

High Diversity of Fungi in Air Particulate Matter

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Fungal spores account for large proportions of air particulate matter, and they influence the hydrological cycle and climate as nuclei for water droplets and ice crystals in clouds, fog and precipitation (Elbert et al., 2007). Moreover, some fungi are major pathogens and allergens. The diversity of airborne fungi is, however, hardly known. The use of molecular genetic methods resolves many limitations of traditional detection methods for the analysis of biological aerosol particles (Després et al., 2007).

In this study, air filter samples were collected with a High Volume Sampler separating fine and coarse particles (aerodynamic cut-off diameter ~3 µm) for one year 2006/2007 in Mainz, Germany. The samples were analyzed for the presence of fungal deoxyribonucleic acid (DNA). All PCR products were cloned and several clones sequenced. The obtained sequences were blasted in the National Center for Biotechnology Information databank to find the closest match and determine the taxonomic identity of the organisms from which the DNA on the filter samples had most likely originated.

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 and more human pathogens and allergens in the respirable fine particle fraction (< 3 µm). Moreover, the ratio of Basidiomycota to Ascomycota was found to be much higher than previously assumed, which might also apply to the biosphere.

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