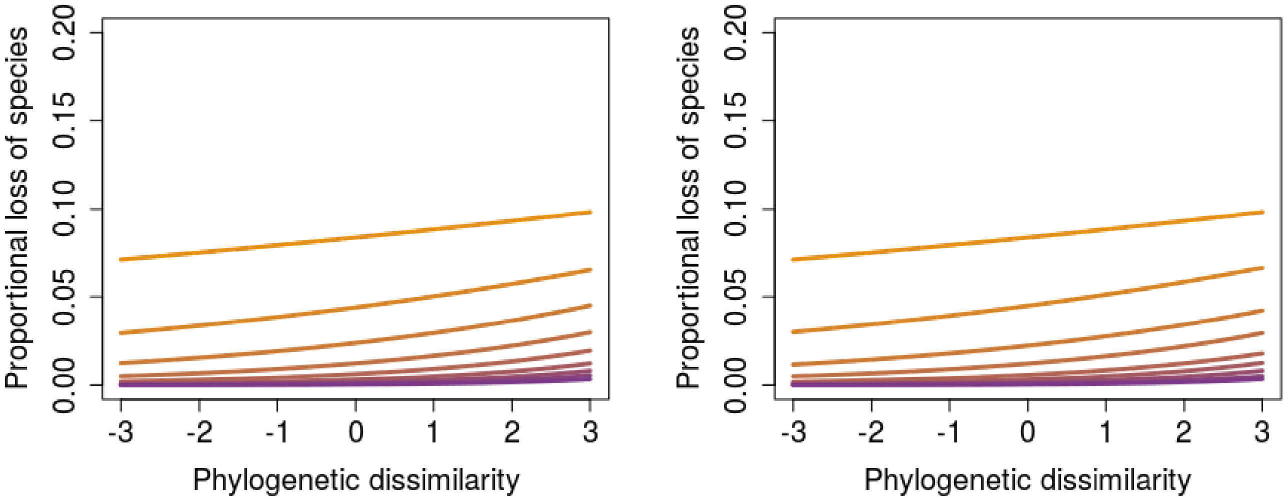
Supplementary Table 8: Blomberg's K statistic for test of phylogenetic signal for the various competitive traits.

Traits	K	Obs. Variance	Random variance	P-value	Z statistic
Growth rate	7.05E-05	66082.2	1127985.0	<0.001	-2.029
Density	8.72E-06	648344.5	1136374.1	0.321	-0.636
Decomposition	7.78E-06	568269.9	1143658.5	0.109	-1.183
Phos	1.10E-05	436053.7	1142499.4	0.094	-1.281
Nag	6.81E-06	697574.9	1139862.8	0.346	-0.570
Lap	2.21E-05	201611.1	1142582.7	0.028	-1.010
BG	4.87E-05	90677.7	1153433.1	0.009	-1.145
CBH	1.05E-05	424732.1	1150123.0	0.142	-0.924
Perox 1	2.61E-04	19569.6	1143686.8	0.091	-0.681
Perox 2	2.99E-05	147414.1	1141161.6	0.001	-2.299
Phenox	6.33E-06	755329.2	1155736.0	0.341	-0.593

Supplementary Table 9: Pairwise correlations between trait and phylogenetic differences among species (N=615).

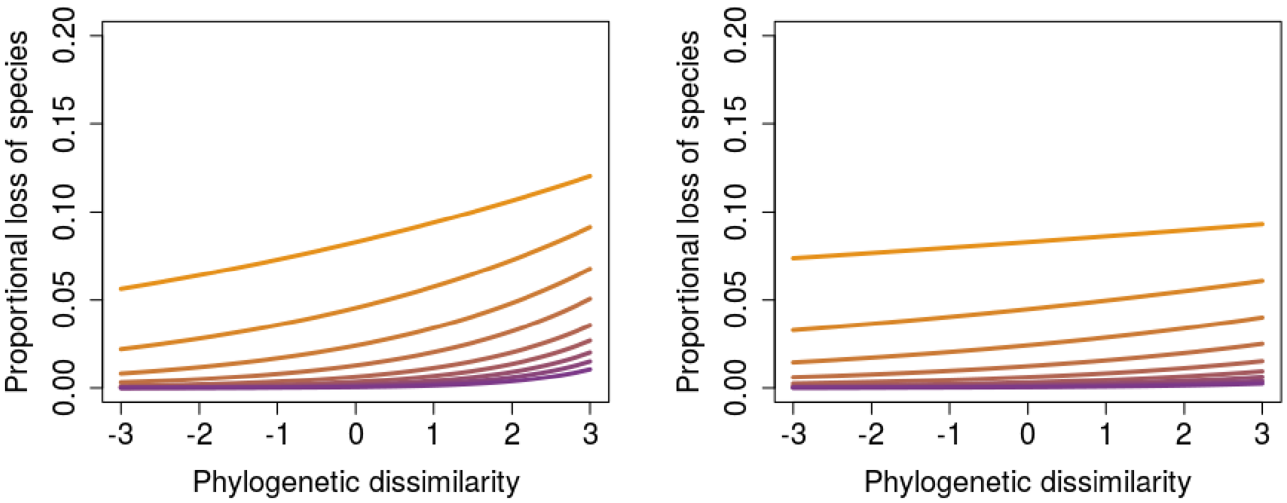
	Phylogeny	Growth rate	Density	Decomp.
Growth rate	0.05**			
Density	0.11	0.01		
Decomp.	-0.01	0.40***	0.00	
Enzymes	0.15***	0.00	0.07	-0.09*
Note:	*p<0.05; **p<0.01; ***p<0.001			

Supplementary Figure 1: Proportional loss of species as a function of four different phylogenetic distance metrics; see Table 6 for details.



(Pairwise substitutions)

(Non-parametric rate smoothing)



(Molecular TimeTree)

(UPGMA)