

Supplementary Information for

The proportion of soil-borne pathogens increases with warming at the global scale

Manuel Delgado-Baquerizo*, Carlos Guerra, Concha Cano-Díaz, Eleonora Egidi, Juntao Wang, Nico Eisenhauer, Brajesh K. Singh, Fernando T. Maestre.

Correspondence to: Manuel Delgado-Baquerizo. E-mail: M.DelgadoBaquerizo@gmail.com

This PDF file includes:

Supplementary Appendixes 1 to 2
Supplementary Figures 1 to 12
Supplementary Tables 1 to 10

Supplementary Appendix 1. Extrapolation uncertainties for our global survey.

We conducted further analyses to quantify the extrapolation uncertainties (dataset accuracy and distribution outliers) in our global survey. This analysis only refers to the dataset used for the mapping and predictions (Fig. 4 and related). In particular, we propose two complementary indicators, based on the environmental variability covered by our global survey (in terms of seven environmental factors including elevation, vegetation type, soil pH, texture and carbon, and mean annual precipitation and temperature), to assess the parameter space covered by our global dataset: (1) First, we calculated the distance of the global environmental space in relation to the convex-hull formed by the standardized set of 235 data points of the original dataset (Supplementary Fig. 8A)⁵⁸⁻⁵⁹. This indicator is especially useful to show the array of environmental characteristics contained in the multidimensional space formed by our data (i.e., convex hull, referring to the smallest convex set in higher dimensional space that contains all of the points present in our dataset)⁵⁸⁻⁵⁹. Our analyses allowed us to assess whether a new environmental condition is an extrapolation or an interpolation in relation to our dataset. To compute the distance to the convex hull, we first standardize the environmental information available for the 235 data points. We then used a quadratic program solver to calculate the environmental distance of any xy pair of coordinates to the convex hull (e.g., to observe how distant the environmental conditions present in Australia are from those covered by our dataset). In this analysis, the closer a prediction to the convex hull, the more reliable this prediction is.

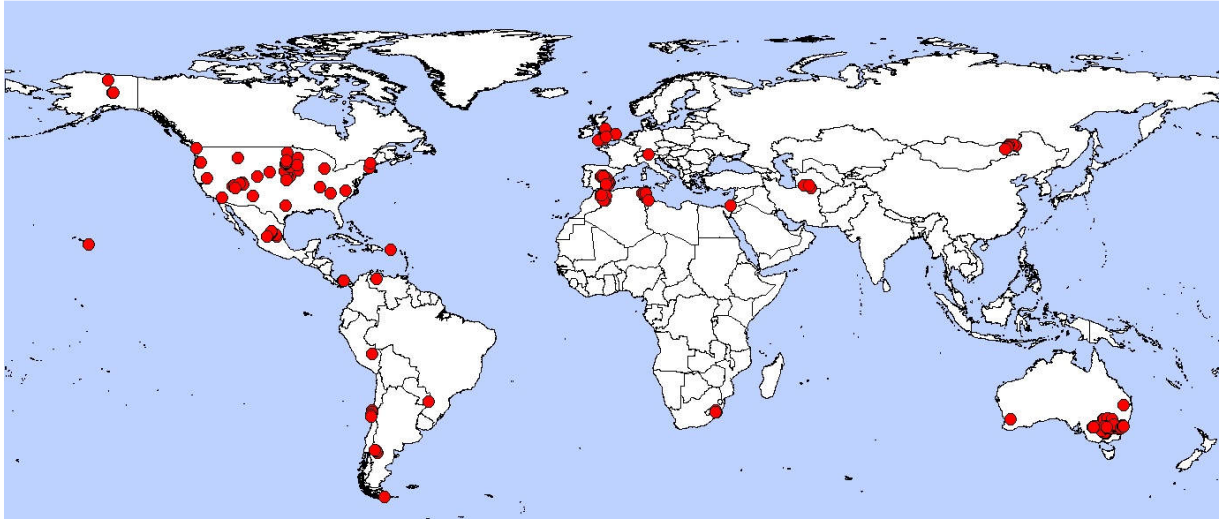
(2) Secondly, we calculated the Mahalanobis distance⁶⁰⁻⁶¹ of all locations to the center of the observed distribution given by the 235 locations (based on seven environmental factors, Supplementary Fig. 8B). This distance is useful to detect outliers in point cloud distributions that are assumed to follow a multivariate Normal distribution⁶⁰⁻⁶¹. When each of the variables is normally distributed, the Mahalanobis distance follows a Chi-squared distribution with d degrees of freedom, where d is the dimension of the multidimensional space ($d =$ seven environmental factors; see above)⁶⁰⁻⁶¹. Supplementary Fig. 8B uses a color gradient to indicate the quantile of the Chi squared distribution with seven degrees of freedom that each xy coordinate belongs to⁶².

Based on these two indicators, we observe that our model is reliable for 72.5% (40.2% with high reliability and 32.3% with moderate reliability) of the considered regions of Earth. Thus, our model is especially reliable for Mediterranean and temperate forests, grasslands, arid ecosystems, and many tropical regions. However, our model is less reliable for Tundra and Boreal forests, as

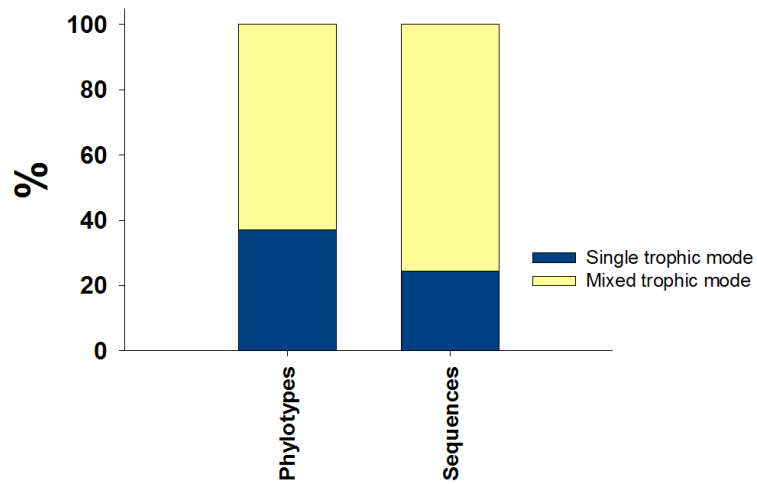
well as in the Southeast Asian ecosystems, and therefore, predictions for these regions need to be considered carefully.

Supplementary Appendix 2. Global maps cross-validation.

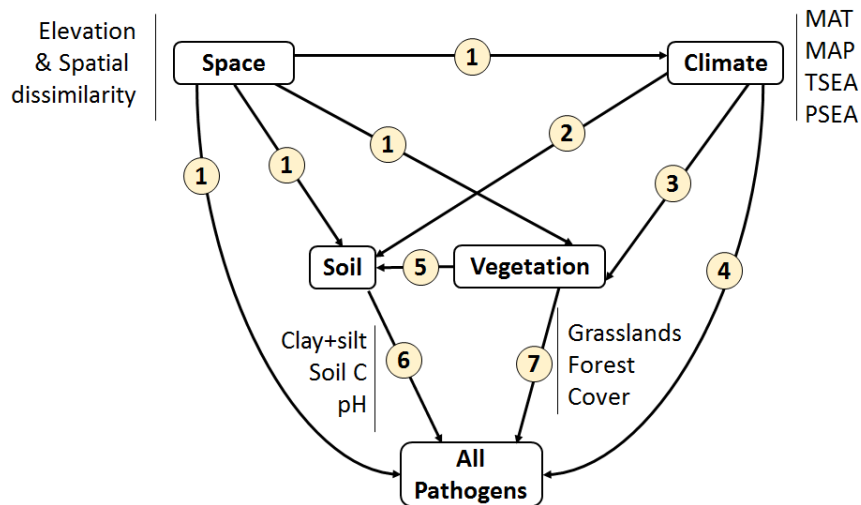
We used data from an independent global survey including 365 soil samples across the globe (Supplementary Fig. 11) to further validate our main map for the distributions of potential plant pathogens⁹. This survey includes soils from contrasting vegetation and climates from six continents and 39 countries. Note that any comparisons between this independent dataset and our dataset need to be considered carefully given methodological differences in the primer sets used (here FITS7/ITS4 vs. ITS3/ITS4⁹). However, soils are comparable in terms of sampling design and soil depth. We obtained information on the relative abundance of potential plant pathogens which was directly available from ref.⁹. We then used the map in Fig. 4A to predict the distribution of the relative abundance of pathogens in ref.⁹ and found positive and significant correlations between information based on our maps and that from that study (Spearman $\rho = 0.41$, $P < 0.001$, $n = 365$). In addition, the relative abundance of pathogens in ref.⁹ was also positively associated with mean annual temperature (Spearman $\rho = 0.50$, $P < 0.001$, $n = 365$), further supporting our results. Finally, we also found a positive and significant association between the relative abundance of the two most dominant pathogens in our database with that in ref.⁹: *Alternaria* ($\rho = 0.25$, $P < 0.001$, $n = 365$) and *Fusarium* ($\rho = 0.38$, $P < 0.001$, $n = 365$). These results are compelling given the fact that our data and those from ref.⁹ were independently generated using different methods. Therefore, these results provide further support for the validity of our global maps as representations of the distribution of the relative abundance of potential plant pathogens across the globe.



Supplementary Figure 1 | Global survey including the 235 locations used in this study.

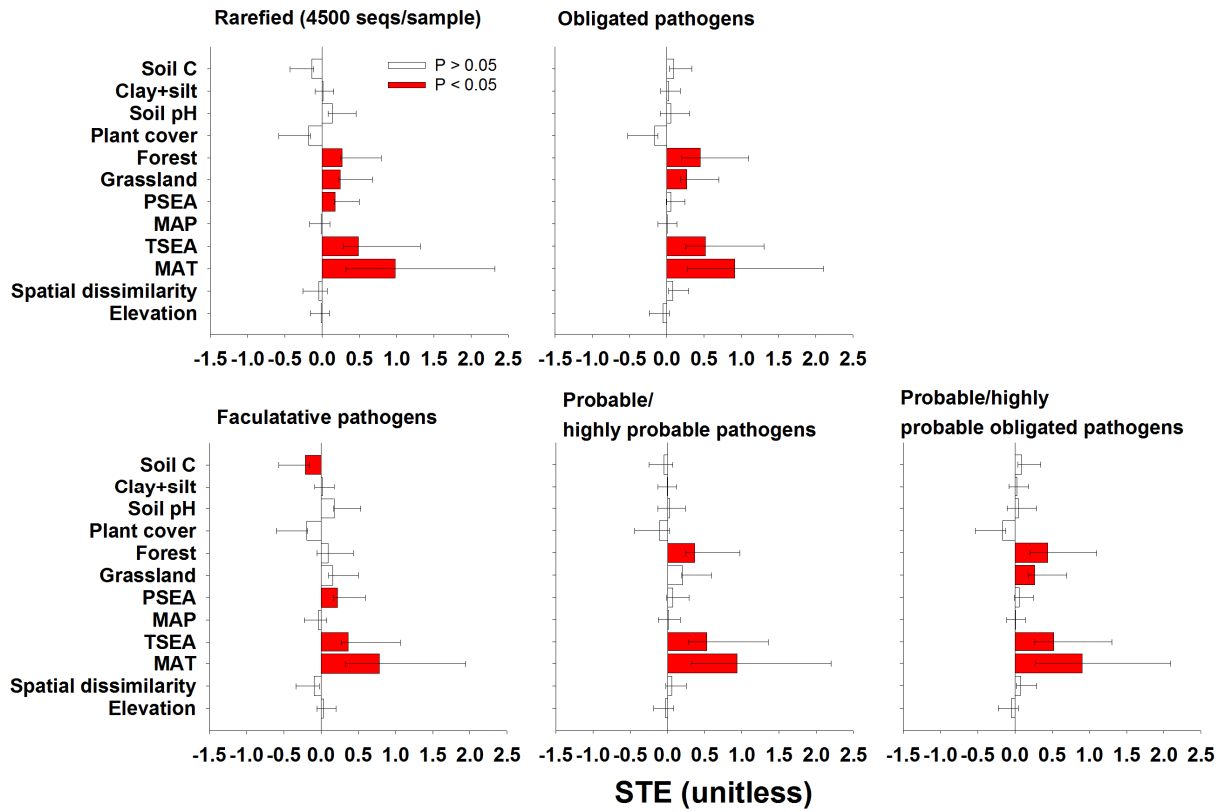


Supplementary Figure 2 | Main pathogenic trophic modes identified across our global survey. A complete list of all the taxa found in our survey can be found in Supplementary Data 1. Single trophic mode = plant pathogens only. Mixed trophic mode includes phylotypes classified as plant pathogen and endophyte and/or saprotrophic fungi.

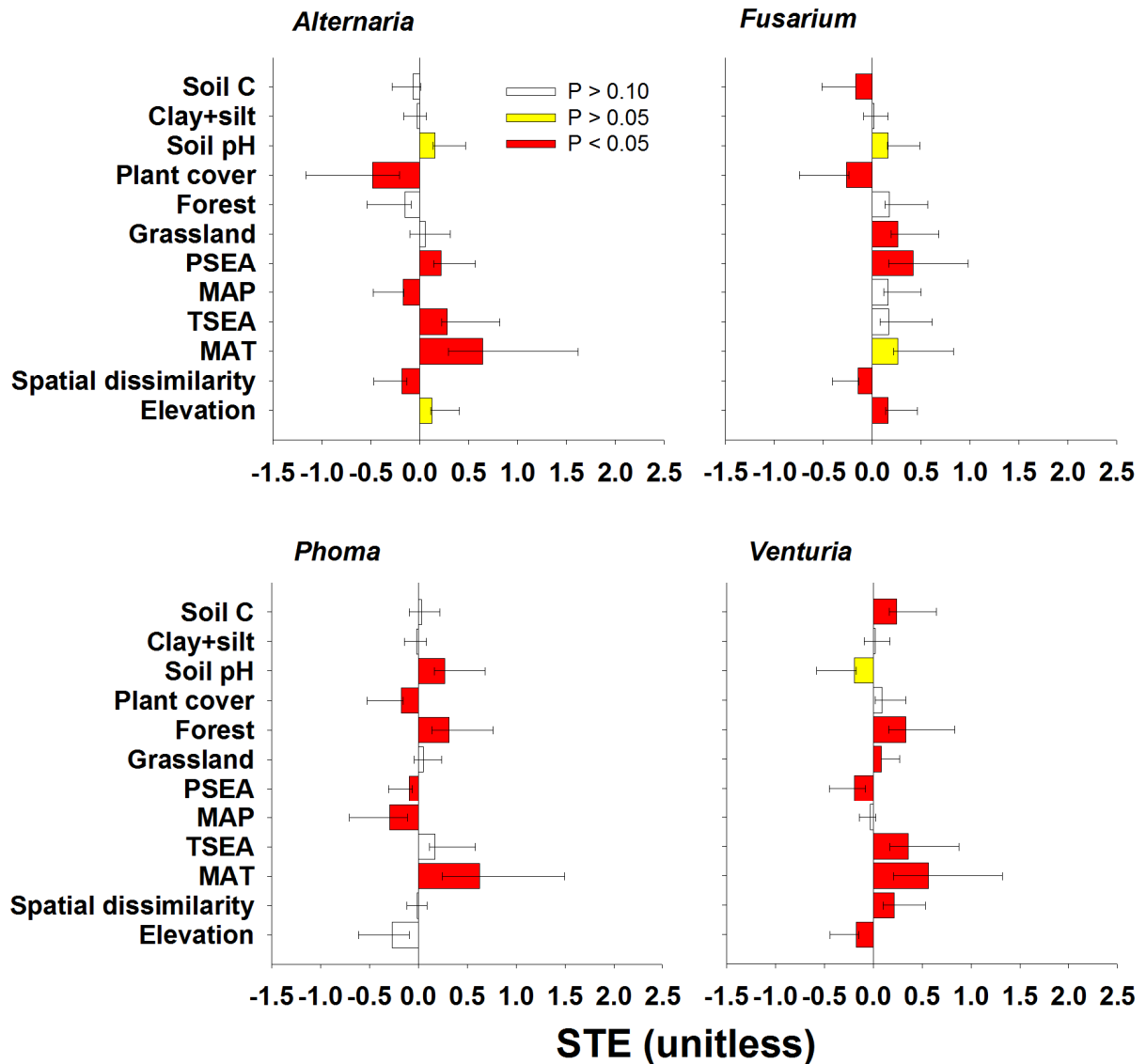


#	Rationale	References
1	Geographical location and altitude are well-known to affect climate, vegetation, soil properties and microbial communities at the global scale.	63-64
2	Climate regulates important soil properties such as pH and texture. For example, wetter locations are expected to have lower pH and higher amount of clay+silt and soil C, because of the higher levels of weathering and organic matter accumulations compared with drier environments.	65-66
3	Climate controls the cover of plants and the type of vegetation in each location. Wetter locations often have higher plant cover and develop forests compared with drier ecosystems.	67-68
4	Climate is also known to regulate the diversity and community composition of soil microbial communities. Precipitation is known to be related with the richness and relative abundance of dominant taxa in soils across the globe. Moreover, temperature is expected to promote the relative abundance of fast-growing opportunistic pathogens.	15, 28, 64, 69
5	Vegetation can influence important soil properties such as pH, soil texture and C. Forests often have lower pH and higher levels of C than grasslands. Moreover, plant cover can influence the capture of small soil particles, reduce the pH of soil via weathering, and increase the amount of soil C via litter inputs.	13, 70-71
6	Soil properties regulate the diversity and community composition of soil fungi.	13, 72-73
7	Vegetation type can influence the relative abundance of soil-born plant pathogens by selecting soil-borne pathogens associated with particular environments.	74-75

Supplementary Figure 3 | *A priori* model showing the rationale behind the direct and indirect effects from climate, vegetation and soil properties on the relative abundance of soil-borne fungal plant pathogens. We grouped the different categories of predictors (climate, soil properties, plants and spatial influence) in the same box in the model for graphical simplicity; these boxes do not represent latent variables. The acronyms for climatic and soil variables are defined in Supplementary Table 1. See Supplementary Fig. 12 for a detailed version of our *a priori* model.



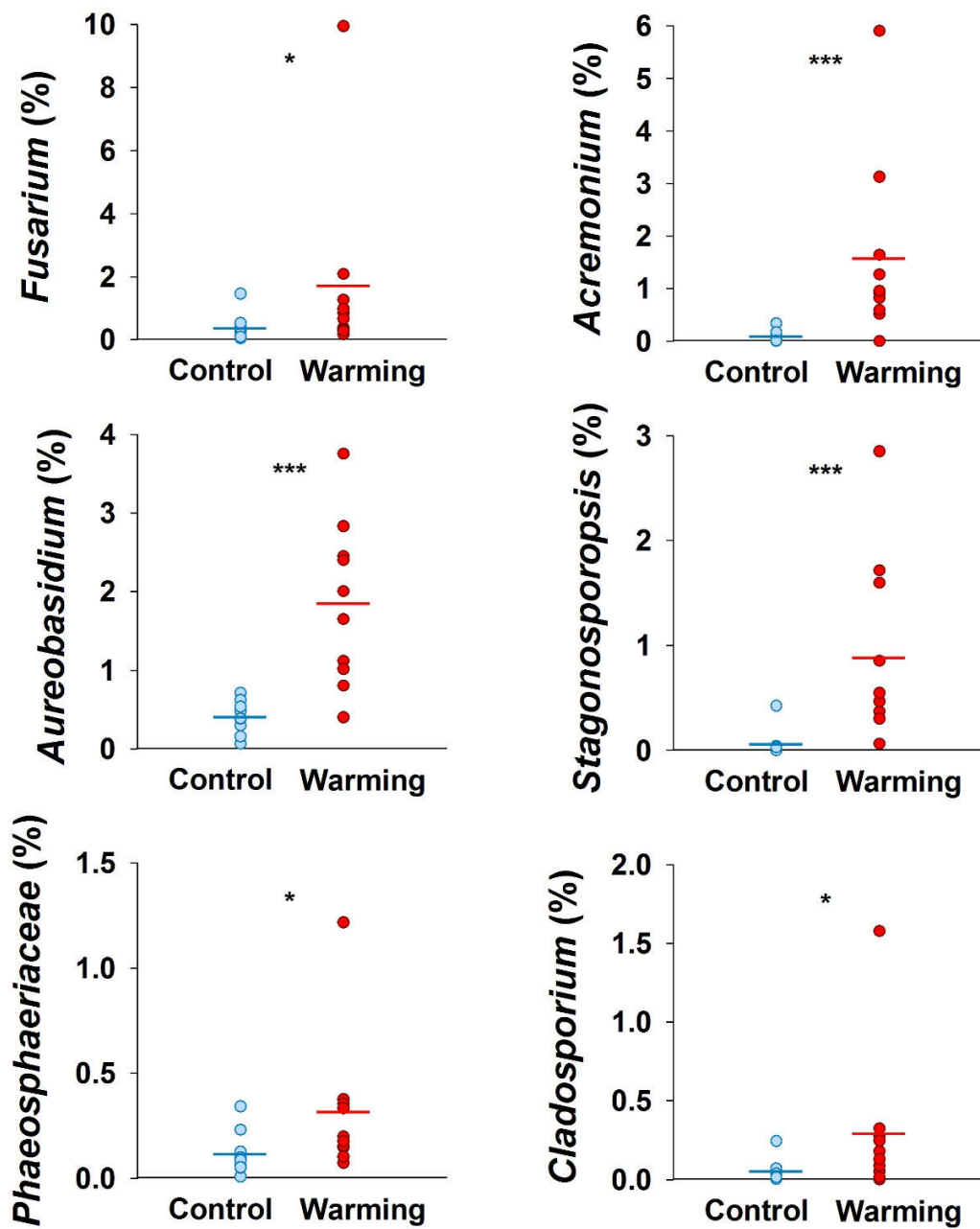
Supplementary Figure 4 | Standardized total effect (STE; \pm bootstrap CI 95%) based on structural equation models showed in Supplementary Tables 3-8. The acronyms for climatic and soil variables are defined in Supplementary Table 1.



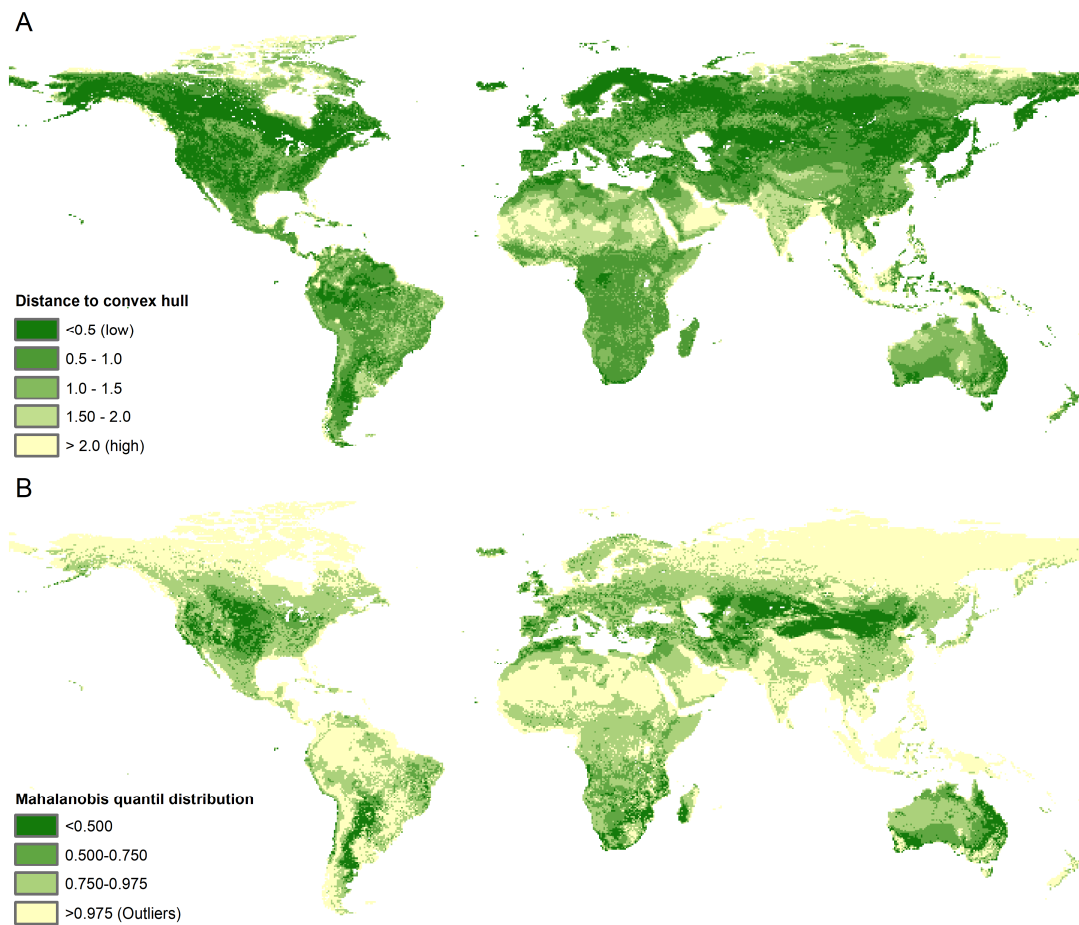
Supplementary Figure 5 | Standardized total effect (STE; \pm bootstrap CI 95%) based on structural equation models for the most abundant pathogen genera (*Alternaria*, *Fusarium*, *Venturia*, and *Phoma*; Fig. 1C). The acronyms for climatic and soil variables are defined in Supplementary Table 1.



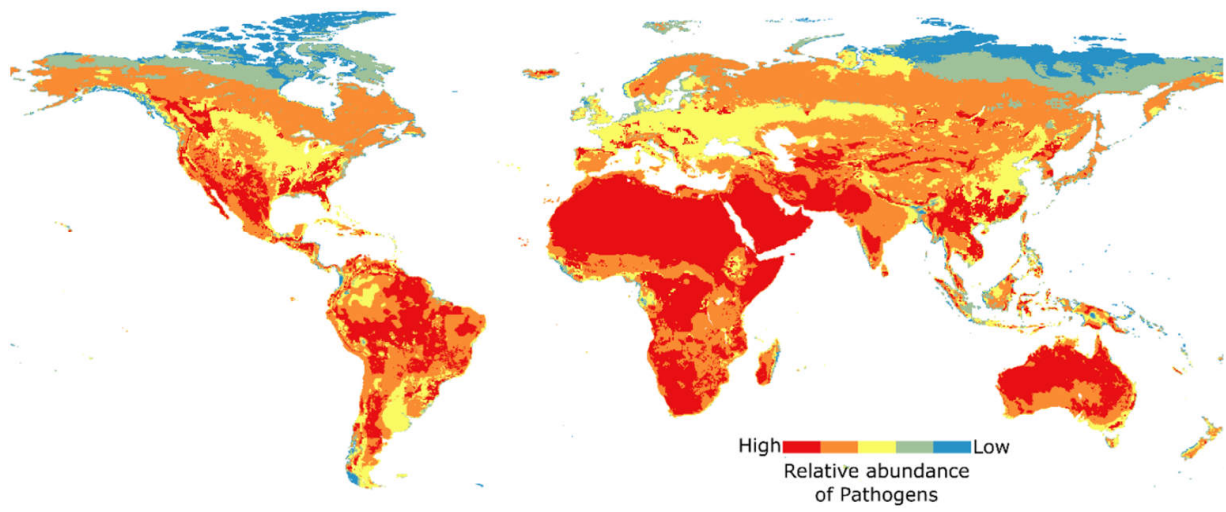
Supplementary Figure 6 | View of an experimental plot of the warming treatment in the field experiment.



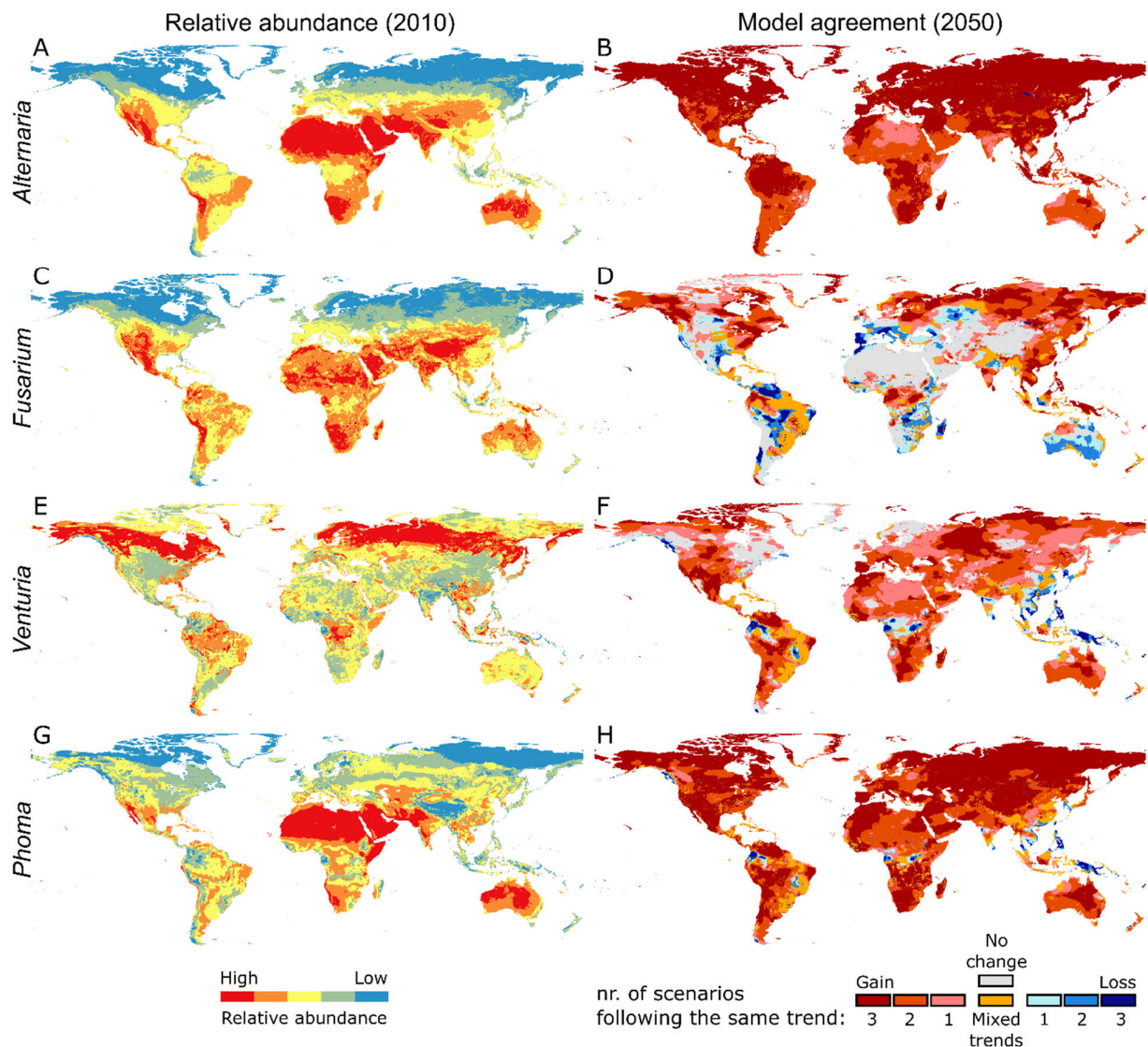
Supplementary Figure 7 | Experimental warming increases the relative abundance of potential plant pathogens. Warming effects on the relative abundance of potential plant pathogens in a nine-year field experiment. The solid lines show the mean values (n = 10). P values as follows: ***P < 0.001; *P < 0.05. The solid lines show the mean values. See Supplementary Table 9 for further statistical details.



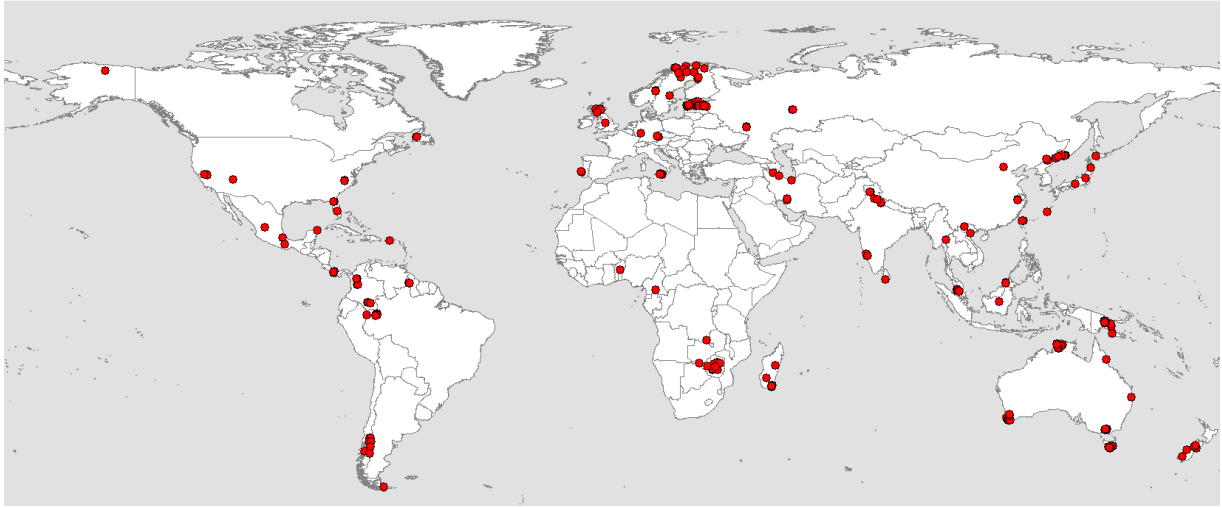
Supplementary Figure 8 | Extrapolation uncertainties for our global survey. Panel (A) includes the distance to the convex hull determined by the original 235 locations. The closer a prediction to the convex hull, the more reliable this prediction is. Panel (B) includes the Chi-squared distribution with seven degrees of freedom calculated based on the Mahalanobis multidimensional distance. See Supplementary Appendix 1 for further details.



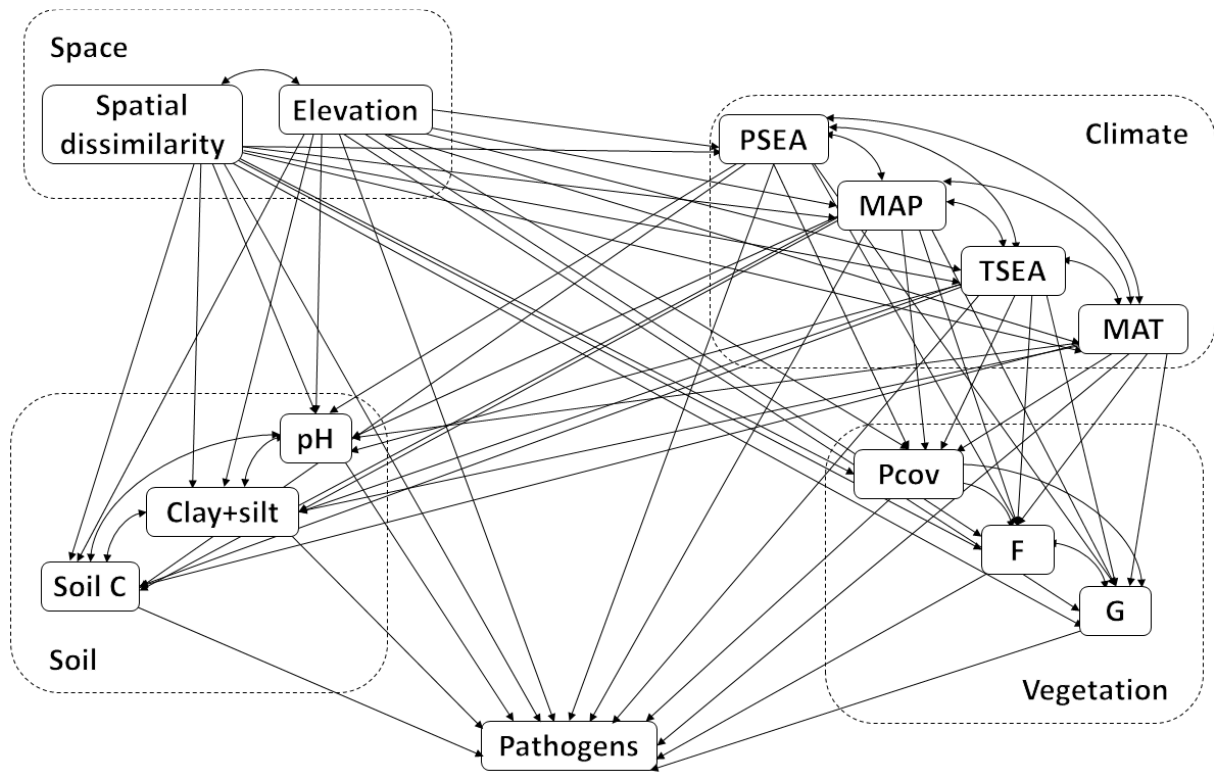
Supplementary Figure 9 | Current relative abundance of potential plant pathogens with single trophic mode (plant pathogens only) across the globe.



Supplementary Figure 10 | Spatial and temporal projections of main genera of fungal soil-borne pathogens. The left column includes the current relative abundance of these pathogens across the globe. The right column includes information on the agreement across the different scenarios considered (mixed reflects areas where different scenarios predict either gain or loss). SSP1 (sustainability), SSP4 (Regional inequality), and SSP5 (Fossil-fueled development). Correlations between observed and predicted values are as follows: *Alternaria* ($P_{Alternaria}$): $R^2=0.27$, $P<0.001$; iii) *Fusarium* ($P_{Fusarium}$): $R^2=0.18$, $P<0.001$; iv) *Phoma* (P_{Phoma}): $R^2=0.37$, $P<0.001$; and vi) *Venturia* ($P_{Venturia}$): $R^2=0.26$, $P<0.05$.



Supplementary Figure 11 | Locations of the global survey in ref.⁹



Supplementary Figure 12 | Detailed version of our *a priori* SEM. Pcov = Plant cover. F = Forests. G = Grasslands.

Supplementary Table 1 | Environmental factors included in our structural equation model.

Group of variables	Label	Variable	Units	Transformation
Pathogens	Pathogens	Relative abundance of potential pathogens	%	log10
Space	Elevation	Elevation	m	
	Spatial dissimilarity	Cross-sites averaged distance dissimilarity (Euclidean distance) based on latitude and longitude (sine and cosine)	Unitless	
Climate	MAT	Mean annual temperature	°C	
	MAP	Mean annual precipitation	mm	
	TSEA	Temperature Seasonality (standard deviation *100)	Unitless	
	PSEA	Precipitation Seasonality (Coefficient of Variation)	%	
Vegetation	Forest (F)	Location supporting forest ecosystems	0/1	
	Grassland (G)	Location supporting grassland ecosystems	0/1	
	Plant cover	Plant cover (vegetation cover)	% * 100	log10
Soil	Clay+silt	Fine texture	%	
	pH	pH	Unitless	log10
	Soil C	Soil carbon	%	log10

Supplementary Table 2 | Details on the structural equation model based on the relative abundance (%) of potential plant pathogens. See Supplementary Table 1 for variable acronyms. Goodness of fit as follows: $\chi^2=0.102$, $P = 0.750$, $df = 1$; Bootstrap $P = 0.647$; RMSEA = 0.00, $P = 0.811$. S.E. = Standard Error.

Parameter			Standardized direct effect	Bootstrap 95% CI Lower bound	Bootstrap 95% CI Upper bound	Bootstrap P-value	Unstandardized direct effect	S.E.
PSEA	←	Spatial dissimilarity	-0.150	-0.263	-0.044	0.018	-0.751	0.338
MAP	←	Spatial dissimilarity	-0.226	-0.313	-0.130	0.001	-22.599	6.966
MAT	←	Spatial dissimilarity	-0.572	-0.668	-0.468	<0.001	-0.656	0.063
TSEA	←	Spatial dissimilarity	0.032	-0.140	0.220	0.726	18.045	40.025
PSEA	←	Elevation	0.221	0.123	0.326	<0.001	0.009	0.003
MAP	←	Elevation	-0.121	-0.216	-0.015	0.063	-0.099	0.057
MAT	←	Elevation	-0.601	-0.684	-0.511	<0.001	-0.006	0.001
TSEA	←	Elevation	0.127	0.017	0.233	0.059	0.589	0.327
Plant cover	←	PSEA	-0.316	-0.405	-0.217	<0.001	-0.004	<0.001
Plant cover	←	MAP	0.605	0.518	0.699	<0.001	<0.001	<0.001
Plant cover	←	MAT	-0.633	-0.812	-0.454	<0.001	-0.031	0.005
Plant cover	←	TSEA	-0.249	-0.411	-0.113	0.002	<0.001	<0.001
Forest	←	PSEA	-0.410	-0.490	-0.329	<0.001	-0.008	0.001
Grassland	←	PSEA	0.211	0.099	0.342	0.001	0.004	0.001
Forest	←	MAP	0.251	0.144	0.356	<0.001	<0.001	<0.001
Grassland	←	MAP	0.014	-0.113	0.136	0.832	<0.001	<0.001
Forest	←	MAT	0.825	0.572	1.049	<0.001	0.070	0.010
Grassland	←	MAT	-0.909	-1.175	-0.616	<0.001	-0.073	0.011
Grassland	←	TSEA	-0.305	-0.543	-0.079	0.023	<0.001	<0.001
Forest	←	TSEA	0.484	0.277	0.683	<0.001	<0.001	<0.001
Plant cover	←	Spatial dissimilarity	-0.111	-0.252	0.032	0.203	-0.006	0.004
Forest	←	Spatial dissimilarity	0.718	0.546	0.879	<0.001	0.070	0.008
Grassland	←	Spatial dissimilarity	-0.643	-0.851	-0.433	<0.001	-0.059	0.009
Plant cover	←	Elevation	-0.396	-0.518	-0.259	<0.001	<0.001	<0.001
Forest	←	Elevation	0.318	0.151	0.492	0.002	<0.001	<0.001
Grassland	←	Elevation	-0.520	-0.732	-0.299	<0.001	<0.001	<0.001
Soil pH	←	PSEA	-0.125	-0.209	-0.042	0.014	<0.001	<0.001
Soil C	←	PSEA	0.042	-0.059	0.150	0.510	<0.001	0.001
Soil pH	←	MAP	-0.457	-0.562	-0.350	<0.001	<0.001	<0.001
Soil C	←	MAP	-0.126	-0.258	0.006	0.119	<0.001	<0.001
Soil pH	←	Plant cover	-0.206	-0.302	-0.113	<0.001	-0.061	0.021
Clay+silt	←	Plant cover	0.433	0.272	0.574	<0.001	31.739	7.105
Soil C	←	Plant cover	0.531	0.385	0.663	<0.001	0.481	0.077

Soil pH	←	MAT	0.329	0.090	0.559	0.023	0.005	0.002
Soil pH	←	Forest	-0.232	-0.357	-0.116	0.002	-0.039	0.013
Clay+silt	←	Forest	-0.263	-0.422	-0.108	0.005	-11.001	4.337
Soil C	←	Forest	0.368	0.196	0.538	<0.001	0.190	0.046
Soil pH	←	Grassland	-0.050	-0.131	0.034	0.315	-0.009	0.012
Clay+silt	←	Grassland	0.086	-0.061	0.225	0.338	3.779	4.217
Soil C	←	Grassland	0.121	0.011	0.258	0.072	0.066	0.042
Soil C	←	MAT	-0.431	-0.750	-0.127	0.019	-0.019	0.006
Soil pH	←	Spatial dissimilarity	-0.232	-0.405	-0.074	0.014	-0.004	0.001
Clay+silt	←	Spatial dissimilarity	0.403	0.221	0.597	0.001	1.639	0.521
Soil C	←	TSEA	-0.379	-0.569	-0.209	0.001	<0.001	<0.001
Soil C	←	Spatial dissimilarity	-0.172	-0.422	0.079	0.256	-0.009	0.005
Soil pH	←	Elevation	0.007	-0.134	0.145	0.912	<0.001	<0.001
Clay+silt	←	Elevation	0.174	0.018	0.344	0.069	0.006	0.004
Soil C	←	Elevation	-0.034	-0.231	0.157	0.762	<0.001	<0.001
Clay+silt	←	MAP	-0.036	-0.180	0.097	0.651	-0.001	0.004
Clay+silt	←	MAT	0.609	0.333	0.901	<0.001	2.160	0.639
Clay+silt	←	TSEA	0.287	0.081	0.497	0.026	0.002	0.001
Soil pH	←	TSEA	0.134	<0.001	0.264	0.102	<0.001	<0.001
Pathogens	←	Clay+silt	0.014	-0.090	0.117	0.806	<0.001	0.001
Pathogens	←	Soil C	-0.144	-0.270	-0.007	0.085	-0.168	0.090
Pathogens	←	Soil pH	0.128	-0.033	0.280	0.193	0.463	0.329
Pathogens	←	PSEA	0.194	0.037	0.353	0.046	0.002	0.001
Pathogens	←	MAP	0.076	-0.104	0.253	0.496	<0.001	<0.001
Pathogens	←	MAT	0.749	0.360	1.150	0.002	0.038	0.009
Pathogens	←	Plant cover	-0.089	-0.291	0.113	0.457	-0.095	0.120
Pathogens	←	Forest	0.339	0.126	0.553	0.010	0.205	0.068
Pathogens	←	Spatial dissimilarity	0.477	0.212	0.743	0.004	0.028	0.008
Pathogens	←	TSEA	0.318	0.019	0.648	0.077	<0.001	<0.001
Pathogens	←	Grassland	0.248	0.064	0.413	0.028	0.158	0.059
Pathogens	←	Elevation	0.433	0.183	0.690	0.002	<0.001	<0.001
Spatial dissimilarity	↔	Elevation	-0.399	-0.473	-0.323	<0.001	-1288.931	227.442
PSEA	↔	MAP	-0.079	-0.177	0.030	0.238	-971.903	804.138
PSEA	↔	MAT	-0.269	-0.411	-0.115	0.006	-29.672	7.462
PSEA	↔	TSEA	0.271	0.079	0.443	0.026	19101.553	4772.195
MAP	↔	MAT	0.061	-0.073	0.180	0.424	137.625	148.566
MAP	↔	TSEA	-0.316	-0.412	-0.198	<0.001	-458145.777	99411.424
MAT	↔	TSEA	-0.830	-0.867	-0.782	<0.001	-10811.730	1107.043
Plant cover	↔	Forest	0.055	-0.068	0.168	0.460	0.003	0.004
Plant cover	↔	Grassland	0.090	-0.062	0.226	0.337	0.006	0.004
Forest	↔	Grassland	-0.635	-0.705	-0.562	<0.001	-0.086	0.010
Soil C	↔	Clay+silt	0.024	-0.083	0.138	0.673	0.088	0.236
Soil C	↔	Soil pH	0.061	-0.077	0.193	0.498	0.001	0.001
Soil pH	↔	Clay+silt	0.126	0.006	0.246	0.085	0.126	0.066

Supplementary Table 3 | Details on the structural equation model based on the relative abundance (%) of all ITS sequences classified as potential plant pathogens on a rarefied OTU table (4500 sequences per sample). See Supplementary Table 1 for variable acronyms. Goodness of fit as follows: $\chi^2=0.102$, $P = 0.750$, $df = 1$; Bootstrap $P = 0.647$; RMSEA = 0.00, $P = 0.811$. S.E. = Standard Error.

Parameter			Standardized direct effect	Bootstrap 95% CI Lower bound	Bootstrap 95% CI Upper bound	Bootstrap P-value	Unstandardized direct effect	S.E.
PSEA	←	Spatial dissimilarity	-0.150	-0.263	-0.044	0.018	-0.751	0.338
MAP	←	Spatial dissimilarity	-0.226	-0.313	-0.130	0.001	-22.599	6.966
MAT	←	Spatial dissimilarity	-0.572	-0.668	-0.468	<0.001	-0.656	0.063
TSEA	←	Spatial dissimilarity	0.032	-0.140	0.220	0.726	18.045	40.025
PSEA	←	Elevation	0.221	0.123	0.326	<0.001	0.009	0.003
MAP	←	Elevation	-0.121	-0.216	-0.015	0.063	-0.099	0.057
MAT	←	Elevation	-0.601	-0.684	-0.511	<0.001	-0.006	0.001
TSEA	←	Elevation	0.127	0.017	0.233	0.059	0.589	0.327
Plant cover	←	PSEA	-0.316	-0.405	-0.217	<0.001	-0.004	<0.001
Plant cover	←	MAP	0.605	0.518	0.699	<0.001	<0.001	<0.001
Plant cover	←	MAT	-0.633	-0.812	-0.454	<0.001	-0.031	0.005
Plant cover	←	TSEA	-0.249	-0.411	-0.113	0.002	<0.001	<0.001
Forest	←	PSEA	-0.410	-0.490	-0.329	<0.001	-0.008	0.001
Grassland	←	PSEA	0.211	0.099	0.342	0.001	0.004	0.001
Forest	←	MAP	0.251	0.144	0.356	<0.001	<0.001	<0.001
Grassland	←	MAP	0.014	-0.113	0.136	0.832	<0.001	<0.001
Forest	←	MAT	0.825	0.572	1.049	<0.001	0.070	0.010
Grassland	←	MAT	-0.909	-1.175	-0.616	<0.001	-0.073	0.011
Grassland	←	TSEA	-0.305	-0.543	-0.079	0.023	<0.001	<0.001
Forest	←	TSEA	0.484	0.277	0.683	<0.001	<0.001	<0.001
Plant cover	←	Spatial dissimilarity	-0.111	-0.252	0.032	0.203	-0.006	0.004
Forest	←	Spatial dissimilarity	0.718	0.546	0.879	<0.001	0.070	0.008
Grassland	←	Spatial dissimilarity	-0.643	-0.851	-0.433	<0.001	-0.059	0.009
Plant cover	←	Elevation	-0.396	-0.518	-0.259	<0.001	<0.001	<0.001
Forest	←	Elevation	0.318	0.151	0.492	0.002	<0.001	<0.001
Grassland	←	Elevation	-0.520	-0.732	-0.299	<0.001	<0.001	<0.001
Soil pH	←	PSEA	-0.125	-0.209	-0.042	0.014	<0.001	<0.001
Soil C	←	PSEA	0.042	-0.059	0.150	0.510	<0.001	0.001
Soil pH	←	MAP	-0.457	-0.562	-0.350	<0.001	<0.001	<0.001
Soil C	←	MAP	-0.126	-0.258	0.006	0.119	<0.001	<0.001
Soil pH	←	Plant cover	-0.206	-0.302	-0.113	<0.001	-0.061	0.021

Clay+silt	←	Plant cover	0.433	0.272	0.574	<0.001	31.739	7.105
Soil C	←	Plant cover	0.531	0.385	0.663	<0.001	0.481	0.077
Soil pH	←	MAT	0.329	0.090	0.559	0.023	0.005	0.002
Soil pH	←	Forest	-0.232	-0.357	-0.116	0.002	-0.039	0.013
Clay+silt	←	Forest	-0.263	-0.422	-0.108	0.005	-11.001	4.337
Soil C	←	Forest	0.368	0.196	0.538	<0.001	0.190	0.046
Soil pH	←	Grassland	-0.050	-0.131	0.034	0.315	-0.009	0.012
Clay+silt	←	Grassland	0.086	-0.061	0.225	0.338	3.779	4.217
Soil C	←	Grassland	0.121	0.011	0.258	0.072	0.066	0.042
Soil C	←	MAT	-0.431	-0.750	-0.127	0.019	-0.019	0.006
Soil pH	←	Spatial dissimilarity	-0.232	-0.405	-0.074	0.014	-0.004	0.001
Clay+silt	←	Spatial dissimilarity	0.403	0.221	0.597	0.001	1.639	0.521
Soil C	←	TSEA	-0.379	-0.569	-0.209	0.001	<0.001	<0.001
Soil C	←	Spatial dissimilarity	-0.172	-0.422	0.079	0.256	-0.009	0.005
Soil pH	←	Elevation	0.007	-0.134	0.145	0.912	<0.001	<0.001
Clay+silt	←	Elevation	0.174	0.018	0.344	0.069	0.006	0.004
Soil C	←	Elevation	-0.034	-0.231	0.157	0.762	<0.001	<0.001
Clay+silt	←	MAP	-0.036	-0.180	0.097	0.651	-0.001	0.004
Clay+silt	←	MAT	0.609	0.333	0.901	<0.001	2.160	0.639
Clay+silt	←	TSEA	0.287	0.081	0.497	0.026	0.002	0.001
Soil pH	←	TSEA	0.134	<0.001	0.264	0.102	<0.001	<0.001
Pathogens	←	Clay+silt	0.015	-0.088	0.119	0.798	<0.001	0.001
Pathogens	←	Soil C	-0.140	-0.265	-0.001	0.097	-0.164	0.090
Pathogens	←	Soil pH	0.138	-0.027	0.291	0.164	0.499	0.330
Pathogens	←	PSEA	0.198	0.040	0.357	0.042	0.002	0.001
Pathogens	←	MAP	0.071	-0.109	0.248	0.527	<0.001	<0.001
Pathogens	←	MAT	0.742	0.352	1.141	0.002	0.038	0.009
Pathogens	←	Plant cover	-0.088	-0.291	0.116	0.463	-0.094	0.121
Pathogens	←	Forest	0.357	0.144	0.570	0.009	0.217	0.068
Pathogens	←	Spatial dissimilarity	0.461	0.197	0.720	0.004	0.027	0.008
Pathogens	←	TSEA	0.312	0.014	0.637	0.085	<0.001	<0.001
Pathogens	←	Grassland	0.262	0.079	0.429	0.021	0.168	0.059
Pathogens	←	Elevation	0.428	0.179	0.682	0.002	<0.001	<0.001
Spatial dissimilarity	↔	Elevation	-0.399	-0.473	-0.323	<0.001	-1288.931	227.442
PSEA	↔	MAP	-0.079	-0.177	0.030	0.238	-971.903	804.138
PSEA	↔	MAT	-0.269	-0.411	-0.115	0.006	-29.672	7.462
PSEA	↔	TSEA	0.271	0.079	0.443	0.026	19101.553	4772.195
MAP	↔	MAT	0.061	-0.073	0.180	0.424	137.625	148.566
MAP	↔	TSEA	-0.316	-0.412	-0.198	<0.001	-458145.777	99411.424
MAT	↔	TSEA	-0.830	-0.867	-0.782	<0.001	-10811.730	1107.043
Plant cover	↔	Forest	0.055	-0.068	0.168	0.460	0.003	0.004
Plant cover	↔	Grassland	0.090	-0.062	0.226	0.337	0.006	0.004
Forest	↔	Grassland	-0.635	-0.705	-0.562	<0.001	-0.086	0.010
Soil C	↔	Clay+silt	0.024	-0.083	0.138	0.673	0.088	0.236
Soil C	↔	Soil pH	0.061	-0.077	0.193	0.498	0.001	0.001
Soil pH	↔	Clay+silt	0.126	0.006	0.246	0.085	0.126	0.066

Supplementary Table 4 | Details on the structural equation model based on the relative abundance (%) of all ITS sequences classified as potential plant pathogens with single trophic mode (plant pathogens only). See Supplementary Table 1 for variable acronyms. Goodness of fit as follows: $\chi^2=0.102$, $P = 0.750$, $df = 1$; Bootstrap $P = 0.647$; RMSEA = 0.00, $P = 0.811$. S.E. = Standard Error.

Parameter			Standardized direct effect	Bootstrap 95% CI Lower bound	Bootstrap 95% CI Upper bound	Bootstrap P-value	Unstandardized direct effect	S.E.
PSEA	←	Spatial dissimilarity	-0.150	-0.263	-0.044	0.018	-0.751	0.338
MAP	←	Spatial dissimilarity	-0.226	-0.313	-0.130	0.001	-22.599	6.966
MAT	←	Spatial dissimilarity	-0.572	-0.668	-0.468	<0.001	-0.656	0.063
TSEA	←	Spatial dissimilarity	0.032	-0.140	0.220	0.726	18.045	40.025
PSEA	←	Elevation	0.221	0.123	0.326	<0.001	0.009	0.003
MAP	←	Elevation	-0.121	-0.216	-0.015	0.063	-0.099	0.057
MAT	←	Elevation	-0.601	-0.684	-0.511	<0.001	-0.006	0.001
TSEA	←	Elevation	0.127	0.017	0.233	0.059	0.589	0.327
Plant cover	←	PSEA	-0.316	-0.405	-0.217	<0.001	-0.004	<0.001
Plant cover	←	MAP	0.605	0.518	0.699	<0.001	<0.001	<0.001
Plant cover	←	MAT	-0.633	-0.812	-0.454	<0.001	-0.031	0.005
Plant cover	←	TSEA	-0.249	-0.411	-0.113	0.002	<0.001	<0.001
Forest	←	PSEA	-0.410	-0.490	-0.329	<0.001	-0.008	0.001
Grassland	←	PSEA	0.211	0.099	0.342	0.001	0.004	0.001
Forest	←	MAP	0.251	0.144	0.356	<0.001	<0.001	<0.001
Grassland	←	MAP	0.014	-0.113	0.136	0.832	<0.001	<0.001
Forest	←	MAT	0.825	0.572	1.049	<0.001	0.070	0.010
Grassland	←	MAT	-0.909	-1.175	-0.616	<0.001	-0.073	0.011
Grassland	←	TSEA	-0.305	-0.543	-0.079	0.023	<0.001	<0.001
Forest	←	TSEA	0.484	0.277	0.683	<0.001	<0.001	<0.001
Plant cover	←	Spatial dissimilarity	-0.111	-0.252	0.032	0.203	-0.006	0.004
Forest	←	Spatial dissimilarity	0.718	0.546	0.879	<0.001	0.070	0.008
Grassland	←	Spatial dissimilarity	-0.643	-0.851	-0.433	<0.001	-0.059	0.009
Plant cover	←	Elevation	-0.396	-0.518	-0.259	<0.001	<0.001	<0.001
Forest	←	Elevation	0.318	0.151	0.492	0.002	<0.001	<0.001
Grassland	←	Elevation	-0.520	-0.732	-0.299	<0.001	<0.001	<0.001
Soil pH	←	PSEA	-0.125	-0.209	-0.042	0.014	<0.001	<0.001
Soil C	←	PSEA	0.042	-0.059	0.150	0.510	<0.001	0.001
Soil pH	←	MAP	-0.457	-0.562	-0.350	<0.001	<0.001	<0.001
Soil C	←	MAP	-0.126	-0.258	0.006	0.119	<0.001	<0.001
Soil pH	←	Plant cover	-0.206	-0.302	-0.113	<0.001	-0.061	0.021

Clay+silt	←	Plant cover	0.433	0.272	0.574	<0.001	31.739	7.105
Soil C	←	Plant cover	0.531	0.385	0.663	<0.001	0.481	0.077
Soil pH	←	MAT	0.329	0.090	0.559	0.023	0.005	0.002
Soil pH	←	Forest	-0.232	-0.357	-0.116	0.002	-0.039	0.013
Clay+silt	←	Forest	-0.263	-0.422	-0.108	0.005	-11.001	4.337
Soil C	←	Forest	0.368	0.196	0.538	<0.001	0.190	0.046
Soil pH	←	Grassland	-0.050	-0.131	0.034	0.315	-0.009	0.012
Clay+silt	←	Grassland	0.086	-0.061	0.225	0.338	3.779	4.217
Soil C	←	Grassland	0.121	0.011	0.258	0.072	0.066	0.042
Soil C	←	MAT	-0.431	-0.750	-0.127	0.019	-0.019	0.006
Soil pH	←	Spatial dissimilarity	-0.232	-0.405	-0.074	0.014	-0.004	0.001
Clay+silt	←	Spatial dissimilarity	0.403	0.221	0.597	0.001	1.639	0.521
Soil C	←	TSEA	-0.379	-0.569	-0.209	0.001	<0.001	<0.001
Soil C	←	Spatial dissimilarity	-0.172	-0.422	0.079	0.256	-0.009	0.005
Soil pH	←	Elevation	0.007	-0.134	0.145	0.912	<0.001	<0.001
Clay+silt	←	Elevation	0.174	0.018	0.344	0.069	0.006	0.004
Soil C	←	Elevation	-0.034	-0.231	0.157	0.762	<0.001	<0.001
Clay+silt	←	MAP	-0.036	-0.180	0.097	0.651	-0.001	0.004
Clay+silt	←	MAT	0.609	0.333	0.901	<0.001	2.160	0.639
Clay+silt	←	TSEA	0.287	0.081	0.497	0.026	0.002	0.001
Soil pH	←	TSEA	0.134	<0.001	0.264	0.102	<0.001	<0.001
Pathogens	←	Clay+silt	0.022	-0.086	0.133	0.729	<0.001	0.001
Pathogens	←	Soil C	0.090	-0.031	0.221	0.221	0.097	0.084
Pathogens	←	Soil pH	0.052	-0.103	0.221	0.558	0.171	0.306
Pathogens	←	PSEA	0.137	0.018	0.259	0.059	0.001	0.001
Pathogens	←	MAP	0.021	-0.155	0.190	0.874	<0.001	<0.001
Pathogens	←	MAT	0.691	0.343	1.024	0.001	0.033	0.009
Pathogens	←	Plant cover	-0.208	-0.391	-0.012	0.081	-0.202	0.112
Pathogens	←	Forest	0.432	0.247	0.615	<0.001	0.240	0.063
Pathogens	←	Spatial dissimilarity	0.445	0.197	0.693	0.003	0.024	0.007
Pathogens	←	TSEA	0.366	0.113	0.616	0.017	<0.001	<0.001
Pathogens	←	Grassland	0.255	0.100	0.394	0.009	0.149	0.055
Pathogens	←	Elevation	0.351	0.145	0.561	0.004	<0.001	<0.001
Spatial dissimilarity	↔	Elevation	-0.399	-0.473	-0.323	<0.001	-1288.931	-1571.899
PSEA	↔	MAP	-0.079	-0.177	0.030	0.238	-971.903	-2261.742
PSEA	↔	MAT	-0.269	-0.411	-0.115	0.006	-29.672	-50.451
PSEA	↔	TSEA	0.271	0.079	0.443	0.026	19101.553	5584.204
MAP	↔	MAT	0.061	-0.073	0.180	0.424	137.625	-137.344
MAP	↔	TSEA	-0.316	-0.412	-0.198	<0.001	-458145.777	-
MAT	↔	TSEA	-0.830	-0.867	-0.782	<0.001	-10811.730	-13473.259
Plant cover	↔	Forest	0.055	-0.068	0.168	0.460	0.003	-0.003
Plant cover	↔	Grassland	0.090	-0.062	0.226	0.337	0.006	-0.003
Forest	↔	Grassland	-0.635	-0.705	-0.562	<0.001	-0.086	-0.106
Soil C	↔	Clay+silt	0.024	-0.083	0.138	0.673	0.088	-0.275
Soil C	↔	Soil pH	0.061	-0.077	0.193	0.498	0.001	-0.001
Soil pH	↔	Clay+silt	0.126	0.006	0.246	0.085	0.126	0.016

Supplementary Table 5 | Direct standardized effects from SEM on the relative abundance (%) of all ITS sequences classified as plant pathogens with a mixed trophic mode (plant pathogen and endophyte and/or saprotrophic fungi). See Supplementary Table 1 for variable acronyms. Goodness of fit as follows: $\chi^2=0.102$, $P = 0.750$, $df = 1$; Bootstrap $P = 0.647$; RMSEA = 0.00, $P = 0.811$. S.E. = Standard Error.

Parameter			Standardized direct effect	Bootstrap 95% CI Lower bound	Bootstrap 95% CI Upper bound	Bootstrap P-value	Unstandardized direct effect	S.E.
PSEA	←	Spatial dissimilarity	-0.150	-0.263	-0.044	0.018	-0.751	0.338
MAP	←	Spatial dissimilarity	-0.226	-0.313	-0.130	0.001	-22.599	6.966
MAT	←	Spatial dissimilarity	-0.572	-0.668	-0.468	<0.001	-0.656	0.063
TSEA	←	Spatial dissimilarity	0.032	-0.140	0.220	0.726	18.045	40.025
PSEA	←	Elevation	0.221	0.123	0.326	<0.001	0.009	0.003
MAP	←	Elevation	-0.121	-0.216	-0.015	0.063	-0.099	0.057
MAT	←	Elevation	-0.601	-0.684	-0.511	<0.001	-0.006	0.001
TSEA	←	Elevation	0.127	0.017	0.233	0.059	0.589	0.327
Plant cover	←	PSEA	-0.316	-0.405	-0.217	<0.001	-0.004	<0.001
Plant cover	←	MAP	0.605	0.518	0.699	<0.001	<0.001	<0.001
Plant cover	←	MAT	-0.633	-0.812	-0.454	<0.001	-0.031	0.005
Plant cover	←	TSEA	-0.249	-0.411	-0.113	0.002	<0.001	<0.001
Forest	←	PSEA	-0.410	-0.490	-0.329	<0.001	-0.008	0.001
Grassland	←	PSEA	0.211	0.099	0.342	0.001	0.004	0.001
Forest	←	MAP	0.251	0.144	0.356	<0.001	<0.001	<0.001
Grassland	←	MAP	0.014	-0.113	0.136	0.832	<0.001	<0.001
Forest	←	MAT	0.825	0.572	1.049	<0.001	0.070	0.010
Grassland	←	MAT	-0.909	-1.175	-0.616	<0.001	-0.073	0.011
Grassland	←	TSEA	-0.305	-0.543	-0.079	0.023	<0.001	<0.001
Forest	←	TSEA	0.484	0.277	0.683	<0.001	<0.001	<0.001
Plant cover	←	Spatial dissimilarity	-0.111	-0.252	0.032	0.203	-0.006	0.004
Forest	←	Spatial dissimilarity	0.718	0.546	0.879	<0.001	0.070	0.008
Grassland	←	Spatial dissimilarity	-0.643	-0.851	-0.433	<0.001	-0.059	0.009
Plant cover	←	Elevation	-0.396	-0.518	-0.259	<0.001	<0.001	<0.001
Forest	←	Elevation	0.318	0.151	0.492	0.002	<0.001	<0.001
Grassland	←	Elevation	-0.520	-0.732	-0.299	<0.001	<0.001	<0.001
Soil pH	←	PSEA	-0.125	-0.209	-0.042	0.014	<0.001	<0.001
Soil C	←	PSEA	0.042	-0.059	0.150	0.510	<0.001	0.001
Soil pH	←	MAP	-0.457	-0.562	-0.350	<0.001	<0.001	<0.001
Soil C	←	MAP	-0.126	-0.258	0.006	0.119	<0.001	<0.001
Soil pH	←	Plant cover	-0.206	-0.302	-0.113	<0.001	-0.061	0.021

Clay+silt	←	Plant cover	0.433	0.272	0.574	<0.001	31.739	7.105
Soil C	←	Plant cover	0.531	0.385	0.663	<0.001	0.481	0.077
Soil pH	←	MAT	0.329	0.090	0.559	0.023	0.005	0.002
Soil pH	←	Forest	-0.232	-0.357	-0.116	0.002	-0.039	0.013
Clay+silt	←	Forest	-0.263	-0.422	-0.108	0.005	-11.001	4.337
Soil C	←	Forest	0.368	0.196	0.538	<0.001	0.190	0.046
Soil pH	←	Grassland	-0.050	-0.131	0.034	0.315	-0.009	0.012
Clay+silt	←	Grassland	0.086	-0.061	0.225	0.338	3.779	4.217
Soil C	←	Grassland	0.121	0.011	0.258	0.072	0.066	0.042
Soil C	←	MAT	-0.431	-0.750	-0.127	0.019	-0.019	0.006
Soil pH	←	Spatial dissimilarity	-0.232	-0.405	-0.074	0.014	-0.004	0.001
Clay+silt	←	Spatial dissimilarity	0.403	0.221	0.597	0.001	1.639	0.521
Soil C	←	TSEA	-0.379	-0.569	-0.209	0.001	<0.001	<0.001
Soil C	←	Spatial dissimilarity	-0.172	-0.422	0.079	0.256	-0.009	0.005
Soil pH	←	Elevation	0.007	-0.134	0.145	0.912	<0.001	<0.001
Clay+silt	←	Elevation	0.174	0.018	0.344	0.069	0.006	0.004
Soil C	←	Elevation	-0.034	-0.231	0.157	0.762	<0.001	<0.001
Clay+silt	←	MAP	-0.036	-0.180	0.097	0.651	-0.001	0.004
Clay+silt	←	MAT	0.609	0.333	0.901	<0.001	2.160	0.639
Clay+silt	←	TSEA	0.287	0.081	0.497	0.026	0.002	0.001
Soil pH	←	TSEA	0.134	<0.001	0.264	0.102	<0.001	<0.001
Pathogens	←	Clay+silt	0.023	-0.087	0.132	0.720	<0.001	0.001
Pathogens	←	Soil C	-0.208	-0.335	-0.079	0.009	-0.260	0.098
Pathogens	←	Soil pH	0.180	0.021	0.326	0.064	0.695	0.358
Pathogens	←	PSEA	0.198	0.044	0.353	0.037	0.002	0.001
Pathogens	←	MAP	0.114	-0.082	0.320	0.348	<0.001	<0.001
Pathogens	←	MAT	0.565	0.196	0.944	0.011	0.031	0.010
Pathogens	←	Plant cover	-0.056	-0.257	0.155	0.652	-0.064	0.131
Pathogens	←	Forest	0.219	0.007	0.429	0.091	0.142	0.074
Pathogens	←	Spatial dissimilarity	0.379	0.127	0.616	0.012	0.024	0.008
Pathogens	←	TSEA	0.212	-0.065	0.530	0.213	<0.001	<0.001
Pathogens	←	Grassland	0.189	0.016	0.351	0.073	0.129	0.064
Pathogens	←	Elevation	0.370	0.134	0.612	0.007	<0.001	<0.001
Spatial dissimilarity	↔	Elevation	-0.399	-0.473	-0.323	<0.001	-1288.931	227.442
PSEA	↔	MAP	-0.079	-0.177	0.030	0.238	-971.903	804.138
PSEA	↔	MAT	-0.269	-0.411	-0.115	0.006	-29.672	7.462
PSEA	↔	TSEA	0.271	0.079	0.443	0.026	19101.553	4772.195
MAP	↔	MAT	0.061	-0.073	0.180	0.424	137.625	148.566
MAP	↔	TSEA	-0.316	-0.412	-0.198	<0.001	-458145.777	99411.424
MAT	↔	TSEA	-0.830	-0.867	-0.782	<0.001	-10811.730	1107.043
Plant cover	↔	Forest	0.055	-0.068	0.168	0.460	0.003	0.004
Plant cover	↔	Grassland	0.090	-0.062	0.226	0.337	0.006	0.004
Forest	↔	Grassland	-0.635	-0.705	-0.562	<0.001	-0.086	0.010
Soil C	↔	Clay+silt	0.024	-0.083	0.138	0.673	0.088	0.236
Soil C	↔	Soil pH	0.061	-0.077	0.193	0.498	0.001	0.001
Soil pH	↔	Clay+silt	0.126	0.006	0.246	0.085	0.126	0.066

Supplementary Table 6 | Details on the structural equation model based on the relative abundance (%) of all ITS sequences classified as probable and highly probable fungal plant pathogens (from both mixed and single trophic modes). See Supplementary Table 1 for variable acronyms. Confidence Ranking are based at the genus level or above as recommended by ref.6. Goodness of fit as follows: $\chi^2=0.102$, $P = 0.750$, $df = 1$; Bootstrap $P = 0.647$; RMSEA = 0.00, $P = 0.811$. S.E. = Standard Error.

Parameter			Standardized direct effect	Bootstrap 95% CI Lower bound	Bootstrap 95% CI Upper bound	Bootstrap P-value	Unstandardized direct effect	S.E.
PSEA	←	Spatial dissimilarity	-0.150	-0.263	-0.044	0.018	-0.751	0.338
MAP	←	Spatial dissimilarity	-0.226	-0.313	-0.130	0.001	-22.599	6.966
MAT	←	Spatial dissimilarity	-0.572	-0.668	-0.468	<0.001	-0.656	0.063
TSEA	←	Spatial dissimilarity	0.032	-0.140	0.220	0.726	18.045	40.025
PSEA	←	Elevation	0.221	0.123	0.326	<0.001	0.009	0.003
MAP	←	Elevation	-0.121	-0.216	-0.015	0.063	-0.099	0.057
MAT	←	Elevation	-0.601	-0.684	-0.511	<0.001	-0.006	0.001
TSEA	←	Elevation	0.127	0.017	0.233	0.059	0.589	0.327
Plant cover	←	PSEA	-0.316	-0.405	-0.217	<0.001	-0.004	<0.001
Plant cover	←	MAP	0.605	0.518	0.699	<0.001	<0.001	<0.001
Plant cover	←	MAT	-0.633	-0.812	-0.454	<0.001	-0.031	0.005
Plant cover	←	TSEA	-0.249	-0.411	-0.113	0.002	<0.001	<0.001
Forest	←	PSEA	-0.410	-0.490	-0.329	<0.001	-0.008	0.001
Grassland	←	PSEA	0.211	0.099	0.342	0.001	0.004	0.001
Forest	←	MAP	0.251	0.144	0.356	<0.001	<0.001	<0.001
Grassland	←	MAP	0.014	-0.113	0.136	0.832	<0.001	<0.001
Forest	←	MAT	0.825	0.572	1.049	<0.001	0.070	0.010
Grassland	←	MAT	-0.909	-1.175	-0.616	<0.001	-0.073	0.011
Grassland	←	TSEA	-0.305	-0.543	-0.079	0.023	<0.001	<0.001
Forest	←	TSEA	0.484	0.277	0.683	<0.001	<0.001	<0.001
Plant cover	←	Spatial dissimilarity	-0.111	-0.252	0.032	0.203	-0.006	0.004
Forest	←	Spatial dissimilarity	0.718	0.546	0.879	<0.001	0.070	0.008
Grassland	←	Spatial dissimilarity	-0.643	-0.851	-0.433	<0.001	-0.059	0.009
Plant cover	←	Elevation	-0.396	-0.518	-0.259	<0.001	<0.001	<0.001
Forest	←	Elevation	0.318	0.151	0.492	0.002	<0.001	<0.001
Grassland	←	Elevation	-0.520	-0.732	-0.299	<0.001	<0.001	<0.001
Soil pH	←	PSEA	-0.125	-0.209	-0.042	0.014	<0.001	<0.001
Soil C	←	PSEA	0.042	-0.059	0.150	0.510	<0.001	0.001
Soil pH	←	MAP	-0.457	-0.562	-0.350	<0.001	<0.001	<0.001
Soil C	←	MAP	-0.126	-0.258	0.006	0.119	<0.001	<0.001
Soil pH	←	Plant cover	-0.206	-0.302	-0.113	<0.001	-0.061	0.021

Clay+silt	←	Plant cover	0.433	0.272	0.574	<0.001	31.739	7.105
Soil C	←	Plant cover	0.531	0.385	0.663	<0.001	0.481	0.077
Soil pH	←	MAT	0.329	0.090	0.559	0.023	0.005	0.002
Soil pH	←	Forest	-0.232	-0.357	-0.116	0.002	-0.039	0.013
Clay+silt	←	Forest	-0.263	-0.422	-0.108	0.005	-11.001	4.337
Soil C	←	Forest	0.368	0.196	0.538	<0.001	0.190	0.046
Soil pH	←	Grassland	-0.050	-0.131	0.034	0.315	-0.009	0.012
Clay+silt	←	Grassland	0.086	-0.061	0.225	0.338	3.779	4.217
Soil C	←	Grassland	0.121	0.011	0.258	0.072	0.066	0.042
Soil C	←	MAT	-0.431	-0.750	-0.127	0.019	-0.019	0.006
Soil pH	←	Spatial dissimilarity	-0.232	-0.405	-0.074	0.014	-0.004	0.001
Clay+silt	←	Spatial dissimilarity	0.403	0.221	0.597	0.001	1.639	0.521
Soil C	←	TSEA	-0.379	-0.569	-0.209	0.001	<0.001	<0.001
Soil C	←	Spatial dissimilarity	-0.172	-0.422	0.079	0.256	-0.009	0.005
Soil pH	←	Elevation	0.007	-0.134	0.145	0.912	<0.001	<0.001
Clay+silt	←	Elevation	0.174	0.018	0.344	0.069	0.006	0.004
Soil C	←	Elevation	-0.034	-0.231	0.157	0.762	<0.001	<0.001
Clay+silt	←	MAP	-0.036	-0.180	0.097	0.651	-0.001	0.004
Clay+silt	←	MAT	0.609	0.333	0.901	<0.001	2.160	0.639
Clay+silt	←	TSEA	0.287	0.081	0.497	0.026	0.002	0.001
Soil pH	←	TSEA	0.134	<0.001	0.264	0.102	<0.001	<0.001
Pathogens	←	Clay+silt	-0.001	-0.105	0.103	0.978	<0.001	0.001
Pathogens	←	Soil C	-0.047	-0.175	0.095	0.600	-0.049	0.083
Pathogens	←	Soil pH	0.027	-0.128	0.185	0.756	0.087	0.301
Pathogens	←	PSEA	0.151	<0.001	0.300	0.100	0.002	0.001
Pathogens	←	MAP	-0.011	-0.199	0.178	0.910	<0.001	<0.001
Pathogens	←	MAT	0.723	0.341	1.091	0.001	0.033	0.009
Pathogens	←	Plant cover	-0.075	-0.292	0.155	0.613	-0.071	0.110
Pathogens	←	Forest	0.388	0.179	0.584	0.002	0.209	0.062
Pathogens	←	Spatial dissimilarity	0.445	0.182	0.720	0.005	0.023	0.007
Pathogens	←	TSEA	0.366	0.084	0.653	0.032	<0.001	<0.001
Pathogens	←	Grassland	0.209	0.033	0.365	0.056	0.118	0.054
Pathogens	←	Elevation	0.401	0.160	0.644	0.004	<0.001	<0.001
Spatial dissimilarity	↔	Elevation	-0.399	-0.473	-0.323	<0.001	-1288.931	227.442
PSEA	↔	MAP	-0.079	-0.177	0.030	0.238	-971.903	804.138
PSEA	↔	MAT	-0.269	-0.411	-0.115	0.006	-29.672	7.462
PSEA	↔	TSEA	0.271	0.079	0.443	0.026	19101.553	4772.195
MAP	↔	MAT	0.061	-0.073	0.180	0.424	137.625	148.566
MAP	↔	TSEA	-0.316	-0.412	-0.198	<0.001	-458145.777	99411.424
MAT	↔	TSEA	-0.830	-0.867	-0.782	<0.001	-10811.730	1107.043
Plant cover	↔	Forest	0.055	-0.068	0.168	0.460	0.003	0.004
Plant cover	↔	Grassland	0.090	-0.062	0.226	0.337	0.006	0.004
Forest	↔	Grassland	-0.635	-0.705	-0.562	<0.001	-0.086	0.010
Soil C	↔	Clay+silt	0.024	-0.083	0.138	0.673	0.088	0.236
Soil C	↔	Soil pH	0.061	-0.077	0.193	0.498	0.001	0.001
Soil pH	↔	Clay+silt	0.126	0.006	0.246	0.085	0.126	0.066

Supplementary Table 7 | Details on the structural equation model based on the relative abundance (%) of potential plant pathogens with single trophic mode (plant pathogen only) and classified as highly probable fungal plant pathogens. See Supplementary Table 1 for variable acronyms. Confidence Ranking are based at the genus level or above as recommended by ref.6. Goodness of fit as follows: $\chi^2=0.102$, $P = 0.750$, $df = 1$; Bootstrap $P = 0.647$; RMSEA = 0.00, $P = 0.811$. S.E. = Standard Error.

Parameter			Standardized direct effect	Bootstrap 95% CI Lower bound	Bootstrap 95% CI Upper bound	Bootstrap P-value	Unstandardized direct effect	S.E.
PSEA	←	Spatial dissimilarity	-0.150	-0.263	-0.044	0.018	-0.751	0.338
MAP	←	Spatial dissimilarity	-0.226	-0.313	-0.130	0.001	-22.599	6.966
MAT	←	Spatial dissimilarity	-0.572	-0.668	-0.468	<0.001	-0.656	0.063
TSEA	←	Spatial dissimilarity	0.032	-0.140	0.220	0.726	18.045	40.025
PSEA	←	Elevation	0.221	0.123	0.326	<0.001	0.009	0.003
MAP	←	Elevation	-0.121	-0.216	-0.015	0.063	-0.099	0.057
MAT	←	Elevation	-0.601	-0.684	-0.511	<0.001	-0.006	0.001
TSEA	←	Elevation	0.127	0.017	0.233	0.059	0.589	0.327
Plant cover	←	PSEA	-0.316	-0.405	-0.217	<0.001	-0.004	<0.001
Plant cover	←	MAP	0.605	0.518	0.699	<0.001	<0.001	<0.001
Plant cover	←	MAT	-0.633	-0.812	-0.454	<0.001	-0.031	0.005
Plant cover	←	TSEA	-0.249	-0.411	-0.113	0.002	<0.001	<0.001
Forest	←	PSEA	-0.410	-0.490	-0.329	<0.001	-0.008	0.001
Grassland	←	PSEA	0.211	0.099	0.342	0.001	0.004	0.001
Forest	←	MAP	0.251	0.144	0.356	<0.001	<0.001	<0.001
Grassland	←	MAP	0.014	-0.113	0.136	0.832	<0.001	<0.001
Forest	←	MAT	0.825	0.572	1.049	<0.001	0.070	0.010
Grassland	←	MAT	-0.909	-1.175	-0.616	<0.001	-0.073	0.011
Grassland	←	TSEA	-0.305	-0.543	-0.079	0.023	<0.001	<0.001
Forest	←	TSEA	0.484	0.277	0.683	<0.001	<0.001	<0.001
Plant cover	←	Spatial dissimilarity	-0.111	-0.252	0.032	0.203	-0.006	0.004
Forest	←	Spatial dissimilarity	0.718	0.546	0.879	<0.001	0.070	0.008
Grassland	←	Spatial dissimilarity	-0.643	-0.851	-0.433	<0.001	-0.059	0.009
Plant cover	←	Elevation	-0.396	-0.518	-0.259	<0.001	<0.001	<0.001
Forest	←	Elevation	0.318	0.151	0.492	0.002	<0.001	<0.001
Grassland	←	Elevation	-0.520	-0.732	-0.299	<0.001	<0.001	<0.001
Soil pH	←	PSEA	-0.125	-0.209	-0.042	0.014	<0.001	<0.001
Soil C	←	PSEA	0.042	-0.059	0.150	0.510	<0.001	0.001
Soil pH	←	MAP	-0.457	-0.562	-0.350	<0.001	<0.001	<0.001
Soil C	←	MAP	-0.126	-0.258	0.006	0.119	<0.001	<0.001
Soil pH	←	Plant cover	-0.206	-0.302	-0.113	<0.001	-0.061	0.021

Clay+silt	←	Plant cover	0.433	0.272	0.574	<0.001	31.739	7.105
Soil C	←	Plant cover	0.531	0.385	0.663	<0.001	0.481	0.077
Soil pH	←	MAT	0.329	0.090	0.559	0.023	0.005	0.002
Soil pH	←	Forest	-0.232	-0.357	-0.116	0.002	-0.039	0.013
Clay+silt	←	Forest	-0.263	-0.422	-0.108	0.005	-11.001	4.337
Soil C	←	Forest	0.368	0.196	0.538	<0.001	0.190	0.046
Soil pH	←	Grassland	-0.050	-0.131	0.034	0.315	-0.009	0.012
Clay+silt	←	Grassland	0.086	-0.061	0.225	0.338	3.779	4.217
Soil C	←	Grassland	0.121	0.011	0.258	0.072	0.066	0.042
Soil C	←	MAT	-0.431	-0.750	-0.127	0.019	-0.019	0.006
Soil pH	←	Spatial dissimilarity	-0.232	-0.405	-0.074	0.014	-0.004	0.001
Clay+silt	←	Spatial dissimilarity	0.403	0.221	0.597	0.001	1.639	0.521
Soil C	←	TSEA	-0.379	-0.569	-0.209	0.001	<0.001	<0.001
Soil C	←	Spatial dissimilarity	-0.172	-0.422	0.079	0.256	-0.009	0.005
Soil pH	←	Elevation	0.007	-0.134	0.145	0.912	<0.001	<0.001
Clay+silt	←	Elevation	0.174	0.018	0.344	0.069	0.006	0.004
Soil C	←	Elevation	-0.034	-0.231	0.157	0.762	<0.001	<0.001
Clay+silt	←	MAP	-0.036	-0.180	0.097	0.651	-0.001	0.004
Clay+silt	←	MAT	0.609	0.333	0.901	<0.001	2.160	0.639
Clay+silt	←	TSEA	0.287	0.081	0.497	0.026	0.002	0.001
Soil pH	←	TSEA	0.134	<0.001	0.264	0.102	<0.001	<0.001
Pathogens	←	Clay+silt	0.025	-0.083	0.136	0.694	<0.001	0.001
Pathogens	←	Soil C	0.093	-0.029	0.225	0.209	0.100	0.084
Pathogens	←	Soil pH	0.044	-0.112	0.213	0.614	0.145	0.306
Pathogens	←	PSEA	0.137	0.018	0.259	0.059	0.001	0.001
Pathogens	←	MAP	0.023	-0.153	0.191	0.861	<0.001	<0.001
Pathogens	←	MAT	0.689	0.344	1.025	0.001	0.032	0.009
Pathogens	←	Plant cover	-0.214	-0.398	-0.018	0.074	-0.208	0.112
Pathogens	←	Forest	0.426	0.240	0.609	<0.001	0.237	0.063
Pathogens	←	Spatial dissimilarity	0.442	0.194	0.690	0.003	0.024	0.007
Pathogens	←	TSEA	0.367	0.115	0.617	0.016	<0.001	<0.001
Pathogens	←	Grassland	0.255	0.100	0.394	0.009	0.149	0.055
Pathogens	←	Elevation	0.351	0.143	0.562	0.004	<0.001	<0.001
Spatial dissimilarity	↔	Elevation	-0.399	-0.473	-0.323	<0.001	-1288.931	227.442
PSEA	↔	MAP	-0.079	-0.177	0.030	0.238	-971.903	804.138
PSEA	↔	MAT	-0.269	-0.411	-0.115	0.006	-29.672	7.462
PSEA	↔	TSEA	0.271	0.079	0.443	0.026	19101.553	4772.195
MAP	↔	MAT	0.061	-0.073	0.180	0.424	137.625	148.566
MAP	↔	TSEA	-0.316	-0.412	-0.198	<0.001	-458145.777	99411.424
MAT	↔	TSEA	-0.830	-0.867	-0.782	<0.001	-10811.730	1107.043
Plant cover	↔	Forest	0.055	-0.068	0.168	0.460	0.003	0.004
Plant cover	↔	Grassland	0.090	-0.062	0.226	0.337	0.006	0.004
Forest	↔	Grassland	-0.635	-0.705	-0.562	<0.001	-0.086	0.010
Soil C	↔	Clay+silt	0.024	-0.083	0.138	0.673	0.088	0.236
Soil C	↔	Soil pH	0.061	-0.077	0.193	0.498	0.001	0.001
Soil pH	↔	Clay+silt	0.126	0.006	0.246	0.085	0.126	0.066

Supplementary Table 8 | R² values for endogenous variables in SEMs from Supplementary Tables 2-7.

Variables	Supplementary Table 2	Supplementary Table 3	Supplementary Table 4	Supplementary Table 5	Supplementary Table 6	Supplementary Table 7
PSEA	0.10	0.10	0.10	0.10	0.10	0.10
MAP	0.04	0.04	0.04	0.04	0.04	0.04
MAT	0.41	0.41	0.41	0.41	0.41	0.41
TSEA	0.01	0.01	0.01	0.01	0.01	0.01
Plant cover	0.67	0.67	0.67	0.67	0.67	0.67
Forest	0.51	0.51	0.51	0.51	0.51	0.51
Grassland	0.34	0.34	0.34	0.34	0.34	0.34
Soil C	0.46	0.46	0.46	0.46	0.46	0.46
Clay+silt	0.18	0.18	0.18	0.18	0.18	0.18
Soil pH	0.61	0.61	0.61	0.61	0.61	0.61
Pathogens	0.25	0.25	0.23	0.22	0.21	0.23

Supplementary Table 9 | Summary for PERMANOVA analyses in Figs. 3 and S7.

Variables	n	Source	df	SS	MS	Pseudo-F	P-value
All pathogens	20	WA	1	2113.3	2113.3	26.557	0.0002
		Res	18	1432.4	79.578		
		Total	19	3545.8			
<i>Alternaria</i>	20	WA	1	968.39	968.39	22.694	0.0003
		Res	18	768.07	42.671		
		Total	19	1736.5			
<i>Fusarium</i>	20	WA	1	8.9913	8.9913	2.0181	0.0498
		Res	18	80.195	4.4553		
		Total	19	89.187			
<i>Acremonium</i>	20	WA	1	11.173	11.173	7.3642	0.0001
		Res	18	27.311	1.5173		
		Total	19	38.484			
<i>Aureobasidium</i>	20	WA	1	10.38	10.38	18.513	0.0001
		Res	18	10.093	0.5607		
		Total	19	20.472			
<i>Stagonosporopsis</i>	20	WA	1	3.4071	3.4071	8.2124	0.001
		Res	18	7.4677	0.41487		
		Total	19	10.875			
<i>Phaeosphaeriaceae</i>	20	WA	1	0.1986	0.19864	3.2576	0.0313
		Res	18	1.0976	6.10E-02		
		Total	19	1.2962			
<i>Cladosporium</i>	20	WA	1	0.2868	0.28683	2.582	0.0209
		Res	18	1.9996	0.11109		
		Total	19	2.2864			
<i>Alternaria</i> (qPCR)	19	WA	1	0.4662	0.46618	5.379	0.0297
		Res	17	1.4733	8.67E-02		
		Total	18	1.9395			

Supplementary Table 10 | Pearson correlations between environmental factors (n = 235).

Variables	Parameters	Elevation	Spatial dissimilarity	MAT	TSEA	MAP	PSEA	Forest	Grassland	Plant cover	Soil C	pH
Spatial dissimilarity	r	-.399**										
	P-value	.000										
MAT	r	-.372**	-.332**									
	P-value	.000	.000									
TSEA	r	.115	-.019	-.689**								
	P-value	.079	.773	.000								
MAP	r	-.031	-.178**	.166*	-.316**							
	P-value	.636	.006	.011	.000							
PSEA	r	.280**	-.238**	-.228**	.284**	-.054						
	P-value	.000	.000	.000	.000	.412						
Forest	r	-.343**	.361**	.270**	-.257**	.119	-.556**					
	P-value	.000	.000	.000	.000	.068	.000					
Grassland	r	.099	-.180**	-.338**	.329**	.079	.338**	-.698**				
	P-value	.131	.006	.000	.000	.230	.000	.000				
Plant cover	r	-.252**	.230**	-.104	-.138*	.628**	-.360**	.260**	.095			
	P-value	.000	.000	.112	.034	.000	.000	.000	.146			
Soil C	r	-.002	.201**	-.155*	-.135*	.281**	-.190**	.241**	-.043	.447**		
	P-value	.975	.002	.017	.038	.000	.003	.000	.516	.000		
Soil pH	r	.109	-.370**	.249**	.080	-.540**	.104	-.271**	-.018	-.620**	-.395**	
	P-value	.095	.000	.000	.224	.000	.113	.000	.787	.000	.000	
Clay+silt	r	-.191**	.121	.062	-.073	.145*	-.069	-.038	.141*	.296**	.035	-.076
	P-value	.003	.063	.342	.263	.026	.290	.559	.031	.000	.592	.247

References (not listed in the main text)

58. Preparata, F.P., Shamos, M.I. Computational Geometry: An Introduction (Springer Science & Business Media, 2012).
59. Ebert, T. et al. IEEE Symposium on Computational Intelligence and Data Mining (CIDM) (2014).
60. Rousseeuw, P.J., van Zomeren, B. C. Unmasking Multivariate Outliers and Leverage Points. *J. Am. Stat. Assoc.* **85**, 633–639 (1990).
61. Jackson, D.A., Chen, Y. Robust principal component analysis and outlierdetection with ecological data. *Environmetrics* **15**, 129–139 (2004).
62. B. P. Mallavan, B. Minasny, A. B. McBratney, in Digital Soil Mapping (Springer, Dordrecht, 2010), Progress in Soil Science, pp. 137–150.
63. Eldridge D.J. et al. Australian dryland soils are acidic and nutrient-depleted, and have unique microbial communities compared with other drylands. *Journal of Biogeography* **45**, 2803-2814 (2018).
64. Maestre F.T. et al. Increasing aridity reduces soil microbial diversity and abundance in global drylands. *Proc Natl Acad Sci U S A.* **112**, 15684-15689 (2015).
65. Delgado-Baquerizo M. et al. Decoupling of soil nutrient cycles as a function of aridity in global drylands. *Nature* **502**, 672–676 (2013).
66. Schlesinger, W.H. Biogeochemistry, an analysis of global change (Academic Press, San Diego, CA, USA, 1996).
67. Jenny, H. Factors of Soil Formation: A System of Quantitative Pedology (Dover Publications, New York, USA, 1941).
68. Vicente-Serrano S.M. et al. Response of vegetation to drought time-scales across global land biomes. *Proc Natl Acad Sci U S A.* **110**, 52-57 (2013).
69. Ochoa-Hueso R. et al. Drought consistently alters the composition of soil fungal and bacterial communities in grasslands from two continents. *Global Change Biology* **24**, 2818-2827 (2017).
70. Delgado-Baquerizo M., Eldridge D. J. Cross-biome drivers of soil bacterial alpha diversity on a worldwide scale. *Ecosystems* 1–12 (2019).
71. Delgado-Baquerizo M. et al. Plant attributes explain the distribution of soil microbial communities in two contrasting regions of the globe. *New Phytologist* **219**, 574–587 (2018).

72. Baldrian, P. Forest microbiome: diversity, complexity and dynamics. *FEMS Microbiology Reviews* **41**, 109–130 (2017).
73. Fierer N. Embracing the unknown: disentangling the complexities of the soil microbiome. *Nature Reviews Microbiology* **15**, 579–590 (2017)
74. Gilbert G.S., Webb, C.O. Phylogenetic signal in plant pathogen-host range. *Proc Natl Acad Sci U S A.* **104**, 4979-4983 (2007).
75. Mitchell, C.E. et al. Effects of elevated CO₂, nitrogen deposition, and decreased species diversity on foliar fungal plant disease. *Global Change Biology* **9**, 438-451 (2003).