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APPENDIX A

Canopy openness as a measure of microclimate at canopy and understory sample sites for radial transects in Cape Tribulation, Australia (*Ecological Archives* E088-035-A1).

APPENDIX B

Indentification and frequency of collection of epifoliar fungi in canopy or understory radial transects from Cape Tribulation, Australia, or San Lorenzo, Panama (*Ecological Archives* E088-035-A2).

APPENDIX C

Calculation of the probability of plant species being free of epifoliar fungi, under the assumption that fungi are host nonselective (*Ecological Archives* E088-035-A3).

APPENDIX D

Logistic regression results for the effect of phylogenetic distance (My), joint relative abundance (JRA), or the interaction (MyxJRA) on the probability that two plant species shared epifoliar fungal symbionts, from radial transects at San Lorenzo, Panama, and Cape Tribulation, Australia (*Ecological Archives* E088-035-A4).

APPENDIX E

Logistic regression results for the effect of canopy fungi (presence/absence of fungi on nearest mature conspecific), juvenile density (number of juveniles in 3-m radius around adult), and percentage of canopy openness on the proportion of juvenile *Cleistanthus myrianthus* colonized by epifoliar fungi at Cape Tribulation, Australia (*Ecological Archives* E088-035-A5).

Ecological Archives E088-035-A1

Gregory S. Gilbert, Don R. Reynolds, and Ariadna Bethancourt. 2007. The patchiness of epifoliar fungi in tropical forests: host range, host abundance, and environment. *Ecology* 88:575–581.

Appendix A. Canopy openness as a measure of microclimate at canopy and understory sample sites for radical transects in Cape Tribulation, Australia.

The openness of the forest canopy provides an integrated measure of variation in irradiation, relative humidity, and temperature. Canopy openness was estimated at each sample point along radial transects in the canopy (using a Nikon fisheye lens camera) and in the understory with a CID-110 Canopy Analyzer (CID Inc., Camas, Washington, USA). Due to failure of the CID-110, hemispherical images could not be collected with the same instruments in both strata. All images were collected under conditions of uniform lighting (early or late in day, overcast conditions). Percent canopy openness was calculated from the digital images using Canopy Analyzer software from CID, Inc.

Light conditions were highly variable across sample points, and distribution of light environments in the canopy and understory were largely non overlapping (Fig. A1).

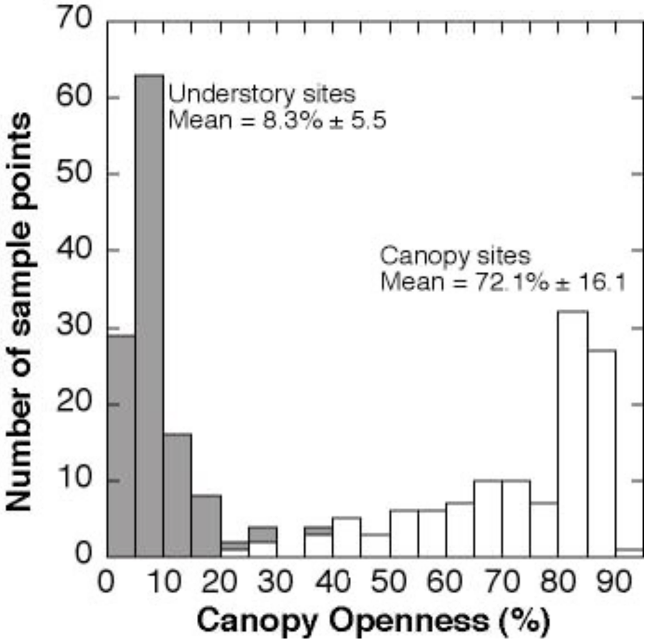

FIG. A1. Distribution of canopy openness in the canopy and understory of radial transect sample points at Cape Tribulation, Australia.

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Appendix B. Identification and frequency of collection of epifoliar fungi in canopy or understory radial transects from Cape Tribulation, Australia, or San Lorenzo, Republic of Panama.

Fungi were identified by D. Reynolds based on morphological characteristics, through examination of fungi from pressed and dried leaves. Observations and measurements of fungal structures were made from dried specimens mounted in lactophenol and examined using Zeiss light microscopes (Carl Zeiss International, Göttingen, Germany) and with a Cambridge scanning electron microscope (Hitachi S-3000N, Hitachi Scientific Instruments, Nitachinaka, Japan). Specimens were compared to type and other collections from world-wide herbaria and from descriptions in relevant literature (Reynolds and Gilbert 2005)(Reynolds, Gilbert, and Bethancourt, *unpublished data*). Specimens from both sites are deposited at the University Herbarium (UC) at the University of California, Berkeley, USA, and from Panama at the Herbarium of the University of Panama.

Cape Tribulation, Australia					
Family	Habit	Fungus	Canopy	Understory	Total
Antennulariellaceae	saprobic	*Antennulariella californica*	0	1	1
Asterinaceae	biotrophic	*Asterina eupomatiae*	1	11	12
Asterinaceae	biotrophic	*Asterina radulafistula*	0	1	1
mitotic ascomycete		*Asterostomella stophani*	0	4	4
Brefeldelliaceae	biotrophic	*Brefeldiella subcuticulosa*	4	16	20
Capnodiaceae	saprobic, honeydew	*Caldariomyces axillatum*	1	14	15
Micropeltidiaceae	saprobic	*Chaetothyrina costaricensis*	1	2	3
Chaetothyriaceae	saprobic	*Chaetothyrium fusisporum*	0	1	1
Chaetothyriaceae	saprobic	*Chaetothyrium strigosum*	0	3	3
Capnodiaceae	saprobic, honeydew	*Conidiocarpus philippensis*	0	1	1
mitotic Ascomycete	saprobic	*Elachopeltis andinas*	0	1	1
mitotic Ascomycete	saprobic	*Enthallopycnidium gouldiae*	0	2	2
mitotic Ascomycete	saprobic	*Hymeniodiopeltis major*	1	1	2
Meliolaceae	biotrophic	*Meliola alstoniae*	1	2	3
Micropelidtaceae	superficial	*Micropeltis bambusina*	0	7	7

Micropelidtaceae	saprobic	*Micropeltis bauhiniae*	1	6	7
Micropeltidiaceae	saprobic	*Micropeltis sp.*	0	3	3
mitotic Ascomycete	saprobic	*Parastigmatellina asiatica*	1	1	2
mitotic Ascomycete	saprobic	*Plectopeltis egenula*	0	2	2
Schizothyriaceae	saprobic	*Plochmopeltis ellisii*	1	1	2
mitotic Ascomycete	saparobic	*Sporidesmium macrurum*	0	4	4
Micropeltidiaceae	saprobic	*Stigmatodothis palawanensis*	0	1	1
Micropelticiaceae	saprobic	*Stomiopeltis gautheriae*	2	0	2
Capnodiaceae	saprobic	*Trichomerium grandisporum*	0	8	8
Antennulariaceae	saprobic	*Trichothallus hawaiiensis*	0	2	2
		Grand Total	14	95	109

San Lorenzo, Panama					
Family	Habit	Fungus	Canopy	Understory	Total
Incertae sedis	saprobic	*Fumiglobus ficina*	0	1	1
Brefeldiellaceae	biotropic	*Brefeldiella brasiliensis*	3	5	8
Chaetothyriaceae	saprobic	*Ciferriusia orientalis*	0	2	2
Capnodiaceae	saprobic	*Conidiocarpus penzigii*	0	1	1
Saccardiaceae	sapraobic	*Cyanodiscus glabrescens*	0	6	6
mitotic Ascomycete	saprobic	*Elachopeltella rubescens*	1	2	3
mitotic Ascomycete	saprobic	*Hansfordiopeltopsis amazonensis*	2	5	7
Coccodiniaceae	saprobic	*Limacinula tenuis*	1	0	1
Meliolaceae	biotrophic	*Meliola protii*	0	1	1
Schizothyriaceae	saprobic	*Metathyriella roupalae*	0	3	3
Micropeltinaceae	saprobic	*Micropeltis bambusina*	0	5	5
Micropeltinaceae	saprobic	*Micropeltis borgorensis*	0	1	1
Micropeltinaceae	saprobic	*Micropeltis caesalpiniae*	0	2	2
Micropeltinaceae	saprobic	*Micropeltis clavispora*	1	0	1
Micropeltinaceae	saprobic	*Micropeltis megasperma*	0	1	1
Micropeltinaceae	saprobic	*Micropeltis aspidiospermae*	0	1	1
Micropeltinaceae	saprobic	*Micropeltis* sp1	0	3	3
Schizothyriaceae	saprobic	*Metathyriella roupalae*	1	3	4
Schizothyriaceae	saprobic	*Plochmopeltis ellisii*	0	1	1
Schizothyriaceae	saprobic	*Schizothyriaceae* immature	6	6	12
		Sterile tufts	0	1	1

Vizellaceae		*Vizella royenae*	2	4	6
		Grand Total	17	54	71

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Ecological Archives **E088-035-A3**

Gregory S. Gilbert, Don R. Reynolds, and Ariadna Bethancourt. 2007. The patchiness of epifoliar fungi in tropical forests: host range, host abundance, and environment. *Ecology* 88:575–581.

Appendix C. Calculation of the probability of plant species being free of epifoliar fungi, under the assumption that fungi are host non-selective.

In order to calculate the probability that plant species of particular abundance would be fungus-free (or have any particular number of fungal collections), we used the binomial distribution as presented in Sokal and Rohlf (1995: pp.71–74), where:

$$\left(\frac{k}{Y}\right)p^{Y}q^{k-Y} = \frac{k!}{Y!(k-Y!)}p^{Y}(1-p)^{k-Y} \qquad \text{(C.1)}$$

where:
k = number of collections of a plant species
Y = number of those collections with epifoliar fungi,
p = proportion of all plant samples that had epifoliar fungi, and
q = 1-p = proportion of all samples with no fungi

For Cape Tribulation p = 109/843 = 0.129 and for San Lorenzo p = 71/564 = 0.126.
For each observed frequency of a plant species at each site, we calculated the probability of observing zero fungi – p(NoFungi) – on a plant species of that frequency.

For each frequency, we then tallied the number of observed species with or without epifoliar fungi. We then used p(NoFungi) in formula (1) to calculate the probability that, under the assumption of host non-selectivity, the observed proportion of plant species of a particular frequency would be free of epifoliar fungi (Fig. C1).

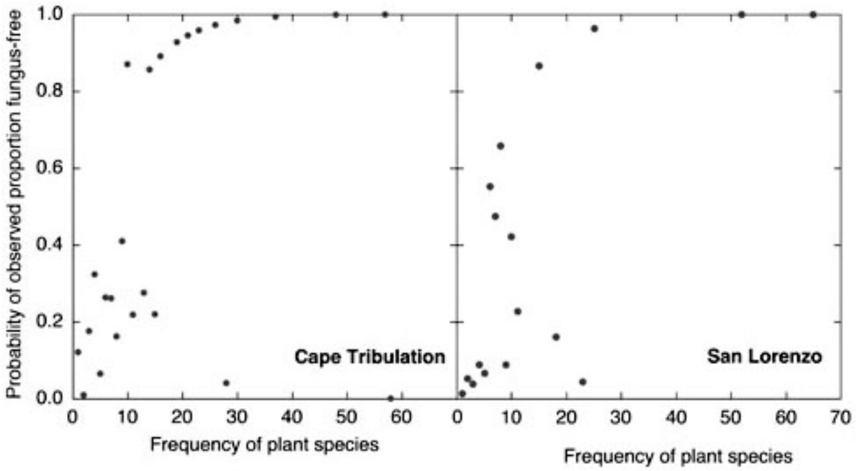

Fig. C1. For both Cape Tribulation, Australia and San Lorenzo, Panama, we observed many more fungus-free species than would be expected by chance under the assumption that fungi are not host selective, as expected if there was local host selectivity. In particular, less common species were less likely to harbor epifoliar fungi than expected by chance.

Probabilities of being fungus free (p(NoFungi)) for a particular species of given frequency, and of the probability of finding the observed number of fungus-free species of that frequency, as used in Fig. C1.

For Cape Tribulation, Australia

Species frequency	p(NoFungi)	Obs. spp. without fungi	Obs. spp with fungi	Total no. spp.	p(that many w/o fungi)
1	0.8707	57	10	67	0.121042
2	0.758118	34	3	37	0.00896
3	0.660094	13	5	18	0.175609
4	0.574743	3	1	4	0.322948
5	0.50429	4	0	4	0.064673
6	0.435723	3	2	5	0.263401
7	0.379384	3	3	6	0.261058
8	0.33033	3	2	5	0.161646
9	0.287618	1	1	2	0.409788
10	0.8707	1	0	1	0.8707
11	0.218049	1	0	1	0.218049
13	0.165307	1	1	2	0.275961
14	0.143932	0	1	1	0.856068
15	0.125322	1	1	2	0.219233
16	0.109118	0	1	1	0.890882
19	0.072028	0	1	1	0.927972
21	0.054606	0	1	1	0.945394
23	0.041398	0	1	1	0.958602
26	0.027326	0	1	1	0.972674
28	0.020717	1	1	2	0.040575
30	0.015706	0	1	1	0.984294
37	0.005958	0	1	1	0.994042
48	0.001299	0	1	1	0.998701
57	0.000374	0	1	1	0.999626
58	0.000325	1	0	1	0.000325

For San Lorenzo, Panama

Species frequency	p(NoFungi)	Obs. spp. without fungi	Obs. spp. with fungi	Total no. spp.	p(that many w/o fungi)
1	0.874113	85	5	90	0.015001

2	0.764074	25	3	28	0.05153
3	0.667888	9	10	19	0.039879
4	0.58381	2	5	7	0.089376
5	0.510316	4	0	4	0.06782
6	0.446074	0	1	1	0.553926
7	0.389919	1	1	2	0.475764
8	0.340834	0	1	1	0.659166
9	0.297927	2	0	2	0.088761
10	0.260422	1	3	4	0.421395
11	0.227639	1	0	1	0.227639
15	0.132898	0	1	1	0.867102
18	0.088761	1	1	2	0.161764
23	0.045296	1	0	1	0.045296
25	0.03461	0	1	1	0.96539
52	0.000915	0	1	1	0.999085
65	0.000159	0	1	1	0.999841

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Appendix D. Logistic regression results for the effect of phylogenetic distance (My), joint relative abundance (JRA), or the interaction (MyxJRA) on the probability that two plant species shared epifoliar fungal symbionts, from radial transects at San Lorenzo, Panama and Cape Tribulation, Australia.

Akaike Information Criterion (AIC), Likelihood Ratio (LR), *P* values of Wald test chi-square estimates for each factor, and percent concordance were used to select the best model for each site. At neither site did phylogenetic distance between plant species pairs contribute significantly to the model. Intercept was always significant ($P \leq 0.004$ for all).

				P values				
Site	Model	AIC	LR	LR	My	JRA	MyxJRA	Conc.%
SanLorenzo	1	787.4	18.7	0.0003	0.5426	0.0067	0.0532	61.4
SanLorenzo	2	789.3	14.8	0.0006	0.6816	0.0001		60.8
SanLorenzo	3	802	0.1	0.8379	0.8374			23.3
SanLorenzo	4	787.4	14.67	0.0001		0.0001		60.4
SanLorenzo	5	762.7	39.4	0.0001		0.0001†		63.3
CapeTrib	1	796	27.2	0.0001	0.5328	0.1944	0.9277	63.6
CapeTrib	2	794	27.2	0.0001	0.4079	0.0001		63.7
CapeTrib	3	818.3	0.9	0.3407	0.3293			34.8
CapeTrib	4	792.7	26.6	0.0001		0.0001		62.7
CapeTrib	5	754.7	64.5	0.0001		0.0001†		71.4

†Model uses log10(joint relative abundance).

At both sites, model 5 was the best, taking the form p(sharing) = expy / (1 + expy) where:
y = 2.0995 + 1.2722 log10JRA (for San Lorenzo)
y = 1.7059 + 1.1563 log10JRA (for Cape Tribulation).
To compare the logistic model predictions to the rates of fungal sharing observed at each site (Fig. 1), we grouped all pairwise joint relative abundances into log-series bins with lower bounds at 0.5x. In each bin, we calculated the proportion of plant pairs that shared fungal taxa.

		San Lorenzo, Panama	Cape Tribulation, Australia

x	Lower bound	No. shared pairs	No. total pairs	Proportion shared	No. shared pairs	No. total pairs	Proportion shared
19	1.91E-06	0	0		0	55	2.85E-06
18	3.82E-06	0	0		0	110	5.71E-06
17	7.63E-06	0	0		1	133	3.42E-05
16	1.53E-05	6	351	0.0171	10	255	0.0001
15	3.05E-05	0	0		9	311	0.0005
14	6.10E-05	11	216	0.0509	9	271	0.0014
13	1.22E-04	42	683	0.0615	28	254	0.0048
12	2.44E-04	17	206	0.0825	14	199	0.0127
11	4.88E-04	20	130	0.1538	13	121	0.0308
10	9.77E-04	8	50	0.1600	13	76	0.0455
9	1.95E-03	4	13	0.3077	6	33	0.0634
8	3.91E-03	0	3	0.0000	4	10	0.0395
7	7.81E-03	0	1	0.0000	0	2	0.0174

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Appendix E. Logistic regression results for the effect of canopy fungi (presence/absence of fungi on nearest mature conspecific), juvenile density (no. juveniles in 3-m radius around adult), and percentage canopy openness on the proportion of juvenile *Cleistanthus myrianthus* colonized by epifoliar fungi at Cape Tribulation, Australia.

Akaike Information Criterion (AIC), Likelihood Ratio (LR), *P* values of Wald test chi-square estimates for each factor, and percentage concordance were used to select the best model. Intercept was always significant ($P \leq 0.042$ for all).

			P values				
Model	AIC	LR Chi-square	LR	Can Fungi	Juv Dens	% open	Conc.%
1	55.7	11.6	0.0089	0.211	0..1366	0.0166	77
2	61.3	5.18	0.0749	0.0969	0.0446		63.9
3	56	9.29	0.0096	0.4875		0.0083	75.2
4	55.2	10.06	0.0065		0.2681	0.0101	72.6
5	62.5	0.85	0.3570	0.3498			23.8
6	60.9	2.42	0.1199		0.1211		47.4
7	54.5	8.82	0.0030			0.007	72.6

Model 7 was the best fit (lowest AIC with high concordance),
taking the form p(juvenile colonized) = expy / (1 + expy) where:
y = -2.8624 + 0.2729(% Canopy Openness).
Fit of this model against the observed data are shown in Fig. E1.

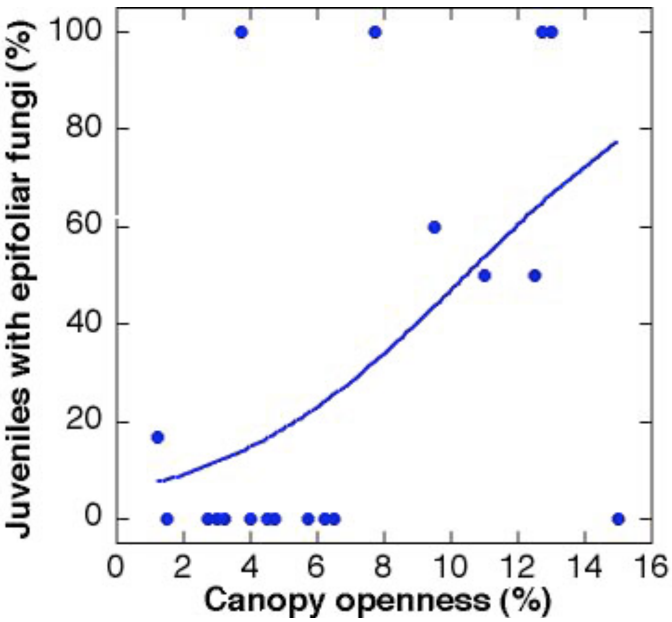

FIG. E1. Increased canopy openness increases the likelihood of epifoliar fungi on understory juveniles of *Cleistanthus myrianthus*. Each point is the percentage of juveniles within 3 m of an adult that were colonized by epifoliar fungi. The solid line indicates the probability that a juvenile would be colonized based on best-fit logistic regression (logit(probability juvenile colonized) = -2.8624 + 0.2729 (canopy openness).

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