A rapid method for the assessment of the macromycota. The fungal community of an evergreen cloud forest as an example

R. Guevara and R. Dirzo

Abstract: The macromycota of an evergreen cloud forest was described using a simple method, intended to minimize taxonomic work but still provide an accurate account of diversity. The method showed that the fungal community in the area is spatially structured and that area sampled limited the recording of fungal richness in this study. Parameters derived from the Clench equation suggest that an area of 1 ha will maximize the proportion of recorded taxa and minimize sampling effort.

Key words: fungal diversity, macrofungal communities, tropical mycoecology, El Triunfo.

Résumé : Les auteurs décrivent le macromycota d'une forêt nebelwald en utilisant une méthode simple, dans le but de minimiser le travail taxonomique tout en fournissant une information précise sur la diversité. La méthode montre que la communauté fongique de cette région est spatialement structurée, et que les surfaces échantillonnées limitent l'enregistrement de la richesse floristique dans cette étude. Les paramètres dérivés de l'équation Clench suggèrent qu'une surface d'un hectare permettrait de maximiser la proportion des espèces enregistrées, tout en minimisant l'effort d'échantillonnage.

Mots clés : diversité fongique, communautés macrofongiques, mycoécologie tropicale, El Triunfo.

[Traduit par la rédaction]

Introduction

During the last decade, fungi have been acknowledged as one of the hyperdiverse groups of living organisms (1). Some attempts have been made to estimate the global diversity of fungi (2), but these provide at best a working figure, and their accuracy is uncertain when based on calculations from a biased data set. Local assessments of diversity from tropical regions may enhance the accuracy of global assessments by allowing correction of parameters and help to reveal the spatial and temporal heterogeneity of fungal communities.

Long-term studies (e.g., 3) have shown considerable year to year variation in the production of macrofungal fruiting bodies. Short-term studies are therefore likely to record a biased sample of the actual diversity of fungi. The current global trend of accelerated habitat transformation is, however, in conflict with long-term diversity assessments at any location other than already protected areas. A strategy that compromises between sampling effort and recorded richness is therefore desirable, especially for tropical fungi that have been little studied. Here we present the results of a survey carried out to explore the diversity of the macromycota in an evergreen cloud forest in southern Mexico.

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Methods

The study area is located in the core I of the Biosphere Reserve El Triunfo. This protected area, under the administration of the Instituto de Historia Natural, is located in the Sierra Madre de Chiapas, Mexico. Samples were collected at the plateau of core I between 1750 and 1900 m above sea level (4). The site is characterized by a relative dry season from mid-November to mid-March, and the peak of the rainy season occurs from June to October (see data for Finca Prusia in 5). The dominant vegetation at the plateau has been characterized as a *Quercus–Matudaea–Hedyosmus–Dendropanax* community with exuberant growth at all strata and with a high density of epiphytes (4).

Ten transects (50 × 2 m each) were randomly distributed within the closed canopy area (CCA). The transects extended perpendicularly from two of the main footpaths in the area. The starting point of each transect was marked 2 m away from the trail into the thick vegetation and the orientation recorded for easy relocation. The main footpaths in core I are marked to show the distance in meters from the field station every 25 m for up to 4 km. On this basis, 20 footpath sections (each 25 m long) were randomly selected within the first kilometre from the field station. Samples were collected from a strip 1 m wide at each side of the main track. A total of 0.1 ha was sampled in each of the contrasting situations of the woodland, open canopy areas (OCA) at the sides of the footpaths, and CCA.

Samples were gathered in May and September 1991. Each transect was carefully scanned once in each season, and every macrofungal fruiting body was recorded. Since individual fruiting bodies do not correspond to individual mycelia, for the purpose of this study a group of morphologically similar and locally aggregated fruiting bodies was recorded as a single individual (a genet). Samples from each genet were characterized, collected, and dried. They were then sorted into families, genera, and "species" on the bases of macroscopic and microscopic features. Emphasis was made on separating the samples into distinctive taxa and no attempt was made to assign binomial names. For the purpose of this study, genets with a high degree of similarity both in macroscopic and microscopic characters were grouped into a single taxon (morphospecies). All samples were de-

Table 1. Summary of the number of genets, morphospecies, genera, families, and diversity indexes of Shannon (*H*) and Simpson (*S*) for the macromycota.

Census	No. of genets	No. of morphospecies	No. of genera	No. of families	Diversity	
					H	*S*
May						
CCA	82	37	26	14	3.21	0.94
OCA	118	38	27	19	3.17	0.94
Overall	200	63	40	21	3.29	0.97
September						
CCA	62	27	24	14	2.3	0.91
OCA	68	30	27	18	3.01	0.93
Overall	130	44	38	21	3.23	0.93

posited in the XALU herbarium (RG-CE-0001 to RG-CE-00330) of Facultad de Biología, Universidad Veracruzana, Xalapa.

The macromycota was characterized based on the number of families, genera, and morphospecies in each season and habitat. Diversity indexes of Shannon and Simpson were calculated, and we used a modified *t* test (6) to compare the values from Shannon's index. Species-accumulation functions were plotted and extrapolated based on the logarithmic model and the Clench equation (see Appendix 1). The Clench equation is a more conservative model than the logarithmic model (7). The Clench equation, however, allowed for the calculation of total expected richness (asymptote *a*/*b*; see Appendix 1, Table A1) and other parameters that predict the sampling effort required to record a *q* fraction of the total richness (t_q) or to drop the probability of adding a new record below a threshold *k* (t_k) (see Appendix 1 for details of the model and derived parameters).

Results

The flora

Floristic analysis of the 10 transects in the CCA showed that *Quercus crispifolia* Trelease, *Nectandra reticulata* Mez., *Trichilia havanensis* Jacq., *Eugenia acapulcensis* Steud., *Piper hispidum* Sw., *Eugenia mexicana* Steud., *Amphiteca* sp., *Cesearia nitida* Jacq., *Icacorea* sp., and *Posoqueria* sp. were the dominant species in the study area. A more detailed floristic analysis is presented elsewhere (8).

Diversity of the macromycota

A summary of the macromycota is presented in Table 1, and a complete list of recorded morphospecies is presented in Appendix 2. A total of 330 genets belonging to 98 morphospecies was recorded, 200 genets (63 morphospecies) in May (82 from CCA and 118 from OCA) and 130 genets (44 morphospecies) in September (62 from CCA and 68 from OCA). Ten morphospecies occurred in both censuses. Thirty-seven and 38 morphospecies were recorded from CCA and OCA, respectively, in May, whereas 27 and 30 morphospecies were recorded from CCA and OCA, respectively, in September. The number of morphospecies common to the two habitats was 12 and 13 in May and September, respectively.

The indexes of Shannon and Simpson revealed high diversity. There were no significant differences between CCA and OCA in May ($t_{110} = 0.24$, $P > 0.50$) and September ($t_{130} = 0.55$, $P > 0.50$) nor between seasons ($t_{294} = 0.28$, $P > 0.50$) for the index of Shannon.

A total of 27 families and 61 genera were recorded. Tricholomataceae was the best represented family (Fig. 1), whereas *Marasmius*, a Tricholomataceae member, was the dominant genus. The analysis showed that Corticiaceae, Agaricaceae, Coprinaceae, Crepidotaceae, and Pluteaceae were only represented in May, whereas Schizophyllaceae, Stereaceae, Entolomataceae, Lycoperdaceae, and Tulostomataceae were only represented in September. On the spatial scale, Auriculariaceae, Tremellaceae, and Hymenochaetaceae were restricted to OCA, whereas Amanitaceae were restricted to CCA.

Extrapolation of the species accumulation functions (Fig. 2 and Appendix 1, Table A1 for statistical values) showed that the accumulation of new records would be expected to increase at a high rate if the sampling effort were increased. Given the limiting effect of the area sampled in this study two parameters derived from the Clench equation are important for consideration in future work (Appendix 1, Table A2). The parameter t_q accounts for the sampling effort necessary to collect a fraction *q* of the total predicted richness and the parameter t_k accounts for the sampling effort necessary to drop the probability of adding a new record to an existing list of morphospecies, below the threshold *k*. To collect 99% ($t_q = 0.99$) of the total predicted richness, it would be necessary to increase sampling effort 18- to 190-fold in the area sampled in this study (Appendix 1, Table A2). On the other hand to drop the probability of adding a new record below the threshold of 0.1% ($t_k = 0.001$), it would be necessary to increase sampling effort two- to eight-fold.

Discussion

The analysis of the macromycota showed that the two contrasting habitats (CCA and OCA) in the study area sustain equally rich communities of macrofungi. Furthermore, the low number of common species between the two habitats and the restriction of some families to only one habitat strongly suggest that the macromycota is spatially structured.

The species accumulation function revealed that the sampling area was limiting for the recording of fungal richness. Based on the Clench equation an area of 1 ha is suggested as the working area that will maximize the proportion of recorded taxa and minimize the sampling effort for the cases of evergreen cloud forests.

This study showed that a rapid assessment of the macromycota based on a standard method has the potential to uncover temporal and spatial structure of the macromycota. The authors see in the proliferation of rapid assessment of the

Fig. 1. Distribution of morphospecies among families by (*a*) seasons (families represented in May (□) and September (■)) and habitats in (*b*) May and (*c*) September (families represented in closed canopy areas (■) and open canopy areas (□)). (1) Xylariaceae; (2) Sarcosomataceae; (3) Auriculariaceae; (4) Tremellaceae; (5) Cantharellaceae; (6) Corticiaceae; (7) Ganodermataceae; (8) Gomphaceae; (9) Hymenochaetaceae; (10) Polyporaceae; (11) Schizophyllaceae; (12) Stereaceae; (13) Agaricaceae; (14) Amanitaceae; (15) Bolbitaceae; (16) Coprinaceae; (17) Cortinariaceae; (18) Crepidotaceae; (19) Entolomataceae; (20) Hygrophoraceae; (21) Pluteaceae; (22) Strophariaceae; (23) Tricolomataceae; (24) Russulaceae; (25) Boletaceae; (26) Lycoperdaceae; (27) Tulustomataceae.

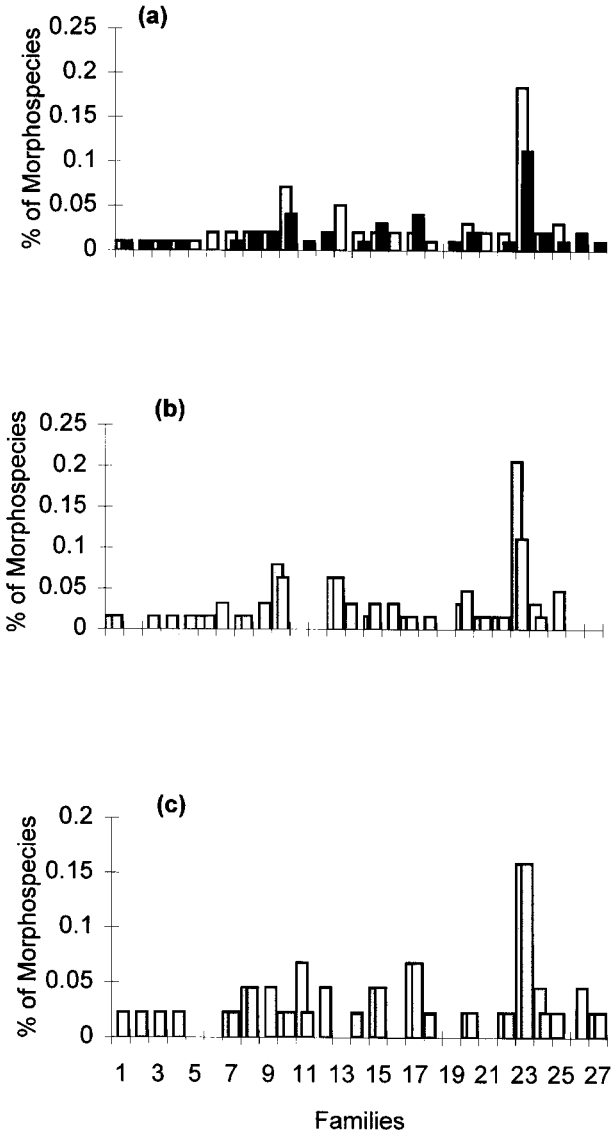
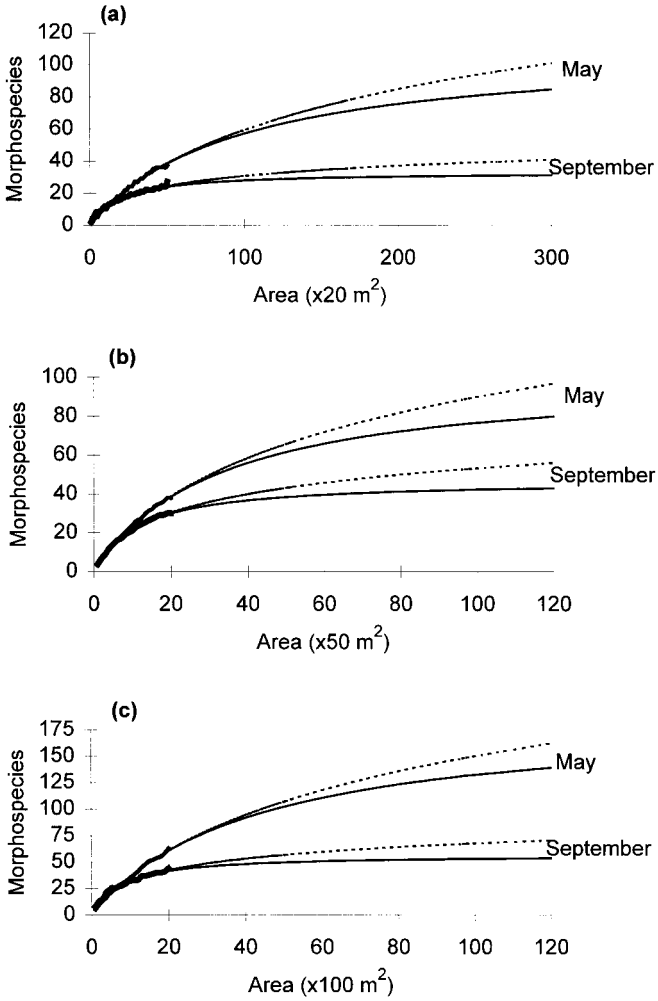


Fig. 2. Observed species-accumulation functions (bold line) and extrapolations from (*a*) closed canopy areas, (*b*) open canopy areas, and (*c*) seasons based on the logarithmic model (broken line) and the Clench equation (solid line).



macromycota a real possibility to uncover the diversity of fungal communities. This kind of study may be particularly useful in tropical regions where time before habitat transformation, budgets, and taxonomic monographs is restricted.

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Appendix 1

Table A1. Statistical summary of estimated parameters for the logarithmic model ($S(t) = 1/z \ln(1 + zat)$). See hard copy where $z = 1 - e^{-b}$ and the Clench equation ($S(t) = at/(1 + bt)$).

	Logarithmic model			Clench equation		
	a	z	R^2	a	b	R^2
May						
CCA	1.19*	0.02*	0.99	1.17*	0.01*	0.99
OCA	3.18*	0.02*	0.99	3.09*	0.03*	0.99
Overall	4.60*	0.01*	0.98	4.47*	0.02*	0.98
September						
CCA	2.23*	0.10*	0.99	1.71*	0.05*	0.98
OCA	4.72*	0.07*	0.99	4.08*	0.09*	0.99
Overall	9.89*	0.06*	0.99	7.62*	0.13*	0.98

*, $P < 0.01$.

Table A2. Summary of extrapolations.

	O	LM	CE	T	$t_q = 0.99$ (ha)	$t_k = 0.001$ (ha)
May						
CCA	37	39	38	112	18.91	0.53
OCA	38	39	39	102	16.35	0.83
Overall	63	61	61	188	20.82	0.93
September						
CCA	27	24	24	33	3.85	0.26
OCA	30	30	30	47	5.73	0.51
Overall	44	42	42	57	3.71	0.41

Note: Values are the observed number of species (O), expected number of species at the actual sampled area as derived from the logarithmic model (LM) and the Clench equation (CE), the total expected richness (T) as derived from the Clench equation (a/b); see Table A1. The sampling effort necessary to record 99% of the predicted richness ($t_q = 0.99$) and to drop the probability of adding a new record below the 0.1% threshold ($t_k = 0.001$) as calculated from $t_q = q/(b(1 - q))$ and $t_k = (1 + (4b/k))^{0.5} - 1]/2b$ (7).

Appendix 2

Table A3. Presence (1) and absence (0) of morphospecies in the sample sites.

			May		September	
			CCA	OCA	CCA	OCA
		Ascomycotina				
Sphaeriales						
Xylariaceae	1	*Xylaria fukeii*	1	1	0	0
	2	*Xylaria polymorphica*	0	0	0	1
Pezizales						
Sarcosomataceae	3	*Sarcosypha* (1)	0	0	0	1
		Basidiomycotina				
Auriculariales						
Auriculariaceae	4	*Auricularia delicata*	0	1	0	0
	5	*Auricularia mesenterica*	0	0	0	1
Tremellaceae	6	*Tremella fusiformis*	0	1	0	0
	7	*Tremella* (1)	0	0	0	1
Aphyllophorales						
Cantharellaceae	8	*Cantarellus cibarius*	0	1	0	0
Corticiaceae	9	*Corticium* (1)	1	0	0	0
	10	*Veluticeps* (1)	0	1	0	0
Ganodermataceae	11	*Ganoderma applanatum*	1	0	0	0
	12	*Ganoderma* (1)	1	0	1	1
Gomphaceae	13	*Gomphus* (1)	0	1	0	0
	14	*Gomphus* (2)	1	0	1	1
	15	*Ramaria stricta*	0	0	1	1
Hymenochaetaceae	16	*Coltricia* (1)	0	1	0	1
	17	*Hymenochaete* (1)	0	1	0	0
	18	*Phellinus* (1)	0	0	1	1
Polyporaceae	19	*Coriolopsis* (1)	0	1	0	0
	20	*Coriolopsis* (2)	1	1	1	0
	21	*Fomes* (1)	1	0	1	0
	22	*Gloeophyllum mexicanum*	0	0	0	1
	23	*Heterobasidion annosum*	1	1	0	0
	24	*Panus*	1	0	0	0
	25	*Polyporus leprieuri*	1	0	0	0
	26	*Polyporus* (1)	0	1	0	0
	27	*Trametes* (1)	0	0	1	0
Schizophyllaceae	28	*Schizophyllum commune*	0	0	0	1
Stereaceae	29	*Cotylidia* (1)	0	0	0	1
	30	*Stereum* (1)	0	0	0	1
Agaricales						
Agaricaceae	31	*Lepiota rubroctinta*	1	1	0	0
	32	*Lepiota clypeolaria*	0	1	0	0
	33	*Leucoagaricus* (1)	1	1	0	0
	34	*Leucocoprinus* (1)	1	1	0	0
	35	*Macrolepiota procera*	1	0	0	0
Amanitaceae	36	*Amanita caesarea*	1	0	0	0
	37	*Amanita pantherina*	1	0	0	0
	38	*Limacella* (1)	0	0	1	0
Bolbitiaceae	39	*Agrocybe* (1)	0	1	0	0
	40	*Bolbitus betulinus*	0	0	1	0
	41	*Conocybe* (1)	0	0	1	1
	42	*Psathyrella smithii*	1	1	0	0
	43	*Psathyrella* (1)	0	0	0	1
Coprinaceae	44	*Coprinus (1)*	0	1	0	0
	45	*Coprinus* (2)	0	1	0	0
Cortinariaceae	46	*Cortinarius* (1)	1	0	1	1

Table A3. (*concluded*).

			May		September	
			CCA	OCA	CCA	OCA
	47	*Cortinarius* (2)	0	0	0	1
	48	*Galerina* (1)	0	0	1	0
	49	*Gymnophyllus subdriophillus*	0	1	0	0
	50	*Inocybe* (1)	0	0	1	1
Crepidotaceae	51	*Crepidotus* (1)	0	1	0	0
Entolomataceae	52	*Entoloma* (1)	0	0	1	0
Hygrophoraceae	53	*Hygrocybe (1)*	0	0	0	1
	54	*Hygrophorus pratensis*	0	1	0	0
	55	*Hygrophorus* (1)	1	1	0	0
	56	*Hygrophorus* (2)	1	1	1	0
Pluteaceae	57	*Pluteus* (2)	1	0	0	0
	58	*Volvariella* (1)	0	1	0	0
Strophariaceae	59	*Nematoloma* (1)	0	0	1	1
	60	*Panaeolus* (1)	1	0	0	0
	61	*Panaeolus* (2)	0	1	0	0
Tricholomataceae	62	*Clitocybe cinerea*	1	0	0	0
	63	*Clitocybe* (1)	1	0	0	1
	64	*Clitocybe* (2)	1	0	0	0
	65	*Crinipellis* (1)	1	0	0	0
	66	*Laccaria laccata*	0	0	1	0
	67	*Lacaria* (1)	0	0	1	1
	68	*Marasmius chiapensis*	0	0	1	1
	69	*Marasmius coherens*	0	1	0	0
	70	*Marasmius guzmanianus*	0	1	0	0
	71	*Marasmius ramealis*	1	1	0	1
	72	*Marasmius* (1)	1	0	0	0
	73	*Marasmius* (2)	1	0	0	0
	74	*Marasmius* (3)	1	0	0	0
	75	*Marasmius* (4)	1	0	0	0
	76	*Marasmius* (5)	1	0	0	0
	77	*Marasmius* (6)	0	1	0	0
	78	*Marasmius* (7)	0	0	1	1
	79	*Marasmius* (8)	0	0	1	0
	80	*Mycena* (1)	1	0	0	0
	81	*Mycena* (2)	0	0	1	0
	82	*Oudemansiella canarii*	1	0	0	0
	83	*Tricholoma terreum*	0	1	0	0
	84	*Tricholoma* (1)	0	0	1	0
	85	*Tricholoma* (2)	0	0	0	1
	86	*Tricholoma* (3)	0	1	0	0
	87	*Tricholoma* (4)	1	1	0	1
Russulales						
Russulaceae	88	*Lactarius indigo*	0	0	1	0
	89	*Russula mexicana*	1	0	0	0
	90	*Russula virecens*	1	1	0	0
	91	*Russula* (1)	0	0	1	1
Boletales						
Boletaceae	92	*Boletus griseus*	0	1	0	0
	93	*Suillus chiapensis*	0	0	1	0
	94	*Tylopilus bailoui*	0	1	0	0
	95	*Tylopilus* (1)	0	1	0	0
		Gasteromycetes				
Lycoperdales						
Lycoperdaceae	96	*Geastrum*	0	0	0	1
	97	*Vascellum*	0	0	0	1
Tulostomatales						
Tulostomataceae	98	*Calostoma cinnabarina*	0	0	1	1