Biodiversity of wood-inhabiting fungi in Israeli pine forests

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Czederpiltz, D. L. L. (Dept. of Plant Pathology, 1630 Linden Dr., Russell Laboratories, University of Wisconsin–Madison, Madison, WI 53706, U.S.A.), K. Wikler (UC Cooperative Extension, 1131 Harbor Bay Parkway, Suite 131, Alameda, CA 94501, U.S.A.), M. R. Rademacher (Nutra-Park Inc., 3225 Deming Way, Suite 140, Middleton, WI 53562, U.S.A.), T. J. Volk (Dept. of Biology, 3024 Cowley Hall, University of Wisconsin–La Crosse, La Crosse, WI 54601, U.S.A.), Y. Hadar (The Hebrew University of Jerusalem, Faculty of Agriculture, P.O. Box 12, Rehovot 76-100, Israel) & J. Micales (Center for Forest Mycology Research, USDA–Forest Service, Forest Products Laboratory, One Gifford Pinchot Drive, Madison, WI 53726, U.S.A.). Biodiversity of wood-inhabiting fungi in Israeli pine forests. Memoirs of The New York Botanical Garden 89: 191-202, 2004.—During the twentieth century the Jewish National Fund (JNF) planted more than 200 million trees in Israel. These newly developing forests provide an opportunity to study the development of fungal communities. This study was initiated to quantify taxa richness and abundance of wood-inhabiting corticioid and polyporoid fungi (including heterobasidiomycetes) in eight even-aged forests dominated by *Pinus halepensis* (Aleppo pine). Four of the stands were 5-15 years of age, and four were 30-45 years of age. Of the four younger stands, three were previously planted to *P. halepensis.* Each stand was sampled by running eight transect lines radiating from a central point, and establishing two dusters of five 25 m^2 plots along each line, for a total sampling area of 2000 m^2 per site. Taxa accumulation curves were generated for each site to assess the completeness of sampling. A total of 78 taxa was observed in all eight sites, with 62 taxa in the four old stands and 53 taxa in the four young stands. The average number of taxa in the old stands was 32, while the average number of taxa in the young stands was 26.

KEY WORDS: Aphyllophorales, Basidiomycete, Corticiaceae, heterobasidiomycete, Israel, Polyporaceae, polypore, species richness

Introduction

Pinus halepensis Mill. (Aleppo pine) is the only pine species native to Israel. Native pine forests, however, are essentially nonexistent in current-day Israel, with only two minor populations remaining. Over the last 100 years, the Jewish National Fund (JNF), which is also known as Keren Kayemeth LeIsrael (KKL), has created huge tracts of new forests in Israel (Figure 1). Planting operations have focused primarily on monocultures and simple polycultures of *P. halepensis,* although a few other native and nonnative species have been used, including *Cupressus sempervirens, Eucalyptus camadulensis, Pinus brutia, P. pinea,* and *Quercus calliprinos.* Over the last two decades, many significant management issues have arisen regarding the occurrence of pests and the effects of drought stress in the newly established forests. In addition, there has been a rapid accumulation of woody debris on the forest floors, which has generated concerns about the fire danger presented by these forests. This study was initiated to gather baseline information about the wood-inhabiting, and potentially wood-decomposing, fungi in *P. halepensis* plantation forests.

While previous studies have yielded useful descriptions of fungi found throughout Israel (Binyamini, 1981, 1982, 1983, 1993). fungal communities have not been systematically inventoried to quantify trends in species richness and abundance. By using plot-based, quantitative sampling methods, this study provides a description of the fungal communities in younger and older *P. halepensis* plantations, as well as a preliminary assessment of the diversity and abundance of wood-inhabiting fungi within each stand.

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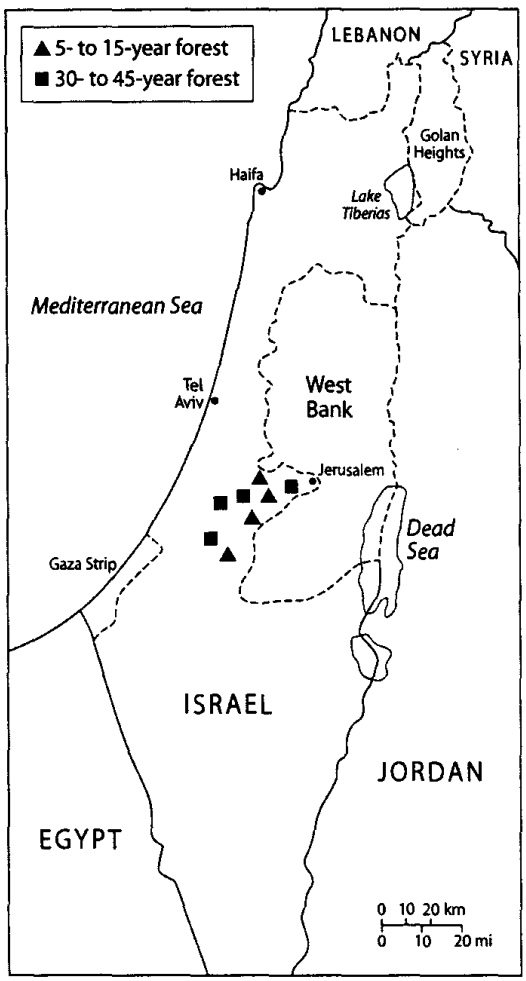


FIG. 1. Map of Israel showing approximate locations of plots.

Because of the persistent nature of their fruiting bodies and their importance in forest ecosystems (Czederpiltz, 2001), our sampling focused on wood-inhabiting fungi that produce polyporoid or conicioid fruiting bodies. These fungi are generally found in the families Polyporaceae and Corticiaceae, which are known to be phylogenetically diverse (Gilbertson & Ryvarden, 1986; Ginns & Lefebvre, 1993; Hibbett et al., 1997). However, some species that produce corticioid or polyporoid fruiting bodies are not found in either the Polyporaceae or the Coniciaceae. These species are heterobasidiomycetes found in orders such as the Tremellales, the Auriculariales, the Dacryomycetales, and the Tulasnellales. Our sampling regime included any species that produced fruiting bodies with either a more or less poroid hymenophore (these species can be found in Gilbertson & Ryvarden, 1986) or a flat, wrinkled, or toothed hymenophore (these species can be found in the works of Ginns & Lefebvre, 1993, or Parmasto, 1997). Because these types of fungi tend to produce inconspicuous fruiting bodies, they are often overlooked in mycological surveys, despite their importance to forest health. This study was therefore intended to provide information about a particular Israeli forest ecosystem, while at the same time contributing to the more universal body of knowledge concerning the occurrence of these little-studied fungi.

Methods

To compare the fungal community both among sites and between treatments, four sampling sites were established in older forests and four were established in younger forests. All sites were chosen from JNF forests in central Israel, where the average annual rainfall is 500-600 mm and the average annual temperature is 17–19°C (Danin & Orshan, 1999). The plots were placed in even-aged stands that were large enough to accommodate our sampling design as described below. The many stands that were planted in narrow patches were not selected as sampling sites. Forest maps were randomly selected from the JNF GIS database until four plots of each age-class were located. The JNF has been planting decreasing numbers of *P. halepensis* over the last two decades due to increasing disease and pest pressure; therefore, we were unable to locate four newly forested stands of *P. halepensis* in the central region of Israel. Thus, two of the young stands selected were composed of *P. halepensis* that regenerated after accidental wildfires in the previous forest stands (all remaining timber was subsequently clear-cut). The third young stand was a *P. halepensis* stand that was replanted after the previous stand had been clear-cut and burned as a management tool in preparation for replanting. The fourth stand was planted in an open section of land that was surrounded by older plantation-forests. This site was burned before planting to clear the preexisting vegetation, and the forest was thinned approximately 10 years after the planting date. The site locations and stand ages are shown in Figure I and are listed in Table I.

The sites were sampled between 5 January and 20 March 2000, with older and younger sites being sampled in alternating order. The sites were sampled in the following order: 1, 5, 2, 6, 3, 7, 4, 8. At each site, two clusters of five plots were established at randomly cho-

TABLE I

SITE LOCATION DATA FOR SELECTED ISRAELI PINE FORESTS. ALL GPS DATA WERE TAKEN AT THE CENTER OF THE SITE. SITES 1–4 WERE DESIGNATED OLDER STANDS, WHILE SITES 5-8 WERE DESIGNATED YOUNGER STANDS.

	Latitude	Longitude	Site history	Age class (years)
Site 1	31°49.141'N	35°00.518'E	Planted 1968	30–45
Site 2	31°47.354'N	35°01.519'E	Planted 1957	30–45
Site 3	31°48.354'N	34°59.424'E	Planted 1963–1964	30–45
Site 4	31°40.365'N	34°53.305'E	Planted 1957	30–45
Site 5	31°47.367'N	34°59.834'E	Regenerated 1994	5–15
Site 6	31°43.188'N	34°51.736'E	Planted 1988	5–15
Site 7	31°48.292'N	35°03.489'E	Regenerated 1995	5–15
Site 8	31°45.482'N	34°52.014'E	Regenerated 1993	5–15

sen points along a set of eight transect lines, all of which radiated from a central point (Fig. 2A). Sampling on multiple, nonparallel lines reduced the possibility of inadvertently picking up preexisting linear trends within the forests, which was particularly important in planted forests. The overall configuration of the plots was chosen for ease of sampling, as well as to allow for an analysis of autocorrelation at various spatial scales. No two sites were closer together than 1.5 km.

Each plot was circular with a 2.8 m radius, and not closer than I m from its nearest neighbor (Fig. 2B), and each cluster of five plots was at least 10 m from the closest neighboring cluster. The clusters were arranged so that a second sampling could be performed within the site without overlapping sampling of plots (this could be done by placing additional clusters on the opposite sides of the transect lines). The plot sizes were chosen to facilitate comparisons between the present data set and a data set of wood-inhabiting fungi in Wisconsin and Michigan compiled by Czederpiltz (2001), in which the sampling units were square 5 × 5 m plots.

All polyporoid and corricioid fungi to 2 m off the ground in each plot were recorded. Unless the fungus was easily identified in the field, it was collected, dried, and identified in the laboratory. Microscopic observations were made using an Olympus BH-2 compound

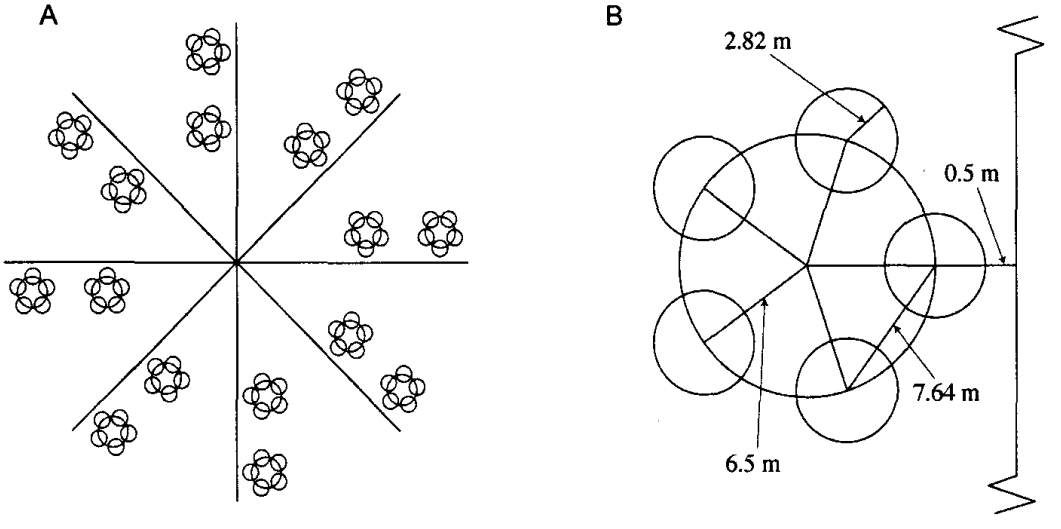


FIG. 2. Plot layout. A. At each site, a plot was constructed that consisted of 16 clusters of five plots, giving a total of 80 plots per site. Each plot had a radius of 2.82 m and an area of 25.0 m^2; a total of 2000 m^2 was therefore sampled at each site. B. Plots were evenly spaced along the circumference of a circle with a radius of 6.5 m (thus producing a "cluster" of five plots), which gave plot boundaries that were separated by at least 1 m.

microscope at 400× and under oil immersion at 1000×. Fruiting bodies were identified to species using morphological characters. When a species could not be matched to a known Latin description, it was assigned to a genus and given a number (e.g., *Sistotrema* sp. #1). Voucher specimens were deposited in the herbarium of the Center for Forest Mycology Research (CFMR) located in the USDA–ForestService Forest Products Laboratory (Madison, Wisconsin). If a fungus was seen frequently within a site, it was given a "field name" specific for that site. Thus, the fungus did not need to be collected repeatedly in any given site, even if its scientific name was not known.

In the laboratory, samples were identified using available keys and descriptions. In many cases the specimens were not identified to species level because of difficulties in designations or because the specimens did not fit any of the described species for a particular genus. Taxa concepts were often broadened to include samples that could represent distinct species. For example, the *Dacrymyces* complex includes at least two distinct species (*D. punctiformis* and *D. capitatus*) and the *Oligoporous* complex includes at least three distinct species (*O. hibernicus, O. inocybe,* and a third, unidentified species). Such variants were grouped into a single taxon because some of the samples blurred the lines between otherwise distinct taxa, and because some of the "field names" turned out to be ambiguous in distinguishing macroscopically similar, but microscopically distinct, taxa. Thus, the total number of taxa and number of taxa present at each site are conservative estimates of the number of species present.

Taxa abundance graphs and taxa accumulation curves were calculated for each site. Taxa abundance graphs were based on the total number of plots in which each taxon was collected per site (Fig. 3); multiple collections of the same fungus within a single plot were ignored. Taxa accumulation curves were used to compare taxa accumulation by plot and by cluster at each site (Fig. 4). as well as to compare average taxa accumulation in old and young forests (Fig. 5). Plot-level accumulation curves were generated based on the number of individual plots in which each taxon was found at a site; multiple collections within a plot were ignored. Likewise, taxa accumulation curves generated with the cluster data were based on the number of dusters in which each taxon was collected, and multiple collections of the same fungus within a duster were ignored.

All accumulation curves were calculated using Sanders's (1968) rarefaction equations as modified by Hurlbert (1971). These equations allow for the exact calculation of the mean species accumulation curve over all possible permutations of sampling order. The equation used to construct an exact mean species accumulation curve is given by Smith et al. (1979) as

$$\hat{s}(m) = \sum_{i=1}^{k}\left[1 - \binom{M - L_i}{m} \Big/ \binom{M}{m}\right]$$

Where:

$\hat{s}(m)$ = the expected number of species encountered after sampling m units

m = the number of "observed" sampling units, from o to M

M = the total number of sampling units

L_i = the number of sampling units in which species i is present

K = the total number of species

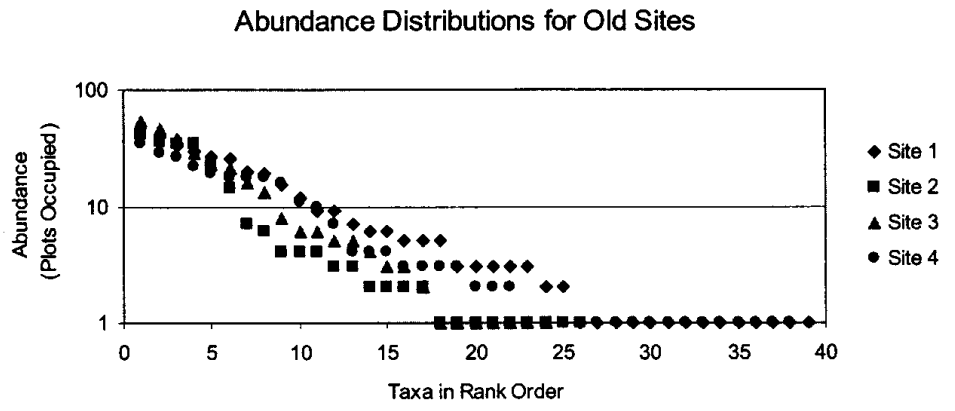
Results

During the course of the study 1888 samples were collected. Of these, 265 were either infertile or in too poor condition to identify. There were also 562 fungal observations recorded in the field, for a total of 2450 data points (combining identifiable collections and observations). In the eight sites combined, there were 78 different taxa (Table 2). Two of the older sites (Site 1 and Site 4) had the greatest number of taxa per site (39 and 38, respectively). The fewest taxa were observed at Site 7 (23 taxa), which was a young stand, and at Site 3 (24 taxa), which was an older stand. There was no significant difference (α = 0.05) between the average taxa richness in the young versus the old stands (ANOVA, P = 0.19), though there is a visible offset in the average young versus old taxa accumulation curves (Fig. 4).

On all but two of the sites, the most dominant taxon occurred in over 50% of the plots, and on one site (Site 7) the dominant taxon, *Peniophora lycii,* occurred in over 75% of the plots (Fig. 3B, Table 2). Interestingly, Site 7 had a conspicuous absence of four taxa (*Ceriporia purpurea, Dacrymyces* complex, *Hyphodontia subalutacea,* and *Crustoderma cornea*) that were common at the other seven sites. There were also certain fungi that were abundant at a particular site, but rare at all other sites. For example, *Radulomyces confluens* occurred in 34% of the plots at Site 1, but in no more than 4% of the plots at any other site. Likewise, *Clavulicium macounii* occurred in 19% of the plots at Site 6, but was absent to rare in all the other sites. In addition, *Phanerochaete sanguinea* occurred in 22.5% of the plots at Site 8, but was absent at every other site.

The taxa accumulation curves indicated that sampling was fairly complete for each site (based on the slope of the curves approaching zero); therefore, increas-

A



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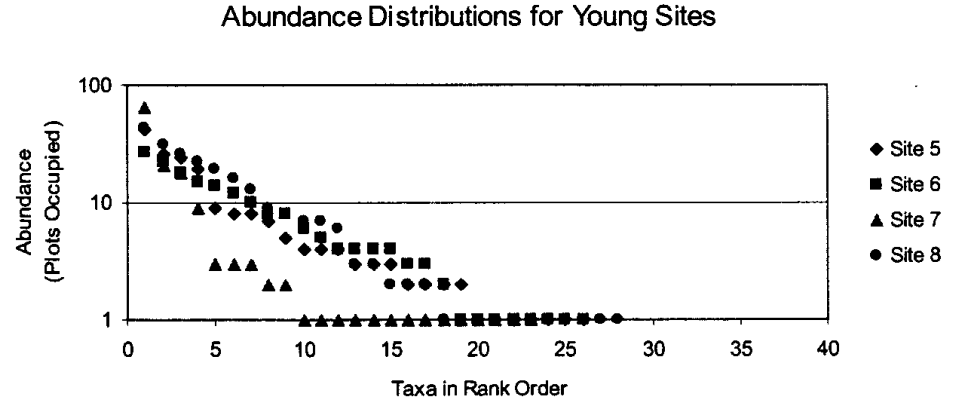


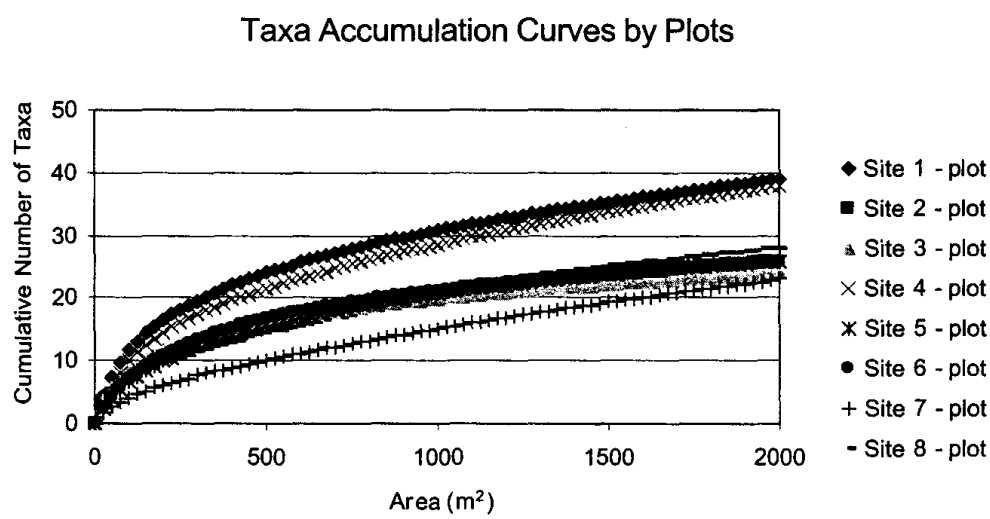
FIG. 3. Abundance distributions for fungal taxa in *Pinus halepensis* forests. Abundance data were based on the number of plots in which a taxon was observed per site, and taxa are listed in rank order of abundance. A. Abundance distributions for the four older sites. B. Abundance distributions for the four younger rites.

ing the sampling area probably would not significantly increase the number of taxa observed (Fig. 4) (Magurran, 1988). Furthermore, the taxa accumulation curves based on the cluster data are essentially indistinguishable from the curves generated using the plot data, suggesting that autocorrelation probably is not a significant issue in this data set (Czederpiltz, 2001). The accumulation curves of all eight plots were shaped similarly, except for that of Site 7, which has a much lower initial slope than any of the other curves. Although the shapes of the curves for Sites 1 and 4 were similar to those from all other sites, the curves for these two sites were larger in magnitude.

Discussion

Despite the dominating host monoculture of Pinus *halepensis* (Fig. 6), the variability in site histories, especially among the young sites, likely contributed to the variability observed in the fungal communities. The site that had experienced the most extensive fire (over 6 km^2 burned) had the most dominant community, with one

A



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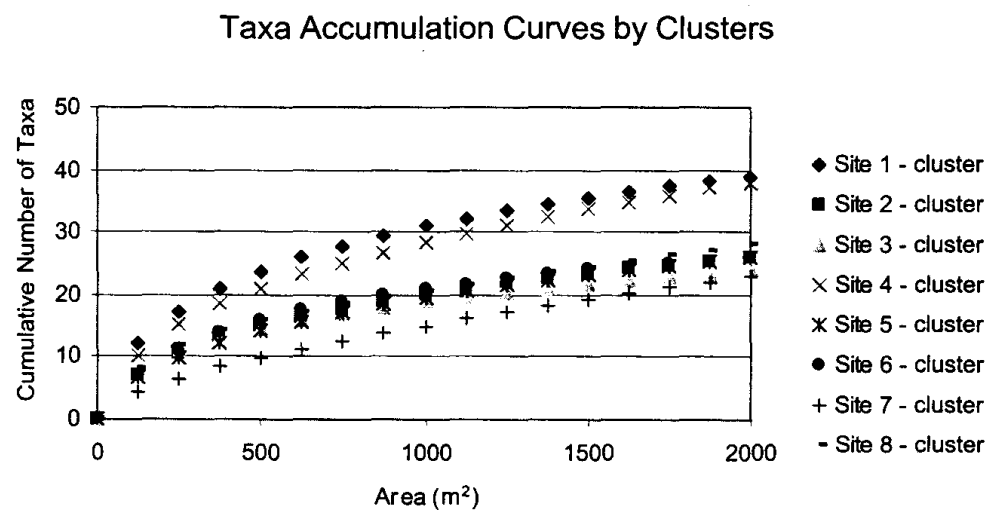

FIG. 4. Taxa accumulation curves for fungal taxa in *Pinus halepensis* forests. All accumulation curves were generated using rarefaction equations, which average over all possible permutations of sampling order. A. Accumulation curves generated using plot data (i.e., area was accumulated in 25 m^2 increments). B. Accumulation curves generated using cluster data (i.e., area was accumulated in 125 m^2 increments).

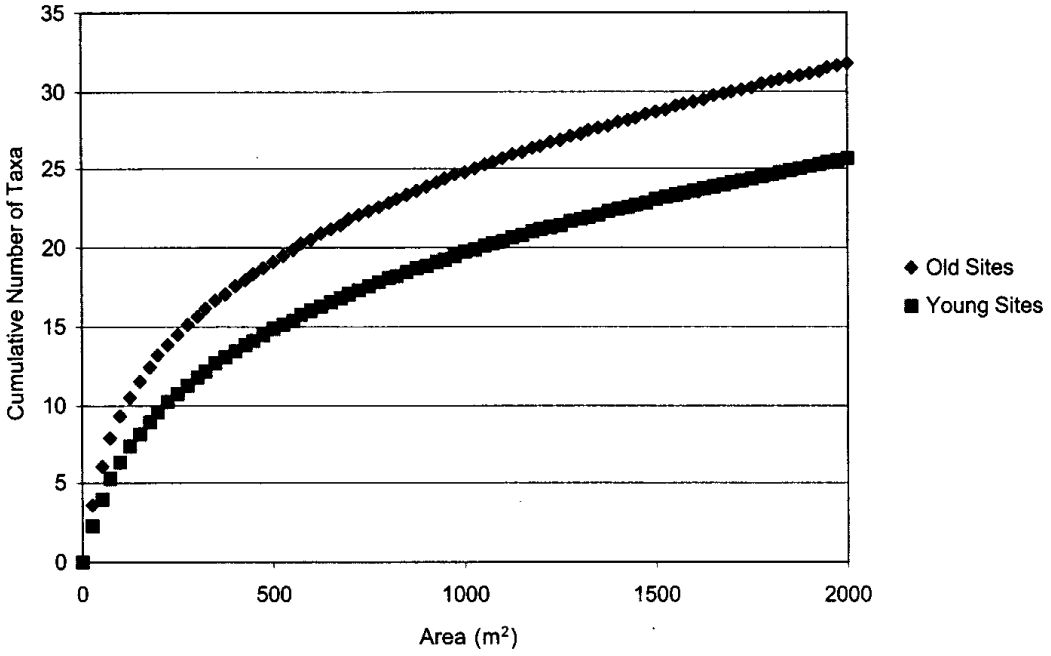

FIG. 5. Average taxa accumulation curves for wood-inhabiting fungi in *Pinus halepensis* forests in old and young sites. These curves were generated by averaging the four accumulation curves for each age class. Plot-based data (see Fig. 3) were used to calculate these curves.

taxon present in over 75% of the plots (Site 7). Interestingly, the abundance of this single taxon (*Peniophora lycii*) correlates to the absence of taxa common in the other seven sites (*Ceriporia purpurea, Dacrymyces complex, Hyphodontia subalutacea,* and *Crustoderma cornea*). This suggests that the most dominant taxon in Site 7 may have flourished in the absence of competition from other potential dominants which have not (re)colonized the site since the fire. Alternatively, this taxon may simply have been well-suited for the particular environmental conditions found at this site.

This degree of single-taxon dominance was not exhibited in any of the other three young forests, perhaps due to remnant fungal populations that survived the less severe burns (none more than 1 km^2 in extent), or perhaps due to faster recolonization because of closer proximity to mature forests. Interestingly, the other young site (Site 5) that experienced a wildfire had a relatively low number of dominant taxa. All sites had six or more taxa that occurred in more than 10 plots, with the exception of Sites 5 and 7 (Site 5 had only four such taxa, and Site 7 had only three) (Fig. 3, Table 2). It should also be noted that in addition to having similar fire histories, Sites 5 and 7 were composed of trees that were younger than those in the other two young stands.

Due to the unique proportion of dominant and rare taxa that was found at Site 7, the taxa accumulation curve for this site has a much lower initial slope than the curves of the other sites. This was true even though the total number of taxa collected at this site was comparable to the number found in Sites 2, 3, 5, 6, and 8. Thus, if sampling had been limited to 1000 m^2 or less, we might have incorrectly concluded that Site 7 was significantly less taxa-rich than the other sites (Fig. 4).

Although species composition of the forest understories was not formally quantified at each site, the two sites with the greatest taxa richness (Sites 1 and 4) had noticeably denser understories than any of the other sites. These understories were primarily composed of *Quercus calliprinos, Rhamnus* sp., *Cistus villosus,* and *Pistacia palacstina.* Thus, it is possible that if the sites had been chosen by understory characteristics rather then by age class, stronger trends in taxa richness may have been observed. In addition, stronger statistical trends in taxa richness would likely have been observed if more sites had been sampled. If variability of taxa richness had

TABLE II

FUNGAL TAXA FOUND IN ISRAELI *PINUS HALEPENSIS* FORESTS, AND THEIR ABUNDANCE AT EACH SITE

	Abundance (number of plots in which taxon was found)										
	30–45 yrs				5–15 yrs				Totals		
Taxa	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Site 8	All sites	Old sites	Young sites
Aleurodiscus dextrinoideocerussatus Moreno, Blanco & Manjon	5	7	1	1	5				19	14	5
Aleurodiscus thoenii (Boidin. Lanquetin & Gilles) Nuñez & Ryvarden		3		4					7	7	
Amphinema byssoides (Pers.:Fr.) J. Erikss.[1]	5	1					2		8	6	2
Amylostereum sp. #1	2				2		1		5	2	3
Antrodia cf. *serialis* (Fr.) Donk							1		1		1
Asterostroma cf. *cervicolor* (Berk. & M. A. Curtis) Massee	1			1	2	1		1	6	2	4
Athelia sp. #1	1								1	1	
Athelia sp. #2			1						1	1	
Basidiodendron cinereum (Bres.) Luck-Allen				1						1	1
Botryobasidium candicans J. Erikss.	3					1			4	3	1
Byssomerulius albostramineus (Torrend) Hjortstam								1	1		1
Ceratobasidium cornigerum (Bourdot) D. P. Rogers	1	4	1	2	1		1		10	8	2
Ceriporia purpurea (Fr.:Fr.) Don	15	36	16	18	19	27		13	144	85	59
Clavulicium macounii (Burt.) J. Erikss. & Boidin ex Parmasto				3		15		3	21	3	18
Coniophora arida (Fr.:Fr.) P. Karst.	7		6	16	4	4	9	9	55	29	26
Coniophora olivacea (Fr.:Fr.) P. Karst.							1		1		1
Corticium roseocarneum (Schwein.) Hjortstam						1	3		4		4
Crustoderma corneum (Bourdot & Galzin) Nakasone	20	4	23	22	8	22		31	130	69	61
Crustoderma dryinum (Berk. & M. A. Curtis) Parmasto								1	1		1
Dacrymyces complex[2]	33	41	29	19	26	8		22	178	122	56
Dacryobolus sudans (Alb. & Schwein.:Fr.) Fr.	1	1							2	2	
Exidia sp. #1	1						1		2	1	1
Exidia sp. #2	1								1	1	
Exidia pithya (Alb. & Schwein.) Fr.	5								5	5	
Exidiopsis calcea (Pers.) K. Wells				1					1	1	
Exidiopsis cf. *grisea* (Pers.) Bourdot & Maire				1					1	1	
Gloeophyllum sepiarium (Wulfen:Fr.) P. Karst.					3				3		3
Gloeophyllum subferrugineum (Berk.) Bondartseva & Singer	3		2		7		2	1	15	5	10
Henningsomyces candidus (Pers.:Fr.) Kuntze	12	3	38	3		10		16	82	56	26
Hyphoderma argillaceum (Bres.) Donk								8	8		8

	Abundance (number of plots in which taxon was found)										
	30–45 yrs				5–15 yrs				Totals		
Taxa	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Site 8	All sites	Old sites	Young sites
Hyphoderma tsugae (Bun) J. Erik. & Å. Strid								1	1		1
Hyphoderma medioburiense (Bun) Donk									0	0	
Hyphoderma praetermissum (P. Karst.) J. Erik. & Å. Strid	40	22	53	18	9	18	3	19	182	133	49
Hyphoderma sp. #1						1	1		2		2
Hyphoderma sambuci (Pen.) Jülich	19	2	6	2	2	3		1	35	29	6
Hyphodermella corrugata (Fr.) J. Erikss. & Ryvarden	26	14	13	27	4	4	1	43	132	80	52
Hyphodontia juniperi (Bourdot & Galzin) J. Erikss. & Hjortstam				1					1	1	
Hyphodontia subalutacea (P. Karst.) J. Erikss.	6	2	5	34	1	14		6	68	47	21
Lachnella alboviolascens (Alb. & Schwein.:Fr.) Fr.	2						1		3	2	1
Litschauerella clematitis (Bourdot & Galzin) J. Erikss. & Ryvarden	1				1				2	1	1
Meruliopsis corium (Pers.:Fr.) Ginns	9			11	3	2	18	2	45	20	25
Oligoporous complex[3]	30	34	46	10	24	8	21	2	175	120	55
Pellidiscus cf. *pallidus* (Berk. & Broome) Donk							1		1		1
Peniophora lycii (Pers.) Höhn. & Litsch.	48	34	21	29	42	12	64	26	276	132	144
Peniophora pini (Schleich.:Fr.) Boidin	6	1	3	2	8	1	3		24	12	12
Phanerochaete sanguinea (Fr.:Fr.) Pouzar				18					18	18	
Phanerochaete tuberculascens Hjortstam	3	2	1				1		7	6	1
Phellinus sp. #1	1								1	1	
Phlebia centrifuga P. Karst								1	1		1
Phlebia deflectans (P. Karst.) Ryvarden	3								3	3	
Phlebiopsis ravenellii (Cooke) Hjortstam								1	1		1
Piloderma cf. *lanatum* (Jülich) J. Erikss. & Hjortstam							1		1		1
Platygloea cf. *decipiens* G. W. Martin				1					1	1	
Polyporus brumalis (Pers.:Fr.) Fr.	3	2	1	4		1			11	10	1
Pulcherricium caeruleum (Lam.:Fr.) Parmasto				1			1		2	1	1
Radulomyces confluens (Fr.:Fr.) M. P. Christ.	27		3		1	3		1	35	30	5
Scopuloides leprosa (Bourdot & Galzin) Boidin et al.					1				1		1
Scytinostroma portentosum (Berk. & M. A. Curtis in Berk.) Donk		1							1	1	
Sebacina epigaea (Berk. & Broome) Bourdot & Galzin		1							1	1	
Sistotrema coroniferum (Höhn. & Litsch.) Donk				1		5			6	1	5
Sistotrema cf. *diademiferum* (Bourdot & Galzin) Donk				1					1	1	

TABLE II

FUNGAL TAXA FOUND IN ISRAELI *PINUS HALEPENSIS* FORESTS, AND THEIR ABUNDANCE AT EACH SITE (*continued*)

	Abundance (number of plots in which taxon was found)										
	30—45 yrs				5–15 yrs				Totals		
Taxa	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Site 7	Site 8	All sites	Old sites	Young sites
Sistotrema sp. #1[4]					1				1		1
Steccherinum fimbriatum (Pers.:Fr.) J. Erikss.[5]		6	5	7		4		7	29	18	11
Subulicium minus Hjortstam	1								1	1	
Subulicystidium longisporum (Pat.) Parmasto			1						1	1	
Thanatephorus cucumeris (A. B. Frank) Donk					1				1		1
Tomentella italica (Sacc.) M. J. Larsen[6]	1	1		4	3	1	1		11	6	5
Tomentellastrum caesiocinera Svrcek	1			1		1			3	2	1
Tomentellopsis cf. *zygodesmoides* (Ellis) Hjortstam		1	4				1	7	13	5	8
Trechispora farinacea (Pers.:Fr.) Liberta	9	1	8	3		6		1	28	21	7
Trechispora microspora (P. Karst.) Liberta				1					1	1	
Trechispora praefocata (Bourdot & Galzin) Liberta			1	1					2	2	
Tubulicrinis calothrix (Pat.) Donk	1							2	3	1	2
Tulasnella sp. # 1				1					1	1	
Tulasnella tomaculum P. Roberts				1					1	1	
Uthatobasidium sp. #1[7]	1	4			2	4		1	12	5	7
Vuilleminia megalospora Bres.				3					3	3	
Xenasma sp. # 1		1		1	4			3	9	2	7
Total number of taxa	38	26	24	38	26	26	23	28	78	62	53

[1] *Amphimema byssoides* includes an albino variation in Site 7, which fits the description of *A. tomentellum* (Bres.) M. P. Christ.

[2] Due to taxonomic problems and difficulties encountered with identification, all *Dacrymyces* species were considered as one taxon.

[3] Includes *Oligoporous hibernicus, Oligoporous inocybe*, and a third *Oligoporous* taxa with cylindrical, rather than allantoid, spores.

[4] Resembles *Sistotrema* sp. B & Jerikss 4452.

[5] A great deal of variation was encountered in this taxon in terms of color and rhizomorph production.

[6] This taxon may include more than one species.

[7] Variation in spore morphology suggests that this taxon may be composed of more than one species.

FIG. 6. Older *Pinus halepensis* forest from the top of Mount Carmel, Israel. Dead branches and light foliage color are from *Sphaeropsis sapinea* colonization.

remained approximately the same, the sampling of one additional replicate (i.e., one additional old and young stand) would have produced a significant p-value ($\alpha = 0.05$) for the difference in taxa richness between forest age classes.

Two additional variables probably had a strong influence on the present data set. There had been a drought in Israel for the two years preceding the sampling, which, compounded by a late onset of winter rains during the collection period, presumably influenced the particular set of fungi that fruited within the field season. Without two collection periods per site during the field season, as well as another entire year of data, the conclusions that can be drawn from the present data have obvious limitations. However, these data document the presence of a diverse group of wood-inhabiting taxa in the plantation-forests, which will help to facilitate future exploration of the wood-decay capabilities of this community.

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