

Fungal diversity in a water-damaged office building before and after remediation

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Abstract

Rationale: Post occupancy-onset asthma was associated with exposure to fungi derived from floor dust in an office building that had a history of water damage. In this study, internal transcribed spacer (ITS) region sequencing was employed to determine if building remediation had any effect on the fungal populations present.

Methods: Floor dust was collected from areas surrounding workstations in an office building in the northeastern United States that had known water incursion before (n=27) and one year following (n=27) building remediation. Genomic DNA was extracted from 5 mg of dust and fungal ITS regions were amplified and Sanger sequenced.

Results: Unicellular yeast species as well as plant-associated fungi belonging to the orders Pleosporales and Capnodiales were among the most abundant fungi detected in floor dust prior to remediation. Following remediation, many of the same species remained the most abundant. Building remediation had little effect on the diversity of fungi present as the Shannon Diversity indices and species richness were not significantly different before and after remediation. Bray-Curtis dissimilarity indices revealed the fungal orders present pre- and post-remediation were 75% similar.

Conclusions: These data suggest that remediation did not significantly alter the fungal diversity within the office building. In addition, it is possible that many of the detected fungi were introduced by passive transfer or anthropogenic disturbance. ITS sequencing has revealed a broad assemblage of fungal species, including previously overlooked yeast species often not detected using traditional culture or quantitative PCR approaches. These data highlight the contribution of yeast species within indoor office environments.

Background

- Workers occupying an office building with documented water damage suffered from building-related respiratory illnesses.
- NIOSH investigated the hazards associated with respiratory morbidity.

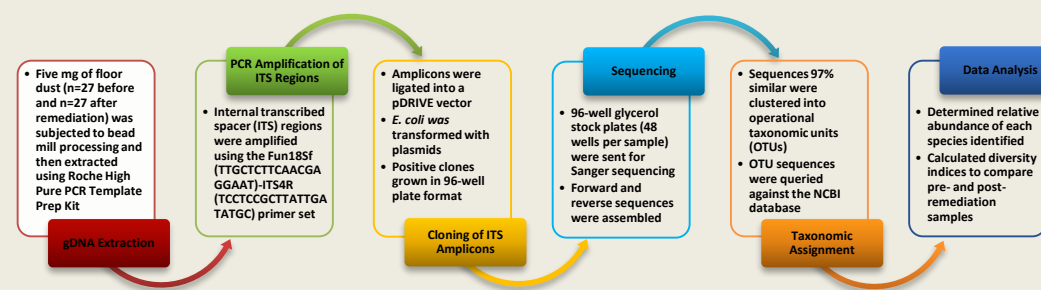
Species in samples	Floor (n = 328)		
	Prevalence No. (%)	Median	Maximum
Yeasts ^b	250 (76.2)	2,400	1.2 × 10 ⁶
<i>Aureobasidium pullulans</i>	175 (53.4)	770	8.0 × 10 ⁴
<i>Epicoecum nigrum</i>	121 (36.9)	400	1.4 × 10 ⁴
<i>Alternaria alternata</i>	70 (21.3)	710	1.1 × 10 ⁴
<i>Phoma herbarum</i> ^b	54 (16.5)	2,850	1.0 × 10 ⁶
<i>Cladosporium sphaerospermum</i>	48 (14.6)	1,100	3.0 × 10 ⁴
<i>Aspergillus niger</i>	30 (9.1)	390	6.1 × 10 ⁴
<i>Chaetomium globosum</i> ^b	27 (8.2)	770	1.4 × 10 ⁴
<i>Cladosporium cladosporioides</i>	19 (5.8)	400	2.9 × 10 ⁴
<i>Fusarium solani</i>	18 (5.5)	400	8.0 × 10 ³
<i>Cladosporium herbarum</i>	16 (4.9)	1,800	1.2 × 10 ⁴
<i>Mucor plumbeus</i> ^b	11 (3.4)	380	3.7 × 10 ⁴
<i>Rhizopus stolonifer</i> ^b	9 (2.7)	370	3.7 × 10 ³
<i>Ulocladium chartarum</i>	6 (1.8)	390	3.6 × 10 ⁴
<i>Stachybotrys chartarum</i> ^b	4 (1.2)	2,200	1.7 × 10 ⁴
<i>Aspergillus flavus</i>	2 (<1)	2,080	3.8 × 10 ³
<i>Chrysomya sitophila</i>	2 (<1)	3,800	3.8 × 10 ³
<i>Penicillium expansum</i>	2 (<1)	1,300	1.5 × 10 ³

^bHydrophilic fungi; all other species in the table are mesophilic fungi.
Park et al., *Environ Health Perspect*, 2008, 116(1):45-50

Study Aim:

- A subset of floor dust samples were analyzed using internal transcribed spacer (ITS) region sequencing to determine the diversity of fungi present before and after remediation

Methods



Results – Relative Abundance

Figure 1.

Relative abundance of the most prevalent orders detected in the 2002 pre- and 2004 post-remediation samples. Shades of red and blue indicate Ascomycota and Basidiomycota orders, respectively. Species belonging to the orders Pleosporales and Capnodiales were prevalent in both pre- and post-remediation samples.

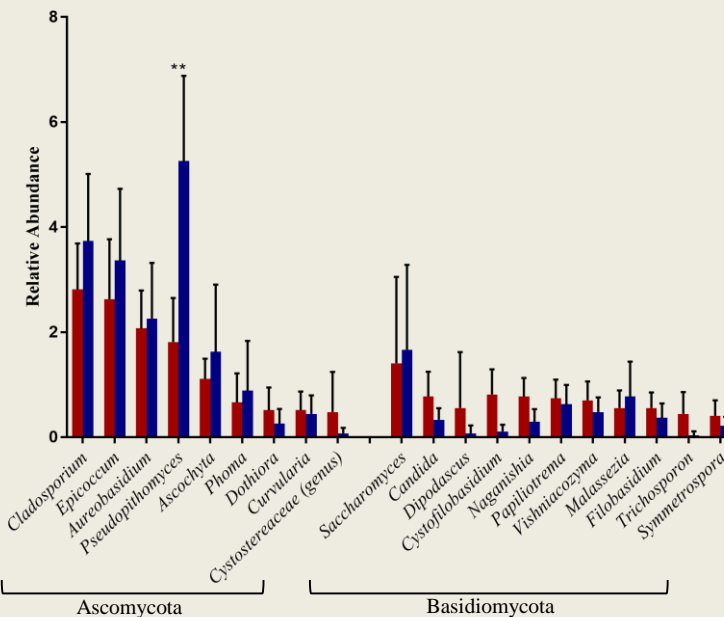
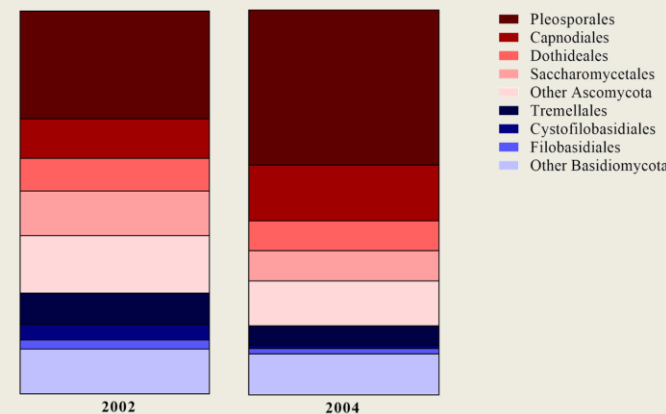


Figure 2.

Twenty most abundant genera detected before (red bars) and 1 year after (blue bars) remediation of the office building. Outdoor and plant-associated fungi, such as *Pseudopithomyces*, *Cladosporium*, *Epicoecum*, and *Aureobasidium* species, were among the most abundant before and after remediation. Other abundant fungi included unicellular yeasts, such as *Saccharomyces*, *Candida*, as well as yeasts belonging to the order Tremellales.

Results – Fungal Diversity Indices

- Species Richness (S):** measure of the number of species in a sample (does not account for abundance)
- Shannon Diversity Index (H):** measure of the species diversity in a given sample population

$$H = - \sum_{i=1}^R p_i \ln p_i$$

where R = number of species and p_i = the relative abundance of individual species

- Bray-Curtis Dissimilarity (BC):** measure of the compositional dissimilarity between 2 populations

$$BC_{ij} = 1 - \frac{2C_{ij}}{S_i + S_j}$$

where C_{ij} = sum of the lesser values for the species common between both sites and S_i & S_j = the total number of specimens counted at both sites

Table 1. Comparison of the fungal diversity indices among pre- and post-remediation samples

	Shannon Diversity Index		Species Richness	Bray-Curtis Dissimilarity	
	Within Each Sample	Within Sample Group	# Species/Sample	Genus Level	Order Level
Pre-remediation (2002)	2.69 ± 0.49	4.39	20.2 ± 7.4	0.373	0.249
Post-remediation (2004)	2.62 ± 0.32	4.03	19.7 ± 4.0		

Student t-test revealed no statistical differences between the Shannon diversity and species richness indices.

Conclusions

- Unicellular yeasts (*Saccharomycetales*, *Tremellales*, *Cystofilobasidiales*, and *Filobasidiales*) and plant-associated fungi (*Pleosporales* and *Capnodiales*) were the most abundant fungi detected in floor dust prior to remediation.
- Many of these fungi remained prevalent even after remediation of the office building.
- Remediation did not have any effect on the fungal diversity observed, as indicated by species richness and diversity indices.
- These data suggest many of the fungi present in the office building may have been passively or anthropogenically introduced.
- These data also demonstrate the presence of many previously overlooked fungi that contribute to indoor exposures, specifically yeasts.

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