

High diversity of fungi in air particulate matter

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Fungal spores can account for large proportions of air particulate matter, and they may potentially influence the hydrological cycle and climate as nuclei for water droplets and ice crystals in clouds, fog, and precipitation. Moreover, some fungi are major pathogens and allergens. The diversity of airborne fungi is, however, not well-known. By DNA analysis we found pronounced differences in the relative abundance and seasonal cycles of various groups of fungi in coarse and fine particulate matter, with more plant pathogens in the coarse fraction and more human pathogens and allergens in the respirable fine particle fraction ($<3\ \mu\text{m}$). Moreover, the ratio of *Basidiomycota* to *Ascomycota* was found to be much higher than previously assumed, which might also apply to the biosphere.

atmospheric aerosol | bioaerosol | DNA analysis | fungal spores

Recent studies have shown that fungal spores and other biological particles can account for large proportions of aerosol particle mass in pristine rainforest air as well as in rural and urban environments (1–5). For example, fungal spores were found to account for up to 45% of coarse particle mass ($>1\ \mu\text{m}$) in tropical rainforest air and up to 4–11% of fine particle mass ($\leq 2.5\ \mu\text{m}$) in urban and rural air (3). Fungi have also been found in clouds, fog, and precipitation where these and other biological particles can act as nuclei for water droplets and ice crystals and can influence precipitation patterns and the Earth's energy budget (e.g., refs. 6–17). On average, the number and mass concentrations of fungal spores in continental boundary layer air are on the order of 10^3 – $10^4\ \text{m}^{-3}$ and approximately $1\ \mu\text{g}\ \text{m}^{-3}$, respectively, and the estimated global emissions of approximately $50\ \text{Tg}\ \text{yr}^{-1}$ are among the largest sources of organic aerosol (1).

Some fungi are major pathogens or allergens for humans, animals, and plants, and air is the primary medium for their dispersal (18–20), but the diversity of fungi in air particulate matter is not well-known. The traditional cultivation, microscopy, and chemical tracer techniques applied in earlier studies were insufficient for a broad coverage of different fungal species, and recently reported first applications of molecular genetic techniques were very limited in scope and methodology as discussed below.

In this study, we investigated and characterized the diversity and frequency of occurrence of fungi in air particulate matter by DNA extraction and sequence analysis of the internal transcribed spacer region (ITS).

Results and Discussion

Over a period of 1 year, coarse and fine particle air filter samples were collected on glass fiber filters with a high-volume sampler and a nominal cut-off diameter of approximately $3\ \mu\text{m}$ (Table S1). The average sampling time was 7 days, corresponding to a sampled air volume of approximately $3,000\ \text{m}^3$, in central Europe. We investigated the diversity of fungi by DNA extraction, amplification (Table S2), and sequence analysis of the internal transcribed spacer region (ITS). Fungal DNA was found in all air samples. As shown in Table 1, the number of different species (species richness, S) detected in the fine particle fraction was not much lower than in the coarse fraction. The Shannon

index (H'), Shannon evenness (E), and Simpson's index (D) values calculated from the frequency of occurrence of the different species were nearly the same for coarse and fine particles (Table 1). These diversity parameter values are similar to the values commonly obtained for fungi in soil and on plants as well as for bacteria in soil (21–23).

The most frequent species (*Cladosporium* sp.) was detected in all air samples except 1. On the other hand, 70% of the detected species were found only in 1 sample (SI Text, and Table S3). The high proportion of species that were found only once and the limited number of investigated samples and DNA amplification products imply that the actual diversity of fungi in the sampled air masses was higher than detected. As shown in Table 1, estimates of the actual species richness (S^*) based on the Chao-1 estimator approach (21, 24) are an approximate factor of 3 higher than the measured species richness values (S), suggesting that the total number of fungal species in the investigated air samples was $>1,000$.

As illustrated in Fig. 1A, nearly all detected fungal species were *Basidiomycota* (BMC, club fungi, 64%) or *Ascomycota* (AMC, sac fungi, 34%), many of which actively eject their spores with aqueous jets or droplets (1). Only approximately 2% of the measured sequences were from *Fungi Incertae Sedis* (FIS, formerly called *Zygomycota*) or other fungi that could not be attributed to a phylum. This is consistent with the predominance of AMC and BMC in the biosphere, where the subkingdom of *Dikarya* (AMC plus BMC) accounts for 98% of the known species in the biological kingdom of *Eumycota* (fungi) (25). The AMC species found in the air samples were distributed over 4 major classes (*Dothideomycetes*, *Eurotiomycetes*, *Leotiomycetes*, and *Sordariomycetes*; Fig. 1B) and about one-third could not be attributed to any class. In contrast, most of the detected BMC species belonged to a single class, the *Agaricomycetes* (Fig. 1C). More information about the taxonomic classes and families of the detected fungi is available online (SI Text) (26).

Fig. 2 shows seasonal variations in the normalized species richness (S_n : number of detected species divided by number of investigated samples), in the ratio of S_n between coarse and fine particles ($S_{n,c}/S_{n,f}$), and in the ratio of S_n between BMC and AMC ($S_{n,BMC}/S_{n,AMC}$). With regard to all fungal species, S_n and $S_{n,c}/S_{n,f}$ exhibited little seasonal variability. AMC and BMC, however, exhibited pronouncedly different values and seasonal cycles of S_n and $S_{n,c}/S_{n,f}$. For AMC, S_n was highest in spring and lowest in summer and $S_{n,c}/S_{n,f}$ was lowest in fall, whereas for BMC both S_n and $S_{n,c}/S_{n,f}$ were highest in fall and lowest in winter. Throughout all seasons, S_n remained higher for BMC

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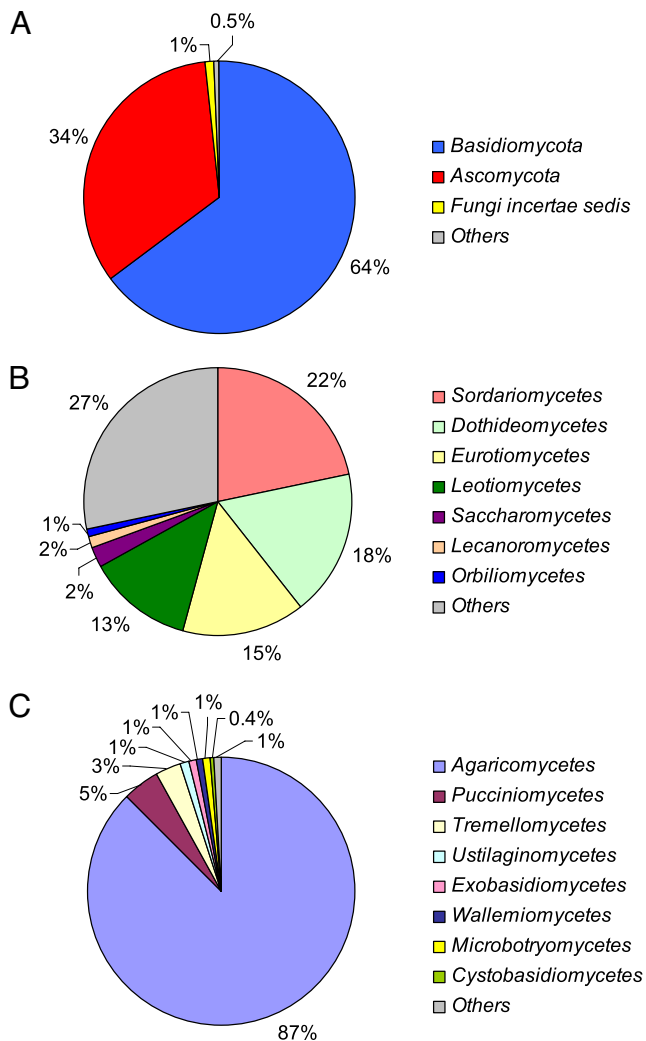


Fig. 1. Species richness of airborne fungi: relative proportions of different phyla (A), different classes of *Ascomycota* (B), and different classes of *Basidiomycota* (C).

than for AMC (Fig. 2A) and $S_{n,c}/S_{n,f}$ remained >1 for BMC but <1 for AMC (Fig. 2B). The ratio of BMC to AMC ($S_{n,BMC}/S_{n,AMC}$) was higher in summer and fall than in spring and winter, and it was higher for coarse than for fine particle samples (Fig. 2C). In other words, most BMC occurred in the coarse particle fraction during summer/fall, whereas most AMC were found in the fine particle fraction during winter/spring. This seems to reflect a predominance of BMC among the mushrooms that form fruiting bodies in summer and fall, and a high proportion of AMC among the molds, endophytes, and epiphytes spreading in winter and spring (27, 28). Statistical analyses (multiple linear regressions) indicate that ambient temperature and relative humidity are positively correlated with the relative proportion of BMC ($R^2 = 0.64$, P value <0.001) and negatively correlated with the relative proportion of AMC ($R^2 = 0.67$, P value <0.001).

Fig. 3 illustrates that the relative frequency of occurrence (*RFO*) of individual species, that is, the proportion of samples in which these species were detected, is independent of the seasonal variability of AMC and BMC species richness. For example, the prominent allergenic AMC species *Cladosporium* sp. and *Alternaria* spp. occurred most frequently in summer and fall, whereas the mold *Penicillium* spp. and the plant pathogen *Blumeria graminis* (mildew) were mostly found in winter and spring. With

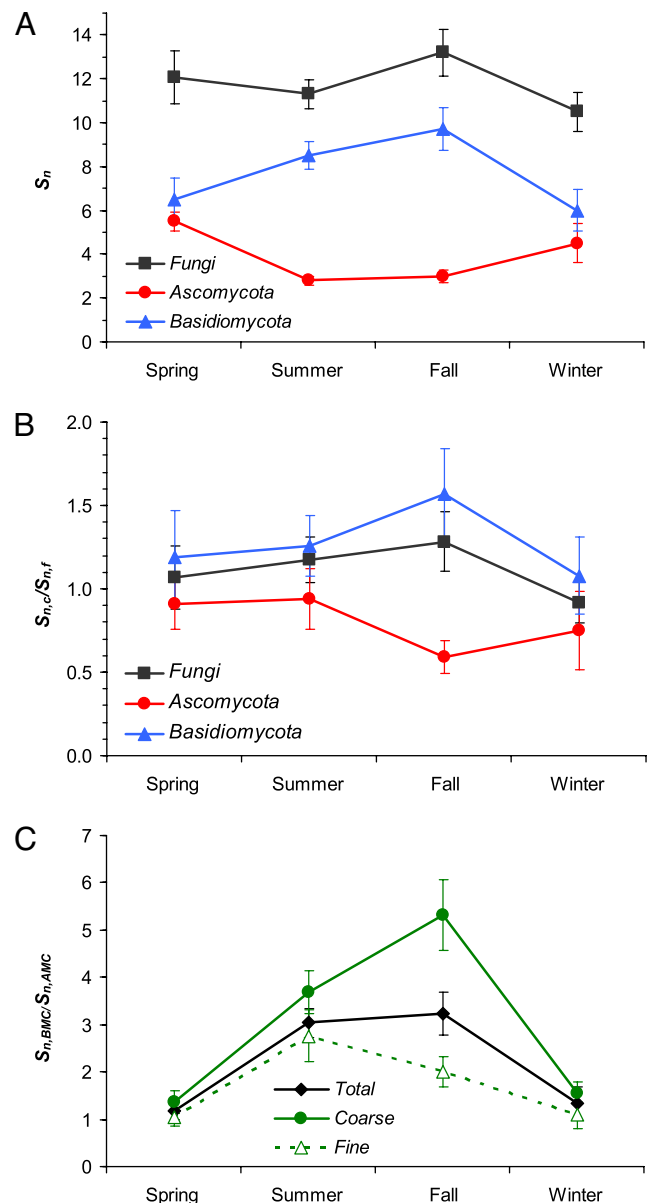


Fig. 2. Seasonal variations in the species richness normalized by the number of investigated air samples (S_n) (A), the ratio of normalized species richness between coarse and fine particles ($S_{n,C}/S_{n,F}$) (B), and the ratio of normalized species richness between *Basidiomycota* and *Ascomycota* ($S_{n,BMC}/S_{n,AMC}$) (C). Error bars illustrate inter-sample variability (relative standard error of the arithmetic mean of the species richness of individual samples).

regard to BMC, the seasonal cycle of S_n was not matched by the *RFO* of any frequently detected species. The fall maximum of BMC species richness is primarily due to species that were found only once and can be attributed to mushroom fruiting and enhanced activity of plant decomposers during that season (27).

Several allergens and pathogens were frequently found in both fine and coarse particle samples (e.g., *Cladosporium* sp., *Alternaria* spp., *Penicillium* spp., and *Aspergillus* spp.). Some plant pathogens, however, were found only or mostly in coarse particle samples (e.g., *Blumeria graminis* and *Puccinia* spp.), whereas some human pathogens were detected only in the fine particle samples (e.g., *Candida tropicalis* and *Wallemia* spp.). Overall, the species richness and cumulative frequency of occurrence of plant pathogens was found to be higher in the coarse particle fraction,

Table 1. Diversity parameters for all fungi, *Basidiomycota* (BMC), *Ascomycota* (AMC), and *Fungi Incertae Sedis* (FIS) found in the investigated air samples (total, coarse, and fine PM)

	Fungi			BMC			AMC			FIS		
Parameter	Total	Coarse	Fine	Total	Coarse	Fine	Total	Coarse	Fine	Total	Coarse	Fine
S	368	227	203	238	160	124	124	62	78	4	3	1
S^*	1136	713	647	658	448	377	500	327	267	9	5	—
H'	5.2	4.8	4.7	4.9	4.5	4.2	4.1	3.3	3.7	1.3	1	—
E	0.88	0.88	0.88	0.88	0.89	0.87	0.84	0.80	0.85	0.96	0.94	—
D	0.01	0.015	0.018	0.015	0.017	0.027	0.033	0.066	0.054	0.1	0.167	—

Species richness (S measured, S^* estimated), Shannon index (H'), Shannon Evenness (E), and Simpson's index (D).

whereas those of human pathogens and allergens were similar or higher in the fine particle fraction. Note that fine particles have longer residence times in the atmosphere (multiple days to weeks) and that they can reach the alveolar region of human lungs upon inhalation, whereas coarse particles are rapidly removed from the atmosphere (sedimentation, scavenging, and precipitation) and are deposited in the upper airways when inhaled. Thus, the scientific investigation and public discussion of climate and health effects are mostly focused on fine aerosol particles (11).

As discussed by Despres et al. (29), fungal DNA detected in aerosol filter samples is most likely to originate from spores which are known to resist environmental stress and survive atmospheric transport (30, 31), whereas DNA in fungal tissue fragments may be rapidly degraded by atmospheric photooxidants. Nevertheless, hyphae and tissue fragments can also be present in coarse and fine air particulate matter (32–34). Moreover, the disruption of fungal spores due to environmental stress may lead to the formation and sampling of smaller fragments, whereas the association of spores with each other or with other

particulate matter may lead to the formation and sampling of larger particles. For example, unicellular fungi (like endophytic fungi) and plant pathogens (rust fungi, powdery mildew) are likely to be associated with plant fragments (35–37).

As outlined above, the species richness and the relative proportion of BMC were generally higher in coarse particle samples, while the species richness and the relative proportion of AMC were higher in fine particle samples. This is consistent with the following basic features of BMC and AMC (26, 38–40): BMC tend to have spores with relatively large aerodynamic diameters ($\approx 5\text{--}10\text{ }\mu\text{m}$), and many of them produce fruiting bodies that may fragment and release large tissue particles. In contrast, AMC are mostly single-celled (yeast) or filamentous (hyphal), and some of the most prominent AMC species like *Cladosporium* sp. and *Penicillium* spp. have spores with small aerodynamic diameters ($\approx 2\text{--}5\text{ }\mu\text{m}$). More information about the differences between coarse and fine particle samples and about fungal spore size is available online ([SI Text](#) and [Table S3, Table S4, Table S5, Table S6, Table S7, and Table S8](#)).

Earlier studies of airborne fungi have mostly not evaluated the diversity of AMC vs. BMC, or they have reported a predominance of AMC (e.g., refs. 41, 42). Most of these studies were based on cultivation techniques and have detected far fewer species (typically $\ll 100$). Lugauskas et al. (43) reported a high number of different fungal species (≈ 430), but for this they had analyzed over 900 aerosol samples collected at multiple locations over several years, corresponding to a normalized species richness of only approximately 0.5 as opposed to ~ 10 from our DNA-based investigations. Over 80% of all known fungi are not cultivable on synthetic media, and fast growing fungi can mask slower growing fungi (44). BMC are often out-competed by the more rapidly growing mold fungi (45), and some AMC like *Cladosporium* can actively inhibit the growth of others by production of inhibitory substances (46). Thus, cultivation-based studies of airborne fungi are likely biased against the detection of BMC (especially by the high abundance of *Cladosporium*).

To our knowledge, only 3 studies have reported DNA analyses of fungi in atmospheric aerosol samples up to now. Boreson et al. (47) found 18 species in urban air (40% AMC, 6% BMC) and 31 species in desert air (65% AMC, 17% BMC), Despres et al. (29) found only 3 AMC and 1 BMC species in several dozens of filter samples of urban, rural, and high-alpine air, and Fierer et al. (48) measured over 1,500 fungal DNA sequences from 5 urban air samples and attributed 97% to AMC but did not specify the species richness. We have tested and applied multiple PCR primer pairs; these and other experimental details were identified as key elements for efficient amplification of DNA from AMC, BMC, and other fungi (see *Materials and Methods*). Consequently, we have been able to detect a wide range of species that are well-known from cultivation-based studies (e.g., *Cladosporium* spp., *Penicillium* spp., *Alternaria* spp., and *Candida* spp.) as well as non cultivable species (e.g., *Blumeria graminis* and *Puccinia* spp.) and previously unknown species as indicated by 136 operational taxonomic units (OTUs) with low NCBI

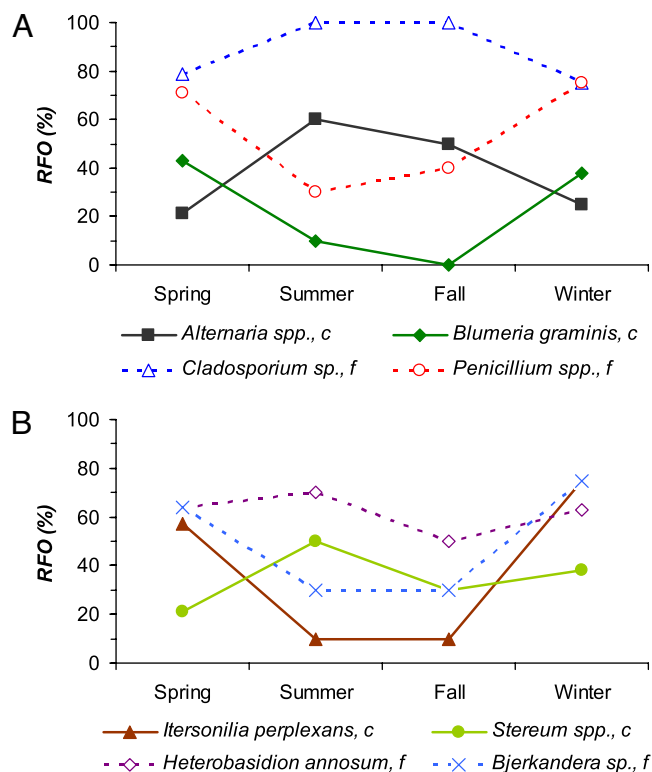


Fig. 3. Seasonal variations in the relative frequency of occurrence (RFO) of selected species of *Ascomycota* (A) and *Basidiomycota* (B) in coarse and fine air particulate matter, respectively (c, f).

similarity scores (<97%). Some of these might also stem from degraded DNA (29), but at least the 21 OTUs that were found in multiple samples are much more likely to represent unknown species. The other DNA-based studies of airborne fungi have neither found the expected high abundance of *Cladosporium* nor a high species richness of BMC, which we suppose to be due to limitations of the applied methods.

Ongoing investigations of aerosol samples from several locations around the world indicate that the species richness of fungi in continental air is generally higher for BMC than for AMC. In contrast, the number and proportion of all fungal species known from the biosphere are higher for AMC ($\approx 60,000$, $\approx 60\text{--}70\%$) than for BMC (25,000–30,000, $\approx 30\text{--}40\%$) (25, 49). Recently, however, Hunt et al. (50) compared culture- and DNA-based analyses of fungi in grassland soil samples and found that 54% of the fungal sequences were from BMC whereas no BMC species could be isolated by plate culturing. Thus, the high proportion of BMC in air as observed in our study (64%) may be explained by one or both of the following hypotheses:

1. BMC may be enriched in the atmosphere relative to the biosphere, because their proportion at the atmosphere-biosphere interface (i.e., on vegetation and soil surfaces) or their efficiency in dispersing spores may be enhanced relative to AMC (dry release vs. active wet discharge with aqueous jets or droplets) (1).
2. The ratio of BMC to AMC in the biosphere may have been underestimated in earlier studies for the reasons outlined above (bias of culture-based techniques, primer selection in DNA-based techniques). In this case, our atmospheric measurement results might reflect the biospheric proportions.

Clearly, our results will need to be complemented by further investigations to confirm or discard the above hypotheses. In any case, however, our data show that the diversity of airborne fungi—and in particular the species richness of BMC—is much higher than indicated by earlier studies.

As many fungal species in the biosphere are still unknown, the detection and characterization of fungi in atmospheric aerosol samples by DNA analysis can help to elucidate the regional and global spread and diversity of fungi. Moreover, DNA analyses also enables efficient and unambiguous identification of other primary biogenic aerosol particles and components [bacteria, animal, and plant fragments, etc., (29)].

Information about the diversity and abundance of airborne fungi and other bioaerosol particles is relevant for many areas of research such as biogeosciences, climate and ecology, human and veterinary medicine, industrial and environmental hygiene, agriculture, bioengineering, and security. Among the key perspectives for future investigations of air particulate matter by DNA analysis are the possible influence of different types of bioaerosols on the hydrological cycle (14, 16, 17), the spread of genetically modified organisms (51), and climate-related changes in the diversity and abundance of fungi and other organisms on local, regional, and global scales (1, 52).

Materials and Methods

Aerosol Sampling. Aerosol samples were collected on glass fiber filters (Pall Corporation, Type A/A, 102-mm diameter) over 1 year in Mainz, Germany (130 m a.s.l., March 2006–April 2007). The sampling station was positioned on a mast at the top of the Max Planck Institute for Chemistry (MPIC, ≈ 5 m above the flat roof of the 3-story building) on the campus of the University of Mainz (49°59′31.36″N 8°14′15.22″E). The air masses sampled at MPIC represent a mix of urban and rural continental boundary layer air in central Europe. A high-volume dichotomous sampler [self-built based on Solomon et al. (53)] was used to separate and collect coarse and fine aerosol particles on a pair of glass fiber filters. The sampler was operated with a rotary vane pump (Becker VT 4.25) at a total flow rate of approximately 300 L min⁻¹, corresponding to a nominal cut-off diameter of ≈ 3 μ m. Coarse particles with aerodynamic diameters larger than the cut-off were collected through a virtual impactor

operated in line with the inlet (≈ 30 L min⁻¹), and fine particles with aerodynamic diameters smaller than the cut-off were collected from the main gas flow perpendicular to the inlet (≈ 270 L min⁻¹).

The sampling period was generally 7 days, corresponding to a sampled air volume of approximately 3,000 m³. A few samples were collected over shorter periods (1–5 days, $\approx 400\text{--}2,000$ m³). A listing of all investigated pairs of air filter samples (42 coarse and 42 fine particle samples) is given in Table S1. Before use, all glass fiber filters were decontaminated by baking at 500°C over night (29). Loaded filters were packed in aluminum foil (also prebaked at 500°C), and stored in a freezer at -80°C until DNA extraction. To detect possible contaminations from the sampler and sample handling, blank samples were taken at regular intervals (≈ 4 weeks). The filters were mounted in the sampler like for regular sampling, but the pump was turned on either not at all (“mounting blanks”) or for only 5 s (“start-up blank”).

DNA Extraction and Amplification. Filter sample aliquots ($\frac{1}{8}\text{--}\frac{1}{4}$) were extracted with a commercial soil extraction kit (LysingMatrixE, Fast DNA Spin Kit for Soil, MP Biomedicals) according to the supplier's instructions with the following modifications: 15-min centrifugation step after the lysis, partly additional 900 μ L buffer and repeated beating and centrifugation. Both generated supernatants were combined for the further extraction process. Finally, the DNA was dissolved in 100 μ L elution buffer. Decontaminated filters were included during the extractions as extraction blanks.

With the DNA extract from each of the filters listed in Table S1, several PCRs were performed to amplify DNA from fungi for sequence analysis. The 50- μ L reaction mixture always contained the template DNA (0.5–2- μ L sample extract), 1 $\times$ PCR buffer, 0.2 mM each dNTP (Roth), 0.33 μ M of each primer (Sigma-Aldrich), and 2.5 units of JumpStart REDTaq DNA polymerase (Sigma-Aldrich). A negative control was included in all PCR runs.

PCR was performed with the primer pairs listed in Table S2 and Fig. S1, respectively. The thermal profile (DNA Engine, Bio-Rad Laboratories) was as follows: initial denaturing at 94°C for 3 min; 35 cycles with denaturing at 94°C for 30 s, annealing at primer pair specific temperature for 30 s (Table S2), elongation at 72°C for 90 s, and a final extension step at 72°C for 5 min.

Fungal DNA was detected in all of the 84 investigated air filter samples, and 200 PCR products were obtained with different primer pairs as specified in Table S1 and Table S2. No DNA was detected in the mounting, start-up, extraction, and PCR blanks, indicating that no contamination occurred during sample handling and analysis in the laboratory.

PCR products were obtained with all primer combinations except for the *Zygomycota*-specific primer pair D (Table S1, Table S2, and Fig. S1). The primer pairs A and F amplified *Basidiomycota* (BMC) as well as *Ascomycota* (AMC) and the primer pairs that were designed to be specific for BMC (B) and AMC (C) indeed amplified only BMC and AMC, respectively. The sequences obtained with the primer pair E which should be specific for *Chytridiomycota* matched with members of the *Pucciniomycetes* (within the BMC) and *Fungi incertae sedis* (formerly *Zygomycota*).

Fungal DNA was also co-amplified with primer pairs (G–I) that were supposed to be specific for animal, insect, and archaea 18S or 16S rDNA (Table S1, Table S2, and Fig. S1). Table S1 gives information on obtained sequences resulting from co-amplification reactions in coarse particle filter extracts. The primer pairs G and H amplified BMC whereas the primer pair I amplified AMC. This primer behavior calls for reevaluation of the primer performance and requires attention before the primer pair is further used in samples that harbor material from different groups of organisms. The obtained fungal 18S sequences confirm knowledge from other studies that the ITS region is a better target region and 18S rDNA analysis often is not able to discriminate between species in environmental samples (54).

Cloning and Restriction Fragment Length Polymorphism. Amplification products for sequencing were cloned using the TOPO TA Cloning Kit (Invitrogen) following the supplier's instructions. Colonies containing inserts were identified by blue-white selection and lysed in 20 μ L water for 10 min at 95°C. The inserts of 12–24 colonies were amplified (“colony PCRs”) using 3 μ L lysate in a 40- μ L reaction. The PCR mixture always contained: 1 $\times$ PCR Buffer, 2.5 mM MgCl₂, 0.25 mM each dNTP (Roth), 0.25 μ M of each primer (Sigma-Aldrich), 1.25 U TaqDNA Polymerase (Invitrogen). PCR was performed with the primer pair M13F-40 and M13R, and the thermal profile was as follows: initial denaturing at 94°C for 5 min; 40 cycles with 94°C for 30 s, annealing at 55°C for 1 min, elongation at 72°C for 1 min, and a final extension step at 72°C for 15 min.

Colony PCR was followed by a restriction fragment length polymorphism (RFLP) analysis to select as many as possible different clones for sequencing. Two microliters of the PCR-products were digested without further purification with 5 U of the enzymes *TaqI*, *HinfI*, or *AluI* (Fermentas). Restriction

fragments were separated by gel electrophoresis in a 3% agarose gel stained with ethidium bromide and the images were documented with the Gel Doc XR system and analyzed with Quantity One software (Bio-Rad Laboratories). On the basis of the resulting restriction fragment patterns, representative colony PCR products with different numbers and sizes of fragments were selected for sequencing.

DNA Sequence Analysis, Taxonomic Attribution, and Statistical Parameters.

DNA sequences were determined with ABI Prism 377, 3100, and 3730 sequencers (Applied Biosystems) using BigDye-Terminator v3.1 chemistry at the DNA Core Facility of the Max Planck Institute for Plant Breeding Research, Cologne. For comparison with known sequences, databank queries using the Basic Local Alignment Search Tool (BLAST) were performed via the website of the National Center for Biotechnology Information (NCBI, <http://www.ncbi.nlm.nih.gov/>). Each sequence was identified to the lowest taxonomic rank common to the top BLAST hits (up to ≈ 100 database sequences with highest similarity and total scores). For 17 of the 1,513 sequences determined in this study, the ITS1 and ITS2 regions matched in different genera. These 17 sequences were assumed to be chimeric results of PCR recombination and were excluded from further analysis.

For each aerosol filter sample, sequences that produced the same BLAST results were pairwise aligned using the program BioEdit (BioEdit 7.05; <http://www.mbio.ncsu.edu/BioEdit/bioedit.html>) and the similarity between them was calculated. Sequences with similarity scores greater than or equal to 97% were clustered into an operational taxonomic unit (OTU). The different OTUs can be regarded as different fungal species, because the sequence variability due to intraspecific ITS divergence is usually $<3\%$ (55). PCR errors can also introduce some sequence variability (56). The approximate 100 PCR cycles typically applied in our study (amplification, colony, and sequencing PCRs) are, however, unlikely to cause substitutions of more than 1% of the base pairs in the measured sequences, because the total error rates of *Taq* polymerase are typically in the range of 10^{-5} – 10^{-4} errors per base pair (57, 58). When sequences obtained by co-amplification with nonfungal primer pairs (18S; G, H, I; Table S2) yielded the same best match results as ITS sequences from the same sample, they were attributed to the same OTU, because they are likely to have the same origin (see Fig. S1).

Table S3 gives an overview of the 368 detected OTUs with corresponding characteristic NCBI sequence accession numbers, taxonomic class and species names, and frequencies of occurrence, that is, numbers of air samples and coarse or fine particle filters, respectively, in which they were detected. Note that some OTUs exhibited high similarity (98–100%) with multiple NCBI sequences attributed to different orders, families, genera, or species, which may be due to database entries with incorrect/inconsistent taxonomic information or high interspecific ITS similarity (e.g., BMC2: *Bjerkandera*

Thanatephorus; BMC3: *Trametes/Tricholoma/Phellinus* sp.). About one-third of the OTUs exhibited less than 97% similarity with NCBI sequences ($<90\%$ for 37 OTUs, 90–96% for 99 OTUs) and may represent species that are unknown or at least not listed in the NCBI database. Alternatively, the measured DNA may have been partially degraded in the air or upon sampling and analysis (59–62). This is, however, not very likely for fungal spores that are known to resist environmental stress and survive atmospheric transport (29). Moreover, 21 OTUs with low best match similarity scores were found in more than 1 sample, which appears unlikely for damaged DNA. Thus, we assume that most if not all OTUs represent different fungal species, and that $\approx 30\%$ of these have not yet been characterized by DNA analysis and listing in the NCBI database.

The detection and apparent frequency of occurrence of different species can also be affected by technical factors like extraction efficiency of DNA, varying rDNA copy number in the species, primer matching and performance, amplification efficiency of the target region, and cloning success. As discussed above, the high proportion of fungal species that were detected only once indicates, that a higher number of samples and clones would have to be investigated for a more complete coverage of species diversity. Thus, the detected and reported numbers and frequencies of occurrence of species, families, and classes should be regarded as a lower limit for the actual diversity and frequency of occurrence of airborne fungi.

To characterize and compare the diversity of fungal species (OTUs) in the investigated air masses, we have calculated the parameters defined in Table S4 for the whole data set and for different subsets (phyla, seasons, etc.). The results are summarized in Table S5, Table S6, and Table S7 and additional information is given in SI Text. Statistical analyses were performed with the software package SPSS (release 16.0.1, SPSS Inc.). *t* tests were performed to confirm statistical significance of discussed differences between seasons, AMC/BMC and coarse/fine particle samples (*P* values <0.05). Multiple linear regressions were performed with species richness values (running mean of 5 consecutive samples) and local air quality data (ZIMEN Luftmessnetz, Rheinland Pfalz, Station Mainz-Mombach: temperature, relative humidity, wind speed and direction, atmospheric pressure, ozone concentration, and rainfall averaged over the sampling periods).

Nucleotide Sequence Accession Numbers. The sequences from the 368 OTUs of the present study have been deposited in the GenBank database under following accession numbers: FJ820489–FJ820856 (Table S9).

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- Elbert W, Taylor PE, Andreae MO, Pöschl U (2007) Contribution of fungi to primary biogenic aerosols in the atmosphere: Wet and dry discharged spores, carbohydrates, and inorganic ions. *Atmos Chem Phys* 7:4569–4588.
- Bauer H, et al. (2008) Significant contributions of fungal spores to the organic carbon and to the aerosol mass balance of the urban atmospheric aerosol. *Atmos Environ* 42:588–593.
- Womilaju TO, Miller JD, Mayer PM, Brook JR (2003) Methods to determine the biological composition of particulate matter collected from outdoor air. *Atmos Environ* 37:4335–4344.
- Held A, et al. (2004) Aerosol size distributions measured in urban, rural and high-alpine air with an electrical low pressure impactor (ELPI). *Atmos Environ* 42:8502–8512.
- Hock N, et al. (2008) Rural continental aerosol properties and processes observed during the Hohenpeissenberg Aerosol Characterization Experiment (HAZE2002). *Atmos Chem Phys* 8:603–623.
- Jaenicke R (2005) Abundance of cellular material and proteins in the atmosphere. *Science* 308: 73–73.
- Christner BC, et al. (2008) Ubiquity of biological ice nucleators in snowfall. *Science* 319:1214.
- Bauer H, et al. (2002) The contribution of bacteria and fungal spores to the organic carbon content of cloud water, precipitation and aerosols. *Atmos Res* 64:109–119.
- Pouleur S, Richard C, Martin JG, Antoun H (1992) Ice nucleation activity in *Fusarium acuminatum* and *Fusarium avenaceum*. *Appl Environ Microbiol* 58:2960–2964.
- Andreae MO, Crutzen PJ (1997) Atmospheric aerosols: Biogeochemical sources and role in atmospheric chemistry. *Science* 276:1052–1058.
- Pöschl (2005) Atmospheric aerosols: Composition, transformation, climate, and health effects. *Angew Chem Int Ed* 44:7520–7540.
- Andreae MO, Rosenfeld D (2008) Aerosol-cloud-precipitation interactions. Part 1. The nature and sources of cloud-active aerosols. *Earth Sci Rev* 89:13–41.
- Rosenfeld D, et al. (2008) Flood or drought: How do aerosols affect precipitation? *Science* 321:1309–1313.
- Möhler O, DeMott PJ, Vali G, Levin Z (2007) Microbiology and atmospheric processes: The role of biological particles in cloud physics. *Biogeosciences* 4:1059–1071.
- Deguillaume L, et al. (2008) Microbiology and atmospheric processes: Chemical interactions of primary biological aerosols. *Biogeosciences* 5:1073–1084.
- Prenni AJ, et al. (2009) Relative roles of biogenic emissions and Saharan dust as ice nuclei in the Amazon basin. *Nature Geoscience* doi:10.1038/ngeo517.
- Pratt KA, et al. (2009) In situ detection of biological particles in cloud ice-crystals. *Nature Geoscience* doi:10.1038/ngeo521.
- Kurup VP, Shen H-D, Banerjee B (2000) Respiratory fungal allergy. *Microbes Infect* 2:1101–1110.
- Adhikari A, Sen MM, Gupta-Bhattacharya S, Chanda S (2004) Airborne viable, non-viable, and allergenic fungi in a rural agricultural area of India: A 2-year study at five outdoor sampling stations. *Sci Total Environ* 326:123–141.
- Brown JKM, Hovmöller MS (2002) Epidemiology—Aerial dispersal of pathogens on the global and continental scales and its impact on plant disease. *Science* 297:537–541.
- Hill TCJ, Walsh KA, Harris JA, Moffett BF (2003) Using ecological diversity measures with bacterial communities. *FEMS Microbiol Ecol* 43:1–11.
- Richard F, Moreau PA, Selosse MA, Gardes M (2004) Diversity and fruiting patterns of ectomycorrhizal and saprobic fungi in an old-growth Mediterranean forest dominated by *Quercus ilex* L. *Can J Bot* 82:1711–1729.
- Maria GL, Sridhar KR (2002) Richness and diversity of filamentous fungi on woody litter of mangroves along the west coast of India. *Curr Sci* 83:1573–1580.
- Chao A (1984) Nonparametric-estimation of the number of classes in a population. *Scand J Stat* 11:265–270.
- James TY, et al. (2006) Reconstructing the early evolution of fungi using a six-gene phylogeny. *Nature* 443:818–822.
- Hibbett DS, et al. (2007) A higher-level phylogenetic classification of the Fungi. *Mycol Res* 111:509–547.
- Levetin E (1990) Studies on airborne basidiospores. *Aerobiologia* 6:177–180.
- Liang-Dong Guo G-RHYW (2008) Seasonal and tissue age influences on endophytic fungi of *Pinus tabulaeformis* (Pinaceae) in the Dongling Mountains, Beijing. *J Integr Plant Biol* 50:997–1003.

Supporting Table S1 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

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Table S1. Overview of air samples (aerosol filter pairs). Sample ID (running number); sampling period and time; sampled air volume; number of DNA sequences obtained with different primer pairs (A-I, Supporting Table S2) and all together from the coarse and fine particle filter samples, respectively (coarse/fine); number of different species (OTUs) of all fungi and of *Ascomycota* (AMC), *Basidiomycota* (BMC), and *Fungi Incertae Sedis* or others (FIS) detected in the whole air sample and in the coarse or fine particle filters, respectively (total/coarse/fine).

Sample ID	Sampling Period	Sampling time (days)	Sampled air volume (m³)	Sequences										Species			
				A	B	C	E	F	G	H	I	All	Fungi	AMC	BMC	FIS	
MZ 1	24.03.06-31.03.06	7.02	3019	10/11	-/12	-/12		8/-	3/-				21/35	29/11/20	7/3/5	22/8/15	
MZ 2	31.03.06-07.04.06	6.95	3057	12/11	-/11	-/9	2/-						14/31	23/8/18	9/4/7	14/4/11	
MZ 4	07.04.06-12.04.06	4.97	2202	12/11	-/10	-/4							12/25	18/8/12	13/6/8	5/2/4	
MZ 9	20.04.06-27.04.06	7.00	3026	37/12	-/11				11/-				48/23	41/34/9	16/14/2	25/20/7	
MZ 10	27.04.06-02.05.06	4.92	2077	11/11	-/11	-/11							11/33	22/10/15	11/5/7	11/5/8	
MZ 11	02.05.06-03.05.06	1.01	444	18/12	-/12				4/-		1/-	23/24	24/16/11	12/6/7		12/10/4	
MZ 15	04.05.06-09.05.06	4.91	2064		6/6	4/7						10/13	12/7/6	6/3/3		6/4/3	
MZ 18	12.05.06-15.05.06	3.02	1321		6/11	7/6						13/17	16/11/8	8/6/4		8/5/4	
MZ 25	22.05.06-23.05.06	0.97	425	10/-	7/9	12/11			3/-			32/20	23/17/10	10/7/6		13/10/4	
MZ 26	23.05.06-30.05.06	6.98	3100	10/-	12/8	4/12			2/-			28/20	31/15/17	12/4/9		18/10/8	1/1/-
MZ 31	01.06.06-06.06.06	4.95	2199		8/9	3/6						11/15	17/10/11	7/3/5		10/7/6	
MZ 35	14.06.06-21.06.06	6.97	2999	31/-	7/8	-/4						38/12	15/12/6	5/5/1		10/7/5	
MZ 36	21.06.06-	0.97	422	11/-	12/7	-/3	3/-		1/-			27/10	25/20/8	4/4/1		21/16/7	

	22.06.06											
MZ 40	27.06.06-04.07.06	6.96	3045	8/-	12/8	3/4	1/-	24/12	18/13/7	5/4/2	13/9/5	
MZ 41	04.07.06-11.07.06	6.96	3019	6/-	8/8	5/5	4/-	23/13	20/13/9	6/5/2	14/8/7	
MZ 45	19.07.06-21.07.06	1.98	872		6/9	4/7		10/16	17/8/11	5/4/3	12/4/8	
MZ 47	26.07.06-02.08.06	6.97	3025	8/-	12/12	-/3		20/15	19/10/12	5/4/2	14/6/10	
MZ 50	02.08.06-09.08.06	6.94	3025	7/-	12/6	4/4	3/-	26/10	24/18/10	7/5/4	17/13/6	
MZ 51	09.08.06-16.08.06	7.01	3060	12/-	8/8	-/5	4/-	24/13	26/15/12	8/4/5	18/11/7	
MZ 52	16.08.06-23.08.06	6.95	3081	8/27	8/-	-/4		2/-	18/31	22/11/12	7/3/5	15/8/7
MZ 54	30.08.06-06.09.06	7.00	3091	16/-	-/8	-/5		16/13	22/12/12	9/5/5	13/7/7	
MZ 59	11.09.06-18.09.06	6.86	2977	13/7	12/12	-/3	3/-	1/-	29/22	27/18/11	8/5/4	19/13/7
MZ 60	18.09.06-25.09.06	7.02	3033		9/9	4/3		13/12	14/10/6	3/2/2	11/8/4	
MZ 62	02.10.06-09.10.06	6.99	3026	12/-	12/9	-/4	2/-	5/-	31/13	26/18/9	5/2/4	20/15/5 1/1/-
MZ 63	09.10.06-16.10.06	6.98	3079	11/12	10/-		6/-		27/12	24/20/5	4/3/2	16/13/3 4/4/-
MZ 66	16.10.06-23.10.06	6.96	2995	9/10	11/5	-/7			20/22	19/12/12	7/3/6	12/9/6
MZ 67	23.10.06-30.10.06	6.97	3028	6/-	12/8	5/4			23/12	25/15/11	7/5/3	18/10/8
MZ 69	02.11.06-09.11.06	7.00	3034	12/11					12/11	16/8/9	6/5/2	10/3/7
MZ 71	16.11.06-23.11.06	6.98	3063	11/11					11/11	12/6/8	6/3/4	6/3/4
MZ 74	23.11.06-30.11.06	6.95	2808		10/11	8/4			18/15	25/14/13	7/5/3	17/9/9 1/-/1
MZ 75	30.11.06-07.12.06	6.95	2992	12/10	-/9	-/3	4/-		16/22	22/10/13	4/1/4	18/9/9
MZ 77	14.12.06-21.12.06	6.98	3011	-/12	9/-	2/-			11/12	14/7/8	5/2/3	9/5/5
MZ 81	28.12.06-04.01.07	7.03	3005	17/10	12/-		2/-		31/10	16/10/6	2/0/2	14/10/4
MZ 82	04.01.07-11.01.07	6.99	3056		6/9	6/7			12/16	23/10/14	9/4/5	14/6/9
MZ 84	18.01.07-25.01.07	7.01	3121		8/10	6/6			14/16	23/10/15	14/6/9	9/4/6
MZ 88	01.02.07-08.02.07	6.99	3056		8/10	7/2			15/12	16/12/7	8/6/2	8/6/5
MZ 90	15.02.07-22.02.07	7.02	2998		8/11	6/6			14/17	22/10/13	15/6/10	7/4/3
MZ 93	22.02.07-01.03.07	6.93	3023		3/4	6/5			9/9	12/7/8	8/4/5	4/3/3
MZ 95	08.03.07-15.03.07	7.00	3025		6/6	6/5			12/11	16/10/8	11/6/5	5/4/3
MZ 97	22.03.07-29.03.07	6.97	3025		8/4	9/5			17/9	21/16/8	11/9/4	10/7/4
MZ 101	05.04.07-12.04.07	7.01	3061	-/1	7/8	4/4			11/13	14/9/9	8/4/6	6/5/3
MZ 103	19.04.07-26.04.07	7.05	3078		7/5	7/5			14/10	12/8/8	5/3/4	7/5/4

Supporting Table S2 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

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Table S2. PCR primer combinations (A-I). Forward and reverse primer names, amplified region/gene, approx. length of the PCR product (number of base pairs, bp), annealing temperature, and references.

Primer pair	Forward	Reverse	Amplified region	Product (bp)	Temperature (°C)	References (SI)
A	ITS5	ITS4	ITS1-5.8S-ITS2	500 - 700	54	(26)
B	ITS5	ITS4B	ITS1-5.8S-ITS2	~900	58	(26, 27)
C	ITS5	ITS4A	ITS1-5.8S-ITS2	~600	55	(26, 27)
D	ITS5	ITS4Z	ITS1-5.8S-ITS2	~700	45	(26, 27)
E	ITS5	ITS4C	ITS1-5.8S-ITS2	~1000	53	(26, 27)
F	ITS1	5.8S	ITS1-5.8S	~300	55	(26, 28)
G	18Sai	18Sbi	18S	1140	55	(29)
H	18S-H17F	18S-H35R	18S	900	58	(30)
I	109f	934r	16S	800	52	(31)

Supporting Table S3 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

Janine Fröhlich-Nowoisky, Daniel A. Pickersgill, Viviane R. Després, and Ulrich Pöschl

Table S3. Operational taxonomic units (OTUs) attributed to Ascomycota (A) and Basidiomycota (B). Operational ID (AMC/BMC and running number); frequency of occurrence (number of air samples and coarse/fine particle filters in which the species was detected); most characteristic NCBI accession numbers sorted by similarity score; taxonomic class and species name according to NCBI data base (if determined). Species names are listed if available from NCBI sequences with similarity scores $\geq 97\%$.

(A)

OTU	Frequency of occurrence			NCBI accession numbers and similarity scores	Class, species
	total	coarse	fine		
AMC1	41	35	37	EU167591 (99-100%), AF455517 (99-100%), AF393712 (99-100%), AF393707 (99-100%)	<i>Dothideomycetes, Cladosporium sp.</i>
AMC2	24	20	8	EF207415 (98-100%), AF455526 (98-100%), EU563125 (99%), EF153017 (98%)	<i>Leotiomycetes, Botryotinia fuckeliana</i> *
AMC3	18	18	0	EU552134 (100%), AJ279463 (100%)	<i>Dothideomycetes, Epicoccum sp.</i> *
AMC4	13	7	7	AF455536 (100%), AF455528 (100%)	<i>Eurotiomycetes, Eurotium sp.</i>
AMC5	12	11	1	EF432293 (99%), AY154712 (99%)	<i>Dothideomycetes, Alternaria sp.</i>
AMC6	12	0	12	FJ008997 (99%)	<i>Eurotiomycetes, Penicillium expansum</i>
AMC7	11	9	3	AF520642 (99%)	<i>mitosporic AMC, Ascochyta sp.</i>
AMC8	11	3	10	DQ426522 (100%), AY373898 (100%), AM158223 (100%)	<i>Eurotiomycetes, Penicillium sp.</i>
AMC9	10	10	0	AB273542 (99%), AB273566 (99%)	<i>Leotiomycetes, Blumeria graminis</i>
AMC10	9	8	2	AY154692 (99%), EF432282 (99%), AY154695 (98%)	<i>Dothideomycetes, Alternaria sp.</i>
AMC11	6	5	4	EU998929 (95%), EF601602 (95%)	
AMC12	6	5	1	EU167608 (99%), AM160630 (99%)	<i>Dothideomycetes, Aureobasidium sp.</i> *
AMC13	6	2	4	AY805550 (100%),	<i>Leotiomycetes, Cistella acuum</i>
AMC14	5	1	4	AM901991 (99%), AF501262 (99%), AF435827 (98%), AF501259 (98%), EU167591 (97%)	
AMC15	5	0	5	EF652038 (99%), EF652039 (98%)	<i>Eurotiomycetes, Aspergillus sp.</i>
AMC16	4	1	3	AY373862 (95%), AF540513 (95%)	
AMC17	4	0	4	AY373851 (100%),	<i>Eurotiomycetes, Aspergillus fumigatus</i>
AMC18	4	0	4	EU288196 (99%)	<i>Saccharomycetes, Candida tropicalis</i>
AMC19	3	3	0	DQ006952 (95%), AF455427 (94%)	<i>Sordariomycetes</i>

AMC20	3	1	2	AY853228 (99%),	<i>Leotiomyces</i> , <i>Naevula minutissima</i>
AMC21	3	0	3	DQ195780 (100%),	<i>Dothideomycetes</i> , <i>Leptospora rubella</i>
AMC22	3	0	3	EF434058 (99%), AJ560686 (99%)	<i>Sordariomycetes</i> , <i>Beauveria bassiana</i>
AMC23	2	2	0	DQ530453 (96%), U04207 (94%)	
AMC24	2	2	0	AM901702 (99%), DQ778909 (99%), AJ488260 (99%), AF459728 (99%), EF652065 (99%)	
AMC25	2	2	0	AJ293875 (100%), AJ888477 (99%),	
AMC26	2	1	2	AY183369 (96%)	<i>Sordariomycetes</i>
AMC27	2	1	1	AM084454 (99%), AF439488 (99%)	<i>Dothideomycetes</i> , <i>Phaeosphaeria juncophila</i>
AMC28	2	1	1	DQ006952 (98%)	<i>Sordariomycetes</i> , <i>Diatrype</i> sp.
AMC29	2	0	2	EU019285 (99%), AB109183 (99%), AY607019 (99%), AY152593 (99%)	<i>Dothideomycetes</i> , <i>Ramularia</i> sp. *
AMC30	2	0	2	AF439504 (96%), AF383951 (91%)	<i>Dothideomycetes</i>
AMC31	2	0	2	EU687059 (92%), AY754945 (91%)	<i>Sordariomycetes</i>
AMC32	2	0	2	EF026143 (99%)	<i>Sordariomycetes</i> , <i>Hypoxyton rubiginosum</i>
AMC33	2	0	2	AM749928 (99%)	<i>Sordariomycetes</i> , <i>Hypoxyton howeanum</i>
AMC34	1	1	0	EU292653 (93%), U57089 (93%), DQ182427 (93%)	<i>Leotiomyces</i>
AMC35	1	1	0	AY634167 (98%), AF486133 (97%), DQ249994 (96%)	
AMC36	1	1	0	DQ679486 (91%), DQ182451 (91%), AY864822 (90%)	
AMC37	1	1	0	EU826481 (99%), EF024754 (99%), EU167600 (99%)	
AMC38	1	1	0	DQ683973 (95%)	
AMC39	1	1	0	DQ683973 (94%)	
AMC40	1	1	0	DQ979719 (92%), AF013225 (91%)	
AMC41	1	1	0	EF159443 (97%), EU552134 (92%), AJ279463 (92%)	
AMC42	1	1	0	AY969725 (92%), AF050278 (83%)	
AMC43	1	1	0	EF521252 (99%), EU035412 (85%)	
AMC44	1	1	0	EU754979 (97%), EU883432 (96%), EU883430 (96%)	<i>mitosporic AMC</i> , <i>Tetracladium</i> sp.
AMC45	1	1	0	EU687056 (93%), EU326188 (89%), EF577238 (89%)	
AMC46	1	1	0	AJ244263 (92%), AY969659 (91%)	
AMC47	1	1	0	EU529999 (95%), EF207415 (89%)	
AMC48	1	1	0	EU167569 (98%), AY357266 (98%), AF279583 (98%)	
AMC49	1	1	0	AB085929 (98%),	<i>mitosporic AMC</i> , <i>Thermomyces lanuginosus</i>
AMC50	1	1	0	EU019284 (97%), AJ301970 (97%), AY154692 (96%), EF432286 (96%)	
AMC51	1	1	0	FJ000399 (98%)	<i>mitosporic AMC</i> , <i>Tumularia aquatica</i>
AMC52	1	1	0	AY387657 (94%), EU848215 (88%)	<i>Dothideomycetes</i>
AMC53	1	1	0	AY961406 (91%), EU885415 (91%)	<i>Dothideomycetes</i>
AMC54	1	1	0	EF420004 (96%), AM262366 (95%), DQ092527 (93%)	<i>Dothideomycetes</i>
AMC55	1	1	0	DQ273287 (89%), EU167596 (86%), EU707892 (85%)	<i>Dothideomycetes</i>
AMC56	1	1	0	AF383957 (100%)	<i>Dothideomycetes</i> , <i>Massarina corticola</i>
AMC57	1	1	0	AM902015 (100%), DQ384571 (99%)	<i>Dothideomycetes</i> , <i>Leptosphaerulina chartarum</i>
AMC58	1	1	0	AY739861 (99%)	<i>Dothideomycetes</i> , <i>Pyrenophora tritici-repentis</i>
AMC59	1	1	0	AF203450 (99%), EF452450 (99%)	<i>Dothideomycetes</i> , <i>Stemphylium</i> sp.
AMC60	1	1	0	EF432300 (100%), AY196988 (100%)	<i>Dothideomycetes</i> , <i>Phaeosphaeria</i> sp.
AMC61	1	1	0	AY681194 (99%), AY681193 (99%)	<i>Sordariomycetes</i> , <i>Neurospora</i> sp.
AMC62	1	1	0	EU918705 (99%), AY681180 (99%)	<i>Sordariomycetes</i> , <i>Sordaria</i> sp.

AMC63	1	1	0	DQ323535 (99%)	<i>Sordariomycetes, Gnomonia leptostyla</i>
AMC64	1	1	0	AF000567 (97%),	<i>Sordariomycetes, Diaporthe sp.</i>
AMC65	1	1	0	U57673 (93%), AB067714 (92%)	<i>Sordariomycetes</i>
AMC66	1	1	0	AY484909 (96%)	<i>Eurotiomycetes</i>
AMC67	1	1	0	AF489434 (98%),	<i>Eurotiomycetes, Penicillium sp.</i>
AMC68	1	1	0	EU035422 (99%)	<i>Eurotiomycetes, Exophiala sp.</i>
AMC69	1	1	0	EF191234 (86%), EF191241 (85%)	<i>Leotiomycetes</i>
AMC70	1	1	0	Z73791 (99%), Z73771 (98%)	<i>Leotiomycetes, Monilinia padi</i>
AMC71	1	1	0	AB193380 (99%)	<i>Leotiomycetes, Sawadaea bicornis</i>
AMC72	1	1	0	EF029230 (96%), AJ430397 (96%)	
AMC73	1	1	0	AY541277 (93%), AJ457152 (89%)	<i>Lecanoromycetes</i>
AMC74	1	0	1	AM262380 (95%), AY075113 (93%)	
AMC75	1	0	1	DQ093661 (99%), AM292050 (99%)	
AMC76	1	0	1	EF029228 (93%), EU639650 (92%)	
AMC77	1	0	1	EU041789 (99%)	<i>mitosporic AMC, Radulidium subulatum</i>
AMC78	1	0	1	AY961406 (92%), EU040234 (91%), EU040233 (91%)	
AMC79	1	0	1	AY345346 (90%), AJ244276 (89%), DQ402525 (89%)	
AMC80	1	0	1	EU852369 (92%), AJ244276 (90%), DQ402525 (89%)	
AMC81	1	0	1	AY354273 (99%), DQ273341 (97%)	
AMC82	1	0	1	EU543253 (96%), AY773457 (95%)	
AMC83	1	0	1	EU707899 (96%), EU167569 (96%), AJ301970 (96%)	
AMC84	1	0	1	AJ496632 (97%)	<i>Dothideomycetes, Phaeosphaeria pontiformis</i>
AMC85	1	0	1	EU040243 (98%), AM176696 (97%)	<i>Dothideomycetes, Toxicocladosporium irritans</i>
AMC86	1	0	1	AJ608969 (99%)	<i>Dothideomycetes, Leptosphaeria sp.</i>
AMC87	1	0	1	AM262352 (96%), AJ244276 (90%)	<i>Dothideomycetes</i>
AMC88	1	0	1	EF060804 (91%)	<i>Sordariomycetes</i>
AMC89	1	0	1	EU686961 (89%), EU164404 (86%), EU552101 (85%)	<i>Sordariomycetes</i>
AMC90	1	0	1	EF212848 (96%), EU167609 (95%)	<i>Sordariomycetes</i>
AMC91	1	0	1	AJ557830 (99%), EU557361 (99%), AY138846 (99%)	<i>Sordariomycetes, Nectria sp. *</i>
AMC92	1	0	1	EU686848 (90%), EU552098 (88%), EF423534 (90%)	<i>Sordariomycetes</i>
AMC93	1	0	1	AY908999 (98%),	<i>Sordariomycetes, Rosellinia corticium</i>
AMC94	1	0	1	AB017661 (95%), AY805591 (94%)	<i>Sordariomycetes</i>
AMC95	1	0	1	AY908993 (99%)	<i>Sordariomycetes, Dicyma pulvinata</i>
AMC96	1	0	1	EU326205 (93%),	<i>Sordariomycetes</i>
AMC97	1	0	1	EF212848 (99%)	<i>Sordariomycetes, Gnomonia rostellata</i>
AMC98	1	0	1	EF447416 (98%), EF447401 (98%)	<i>Sordariomycetes, Valsa sp. *</i>
AMC99	1	0	1	DQ402530 (94%), AB208110 (93%)	<i>Sordariomycetes</i>
AMC100	1	0	1	DQ459870 (99%), DQ459868 (98%)	<i>Sordariomycetes, Fusarium sp.</i>
AMC101	1	0	1	AB027382 (99%),	<i>Sordariomycetes, Beauveria bassiana</i>
AMC102	1	0	1	AF455478 (100%)	<i>Sordariomycetes, Arthrinium sp.</i>
AMC103	1	0	1	AY373910 (100%)	<i>Eurotiomycetes, Penicillium digitatum</i>
AMC104	1	0	1	EF634441 (99%)	<i>Eurotiomycetes, Penicillium brevicompactum</i>
AMC105	1	0	1	DQ681321 (99%), DQ681325 (99%)	<i>Eurotiomycetes, Penicillium sp.</i>
AMC106	1	0	1	AF033491 (98%), AF033490 (98%), EF669708 (98%)	<i>Eurotiomycetes, Penicillium sp. *</i>
AMC107	1	0	1	EU833220 (95%), AF125937 (96%)	<i>Eurotiomycetes</i>
AMC108	1	0	1	AF033453 (98%), AF033452 (98%)	<i>Eurotiomycetes, Penicillium sp.</i>
AMC109	1	0	1	AB263742 (97%), AB086631 (97%)	<i>Eurotiomycetes, Paecilomyces sp.</i>
AMC110	1	0	1	EF029810 (92%), AB175237 (86%)	<i>Eurotiomycetes</i>

AMC111	1	0	1	AF033387 (99%), AF033386 (99%)	<i>Eurotiomycetes, Geosmithia</i>
AMC112	1	0	1	AJ131688 (97%)	<i>Eurotiomycetes, Chrysosporium lobatum</i>
AMC113	1	0	1	AY781221 (99%),	<i>Orbiliomycetes, Dactylaria sp.</i>
AMC114	1	0	1	EU040232 (91%), EF093148 (91%)	<i>Leotiomycetes</i>
AMC115	1	0	1	EU292504 (95%), DQ093752 (95%)	<i>Leotiomycetes</i>
AMC116	1	0	1	AY590782 (99%)	<i>Leotiomycetes, Chalara microchona</i>
AMC117	1	0	1	EF207423 (97%), EF153017 (97%)	<i>Leotiomycetes, Monilinia sp.</i>
AMC118	1	0	1	AY787711 (99%)	<i>Leotiomycetes, Lachnum sp.</i>
AMC119	1	0	1	AJ430221 (98%)	<i>Leotiomycetes, Lachnum virgineum</i>
AMC120	1	0	1	AJ430398 (98%)	<i>Leotiomycetes, Pezizella amentii</i>
AMC121	1	0	1	AY266169 (100%), AY266145 (100%)	<i>Leotiomycetes, Oculimacula sp.</i>
AMC122	1	0	1	AF410838 (99%)	<i>Lecanoromycetes, Parmelia sulcata</i>
AMC123	1	0	1	AY923248 (95%), AM850055 (94%)	<i>Saccharomycetes</i>
AMC124	1	0	1	AM279255 (99%)	<i>Saccharomycetes, Candida deformans</i>

* Some of the characteristic NCBI accession numbers correspond to different genera.

(B)

OTU	Frequency of occurrence			NCBI accession numbers and similarity scores	Class, species
	total	coarse	fine		
BMC1	30	12	26	AF455496 (99-100%), X70027 (99%), DQ384592 (99%)	<i>Agaricomycetes, Heterobasidion annosum</i>
BMC2	29	22	21	AJ006672 (99%), AF455463 (99%), AF455461 (99%), DQ060096 (99%), EF155506 (99%), AY633927 (99%), AF455421 (99%), AF455454 (99%), AJ279471 (99%), AJ279465 (99%)	<i>Agaricomycetes, Bjerkandera sp. *</i>
BMC3	25	16	19	AY309018 (99%), AF139961 (99%), AB158314 (99%), AF139961 (99%), AY089738 (99%), AF455529 (99%), DQ311085 (99%)	<i>Agaricomycetes, Trametes sp. *</i>
BMC4	22	14	9	AY787677 (98-99%), AY208796 (98%), AF210821 (97%-98%)	<i>Agaricomycetes, Peniophora sp.</i>
BMC5	19	14	9	AY854063 (99%), AM269810 (99%), DQ000294 (99%)	<i>Agaricomycetes, Stereum sp.</i>
BMC6	17	16	1	AB072233 (99%)	<i>Tremellomycetes, Itersonilia perplexans</i>
BMC7	13	13	0	DQ398959 (97%, 99%)	<i>Agaricomycetes, Vuilleminia comedens</i>
BMC8	12	6	7	AY271810 (98%), AY854087 (98%), AF455458 (97%)	<i>Agaricomycetes, Phlebia sp. *</i>
BMC9	8	7	3	AY015438 (100%), AB030351 (100%), AY070003 (100%)	<i>Microbotryomycetes, Sporobolomyces roseus</i>
BMC10	8	3	5	AY840572 (100%), AF516556 (99%)	<i>Agaricomycetes, Trametes sp.</i>
BMC11	7	5	4	DQ200924 (99%)	<i>Agaricomycetes, Botryobasidium subcoronatum</i>
BMC12	6	3	3	DQ093653 (99%), DQ093737 (99%), AB301610 (99%), AF345820 (99%), DQ899094 (99%), AB286935 (99%)	<i>Agaricomycetes, Sistotrema sp. *</i>
BMC13	6	3	3	AM084814 (99%), EU918698 (94%), DQ118417 (94%)	<i>Agaricomycetes</i>
BMC14	5	4	1	AM160645 (99%),	<i>Cystobasidiomycetes, Sporobolomyces coprosmae</i>
BMC15	5	2	3	EU047805 (99%)	<i>Agaricomycetes, Phanerochaete sordida</i>
BMC16	5	1	4	EU118668 (98%)	<i>Agaricomycetes, Steccherinum fimbriatum</i>
BMC17	4	4	0	AF026586 (99%), AF334912 (98%)	<i>Agaricomycetes, Peniophora sp. *</i>
BMC18	4	4	0	EU118651 (95%), AF210821 (95%)	<i>Agaricomycetes</i>
BMC19	4	3	2	DQ347490 (99%), AY558617 (97%)	<i>Agaricomycetes, Fuscoporia ferrea</i>
BMC20	4	3	1	AF347080 (88%), AY641458 (84%), AF347092 (83%)	<i>Agaricomycetes</i>
BMC21	4	3	1	AJ437602 (99%)	<i>Agaricomycetes, Serpula himantoides</i>
BMC22	4	3	1	AB072232 (99%)	<i>Tremellomycetes, Udeniomyces pannonicus</i>

BMC23	4	2	2	DQ340338 (99%)	<i>Agaricomycetes, Hyphodontia alutacea</i>
BMC24	4	0	4	DQ384584 (98%)	<i>Agaricomycetes, Phlebia tremellosa</i>
BMC25	3	3	0	AY633927 (88%), AY089741 (88%), AF455461(87%), EU118655 (84%)	<i>Agaricomycetes</i>
BMC26	3	3	0	DQ868345 (99%), DQ868346 (98%)	<i>Agaricomycetes, Baeospora sp.</i>
BMC27	3	2	1	AY271810 (85%), AY219390 (83%), EU118665 (83%)	<i>Agaricomycetes</i>
BMC28	3	2	1	DQ097370 (98%), AY354227 (98%)	<i>Agaricomycetes, Strobilurus sp. *</i>
BMC29	3	2	1	AM076640 (99%), AM712271 (98%)	<i>Agaricomycetes, Psathyrella sp.</i>
BMC30	3	2	1	AM269811 (100%), AF533962 (99%)	<i>Agaricomycetes, Stereum sp.</i>
BMC31	3	2	1	EU326210 (90%), AF516524 (89%)	<i>Agaricomycetes</i>
BMC32	3	2	1	AY781266 (100%)	<i>Agaricomycetes, Phanerochaete sordida</i>
BMC33	3	2	1	AY558616 (97%)	<i>Agaricomycetes, Fuscoporia ferruginosa</i>
BMC34	3	2	1	AB032638 (99%), AY242817 (98%)	<i>Tremellomycetes, Dioszegia sp.</i>
BMC35	3	1	3	AB084621 (98%), AY787676 (98%)	<i>Agaricomycetes, Phlebia uda</i>
BMC36	3	1	2	DQ822818 (97%), AF335450 (85%), EU669216 (84%)	<i>Agaricomycetes</i>
BMC37	3	1	2	AM902093 (99%), EU877759 (98%), EU436684 (98%)	<i>Agaricomycetes, Coprinellus sp. *</i>
BMC38	3	1	2	AJ006684 (99%)	<i>Agaricomycetes, Ceriporiopsis gilvescens</i>
BMC39	3	1	2	EU118659 (97%), AY805620 (97%)	<i>Agaricomycetes, Phlebiella sp.</i>
BMC40	3	0	3	AY302514 (100%), AY302534 (99%)	<i>Wallemiomycetes, Wallemia muriae</i>
BMC41	3	0	3	AY969566 (86%), AY641458 (84%), DQ411529 (83%)	<i>Agaricomycetes</i>
BMC42	3	0	3	AY854075 (99%), DQ112557(99%)	<i>Agaricomycetes, Morganella pyriformis</i>
BMC43	2	2	1	DQ873601 (99%)	<i>Agaricomycetes, Hyphodontia abieticola</i>
BMC44	2	2	0	AM901851 (91%), DQ340326 (89%)	<i>Agaricomycetes</i>
BMC45	2	2	0	DQ367906 (94%), AY634136 (80%), AF335450 (80%), AY669602 (80%)	<i>Agaricomycetes</i>
BMC46	2	2	0	AF518588 (99%), AF334899.1 (98%)	<i>Agaricomycetes, Resinicium sp. *</i>
BMC47	2	2	0	AB074655 (99%), DQ851582 (99%), DQ459375 (99%), AF026622 (99%)	<i>Agaricomycetes</i>
BMC48	2	2	0	DQ444863 (99%), AY787215 (99%)	<i>Agaricomycetes, Nematoloma sp. *</i>
BMC49	2	2	0	AY293129 (99%), DQ520099 (99%), AY293130 (99%)	<i>Agaricomycetes, Exidia sp. *</i>
BMC50	2	2	0	DQ520099 (99%),	<i>Agaricomycetes, Auricularia auricula-judae</i>
BMC51	2	2	0	EU158830 (98%), AY336782 (98%), AY336765 (98%)	<i>Agaricomycetes, Antrodia sp. *</i>
BMC52	2	2	0	AM901975 (99%), AY781273 (98%), AM269816 (98%)	<i>Agaricomycetes, Trichaptum sp.</i>
BMC53	2	2	0	DQ365617 (99%), AJ408372 (99%)	<i>Agaricomycetes, Ramaria stricta</i>
BMC54	2	2	0	AF444418 (99%), AF444417 (99%)	<i>Tremellomycetes</i>
BMC55	2	2	0	AF468041 (99%), AF468040 (99%)	<i>Pucciniomycetes, Puccinia sp.</i>
BMC56	2	1	2	DQ093750 (94%), DQ873618 (93%), DQ384575 (93%), AB084616 (91%)	<i>Agaricomycetes</i>
BMC57	2	1	2	AM902071 (99%), AY781263 (98%), AF210821 (97%)	<i>Agaricomycetes, Peniophora sp.</i>
BMC58	2	1	2	AF444402 (99%)	<i>Tremellomycetes, Udeniomyces pyricola</i>
BMC59	2	1	1	U85790 (97%), U85794 (97%)	<i>Agaricomycetes, Fibulorhizoctonia sp.</i>
BMC60	2	1	1	AJ890441 (83%), EU113196 (82%), AM901850 (81%),	<i>Agaricomycetes</i>
BMC61	2	1	1	AF310096 (99%), AF310095 (99%)	<i>Agaricomycetes, Gloeocystidiellum porosum</i>
BMC62	2	1	1	AY219361 (99%)	<i>Agaricomycetes, Ceriporiopsis pannocincta</i>
BMC63	2	1	1	DQ411529 (99%)	<i>Agaricomycetes, Trechispora alnicola</i>
BMC64	2	1	1	AF145571 (99%)	<i>Agaricomycetes, Schizopora paradoxa</i>
BMC65	2	1	1	EF068136 (88%), EU826014 (86%)	<i>Agaricomycetes</i>
BMC66	2	1	1	AM922292 (82%), AM410637 (82%)	<i>Microbotryomycetes</i>
BMC67	2	1	1	DQ157700 (99%)	<i>Ustilaginomycetes, Ustilago maydis</i>
BMC68	2	0	2	AF455461 (91%), AY271810 (91%)	<i>Agaricomycetes</i>
BMC69	2	0	2	AF518763 (99%), AF533963 (99%)	<i>Agaricomycetes, Polyporus sp. *</i>

BMC70	2	0	2	EF174452 (99%), AY265847 (99%)	<i>Agaricomycetes</i> , <i>Sarcomyxa</i> sp. *
BMC71	2	0	2	AF087487 (99%)	<i>Agaricomycetes</i> , <i>Phlebiopsis gigantea</i>
BMC72	2	0	2	EU326210 (92%), EU661877 (91%)	<i>Agaricomycetes</i>
BMC73	2	0	2	AF347089 (98%)	<i>Agaricomycetes</i> , <i>Trechispora farinacea</i>
BMC74	2	0	2	EU118665 (99%)	<i>Agaricomycetes</i> , <i>Scopuloides hydnoides</i>
BMC75	1	1	0	AF026586 (97%), DQ915464 (97%)	<i>Agaricomycetes</i> , <i>Peniophora</i> sp. *
BMC76	1	1	0	AM922290 (87%), AY841862 (85%), AF444322 (85%), EU218894 (84%),	
BMC77	1	1	0	AM084814 (99%), EU918698 (94%), DQ118417 (93%)	<i>Agaricomycetes</i>
BMC78	1	1	0	AY633927 (90%), EU118654 (89%), EU118653 (89%)	<i>Agaricomycetes</i>
BMC79	1	1	0	AM901974 (91%), DQ398959 (91%), AF139961 (84%)	<i>Agaricomycetes</i>
BMC80	1	1	0	DQ367906 (90%), AY174809 (79%), DQ112621 (84%)	<i>Agaricomycetes</i>
BMC81	1	1	0	EU003034 (84%), DQ411529 (83%)	<i>Agaricomycetes</i>
BMC82	1	1	0	AY969526 (94%), AY641458 (84%), AF347080 (84%)	<i>Agaricomycetes</i>
BMC83	1	1	0	AY969397 (96%), U66450 (94%), EU669216 (86%)	<i>Agaricomycetes</i>
BMC84	1	1	0	AY288099 (87%), AF440673 (86%), AJ606042 (85%)	<i>Agaricomycetes</i>
BMC85	1	1	0	DQ278949 (95%), EU622841 (87%), DQ672336 (86%)	<i>Agaricomycetes</i>
BMC86	1	1	0	DQ915469 (90%), DQ899095 (84%)	<i>Agaricomycetes</i>
BMC87	1	1	0	DQ273371 (91%), DQ309138 (91%), AY805624 (88%)	<i>Agaricomycetes</i>
BMC88	1	1	0	DQ490645 (89%), DQ026258 (89%), U66435 (82%), AM999704 (81%)	<i>Agaricomycetes</i>
BMC89	1	1	0	AM999723 (100%), AF394919 (90%), AJ534710 (88%)	<i>Agaricomycetes</i>
BMC90	1	1	0	DQ851579 (98%), DQ115781 (98%), DQ115779 (98%)	<i>Agaricomycetes</i>
BMC91	1	1	0	AY219355 (91%), EU118655 (87%), EU118648 (85%),	<i>Agaricomycetes</i>
BMC92	1	1	0	AY219392 (83%), EU118656 (83%), EU118662 (82%)	<i>Agaricomycetes</i>
BMC93	1	1	0	AM902085 (99%), EU118655 (91%), DQ912694 (91%), EU118648 (88%)	<i>Agaricomycetes</i>
BMC94	1	1	0	AB210074 (88%), EF577058 (87%), AY633927 (87%), AY463486 (86%)	<i>Agaricomycetes</i>
BMC95	1	1	0	AY805625 (92%), EF687930 (91%)	<i>Agaricomycetes</i>
BMC96	1	1	0	DQ241782 (94%), U66438 (93%), EU118621 (88%)	<i>Agaricomycetes</i>
BMC97	1	1	0	AY382822 (99%), DQ234537 (99%)	<i>Agaricomycetes</i> , <i>Tomentella</i> sp. *
BMC98	1	1	0	EU301643 (86%), EU118655 (86%), EU918713 (86%)	<i>Agaricomycetes</i>
BMC99	1	1	0	D85631 (95%), EF025042 (95%), EF024029 (95%), DQ873594 (95%)	<i>Agaricomycetes</i>
BMC100	1	1	0	DQ444856 (98%), AY916753 (98%), AY916719 (98%)	<i>Agaricomycetes</i>
BMC101	1	1	0	AY219404 (99%), AB084592 (99%), EU670846 (99%), AF334913 (99%)	<i>Agaricomycetes</i>
BMC102	1	1	0	AB267393 (92%), EU669216 (87%)	<i>Agaricomycetes</i>
BMC103	1	1	0	DQ873655 (91%), AY228345 (83%), AM901941 (82%), EU118621 (82%),	<i>Agaricomycetes</i>
BMC104	1	1	0	DQ117964 (86%), U66430 (85%), EU669363 (85%)	<i>Agaricomycetes</i>
BMC105	1	1	0	AY558594 (90%), AY251309 (89%)	<i>Agaricomycetes</i>
BMC106	1	1	0	DQ309229 (88%), DQ481971 (88%), EU846251 (87%)	<i>Agaricomycetes</i>
BMC107	1	1	0	AB084488 (100%), AF289069 (100%)	<i>Agaricomycetes</i> , <i>Panellus stypticus</i>
BMC108	1	1	0	AY771606 (99%), DQ437681 (98%)	<i>Agaricomycetes</i> , <i>Collybia</i> sp. *

BMC109	1	1	0	EU669216 (96%), AM902078 (95%), EU486440 (95%),	<i>Agaricomycetes</i>
BMC110	1	1	0	DQ093734 (100%), AM113456 (97%), AF335444 (95%)	<i>Agaricomycetes</i>
BMC111	1	1	0	AF377194 (99%)	<i>Agaricomycetes, Tricholoma sp.</i>
BMC112	1	1	0	AF345811 (97%)	<i>Agaricomycetes, Lacrymaria velutina</i>
BMC113	1	1	0	DQ403253 (99%)	<i>Agaricomycetes, Panaeolus sp.</i>
BMC114	1	1	0	AY228340 (90%), EF530937 (88%)	<i>Agaricomycetes</i>
BMC115	1	1	0	AY540327 (99%), AY540332 (99%)	<i>Agaricomycetes, Pleurotus sp.</i>
BMC116	1	1	0	EF218784 (97%), DQ474576 (96%)	<i>Agaricomycetes, Lactarius sp.</i>
BMC117	1	1	0	DQ384592 (96%), X70027 (96%)	<i>Agaricomycetes</i>
BMC118	1	1	0	AF533962 (95%), AM269811 (94%)	<i>Agaricomycetes</i>
BMC119	1	1	0	AY805604 (99%), AY781246 (98%)	<i>Agaricomycetes, Amylostereum sp.</i>
BMC120	1	1	0	EU118638 (98%)	<i>Agaricomycetes, Junghuhnia nitida</i>
BMC121	1	1	0	EU084665 (100%), DQ647827 (99%)	<i>Agaricomycetes, Paxillus sp.</i>
BMC122	1	1	0	EF218744 (99%), AJ889934 (99%), DQ066404 (99%)	<i>Agaricomycetes, Xerocomus sp.</i>
BMC123	1	1	0	AJ272404 (99%)	<i>Agaricomycetes, Suillus bovinus</i>
BMC124	1	1	0	AJ437601 (99%)	<i>Agaricomycetes, Serpula lacrymans</i>
BMC125	1	1	0	AJ420946 (100%)	<i>Agaricomycetes, Gloeophyllum sepiarium</i>
BMC126	1	1	0	AJ889982 (99%), AY874382 (99%)	<i>Agaricomycetes, Tomentella sp.</i>
BMC127	1	1	0	AJ966746 (98%), DQ979014 (95%)	<i>Agaricomycetes, Geastrum sp. *</i>
BMC128	1	1	0	AF291279 (99%)	<i>Agaricomycetes, Exidia truncata</i>
BMC129	1	1	0	AY805609 (99%), AY509555 (98%)	<i>Agaricomycetes, Exidia sp.</i>
BMC130	1	1	0	AM901944 (100%), AF516524 (96%), EU661877 (96%)	<i>Agaricomycetes</i>
BMC131	1	1	0	AF126896 (99%), AF126884 (99%)	<i>Agaricomycetes, Antrodiella sp.</i>
BMC132	1	1	0	EF088657 (100%), EU840622 (99%)	<i>Agaricomycetes, Laetiporus sp.</i>
BMC133	1	1	0	AY336772 (99%), AF255198 (99%), AF255199 (99%)	<i>Agaricomycetes, Coriolopsis sp. *</i>
BMC134	1	1	0	EU294161 (99%)	<i>Agaricomycetes, Piptoporus betulinus</i>
BMC135	1	1	0	EU118630 (99%)	<i>Agaricomycetes, Hyphodermella corrugata</i>
BMC136	1	1	0	AY513227 (97%)	<i>Agaricomycetes, Lentinellus cochleatus</i>
BMC137	1	1	0	EU118651 (97%), AF210821 (94%)	<i>Agaricomycetes, Peniophora sp.</i>
BMC138	1	1	0	AF506470 (99%)	<i>Agaricomycetes, Scytinostroma portentosum</i>
BMC139	1	1	0	AF518571 (96%), AF026607 (96%), DQ457625 (95%)	<i>Agaricomycetes</i>
BMC140	1	1	0	EF060012 (99%), EF060011 (99%)	<i>Agaricomycetes, Ganoderma sp.</i>
BMC141	1	1	0	AF347080 (93%), AF347081 (91%)	<i>Agaricomycetes</i>
BMC142	1	1	0	AB210074 (99%)	<i>Agaricomycetes, Phlebia acanthocystis</i>
BMC143	1	1	0	EU872426 (94%), AY219365 (87%)	<i>Agaricomycetes</i>
BMC144	1	1	0	DQ340340 (96%)	<i>Agaricomycetes</i>
BMC145	1	1	0	DQ340310 (99%)	<i>Agaricomycetes, Hyphodontia nespori</i>
BMC146	1	1	0	DQ340311 (99%)	<i>Agaricomycetes, Hyphodontia hastata</i>
BMC147	1	1	0	DQ340341 (99%)	<i>Agaricomycetes, Hyphodontia subaluctata</i>
BMC148	1	1	0	EU118631 (99%)	<i>Agaricomycetes, Hyphodontia alutaria</i>
BMC149	1	1	0	EU118653 (97%), AY219351 (97%)	<i>Agaricomycetes, Phanerochaete sp.</i>
BMC150	1	1	0	EU622846 (99%)	<i>Agaricomycetes, Limonomyces roseipellis</i>
BMC151	1	1	0	DQ677498 (98%)	<i>Agaricomycetes, Hyphoderma mutatum</i>
BMC152	1	1	0	AJ534294 (99%)	<i>Agaricomycetes, Hyphoderma setigerum</i>
BMC153	1	1	0	EU118609 (99%)	<i>Agaricomycetes, Candelabrochaete septocystidia</i>
BMC154	1	1	0	EU811510 (99%), EF024029 (99%)	<i>Agaricomycetes</i>
BMC155	1	1	0	AY558599 (95%), AY624992 (95%)	<i>Agaricomycetes</i>
BMC156	1	1	0	AY558616 (98%)	<i>Agaricomycetes, Fuscoporia ferruginosa</i>
BMC157	1	1	0	AB105437 (99%), AY821994 (99%)	<i>Tremellomycetes</i>
BMC158	1	1	0	DQ317359 (99%), AB105438 (99%)	<i>Tremellomycetes, Cryptococcus sp.</i>
BMC159	1	1	0	DQ460724 (93%), AY956552 (93%),	<i>Pucciniomycetes</i>

				AY956563 (93%)	
BMC160	1	1	0	EU014070 (89%), EU014062 (89%)	<i>Pucciniomycetes</i>
BMC161	1	1	0	DQ417401 (93%), AY956560 (93%)	<i>Pucciniomycetes</i>
BMC162	1	1	0	AB192988 (99%)	<i>Pucciniomycetes</i> , <i>Puccinia tanacetii</i>
BMC163	1	1	0	EF635898 (99%)	<i>Pucciniomycetes</i> , <i>Puccinia rupestris</i>
BMC164	1	1	0	U57351 (90%), DQ250744 (88%)	<i>Pucciniomycetes</i>
BMC165	1	1	0	EU014070 (97%),	<i>Pucciniomycetes</i> , <i>Uromyces trifolii-repentis</i>
BMC166	1	1	0	AF180189 (99%),	<i>Pucciniomycetes</i> , <i>Uromyces pisi</i>
BMC167	1	1	0	DQ087231 (99%)	<i>Pucciniomycetes</i> , <i>Thekopsora areolata</i>
BMC168	1	1	0	AF125178 (99%)	<i>Pucciniomycetes</i> , <i>Melampsorium hiratsukanum</i>
BMC169	1	1	0	AY854976 (99%), DQ025481 (99%)	<i>Exobasidiomycetes</i> , <i>Tilletiopsis</i> sp.
BMC170	1	1	0	U00973 (99%), DQ831012 (99%)	<i>Ustilaginomycetes</i>
BMC171	1	1	0	DQ875355 (96%)	<i>Ustilaginomycetes</i>
BMC172	1	0	1	AJ866976 (88%), AM901979 (88%), DQ317357 (88%)	
BMC173	1	0	1	AY328913 (99%)	<i>Wallemiomycetes</i> , <i>Wallemia sebi</i>
BMC174	1	0	1	EU118659 (83%), EU118658 (83%), AY605709 (81%)	<i>Agaricomycetes</i>
BMC175	1	0	1	AY254876 (94%), AF347080 (92%)	<i>Agaricomycetes</i>
BMC176	1	0	1	AY641458 (91%), DQ411529 (86%), EU003034 (85%)	<i>Agaricomycetes</i>
BMC177	1	0	1	AY969535 (87%), DQ411529 (85%), AY641458 (84%)	<i>Agaricomycetes</i>
BMC178	1	0	1	AY641458 (84%), DQ411529 (84%), AM902006 (82%)	<i>Agaricomycetes</i>
BMC179	1	0	1	DQ060097 (91%), AF455461 (91%)	<i>Agaricomycetes</i>
BMC180	1	0	1	AF455461 (91%), DQ060096 (90%)	<i>Agaricomycetes</i>
BMC181	1	0	1	EU003034 (93%), DQ411529 (85%), AY969566 (84%)	<i>Agaricomycetes</i>
BMC182	1	0	1	DQ309120 (99%), AM084802 (95%), DQ397337 (93%)	<i>Agaricomycetes</i>
BMC183	1	0	1	EF381671 (99%), DQ102418 (82%)	<i>Agaricomycetes</i>
BMC184	1	0	1	AY254874 (88%), AF394919 (86%)	<i>Agaricomycetes</i>
BMC185	1	0	1	EU113196 (82%), AY461837 (82%), AM076643 (82%), AF462637 (80%)	<i>Agaricomycetes</i>
BMC186	1	0	1	L43380 (84%), AY433812 (83%), EU118648 (82%)	<i>Agaricomycetes</i>
BMC187	1	0	1	AY219393 (92%), AF087487 (91%), EU118657 (90%)	<i>Agaricomycetes</i>
BMC188	1	0	1	AY513231 (89%), AY534580 (86%), AF454422 (84%)	<i>Agaricomycetes</i>
BMC189	1	0	1	AF310090 (95%), AY513224 (83%), AF336150 (81%)	<i>Agaricomycetes</i>
BMC190	1	0	1	EU819413 (90%), DQ149727 (90%), DQ097876 (88%)	<i>Agaricomycetes</i>
BMC191	1	0	1	DQ672292 (90%), AY456375 (88%), DQ979014 (84%),	<i>Agaricomycetes</i>
BMC192	1	0	1	EU292660 (87%), EU118617 (85%)	<i>Agaricomycetes</i>
BMC193	1	0	1	AJ006683 (84%), AB210075 (84%)	<i>Agaricomycetes</i>
BMC194	1	0	1	DQ493754 (98%), U85798 (97%)	<i>Agaricomycetes</i> , <i>Fibulorhizoctonia</i> sp.
BMC195	1	0	1	DQ276871 (97%)	<i>Agaricomycetes</i> , <i>Fibulorhizoctonia</i> sp.
BMC196	1	0	1	DQ276871 (88%), U85798 (87%)	<i>Agaricomycetes</i>
BMC197	1	0	1	AM922223 (88%), EF493272 (92%)	<i>Agaricomycetes</i>
BMC198	1	0	1	AM712272 (96%), EU292654 (93%)	<i>Agaricomycetes</i>
BMC199	1	0	1	DQ534576 (100%), EU661888 (99%)	<i>Agaricomycetes</i> , <i>Plicaturopsis</i> sp. *
BMC200	1	0	1	AY461832 (97%), EU622272 (97%)	<i>Agaricomycetes</i> , <i>Coprinellus</i> sp. *
BMC201	1	0	1	EU819413 (88%), DQ149728 (88%), EU669216 (87%)	<i>Agaricomycetes</i>
BMC202	1	0	1	AY176379 (99%)	<i>Agaricomycetes</i> , <i>Lepiota lilacea</i>

BMC203	1	0	1	EU669311 (89%), AY228340 (88%)	<i>Agaricomycetes</i>
BMC204	1	0	1	AY781254 (95%), AF533962 (89%)	<i>Agaricomycetes</i>
BMC205	1	0	1	EU301643 (99%), EU273517 (99%)	<i>Agaricomycetes, Irpex lacteus</i>
BMC206	1	0	1	EU118669 (97%)	<i>Agaricomycetes, Steccherinum ochraceum</i>
BMC207	1	0	1	DQ112556 (99%)	<i>Agaricomycetes, Vascellum sp.</i>
BMC208	1	0	1	AJ617490 (94%), AB067724 (92%)	<i>Agaricomycetes</i>
BMC209	1	0	1	EF218819 (99%), TTU83486 (98%)	<i>Agaricomycetes, Thelephora sp.</i>
BMC210	1	0	1	AY382822 (98%)	<i>Agaricomycetes, Tomentella sp.</i>
BMC211	1	0	1	AY382822 (96%)	<i>Agaricomycetes</i>
BMC212	1	0	1	EU661877 (99%), AF516525 (99%)	<i>Agaricomycetes</i>
BMC213	1	0	1	EF011121 (98%)	<i>Agaricomycetes, Oxyporus populinus</i>
BMC214	1	0	1	AJ006673 (99%), DQ060097 (99%)	<i>Agaricomycetes, Bjerkandera sp.</i>
BMC215	1	0	1	AF454430 (98%)	<i>Agaricomycetes, Auriscalpium vulgare</i>
BMC216	1	0	1	AF347104 (100%), AM269816 (98%)	<i>Agaricomycetes, Trichaptum sp.</i>
BMC217	1	0	1	AJ006679 (99%)	<i>Agaricomycetes, Skeletocutis nivea</i>
BMC218	1	0	1	AF516528 (99%), EU661877 (99%), AY494980 (98%)	<i>Agaricomycetes, Polyporus sp.*</i>
BMC219	1	0	1	AF347080 (97%), AF347081 (97%)	<i>Agaricomycetes, Trechispora sp.</i>
BMC220	1	0	1	AF347080 (87%), AY254876 (85%)	<i>Agaricomycetes</i>
BMC221	1	0	1	DQ411529 (94%)	<i>Agaricomycetes</i>
BMC222	1	0	1	AF347093 (100%)	<i>Agaricomycetes, Porpomyces mucidus</i>
BMC223	1	0	1	DQ365649 (91%), EU624408 (88%)	<i>Agaricomycetes</i>
BMC224	1	0	1	AJ408375 (98%), AJ408374 (97%)	<i>Agaricomycetes, Ramaria decurrens</i>
BMC225	1	0	1	AB210074 (95%), EU118656 (93%), EU118665 (90%)	<i>Agaricomycetes</i>
BMC226	1	0	1	DQ873609 (98%)	<i>Agaricomycetes, Hyphodontia barba-jovis</i>
BMC227	1	0	1	DQ873618 (99%)	<i>Agaricomycetes, Hyphodontia floccosa</i>
BMC228	1	0	1	DQ873614 (99%)	<i>Agaricomycetes, Hyphodontia crustosa</i>
BMC229	1	0	1	AF475150 (79%), AF475147 (78%)	<i>Agaricomycetes</i>
BMC230	1	0	1	AB361645 (100%)	<i>Agaricomycetes, Phanerochaete chrysosporium</i>
BMC231	1	0	1	DQ911612 (97%)	<i>Agaricomycetes, Haplotrichum conspersum</i>
BMC232	1	0	1	AF429426 (99%)	<i>Agaricomycetes, Hypochnicium geogenium</i>
BMC233	1	0	1	DQ647507 (100%), DQ873599 (99%)	<i>Agaricomycetes, Hyphoderma puberum</i>
BMC234	1	0	1	AM747290 (100%), DQ822795 (99%)	<i>Agaricomycetes</i>
BMC235	1	0	1	DQ200924 (96%)	<i>Agaricomycetes</i>
BMC236	1	0	1	DQ267124 (97%)	<i>Agaricomycetes, Botryobasidium botryosum</i>
BMC237	1	0	1	AY081045 (93%), AY854976 (93%)	<i>Exobasidiomycetes</i>
BMC238	1	0	1	AF505782 (99%), DQ480098 (99%)	<i>Agaricomycetes, Gymnopus sp.</i>

* Some of the characteristic NCBI accession numbers correspond to different genera.

Supporting Table S4 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

Janine Fröhlich-Nowoisky, Daniel A. Pickersgill, Viviane R. Després, and Ulrich Pöschl

Table S4. Statistical parameters.

Symbol	Quantity/Definition
D	Simpson's index [†] , $D = \sum_{i=1}^S \frac{n_i (n_i - 1)}{N(N - 1)}$
E	Shannon evenness, $E = H' / \ln S$
H'	Shannon index, $H' = - \sum_{i=1}^S P_i \ln P_i$
n	Number of investigated samples
n_i	Frequency of occurrence of an individual species i (number of samples in which species i was detected)
N	Cumulative frequency of occurrence of investigated species, $N = \sum_{i=1}^S n_i$
P_i	Relative proportion of an individual species i , $P_i = n_i / N$
RFO	Relative frequency of occurrence of a species or group of species
S	Species richness measured (number of detected species)
S^*	Species richness estimated with the Chao-1 approach, [‡] $S^* = S + a^2 / (2 b)$, a = number of species detected only once (singletons), b = number of species detected twice (doubletons)
S_n	Species richness normalized by the number of investigated samples, $S_n = S / n$

[†] (32), [‡](32,33)

Supporting Table S5 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

Janine Fröhlich-Nowoisky, Daniel A. Pickersgill, Viviane R. Després, and Ulrich Pöschl

Table S5. Taxonomic classes of Ascomycota (A) and Basidiomycota (B).

Relative frequency occurrence (*RFO*; proportion of total/coarse/fine particle samples in which the class was detected) for different seasons and overall; number of different families and species (total/coarse/fine; n.a. = not available; n.d. = not determined). The number of air samples (filter pairs of fine and coarse particles) collected in spring (Mar-May), summer (Jun-Aug), fall (Sep-Nov) and winter (Dec-Feb) were 14, 10, 10, and 8, respectively.

(A)

AMC class	RFO (%)					Families	Species
	Spring	Summer	Fall	Winter	Overall		
<i>Dothideomycetes</i>	100/100/93	100/100/100	100/100/100	88/63/75	98/93/93	6/6/5	22/14/12
<i>Eurotiomycetes</i>	79/36/79	50/10/40	70/20/60	100/38/75	74/26/64	2/2/1	18/5/15
<i>Lecanoromycetes</i>	14/7/7	0/0/0	0/0/0	0/0/0	5/2/2	1/n.d./1	2/1/1
<i>Leotiomycetes</i>	78/71/57	70/50/20	90/90/20	75/75/50	78/71/38	4/4/3	16/8/11
<i>Orbiliomycetes</i>	7/0/7	0/0/0	0/0/0	0/0/0	2/0/2	1/0/1	1/0/1
<i>Saccharomycetes</i>	14/0/14	0/0/0	10/0/10	25/0/25	12/0/12	1/0/1	3/0/3
<i>Sordariomycetes</i>	71/36/43	30/10/30	50/0/50	63/13/63	55/17/45	8/5/7	27/8/21
Unknown	86/71/57	80/50/50	80/40/50	75/63/38	81/57/50	n.a./n.d	35/24/14

(B)

BMC class	RFO (%)					Families	Species
	Spring	Summer	Fall	Winter	Overall		
<i>Agaricomycetes</i>	100/100/100	100/100/100	100/100/100	100/100/100	100/100/100	33/31/20	208/134/112
<i>Cystobasidiomycetes</i>	7/7/0	30/20/10	10/10/0	0/0/0	12/10/2	n.a.	1/1/1
<i>Exobasidiomycetes</i>	0/0/0	0/0/0	0/0/0	25/13/13	5/2/2	1/1/1	2/1/1
<i>Microbotryomycetes</i>	14/14/0	50/50/20	0/0/0	25/0/25	21/17/10	n.d.	2/2/2
<i>Pucciniomycetes</i>	14/14/0	10/10/0	30/30/0	0/0/0	14/14/0	2/2/0	11/11/0
<i>Tremellomycetes</i>	71/64/7	40/30/20	20/10/10	88/88/0	55/48/10	n.a.	7/7/4
<i>Ustilaginomycetes</i>	7/7/0	30/20/10	0/0/0	0/0/0	10/7/2	2/2/1	3/3/1
<i>Wallemiomycetes</i>	0/0/0	0/0/0	20/0/20	13/0/13	7/0/7	n.a.	2/0/2
Unknown	0/0/0	10/10/0	10/0/10	0/0/0	5/2/2	n.d.	2/1/1

Supporting Table S6 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

Janine Fröhlich-Nowoisky, Daniel A. Pickersgill, Viviane R. Després, and Ulrich Pöschl

Table S6. Taxonomic families of Ascomycota (A) and Basidiomycota (B).

Number of species (OTUs) detected in the air samples and coarse or fine particle filters, respectively (total/coarse/fine). Note that with regard to the definition of families the NCBI taxonomy as applied here may deviate from that of other data bases (e.g., Mycobank).

(A)

AMC Family	Species
<i>Apiosporaceae</i>	1/0/1
<i>Chaetomiaceae</i>	1/0/1
<i>Cordycipitaceae</i>	2/0/2
<i>Davidiellaceae</i>	1/1/1
<i>Dermateaceae</i>	2/1/2
<i>Diatrypaceae</i>	2/2/1
<i>Dothioraceae</i>	2/2/1
<i>Erysiphaceae</i>	2/2/0
<i>Gnomoniaceae</i>	2/1/1
<i>Herpotrichiellaceae</i>	1/1/0
<i>Hyaloscyphaceae</i>	4/1/4
<i>Leptosphaeriaceae</i>	2/1/1
<i>Massarinaceae</i>	1/1/0
<i>Orbiliaceae</i>	1/0/1
<i>Parmeliaceae</i>	1/0/1
<i>Phaeosphaeriaceae</i>	4/2/3
<i>Pleosporaceae</i>	5/5/2
<i>Saccharomycetaceae</i>	1/0/1
<i>Sclerotiniaceae.</i>	3/2/2
<i>Sordariaceae</i>	2/2/0
<i>Trichocomaceae</i>	16/4/14
<i>Valsaceae</i>	2/1/1
<i>Xylariaceae</i>	6/1/6

(B)

BMC Family	Species
<i>Agaricaceae</i>	3/2/2
<i>Atheliaceae</i>	5/1/5
<i>Auriculariaceae</i>	1/1/0
<i>Auriscalpiaceae</i>	2/1/1
<i>Bolbitiaceae</i>	1/1/0
<i>Boletaceae</i>	1/1/0
<i>Bondarzewiaceae</i>	2/2/1
<i>Botryobasidiaceae</i>	3/1/3
<i>Corticaceae</i>	33/22/19
<i>Entolomataceae</i>	2/1/1
<i>Entylomataceae</i>	2/1/1
<i>Exidiaceae</i>	2/2/0
<i>Ganodermataceae</i>	1/1/0
<i>Gastraceae</i>	1/1/0
<i>Gloeocystidiellaceae</i>	1/1/1
<i>Gloeophyllaceae</i>	1/1/0
<i>Gomphaceae</i>	3/1/2
<i>Hymenochaetaceae</i>	5/5/3
<i>Lachnocladiaceae</i>	8/8/3
<i>Lycoperdaceae</i>	3/0/3
<i>Meruliaceae</i>	1/0/1
<i>Phanerochaetaceae</i>	1/1/0
<i>Paxillaceae</i>	1/1/0
<i>Pleurotaceae</i>	1/1/0
<i>Polyporaceae</i>	4/1/3
<i>Pucciniaceae</i>	7/7/0
<i>Pucciniastraceae</i>	2/2/0
<i>Russulaceae</i>	1/1/0
<i>Serpulaceae</i>	2/2/1

<i>Steccherinaceae</i>	4/2/3
<i>Stereaceae</i>	5/4/3
<i>Strophariaceae</i>	1/1/0
<i>Suillaceae</i>	1/1/0
<i>Thelephoraceae</i>	4/1/3
<i>Trechisporaceae</i>	7/2/6
<i>Tricholomataceae</i>	10/7/4
<i>Urocystaceae</i>	1/1/0
<i>Ustilaginaceae</i>	2/2/1

Supporting Table S7 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

Janine Fröhlich-Nowoisky, Daniel A. Pickersgill, Viviane R. Després, and Ulrich Pöschl

Table S7. Relative frequency occurrence (*RFO*) of selected species from *Ascomycota* and *Basidiomycota* (proportion of total/coarse/fine particle samples in which the species were detected) for different seasons and overall.

Species	<i>RFO</i> (%)				
	Spring	Summer	Fall	Winter	Overall
AMC					
<i>Alternaria spp.</i>	21/21/0	70/60/20	50/50/0	38/25/13	43/38/7
<i>Blumeria graminis.</i>	43/43/0	10/10/0	0/0/0	38/38/0	24/24/0
<i>Cladosporium sp.</i>	100/93/79	100/100/100	100/90/100	88/38/75	98/83/88
<i>Penicillium spp.</i>	71/21/71	30/0/30	50/10/40	75/0/75	55/10/55
<i>Eurotium sp.</i>	36/21/21	0/0/0	20/10/10	75/38/38	31/17/17
BMC					
<i>Heterobasidion annosum</i>	79/36/64	70/10/70	70/40/50	63/25/63	71/28/62
<i>Itersonilia perplexans</i>	57/57/0	10/10/0	10/10/10	75/75/0	40/38/2
<i>Stereum spp.</i>	43/21/21	50/50/20	40/30/30	63/38/25	48/33/24

Supporting Table S8 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

Janine Fröhlich-Nowoisky, Daniel A. Pickersgill, Viviane R. Després, and Ulrich Pöschl

Table S8. Exemplary geometric and aerodynamic diameters and shapes of fungal spores.

Species	Geometric diameter (μm), shape	Aerodynamic diameter (μm)	References (SI)
<i>Aspergillus spp.</i>	2-3.5, near-spherical	2.5-3.7	(23, 34)
<i>Cladosporium spp.</i>	3-8 $\times$ 2-5, ovoid, lemon-shaped, oblong, near-spherical	1.8-2.3	(23, 35, 36, 37)
<i>Penicillium spp.</i>	3-6, near-spherical	3.0-3.7	(34, 35)
Basidiospores	5-15, elliptic, oblong	6.8	(38, 39)
<i>Itersonilia perplexans</i>	10-12 $\times$ 10-13		(40)
Smut spores		9.7	(34)
Rust spores (<i>Puccinia spp.</i>)	> 20		(9, 41)

Supporting Table S9 for the Manuscript “High Diversity of Fungi in Air Particulate Matter”

Janine Fröhlich-Nowoisky, Daniel A. Pickersgill, Viviane R. Després, and Ulrich Pöschl

Table S9. NCBI accession numbers of the present study attributed to the operational taxonomic units (OTUs).

NCBI accession number	OTU ID	NCBI accession number	OTU ID	NCBI accession number	OTU ID	NCBI accession number	OTU ID
FJ820489	BMC172	FJ820581	BMC126	FJ820673	BMC155	FJ820765	AMC10
FJ820490	BMC40	FJ820582	BMC127	FJ820674	BMC19	FJ820766	AMC57
FJ820491	BMC173	FJ820583	BMC49	FJ820675	BMC65	FJ820767	AMC5
FJ820492	BMC75	FJ820584	BMC128	FJ820676	BMC156	FJ820768	AMC58
FJ820493	BMC76	FJ820585	BMC50	FJ820677	BMC33	FJ820769	AMC59
FJ820494	BMC77	FJ820586	BMC10	FJ820678	BMC54	FJ820770	AMC3
FJ820495	BMC2	FJ820587	BMC129	FJ820679	BMC157	FJ820771	AMC60
FJ820496	BMC25	FJ820588	BMC31	FJ820680	BMC6	FJ820772	AMC27
FJ820497	BMC78	FJ820589	BMC130	FJ820681	BMC22	FJ820773	AMC21
FJ820498	BMC3	FJ820590	BMC51	FJ820682	BMC58	FJ820774	AMC88
FJ820499	BMC79	FJ820591	BMC131	FJ820683	BMC34	FJ820775	AMC31
FJ820500	BMC174	FJ820592	BMC132	FJ820684	BMC158	FJ820776	AMC89
FJ820501	BMC36	FJ820593	BMC213	FJ820685	BMC66	FJ820777	AMC19
FJ820502	BMC80	FJ820594	BMC38	FJ820686	BMC9	FJ820778	AMC28
FJ820503	BMC44	FJ820595	BMC62	FJ820687	BMC159	FJ820779	AMC92
FJ820504	BMC81	FJ820596	BMC133	FJ820688	BMC55	FJ820780	AMC26
FJ820505	BMC41	FJ820597	BMC134	FJ820689	BMC161	FJ820781	AMC32
FJ820506	BMC82	FJ820598	BMC214	FJ820690	BMC162	FJ820782	AMC93
FJ820507	BMC176	FJ820599	BMC135	FJ820691	BMC163	FJ820783	AMC95
FJ820508	BMC177	FJ820600	BMC215	FJ820692	BMC160	FJ820784	AMC61
FJ820509	BMC178	FJ820601	BMC136	FJ820693	BMC164	FJ820785	AMC62
FJ820510	BMC83	FJ820602	BMC4	FJ820694	BMC165	FJ820786	AMC96
FJ820511	BMC20	FJ820603	BMC13	FJ820695	BMC166	FJ820787	AMC63
FJ820512	BMC84	FJ820604	BMC17	FJ820696	BMC167	FJ820788	AMC64
FJ820513	BMC85	FJ820605	BMC57	FJ820697	BMC168	FJ820789	AMC98
FJ820514	BMC181	FJ820606	BMC18	FJ820698	BMC14	FJ820790	AMC65
FJ820515	BMC86	FJ820607	BMC137	FJ820699	BMC169	FJ820791	AMC99
FJ820516	BMC87	FJ820608	BMC138	FJ820700	BMC170	FJ820792	AMC100
FJ820517	BMC45	FJ820609	BMC139	FJ820701	BMC171	FJ820793	AMC22
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FJ820519	BMC89	FJ820611	BMC217	FJ820703	BMC182	FJ820795	AMC15
FJ820520	BMC185	FJ820612	BMC140	FJ820704	BMC183	FJ820796	AMC8

FJ820521	BMC90	FJ820613	BMC63	FJ820705	BMC72	FJ820797	AMC103
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FJ820523	BMC92	FJ820615	BMC35	FJ820707	BMC237	FJ820799	AMC105
FJ820524	BMC93	FJ820616	BMC186	FJ820708	BMC68	FJ820800	AMC66
FJ820525	BMC27	FJ820617	BMC189	FJ820709	BMC199	FJ820801	AMC67
FJ820526	BMC56	FJ820618	BMC216	FJ820710	BMC197	FJ820802	AMC6
FJ820527	BMC187	FJ820619	BMC53	FJ820711	BMC192	FJ820803	AMC106
FJ820528	BMC225	FJ820620	BMC69	FJ820712	BMC210	FJ820804	AMC17
FJ820529	BMC94	FJ820621	BMC218	FJ820713	BMC211	FJ820805	AMC109
FJ820530	BMC12	FJ820622	BMC208	FJ820714	BMC204	FJ820806	BMC238
FJ820531	BMC95	FJ820623	BMC201	FJ820715	BMC179	FJ820807	AMC110
FJ820532	BMC96	FJ820624	BMC229	FJ820716	BMC180	FJ820808	AMC68
FJ820533	BMC46	FJ820625	BMC5	FJ820717	BMC184	FJ820809	AMC113
FJ820534	BMC188	FJ820626	BMC118	FJ820718	BMC120	FJ820810	AMC69
FJ820535	BMC97	FJ820627	BMC30	FJ820719	BMC112	FJ820811	AMC114
FJ820536	BMC190	FJ820628	BMC223	FJ820720	BMC111	FJ820812	AMC115
FJ820537	BMC98	FJ820629	BMC224	FJ820721	BMC200	FJ820813	AMC116
FJ820538	BMC99	FJ820630	BMC222	FJ820722	AMC11	FJ820814	AMC2
FJ820539	BMC100	FJ820631	BMC175	FJ820723	AMC34	FJ820815	AMC70
FJ820540	BMC101	FJ820632	BMC73	FJ820724	AMC35	FJ820816	AMC118
FJ820541	BMC47	FJ820633	BMC219	FJ820725	AMC23	FJ820817	AMC119
FJ820542	BMC191	FJ820634	BMC220	FJ820726	AMC52	FJ820818	AMC13
FJ820543	BMC102	FJ820635	BMC141	FJ820727	AMC36	FJ820819	AMC20
FJ820544	BMC103	FJ820636	BMC143	FJ820728	AMC37	FJ820820	AMC9
FJ820545	BMC104	FJ820637	BMC74	FJ820729	AMC38	FJ820821	AMC71
FJ820546	BMC105	FJ820638	BMC7	FJ820730	AMC39	FJ820822	AMC73
FJ820547	BMC59	FJ820639	BMC39	FJ820731	AMC40	FJ820823	AMC122
FJ820548	BMC194	FJ820640	BMC23	FJ820732	AMC41	FJ820824	AMC123
FJ820549	BMC195	FJ820641	BMC226	FJ820733	AMC42	FJ820825	AMC18
FJ820550	BMC37	FJ820642	BMC43	FJ820734	AMC43	FJ820826	AMC94
FJ820551	BMC198	FJ820643	BMC144	FJ820735	AMC44	FJ820827	AMC111
FJ820552	BMC60	FJ820644	BMC145	FJ820736	AMC74	FJ820828	AMC82
FJ820553	BMC106	FJ820645	BMC227	FJ820737	AMC45	FJ820829	AMC120
FJ820554	BMC28	FJ820646	BMC228	FJ820738	AMC46	FJ820830	AMC78
FJ820555	BMC107	FJ820647	BMC64	FJ820739	AMC75	FJ820831	AMC107
FJ820556	BMC70	FJ820648	BMC146	FJ820740	AMC47	FJ820832	AMC102
FJ820557	BMC26	FJ820649	BMC147	FJ820741	AMC72	FJ820833	AMC124
FJ820558	BMC108	FJ820650	BMC148	FJ820742	AMC76	FJ820834	AMC112
FJ820559	BMC109	FJ820651	BMC15	FJ820743	AMC48	FJ820835	AMC33
FJ820560	BMC110	FJ820652	BMC32	FJ820744	AMC49	FJ820836	AMC77
FJ820561	BMC29	FJ820653	BMC230	FJ820745	AMC53	FJ820837	AMC91
FJ820562	BMC202	FJ820654	BMC149	FJ820746	AMC50	FJ820838	AMC90
FJ820563	BMC113	FJ820655	BMC231	FJ820747	AMC16	FJ820839	AMC30
FJ820564	BMC114	FJ820656	BMC212	FJ820748	AMC24	FJ820840	AMC86
FJ820565	BMC203	FJ820657	BMC232	FJ820749	AMC25	FJ820841	AMC84
FJ820566	BMC115	FJ820658	BMC150	FJ820750	AMC79	FJ820842	AMC108
FJ820567	BMC48	FJ820659	BMC151	FJ820751	AMC81	FJ820843	AMC97
FJ820568	BMC61	FJ820660	BMC152	FJ820752	AMC7	FJ820844	AMC117
FJ820569	BMC116	FJ820661	BMC233	FJ820753	AMC14	FJ820845	AMC121
FJ820570	BMC1	FJ820662	BMC153	FJ820754	AMC12	FJ820846	AMC101

FJ820571	BMC117	FJ820663	BMC154	FJ820755	AMC51	FJ820847	BMC193
FJ820572	BMC42	FJ820664	BMC205	FJ820756	AMC29	FJ820848	BMC67
FJ820573	BMC207	FJ820665	BMC16	FJ820757	AMC83	FJ820849	F1
FJ820574	BMC121	FJ820666	BMC206	FJ820758	AMC80	FJ820850	F2
FJ820575	BMC122	FJ820667	BMC119	FJ820759	AMC54	FJ820851	FIS1
FJ820576	BMC123	FJ820668	BMC71	FJ820760	AMC85	FJ820852	FIS2
FJ820577	BMC21	FJ820669	BMC234	FJ820761	AMC55	FJ820853	FIS3
FJ820578	BMC124	FJ820670	BMC11	FJ820762	AMC1	FJ820854	FIS4
FJ820579	BMC125	FJ820671	BMC235	FJ820763	AMC87	FJ820855	BMC142
FJ820580	BMC209	FJ820672	BMC236	FJ820764	AMC56	FJ820856	BMC24

Supporting Information

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SI Text

Taxonomic classes and families. According to the best match sequences and taxonomy used in the NCBI database, the 368 OTUs or fungal species detected in this study have been attributed to 3 phyla, 15 classes, and 61 families. The species richness and proportions of the different phyla and classes are described and discussed in the main manuscript. Additional information about the taxonomic classes and families is given below.

Basidiomycotic classes and families. Of the 15 accepted classes of BMC (1), 8 classes were found in the investigated aerosol samples (Table S3 and Table S5). Of the 238 detected BMC species, 208 can be attributed to the most species rich class of BMC, the *Agaricomycetes*. The proportion of *Agaricomycetes* among the different species of BMC found in the atmospheric samples (~87%) was even higher than in the biosphere, where *Agaricomycetes* (~16,000–20,000 species) account for approximately 50% of the known BMC species (2). They act as decomposers (decompose lignin and cellulose), pathogens, parasites, and symbionts of both plants (trees, shrubs, and grasses) and animals (e.g., insects) (3–5). Some species of *Agaricomycetes* are edible whereas others produce secondary metabolites that make them hallucinogenic or toxic (2). A diverse array of fruiting bodies like gilled mushrooms, chanterelles, stinkhorns, false truffles, puffballs, corticoid fungi and coral fungi are produced from members of this class (6). *Agaricomycetes* were found in all coarse particles samples (134 species) and in all fine particles samples (112 species), that is, the *RFO* of this class was 100% throughout all seasons (Table S5). Thirty-eight species of the *Agaricomycetes* occurred in both coarse and fine particle samples.

Compared to the *Agaricomycetes*, all other classes of BMC exhibited much lower species richness and lower *RFO* values (Table S5). Two classes were found only in coarse or only in fine particle samples. *Pucciniomycetes* were detected only in the coarse particle samples (*RFO* 14%). In contrast to the *Agaricomycetes*, the proportion of *Pucciniomycetes* among the different species of BMC found in the atmospheric samples (~5%) was substantially lower than in the biosphere, where *Pucciniomycetes* account for approximately 30% of the known BMC species (7). They are parasites of animals and fungi as well as obligate pathogens of ferns, conifers, flowering plants, cereal grains, legumes, and trees such as apple, where they can cause extensive reduction in yield and even host death (7–9). Most *Pucciniomycetes* (~7,000 species or ~90%) belong to a single order, the *Pucciniales* or plant parasitic rust fungi (7), which was indeed the only type of *Pucciniomycetes* found in the investigated air samples. *Wallemiomycetes* could be detected only in fine particle samples (*RFO* 7%). This class includes only 3 species of xerophilic molds from the genus *Wallemia*, 2 of which we found (*W. sebi* and *W. muriae*). They are mutualists of plants, green algae, bryophytes, and cyanobacteria, and they can act as decomposers and pathogens of plants, animals, and other fungi (10–12).

Of the 38 detected BMC families, 33 belonged to the class of *Agaricomycetes*. As shown in Table S6, the most species rich BMC family was *Corticaceae* with 33 different species (mostly wood decaying fungi). Species from this and 19 other families occurred in coarse as well as in fine particle samples (*Hymenochaetaeaceae*, *Lachnocladiaceae*, *Tricholomataceae*, etc.). Sixteen families were found only in coarse particle samples (*Bolbitiaceae*, *Pleurotaceae*, *Suillaceae*, etc.), and 2 families were found only in fine particle samples (*Lycoperdaceae* and *Meruliaceae*). With regard to families, the taxonomic attribution according to

the NCBI database applied in this study is often not in agreement with the Mycobank taxonomy. For example, only 2 of the 33 species attributed to the *Corticaceae* according to NCBI would be attributed to this family according to Mycobank. In view of the taxonomic uncertainties, we have not calculated *RFO* values for the families.

Ascomycotic classes and families. Of the 15 accepted classes of AMC (1), 7 classes were found in the investigated aerosol samples (Table S3 and Table S5). The most species rich class of AMC were the *Sordariomycetes* (27 of 124 detected AMC species), which include plant pathogens and endophytes, animal pathogens, and mycoparasites (13). *Sordariomycetes* were found in 19 fine particle samples (21 species) and in 7 coarse particle samples (8 species), corresponding to *RFO* values of 45% and 17%, respectively (Table S5). The AMC class with the highest *RFO* (98%) was the *Dothideomycetes* (22 species). This class contains several allergenic fungi and plant pathogens, endophytes or epiphytes of living plants, and also saprobes degrading cellulose and other complex carbohydrates in dead or partially digested plant matter, in leaf litter, or dung (14).

Two more AMC classes with high species richness and frequency of occurrence were the *Leotiomyces* (16 species, *RFO* 78%), which are the largest nonlichen-forming group of fungi (15), and the *Eurotiomycetes* (18 species, *RFO* 74%), including well-known molds like *Penicillium* spp. No taxonomic class attribution was available for 35 (partly mitosporic) AMC.

Of the 23 detected AMC families, 13 were found in both coarse and fine particle samples (e.g., *Davidiellaceae*, *Sclerotiniaceae*, and *Trichocomaceae*), 6 were found only in fine particle samples (e.g., *Orbiliaceae*, and *Saccharomycetaceae*), and 4 were found only in coarse particle samples (e.g., *Erysiphaceae*, Table S6). The most species rich AMC family were the *Trichocomaceae* (16 species), which include the molds *Aspergillus* and *Penicillium*.

Coarse versus fine particle samples and fungal spore size. Fungal DNA was found in both the coarse and the fine aerosol particle samples that had been collected with a nominal cut-off diameter of approximately 3 μm as detailed in the main manuscript. Overall, the species richness and relative frequency of occurrence of fungal species in coarse and fine particle samples were of similar magnitude. Of the fungi, 165 were found only in coarse particle samples, and 141 were found only in fine particle samples; 62 species were detected in both types of samples (Table S3 and Table S7).

Fungal spores are usually in the size range of 1–50 μm (16) and have been found in coarse as well as in fine aerosol particle samples (17–20). The aerodynamic behavior of a particle depends on its size, density, shape, and structure, and the aerodynamic diameter is defined as the diameter of an equivalent spherical particle with a density of 10^3 kg m^{-3} that has the same aerodynamic behavior as the investigated particle. The shape of fungal spores, however, is often nonspherical and their density can be lower than the reference density. Therefore, the aerodynamic diameter of fungal spores is often smaller than the size of their geometric envelope. Exemplary properties and aerodynamic diameters of spores from different fungal species are given in Table S8.

The aerodynamic diameter of spores, however, does not only depend on the fungal species from which they are emitted but also on their biological age and on ambient conditions. For example, the diameter of *Penicillium* spores typically increases with age (2.3–2.6 μm) (21), freshly released spores are usually larger than spores that have been airborne for a longer time (22),

and the size of spores can increase with the ambient relative humidity (23, 24). The effects outlined above can lead to the deposition of DNA from fungi with spore diameters $>3\ \mu\text{m}$ in the investigated fine particle samples as well as to the deposition of DNA from fungi with spore diameters $<3\ \mu\text{m}$ in the coarse particle samples.

Besides the uncertainties and variability related to the type and size of aerosol particles carrying fungal DNA, the distinction between coarse and fine particles is also affected by imperfections of the aerosol sampling techniques. The nominal cut-off diameter of the applied high-volume sampler cannot be regarded as a sharp limit; it is just the midpoint of the collection efficiency curve of the virtual impactor which extends over several micrometers (25). Thus, particles that are a couple of micrometers smaller or larger than the nominal cut-off diameter can be deposited on both the coarse and the fine particle filters. Moreover, the operating principles of the applied high-volume sampler imply that approximately 10% of the fine particulate matter in the sampled air mass is deposited on the coarse particle sample. As a consequence, fungi that occur with high frequency in the fine particle fraction are likely to be detected also in the coarse particle samples and the following points should be taken

as a guideline for the interpretation of the measurement results reported above:

1. Zero or very low *RFO* values in the fine particle fraction indicate that the detected fungal species had been present in the sampled air masses as particles (spores) with aerodynamic diameters larger than approximately $3\ \mu\text{m}$. Examples from Table S7 are *Blumeria graminis* and *Itersonilia perplexans*. Moreover, members of the order *Pucciniales* (rust fungi) are known to have large spores (up to $>20\ \mu\text{m}$) and were found only in coarse particle samples (9).
2. High *RFO* values in the fine and in the coarse particle fraction or high/medium *RFO* values in the fine and lower *RFO* values in the coarse particle fraction indicate that the detected fungal species had been present in the sampled air masses as particles (spores) with aerodynamic diameters of approximately $3\ \mu\text{m}$ or less. Examples from Table S7 are *Cladosporium* sp., *Penicillium* spp., and *Heterobasidion annosum*.
3. Medium *RFO* values of similar magnitude in the fine and in the coarse particle fraction indicate that the detected fungal species had been present in the sampled air masses as particles (spores) with aerodynamic diameters around approximately $3\ \mu\text{m}$ (or as larger and smaller particles with similar abundance). Examples from Table S7 are *Eurotium* sp. and *Stereum* spp.

1. Hibbett DS, et al. (2007) A higher-level phylogenetic classification of the Fungi. *Mycol Res* 111:509–547.
2. Hibbett DS (2006) A phylogenetic overview of the Agaricomycotina. *Mycologia* 98:917–925.
3. Aanen DK, et al. (2002) The evolution of fungus-growing termites and their mutualistic fungal symbionts. *Proc Natl Acad Sci USA* 99:14887–14892.
4. Read D (1997) Mycorrhizal fungi—the ties that bind. *Nature* 388:517–518.
5. Smith SE, Read DJ (1997) *Mycorrhizal Symbiosis*, (Academic, London).
6. Hibbett DS (2007) After the gold rush, or before the flood? Evolutionary morphology of mushroom-forming fungi (Agaricomycetes) in the early 21st century. *Mycol Res* 111:1001–1018.
7. Aime MC, et al. (2006) An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. *Mycologia* 98:896–905.
8. Frieders EM, McLaughlin, David Ja, Szabo LJ (2008) Pucciniomycotina (formerly Urediniomycetes). A diverse group of fungi, including rusts, yeasts, smut-like and jelly-like fungi. <http://tolweb.org/Pucciniomycotina/20528/> 2008.02.21 in The Tree of Life Web Project, <http://tolweb.org/>.
9. Anikster Y, Eilam T, Bushnell WR, Kosman E (2005) Spore dimensions of Puccinia species of cereal hosts as determined by image analysis. *Mycologia* 97:474–484.
10. Matheny PB, et al. (2007) Contributions of rpb2 and tef1 to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). *Mol Phylogenet Evol* 43:430–451.
11. Wood GM, et al. (1990) Studies on a toxic metabolite from the mold *Wallemia*. *Food Addit Contamin* 7:69–77.
12. Zalar P, de Hoog GS, Schroers HJ, Frank JM, Gunde-Cimerman N (2005) Taxonomy and phylogeny of the xerophilic genus *Wallemia* (Wallemiomycetes and Wallemiales, cl. et ord. nov.). *Ant Leeuw Int J G* 87:311–328.
13. Zhang N, Sung G-H (2008) Sordariomycetes. <http://tolweb.org/Sordariomycetes/29050/> 2008.01.14 in The Tree of Life Web Project, <http://tolweb.org/>.
14. Schoch CL, et al. (2006) A multigene phylogeny of the Dothideomycetes using four nuclear loci. *Mycologia* 98:1041–1052.
15. Wang Z, et al. (2006) Toward a phylogenetic classification of the Leotiomycetes based on rDNA data. *Mycologia* 98:1065–1075.
16. Gregory PH (1973) *The Microbiology of the Atmosphere*, (Leonard Hill Books, Aylesbury).
17. Bauer H, et al. (2002) The contribution of bacteria and fungal spores to the organic carbon content of cloud water, precipitation and aerosols. *Atmos Res* 64:109–119.
18. Elbert W, Taylor PE, Andreae MO, Pöschl U (2007) Contribution of fungi to primary biogenic aerosols in the atmosphere: Wet and dry discharged spores, carbohydrates, and inorganic ions. *Atmos Chem Phys* 7:4569–4588.
19. Battarbee JL, Rose NL, Long XZ (1997) A continuous, high resolution record of urban airborne particulates suitable for retrospective microscopical analysis. *Atmos Environ* 31:171–181.
20. Womilolo TO, Miller JD, Mayer PM, Brook JR (2003) Methods to determine the biological composition of particulate matter collected from outdoor air. *Atmos Environ* 37:4335–4344.
21. Kanaani H, Hargreaves M, Ristovski Z, Morawska L (2007) Performance assessment of UVAPS: Influence of fungal spore age and air exposure. *J Aerosol Sci* 38:83–96.
22. Reponen T, et al. (1994) Comparison of concentrations and size distributions of fungal spores in buildings with and without mold problems. *J Aerosol Sci* 25:1595–1603.
23. Reponen T, et al. (1996) Effect of relative humidity on the aerodynamic diameter and respiratory deposition of fungal spores. *Atmos Environ* 30:3967–3974.
24. Liao CM, et al. (2004) Temporal/seasonal variations of size-dependent airborne fungi indoor/outdoor relationships for a wind-induced naturally ventilated airspace. *Atmos Environ* 38:4415–4419.
25. Solomon PA, Moyers JL, Fletcher RA (1983) High-volume dichotomous virtual impactor for the fractionation and collection of particles according to aerodynamic size. *Aerosol Sci Tech* 2:455–464.
26. White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In *PCR Protocols: A Guide to Methods and Applications*, eds Innis MA, Gelfand DH, Sninsky JJ, White TJ (Academic, San Diego), pp 315–322.
27. Nikolcheva LG, Bärlocher F (2004) Taxon-specific fungal primers reveal unexpectedly high diversity during leaf decomposition in a stream. *Mycol Prog* 3:41–49.
28. Fierer N, Jackson JA, Vilgalys R, Jackson RB (2005) Assessment of soil microbial community structure by use of taxon-specific quantitative PCR assays. *Appl Environ Microbiol* 71:4117–4120.
29. Whiting MF, et al. (1997) The Strepsiptera problem: Phylogeny of the holometabolous insect orders inferred from 18S and 28S ribosomal DNA sequences and morphology. *Syst Biol* 46:1–68.
30. Heraty J, Hawks D, Kostecki JS, Carmichael A (2004) Phylogeny and behaviour of the Gollumiellinae, a new subfamily of the ant-parasitic Eucharitidae (Hymenoptera: Chalcidoidea). *Syst Entomol* 29:544–559.
31. Grosskopf R, Janssen PH, Liesack W (1998) Diversity and structure of the methanogenic community in anoxic rice paddy soil microcosms as examined by cultivation and direct 16S rRNA gene sequence retrieval. *Appl Environ Microbiol* 64:960–969.
32. Hill TCJ, Walsh KA, Harris JA, Moffett BF (2003) Using ecological diversity measures with bacterial communities. *FEMS Microbiol Ecol* 43:1–11.
33. Chao A (1984) Nonparametric-estimation of the number of classes in a population. *Scand J Stat* 11:265–270.
34. Adhikari A, et al. (2006) Correlation of ambient inhalable bioaerosols with particulate matter and ozone: A two-year study. *Environ Pollut* 140:16–28.
35. Gorny RL, et al. (2002) Fungal fragments as indoor air biocontaminants. *Appl Environ Microbiol* 68:3522–3531.
36. Zalar P, et al. (2007) Phylogeny and ecology of the ubiquitous saprobe *Cladosporium sphaerospermum*, with descriptions of seven new species from hypersaline environments. *Stud Mycol* 58:157–183.
37. Grinshpun SA, et al. (2005) Collection of airborne spores by circular single-stage impactors with small jet-to-plate distance. *J Aerosol Sci* 36:575–591.
38. Helbling A, Brander KA, Horner WE, Lehrer SB (2002) in *Fungal Allergy and Pathogenicity*, eds Breitenbach M, Cramer R, Lehrer SB (Karger, Basel), Vol. 81, pp. 28–47.
39. Ingold CT (1971) *Fungal Spores. Their Liberation and Dispersal*, (Clarendon Press, Oxford).
40. Sowell G, Korf RP (1960) An emendation of the genus *Itersonilia* based on studies of morphology and pathogenicity. *Mycologia* 52:934–945.
41. Teodoro NG, Gomez ET (1926) Coffee diseases and their control. *Philippine Agric Rev* 19:249–257.



Fig. S1. Binding sites of the applied primers on the fungal rRNA gene: schematic illustration of the ITS regions and the 18S, 5.8S, and 28S rRNA region (not to scale).

Other Supporting Information Files

[Table S1 \(PDF\)](#)

[Table S2 \(PDF\)](#)

[Table S3 \(PDF\)](#)

[Table S4 \(PDF\)](#)

[Table S5 \(PDF\)](#)

[Table S6 \(PDF\)](#)

[Table S7 \(PDF\)](#)

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[Table S9 \(PDF\)](#)