The following supplement accompanies the article

Role of functional trait variability in the response of individual phytoplankton species to changing environmental conditions in a coastal upwelling zone

Jaime Otero*, Antonio Bode, Xosé Antón Álvarez-Salgado, Manuel Varela

*Corresponding author: jotero@iim.csic.es

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Table S1. List of species used in the analyses including mean abundance, cell size and trait data information. Species names according to the World Register of Marine Species (http://www.marinespecies.org).

ID	Species (Code)	Mean abundance ±SD (cells ml^{-1})	Cell biomass (pg C)	Cell biovolume (μm^3)	μ_{max}	T_{opt}	V_{max}^N	Traits source(s)
	Diatoms							
1	*Asterionellopsis glacialis* (ASTGLA)	7.79 ± 60.51	167	1544	1.64	23.17	7.04e−07	[1, 2]
5	*Cerataulina pelagica* (CERPEL)	2.02 ± 19.27	3052	37885				
6	*Chaetoceros affinis* (CHAAF)	18.85 ± 107.38	32	243	1.50	23.78		[1]
7	*Chaetoceros compressus* (CHACOM)	5.61 ± 34.95	109	966				
8	*Chaetoceros curvisetus* (CHACUR)	4.76 ± 48.16	142	1295				
9	*Chaetoceros decipiens* (CHADEC)	0.61 ± 2.19	252	2445				
10	*Chaetoceros debilis* (CHADEL)	0.39 ± 2.31	200	1886				
11	*Chaetoceros didymus* (CHADID)	3.11 ± 12.00	288	2830	1.44	21.20		[1]
12	*Chaetoceros gracilis* (CHAGRA)	2.98 ± 16.36	17	117	2.08	26.79		[1]
13	*Chaetoceros socialis* (CHASOC)	181.20 ± 697.39	28	210				
14	*Chaetoceros spp.* (CHASPP)	18.56 ± 67.91	282	2771				
16	*Dactyliosolen fragilissimus* (DACFRA)	3.17 ± 25.89	528	5539	0.85	17.24		[1]
17	*Detonula pumila* (DETPUM)	7.05 ± 26.55	475	4924				
22	*Ginardia delicatula* (GUIDEL)	8.19 ± 33.87	601	6386				
23	*Ginardia striata* (GUISTRI)	2.12 ± 18.03	4099	52227				

27	*Lauderia annulata* (LAUANN)	2.02 ± 10.37	3411	42767	1.40	15.10		[3]
28	*Leptocylindrus danicus* (LEPDAN)	74.95 ± 414.78	107	942	1.53	27.61		[1]
29	*Leptocylindrus minimus* (LEPMIN)	4.33 ± 19.68	18	127				
30	*Navicula transitans* (NAVTRA)	0.62 ± 0.88	889	9827				
31	*Nitzschia longissima* (NITLON)	4.10 ± 9.27	44	347			3.48e−07	[2]
32	*Nitzschia longissima petite* (NITLOP)	10.05 ± 85.58	44	347			3.48e−07	[2]
33	*Paralia sulcata* (PARSUL)	0.12 ± 0.41	386	3912				
35	*Proboscia alata* (PROALA)	1.60 ± 7.32	3648	46012				
40	*Pseudo-nitzschia delicatissima* (PSEDEL)	10.07 ± 39.06	29	221				
41	*Pseudo-nitzschia pungens* (PSEPUN)	21.98 ± 67.76	185	1730	0.45	22.59	1.75e−05	[1, 2]
42	*Rhizosolenia imbricata* (RHIIMB)	0.38 ± 0.83	8863	120634				
43	*Rhizosolenia setigera* (RHISET)	0.82 ± 8.07	2442	29708	0.95	17.15		[1]
45	*Skeletonema costatum* (SKECOS)	20.35 ± 215.02	34	261	1.50	23.44	9.01e−07	[1, 2]
47	*Thalassiosira angulata* (THAANG)	0.86 ± 5.82	1156	13103	1.13	17.00		[3]
48	*Thalassiosira antartica* (THAANT)	2.79 ± 17.05	290	2849				
49	*Thalassiosira anguste-lineata* (THAAUG)	0.22 ± 1.14	1366	15731				
50	*Thalassiosira levanderi* (THALEV)	18.68 ± 246.97	27	200				
51	*Thalassionema nitzschioides* (THANIT)	2.22 ± 8.07	188	1761	1.52	23.04		[1]
52	*Thalassiosira oestrupii* (THAOES)	1.05 ± 7.91	74	628				
53	*Thalassiosira rotula* (THAROT)	1.46 ± 5.78	1474	17099	0.99	19.84	1.92e−06	[1, 4]
	Dinoflagellates							
2	*Ceratium furca* (CERFUR)	0.08 ± 0.24	2418	22862	0.40	22.70		[1]
3	*Ceratium fusus* (CERFUS)	0.04 ± 0.12	1215	10450	0.36	20.81		[1]
4	*Ceratium lineatum* (CERLIN)	0.56 ± 5.76	1306	11350	0.23	21.51		[1]
19	*Dinophysis acuminata* (DINACU)	0.11 ± 0.37	1874	17119				
24	*Gyrodinium spirale* (GYRSPI)	0.32 ± 0.52	2354	22184				
25	*Heterocapsa niei* (HETNIE)	6.52 ± 16.29	67	379				
26	*Katodinium glaucum* (KATGLA)	1.66 ± 17.05	290	2030				
36	*Prorocentrum balticum* (PROBAL)	3.85 ± 32.19	39	200				
37	*Protoperidinum bipes* (PROBIP)	0.17 ± 0.38	275	1912				
38	*Prorocentrum micans* (PROMIC)	1.46 ± 17.27	2213	20673	0.55	23.56	1.13e−04	[1, 2]
39	*Prorocentrum minimum* (PROMIN)	0.91 ± 6.44	39	200	0.78	23.34	2.45e−06	[1, 2]
44	*Scrippsiella trochoidea* (SCRTRO)	1.72 ± 7.72	597	4645	0.47	15.73		[1]

54	*Torodinium robustum* (TORROB)	0.38 ± 0.63	921	7621			
	Cryptophytes						
15	Cryptophyceae (CRYPTO)	88.86 ± 187.93	31	188			
	Chrysophytes						
18	*Dictyocha fibula* (DICFIB)	0.12 ± 0.36	334	2723			
20	*Distephanus speculum* (DISSPE)	0.30 ± 1.08	334	2723			
	Euglenophytes						
21	*Eutreptiella spp.* (EUTSPP)	0.20 ± 0.49	437	3666			
	Prymnesiophytes						
34	*Phaeocystis pouchetii* (PHAPOU)	10.23 ± 54.94	12	65	2.29	17.45	[1]
	Incertae sedis						
46	*Solenicola setigera* (SOLSET)	13.27 ± 48.01	30	182			

References

[1] Thomas MK, Kremer CT, Litchman E (2016) Environment and evolutionary history determine the global biogeography of phytoplankton temperature traits. Global Ecol Biogeogr 25:75−86

[2] Edwards KF, Klausmeier CA, Litchman E (2015) Nutrient utilization traits of phytoplankton. Ecology 96:2311

[3] Chen B, Laws EA (2017) Is there a difference of temperature sensitivity between marine phytoplankton and heterotrophs? Limnol Oceanogr 62:806−817

[4] Marañón E, Cermeño P, López-Sandoval DC, Rodríguez-Ramos T, Sobrino C, Huete-Ortega M, Blanco JM, Rodríguez J (2013) Unimodal size scaling of phytoplankton growth and the size dependence of nutrient uptake and use. Ecol Lett 16:371−379

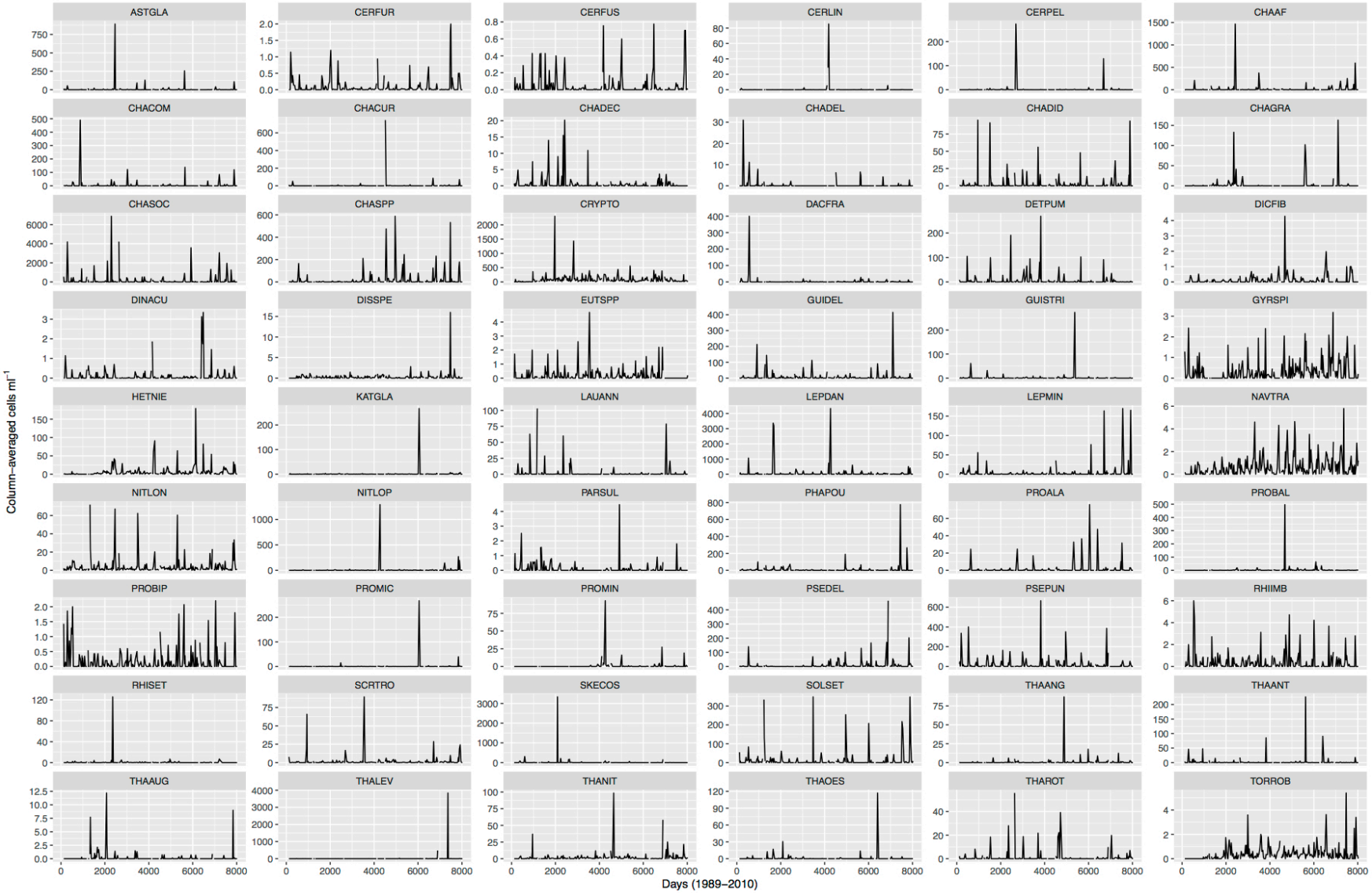


Fig. S1. Time series of column-averaged abundance (cells ml^{-1}) for each species. Codes on top of each panel as in Table S1.

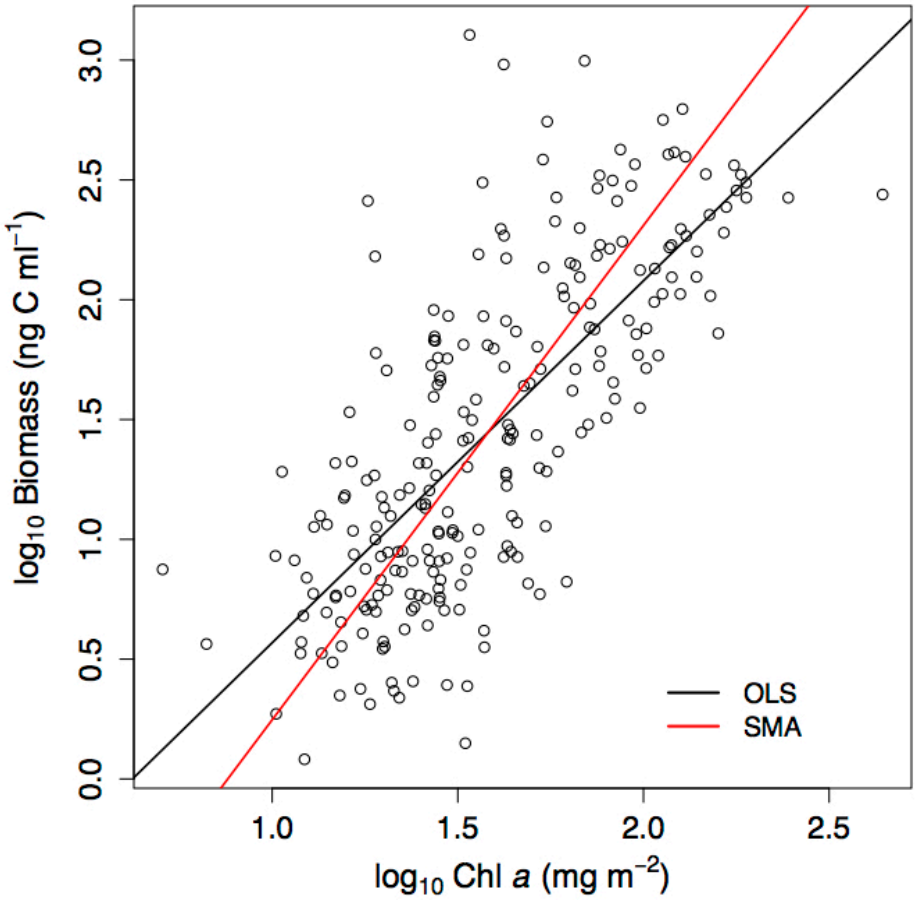


Fig. S2. Relationship between water column-integrated chlorophyll *a* recorded in each sampled day and total biomass for the 54 species. Shown are the ordinary least squares (OLS) regression line, and model II regression by the standardized major-axis (SMA) method. N = 243, $r^2 = 0.54$, $p < 0.0001$.

Table S2. Summary table of the GAMMs fitted to the hydrographic variables. CI = 95% confidence intervals; SE = standard error; edf = estimated degrees of freedom. The corresponding partial plots are shown in Fig. 2 in the main text.

Variable	Effects	Estimate	CI	SE	F-value	t-value	edf	P-value
Upwelling[1]								
(N = 7957)	α	0.026		0.027		0.97		0.33
(R^2_{adj} = 0.07)	f_1				27.56		3.92	< 0.0001
	f_2				0.003		1.08	0.94
	ϕ	0.64	0.62; 0.66					
SST[2]								
(N = 234)	α	14.75		0.08		189.5		< 0.0001
(R^2_{adj} = 0.70)	f_1				84.80		3.73	< 0.0001
	f_2				2.62		1.53	0.19
	Range	20.61	14.19; 29.93					
Nitrate[2]								
(N = 249)	α	140.37		5.11		27.48		< 0.0001
(R^2_{adj} = 0.27)	f_1				16.09		3.65	< 0.0001
	f_2				1.42		1.65	0.142
	Range	15.75	10.38; 23.89					
Chlorophyll *a*[2]								
(N = 254)	α	1.58		0.02		78.54		< 0.0001
(R^2_{adj} = 0.16)	f_1				10.07		3.11	< 0.0001
	f_2				3.72		1.67	0.13
	Range	9.13	4.73; 17.65					

[1]Observations were made sequentially over time (t), thus, an auto-regressive model of order 1 allowing for within-year auto-correlation between the residuals (ϵ) was evaluated, i.e.,$\epsilon_t = \phi\epsilon_{t-1} + \eta_t$, where ϕ is the autocorrelation term of order 1, and η_t are identical, independently distributed errors (Pinheiro & Bates 2000).

[2]Observations were irregularly spaced, thus, in these cases it was evaluated the inclusion of an exponential spatial correlation model that can accommodate the imbalance in time and estimates the distance (Range, in days) between pairs of correlated points (Pinheiro & Bates 2000). The inclusion of a nugget effect was not needed in any case as indicated by likelihood ratio tests.

Table S3. Summary table of the GAMMs fitted to the total abundance and total biomass. CI = 95% confidence intervals; SE = standard error; edf = estimated degrees of freedom. The corresponding partial plots are shown in Fig. 3 in the main text.

Variable	Effects	Estimate	SE	F-value	t-value	edf	P-value
Abundance[1]							
(N = 245)	α	2.37	0.03		75.61		< 0.0001
(R^2_{adj} = 0.29)	f_1			24.24		3.74	< 0.0001
	f_2			2.14		1.80	0.137
Biomass[1]							
(N = 245)	α	1.45	0.04		41.76		< 0.0001
(R^2_{adj} = 0.36)	f_1			34.29		3.67	< 0.0001
	f_2			2.24		1.82	0.109

[1]Note that including an autocorrelation structure was not necessary in either model according to likelihood ratio tests.

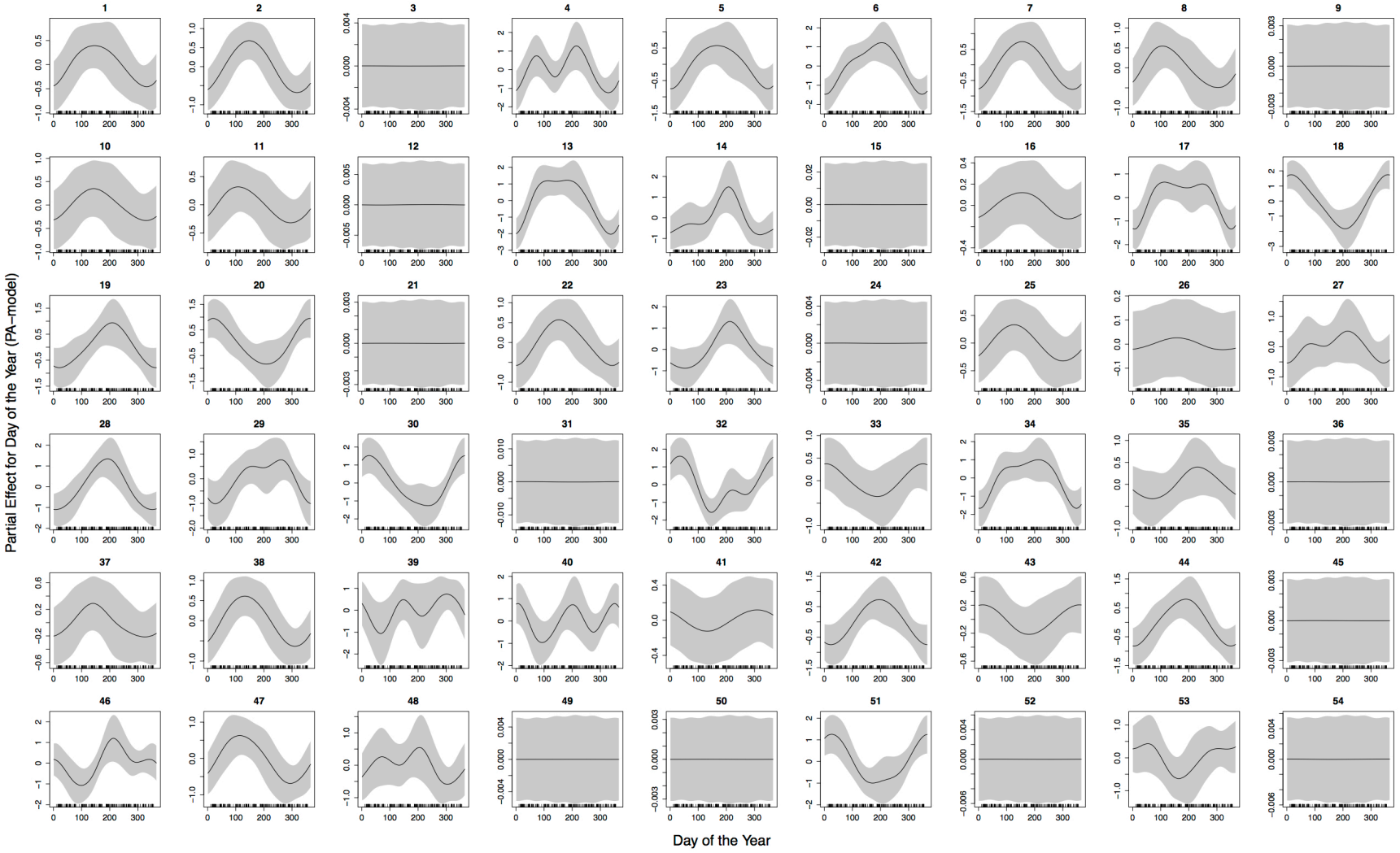


Fig. S3. Plots showing the partial effect of the Day of the Year for each species for the occurrence (presence/absence, PA) model. Numbers on top of each panel as ID column in Table S1.

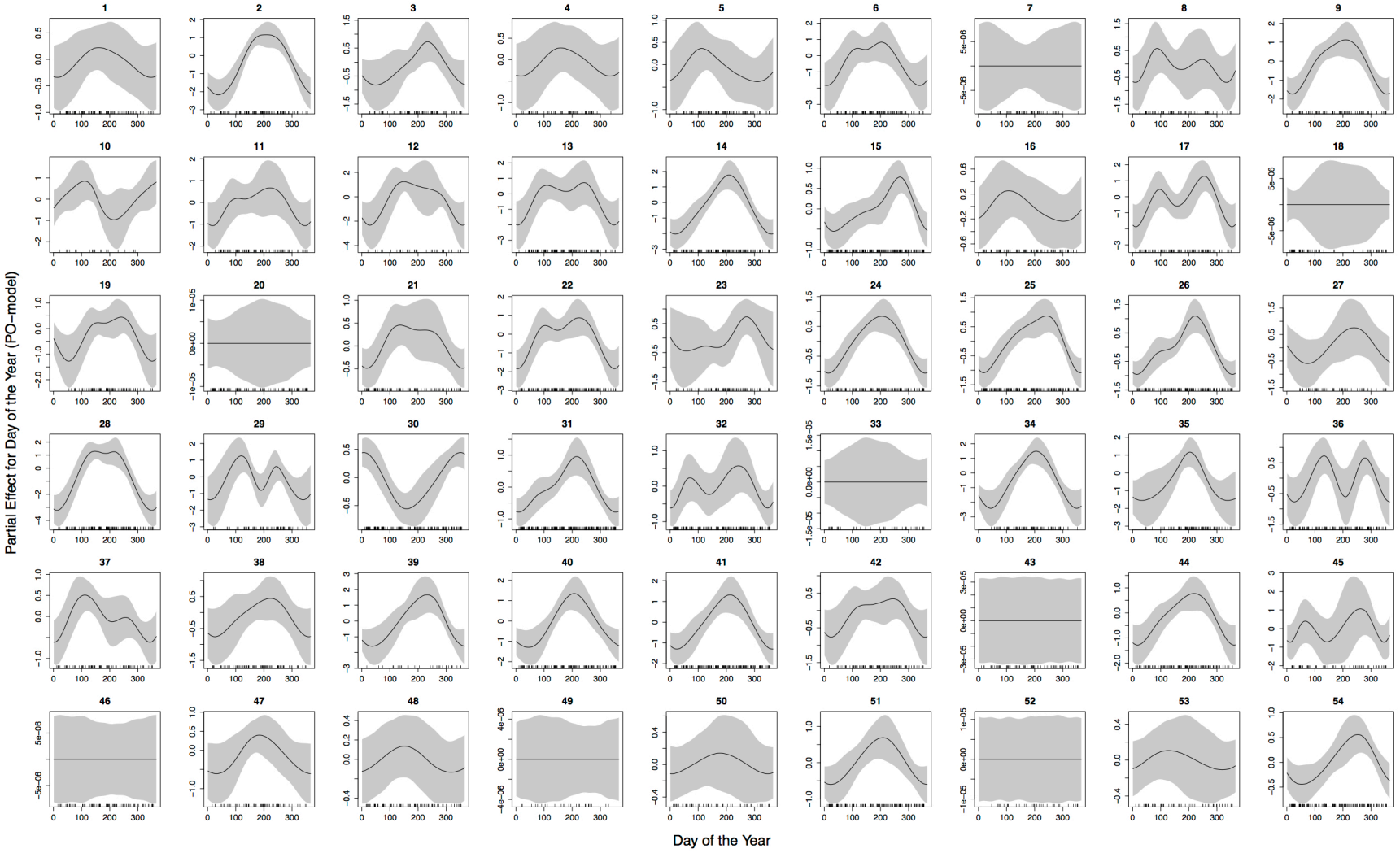


Fig. S4. Plots showing the partial effect of the Day of the Year for each species for the log-normal abundance (i.e. positive counts, PO) model. Numbers on top of each panel as ID column in Table S1.

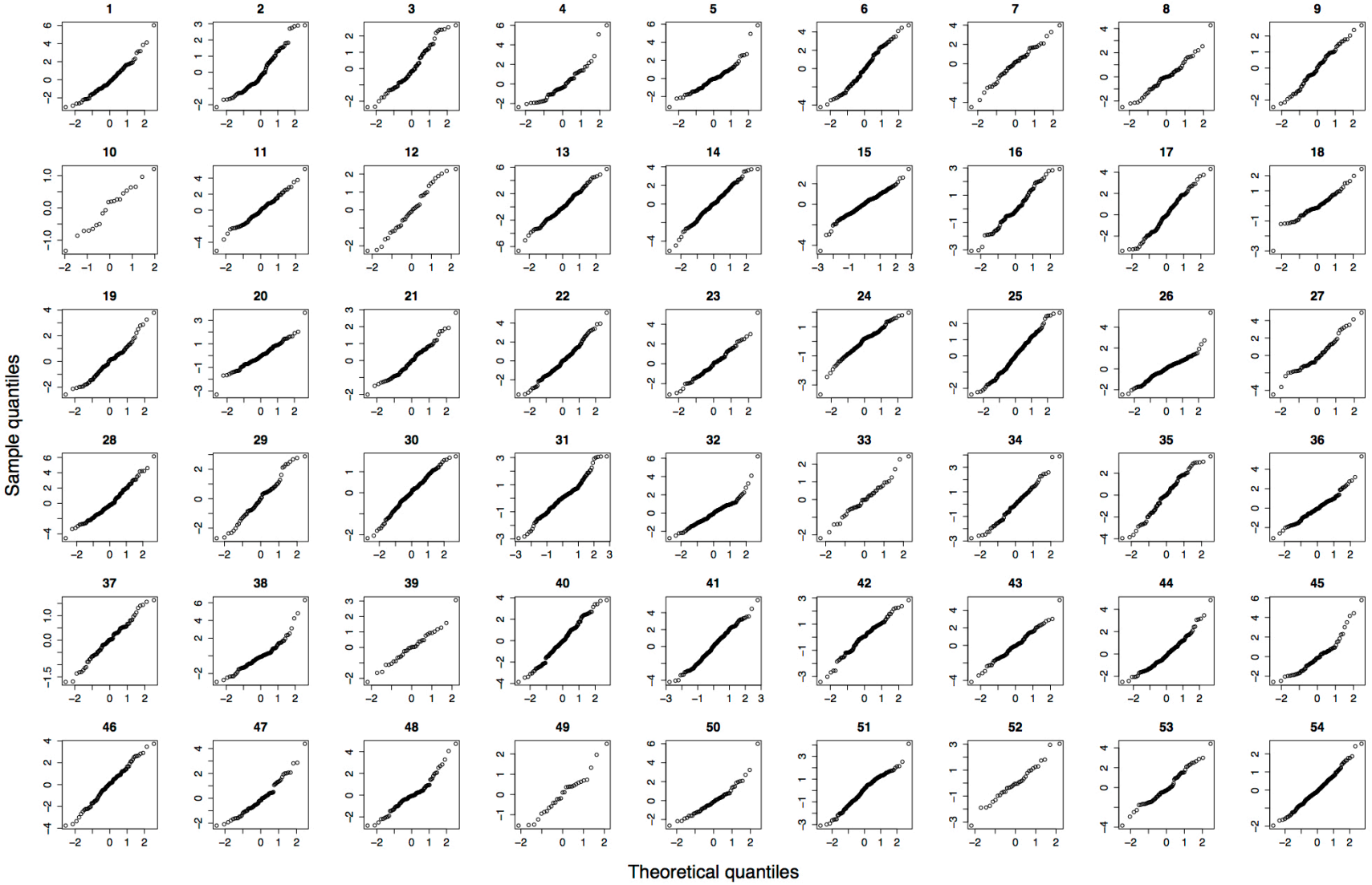


Fig. S5. Normal QQ plots of the Pearson residuals from each abundance model. Numbers on top of each panel as ID column in Table S1.

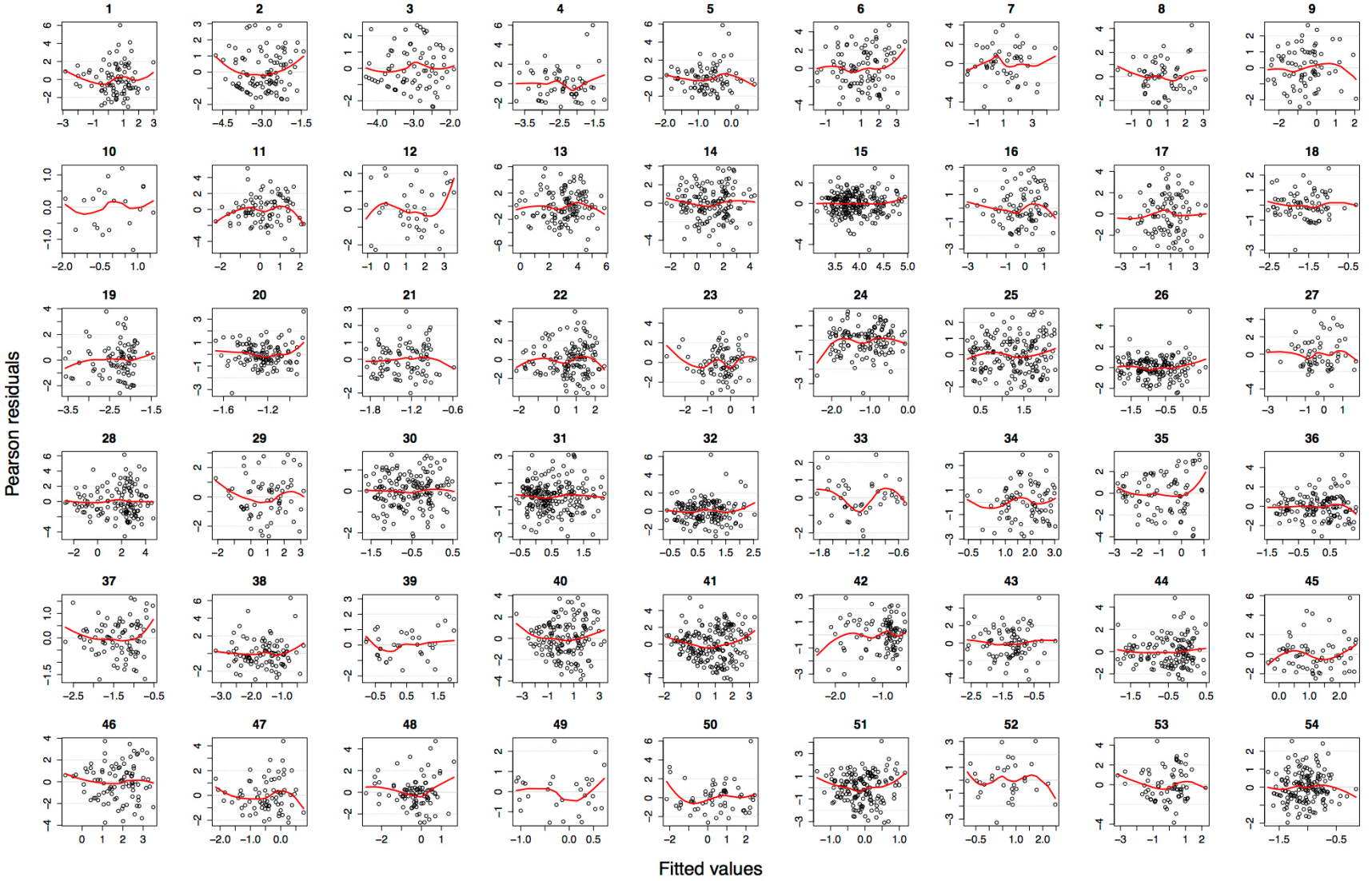


Fig. S6. Pearson residuals against fitted values from each abundance model. Numbers on top of each panel as ID column in Table S1. The red lines show a loess smoother.

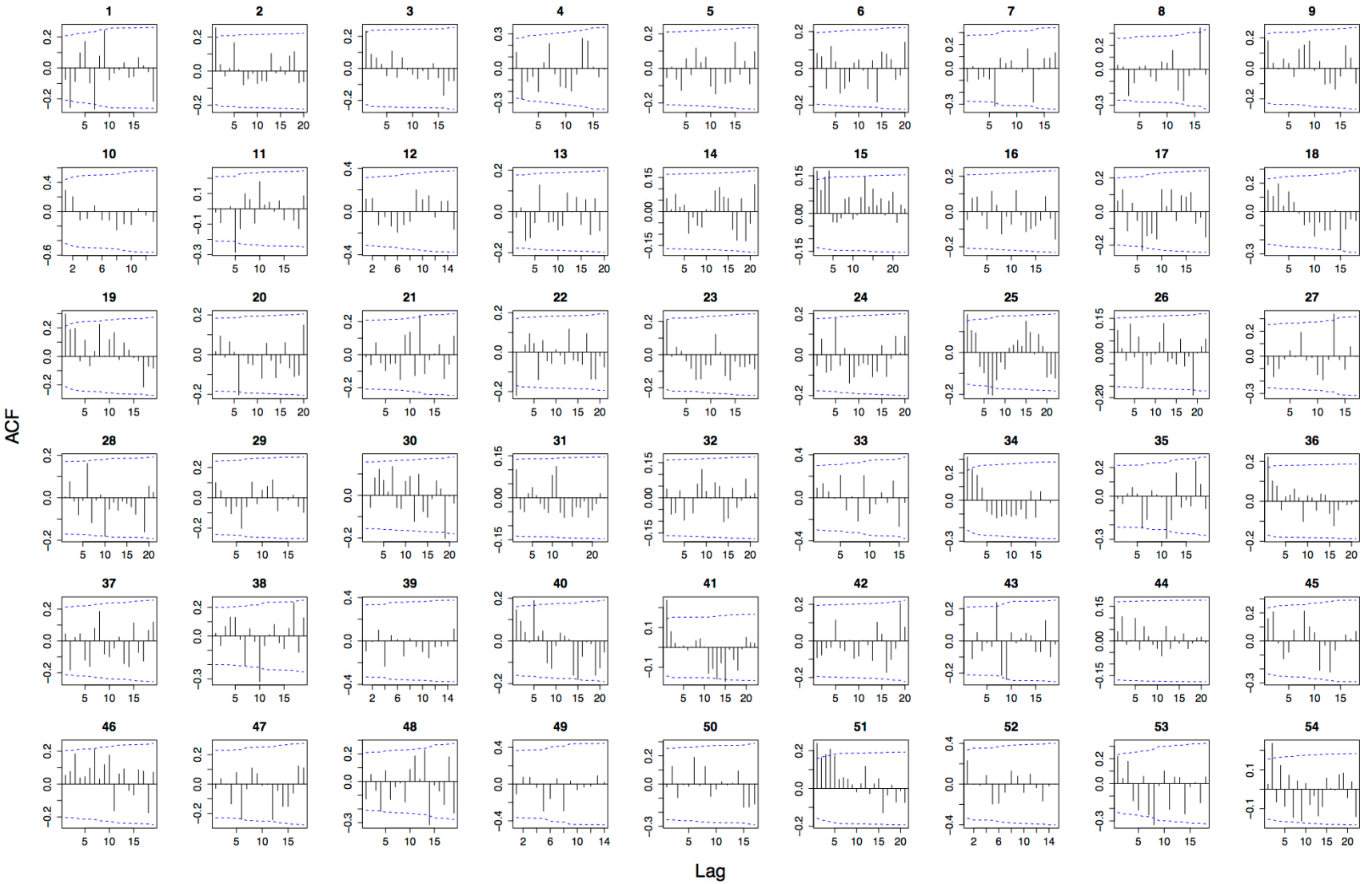


Fig. S7. Autocorrelation function of the Pearson residuals from each abundance model. Numbers on top of each panel as ID column in Table S1. Note that variograms fitted to the Pearson residuals lead to the same conclusion of no remaining autocorrelation.

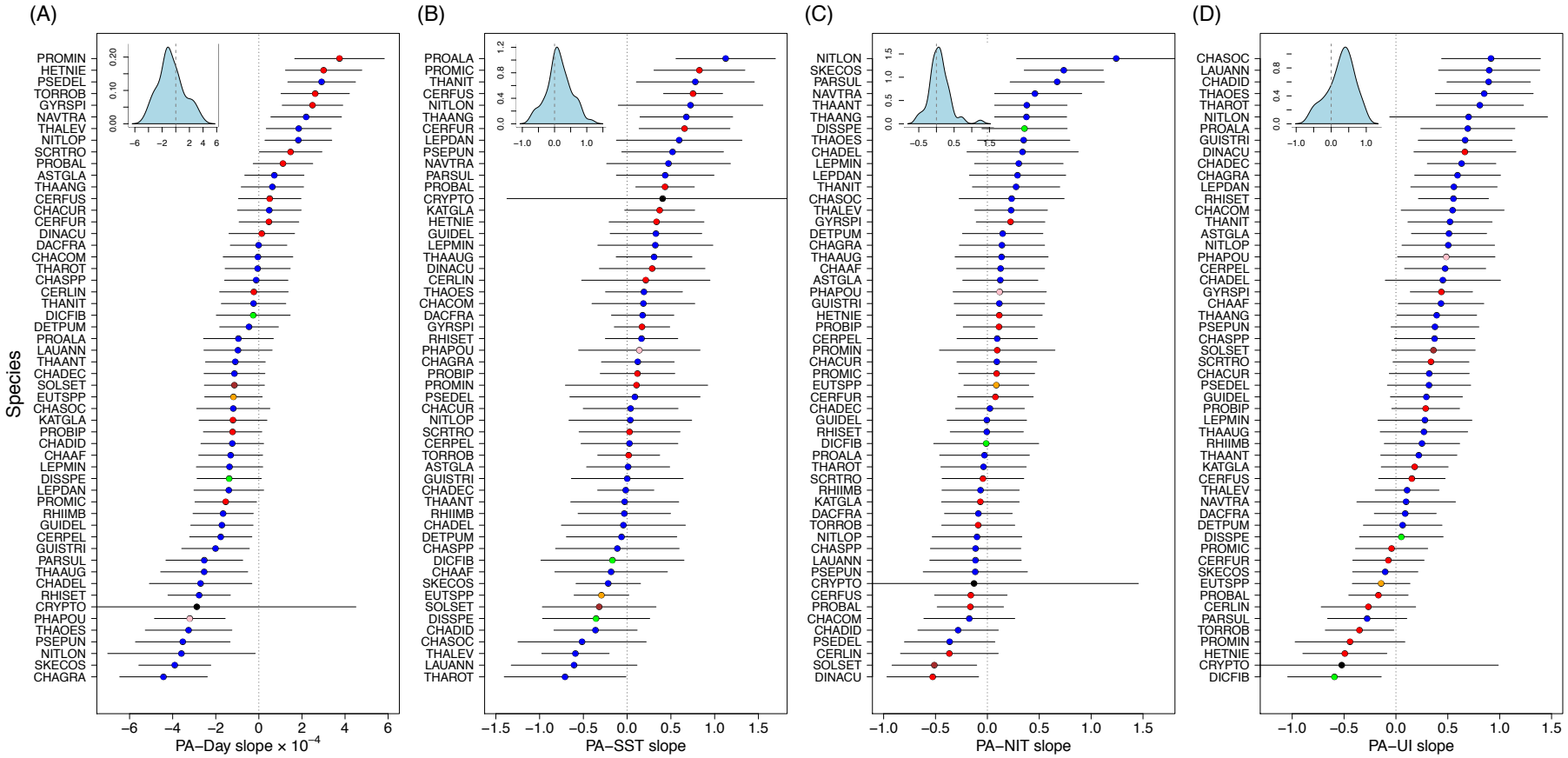
Table S4. Summary table of SMA regressions of the species-specific parametric coefficients for the occurrence and abundance models with cell size. Note that cell size was $\log_{10}$-transformed prior to analyses. See the corresponding plots in Fig. 4 in the main text.

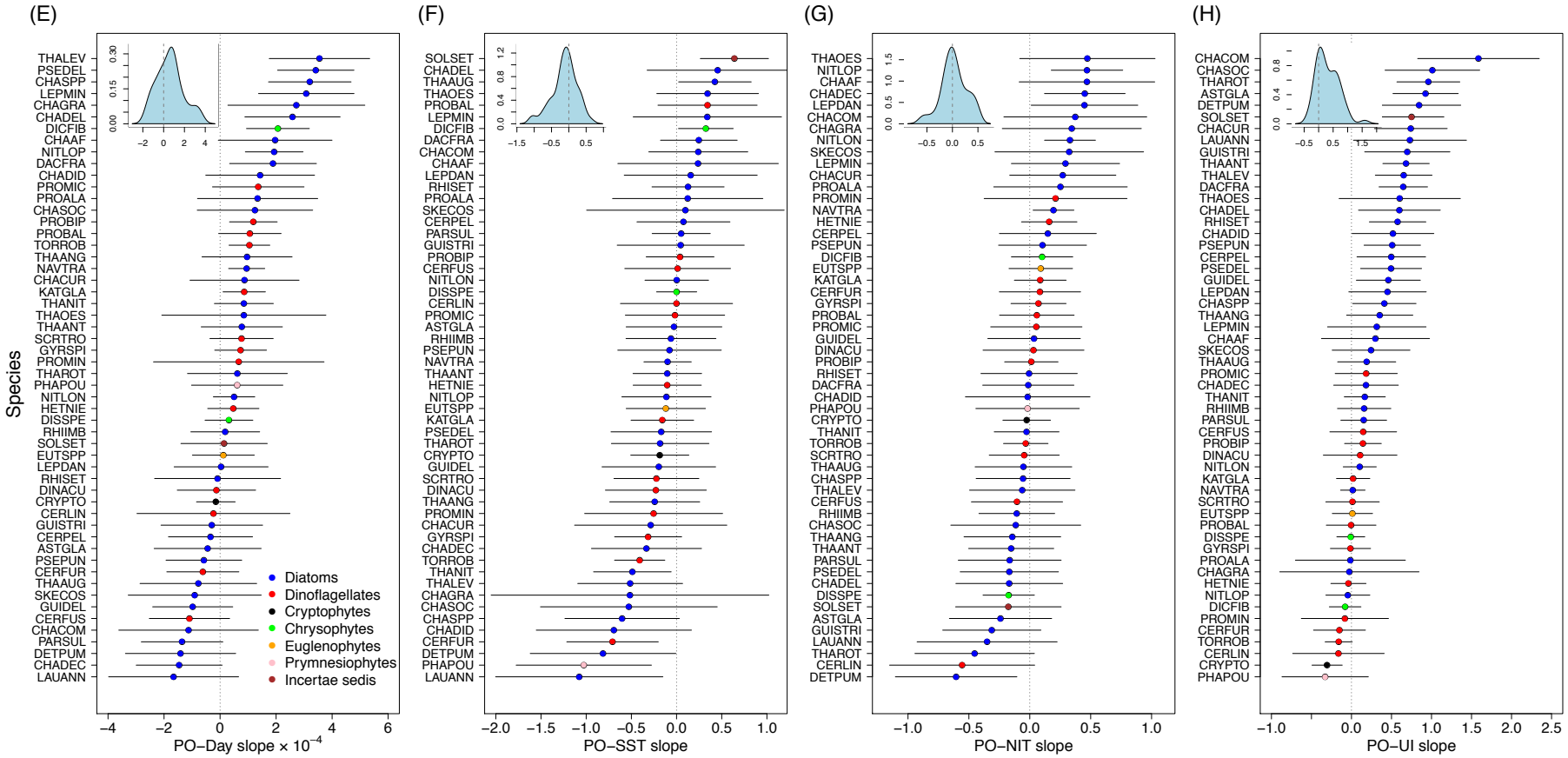
Sub-model	Model II regression	Intercept (±95%CI)	Slope (±95%CI)	R^2	p-value
Occurrence					
	Days ~ cell size	−8.35 (−10.78, −6.57)	2.27 (1.73, 2.99)	0.002	0.763
	SST ~ cell size	−1.42 (−1.91, −1.05)	0.46 (0.35, 0.61)	0.019	0.317
	NIT ~ cell size	1.29 (1.00, 1.67)	−0.36 (−0.47, −0.27)	0.024	0.267
	UI ~ cell size	−1.27 (−1.76, −0.90)	0.46 (0.35, 0.60)	0.013	0.419
Abundance					
	Days ~ cell size	5.82 (4.65, 7.33)	−1.54 (−1.99, −1.20)	0.147	0.004
	SST ~ cell size	1.34 (0.99, 1.80)	−0.43 (−0.57, −0.33)	0.002	0.744
	NIT ~ cell size	1.04 (0.81, 1.34)	−0.30 (−0.39, −0.23)	0.140	0.005
	UI ~ cell size	−1.25 (−1.74, −0.88)	0.46 (0.35, 0.61)	0.001	0.796

Table S5. Coefficients of SMA regressions of growth rate, optimum temperature for growth T_{opt}, and maximum rate of nitrogen uptake with cell size. Note that μ_{max}, V_{max}^N, and cell size were $\log_{10}$-transformed prior to analyses. See the corresponding plots in Fig. S9.

Model II regression		Intercept (±95%CI)	Slope (±95%CI)	R^2	p-value
μ_{max}	~ cell size	1.07 (0.71, 1.63)	−0.32 (−0.48, −0.22)	0.294	0.013
T_{opt}	~ cell size	35.14 (30.31, 42.53)	−4.07 (−6.22, −2.67)	0.221	0.036
V_{max}^N	~ cell size	−9.03 (−12.48, −7.33)	1.10 (0.54, 2.21)	0.423	0.081

Fig. S8. Increasing order of species-specific slopes for the occurrence (A-D) and abundance (E-H) models. Shown are the individual probabilities of occurrence over the study period (A) and in response to SST (B), nitrate concentration (C), and upwelling index (D). Positive slopes indicate that the probability of occurrence increase in response to an increase of a given predictor. Panels E-H show the rates of change in abundance with time (E), SST (F), nitrate concentration (G), and upwelling index (H). Error bars are 95% Wald confidence intervals. The insets depict the distribution of each slope. Species' codes are as in Table S1.




(E)
(F)
(G)
(H)
Species
PO−Day slope × 10^−4
PO−SST slope
PO−NIT slope
PO−UI slope
Diatoms
Dinoflagellates
Cryptophytes
Chrysophytes
Euglenophytes
Prymnesiophytes
Incertae sedis

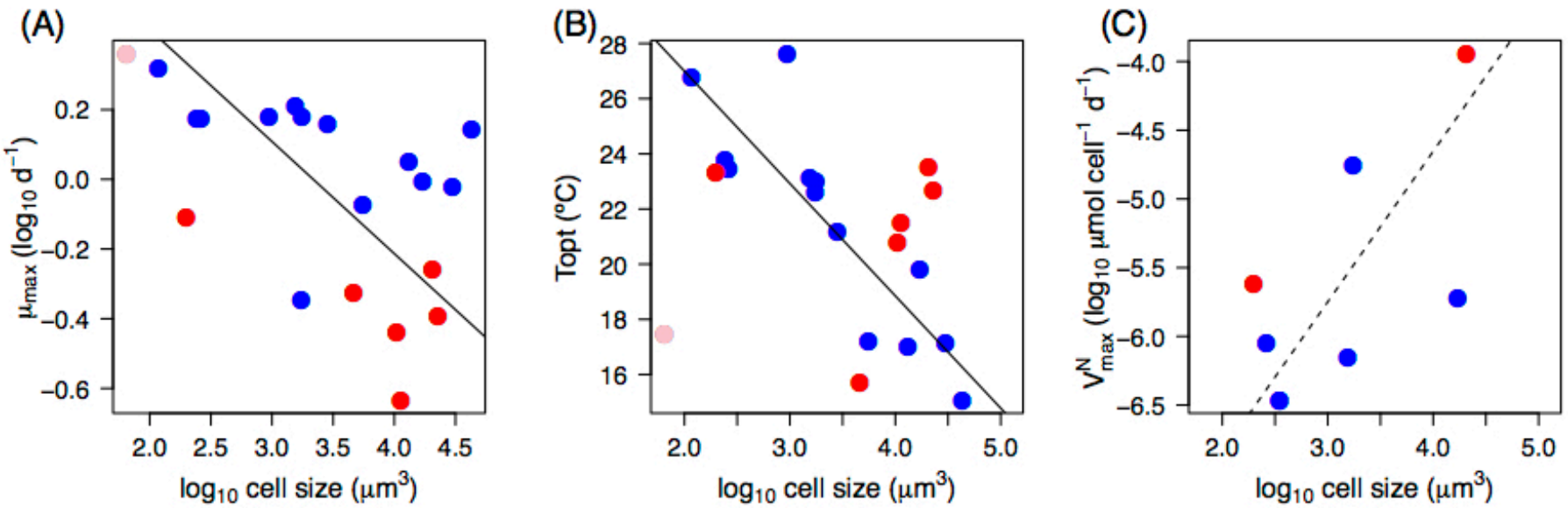


Fig. S9. Scaling relationships between functional traits and cell size. (A) Maximum growth rate, (B) optimum temperature for growth, and (C) maximum rate of nitrogen uptake. Lines show regression fits by the SMA method where the dashed line indicates p-value > 0.05. Numerical results for each model are shown in Table S5. Colour codes as in Fig. S8.

Table S6. Summary table of SMA regressions of the species-specific parametric coefficients for the occurrence and abundance models with μ_{max}. Prior to analyses, μ_{max} was adjusted to account for cell size, that is, we used as a predictor the residuals of the SMA regression of μ_{max} with cell volume shown in Table S5. See the corresponding plots in Fig. 5 and Fig. 6 in the main text.

Sub-model	Model II regression	Intercept (±95%CI)	Slope (±95%CI)	R^2	p-value
Occurrence					
	Days ~ μ_{max}	−0.88 (−2.17, 0.44)	−7.49 (−12.05, −4.66)	0.008	0.714
	SST ~ μ_{max}	0.19 (−0.08, 0.45)	−1.70 (−2.68, −1.07)	0.081	0.225
	NIT ~ μ_{max}	0.06 (−0.10, 0.22)	0.91 (0.57, 1.47)	0.009	0.684
	UI ~ μ_{max}	0.33 (0.19, 0.48)	1.40 (0.99, 1.99)	0.477	0.001
Abundance					
	Days ~ μ_{max}	0.41 (−0.34, 1.17)	−4.24 (−6.83, −2.63)	0.003	0.823
	SST ~ μ_{max}	−0.23 (−0.47, 0.002)	−1.48 (−2.36, −0.93)	0.063	0.286
	NIT ~ μ_{max}	0.004 (−0.16, 0.16)	−1.03 (−1.63, −0.65)	0.080	0.226
	UI ~ μ_{max}	0.29 (0.15, 0.45)	1.36 (0.94, 1.97)	0.424	0.002

Table S7. Summary table of SMA regressions of the species-specific parametric SST and UI coefficients for the occurrence models, and NIT and UI coefficients for the abundance models with T_{opt} and V_{max}^{N}. Prior to analyses, Topt and V_{max}^{N} were adjusted to account for cell size, that is, we used as predictors the residuals of the SMA regression of T_{opt} and V_{max}^{N} with cell size shown in Table S5. See the corresponding plots in Fig. 7 in the main text.

Sub-model	Model II regression	Intercept (±95%CI)	Slope (±95%CI)	R^2	p-value
Occurrence					
	SST ~ T_{opt}	0.18 (−0.06, 0.43)	0.12 (0.08, 0.19)	0.130	0.118
	UI ~ V_{max}^{N}	0.29 (0.03, 0.55)	−0.59 (−1.05, −0.34)	0.637	0.018
Abundance					
	NIT ~ V_{max}^{N}	0.10 (−0.16, 0.36)	0.42 (0.20, 0.87)	0.372	0.108
	UI ~ V_{max}^{N}	0.35 (0.04, 0.67)	−0.56 (−1.11, −0.28)	0.437	0.074