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Partitioning the effects of plant diversity on ecosystem functions at different trophic levels

*Ecological Monographs*

## SUPPORTING INFORMATION: APPENDIX S1

### Section S1: Supplementary Methods

Table S1 PaNDiv experimental species.

Species	resource economics	group
<i>Dactylis glomerata</i>	fast	grass
<i>Holcus lanatus</i>	fast	grass
<i>Lolium perenne</i>	fast	grass
<i>Poa trivialis</i>	fast	grass
<i>Anthriscus sylvestris</i>	fast	herb
<i>Crepis biennis</i>	fast	herb
<i>Galium album</i>	fast	herb
<i>Heracleum sphondylium</i>	fast	herb
<i>Rumex acetosa</i>	fast	herb
<i>Taraxacum officinale</i>	fast	herb
<i>Anthoxanthum odoratum</i>	slow	grass
<i>Bromus erectus</i>	slow	grass
<i>Festuca rubra</i>	slow	grass
<i>Helictotrichon pubescens</i>	slow	grass
<i>Achillea millefolium</i>	slow	herb
<i>Centaurea jacea</i>	slow	herb
<i>Daucus carota</i>	slow	herb
<i>Plantago media</i>	slow	herb
<i>Prunella grandiflora</i>	slow	herb
<i>Salvia pratensis</i>	slow	herb

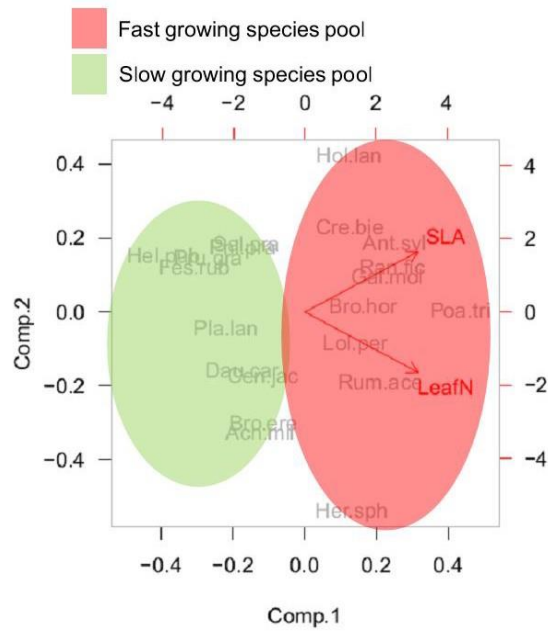


Figure S1 PCA categorizing the experimental species as fast and slow growing based on their values of SLA and leaf nitrogen. By combining only fast, only slow and fast with slow species we created plant communities that span a gradient of average growth strategy along the leaf economics spectrum.

Table S2 number of unique species compositions per species richness and community composition used in the PaNDiv experiment. In order to create a gradient in functional composition and functional diversity (based on the functional trait SLA), communities containing only fast, only slow and a mixture of both, fast and slow species were created. Of each diversity x functional composition combination there were 10 communities, except for the 20 species plots. In total there were 84 species combinations. The twenty species plots were not unique in their species composition as the total species pool. Each of the combination was planted 4 times, once with a control treatment, once with a fungicide treatment, once with a nitrogen treatment and once with both fungicide and nitrogen treatment. The numbers in the brackets are the number of combinations used for the SLA and LDMC measurements.

Richness Composition	1	4	8	20	Total
fast	10 (10)	10 (5)	10 (5)	-	30 (20)
mixed	-	10 (5)	10 (5)	4	24 (14)
slow	10 (10)	10 (5)	10 (5)	-	30 (20)
Total	20 (20)	30 (15)	30 (15)	4	<b>84 (54)</b>

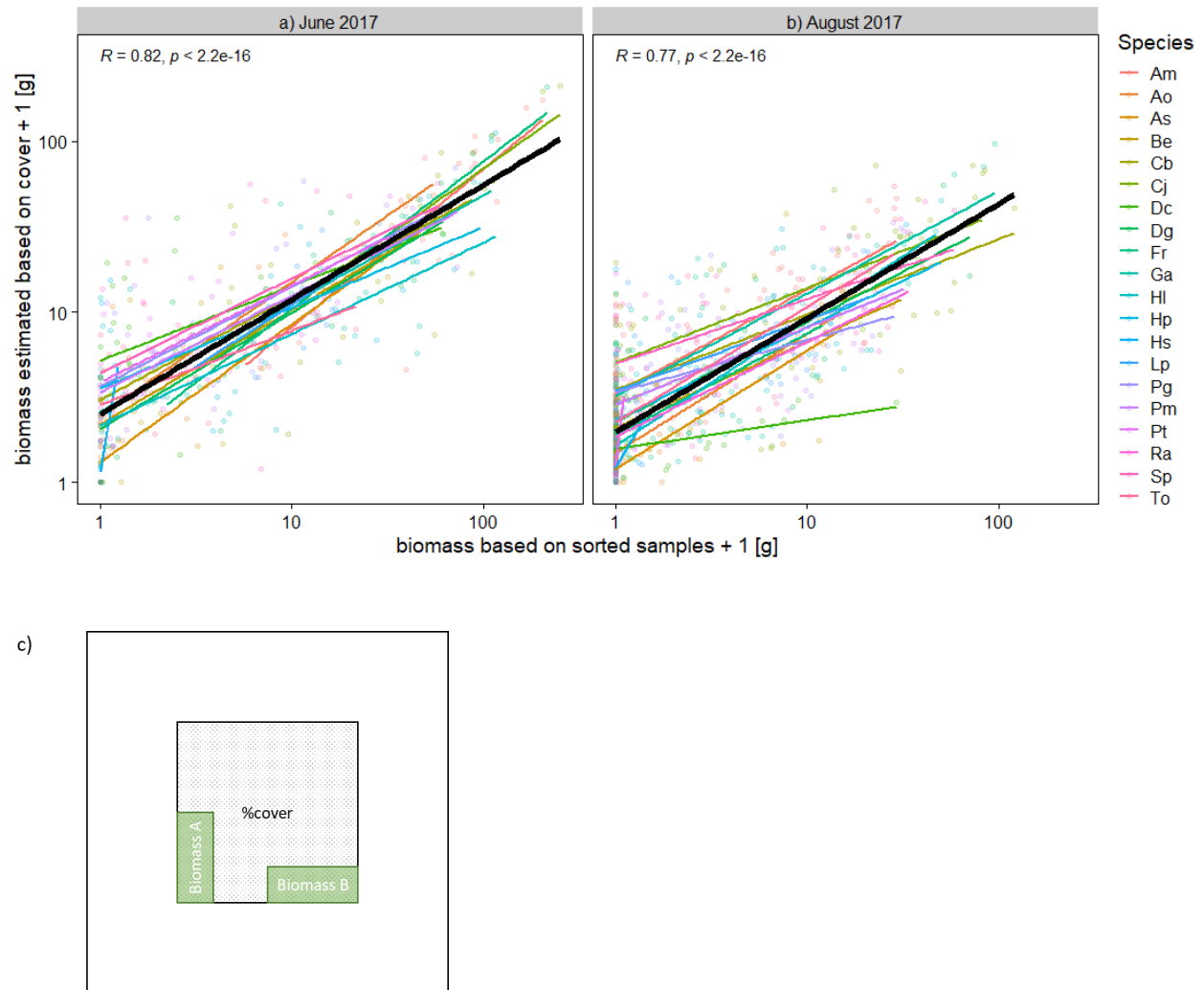


Figure S2 correlation between biomass calculated based on total plot biomass and visual estimates of abundance of each species and biomass per species from sorted samples from a) June and b) August 2017. c) Note that abundance was measured in the central square meter of the plots, while biomass samples were taken on two subplots (20cm x 50cm) within the central square meter. In August we sorted one sample per plot for 216 plots, while in June we sorted both samples per plot for 84 plots. Sorting only one sample led to a less precise correlation, as we do not account for spatial heterogeneity in the plots.

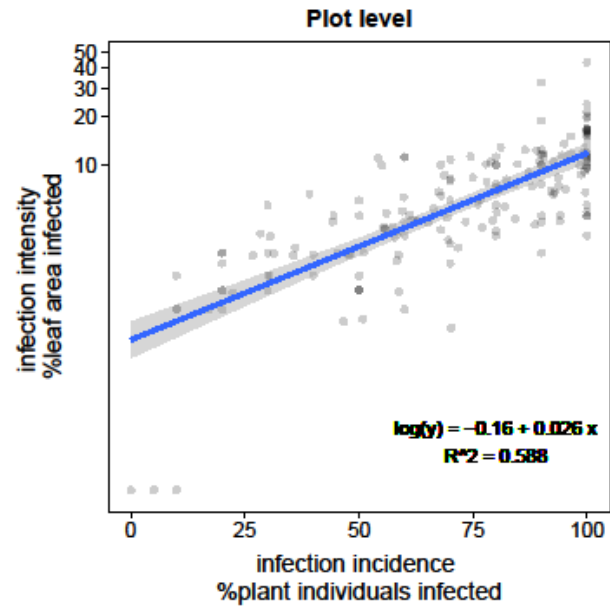


Figure S3 Correlation between community weighted mean of infection intensity based on % leaf area infected and community weighted mean of infection incidence based on % infected individuals. Data from fall 2018, as damaged leaf area was only assessed in fall 2018.

## Calculations of additive partitioning

Table S3 expresses Figure 2 mathematically. The first column contains all the terms used for additive partitioning when comparing the observed plant community with the expected plant community as it is done by Loreau and Hector (2001). The second column contains all the terms used for additive partitioning when comparing the intermediate to the expected community, only considering intraspecific. Note that we assume  $F_{mix\ i}$  to be equal to  $F_{mono\ i}$  and because of this  $RF_{O\ i}$  is equal to  $a_i$ , which then is the reason for zero complementarity effect ( $a_i - \frac{1}{N}$  illustrates the zero sum game as explained by Fox (2005)). The third column contains all the terms used for additive partitioning when comparing the observed to the intermediate community, only considering interspecific shifts. Note that we assume  $RF_{E\ i}$  to be  $a_i$  instead of  $1/N$ .

	Additive partitioning sensu Loreau and Hector (2001)	Tripartite partitioning sensu Fox (2005)	
var.	Total effect	interspecific shifts only	intraspecific shifts only
N			
$a_i$			
$F_{mono\ i}$			
$F_{mix\ i}$		$F_{mono\ i}$	
$F_{O\ i}$	$F_{mix\ i} * a_i$	$F_{mono\ i} * a_i$	$F_{mix\ i} * a_i$
$F_O$	$\sum_i F_{O\ i} * a_i = CWM(F_{O\ i})$	$\sum_i F_{mono\ i} * a_i = CWM(F_{mono\ i})$	$\sum_i F_{O\ i} * a_i = CWM(F_{O\ i})$
$RF_{E\ i}$	$\frac{1}{N}$	$\frac{1}{N}$	$a_i$
$RF_{O\ i}$	$\frac{F_{O\ i}}{F_{mono\ i}} = \frac{F_{mix\ i} * a_i}{F_{mono\ i}}$	$\frac{F_{O\ i}}{F_{mono\ i}} = \frac{F_{mono\ i} * a_i}{F_{mono\ i}} = a_i$	$\frac{F_{O\ i}}{F_{mono\ i}} = \frac{F_{mix\ i} * a_i}{F_{mono\ i}}$
$F_{E\ i}$	$RF_{O\ i} * F_{mono\ i} = \frac{F_{mono\ i}}{N}$	$RF_{O\ i} * F_{mono\ i} = \frac{F_{mono\ i}}{N}$	$RF_{O\ i} * F_{mono\ i} = a_i * F_{mono\ i}$

$F_E$	$\sum_i F_{Ei} = \sum_i RF_{Ei} * F_{mono\ i} = \sum_i \frac{F_{mono\ i}}{N} = \overline{F_{mono\ i}}$	$\sum_i F_{Ei} = \sum_i RF_{Ei} * F_{mono\ i} = \sum_i \frac{F_{mono\ i}}{N} = \overline{F_{mono\ i}}$	$\sum_i F_{Ei} = \sum_i RF_{Ei} * F_{mono\ i} = \sum_i a_i * F_{mono\ i}$
$\Delta RF_i$	$RF_{Oi} - RF_{Ei}$ $= \frac{F_{Oi}}{F_{mono\ i}} - \frac{1}{N} = \frac{F_{mix\ i} * a_i}{F_{mono\ i}} - \frac{1}{N}$	$RF_{Oi} - RF_{Ei}$ $= a_i - \frac{1}{N}$	$RF_{Oi} - RF_{Ei}$ $= \frac{F_{Oi}}{F_{mono\ i}} - a_i = \frac{F_{mix\ i} * a_i}{F_{mono\ i}} - a_i$
$\Delta F$	$= N * \overline{\Delta RT_i} * \overline{F_{mono\ i}} + N * cov(\Delta RF_i, F_{mono\ i})$ <b>= complementarity + selection</b>	$= N * \overline{\Delta RT_i} * \overline{F_{mono\ i}} + N * cov(\Delta RF_i, F_{mono\ i})$ <b>= complementarity + selection</b>	$= N * \overline{\Delta RT_i} * \overline{F_{mono\ i}} + N * cov(\Delta RF_i, F_{mono\ i})$ <b>= complementarity + selection</b>
CE	$N * \overline{\Delta RF_i} * \overline{F_{mono\ i}}$ $= N * \frac{\overline{F_{mix\ i} * a_i}}{F_{mono\ i}} - \frac{1}{N} * \overline{F_{mono\ i}}$ <b>= complementarity effect</b>	$N * \overline{\Delta RF_i} * \overline{F_{mono\ i}}$ $= N * a_i - \frac{1}{N} * \overline{F_{mono\ i}}$ <b>= <math>N * 0 * \overline{F_{mono\ i}} = 0</math></b>	$N * \overline{\Delta RF_i} * \overline{F_{mono\ i}}$ $= N * \frac{\overline{F_{mix\ i} * a_i}}{F_{mono\ i}} - a_i * \overline{F_{mono\ i}}$ <b>= trait independent complementarity effect</b> <b>= complementarity effect</b>
SE	$N * cov(\Delta RT_i, F_{mono\ i})$ $= \sum_i (\Delta RF_i - \overline{\Delta RF_i}) * (F_{mono\ i} - \overline{F_{mono\ i}})$ $= \sum_i ((\frac{F_{mix\ i} * a_i}{F_{mono\ i}} - \frac{1}{N}) - (\frac{\overline{F_{mix\ i} * a_i}}{F_{mono\ i}} - \frac{1}{N})) * (F_{mono\ i} - \overline{F_{mono\ i}})$ <b>= selection effect</b>	$N * cov(\Delta RF_i, F_{mono\ i})$ $= \sum_i (\Delta RF_i - \overline{\Delta RF_i}) * (F_{mono\ i} - \overline{F_{mono\ i}})$ $= \sum_i ((a_i - \frac{1}{N}) - (a_i - \frac{1}{N})) * (F_{mono\ i} - \overline{F_{mono\ i}})$ <b>= dominance effect</b> <b>= interspecific selection effect</b>	$N * cov(\Delta RT_i, T_{mono\ i})$ $= \sum_i (\Delta RF_i - \overline{\Delta RF_i}) * (F_{mono\ i} - \overline{F_{mono\ i}})$ $= \sum_i ((\frac{F_{mix\ i} * a_i}{F_{mono\ i}} - a_i) - (\frac{\overline{F_{mix\ i} * a_i}}{F_{mono\ i}} - a_i)) * (F_{mono\ i} - \overline{F_{mono\ i}})$ <b>= trait dependent complementarity effect</b> <b>= intraspecific selection effect</b>

## Dealing with missing data

Since our plant communities are sown at equal abundances, the expected contribution of the species in a polyculture ( $RF_{e_i}$ ) is  $1/\text{plant diversity}$ . Despite resowing, two species, *Heracleum sphondylium* L. and *Anthriscus silvestris* (L.) Hoffm. did not establish in many plots, most likely unrelated to the experimental treatments. We therefore excluded the two species completely and adjusted plant diversity for the calculation of additive partitioning. In many cases the effect sizes of complementarity and selection was unchanged when the two species were excluded, but selection and complementarity effects for biomass were smaller when they were excluded (Figure S4).

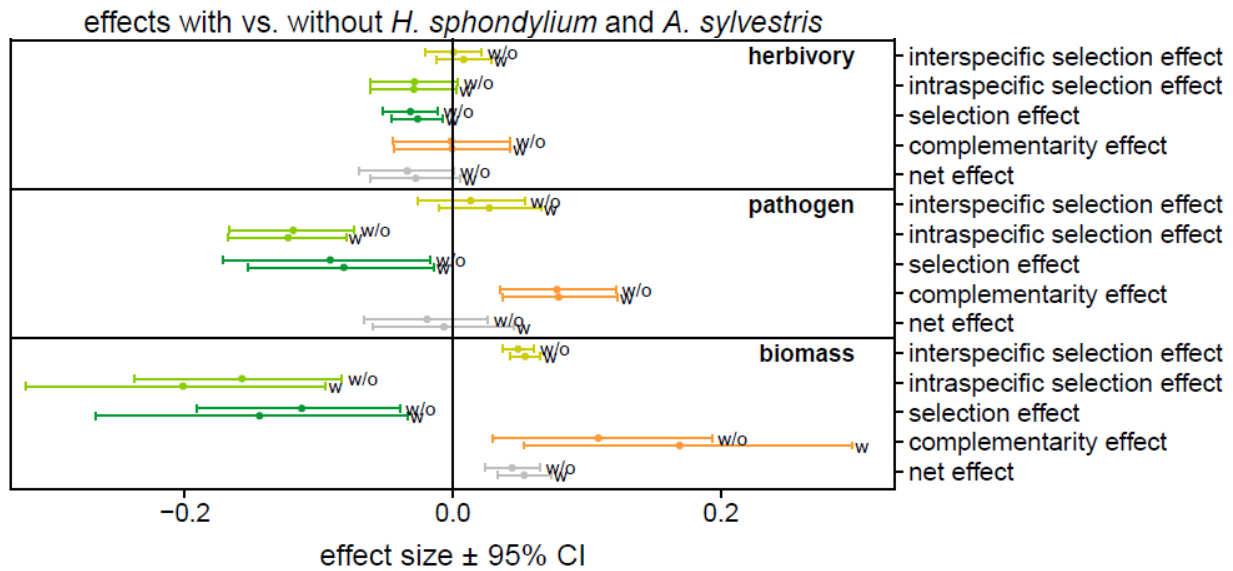


Figure S4 Comparison of intercept only models when *Heracleum sphondylium* L. and *Anthriscus silvestris* (L.) Hoffm. were included (w) or excluded (w/o) in the analysis. Including them leads to an overestimation of complementarity and selection effect for biomass, but does not change the results of other functions much.

We could not measure traits or consumer damage for species with zero or very low abundance in a plot. We therefore used the monoculture values for these species instead. This is a conservative approach because it assumes that there is no effect of diversity on the functioning of these species. The net effect was not altered by this, because species at low abundance hardly contribute to overall community functioning. The contribution of these species to selection due to intraspecific shifts

remains the same and because we used monoculture values, they could not contribute to interspecific shifts.

We had a few cases with missing monoculture values (traits) and measurements of zero in monocultures (infection, herbivory, pathogens). Both cases cause problems when calculating additive partitioning. The measurements of zero were set to half of the minimum of all the other monocultures, to obtain a reasonably small value, without inflating the calculations of complementarity and selection effects. We had two cases of missing monoculture biomass values due to lost samples (2 out of 400 samples [80 monocultures x 5 sampling period]) and in total four missing values for herbivory, pathogens and traits, because the leaf material was dead after the mowing and had not grown back enough for measurements. In case of missing monoculture values, we predicted the values. We modeled the monoculture values as a function of species, sampling period, nitrogen and fungicide treatment and the interaction between species and sampling period. We then predicted the missing monoculture values from these models.



Table S4 expected correlations between the diversity effects of different functions in Figure 7 .  
First column indicates which panel in Figure 7 the expectation refers to.

Panel	Expectation	Reference
b, c	Pathogenic fungi and herbivorous insects cause biomass loss. The more damage by pathogenic fungi and herbivorous insects we observe in the field, the higher the biomass loss should be and diversity effects of biomass production should be negatively related to diversity effects of pathogen infection and herbivory.	Seabloom et al. 2017, Cappelli et al. 2020
e	Pathogenic fungi and herbivorous insects are both primary consumer of plants and many theories about the drivers of infection and herbivory, which are identical for both. There are for example plant characteristics linking to both high infection and high herbivory.	(Raffa et al. 2019, Cappelli et al. 2020, Schädler et al. 2003)

Section S2: Supplementary Results

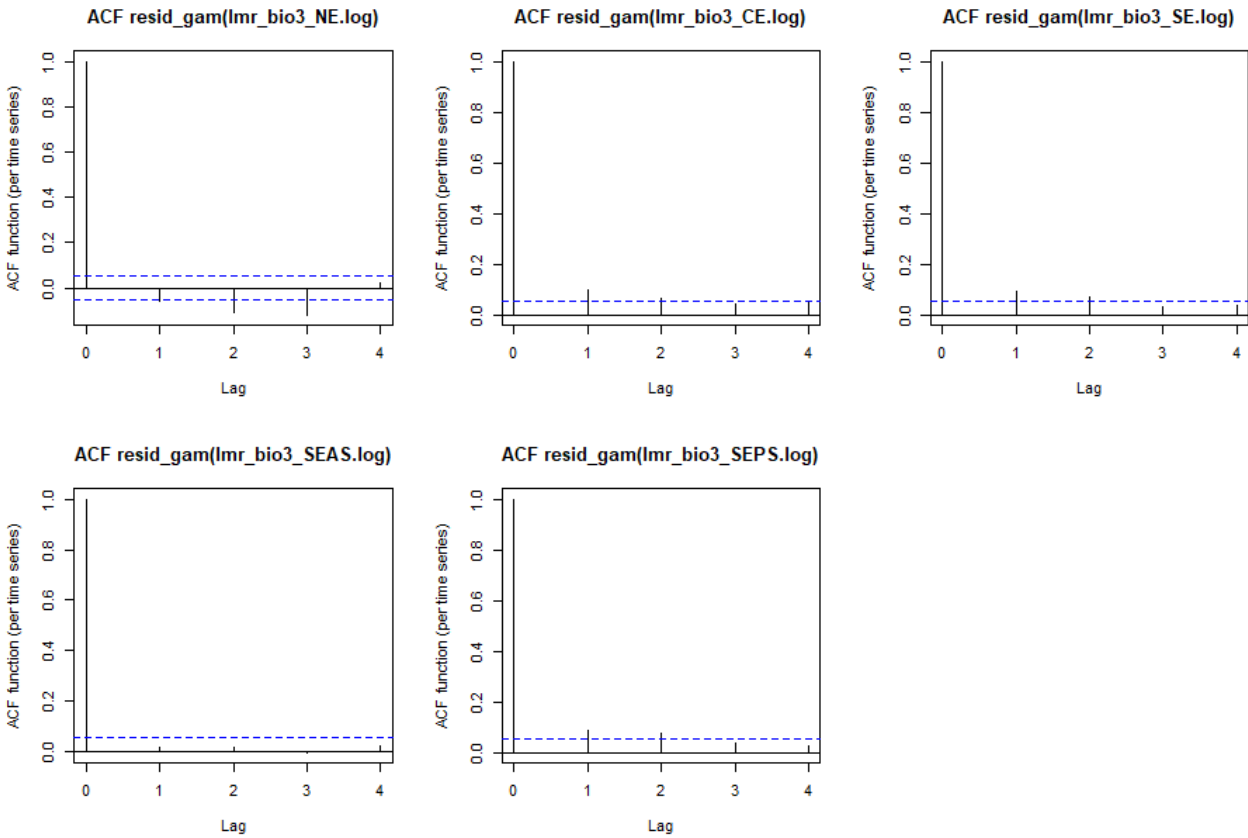


Figure S5 Autocorrelation figures for the mixed effects models of the biodiversity effects for biomass.

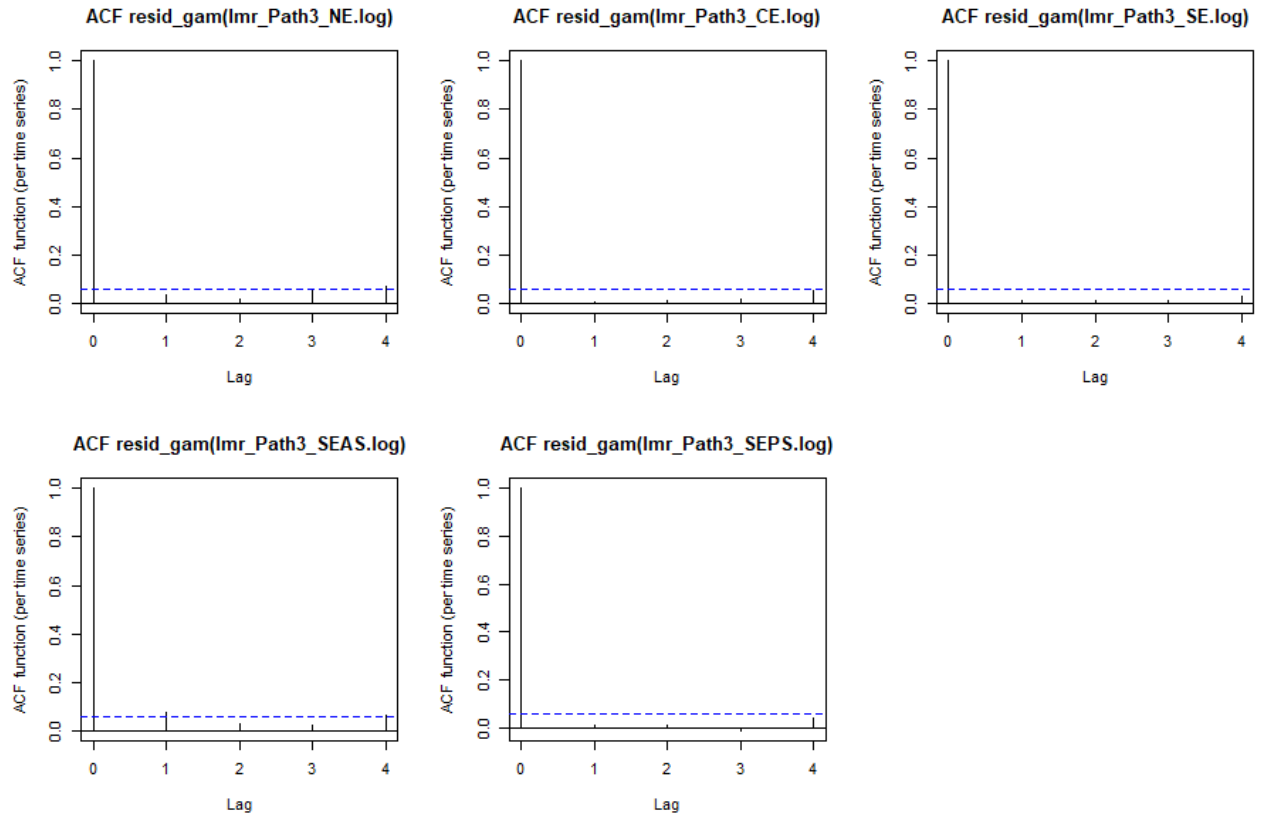


Figure S6 Autocorrelation figures for the mixed effects models of the biodiversity effects for pathogen infection.

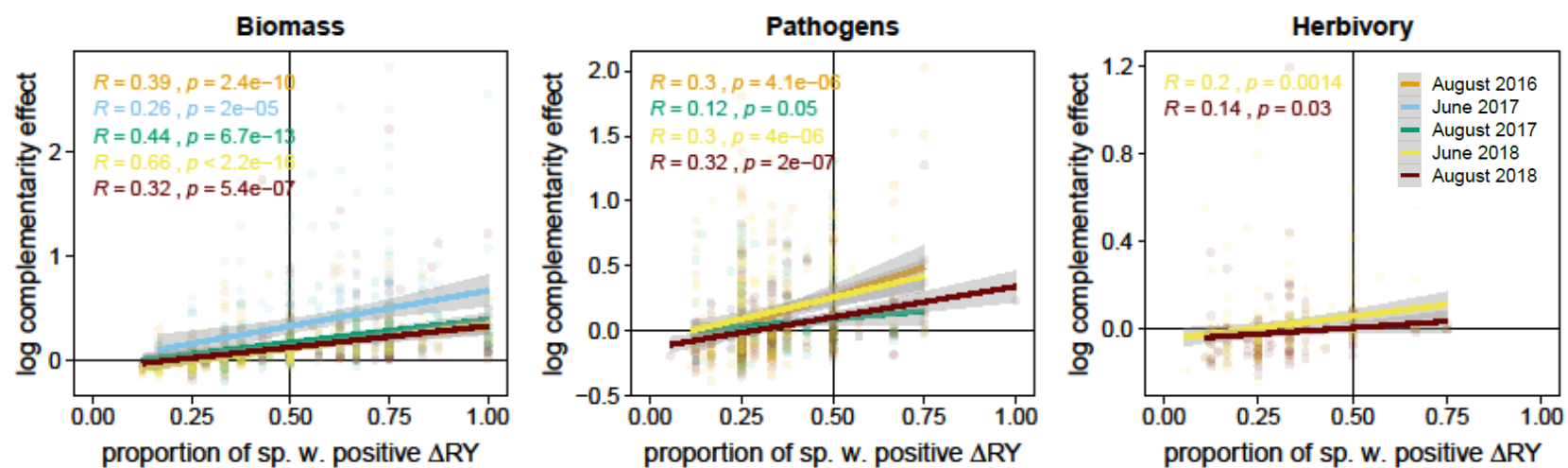


Figure S7 The proportion of species which increase their functioning in polycultures relative to monocultures increased complementarity effects. The proportion of species with positive  $\Delta RY$  explained between 12 and 44% of the variation in complementarity effects in a Pearson correlation. Note that there are cases where a minority of all species in the polyculture were able to drive positive complementarity (top left corner of the graphs).

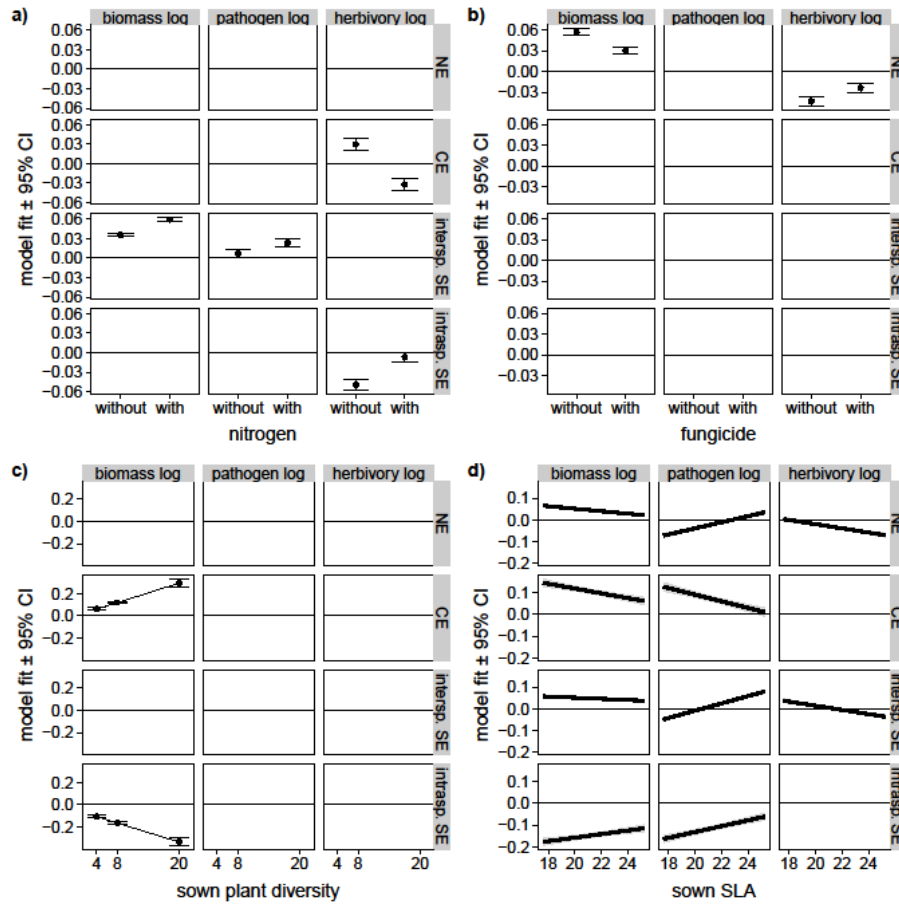


Figure S8 significant effect of a) nitrogen, b) fungicide, c) sown plant species richness and d) sown specific leaf area (SLA) on net effect, complementarity effect, intra- and interspecific selection effect of biomass, pathogen and herbivory. Estimates and CI obtained from the effects package (Fox 2003). When no effect was plotted, it was not included in the best model, which means it was not significant.

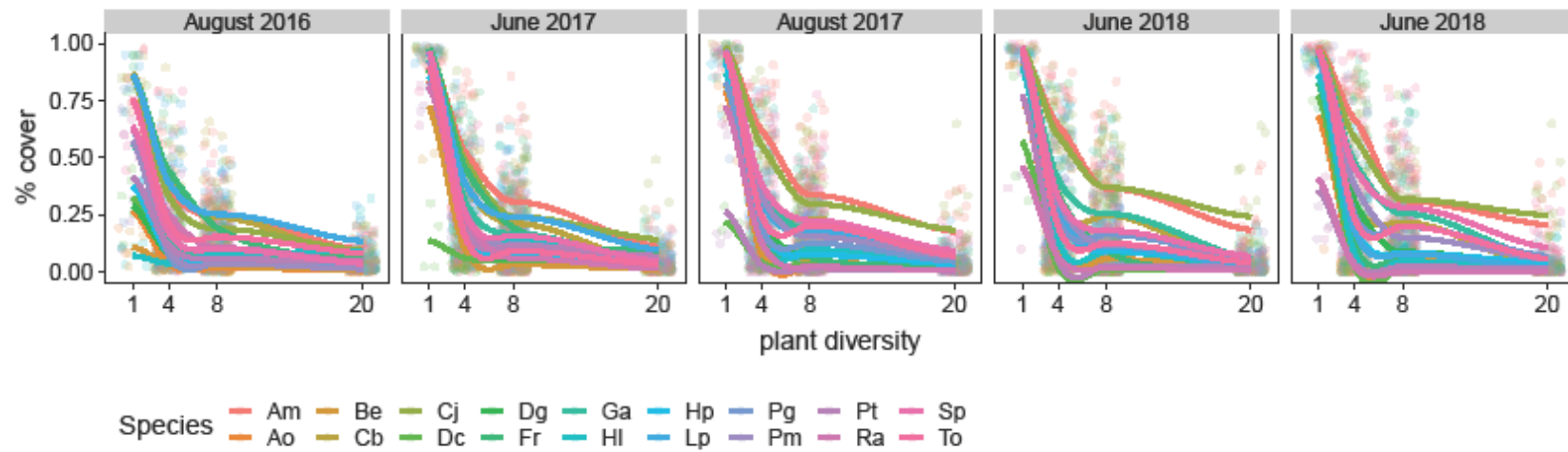


Figure S9 The relationship between plant species abundances and plant species richness in a plot per species. The strongest decrease in abundance occur between the plots with one and four species.

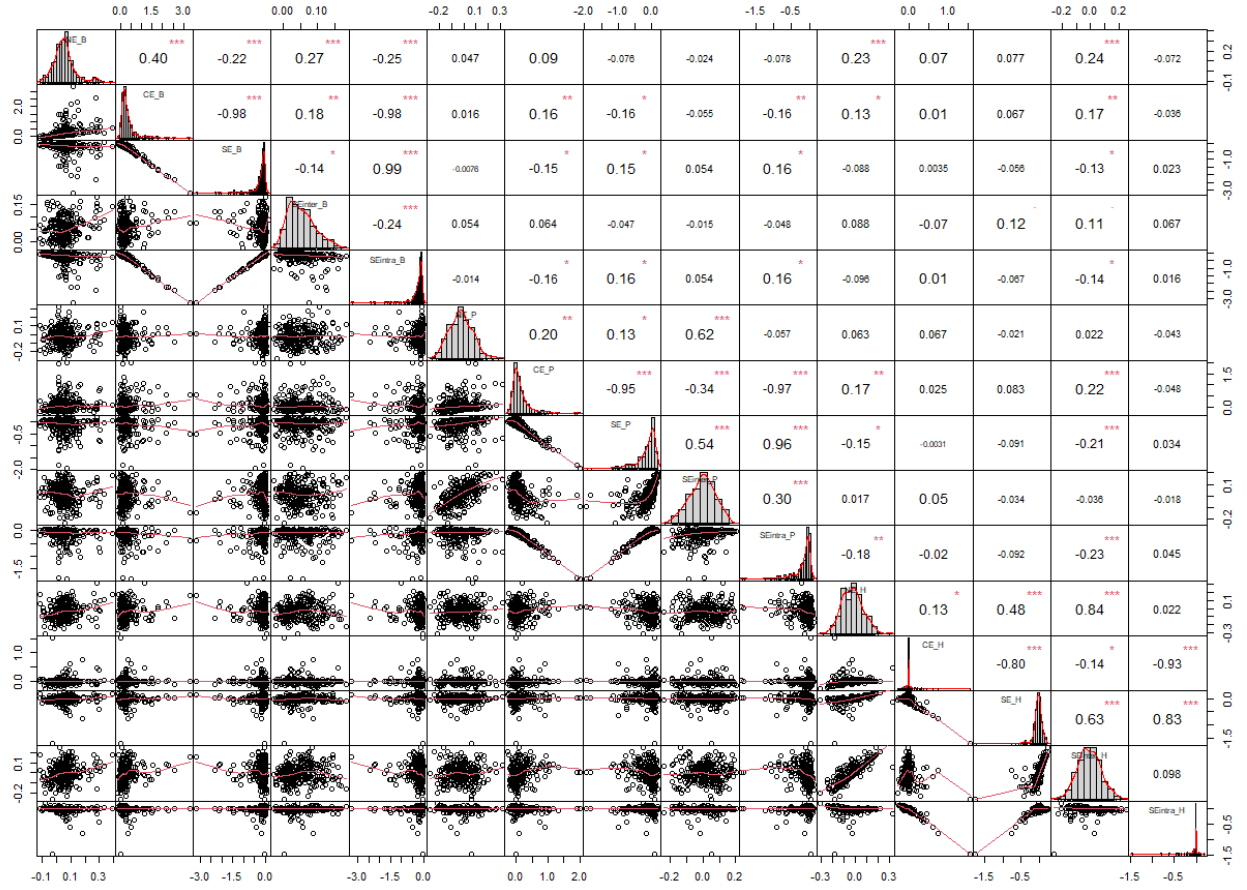


Figure S10 correlations between net effect, selection effect and complementarity effect of all functions (means over the sampling periods)

Table S5 Biodiversity effects on biomass production. Linear mixed effects models results.

	Biomass net effect log esti- mate					complementarity effect log esti- mate					selection effect log esti- mate					interspecific selection effect log esti- mate					intraspecific selection effect log esti- mate				
Fixed Effects	SE	Df	X2	p-value		SE	Df	X2	p-value		SE	Df	X2	p-value		SE	Df	X2	p-value		SE	Df	X2	p-value	
Intercept	0.0433	0.0094				0.1054	0.0355				-0.125	0.0485				0.0474	0.0054				-0.147	0.0318			
Nitrogen			1	-1.609	1.000			1	0.785	0.376			1	-5.993	1.000	0.024	0.008	1	5.906	0.015 *			1	1.425	0.233
Fungicide	-0.027	0.008	1	10.815	0.001 **			1	2.074	0.150	0.014	0.029	1	3.964	0.046 *			1	0.225	0.635			1	0.169	0.681
Plant Diversity			1	1.889	0.169	0.057	0.012	1	20.623	0.000 ***	-0.055	0.011	1	23.479	0.000 ***			1	0.609	0.435	-0.055	0.011	1	25.852	0.000 ***
Sown SLA	-0.022	0.007	1	11.717	0.001 ***	-0.042	0.017	1	5.895	0.015 *			1	2.091	0.148	-0.010	0.004	1	5.615	0.018 *	0.031	0.016	1	3.880	0.049 *
MPD of Sown SLA			1	0.010	0.922			1	0.111	0.739			1	0.115	0.734			1	0.006	0.939			1	0.076	0.783
Random Effects	Var	SD				Var	SD				Var	SD				Var	SD				Var	SD			
1 Block	0.0001	0.0118				0.0004	0.0210				0.0002	0.0151				0.0000	0.0069				0.0004	0.0212			
1 Plot	0.0037	0.0605				0.0155	0.1244				0.0116	0.1078				0.0010	0.0322				0.0115	0.1073			
1 composition	0.0006	0.0252				0.0000	0.0001				0.0000	0.0000				0.0001	0.0116				0.0000	0.0000			
1 compsoth x Harvest						0.0219	0.1480				0.0210	0.1447				0.0006	0.0254				0.0204	0.1430			
1 Harvest	0.0000	0.0062				0.0000	0.0000				0.0000	0.0008				0.0000	0.0007				0.0021	0.0461			
1 Harvest-F						0.0132	0.1150				0.0129	0.1137				0.0001	0.0079				0.0068	0.0825			
Fungicide Harvest						0.0030	0.0551				0.0037	0.0609				0.0001	0.0119				0.0032	0.0568			
1 Harvest-N	0.0003	0.0168				0.0041	0.0637				0.0042	0.0645				0.0000	0.0029				0.0028	0.0527			
Nitrogen Harvest	0.0006	0.0248				0.0072	0.0849				0.0069	0.0831				0.0003	0.0164				0.0063	0.0793			

Table S6 Biodiversity effects on pathogen infection. Linear mixed effects models results.

	Pathogen Infection net effect log esti- mate					complementarity effect log esti- mate					selection effect log esti- mate					interspecific selection effect log esti- mate					intraspecific selection effect log esti- mate				
Fixed Effects	SE	Df	X2	p-value	SE	Df	X2	p-value	SE	Df	X2	p-value	SE	Df	X2	p-value	SE	Df	X2	p-value					
Intercept	-0.019	0.0199			0.0747	0.0183			-0.087	0.0316			0.0154	0.0164			-0.112	0.0196							
Nitrogen			1	0.007	0.932		1	1.648	0.199		1	2.501	0.114	0.016	0.007	1	5.469	0.019 *		1	1.127	0.288			
Fungicide			1	3.707	0.054		1	1.766	0.184		1	2.206	2.206			1	0.322	0.570		1	0.382	0.537			
Plant Diversity			1	1.381	0.240		1	0.174	0.677		1	0.818	0.366			1	0.052	0.820		1	1.258	0.262			
Sown SLA	0.053	0.010	1	22.885	0.000 ***	-0.058	0.017	1	9.856	0.002 **	0.111	0.019	1	31.020	0.000 ***	0.064	0.009	1	39.642	0.000 ***	0.051	0.017	1	9.269	0.002 **
MPD of Sown SLA			1	0.050	0.823		1	0.003	0.958		1	0.037	0.848			1	-0.053	1.000		1	0.026	0.871			
Random Effects	Var	SD			Var	SD			Var	SD			Var	SD			Var	SD							
1 Block	0.0000	0.0000			0.0002	0.0137			0.0004	0.0190			0.0000	0.0000			0.0004	0.0201							
1 Plot	0.0034	0.0585			0.0232	0.1524			0.0211	0.1452			0.0023	0.0484			0.0162	0.0162							
1 composition	0.0020	0.0449			0.0019	0.0431			0.0000	0.0001			0.0006	0.0245			0.0000	0.0000							
1 compotion x Harvest									0.0186	0.1362			0.0040	0.0632			0.0146	0.1209							
1 Harvest	0.0018	0.0426			0.0010	0.0317			0.0039	0.0626			0.0012	0.0351			0.0000	0.0000							
1 Harvest-F					0.0000	0.0000							0.0001	0.0086			0.0011	0.0334							
Fungicide Harvest					0.0087	0.0933							0.0011	0.0325			0.0055	0.0738							
1 Harvest-N																									
Nitrogen Harvest																									



Table S7 Biodiversity effects on insect herbivory. Linear mixed effects models results.

Fixed Effects	Herbivory net effect log					complementarity effect log					selection effect log					interspecific selection effect log					intraspecific selection effect log				
	esti- mate	SE	Df	X2	p-value	esti- mate	SE	Df	X2	p-value	esti- mate	SE	Df	X2	p-value	esti- mate	SE	Df	X2	p-value	esti- mate	SE	Df	X2	p-value
Intercept	-0.033	0.0158				-0.001	0.0203				-0.031	0.0097				0.0004	0.0098				-0.028	0.0149			
Nitrogen			1	0.702	0.402			1	24.035	0.000 ***	0.049	0.012	1	15.771	0.000 ***			1	2.910	0.088	0.042	0.010	1	15.703	0.000 ***
Fungicide	0.019	0.008	1	5.452	0.020 *			1	0.799	0.371	0.028	0.012	1	5.218	0.022 *			1	0.941	0.332			1	1.680	0.195
Plant Diversity			1	0.613	0.434			1	0.071	0.789			1	0.863	0.353			1	0.003	0.957			1	2.384	0.123
Sown SLA	-0.037	0.012	1	8.857	0.003 ***			1	1.418	0.234	-0.046	0.013	1	10.741	0.001 **	-0.036	0.012	1	9.264	0.002 **			1	2.271	0.132
MPD of Sown SLA			1	0.025	0.875			1	0.011	0.918			1	0.036	0.851			1	0.005	0.942			1	0.049	0.825
Random Effects	Var	SD				Var	SD				Var	SD				Var	SD				Var	SD			
1 Block	0.0004	0.0196				0.0010	0.0308				0.0001	0.0082				0.0001	0.0111				0.0004	0.0190			
1 Plot	0.0037	0.0610				0.0083	0.0909				0.0085	0.0923				0.0031	0.0554				0.0060	0.0776			
1 composition	0.0033	0.0579				0.0000	0.0000				0.0013	0.0366				0.0025	0.0502				0.0001	0.0090			
1 composotion x Harvest											0.0039	0.0623				0.0017	0.0415								
1 Harvest	0.0003	0.0167				0.0005	0.0230				0.0000	0.0000				0.0000	0.0000				0.0002	0.0144			
1 Harvest-F																0.0001	0.0098								
Fungicide Harvest																0.0006	0.0251								
1 Harvest-N																									
Nitrogen Harvest																									

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