



## Effect of tree host species on fungal community composition in a tropical rain forest in Panama

ASTRID FERRER<sup>1,3\*</sup> and GREGORY S. GILBERT<sup>2,3</sup> <sup>1</sup>College of Environmental Science and Forestry, State University of New York, 1 Forestry Drive, N.Y. 13210 U.S.A. <sup>2</sup>Department of Environmental Studies, University of California, 1156 High S.T., Santa Cruz, CA 95064, U.S.A. and <sup>3</sup>Smithsonian Tropical Research Institute, Apartado 2072, Balboa, Ancón, Republic of Panamá

**Abstract.** To determine whether host species influence the composition of fungal communities, the ascomycetes and basidiomycetes present on three tree species (*Prioria copaifera* (Fabaceae), *Quararibea asterolepis* (Bombacaceae), and *Trichilia tuberculata* (Meliaceae)) were sampled on the 50-ha Forest Dynamics Project plot in lowland moist tropical forest on Barro Colorado Island, Panama. The most abundant fungal morphotypes of both ascomycetes and basidiomycetes were generalists found on all three hosts, but detrended correspondence analysis revealed distinct differences in fungal community composition among

host trees. These differences among hosts were constant across census years. Randomization tests revealed that there were significantly fewer host-generalist fungi than expected for ascomycetes but not for basidiomycetes. These results indicate that host composition plays a role in structuring both ascomycete and basidiomycete fungal communities, but that the most successful fungal morphotypes are capable of colonizing multiple host species.

**Key words.** Fungal diversity, host preference, wood-inhabiting fungi.

### INTRODUCTION

Fungi are the major agents of wood decomposition and nutrient cycling in forest ecosystems (Boddy & Watkinson, 1995). The activity of wood-decaying fungi is particularly striking in the tropics where high turnover rates of biomass are evident from the low accumulation of organic matter on the forest floor relative to the enormous amount of litter fall (Scheffer & Duncan, 1947; Kurihara & Kikkawa, 1986). Despite the great importance of fungi to forest biomass decomposition, our current understanding of the patterns of community structure, diversity, host specificity, and distribution of wood-inhabiting fungi is very limited.

Tropical rain forests are known to harbour high tree diversity, and it has been suggested that

this diversity may in turn support high fungal diversity (Lodge & Cantrell, 1995; Lodge, 1997). In theory, the greater variety of different wood resources found in species-rich forest should provide a greater number of niches for fungal species. The relationship between plant diversity and fungal diversity, however, may not be linear. As host diversity increases, opportunities for specialization may diminish because the probability of successful colonization decreases as hosts become increasingly rare. Novotny *et al.* (2002) recently found support for such a nonlinear association between the diversity of hosts and their dependent organisms in a study of plant host dependent insects. They found that for an analysis of diet preferences of leaf-chewing insects in Papua New Guinea, insects that fed on a single host tree species were rare, with most insects feeding on several closely related congeneric species.

\* Corresponding author. E-mail: astridferrer@hotmail.com

Even if fungi are not host specialized, they may show host preferences (defined as nonrandom production of fruiting bodies among potential host species). Host preference can be determined by: (1) host abundance (influencing dispersal success) (2) intrinsic properties of the host, or (3) the microenvironmental conditions where particular hosts are found. Recent studies provide some limited evidence for host preferences among tropical basidiomycetes. Lindblad (2000) explored the host ranges of wood inhabiting fungi in Santa Rosa National Park, Guanacaste, Costa Rica. Her study indicated that although most wood-inhabiting fungi have broad host ranges, specialization increased for host trees with high abundance. Similarly, Gilbert *et al.* (2002) found little evidence for host specialization in a diverse tropical forest, but argued that the higher diversity of fungi present on common tree species in a forest plot in Panama may be due to the presence of more specialized fungi on those hosts. There have been few comparable studies of host preference among ascomycetes, but, Lodge & Cantrell (1995) suggested that endophytic xylariaceous fungi have broad host ranges.

The suggested wide distribution patterns, and limited host preferences for decomposer fungi are in contrast with recent findings for ectomycorrhizal fungi. These indicate that individual fungal taxa can show fine scale distribution patterns (Horton & Bruns, 2001), and that host-specificity in some systems is remarkably high (Bidartondo & Bruns, 2002). Differences in specificity between these fungal groups may reflect different mechanisms of interaction between fungi and live host tissue that are absent from wood.

Studies of the host preferences of decomposing fungi, however, have been limited by our ability to identify and sample large numbers of dead host trees. In this study, we sampled intensively the community of both basidiomycetes and ascomycetes colonizing three relatively abundant host trees during three years in the lowland moist tropical forest on Barro Colorado Island, Panama.

Specifically, we address the following questions: (1) Are there differences in the species richness of wood-inhabiting fungi that colonize dead trees and branches of three common tree species in moist tropical forest? (2) Do wood-inhabiting fungi show evidence for host preference indicated

by a nonrandom distribution pattern among tree species? (3) Does the ascomycete community structure mirror that of basidiomycetes?

## METHODS

### Study site

The study was conducted on Barro Colorado Island (BCI), Republic of Panama (9°10'N, 79°51'W). The island has a semideciduous forest with an average rainfall of 2600 mm and a pronounced dry season from January through April (Windsor, 1990). The 50-ha Forest Dynamics Project (FDP) plot of BCI was established in old-growth forest on a plateau in the middle of the island. Since its establishment in 1980, all trees ( $\geq 1$  cm d.b.h.) on the plot have been tagged, mapped, identified, and measured in censuses completed in 1982, 1985, 1990, 1995, and 2000. The plot has been described in detail by Hubbell & Foster (1983). Any individual of the 304 tree species on the plot can be identified from its tag or location, even if the tree is dead and decomposing.

### Tree species

We studied the fungal communities associated with the trunks and branches of three tree species *Prioria copaifera* Griseb., *Quararibea asterolepis* Pitt., and *Trichilia tuberculata* C.DC., that differ in abundance in the FDP plot on BCI. *Prioria copaifera* (Fabaceae, Caesalpinioideae) is a legume tree up to 40 m tall and 150 cm diameter at breast height (d.b.h.) (Croat, 1978). The wood is soft, with a wood specific gravity of 0.40 (Hess *et al.*, 1950). Within the FDP plot, *Prioria* is located mostly in the southern part of the plot; outside the plot it is more common along the shore on the southern side of the island (Croat, 1978). *Quararibea asterolepis* (Bombacaceae) is a tree up to 30 m tall, 75 cm d.b.h., and buttressed to 2 m. The wood is moderately heavy with a wood specific gravity of 0.45 (Muller-Landau, personal communication). On BCI in the 50-ha FDP plot *Quararibea* is more common in the eastern part of the plot (Croat, 1978). *Trichilia tuberculata* C.DC. (Meliaceae) is a tree up to 30 m tall and 70 cm d.b.h. The wood is hard, heavy, and with a wood specific gravity of 0.61 (Muller-Landau, personal communication). It is the most

**Table 1** Number of trees visited in the 1994, 1996, 1997, and 1998 census in the 50-ha FDP and information on decomposition rates

Host species	1994		1996		1997	1998
	# of dead trees	# of live trees	# of dead trees (that died between 1990–1996)	% Completely decomposed in 1996	# of live trees	# of live trees
<i>Prioria copaifera</i>	—	—	41	68%	183	180
<i>Quararibea asterolepis</i>	30	100	40	45%	182	—
<i>Trichilia tuberculata</i>	30	65	71	14%	176	—

abundant tree species in the FDP plot; outside the plot it is a common species of the older forest.

### Fungal diversity

Fungal censuses were undertaken during the early rainy season in two years from July to September in 1996 and in 1997. In the first fungal census, we visited trees of *Prioria*, *Quararibea*, and *Trichilia* that were found dead during the most recent tree census in 1995 (Table 1). At the second fungal census, we visited trees ( $\geq 200$  mm d.b.h.) of the focal species that were found alive in the 1995 tree census.

In both fungal censuses, we collected fruiting bodies of all perennial, macroscopic fungi in the taxonomic groups of basidiomycetes and ascomycetes found growing on identifiable woody substrates (dead or live trunks and branches). An important caveat to this study is that fruiting body appearance may not be correlated with actual fungal abundance on the host (as has been found for ectomycorrhizal species (Horton & Bruns, 2001). Nonetheless, we focused on basidiomycetes and ascomycetes because the fruiting bodies of these groups are visible and persist for months or years. Estimates of diversity for these groups are therefore less likely to be greatly underestimated by seasonality in fruiting phenology. Nonetheless, given the time frame and sample size used in this study, we have likely underestimated total fungal diversity. Fruiting bodies were dried and stored for identification. Identification was made using macroscopic morphology and microscopic characteristics (Ryvarden & Johansen, 1980; Gilbertson &

Ryvarden, 1986; Ju & Rogers, 1996), through consultation with appropriate literature, and comparison with herbarium specimens at the Universidad de Costa Rica, San José (USJ), and Washington State University, Pullman (WSP). The collections will be deposited at the Herbarium of University of Panama with a duplicate of each species sent to SUNY-ESF College of Environmental Science and Forestry's Herbarium (SYRF). Here we use classification of material into fungal morphotypes. An incomplete list of species names attributed to these morphotypes appears in Appendix 1 (To be published ONLY on the web, with URL inserted here). Multiple fruiting bodies of the same fungal morphotype on an individual tree host were considered one collection.

We used Fisher's alpha index to characterize morphotype diversity based on the total number of collections and the number of fungal morphotypes on each host tree (Magurran, 1988). Morphotype accumulation curves were generated from the mean morphotype richness of 100 randomized repeats of the sample ordered using the program EstimateS 5 (Colwell, 1997). To compare species richness among samples of unequal size, the Coleman rarefaction index was calculated from a random sample of equal size for each tree species.

Temporal changes in community composition were investigated by comparing fungal census information collected in three years. In addition to the 1996 and 1997 fungal censuses, we used data taken in 1994 for *Trichilia* and *Quararibea* and in 1998 for *Prioria*. In 1994, 30 of the largest individuals that died between 1985 and 1990 were censused along with an additional 100 individuals

of *Quararibea* and 65 individuals of *Trichilia* that were known to be alive in 1990 (Gilbert *et al.*, 2002). For *Prioria*, an additional census was undertaken in 1998 where 180 *Prioria* trees recorded alive in the 1995 tree census were visited (Table 1). To determine how fungal community composition varied among hosts across census years, detrended correspondence analysis (DCA) was performed using the program PC-ORD version 3.18 (McCune & Mefford, 1997) to analyse a matrix of relative abundance of fungi for each host tree species at each census. Each census included trees that were found dead for the first time in that census year. Fungal morphotypes that were collected only once (singletons) were excluded from ordination analysis but are included in measures of fungal diversity.

### Host preference

To compare the similarity of species occurrence among host tree species, the Sørensen qualitative (presence-absence) index was used (Magurran, 1988). Patterns of host preference were explored using data pooled from the three fungal censuses. To standardize collecting effort across species, 76 collections were randomly selected ( $n = 100$  randomization) from *Trichilia* and *Prioria* for comparison with the total of 76 collections made for *Quararibea*. Fungal morphotypes were arranged according to the number of hosts they colonized. To evaluate if fungi with broad host ranges are also the most abundant on each host species, the mean number of collections per host was plotted against the number of host species on which it was found. In addition, for each host species the proportion of fungi that were found only on that host, two hosts, or on all three hosts was determined.

To estimate whether the number of ascomycete and basidiomycete fungi that were (or were not) apparently 'host generalists' (defined as fungal morphotypes found on all three host species), was significantly different from that expected at random we performed the following test. Using the database of fungal morphotype collections, we randomly reordered morphotypes with respect

to host maintaining the same number of collections per morphotype as in the original collections. After repeating this randomization 100 times we tabulated the expected number of morphotypes encountered on each host. A statistical comparison of the actual number of morphotypes found on each host with this expected number was made using a *Z*-test (Zar, 1999).

## RESULTS

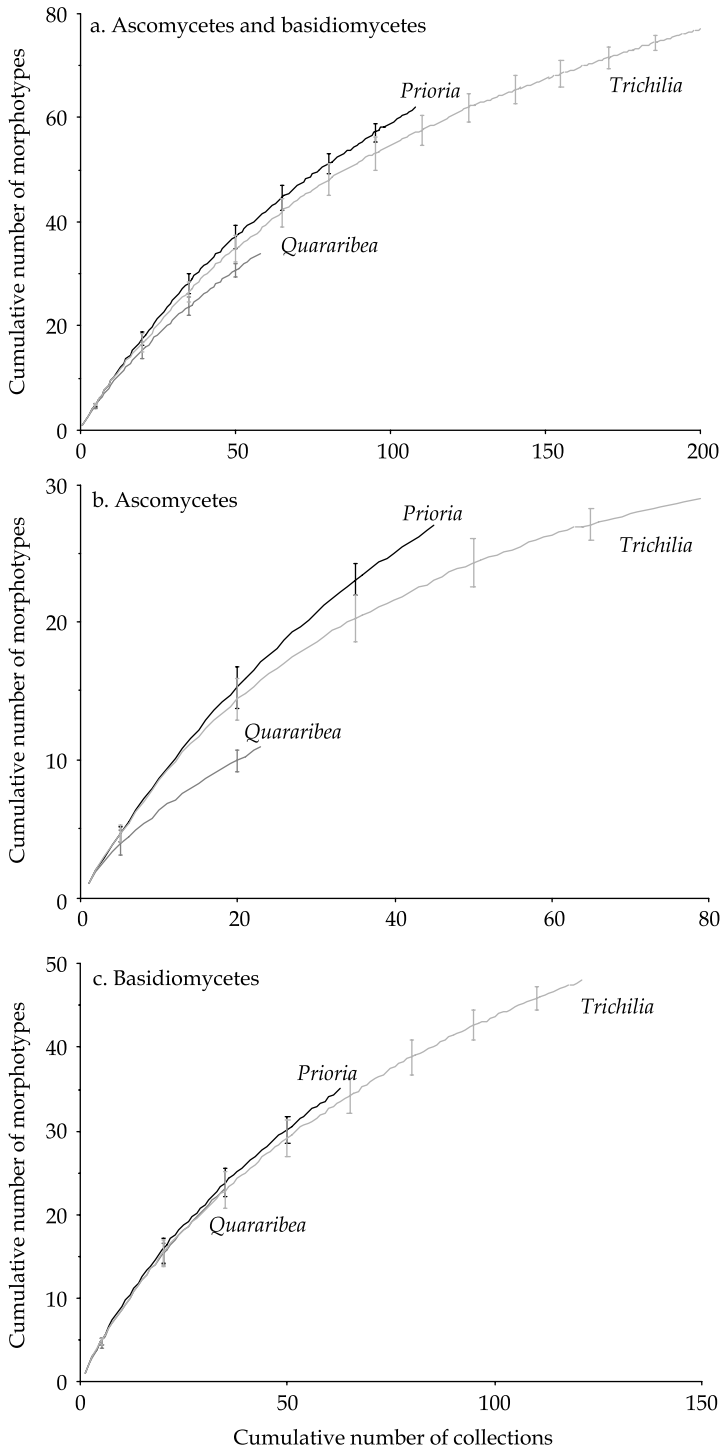
### Host availability

For wood-inhabiting fungi, the abundance of host material is not just determined by the size and number of dead individuals, but also by the length of time dead trees remain undecomposed. Decomposition rates are particularly high in the humid tropics, and a large number of trees that were known to have died during the intercensus period of 1990–95 were completely decomposed by 1996. Tree decomposition rate appears to be associated with wood density. Turnover for *Prioria* (wood specific gravity of 0.40) was remarkably fast with 68% of the dead trees completely decomposed whereas only 14% of *Trichilia* (wood specific gravity of 0.61) trees disappeared over the same period, and 45% of *Quararibea* (wood specific gravity of 0.45).

### Fungal diversity

The total fungal richness (ascomycetes and basidiomycetes) associated with *Prioria*, *Quararibea*, and *Trichilia* was very high, as evidenced by morphotype accumulation curves that did not reach an asymptote (Fig. 1a). Fisher's alpha and rarefaction estimate gave comparable results; *Quararibea* had the lowest fungal diversity index while indices for *Trichilia* and *Prioria* were similar (Table 2). In general, for all the host species, fruiting bodies of basidiomycetes were more common than ascomycetes (Table 2). Basidiomycete diversity indices were also higher, in the case of *Quararibea*, more than three times higher than ascomycete diversity (Table 2). Variation among the hosts in levels of diversity

**Fig. 1** Observed morphotype accumulation curves of wood-inhabiting (a) ascomycetes and basidiomycetes (combined) (b) ascomycetes, and (c) basidiomycetes based on the mean of 100 randomized orderings of sample number.



**Table 2** Number of collections and morphotypes on each host species, associated Fisher's alpha, and expected number of morphotypes in a rarefied sample

Host species	Ascomycetes & Basidiomycetes			Ascomycetes			Basidiomycetes			
	Collections 1996 & 1997	Morphotypes ( <i>n</i> )	Fisher's alpha	E(35)	% Collections	Fisher's Alpha	E(23)	% Collections	Fisher's Alpha	E(23)
	<i>Prioria copaifera</i>	103	62	60.5	39.9	42.7	28.5	16.6	57.3	32.4
<i>Quararibea asterolepis</i>	55	34	34.0	32.3	39.6	8.2	10.65	60.4	29.1	17.0
<i>Trichilia tuberculata</i>	199	77	45.8	36.6	39.5	16.5	15.19	60.5	29.4	16.8

were similar for basidiomycetes and ascomycetes. *Prioria* had the highest diversity followed by *Trichilia* then *Quararibea* for both groups of fungi (Table 2).

Ascomycete morphotype accumulation curves did not reach an asymptote (Fig. 1b). *Prioria* had the highest morphotype richness, and *Quararibea* was significantly lower than the other two species (Table 2). Morphotype accumulation curves and diversity indices for basidiomycetes were very similar for the three host species (Fig. 1c, Table 2). The accumulation curves were very steep, so more sampling is necessary before reliable estimates of total richness can be obtained.

For both ascomycetes and basidiomycetes, most fungi were rare. Singletons (fungal morphotypes collected once) accounted for 45% of basidiomycete fungal morphotypes and 40% for ascomycetes. Nonetheless, considering both basidiomycetes and ascomycetes, at least one common morphotype was found on each host, accounting for up to 25% of the collection on *Quararibea*, 12% on *Trichilia* and 10% on *Prioria* (Data not shown).

### Similarity between host tree species

For both basidiomycetes and ascomycetes, the composition of fungal communities were most similar between *Prioria* and *Trichilia*, and least for *Prioria* and *Quararibea* (Table 3). The same pattern was found using the Morisita-Horn index that takes into account the abundance of each morphotype (Data not shown).

The DCA ordination of ascomycetes and basidiomycetes together indicates a strong degree of host species preference by wood-inhabiting fungi (Fig. 2a). The first axis had a considerably higher eigenvalue (0.72) compared to the two subsequent axes (0.26 and 0.11) (Table 4). The first ordination axis clearly separated fungal communities according to host species (Fig. 2a). Axis 2 and Axis 3 did not reveal any clear separation among host species.

The DCA ordination for ascomycetes also revealed a distinct distribution of the species in ordination space (Fig. 2b), yielding a similar pattern to the ordination of ascomycetes and basidiomycetes combined (Table 4 and Fig. 2b). Almost the same pattern was observed with basidiomycetes communities (Fig. 2c).

**Table 3** Similarity among hosts for ascomycete and basidiomycete communities based on Sørensen similarity index

Host pairs		Sørensen index	
		Ascomycetes	Basidiomycetes
<i>Prioria</i>	<i>Trichilia</i>	0.40	0.32
<i>Quararibea</i>	<i>Trichilia</i>	0.29	0.20
<i>Prioria</i>	<i>Quararibea</i>	0.19	0.17

**Table 4** Summary of the DCA ordination for fungi found on *Prioria*, *Quararibea* and *Trichilia* hosts. Ordination was performed separately for ascomycetes, basidiomycetes, and all fungi combined

	Ascomycetes &								
	Basidiomycetes			Ascomycetes			Basidiomycetes		
	Axis1	Axis 2	Axis3	Axis1	Axis2	Axis3	Axis1	Axis2	Axis3
Eigenvalue	0.72	0.26	0.11	0.83	0.37	0.04	0.67	0.37	0.14
Length of gradient	4.35	2.02	1.76	5.79	2.65	2.21	3.54	2.71	1.98

### Host preference–abundance relationships

A total of 111 fungal morphotypes were found using 76 randomly chosen collections from each of the three host species. Of these morphotypes, 40 were ascomycetes and 71 basidiomycetes. Only one morphotype of ascomycetes (*Hypoxylon stygium* (Lév.) Sacc.) and four of basidiomycetes (*Rigidoporus lineatus* (Pers.) Ryvarden, *Datronia caperata* (Berk.) Ryvarden, *Tinctoporellus epimilitinus* (Berk. & Broome) Ryvarden and *Rigidoporus vinctus* (Berk.) Ryvarden) were found on all three host species. This is significantly fewer than expected at random for ascomycetes, and marginally significant for basidiomycetes (Table 5).

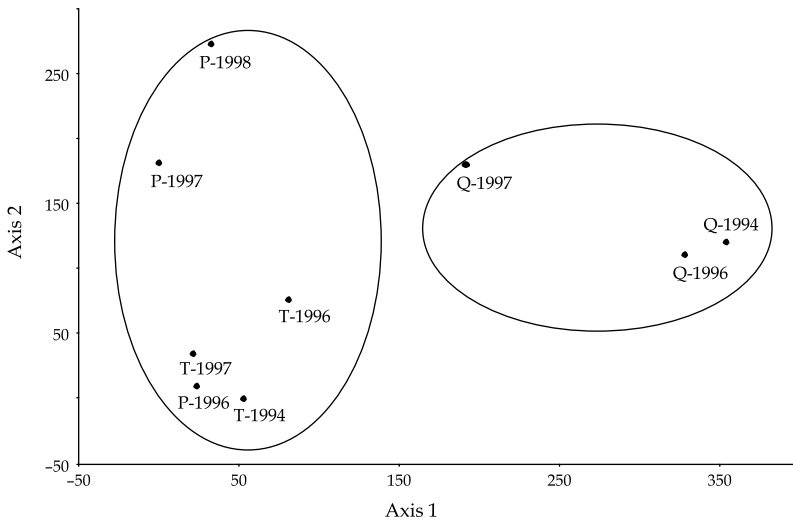
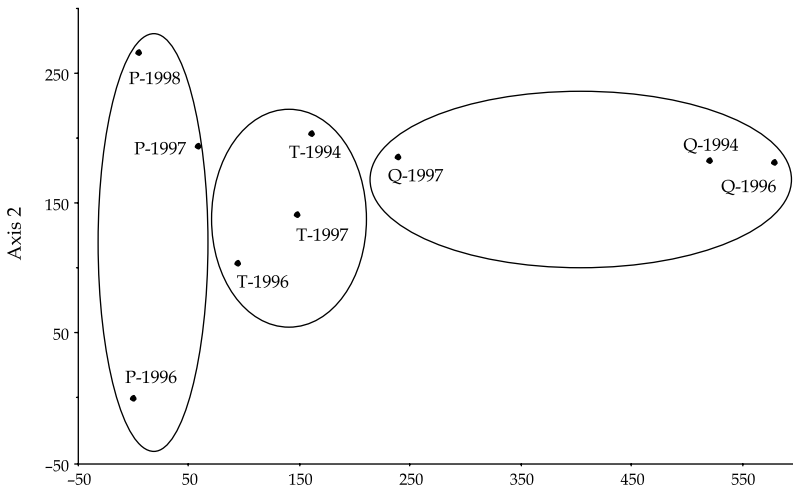
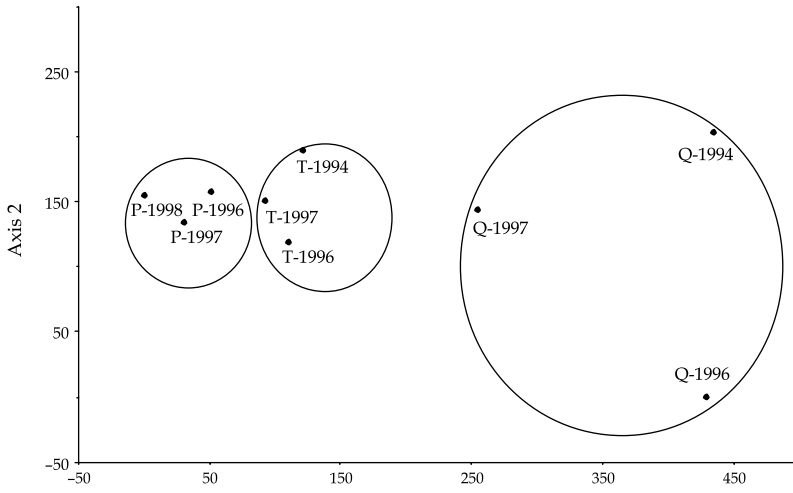
Generalist ascomycete morphotypes made up the smallest proportion of all fungal collections whereas the assemblage of morphotypes present on a single host made up the largest proportion of the fungal collection for each host species (Fig. 3). This pattern is particularly evident for *Quararibea* with almost 80% of the fungi collected from this host found only on *Quararibea*. In addition, fungal morphotypes found only on *Quararibea* were collected more frequently than those shared with two or more hosts.

For basidiomycetes, the four generalist morphotypes, found on all three hosts make up a relatively large proportion of the total fungal collections on *Prioria* and *Trichilia* (22 and 28%) (Fig. 4). These generalist basidiomycetes morphotypes attain a larger mean number of collections on *Prioria* and *Trichilia* (Fig. 4) than on *Quararibea*. Fungi restricted to *Quararibea* made up the largest proportion of total collections on that host (63%), a higher proportion than in the equivalent category for *Prioria* and *Trichilia* (48 and 50%).

## DISCUSSION

### Decay rate of host trees

High decomposition rates of tropical trees have been reported before for BCI. Lang & Knight (1979) found that trees died and completely decomposed during the 10 years intercensus period of their permanent plots. They established a decay constant for all tree species of 10–36 cm in diameter of 0.46/year and reported that this is the largest value found in the literature. They also argued that this value is species specific and





**Table 5** Expected and observed number of generalist fungi found on *Prioria*, *Quararibea*, and *Trichilia*

	No. of collections per tree species (total no. of collections)	Total no. of morphotypes	No. of generalist morphotypes found	No. of generalist morphotypes expected	<i>P</i>
Ascomycetes	30 (90)	40	1	5.68 ( $\pm 1.3$ )	0.0002
Basidiomycetes	46 (138)	71	4	6.31 ( $\pm 1.5$ )	0.061

dependent on bole diameter. The high rate of decay of *Prioria* is probably related to its low wood density compared to *Trichilia* for which a large proportion of the dead trees remained extant at the end of the study. However many other characteristics of wood, such as the presence of chemicals with antifungal activity; water holding capacity; and nutrient content, may affect the rate of decomposition (Rayner & Boddy, 1988; Blanchette, 1991; Worrall *et al.*, 1997). Gilbert (2002) conducted a literature survey of 95 species of tropical American woods and found that both wood density and terpene presence have a strong influence on decay rates. Low density wood without terpenes is most susceptible to rapid decay whereas high density wood with terpenes is extremely resistant. High density without terpenes and low density with terpenes were intermediate. Unfortunately, we lack information on the terpene content of wood of the three species studied here.

### Host species effects on fungal community composition

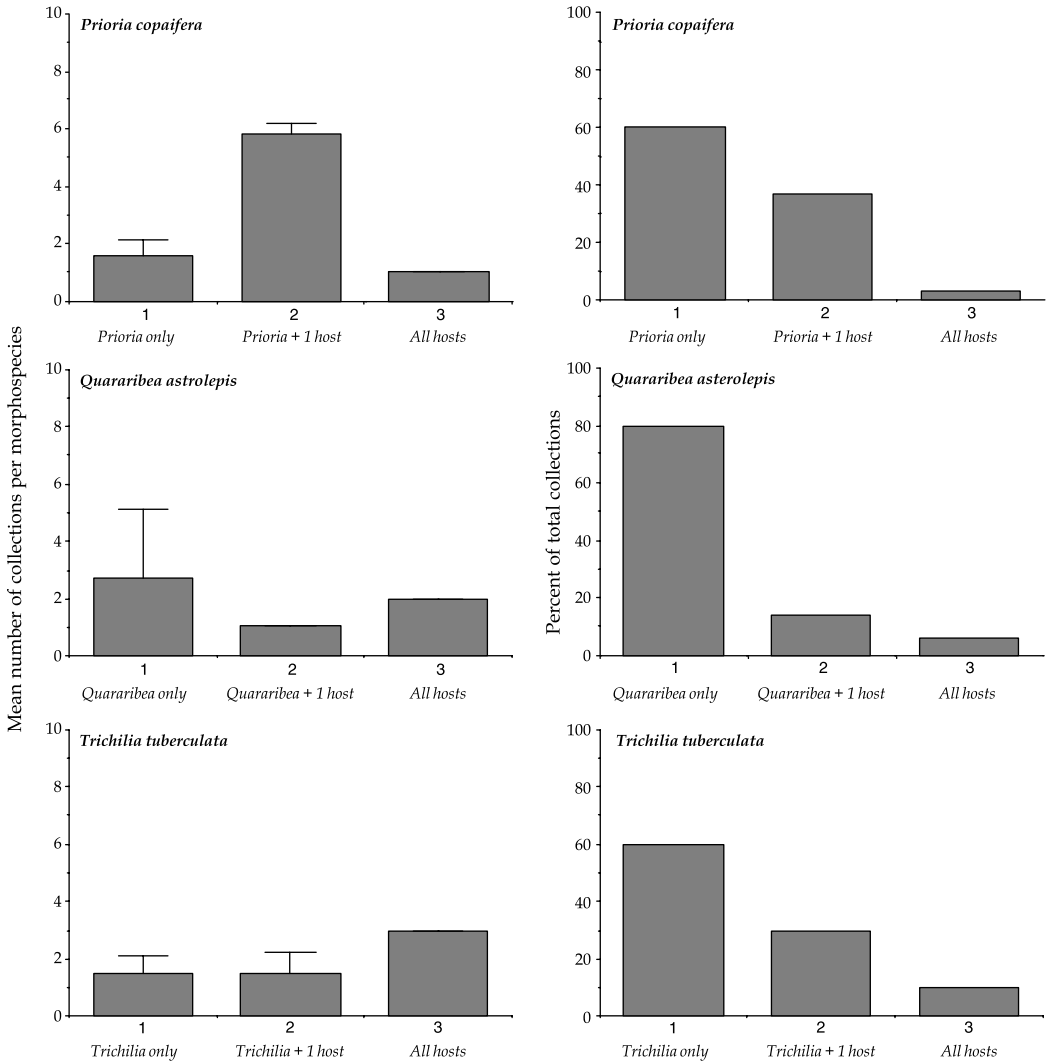
*Prioria*, the species with the lowest abundance among the studied host species within the plot, harboured the highest diversity of ascomycete and basidiomycete fungi. However, while *Prioria* is a species with relatively low density in the 50-ha FDP plot; it is a more abundant species at a larger landscape scale. On BCI it is common around Wheeler and AMNH trails 1 km from the southern boundary of the plot. Furthermore, in a forest stand at Gigante Peninsula 5 km from the 50-ha FDP plot on BCI, *Prioria* is a domi-

nant tree species composing up to 14% of the tree individuals. Elsewhere in the Panama Canal watershed *Prioria* is common along river margins and in seasonally inundated swamps accounting for up to 90% of tree individuals at some sites (Echevarría & Varón, 1988; Grauel *et al.*, 2000). Depending upon the dispersal characteristics of fungi, the potentially colonizable host population size of *Prioria* for fungi present in the plot may therefore be quite large. Unfortunately we know very little about the dispersal abilities of fungal species in natural forests. Although spore dispersal distances by air-borne fungi are generally thought to be short but unspecified (Fitt *et al.*, 1987; Malloch & Blackwell, 1992; Dix & Webster, 1995), spores of *Heterobasidium annosum* are known to travel 50–500 km from their source (Kallio, 1970).

Contrary to predictions based on local host abundance, *Trichilia* did not harbour the highest fungal diversity in this study. However, it is possible that fungal diversity was more strongly underestimated on this relative to the other hosts. This is because decay proceeds slowly in *Trichilia*. It seems likely that as trunk decay proceeds, more fungal fruiting bodies may begin to appear (Bader *et al.*, 1995). Some fungal species may not initiate sexual reproduction until more of the host is colonized, and some slow-growing fungi may require more time to develop their fruiting bodies. In contrast, in *Prioria*, fungi will need to fruit and disperse in a short period before the trunk disappears.

Wood density does not seem to be the dominant factor in determining fungal preferences because *Quararibea*, the species with intermediate

**Fig. 2** DCA ordination of the host tree species at each census based on the composition of wood-inhabiting fungi for: (a) ascomycetes and basidiomycetes (combined), (b) ascomycetes, and (c) basidiomycetes. Notation is as follows: *Prioria copaifera* (P), *Quararibea asterolepis* (Q), and *Trichilia tuberculata* (T) followed by the year.

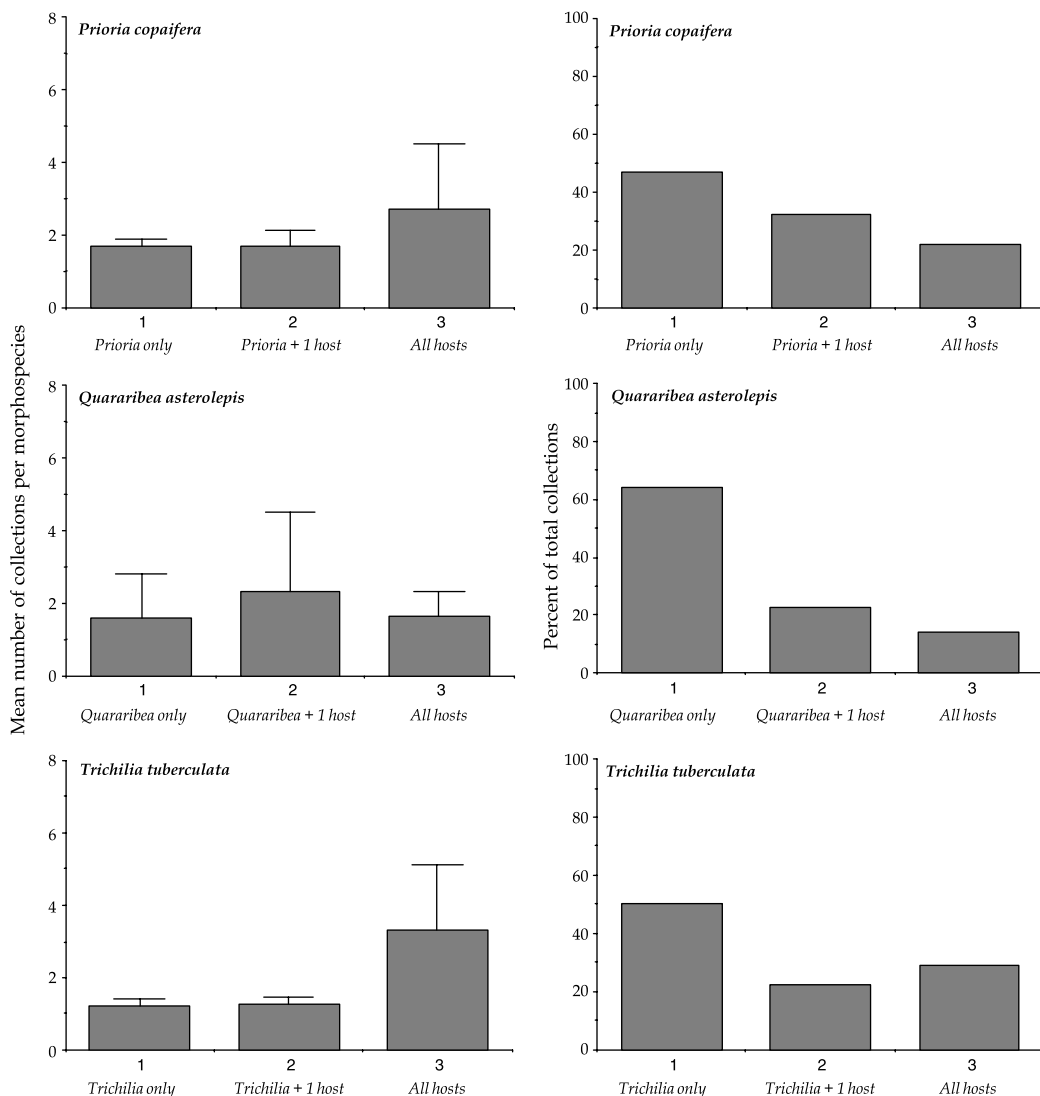


**Fig. 3** Left panels: Mean number of collections ( $\pm 1$  SD) of morphospecies of wood-inhabiting ascomycetes made from the focal host species, for morphospecies that occurred on a single host (1), two hosts (2), or on all three hosts (3). Right panels: Per cent of total collections found on one, two or three host species.

wood density, harboured the most dissimilar fungal community. Remarkably, *Trichilia* and *Prioria* share more fungal morphotypes and their communities are more alike despite very different wood densities. Concentrations of nutrients or defensive compounds in *Quararibea* wood may differ from that of the other host species, preventing it from being colonized by certain groups of fungi. Unfortunately few studies have looked

in detail at wood structure and its chemical constituents in tropical tree species. For temperate trees, there are indications that the presence of tannins may be toxic to fungi and other microorganisms and also that some fungi may be able to detoxify tannins (Scalbert, 1991).

An additional concern not addressed in this study is the geographical basis to host specificity. Although fungi may show host preferences on



**Fig. 4** Left panels: Mean number of collections ( $\pm 1$  SD) of morphospecies of wood-inhabiting basidiomycetes made from the focal host species, for morphospecies that occurred on a single host (1), two hosts (2), or on all three hosts (3). Right panels: Per cent of total collections found on one, two or three host species.

BCI it is unclear whether host requirements are fixed across the range. More intensive sampling of tropical wood-inhabiting fungi over a broad geographical area may detect patterns of local host preferences within a range distribution that exceeds that of individual host trees. This appears to be the case for two basidiomycete fungi *Rigidoporus lineatus* and *Datronia caperata*.

In earlier work on BCI they were the most common species found on all woody substrates sampled in five 500-m  $\times$  10-m transects (Gilbert *et al.*, 2002). These two species have been found in other areas of Panama. They have been found associated with *Prioria* at sites close to BCI, but were absent from *Prioria*-dominated forest in eastern Panama. In Santa Rosa National Park,

Costa Rica, Lindblad (2000) found that *D. caperata* exploits multiple hosts and attains high abundance. In contrast in Panama, *D. caperata* has been found in mangroves on the Caribbean coast where it is restricted to only one of three available hosts (Gilbert *et al.*, 2002).

Therefore, our understanding of host preference is incomplete. In this study many fungal morphotypes were present on a single host but were also encountered only a few times. We cannot test the host preference of these fungi. This problem is also apparent from a census of polypores conducted at the same site in 1993, where 46 fungal morphotypes were found on 39 host species (Gilbert *et al.*, 2002). With an almost one-to-one ratio of fungal morphotypes to host species it is difficult to say whether these fungi were specialists or generalists. For example in 1993, *Rigidoporus microporus* and *Rigidoporus* sp. no. 94 were collected just once on *Quararibea*; additional collections in 1994, 1996, and 1997 were only made in *Quararibea* suggesting host preference for these rare fungi. A high degree of host preference is also reflected in the consistent interannual grouping of fungal communities found on different populations of a single host tree sampled in different years. This would not be expected from colonization at random.

#### Variation in community structure between basidiomycetes and ascomycetes

Patterns of diversity were remarkably similar between ascomycetes and basidiomycetes. Among host trees, the diversity of both fungal classes were highest on *Prioria* and lowest on *Quararibea*. Both fungal groups were characterized by a large proportion of rare morphotypes. Wood-inhabiting basidiomycetes were more diverse than ascomycete fungi. This is in common with patterns found in temperate areas where ascomycetes comprise less than 20% of all fungal species (Bujakiewicz, 1994). A similar result was obtained when studying *Prioria* in five different forest stands in Panama. In four stands ascomycetes were less diverse than basidiomycetes, and their first-ranked morphotypes attained high dominance (Ferrer, unpublished data). In the present study, differences in ascomycete diversity were more pronounced among the tree species than they were for basidiomycetes (Fig. 1b) with a clearly

less steep ascomycete species accumulation curve for *Quararibea*. This pattern arises from the high dominance of a few morphotypes.

Our study showed that tropical fungal communities are dominated by fungi that have wide host ranges. Many of the morphotypes collected here have also been described from the polypore flora of East Africa (Ryvarden & Johansen, 1980). Nonetheless, in the local context, some fungi seem to prefer particular host tree species on BCI. Host preference is difficult to measure and more sampling over more years is needed since most of the host trees occur at low densities in the stand (frequency < 1 individual/ha). Mortality rates for larger trees (= 10 cm d.b.h.) rarely exceed 2%/year (Leigh, 1999) and therefore the number of available dead trunks for individual host species may be only 0.01/ha/year. This is perhaps the greatest constraint on our ability to make extrapolations to estimate the global diversity of wood-inhabiting fungi.

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#### SUPPLEMENTARY MATERIAL

The following material is available from: <http://www.blackwellpublishing.com/products/journals/suppmat/DDI/DDI039/DDI039sm.htm>

**Table S1.** Number of collections of Basidiomycete and Ascomycete morphotypes found on each host species in 1994, 1996, and 1997. In the present study, fungal collections were only classified to morphotypes, although some ascomycetes and basidiomycetes have now been identified to species. Morphotype assignments were made from comparison of macroscopic and microscopic characteristics.

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