Functional and causal relationships between indoor and outdoor airborne fungi

De-Wei Li and Bryce Kendrick

Abstract: From May to October, relationships of total numbers of airborne fungal propagules between indoor and outdoor sampling sites were very strong, particularly for *Alternaria* and *Leptosphaeria*, while that for unidentified ascospores was positive but to a lesser degree. Indoor and outdoor counts of *Cladosporium*, *Epicoccum*, *Ganoderma*, unidentified spores, hyphal fragments, and biodiversity (total number of fungal genera) were also significantly positively related. There appeared to be no functional relationship between *Aspergillus/Penicillium* conidia in indoor and outdoor air. From November to April, indoor and outdoor counts of *Alternaria*, *Ganoderma*, and hyphal fragments displayed negative relationships, but there was a positive correlation for *Cladosporium*, *Epicoccum*, *Leptosphaeria*, unidentified ascospores, total fungal spores, unidentified spores, and biodiversity. Once again, no functional relationship was detected between *Aspergillus/Penicillium* indoors and outdoors. The functional relationships of airborne fungi with indoor environmental factors are examined and discussed. A lack of causal relationships, as detected by path analysis, indicates that airborne spores of *Alternaria*, *Leptosphaeria*, unidentified ascospores, *Coprinus*, and *Ganoderma* came mainly from outdoor sources. All path models fitted this hypothesis well, except for *Aspergillus/Penicillium*. On the other hand, path analysis suggested that there were probably indoor sources of *Cladosporium*, *Epicoccum*, *Aspergillus/Penicillium*, unidentified basidiospores, and unidentified spores. Most of the models explained a large proportion of variance of indoor airborne fungi.

Key words: airborne fungal spores, redundancy analysis, path analysis.

Résumé : De mai à octobre, les relations des nombres totaux de propagules fongiques dans l'air, sur des sites d'échantillonnage localisés à l'intérieur et à l'extérieur, sont très fortes, particulièrement pour les *Alternaria* et les *Leptosphaeria*, alors qu'elles sont positives pour des ascospores non-identifiées, mais à un moindre degré. Les décomptes, à l'intérieur et à l'extérieur, des *Cladosporium*, *Epicoccum*, *Ganoderma*, des spores non-identifiées, des fragments d'hyphes ainsi que la biodiversité (nombre total de genres fongiques) montrent également une relation positive. Il ne semble pas y avoir de relation fonctionnelle entre les conidies des *Aspergillus/Penicillium* à l'intérieur et à l'extérieur. De novembre à avril, les décomptes, à l'intérieur et à l'extérieur, des *Alternaria*, *Ganoderma*, et des fragments d'hyphes montrent des relations négatives, mais il n'y a pas de corrélation positive pour les *Cladosporium*, *Epicoccum*, *Leptosphaeria*, les ascospores non-identifiées, les nombres totaux de spores fongiques, les spores non-identifiées et la biodiversité. Encore une fois, aucune relation fonctionnelle n'a pu être décelée pour les *Aspergillus/Penicillium*, à l'intérieur et à l'extérieur. Les auteurs examinent et discutent les relations fonctionnelles des champignons portés dans l'air avec les facteurs environnementaux prévalant à l'intérieur. L'absence de relation causale, tel que décelé par l'analyse des sentiers (Path Analysis), indique que les spores portées dans l'air des *Alternaria*, *Leptosphaeria*, d'ascospores non-identifiées, de *Coprinus* et de *Ganoderma* proviennent principalement de sources externes. Tous les modèles de sentiers supportent bien cette hypothèse sauf pour les *Aspergillus/Penicillium*. D'autre part, l'analyse des sentiers suggère qu'il y a probablement des sources internes de *Cladosporium*, *Epicoccum*, *Aspergillus/Penicillium*, de basidispores non-identifiées et de spores non-identifiées. La plupart des modèles expliquent un forte proportion de la variance des spores portées dans l'air, à l'intérieur.

Mots clés : spores fongiques portées dans l'air, analyse de redondance, analyse des sentiers.
[Traduit par la rédaction]

Introduction

Fungi are ubiquitous in indoor environments (van Bronswijk et al. 1986), and the indoor environment itself is a complex ecosystem (Tobin et al. 1987). Indoor air quality is becoming an important public health issue. The significance of airborne fungi in inciting allergies in human beings has been recognized (Misra and Jamil 1991), as has their role as important constituents of indoor bioaerosols in some cases of sick building syndrome. It has been estimated by the World Health Organization (1983) that 15–20% of all new buildings will have problems with sick building syndrome.

Airborne fungi found indoors originate both from outdoor air and from various indoor sources. In Austria, significant correlations were found between the airborne fungi of indoor and outdoor environments (Ebner et al. 1992), but numerous fungi can also originate indoors (Sneller 1984) and these can

Received March 2, 1995.

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play a critical role in the indoor environment. Lehtonen et al. (1993) found that from spring to fall, fungal spores in the outdoor air are a principal source of those found indoors, and that spore concentrations indoors are therefore mainly reflections of those recorded outdoors. However, in winter, in areas where the ground is covered by snow, indoor spore counts are higher than those outdoors (Pasanen et al. 1990; Reponen et al. 1992). Ebner et al. (1992) noted that at high altitude (1905 m), concentrations of indoor airborne fungi were double those outdoors over a 1-year observation period but did not provide very satisfactory explanations. Only a few studies were conducted on both indoor and outdoor airborne fungi at the same time in the same area to determine the relationship between the two populations (Ebner et al. 1992). The extent to which fungal spores in outdoor air infiltrate buildings is not fully understood (Ligocki et al. 1993). The relationships between populations of airborne fungal spores found indoors and those found outdoors remain to be fully defined.

The objectives of this study were to determine the functional and causal relationships between indoor and outdoor airborne fungi and to probe the origins of indoor airborne fungi using redundancy analysis and path analysis.

Materials and methods

Fifteen residences were chosen as indoor air-sampling sites in Kitchener–Waterloo, Ont. The study was carried out from December 1991 to September 1993. The sampling was carried out every month for at least 1 year in 10 residences and for 6–9 months in the remainder, either because the patients withdrew from the study or because the houses were sold. Allergic patients lived in 12 of the 15 residences. In each residence, on each sampling date, air samples were taken at six sites: living room, kitchen, bedroom, bathroom, family room, and outside. In apartments, air samples were taken from only five sites, because they had no family room. Samples were taken between 1:00 p.m. and 9:30 p.m. At each site, three 10-min samples were taken with a Samplair-MK1 or -MK2 particle sampler (Allergenco, San Antonio, Tex.). Three samplers drawing 9.0, 15.0, and 15.5 L air/min (factory calibration) were used in this study. Samplers were put on a table 50–80 cm in height during indoor sampling. For outdoor sampling the sampler was placed on the ground. To avoid confounding sampler and room effects, the samplers were randomly assigned to the different sampling sites on each sampling date. The participants were requested to perform only routine daily activities during the sampling periods. At each sampling site and date, temperature (T) and relative humidity (RH) were recorded, and the presence of plants, pets, and carpets in sampling rooms was noted. Residential characteristics and patient data were obtained from questionnaires, allergy diaries, and by visual inspection.

The 75 × 25 mm glass slides used in sampling were coated with a thin layer of a mixture of 90% vaseline and 10% high melting point wax (w/w). For counting purposes the cover slip was mounted with polyvinyl alcohol – lactophenol. All fungal spores were counted and identified under the 40× or 100× objective of a Nikon light microscope equipped with phase contrast optics. The following numerical data were collected and analyzed: (*i*) conidia of *Alternaria*, *Aspergillus/Penicillium*, *Cladosporium*, and *Epicoccum*; ascospores of *Leptosphaeria*; basidiospores of *Coprinus* and *Ganoderma*; (*ii*) other ascospores and basidiospores that could not be identified to genus; and (*iii*) hyphal fragments, unidentified spores, total fungal spores, and total number of fungal genera (number of identifiable fungal genera by spore morphology) represented. Since the spores of *Aspergillus* and *Penicillium* cannot be distinguished under the light microscope, these two genera were recorded as one pooled taxon.

The distribution of the data was checked for homogeneity of variance by plotting the residuals against estimated values before the analysis, and among the 45 variables (Table 1), indoor *Aspergillus/Penicillium*, indoor *Cladosporium*, allergy history (years of allergy from first episode to the present), outdoor unidentified fungal spores, and total fungal spores were log transformed to improve normality.

The functional and causal relationships of indoor fungal spores with environmental factors, including their outdoor counterparts, were analyzed by redundancy analysis (RDA) and path analysis using CANOCO 3.10 and AMOS™ 3.1 software (ter Braak 1992; Arbuckle 1992). The full data file of 48 by 2307 is beyond the capacities of CANOCO 3.10 and AMOS™ 3.1 software. Therefore, before RDA and path analysis, Pearson correlation and Bonferroni adjusted probabilities matrices were computed using SYSTAT. The significant pairs of variables were chosen for further analysis. For RDA, the data for a full year could not be analyzed with CANOCO because of the limitation of the software. The data was therefore split into two halves, growing season (May–October) and non-growing season (November–April), for analysis. The correlation matrix was used as a data file for all path analysis to circumvent the limitations of the AMOS™ 3.1 software. According to the modification indices, all the causal models constructed in the present study would not be improved substantially by adjusting the paths between factors.

Seasonal patterns of indoor and outdoor airborne fungal spores and characteristics of these spores in the residences were presented in two other papers (Li and Kendrick 1995*a*, 1995*b*).

Results

Functional relationships of indoor spores to those outdoors and to indoor environmental factors

Growing season (May–October)

RDA is the canonical form of principal components analysis and the technique selecting the linear combination of environmental variables that gives the smallest total residual sum of squares (Jongman et al. 1987). In the diagrams (Figs. 1 and 2) derived from RDA in this study, solid arrows represent the indoor fungal spores, and broken arrows represent outdoor fungal spores and indoor environmental factors. The cosine of the angle between a broken arrow and a solid arrow is an approximation of the correlation coefficient between the variables. Arrows pointing in almost the same direction indicated a highly positive correlation, arrows at right angles indicate nearly zero correlation, and arrows pointing in opposite directions indicate a highly negative correlation (ter Braak and Prentice 1988). The functional relationships of indoor (IN) spores to those outdoors (OUT) and to indoor environmental factors were compared. The first axis is defined by total fungal spores IN and OUT, and *Cladosporium* IN, and the second axis is defined by *Alternaria* IN and OUT and the characteristics of residences. Canonical axes 1 and 2 explained 93.5% and 4.5% of the variance in the species–environment (or IN–OUT) relations, respectively (Table 2). Axis 1 was defined as highly significant when tested by the Monte Carlo permutation test. Axis 2 was not significant. The eigenvalue of axis 1 is 0.563 and of axis 2 is 0.027.

Alternaria, *Leptosphaeria*, and total fungal spores IN and

Table 1. Variables surveyed.

Variable	Abbr.	Unit or rank
Symptom (18 categories)	LS	0–3/category
Alternaria	A	Spores/m^3
Air conditioner	AC	0, 1
Age	AG	Year
Unidentified ascospores	AS	Spores/m^3
Unidentified basidiospores	B	Spores/m^3
Cat	CA	No.
Cleanliness	CL	0–4
Coprinus	CO	Spores/m^3
Carpet	CT	0, 1
Season	D	0 (Nov.–April), 1 (May–Oct.)
Dog	DO	No.
Dampness	DP	0, 1
Epicoccum	E	Spores/m^3
Filter	F	0, 1
Ganoderma	G	Spores/m^3
Gender	GD	0 (m), 1 (f)
Genera	GE	No. of genera
Hyphal fragments	H	No./m^3
House age	HA	Year
Humidifier	HF	0, 1
Heating system (forced air)	HS	0, 1
Leptosphaeria	L	Spores/m^3
Aspergillus/Penicillium	LAP or AP	Spores/m^3
Cladosporium	LC or C	Spores/m^3
History of illness	LHI or HI	Year
Outdoor fungal genera	LOG1 or OGE	No.
Outdoor hyphal fragments	LOH or OH	No./m^3
Outdoor unidentified spores	LOU or OU	Spores/m^3
Total fungal spores	LTO or TO	Spores/m^3
Outdoor *Alternaria*	OA	Spores/m^3
Outdoor *Aspergillus/Penicillium*	OAP	Spores/m^3
Outdoor unidentified ascospores	OAS	Spores/m^3
Outdoor unidentified basidiospores	OB	Spores/m^3
Outdoor *Cladosporium*	OC	Spores/m^3
Outdoor *Coprinus*	OCO	Spores/m^3
Outdoor *Epicoccum*	OE	Spores/m^3
Outdoor *Leptosphaeria*	OL	Spores/m^3
Outdoor total fungal spores	OT	Spores/m^3
Plants	PT	No. of pots
Relative humidity	RH	%
Rooms	R	Bathroom, bedroom, family room, and living room
Smoking	SK	0, 1
Temperature	T	°C
Types of residence	TH	Apartment, detached house, and town house (row house)
Unidentified fungal spores	U	Spores/m^3

OUT showed strong relationships (Fig. 1). A moderately positive relationship was shown between *Cladosporium*, *Ganoderma*, unidentified spore, hyphal fragment, and total fungal genera IN and OUT. *Epicoccum* and unidentified ascospores IN and OUT were also positively related but to a lesser degree. *Coprinus* and unidentified basidiospores IN and OUT also displayed positive relationships, but since the solid arrows of *Coprinus* OUT and unidentified basidiospores were short, the relationships indicated by these arrows could be nonsignificant. There was no functional relationship between *Aspergillus/Penicillium* IN and OUT (Fig. 1).

The lengths of the solid and broken arrows show the most common fungal spores IN and OUT to be in the same descending order of importance: *Leptosphaeria* ascospores, total spores, *Cladosporium* conidia, and *Alternaria* conidia.

Fig. 1. Redundancy analysis ordination biplot showing outdoor airborne fungi and meteorological factors (broken arrows) and indoor airborne fungi (solid arrows) from May to October. CT, carpet; DP, dampness; F, air filter; HF, humidifier; HS, forced air heating system; PT, house plants; RH, indoor relative humidity; T, indoor temperature; Alt, indoor *Alternaria*; As/pen, indoor *Aspergillus/Penicillium*; Asc, indoor unidentified ascospores; Basi, indoor unidentified basidiospores; Cla, indoor *Cladosporium*; Cop, indoor *Coprinus*; Epi, indoor *Epicoccum*; Gano, indoor *Ganoderma*; Gen, indoor total genera; Hy, indoor hyphal fragments; Lept, indoor *Leptosphaeria*; Tot, indoor total fungal spores; Uni, indoor unidentified spores; OA, outdoor *Alternaria*; OAP, outdoor *Aspergillus/Penicillium*; OU, outdoor unidentified ascospores; OB, outdoor unidentified basidiospores; OC, outdoor *Cladosporium*; OCO, outdoor *Coprinus*; OE, outdoor *Epicoccum*; OG, outdoor *Ganoderma*; OGE, outdoor total genera; OH, outdoor hyphal fragments; OL, outdoor *Leptosphaeria*; OT, outdoor total fungal spores; OU, unidentified spores.

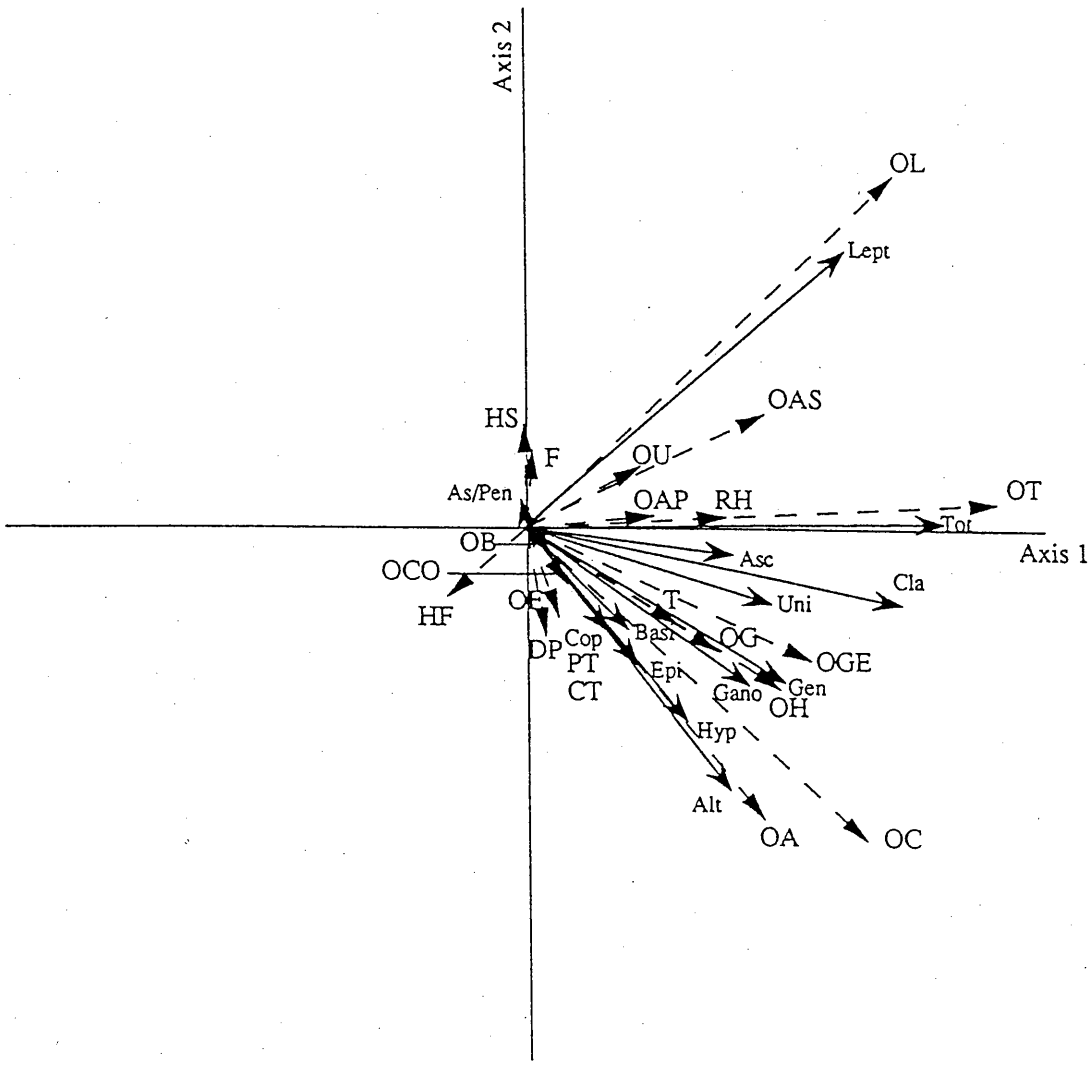
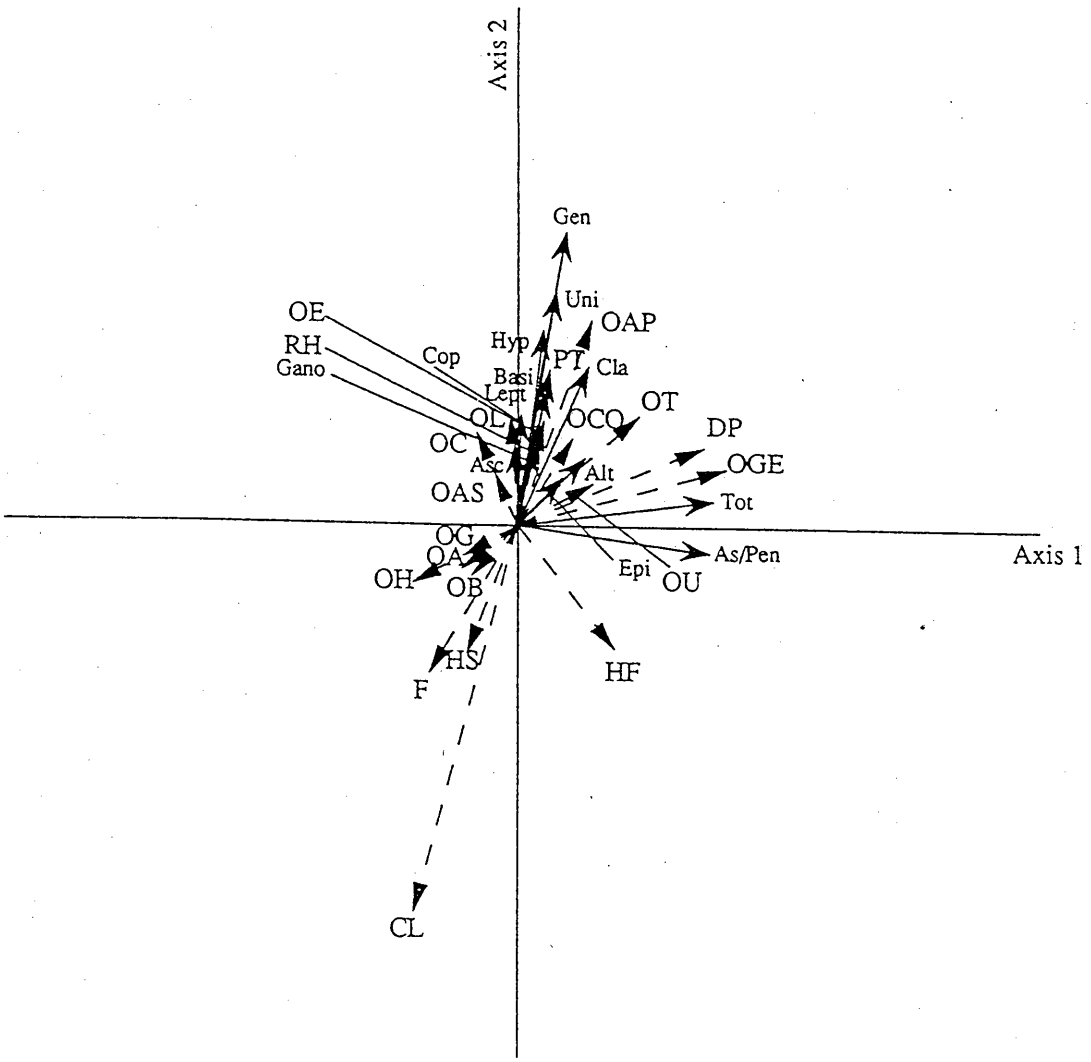


Table 2. Summary of redundancy analysis of airborne fungal spores indoors and outdoors and indoor environmental factors in the Kitchener–Waterloo area.

	Growing season		Nongrowing season	
	Axis 1	Axis 2	Axis 1	Axis 2
Eigenvalues	0.563**	0.027ns	0.133*	0.002ns
Species–environment correlations	0.808	0.642	0.368	0.424
Percentage variance				
Species data	56.3	2.7	13.3	0.3
Specis–environment relation	93.5	4.5	98.0	1.7
Length of gradient	1.88		1.45	

Fig. 2. Redundancy analysis ordination biplot showing outdoor airborne fungi and meteorological factors (broken arrows) and indoor airborne fungi (solid arrows) from November to April. Cl, cleanliness; DP, dampness; F, air filter; HF, humidifier; HS, forced air heating system; PT, house plants; RH, indoor relative humidity; T, indoor temperature; Alt, indoor *Alternaria*; As/pen, indoor *Aspergillus/Penicillium*; Asc, indoor unidentified ascospores; Basi, indoor unidentified basidiospores; Cla, indoor *Cladosporium*; Cop, indoor *Coprinus*; Epi, indoor *Epicoccum*; Gano, indoor *Ganoderma*; Gen, indoor total genera; Hy, indoor hyphal fragments; Lept, indoor *Leptosphaeria*; Tot, indoor total fungal spores; Uni, indoor unidentified spores; OA, outdoor *Alternaria*; OAP, outdoor *Aspergillus/Penicillium*; OU, outdoor unidentified ascospores; OB, outdoor unidentified basidiospores; OC, outdoor *Cladosporium*; OCO, outdoor *Coprinus*; OE, outdoor *Epicoccum*; OG, outdoor *Ganoderma*; OGE, outdoor total genera; OH, outdoor hyphal fragments; OL, outdoor *Leptosphaeria*; OT, outdoor total fungal spores; OU, unidentified spores.



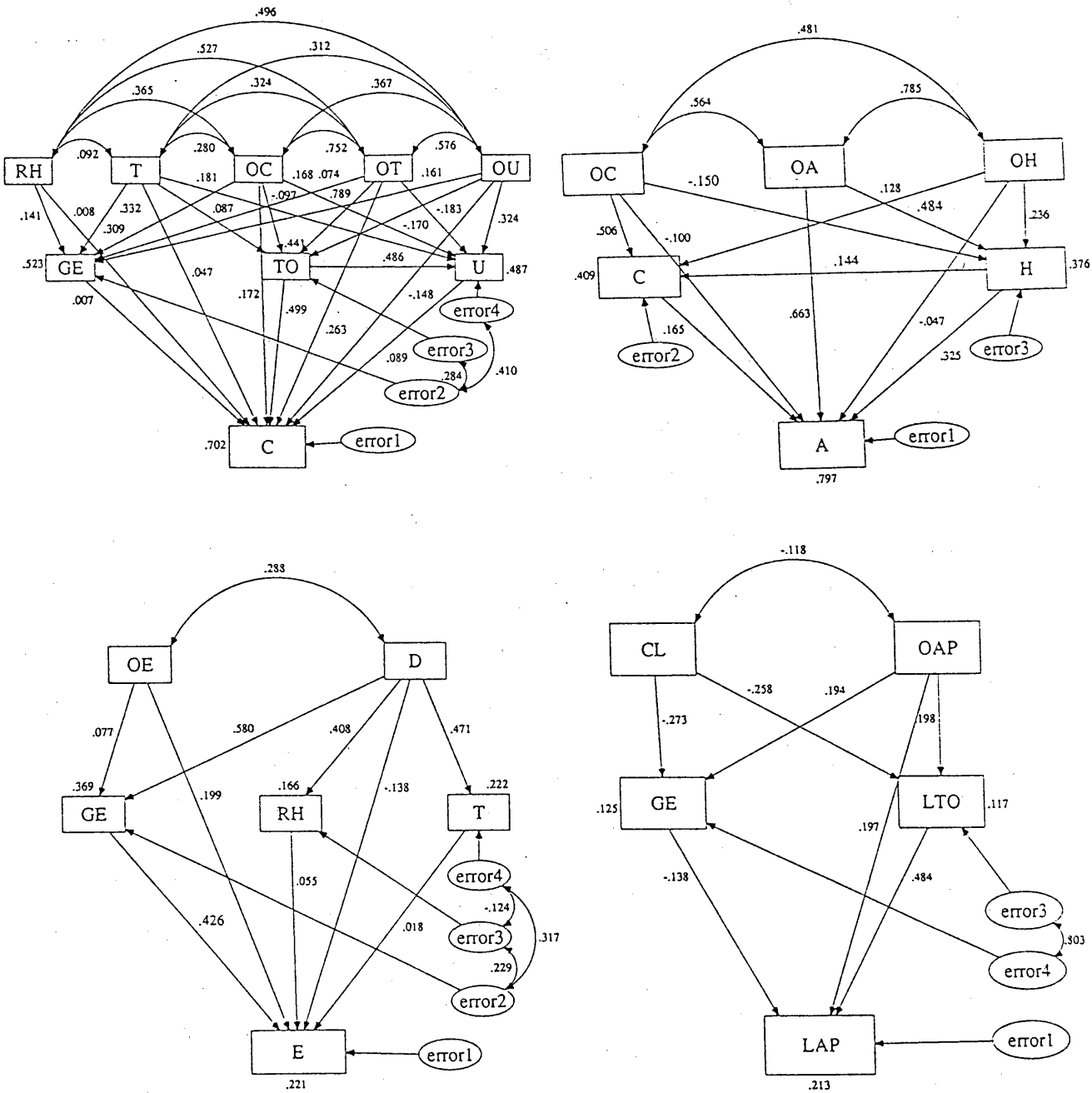
Of the indoor environmental factors, RH, T, carpet, house plants, and dampness (home dampness is defined as moulds visible to naked eyes, water damage, or water in basement (Brunekreef et al. 1989)) appeared to be the most important factors in descending order. Relative humidity and temperature were found to be positively related with all indoor fungal taxa except *Aspergillus/Penicillium*. Dampness, house plants, and carpet were positively related with all fungal groups except *Leptosphaeria*. House plants and carpet were not related to *Leptosphaeria*, while dampness had a negative relationship to this fungus. Humidifier, forced-air heating system, and filter did not appear to be correlated with airborne fungal taxa indoors or were negatively correlated.

Nongrowing season (November–April)

The first axis is mainly defined by *Aspergillus/Penicillium* IN, total fungal spores IN, total fungal taxa OUT, and dampness; the second axis by cleanliness and total fungal taxa IN. Canonical axes 1 and 2 account for 98.0% and 1.7% of variance in the species–environment (or IN–OUT) relations, respectively (Table 2). Axis 1 was assessed to be statistically significant by unrestricted Monte Carlo permutation test ($P = 0.05$). Axis 2 was not significant. The eigenvalue of axis 1 is 0.133 and of axis 2 is 0.002. The eigenvalues of both axes were much lower than those from the growing season.

Leptosphaeria IN and OUT exhibited a close relationship.

Fig. 3. Causal relationships of *Cladosporium*, *Alternaria*, *Epicoccum*, and *Aspergillus/Penicillium* indoors with their counterparts outdoors and main environmental factors. A, *Alternaria*; C, *Cladosporium*; CL, cleanliness; D, seasons; E, *Epicoccum*; GE, indoor total genera; H, hyphal fragments; LAP, logged indoor *Aspergillus/Penicillium*; LTO, logged indoor total spores; OA, outdoor *Alternaria*; OAP, outdoor *Aspergillus/Penicillium*; OC, outdoor *Cladosporium*; OE, outdoor *Epicoccum*; OH, outdoor hyphal fragments; OT, outdoor total spores; OU, outdoor unidentified spores; RH, relative humidity; T, indoor temperature; TO, indoor total spores; U, unidentified spores.



The relationships between *Cladosporium*, *Epicoccum* and unidentified ascospores IN and OUT were also positive (Fig. 2). Total fungal spores IN and OUT were positively related, as were unidentified spores IN and OUT, but the outdoor arrow was much shorter. *Coprinus* and unidentified basidiospores IN and OUT also demonstrated positive relationships, but since both arrows are quite short, the directions shown could be nonsignificant. The relationship of total fungal genera IN and OUT was positive but weak. Hyphal fragments IN and OUT displayed a negative relationship. *Alternaria* and *Ganoderma* IN and OUT displayed a negative relationship also, but the relatively short arrows suggest that the relationship was not well defined. No relationship between *Aspergillus/Penicillium* IN and OUT was detected in the nongrowing season (Fig. 2).

The lengths of the solid arrows suggest that the most important aspects of fungal propagules indoors were, in descending order, total fungal genera, unidentified fungal spores, total spores, *Aspergillus/Penicillium*, and hyphal fragments (Fig. 2). The broken arrow representing fungal

genera OUT suggests that the most important aspects, in descending order, were *Aspergillus/Penicillium*, total fungal genera, and total fungal spores.

Among indoor environmental factors, the most important factors were, in descending order, cleanliness, filter, humidifier, heating system, house plants, and dampness. Dampness was positively correlated with all fungal taxa, though its relationships to total fungal spores and *Aspergillus/Penicillium* were most significant. House plants had positive relationships to most fungal taxa IN except *Aspergillus/Penicillium* (Fig. 2). Cleanliness, filter, and forced-air heating system were negatively related to most of the fungal taxa IN. Humidifier was positively related to *Aspergillus/Penicillium* IN and total fungal spores IN, and negatively related to other fungal factors. The importance of RH and T as influences on the indoor airborne fungal spora was lower in the nongrowing season than in the growing season.

Causal relationships of outdoor spores and indoor environmental factors on indoor spore levels

Path analysis is a statistical technique that partitions correlations into direct and indirect effects and claims to differentiate between correlation and causation (Afifi and Clark 1984; Hayduk 1987). It partitions the simple correlations among a set of variables according to a specific functional hypothesis to produce a working model of their causal relationships, i.e., the path diagram (Fig. 3) (Kingsolver and Schemske 1991; Mitchell 1992). One-headed arrows in a path diagram represent direct effects of one variable on another, two-headed arrows represent unanalyzed correlations, and arrows not originating at a variable represent residual variance (Li 1975). Because path coefficients are independent of units of measurement, the relative importance of causal relationships may be determined (Li 1975).

Cladosporium

Total fungal genera, total spores IN, and unidentified spores were chosen as endogenous variables and their random error variables (*e*), *Cladosporium* OUT, total spores OUT, unidentified spores OUT, T IN, and RH IN as exogenous variables to develop a causal model for *Cladosporium* IN (Fig. 3). The variables were chosen in this analysis as explanatory variables all possessing direct effects and with RH IN, T IN, *Cladosporium* OUT, total spores OUT, and unidentified spores OUT as explanatory variables having indirect effects also on the spore population of *Cladosporium* (Fig. 3).

The path coefficient of the path arrow in the model illustration is represented by p, the subscript $p_{c\text{-}to}$ means the path from total fungal spores to *Cladosporium*. Path coefficients correspond to the standardized partial regression coefficients of multiple regressions, so they indicate what the analysis claims is the direct causal influence of one variable on the variation observed in another (Li 1975; Kingsolver and Schemske 1991). The values beside the endogenous variable boxes are the variances of the variables explained in the model.

The model described 70.2% of the variance of the spore count of *Cladosporium* IN. Most of the path coefficients in this model were significantly different from zero, but $p_{ge\text{-}ot}$, $p_{c\text{-}ge}$, and $p_{c\text{-}rh}$ were nonsignificant (Fig. 3). Total spores IN ($p_{c\text{-}to} = 0.499$), total spores OUT ($p_{c\text{-}ot} = 0.263$), *Cladosporium* OUT ($p_{c\text{-}oc} = 0.172$), and unidentified spores OUT ($p_{c\text{-}ou} = -0.148$) were, in descending order, the most important factors directly influencing the spore concentration of *Cladosporium* IN. Indoor T ($p_{c\text{-}t} = 0.047$) and unidentified fungal spores IN ($p_{c\text{-}u} = 0.089$) had a weak influence on *Cladosporium*. The causal effects of RH and of total fungal genera on *Cladosporium* were not significant. *Cladosporium* OUT, total spores OUT, unidentified spores OUT, and temperature IN not only had direct causal effects but also indirect effects through total fungal spores IN and unidentified fungal spores IN on *Cladosporium* IN.

The causal model overall fitted the hypothesis: $\chi^2 = 4.263$, df = 2, $P = 0.119$. Examination of the solution of the path analysis indicated that the parameter estimates (unstandardized path coefficients) had acceptable standard errors.

Alternaria

Five factors were selected as explanatory variables to generate a causal model for *Alternaria* (Fig. 3). Three of them, *Alternaria* OUT, *Cladosporium* OUT, and hyphal fragments OUT, were exogenous variables having both direct and indirect causal influences on the spore population of *Alternaria* IN. Another two variables, *Cladosporium* IN and hyphal fragments IN, were endogenous variables having direct impacts on *Alternaria* IN. All the path coefficients were statistically significantly different from zero, except $p_{a\text{-}oh}$.

Alternaria OUT showed a strong positive direct causal effect on its counterpart indoors ($p_{a\text{-}oa} = 0.663$) (Fig. 3). Next came hyphal fragments IN ($p_{a\text{-}h} = 0.325$). The direct causal effects of *Cladosporium* IN and hyphal fragments IN were positive on *Alternaria* IN, and those of *Cladosporium* OUT were negative. Hyphal fragments OUT did not have significant direct effect on *Alternaria* IN, but their indirect effect was significantly positive through hyphal fragments IN ($p_{h\text{-}oh} = 0.236$). *Cladosporium* IN ($p_{a\text{-}c} = 0.165$) and *Cladosporium* OUT ($p_{a\text{-}oc} = -0.100$) unanticipatedly showed causal effects on *Alternaria* IN.

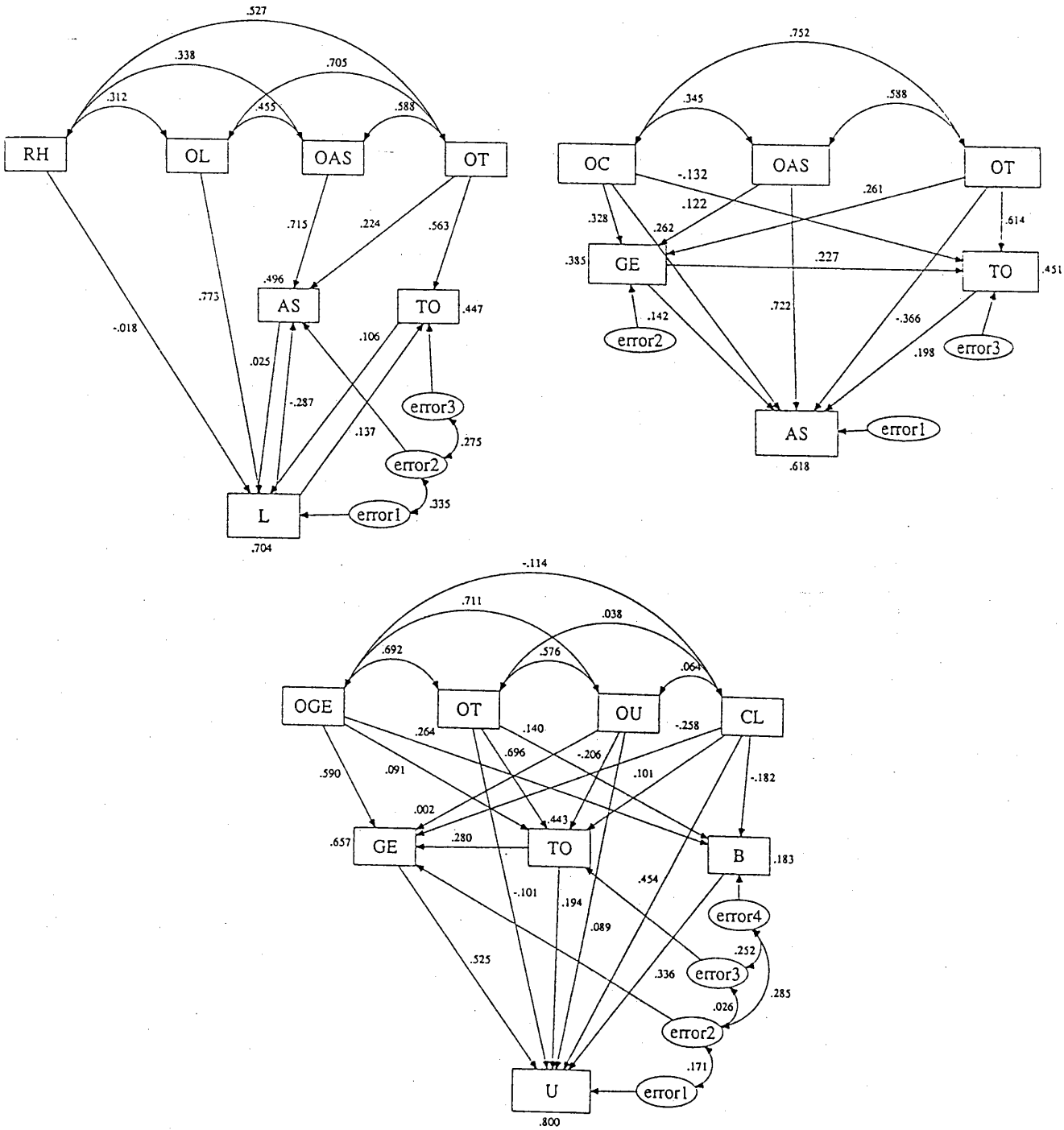
The causal model interpreted a very large proportion (79.7%) of the variance of indoor *Alternaria*. The overall fit of the causal model was very good: $\chi^2 = 1.632$, df = 1, $P = 0.201$.

Epicoccum

The causal model for *Epicoccum* IN incorporated five factors: *Epicoccum* OUT, temperature IN, RH IN, total fungal genera IN, and season (Fig. 3). *Epicoccum* OUT and season were chosen as exogenous explanatory variables with both direct and indirect causal effects on *Epicoccum* IN. Temperature IN, RH IN, and total genera IN were chosen as endogenous variables that had direct effects on *Epicoccum* IN. The model overall fitted the hypothesis: $\chi^2 = 4.735$, df = 2, $P = 0.094$, but only 22.1% of the variance of *Epicoccum* IN was explained by the model.

Among the direct effects on *Epicoccum* IN, all factors were significant except season (Fig. 3). In descending order of importance were the causal effects of total genera ($p_{e\text{-}ge} = 0.426$), *Epicoccum* OUT ($p_{e\text{-}oe} = 0.199$), RH IN ($p_{e\text{-}rh} = 0.055$), and temperature IN ($p_{e\text{-}t} = 0.018$). The direct effects were all positive. The direct causal effects of RH IN and temperature IN on *Epicoccum* IN were very weak, but the paths were significant.

Fig. 4. Causal relationships of *Leptosphaeria*, unidentified ascospores and unidentified spores indoors with their counterparts outdoors and main environmental factors. AS, indoor unidentified ascospores; B, indoor unidentified basidiospores; CL, cleanliness; GE, indoor total genera; L, indoor *Leptosphaeria*; OAS, outdoor unidentified ascospores; OC, outdoor *Cladosporium*; OGE, outdoor total genera; OL, outdoor *Leptosphaeria*; OT, outdoor total spores; OU, outdoor unidentified spores; RH, indoor relative humidity; TO, indoor total spores; U, indoor unidentified spores.



Aspergillus/Penicillium

The causal model was constructed using four factors: *Aspergillus/Penicillium* OUT, total fungal spores IN, total genera IN, and cleanliness, in addition to *Aspergillus/Penicillium* IN (Fig. 3). *Aspergillus/Penicillium* OUT and cleanliness were exogenous variables. *Aspergillus/Penicillium* OUT was an explanatory factor with both direct and indirect effects on indoor *Aspergillus/Penicillium*, while cleanliness had only an indirect effect. Total fungal spores and total genera were endogenous variables with direct causal influences on *Aspergillus/Penicillium* IN.

All the path coefficient estimates were significant. In descending order, the importance of causal effects on *Aspergillus/Penicillium* IN were found to be total fungal spores IN ($p_{\text{lap-lto}} = 0.484$), *Aspergillus/Penicillium* OUT ($p_{\text{lap-oap}} = 0.197$), and total genera IN ($p_{\text{lap-ge}} = -0.138$). The effect of *Aspergillus/Penicillium* OUT was positive, while that of total genera IN was negative.

The causal model did not fit the hypothesis statistically: $\chi^2 = 7.019$, df = 1, $P = 0.008$, and only 21.3% of the variance of *Aspergillus/Penicillium* IN was explained by the model.

Leptosphaeria

Four exogenous factors, RH IN, *Leptosphaeria* OUT, unidentified ascospores OUT, and total spores OUT, and two endogenous variables, unidentified ascospores IN and total fungal spores IN, were chosen to establish a causal model for *Leptosphaeria* IN (Fig. 4). *Leptosphaeria* OUT, RH IN, unidentified ascospores IN, and total fungal spores IN were explanatory variables with direct causal effects on *Leptosphaeria* IN, while unidentified ascospores OUT and total spores OUT had only indirect effects. The direct effects of unidentified ascospores IN and RH IN were not significant.

The strongest direct effect on *Leptosphaeria* IN was found to be that of its outdoor counterpart that was highly significantly positive ($p_{l\text{-}ol} = 0.773$). The second important factor was total spores IN ($p_{l\text{-}to} = 0.106$), but the positive effect was at a much lower level. Since both the direct effects of unidentified ascospores IN and of total fungal spores IN were nonsignificant or trivial, the indirect effects of total fungal spores OUT and unidentified ascospores OUT through unidentified ascospores IN and total fungal spores IN were very slight.

The causal model interpreted a large portion (70.4%) of variance of indoor *Leptosphaeria*. The overall fit of the causal model was very good: $\chi^2 = 8.191$, df = 4, $P = 0.085$.

Unidentified ascospores

The causal model for unidentified ascospores was constructed with unidentified ascospores OUT, total spores OUT, and *Cladosporium* OUT as exogenous variables with both direct and indirect effects, and total spores IN and total genera IN as endogenous variables with direct effects on unidentified ascospores IN (Fig. 4).

The overall fit of the causal model was good: $\chi^2 = 3.711$, df = 1, $P = 0.054$. A large fraction of the variance (61.8%) of unidentified ascospores IN was explained by the causal model. All the effects, including both direct and indirect, on unidentified ascospores IN were statistically significantly different from zero.

Unidentified ascospores OUT constituted the most important factor ($p_{as\text{-}oas} = 0.722$) with positive direct causal influence on their indoor counterpart. Following the direct effect of unidentified ascospores OUT were total fungal spores OUT ($p_{as\text{-}to} = -0.366$), *Cladosporium* OUT ($p_{as\text{-}oc} = 0.262$), total fungal spores IN ($p_{as\text{-}to} = 0.198$), and total genera IN ($p_{as\text{-}ge} = 0.142$), in descending order.

Coprinus

Coprinus OUT, total genera OUT, and RH IN were chosen as explanatory exogenous variables with both direct and indirect effects, and unidentified fungal spores IN and total genera IN as endogenous variables with direct effects on *Coprinus* IN (Fig. 4). The causal model was generated with these four factors in addition to *Coprinus* IN. Not all the effects of the model were significant. RH IN appeared to lack significant causal effects on *Coprinus* IN both directly and indirectly, and its indirect effect through total genera IN was also nonsignificant. The backward effect of *Coprinus* IN on unidentified fungal spores IN was not significant. The rest of the path influences were statistically significant. Over half of the variance (52.3%) of *Coprinus* IN was explained by the five factors in the model. Among the direct effects, *Coprinus* OUT was the strongest positive one ($p_{co\text{-}oco} = 0.508$). The second was total genera IN ($p_{co\text{-}ge} = 0.322$). Next to these two factors were those of unidentified fungal spores IN ($p_{co\text{-}u} = 0.135$) and total genera OUT ($p_{co\text{-}oge} = -0.092$). The direct effect of total genera OUT was negative and unimportant. The overall fit of the causal model was well defined: $\chi^2 = 0.853$, df = 1, $P = 0.356$.

Ganoderma

The causal model for *Ganoderma* IN was erected with *Ganoderma* OUT, total spores OUT, and temperature IN as exogenous factors, and unidentified fungal spores IN, total spores IN, and total genera IN as endogenous variables (Fig. 5). The causal model fitted the hypothetical model very well: $\chi^2 = 3.167$, df = 2, $P = 0.205$. A high percentage (71.1%) of the variance of *Ganoderma* IN was explained by this model.

All the causal effects, both direct and indirect, in the model were significant, except that of temperature IN. *Ganoderma* OUT contributed most to *Ganoderma* IN ($p_{g\text{-}og} = 0.672$). Compared with *Ganoderma* OUT, the direct contributions of the rest of the variables to *Ganoderma* IN were trivial or absent (Fig. 5).

Unidentified basidiospores

Five factors in addition to unidentified basidiospores IN were selected to construct the causal model. Unidentified basidiospores OUT, *Coprinus* OUT, and unidentified spores IN were exogenous variables with direct and indirect effects on unidentified basidiospores IN, and total genera IN and total spores IN were endogenous variables with direct effects (Fig. 5).

The most important direct effects were those of unidentified basidiospores OUT ($p_{b\text{-}ob} = 0.356$) and unidentified spores OUT ($p_{b\text{-}u} = 0.406$). The direct influences of the remainder were nonsignificant. Since the effects of total genera IN and total spores IN were nonsignificant. all the indirect effects through them were nonsignificant. According to the path coefficients, unidentified spores IN played a bigger role than unidentified basidiospores OUT in affecting basidiospores IN.

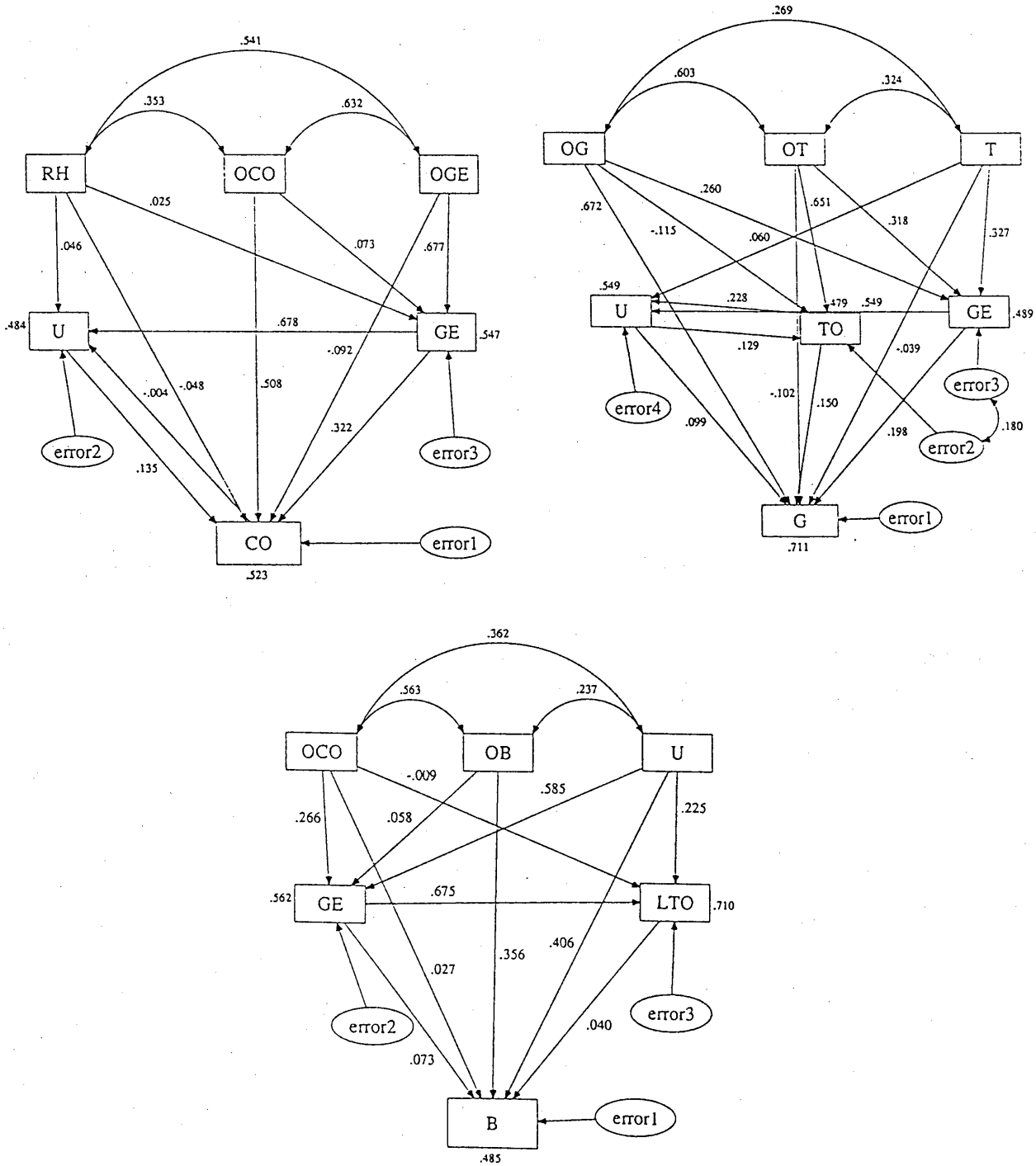
The overall fit of the causal model was very good: $\chi^2 = 0.877$, df = 1, $P = 0.349$. A moderate proportion (48.5%) of the variance of *Ganoderma* IN was explained by this model.

Unidentified fungal spores

The causal model comprised four exogenous variables: unidentified spores OUT, total spores OUT, total genera OUT, and cleanliness, which had direct and indirect effects on unidentified spores IN, and three endogenous variables, unidentified basidiospores IN, total spores IN, and total genera IN, with direct effects (Fig. 4).

The overall fit of the causal model was very good: $\chi^2 =$

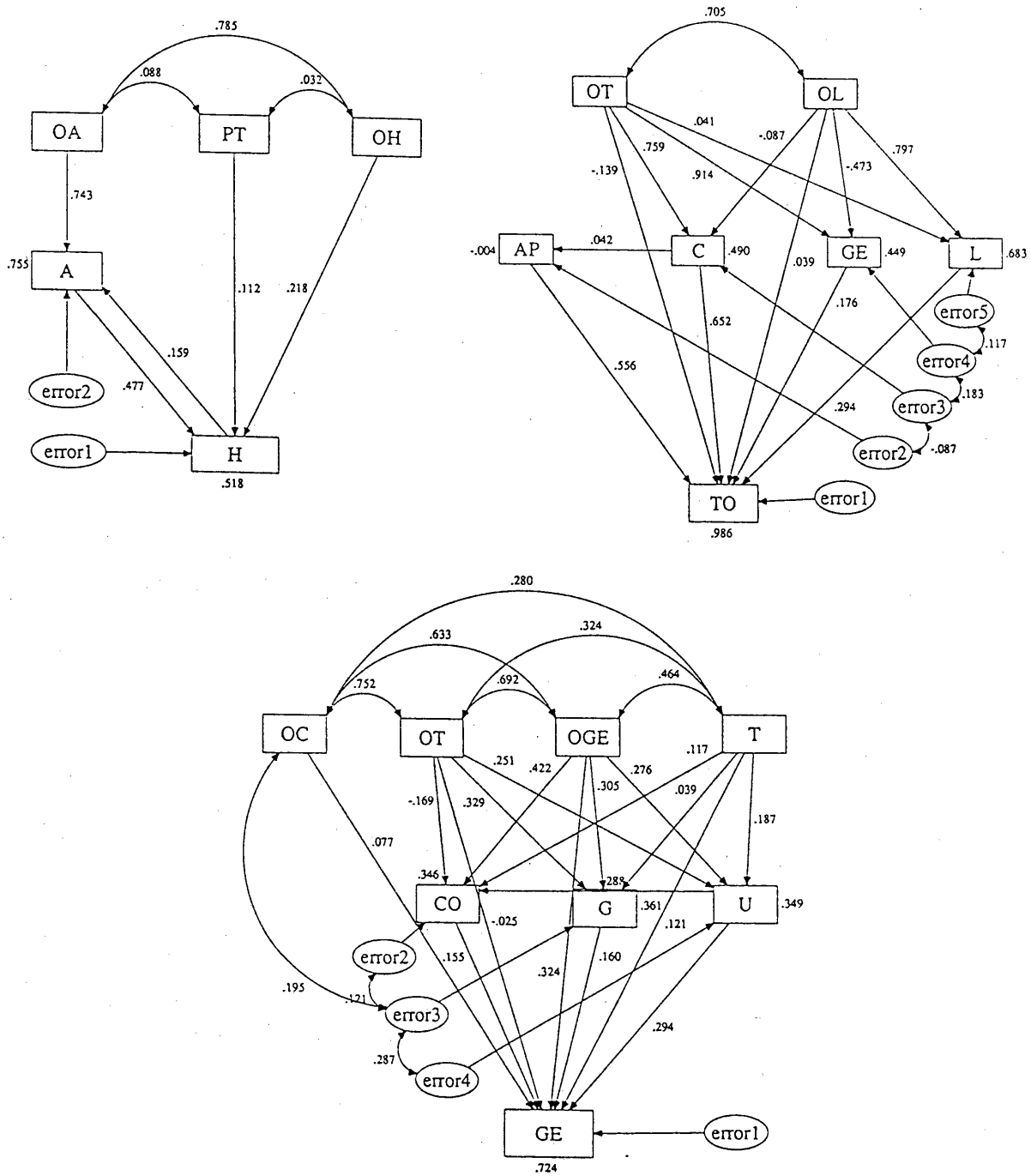
Fig. 5. Causal relationships of *Coprinus*, *Ganoderma*, and unidentified basidiospores indoors with their counterparts outdoors and main environmental factors. B, indoor unidentified basidiospores; CO, indoor *Coprinus*; G, indoor *Ganoderma*; GE, indoor total genera; LTO, logged indoor total spores; OB, outdoor unidentified spores; OCO, outdoor *Coprinus*; OG, outdoor *Ganoderma*; OGE, outdoor total genera; OT, outdoor total spores; RH, indoor relative humidity; T, indoor temperature; TO, indoor total spores; U, indoor unidentified spores.



3.764, df = 1, $P = 0.052$. It is only marginally upgraded by modifying the paths of the model in accordance with the modification indices. A large percentage (80.0%) of the variance of unidentified spores IN was interpreted by this model. The path coefficients of the model were all statistically significantly different from zero, except those for unidentified spores OUT and total genera IN.

Total genera IN ($p_{u\text{-}ge} = 0.525$), cleanliness ($p_{u\text{-}cl} = 0.454$), and unidentified basidiospores IN ($p_{u\text{-}b} = 0.336$) were found to possess the strongest positive effects on unidentified spores IN. The causal effect of unidentified spores OUT on their counterparts indoors was much less important ($p_{u\text{-}ou} = 0.089$) than these three factors. The effects of the other variables were slight (Fig. 4).

Fig. 6. Causal relationships of total spores indoors, hyphal fragments and fungal biodiversity with their counterparts outdoors and main environmental factors. A, indoor *Alternaria*; AP, indoor *Aspergillus/Penicillium*; C, indoor *Cladosporium*; CO, indoor *Coprinus*; G, indoor *Ganoderma*; GE, indoor total genera; H, indoor hyphal fragments; L, indoor *Leptosphaeria*; OA, outdoor *Alternaria*; OC, outdoor *Cladosporium*; OGE, outdoor total genera; OH, outdoor hyphal fragments; OL, outdoor *Leptosphaeria*; OT, outdoor total spores; PT, house plants; T, indoor temperature; TO, indoor total spores; U, indoor unidentified spores.



Total spores

Two exogenous factors, total spores OUT and *Leptosphaeria* OUT, and five endogenous factors, *Cladosporium* IN, *Aspergillus/Penicillium* IN, total genera IN, *Leptosphaeria* IN, and total spores IN, were designated for the causal model (Fig. 6). The exogenous variables showed direct and indirect paths through *Cladosporium* IN, total genera IN, and *Leptosphaeria* IN, and direct paths to total spores IN.

Interestingly enough, total spores IN and total spores OUT did not show profound causal relationships. In the model, endogenous factors showed significant causal effects on total spores IN. The most influential two were *Cladosporium* IN ($p_{to\text{-}c}$ = 0.622) and *Aspergillus/Penicillium* IN ($p_{to\text{-}ap}$ = 0.556). Following these two were *Leptosphaeria* IN, total genera IN, total spores OUT, and *Leptosphaeria* OUT, in descending order. The indirect causal influences of

total spores OUT through *Cladosporium* IN and total genera IN on total spores IN were highly significant. Almost all the variance (98.6%) of total spores IN was explained by the model, mainly by indoor *Cladosporium*, *Aspergillus/Penicillium*, and *Leptosphaeria*. The overall fit of the causal model was excellent: $\chi^2 = 7.052$, df = 4, $P = 0.133$. The model here seems to reflect the additive effects of the major taxa.

Hyphal fragments

The causal model was composed of hyphal fragments OUT, house plants, and *Alternaria* OUT as exogenous variables, and *Alternaria* IN as endogenous variable. The path of *Alternaria* OUT to *Alternaria* IN was indirect, and those of the remainder were direct (Fig. 6). Overall, the model fitted the hypothetical model very well: $\chi^2 = 3.088$, df = 2, $P = 0.214$. All the paths in the model were significant. The model interpreted 51.8% of the variance of hyphal fragments IN.

Alternaria IN showed the greatest direct influence on hyphal fragments IN ($p_{h\text{-}a} = 0.477$), greater than that of hyphal fragments OUT ($p_{h\text{-}oh} = 0.218$). The plants in residences had a significant causal effect on hyphal fragments IN, although their effects were far less than those of *Alternaria* IN and hyphal fragments OUT ($p_{h\text{-}pt} = 0.112$). *Alternaria* OUT had a strong indirect influence on hyphal fragments IN through *Alternaria* IN. The effects between *Alternaria* IN and hyphal fragments IN were mutual, since hyphal fragments IN showed a significant backward effect on *Alternaria* IN ($p_{a\text{-}h} = 0.159$), but its effect was much smaller than that of *Alternaria* IN (Fig. 6).

Fungal diversity

Total genera OUT, total spores OUT, *Cladosporium* OUT, and temperature IN were chosen as exogenous variables, and *Coprinus* IN, *Ganoderma* IN, and unidentified spores IN, as endogenous variables in addition to total genera IN, to generate the causal model (Fig. 6). All path coefficients were statistically significantly different from zero, except those of temperature IN to *Ganoderma* IN and total spores OUT to total genera IN.

Among the direct causal effects on indoor fungal diversity, that of fungal diversity OUT was the most important ($p_{ge\text{-}oge} = 0.324$). Next came unidentified spores IN ($p_{ge\text{-}u} = 0.294$), *Ganoderma* IN ($p_{ge\text{-}g} = 0.160$), *Coprinus* IN ($p_{ge\text{-}ge} = 0.155$), and temperature IN ($p_{ge\text{-}t} = 0.121$). The indirect effect of total genera OUT through *Coprinus* IN on total genera IN ($p_{co\text{-}oge} = 0.422$) appeared to be relatively important.

The causal model explained most (72.4%) of the variance of fungal diversity IN. The overall fit of the causal model was very well defined: $\chi^2 = 0.637$, df = 2, $P = 0.727$.

Discussion

Since residents all open windows in summer, this is one of the major reasons why much stronger functional relationships were found between indoor and outdoor airborne fungi in summer (Figs. 1 and 2). Another reason is that the period from May to October is the season favourable to fungal growth outdoors. During that period, airborne fungi were present in much higher numbers and biodiversity than from November to April. Therefore, from May to October, there were more fungal spores outside and it was much easier for them to infiltrate residences through open windows. The very strong relationships between airborne fungi indoors and outdoors at this time largely masked the importance of the relationships of indoor airborne fungi with indoor environmental factors. Relative humidity was defined as the most important indoor environmental factor in the growing season. This result was similar to one obtained outdoors in a previous study in the same area (Li and Kendrick 1994).

From November to April, outdoor temperatures were low, and the growth of fungi outdoors was largely inhibited. For much of the time the ground was covered by snow, which eliminated most resuspension of fungal propagules. Meanwhile, temperatures that remained within growing range indoors permitted growth wherever locally high humidity and appropriate substrates were found. It is obvious that the functional relationships between indoor and outdoor airborne fungi were reduced dramatically from November to April, but negative functional relationships between indoor airborne fungi and indoor environmental factors were enhanced, especially cleanliness, forced air heating systems, and other factors related to heating systems. Su et al. (1992) found that elevated concentrations of soil fungi were significantly associated with dirt floors, crawl-space type of basements, and gas stoves. Their results from dirt floors were similar to our results concerning cleanliness. Dampness was an important factor detected by RDA in both growing and nongrowing seasons, but it failed to show significance in correlation analysis and was therefore excluded from path analysis. One of the reasons is that temporary incidences of dampness could not be monitored by a monthly survey. Another one is that negative intercorrelated factors could mask the true effect of dampness on airborne fungal spores.

Direct cause and effect relationships of airborne fungi indoors with their counterparts outdoors and indoor environmental factors are difficult to determine because the factors are often intercorrelated, and this could mask the true cause–effect relationships. High correlations and functional relations do not necessarily guarantee high causal relations. Basta et al. (1993) noted that correlation analysis may inadequately describe relationships because correlation does not ensure that a direct cause and effect relationship exists.

Cladosporium

The correlation coefficient ($r = 0.601$) and RDA analysis of *Cladosporium* suggested that the indoor and outdoor spore populations had very strong relationships, but according to path analysis, outdoor spores did not have a strong direct impact on those indoors (Fig. 3). This is not the result anticipated from exploratory analysis. The model was restructured in several different ways, but the results did not change substantially.

One explanation is that *Cladosporium* indoors was not mainly from outdoor sources at all but from indoor sources. *Cladosporium cladosporioides* (Fries) de Vries and *Cladosporium herbarum* Link ex Fries et al. were common on wallpaper, paint, and other surfaces of building materials in homes (van Bronswijk et al. 1986; Moriyama et al. 1992). *Cladosporium* was the second most common fungus detected on internal walls of buildings and houses (Lim et al. 1989) and the most dominant one in damp residences and in old

rural houses (Pasanen 1992). It was also dominant in house dust (Gravesen 1978; Ishii et al. 1979; Calvo et al. 1982; Hamada and Yamada 1991). Pasanen et al. (1992) stated that airborne *Cladosporium* conidia were mainly derived from indoor sources. These results are supported by the present study. A second possible explanation is that the distribution of *Cladosporium* indoors interacted strongly with some other factors, reducing the direct causal influence of outdoor populations.

The causal influence of total spores IN on *Cladosporium* was indirect, arising from factors having effects on both *Cladosporium* and total spores. Moreover, *Cladosporium* was such a large proportion of the outdoor air spora. Airborne *Cladosporium* can be found year-round both indoors and outdoors. This is the reason fungal total genera did not have a significant path to indoor *Cladosporium*. Although RH IN has no significant causal influence on *Cladosporium*, this does not mean that humidity is unimportant. The presence of moisture on surfaces or of locally saturated atmospheres are determining factors for fungal growth. The RH of the indoor air probably did not reflect the true humidity on parts of the interior surface of the residences for several reasons: (*i*) water condensation often occurs on surfaces such as unshielded cold water pipes in walls and false ceilings, cold surfaces on windows, window frames, and even outer walls in winter; (*ii*) periodic high humidity and condensation normally occur in bathrooms, laundry rooms, and kitchens; (*iii*) moisture from outside sometimes infiltrates houses through structural defects; (*iv*) accidental water spills or plumbing leaks can soak carpets and take several days to dry out; (*v*) flooded basements are not uncommon in early spring during runoff in various parts of North America; and (*vi*) basement walls that are insulated inside the foundation.

Alternaria

The results from correlation (r = 0.836), RDA, and path analysis were mutually consistent concerning the relationship of *Alternaria* IN with the same genus outdoors. The result of path analysis suggested that *Alternaria* IN is derived mainly from outdoor sources (Fig. 3). When the conidia of *Alternaria* are released, parts of conidiophores frequently break off with them: airborne conidia were observed with a piece of conidiophore attached. After release, the spores and the conidiophore fragment often apparently separate. The conidiophore pieces were counted as hyphal fragments. The quite strong causal impact from hyphal fragments can be understood, in part, as a result of this phenomenon. Another possible reason is that a large proportion of airborne hyphae belonged to *Alternaria*, since no causal influence of hyphal fragments on other fungal taxa was found. The causal effects of *Cladosporium* IN and OUT on *Alternaria* were unexpected and are difficult to interpret. These two genera do not share the same teleomorph. Since the relationships were not strong and contributed only 1% of variance of *Alternaria*, they may simply represent noise in the model or in other words a pseudocausal relationship. Another possibility is that the relationships between *Cladosporium* and *Alternaria* are biologically significant, such as their exploiting the same substrates in a mutual or successional way. Both *Cladosporium* and *Alternaria* are common moulds growing on foods, such as tomatoes, lemons, and peaches, and building materials (van Bronswijk et al. 1986; Frazier and Westhoff 1988; Northolt and Soentoro 1988). Food spoilage often involves a succession of organisms (Frazier and Westhoff 1988). Grant et al. (1989) have suggested that mould species appear on moist building substrates in a certain succession. In natural environments, *Cladosporium cladosporioides* and *Alternaria alternata* may suppress the white mould *Sclerotinia sclerotiorum* (Boland and Hunter 1988). Traquair et al. (1983) found that *Cladosporium uredinicola* Spegazzini hyperparasitized *Puccinia violae* (Schumacher) De Candolle. A *Cladosporium* sp. was found to be an antagonist of *Sphaerotheca fuliginea* on zucchini (Minuto et al. 1991). However, we do not as yet have enough information to fully explain the relationships between *Cladosporium* and *Alternaria*, which need to be further investigated.

Epicoccum

The correlation (r = 0.281), RDA and path analysis all showed that the relationship between indoor and outdoor spores was not strong. The outdoors was not, apparently, a major source of the spores recovered indoors (Fig. 3). It is quite possible that the spores of *Epicoccum* were brought inside residences with vegetables, or on clothes or tools after garden cultivation, weeding, pruning, lawn mowing, or hedge trimming. Pasanen et al. (1989) noted that fungal spores were carried into homes on people's clothes. However, indoor sources cannot be excluded. Fuel wood chips and firewood were important indoor sources for airborne fungal spores indoors (Hellenbrand and Reade 1992). This has relevance to the present study, since fireplaces were used in winter in over half of the residences surveyed. The very strong path from total genera to *Epicoccum* IN reflected unknown factors having effects on both, since only 22.1% of variance was explained by this model.

Aspergillus/Penicillium

Both correlation (r = 0.037) and RDA analysis (Figs. 1 and 2) showed almost no relationship between indoor and outdoor spores. Since the causal model of *Aspergillus/Penicillium* did not fit the hypothesis well, the weak causal path from outdoors to indoors could not be considered reliable. Some authors have considered that the most important thing was the biological meaning of the model, not its overall fit (Arbuckle 1992). Thus, rejection of a model on a purely statistical basis, particularly with a large sample size, is not necessarily a condemnation (Arbuckle 1992). In the present study, 12 of 13 models fitted the hypotheses very well. These results suggested that indoor substrates were important sources contributing to indoor airborne spore concentrations of *Aspergillus* and *Penicillium*. Sneller (1984) also suggested that *Penicillium* and *Aspergillus* were of endogenous origin. Both genera were found to be the most common fungi growing on indoor substrates (Gravesen 1978; Ishii et al. 1979; Calvo et al. 1982; van Bronswijk et al. 1986; Lim et al. 1989; Hamada and Yamada 1991; Moriyama et al. 1992).

Leptosphaeria

A close relationship between the airborne ascospores of *Leptosphaeria* indoors and outdoors was confirmed by correlation (r = 0.826), RDA, and path analysis. Furthermore,

path analysis found that the population of *Leptosphaeria* ascospores indoors was mostly determined directly by those outdoors. Unidentified ascospores did not have a significant causal influence on *Leptosphaeria*. Rather, *Leptosphaeria* had a significant direct negative effect on unidentified ascospores. This result suggested that some unidentified ascospores actually belonged to *Leptosphaeria*. When the spores of *Leptosphaeria* were numerous, they could be identified with confidence. Small numbers of spores, especially immature ones, cause uncertainty and therefore were more likely to be categorized as unidentified ascospores.

Since outdoor sources were the major source of *Leptosphaeria* indoors, it is clear why RH did not show any significant causal influence. However, a highly positive relationship between RH outdoors and ascospore counts of *Leptosphaeria* outdoors was found in Kitchener–Waterloo, Ont. (Li and Kendrick 1994). The relationship between *Leptosphaeria* and total spores was mutual. *Leptosphaeria* spores formed a part of total spores and in return total spores reflected an indirect effect on *Leptosphaeria* from an unknown factor influencing both. One possible suggestion is that the unknown factor may be conidia of the anamorphs of unidentified ascomycetes among the total spores.

Unidentified ascospores

The high correlation ($r = 0.728$) between indoor and outdoor unidentified ascospores was detected by path analysis as a very strong causal effect of ascospores outdoors on those indoors. RDA analysis showed a good relationship between those indoors and outdoors, but not as close as that emerging from correlation and path analysis. The close relations of ascospores indoors with other environmental factors could conceal the relationship between ascospores IN and OUT. These results suggested that indoor sources were an inconsequential source of indoor ascospores.

In the path model, the causal effects of *Cladosporium* OUT, total genera IN, total spores IN, and total spores OUT on unidentified ascospores IN appear to be due largely to the relationships of ascospores with conidia of their anamorphs. The holomorphs of *Cladosporium* are *Mycosphaerella*, *Venturia*, and *Apiosporina* (Sivanesan 1984; Hanlin 1990) and the teleomorphs of some species of these holomorphs are difficult to identify by spore morphology alone. The negative path coefficients from total spores OUT to unidentified ascospores may be due to a strong interaction of total spores OUT with another unidentified factor.

Coprinus

A close relation between *Coprinus* basidiospores indoors and outdoors was detected by all three methods of analysis. The relationship was of a cause and effect type. It was obvious that the main sources of *Coprinus* basidiospores indoors were outside the residences. This explains why the effect of indoor RH was not significant. As for the lack of significant causal relations found between RH and airborne fungi originating from indoor sources, such as *Cladosporium* and *Aspergillus/Penicillium*, one of the reasons was that overall indoor RH in Kitchener–Waterloo, Ont. did not fluctuate as it did outdoors. Relative humidity near indoor fungal substrates could be more important to indoor spores. The effect of total genera OUT was trivial, and an unknown interaction related to it was responsible for the negative path coefficient. The effect of total genera IN meant that *Coprinus* occurred during the season in which fungal biodiversity was high. The causal influence of unidentified spores may imply that *Coprinus* might have unidentified anamorphs that figured in the overall spore counts. Watling (1979) reported two kinds of arthroconidia for *Coprinus* and both lack any special characteristics that would make identification possible.

Ganoderma

There was a lack of correlation between indoor and outdoor basidiospores of *Ganoderma* from November to April. According to the path analysis, *Ganoderma* IN came mainly from outdoor sources (Fig. 5). Considering the characteristics and the size of the basidioma of *Ganoderma*, it is virtually impossible that *Ganoderma* grew indoors naturally. The effects from other fungal factors were not strong, but they may reveal the effects of a factor not included in the model. Anamorphs of *Ganoderma* recorded as gasterospores by Kendrick and Watling (1979) may be another reason, though this possibility is presumably small, because most gasterospores develop inside the trama of the teleomorph fruiting body (Steyaert 1967). One of the possible reasons is that *Ganoderma* IN in certain periods was more strongly represented by the spores accumulated in dust or other reservoirs indoors than new inputs from outdoor sources. The indoor factors determining spore resuspension of *Ganoderma* may have masked the relationship between the spore indoors and outdoors in these periods.

Unidentified basidiospores

According to the path analysis, outdoor unidentified basidiospores were an important source for those indoors but not as important as unidentified spores (Fig. 5). Numerous basidiospores cannot be identified with certainty even as basidiospores, and there are numerous connections between anamorphs and teleomorphs of basidiomycetes (Kendrick and Watling 1979). These conidia are in most cases difficult or impossible to identify by spore morphology alone.

A close correlation of unidentified basidiospores and total genera was detected ($r = 0.526$), but this was recognized by the path analysis as noncausal. This is due to intercorrelations among the variables. Since only about 50% of variance was interpreted by the model, some determining factors were not among those investigated. The causal factor screen should be reorganized to include other factors that might then be recognized as of genuine importance.

Unidentified spores

Both correlation analysis and RDA analysis showed that there was a fair correlation between unidentified spores indoors and outdoors, but path analysis showed only a weak causal influence from outdoors to indoors (Fig. 4). In addition to the fact that 80% of variance was explained by the model, the results suggested that there was a major source indoors. The first factor is total genera. It was apparent that the higher the fungal diversity, the more spores remain unidentified. Unidentified spores were always a small portion of the total spores in our survey. Normal house-cleaning may reduce many common fungi quite efficiently, but this serves to increase the proportion of unidentified spores rela-

tive to the known ones. Meanwhile, indoor fungal sources are sometimes missed or neglected by normal cleaning (e.g., house plants, soil in pots).

Total spores

The path model supported the path models related to the fungal taxa in the model for indoor total spores (Fig. 6). The lack of prominent causal relationship between total spores indoors and outdoors was due to the overwhelming influence of *Cladosporium*. *Cladosporium* contributed almost 40% to total spores (Li and Kendrick 1995). Total spores OUT showed a very strong causal impact on *Cladosporium* IN, but because less than 50% of the variance of *Cladosporium* was explained in the model, there is a good possibility that indoor sources exist for *Cladosporium*. There was no significant causal relationship between *Cladosporium* and *Aspergillus/Penicillium*. One possible explanation was that the three genera are not parts of the same holomorph (Kendrick et al. 1979; Hawksworth et al. 1983; Sivanesan 1984; Hanlin 1990). The model also suggested that *Aspergillus/Penicillium* primarily originated from indoor sources, which confirmed the results from correlation analysis and RDA analysis.

Hyphal fragments

According to the RDA analysis, from May to October indoor and outdoor hyphal fragments were highly correlated but from November to April were very weakly negatively correlated. Overall the relation was quite close to the result of correlation analysis ($r = 0.544$), but path analysis showed it to be of a strong cause and effect type. The model also proposed that *Alternaria* was an important source of hyphal fragments in the air (Fig. 6). Indoor substrates for many common indoor fungi could also have contributed to indoor hyphal fragments. House plants seem to be an indoor source of hyphal fragments and indirectly to be a substrate of *Alternaria* and other plant-inhabiting fungi. Botzenhart et al. (1984) showed that green plants in buildings could increase the concentrations of airborne fungal spores. Burge et al. (1982) found that watering plants and the presence of a fan slightly increased airborne conidia levels of *Cladosporium*, *Penicillium*, *Alternaria*, *Epicoccum*, and *Pithomyces* in homes. Wyse and Malloch (1970) observed a large number of *Penicillium*, *Epicoccum*, and *Alternaria* on bark of Christmas trees, but these fungi failed to become airborne. These results suggest that more research on house plants is necessary.

Fungal diversity

The relationship between total genera indoors and outdoors was at different levels: very strong versus very weak in growing versus nongrowing seasons (Figs. 1 and 2). Overall the relationship was close according to the correlation analysis ($r = 0.737$). Total genera OUT was listed as the most important factor influencing total genera IN (Fig. 6), but its causal influence was not strong according to its path coefficient ($p_{ge\text{-}oge} = 0.324$). Airborne fungi originating from indoor sources were responsible for an important part of biodiversity indoors. Higher percentages of unidentified spores meant a greater chance for higher fungal biodiversity indoors. The causal impact of temperature IN was weak, but statistically significant. In warm temperatures, more fungi can flourish.

Many endogenous fungi do not appear to follow any recognizable seasonal or climatic pattern and can be important to the mould-sensitive patient. Endogenous airborne fungi should be studied intensively to elucidate their significance to public health. In the meanwhile, the causal effects of indoor environmental factors on airborne fungi with endogenous origin, such as *Cladosporium* and *Aspergillus/Penicillium*, should be studied in detail.

Acknowledgments

Financial support from the Institute for Risk Research, University of Waterloo, to both authors and an operating grant from the Natural Sciences and Engineering Research Council of Canada to Professor B. Kendrick are acknowledged with thanks. We are grateful to Dr. H.A. Burge, Dr. D.M. Wyse, Dr. W. Taylor, Dr. B. Warner, and Mr. S. Barnette for comments and discussions.

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