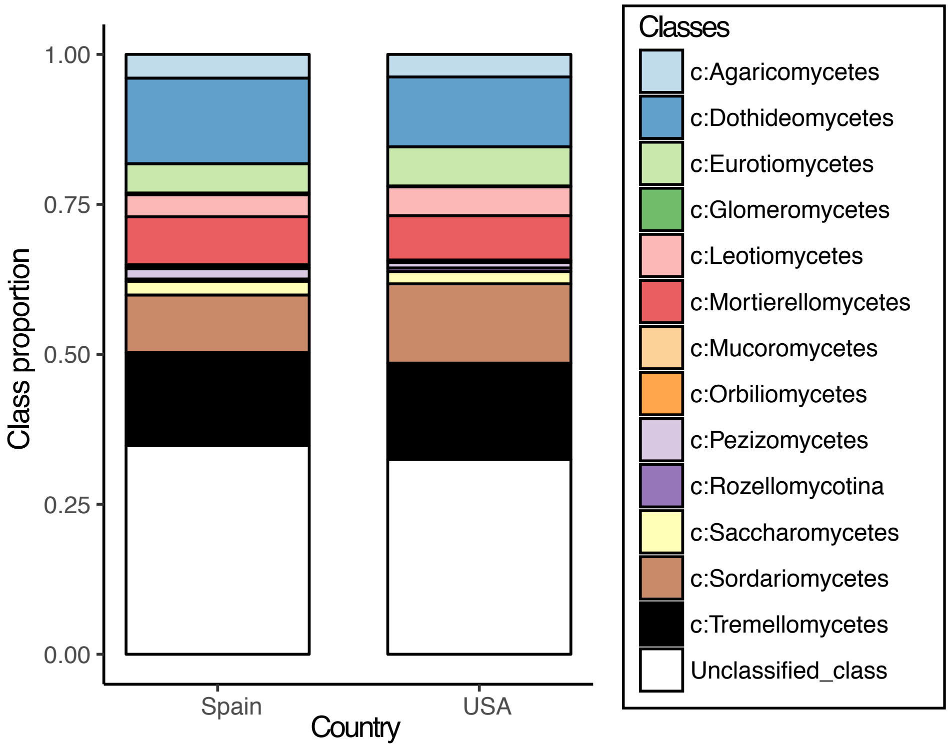

Figure S1. Taxonomic profile of major classes of fungi separated by country of origin (Spain and USA), as classified by Unite, and summing the relative abundances of the samples from each country.

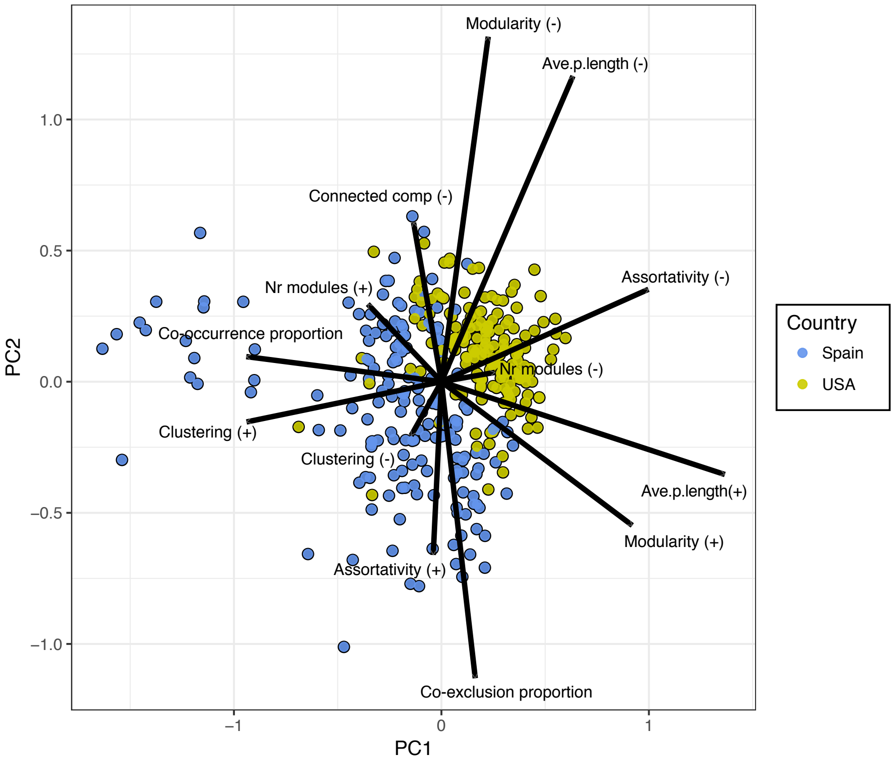

Figure S2. PCA of log-transformed scaled network properties separated by Country of procedence (Spain and USA).

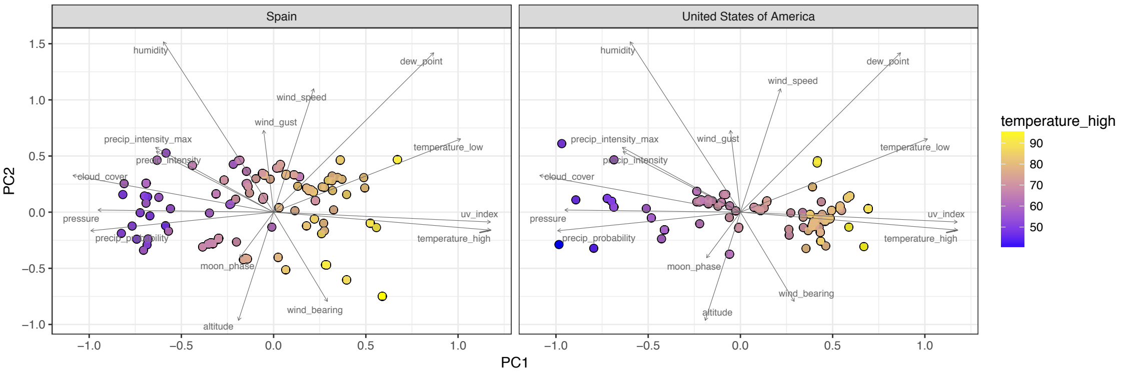

Figure S3. PCA of log-transformed scaled environmental variables separated by Country of procedence (Spain and USA).

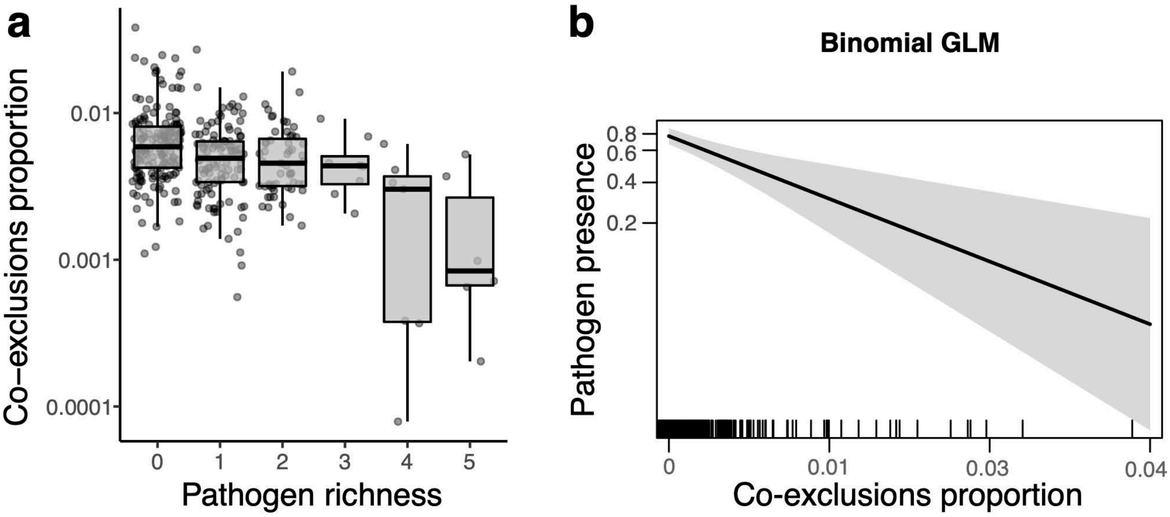

Figure S4. Relationship between fungal pathogen richness and co-exclusions proportion of the network. **a)** Boxplot of co-exclusions proportion at different pathogen richnesses (see Table S3 for a detailed list of the vine pathogens considered). **b)** Probability of fungal pathogen presence at different co-exclusions proportion values.

	Spain			USA		
Network property	**min**	**max**	**mean**	**min**	**max**	**mean**
Co-occurrence proportion	0.116	0.405	0.187	0.086	0.216	0.130
Clustering (+)	0.446	0.934	0.595	0.344	0.670	0.463
Modularity (+)	0.003	0.427	0.140	0.081	0.316	0.178
Nr modules (+)	2.000	21.000	4.846	2.000	12.000	3.817
Ave.p.length (+)	1.189	2.134	1.643	1.574	1.889	1.755
Assortativity (+)	0.078	0.735	0.237	0.072	0.470	0.216
Co-exclusion proportion	0.000	0.038	0.007	0.001	0.015	0.005
Clustering (-)	0.000	0.232	0.019	0.000	0.027	0.004
Connected comp (-)	1.000	6.000	1.914	1.000	9.000	1.977
Modularity (-)	0.002	0.616	0.231	0.065	0.840	0.383
Nr modules (-)	2.000	215.000	24.417	5.000	130.000	29.543
Ave.p.length (-)	2.000	3.891	2.935	1.231	4.116	3.379
Assortativity (-)	-0.798	-0.111	-0.417	-0.573	-0.016	-0.263

Table S1. Summary of ranges (min, max, mean) for network properties.

Variable	ANOVA p	Net. Property
Country	0.0000	Assortativity (-)
	0.0000	Ave.p.length (-)
	0.0000	Ave.p.length (+)
	0.0001	Co-exclusion proportion
	0.0000	Co-occurrence proportion
	0.0011	Nr modules (+)
	0.0000	Modularity (-)
	0.0000	Modularity (+)
	0.0000	Clustering coeff (-)
	0.0000	Clustering coeff (+)
interaction CxM	0.0048	Assortativity (-)
	0.0076	Ave.p.length (-)
	0.0000	Ave.p.length (+)
	0.0000	Co-occurrence proportion
	0.0049	Nr modules (-)
	0.0044	Nr modules (+)
	0.0035	Modularity (+)
	0.0001	Clustering coeff (+)
Management type	0.0001	Assortativity (-)
	0.0001	Assortativity (+)
	0.0000	Ave.p.length (+)
	0.0039	Connected components (-)
	0.0000	Co-exclusion proportion
	0.0000	Co-occurrence proportion
	0.0000	Modularity (+)
	0.0165	Clustering coeff (-)
	0.0000	Clustering coeff (+)

Table S2. Significant results from two-way ANOVA (Country x Management type) for network properties

Disease	**Pathogen sp.**	**presence**
Armillaria root rot	*Armillaria mellea*	present
Aspergillus rot	*Aspergillus carbonarius*	present
Black foot disease	*Ilyonectria robusta*	present
Black foot disease	*Campylocarpon fasciculare*	present
Black foot disease	*Ilyonectria liriodendri*	present
Black foot disease	*Dactylonectria estremocensis*	present
Black foot disease	*Campylocarpon pseudofasciculare*	not present
Botryosphaeria dieback	*Botryosphaeria dothidea*	present
Botryosphaeria dieback	*Lasiodiplodia missouriana*	present
Botryosphaeria dieback	*Neofusicoccum parvum*	present
Botryosphaeria dieback	*Neofusicoccum australe*	not present
Botrytis bunch rot	*Botrytis cinerea*	not present
Esca Complex	*Phaeomoniella chlamydospora*	present
Esca Complex	*Phaeoacremonium minimum*	present
Esca Complex	*Phaeoacremonium hispanicum*	present
Esca Complex	*Fomitiporia aethiopica*	not present
Esca Complex	*Phaeoacremonium inflatipes*	not present
Esca Complex	*Stereum hirsutum*	not present
Eutypa dieback	*Eutypella citricola*	present
Eutypa dieback	*Cryptovalsa ampelina*	present
Eutypa dieback	*Diatrype stigma*	present
Eutypa dieback	*Eutypa lata*	not present
Petri disease	*Cadophora luteo-olivacea*	present
Phomopsis dieback	*Diaporthe ampelina*	present
Verticillium wilt	*Verticillium dahliae*	present

Table S3. Disease and pathogen list considered. Presence of that particular pathogen in our dataset is included.

Table S4. Sample and metadata list (country and management, more in BioProject *PRJNA590645*)